STUDIES ON INDOOR FUNGI

by

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A thesis submitted in conformity with the requirements

for the degree of Doctor of Philosophy in Mycology,

Graduate Department of Botany in the University of Toronto

When I heard the learn'd astronomer,
When the proofs, the figures, were ranged in columns before
me,
When I was shown the charts and diagrams, to add, divide, and
measure them,
When I sitting heard the astronomer where he lectured with
much applause in the lecture-room,
How soon unaccountable I became tired and sick,
Till rising and gliding out I wander'd off by myself,
In the mystical moist night-air, and from time to time,
Look'd up in perfect silence at the stars.

Walt Whitman, "Leaves of Grass", 1855

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2001

ABSTRACT

Fungi are among the most common microbiota in the interiors of buildings, including homes. Indoor fungal contaminants, such as dry-rot, have been known since antiquity and are important agents of structural decay, particularly in Europe. The principal agents of indoor fungal contamination in North America today, however, are anamorphic (asexual) fungi mostly belonging to the phyla Ascomycota and Zygomycota, commonly known as "moulds".

Broadloom dust taken from 369 houses in Wallaceburg, Ontario during winter, 1994, was serial dilution plated, yielding approximately 250 fungal taxa, over 90% of which were moulds. The ten most common taxa were: *Alternaria alternata*, *Aureobasidium pullulans*, *Eurotium herbariorum*, *Aspergillus versicolor*, *Penicillium chrysogenum*, *Cladosporium cladosporioides*, *P. spinulosum*, *Cl. sphaerospermum*, *As. niger* and *Trichoderma viride*. Chi-square association analysis of this mycoflora revealed several ecological groups including phylloplane-, soil-, and xerophilic food-spoilage fungi.

Genotypic variation was investigated in two common dust-borne species, *Penicillium brevicompactum* and *P. chrysogenum*. Nine multilocus haplotypes comprising 75 isolates of *P. brevicompactum* from 50 houses were detected by heteroduplex mobility assay (HMA) of polymorphic regions in beta-tubulin (benA), nuclear ribosomal RNA spanning the internal transcribed spacer regions (ITS1-2) and histone 4 (his4) genes. Sequence analysis of the benA and rDNA loci showed two genetically divergent groups. Authentic strains of *P. brevicompactum* and *P. stoloniferum* clustered together in the predominant clade, accounting for 86% of isolates. The second lineage contained 14% of isolates, and included collections from the rotting fruit bodies of macrofungi.

Similarly, 5 multilocus haplotypes based on acetyl coenzyme-A synthase (acuA), benA, ITS1-2 and thioredoxin reductase (trxB) genes comprised 198 isolates of *P. chrysogenum* obtained from 109 houses. A strictly clonal pattern of inheritance was observed, indicating the absence of recombination. Phylogenetic analyses of allele sequences segregated the population into three divergent lineages, encompassing 90%, 7% and 3% of the house dust isolates, respectively. Type isolates of *P. chrysogenum* and its synonym *P. notatum* clustered within the secondary lineage, confirming this synonymy. No isolates of nomenclatural status clustered within the predominant lineage; however, this clade contained Alexander Fleming's historically noteworthy penicillin-producing strain from 1929. Similarly, there was no available name for the minor lineage.

ACKNOWLEDGEMENTS

I am profoundly grateful to my advisors, Dave Malloch and Neil Straus, for their thoughtful mentorship, both intentional and unintentional, on all matters of science and life. They have given me gifts of their patience and wisdom that I cannot repay. I thank the members of my supervisory committee, Jim Anderson, David Miller and Richard Summerbell, for their gentle encouragement and sincere enthusiasm which helped me to stay on-track. Linda Kohn and Keith Seifert are thanked for their excellent and thoughful feedback on the thesis in conjunction with the senate oral examination.

I could not have completed this thesis nor the research it presents without the friendship, dedication and benevolence of Brenda Koster, Bess Wong and Wendy Untereiner.

I have laughed, cried and grown immeasurably from my friendships and discussions, often over beer, pizza or #49, with my fellow graduate students Jacquie Bede, Cameron Currie, Laurie Ketch and Simona Margaritescu, along with many others. I am grateful for the assistance of Len Hutchison, Brett Couch, Wendy Malloch, Colleen McGee, Emily Taylor and Megan Weibe during the early stages of this work. More recently, Michael Warnock helped with proofreading and correcting this thesis. Barry Neville and Shanelle Lum kindly kept me informed of many news items on indoor fungi that otherwise I would certainly have missed. Carolyn Babcock and Steve Peterson graciously provided cultures. I thank John Pogacar for insightful conversations on building science and for help in final thesis preparation. Financial support was provided by NSERC as operating grants and a strategic grant to DM and NS, and a doctoral scholarship to JS. Jim Gloer generously funded my early mycological training.

Wieland Meyer has been a superlative collaborator on the aspects of this project involving DNA fingerprinting of *Penicillium chrysogenum*. Steve Peterson, John Pitt and Rob Samson are thanked for many insightful discussions on *Penicillium* taxonomy.

I owe the greatest debt of gratitude to my parents, Kay and Alex Scott, for nurturing my ecclectic interests from a very young age, for their compassion and understanding of the many turns my life has taken, and for the unconditional freedom, support and love that they have given me as I have pursued my dreams. For all this and much more, I dedicate this thesis to them.

On a muggy, summer day when I was a very young boy, my cousin, Jim Guillet inspired me to study biology. As we stood together in my grandmother's garden, Jim explained that the stems of the rhubarb plant could be eaten but that the leaves could not, because they were poisonous. How could it be so? And why? I stared in utter disbelief and hotly challenged this absurd idea, while my parents, grimacing, looked on. I stopped just short of biting into a leaf myself to see its effect. In the very many intervening years since, I have reflected on our exchange countless times. Jim, perhaps unintentionally, taught me four very valuable lessons that day: 1) Nature is fascinating and intricate, her properties and processes are rarely apparent or intuitive; 2) Never be afraid to question any notion proffered as fact, no matter how high the authority; 3) Science embodies a set of methods that can provide insight into the delicate inner workings of Nature when applied thoughtfully and skillfully; and above all, 4) Don't eat rhubarb leaves.

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LIST OF ABBREVIATED TERMS

acuA	Acetyl Co-Enzyme A Synthase gene
AFLP	Amplified Fragment Length Polymorphism
AIHA	American Industrial Hygiene Association
ASHRAE	American Society for Heating, Refrigeration and Air-Conditioning Engineers
ASHVE	American Society for Heating and Ventilation Engineers
benA	Beta-tubulin gene
bp	Base pairs
CFM	Cubic feet (of air) per minute (per person)
CFU	Colony Forming Unit
CI	Consistency Index
CMHC	Canada Mortgage and Housing Corporation
CSA	Creatine sucrose agar (*see* Frisvad, 1985)
CYA	Czapek's yeast autolysate agar (*see* Malloch, 1981)
DG18	Dichloran 18 % Glycerol agar (*see* Hocking and Pitt, 1980)
DGGE	Denaturing Gradient Gel Electrophoresis
DNA	Deoxyribonucleic acid
ds	Double stranded
GM	General Motors Corporation
his4	Histone 4 gene
HDX	Heteroduplexed DNA structure
HGE	Horizontal gel electrophoresis
HMA	Heteroduplex mobility assay
HP	Hypersensitivity pneumonitis
HVAC	Heating, Ventilating and Air-Conditioning
IAQ	Indoor Air Quality
ICPAT	International Commission on *Penicillium* and *Aspergillus* Taxonomy
ILD	Incongruence Length Difference test
ISIAQ	International Society for Indoor Air Quality and Climate
ITS	Internal transcribed spacer region, nuclear rDNA
kbp	Kilo-base pairs
MLA	Modified Leonian's agar (*see* Malloch, 1981)
NAT	N-acryolyltrishydroxymethylaminomethane
NCU-2	Names in Current Use in the Trichocomaceae (*see* Pitt and Samson, 1993)
OPEC	Organization of Petroleum Exporting Countries
OTU	Operational Taxonomic Unit
PAW-I	First International *Penicillium* and *Aspergillus* Workshop
PAW-II	Second International *Penicillium* and *Aspergillus* Workshop
PAW-III	Third International *Penicillium* and *Aspergillus* Workshop
PAG	Polyacrylamide gel
PCR	Polymerase Chain Reaction
PHT	Partition Homogeneity Test
RAPD	Random-Amplified Polymorphic DNA
rDNA	DNA subrepeat encoding nuclear ribosomal RNA
RFLP	Restriction Fragment Length Polymorphism
RI	Retention Index

LIST OF ABBREVIATED TERMS (cont'd)

rRNA	Ribosomal ribonucleic acid
ss	Single stranded
SSCP	Single Strand Conformation Polymorphism
TAE	Tris-acetate-EDTA (*see* Sambrook et al., 1989)
TBE	Tris-borate-EDTA (*see* Sambrook et al., 1989)
TEMED	N,N,N',N'-tetramethyl-ethylenediamine
trxB	Thioredoxin reductase gene
UFFI	Urea-formaldehyde foam insulation
UPGMA	Unweighted pair group method using arithmetic averages
USD	US dollars
USDA	United States Department of Agriculture
V8A	V8 Juice agar (Malloch, 1981)
VGE	Vertical gel electrophoresis
VNTR	Variable-number tandem repeat
VOCs	Volatile organic compounds
WWII	World War II

Acronyms of herbaria and culture collections follow Holmgren et al. (1990) and Takishima et al. (1989).

LIST OF NOMENCLATURAL ABBREVIATIONS

ABSI CORY	Absidia corymbifera
ABSI SP__	Absidia sp.
ACRE BUTY	Acremonium butyri
ACRE FURC	Acremonium furcatum
ACRE KILI	Acremonium kiliense
ACRE RUTI	Acremonium rutilum
ACRE SCLE	Acremonium sclerotigenum
ACRE SP__	Acremonium sp.
ACRE STRI	Acremonium strictum
ALTE ALTE	Alternaria alternata
ALTE CITR	Alternaria citri
ALTE SP__	Alternaria sp.
ALTE TENU	Alternaria tenuissima
APIO MONT	Apiospora montagnei
APIO SP__	Apiospora sp.
ASPE CAND	Aspergillus candidus
ASPE CERV	Aspergillus cervinus
ASPE CLAV	Aspergillus clavatus
ASPE FLAP	Aspergillus flavipes
ASPE FLAV	Aspergillus flavus
ASPE FUMI	Aspergillus fumigatus
ASPE GLAU	Aspergillus glaucus
ASPE NIGE	Aspergillus niger
ASPE NIVE	Aspergillus niveus
ASPE OCHR	Aspergillus ochraceus
ASPE ORNA	Aspergillus ornatus
ASPE ORYZ	Aspergillus oryzae
ASPE PARS	Aspergillus parasiticus
ASPE PARX	Aspergillus paradoxus
ASPE PENI	Aspergillus penicilloides
ASPE REST	Aspergillus restrictus
ASPE SCLE	Aspergillus sclerotiorum
ASPE SP__	Aspergillus sp.
ASPE SYDO	Aspergillus sydowii
ASPE TAMA	Aspergillus tamarii
ASPE TERR	Aspergillus terreus
ASPE USTU	Aspergillus ustus
ASPE VERS	Aspergillus versicolor
ASPE WENT	Aspergillus wentii
AURE PULL	Aureobasidium pullulans
BASI DIOM	basidiomycete
BLAS SP__	Blastobotrys sp.
BOTR ALLI	Botrytis allii
BOTR CINE	Botrytis cinerea
BOTR PILU	Botryotrichum piluliferum
BOTR SP__	Botrytis sp.
CAND SP__	Candida sp.
CHAE AURE	Chaetomium aureum
CHAE CIRC	Chaetomium circinatum
CHAE COCH	Chaetomium cochliodes
CHAE FUNI	Chaetomium funicola
CHAE GLOB	Chaetomium globosum
CHAE NOZD	Chaetomium nozdrenkoae
CHAE SP__	Chaetomium sp.
CHAE SUBS	Chaetomium subspirale
CHRN SITO	Chrysonilia sitophila
CHRN SP__	Chrysonilia sp.
CHRS SP__	Chrysosporium sp.
CLAD CHLO	Cladosporium chlorocephalum
CLAD CLAD	Cladosporium cladosporioides
CLAD HERB	Cladosporium herbarum
CLAD MACR	Cladosporium macrocarpum
CLAD SP__	Cladosporium sp.
CLAD SPHA	Cladosporium sphaerospermum
COCH GENI	Cochliobolus geniculatus
COCH SATI	Cochliobolus sativus
CONI FUCK	Coniothyrium fuckelii
CONI SP__	Coniothyrium sp.
CONI SPOR	Coniothyrium sporulosum
CUNN SP__	Cunninghamella sp.
CURV PRAS	Curvularia prasadii
CURV PROT	Curvularia protuberata
CURV SENE	Curvularia senegalensis
CYLI SP__	Cylindrocarpon sp.
DIPL SPIC	Diplococcium spicatum
DORA MICR	Doratomyces microsporus
DOTH CZSP	Dothichiza sp.
DOTH LASP	Dothiorella sp.
DREC BISE	Drechslera biseptata
DREC SP__	Drechslera sp.
EMER NIDU	Emericella nidulans
EMER SP__	Emericella sp.
EMER VARI	Emericella variecolor
EPIC NIGR	Epicoccum nigrum
EPIC SP__	Epicoccum sp.
EUPE OCHR	Eupenicillium ochrosalmonium
EURO AMST	Eurotium amstelodami
EURO CHEV	Eurotium chevalieri
EURO HERB	Eurotium herbariorum
EURO RUBR	Eurotium rubrum
EURO SP__	Eurotium sp.
EXOP JEAN	Exophiala jeanselmei
EXOP SP__	Exophiala sp.
FUSA EQUI	Fusarium equiseti
FUSA FLOC	Fusarium flocciferum
FUSA OXYS	Fusarium oxysporum
FUSA SP__	Fusarium sp.
GEOM PANN	Geomyces pannorum
GEOM SP__	Geomyces sp.
GEOT CAND	Geotrichum candidum
GILM HUMI	Gilmaniella humicola
GLIO MUFE	Gliomastix murorum v. felina
GLIO MUMU	Gliomastix murorum v. murorum
GLIO MURO	Gliomastix murorum
GLIO ROSE	Gliocladium roseum
GLIO SP__	Gliocladium sp.
GLIO VIRE	Gliocladium virens
GRAP SP__	Graphium sp.
HAIN LYTH	Hainesia lythri
HORM DEMA	Hormonema dematioides
HORT WERN	Hortaea werneckii
HUMI FUSC	Humicola fuscoatra
HYAL SP__	Hyalodendron sp.
LECY HOFF	Lecythophora hoffmannii
LECY SP__	Lecythophora sp.
LEPT AUST	Leptosphaerulina australis
MICR OLIV	Microsphaeropsis olivaceus
MICR SP__	Microsphaeropsis sp.
MONA RUBE	Monascus ruber
MONI SP__	Moniliella sp.
MRTR AMAT	Mortierella ramanniana v. autotrophica
MUCO CIRC	Mucor circinelloides
MUCO HIEM	Mucor hiemalis
MUCO MUCE	Mucor mucedo
MUCO PLUM	Mucor plumbeus
MUCO RACE	Mucor racemosus
MUCO SP__	Mucor sp.
MYRO CINC	Myrothecium cinctum
MYRO OLIV	Myrothecium olivaceum
MYRO RORI	Myrothecium roridum
MYRO SP__	Myrothecium sp.
NEOS SP__	Neosartorya sp.
NIGR SPHA	Nigrospora sphaerica

LIST OF NOMENCLATURAL ABBREVIATIONS (cont'd)

OIDI RHOD	Oidiodendron rhodogenum
OIDI SP__	Oidiodendron sp.
OPHI SP__	Ophiostoma sp.
OPHI TENE	Ophiostoma tenellum
PAEC FULV	Paecilomyces fulva
PAEC FUMO	Paecilomyces fumosoroseus
PAEC INFL	Paecilomyces inflatus
PAEC SP__	Paecilomyces sp.
PAEC VARI	Paecilomyces variotii
PENI ATRA	Penicillium atramentosum
PENI AURA	Penicillium aurantiogriseum
PENI BREV	Penicillium brevicompactum
PENI CANE	Penicillium canescens
PENI CHRY	Penicillium chrysogenum
PENI COMM	Penicillium commune
PENI COPR	Penicillium coprophilum
PENI CORY	Penicillium corylophilum
PENI CRUS	Penicillium crustosum
PENI CTNG	Penicillium citreonigrum
PENI CTRM	Penicillium citrinum
PENI DECU	Penicillium decumbens
PENI DIGI	Penicillium digitatum
PENI ECHI	Penicillium echinulatum
PENI EXPA	Penicillium expansum
PENI FUNI	Penicillium funiculosum
PENI GLAN	Penicillium glandicola
PENI GRIS	Penicillium griseofulvum
PENI HIRS	Penicillium hirsutum
PENI IMPL	Penicillium implicatum
PENI ISLA	Penicillium islandicum
PENI ITAL	Penicillium italicum
PENI JANT	Penicillium janthinellum
PENI MELI	Penicillium melinii
PENI MICZ	Penicillium miczynskii
PENI OXAL	Penicillium oxalicum
PENI PURP	Penicillium purpurogenum
PENI RAIS	Penicillium raistrickii
PENI REST	Penicillium restrictum
PENI ROQU	Penicillium roquefortii
PENI SIMP	Penicillium simplicissimum
PENI SP__	Penicillium sp.
PENI SP01	Penicillium sp. #1
PENI SP13	Penicillium sp. #13
PENI SP26	Penicillium sp. #26
PENI SP35	Penicillium sp. #35
PENI SP38	Penicillium sp. #38
PENI SP44	Penicillium sp. #44
PENI SP52	Penicillium sp. #52
PENI SP64	Penicillium sp. #64
PENI SP84	Penicillium sp. #84
PENI SP87	Penicillium sp. #87
PENI SPIN	Penicillium spinulosum
PENI VARI	Penicillium variabile
PENI VERR	Penicillium verrucosum
PENI VIRI	Penicillium viridicatum
PENI VULP	Penicillium vulpinum
PENI WAKS	Penicillium waksmanii
PEST PALU	Pestalotiopsis palustris
PEST SP__	Pestalotiopsis sp.
PHIA FAST	Phialophora fastigiata
PHIA SP__	Phialophora sp.
PHOM CHRY	Phoma chrysanthemicola
PHOM EUPY	Phoma eupyrena
PHOM EXIG	Phoma exigua
PHOM FIME	Phoma fimeti
PHOM GLOM	Phoma glomerata
PHOM HERB	Phoma herbarum
PHOM LEVE	Phoma leveillei
PHOM MEDI	Phoma medicaginis
PHOM SP__	Phoma sp.
PITH CHAR	Pithomyces chartarum
PITH SP__	Pithomyces sp.
PYRE SP__	Pyrenochaeta sp.
PYTH SP__	Pythium sp.
RHIZ ORYZ	Rhizopus oryzae
RHIZ STOL	Rhizopus stolonifer
SCOL CONS	Scolecobasidium constrictum
SCOP BREV	Scopulariopsis brevicaulis
SCOP BRUM	Scopulariopsis brumptii
SCOP CAND	Scopulariopsis candida
SCOP CHAR	Scopulariopsis chartarum
SCOP FUSC	Scopulariopsis fusca
SCOP SP__	Scopulariopsis sp.
SCYT SP__	Scytalidium sp.
SORD SP__	Sordaria sp.
SPHA SP__	Sphaeropsis sp.
SPOR PRUI	Sporotrichum pruinosum
SPOR THSP	Sporothrix sp.
SPRB SP__	Sporobolomyces sp.
STAC CHAR	Stachybotrys chartarum
STAC PARV	Stachybotrys parvispora
STEM BOTR	Stemphylium botryosum
STEM SOLA	Stemphylium solani
STEM SP__	Stemphylium sp.
SYNC RACE	Syncephalastrum racemosum
SYNC SP__	Syncephalastrum sp.
SYNC VERR	Syncephalastrum verruculosum
TALA FLAV	Talaromyces flavus
TALA TRAC	Talaromyces trachyspermus var. macrocarpus
THAM ELEG	Thamnidium elegans
TOLY SP__	Tolypocladium sp.
TORU HERB	Torula herbarum
TRIC ASPE	Trichocladium asperum
TRIC HARZ	Trichoderma harzianum
TRIC KONI	Trichoderma koningii
TRIC POLY	Trichoderma polysporum
TRIC ROSE	Trichothecium roseum
TRIC SP__	Trichoderma sp.
TRIC VIRI	Trichoderma viride
TRPH TONS	Trichophyton tonsurans
TRUN ANGU	Truncatella angustata
ULOC ATRU	Ulocladium atrum
ULOC CHAR	Ulocladium chartarum
ULOC SP__	Ulocladium sp.
VERT SP__	Verticillium sp.
WALL SEBI	Wallemia sebi
WARD HUMI	Wardomyces humicola
YEAS T___	yeast
ZETI HETE	Zetiasplozna heteromorpha

CHAPTER 1. INTRODUCTION

Fungi inhabit nearly all terrestrial environments. In this regard, the interiors of human dwellings and workspaces are no exception. The mould flora of human-inhabited indoor environments consists of a distinctive group of organisms that collectively are not normally encountered elsewhere. The biology and taxonomy of selected members of the fungal flora of household dust are the focus of the research and discussion presented in this thesis.

Household dust itself is not a substance that evokes a rich sense of practical or historical importance aside from its relentless contribution to the stereotypical plight of suburban housewives obsessed with its elimination. Shakespeare used *dust* as a metaphor to evoke the cyclical nature of life, and the fact that neither class nor creed exempts us from this binding cycle. The spirit of Shakespeare's metaphor provides a fitting framework within which to study the substance itself, as a thriving and complex community comprising a vast diversity of organisms whose lives secretly parallel our own.

THE BIOLOGY OF HOUSE DUST

Dust formation occurs as a result of the ongoing elutriation of airborne organic and inorganic particulate matter that originates from a multiplicity of indoor and outdoor sources. House dust is a fibrous material composed primarily of a matrix of textile fibres, hairs and shed epithelial debris (Bronswijk, 1981). The majority of particles comprising household dust fall within the size range from 10^{-3} to 1 mm (ibid.). Airborne particles smaller than this (e.g. smoke, fumes, etc.) tend to behave as a colloidal system and do not sediment efficiently even in still air due to their relative buoyancy; thus, their presence within dust is often a function of filtration, diffusion or electrostatic effects (Cox and Wathes, 1995).

The large daily influx of organic debris to the dust of inhabited houses provides a rich primary nutrient source that supports an intricate microcommunity encompassing three kingdoms of organisms: animals (arthropods, and to some extent larger animals such as rodents, etc.), bacteria and fungi (Bronswijk, 1981; Harvey and May, 1990; Harving et al., 1993; Hay et al., 1992a, 1992b; Miyamoto et al., 1969; Samson and Lustgraaf, 1978; Sinha et al., 1970). The fibrous nature of a stable dust matt composed predominantly of hygroscopic fibres acts to harvest atmospheric moisture and simultaneously provides shelter from desiccation for the organisms contained within. While the variety of fibres themselves (particularly cellulosic fibres) may serve as sources of carbon nutrition for the heterotrophic dust inhabitants, a more readily available source of organic carbon and nitrogen comes from food crumbs and excoriated epithelia. Although the latter makes up a considerable mass-fraction of house dust, its microbial availability is largely limited to non-keratin proteins and lipids due to the refractory nature of keratin itself (Currah, 1985). Plant pollen arising from the phylloplane likely provide additional nutritional input to the house dust ecosystem (Bronswijk, 1981). Bronswijk (1981) compiled a list of taxa of different groups of dust-borne organisms based on reports by numerous workers. The fauna in her inventory included isopods (5 taxa), roaches (47 taxa), lepismatids (8 taxa), psocopterans (20 taxa) and mites (147 taxa), while the microbiota was dominated by fungi (163 taxa) with only few bacterial taxa (8).

INTERACTIONS BETWEEN MITES AND FUNGI

Bronswijk (1981) speculated considerably on trophic interactions between microarthropods and fungi within dust-bound habitats. She suggested that xerophilic fungi, notably *Wallemia sebi* and members of the *Aspergillus glaucus* series were responsible for the hydrolysis of fats in dustborne dander, facilitating the consumption of these materials by various mite species. Bronswijk (1981) further proposed that *Acremonium*, *Penicillium* and *Scopulariopsis* along with mesophilic species of *Aspergillus* provided food for oribatid mites by the colonization of crumbs and other food debris. Samson and Lustgraaf (1978) demonstrated an association between *Dermatophagoides pteronyssinus* and the microfungi *Aspergillus penicillioides* and *Eurotium halophilicum* whereby these fungi frequently co-occurred with certain dust-borne mite species, and the mites preferred consuming materials upon which the fungi had grown. Hay and co-workers (1992a) showed antigenic cross-reactivity between *Aspergillus penicillioides* and the mite *D. pteronyssinus*, however these workers later suggested that this associate may have been an artifact of laboratory culture conditions under which the mites were reared (Hay et al., 1992b)[1].

FUNGI IN HOUSEHOLD DUST

The fungal component of dust biodiversity probably remains underestimated since only a few studies to date have provided thorough mycological characterizations of house dust (Davies, 1960; Gravesen, 1978a; Lustgraaf and Bronswijk, 1977; Ostrowski, 1999; Schober, 1991). An analysis of dust from 60 households in the Netherlands by Hoekstra and co-workers (1994)

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[1] I have observed dramatic overgrowths on the cadavers of predatory mites (Macrochaelidae) from composting marine seaweeds incubated in moist chamber culture by a mould species that compared to *P. olsonii*. Similarly, fungus-feeding mites occurring as inquilines in laboratory cultures of leaf-cutting ants of the tribe Attini often become overgrown by *Penicillium* spp., when incubated under damp chamber conditions. In the latter case, it is reasonably clear that Penicillia are uncommon allochthonous members of the fungal flora of the fungal gardens of leaf-cutting ants. The colonisation of these mites by *Penicillium* is most likely an artifact of high arthropod population density under unnatural conditions of laboratory culture, and neither supports an hypothetical role for *Penicillium* in the mite lifecycles nor suggests that *Penicillium* is important in the nutrient cycling of this system.

revealed 108 fungal species in 54 genera using V8 juice agar and Dichloran 18 % glycerol agar (DG18) as isolation media. Species recovery showed temporal variation in samples taken 6 wks apart. Also, considerable variation was observed according to the isolation media used. A similar study by Ostrowski (1999) from 219 households in the Netherlands reported 143 fungal taxa of which 113 were also observed in air samples taken from kitchen areas, where the highest level of fungal species diversity was observed.

Innumerable reservoirs of fungal material exist outdoors that may contribute to the fungal burden of indoor air and dust according to the continuous input of outdoor air into indoor environments. Levels of phylloplane fungal spores in indoor air are typically correlated with prevailing weather conditions, including wind speed and precipitation that are responsible for mediating spore release in the outdoor environment (Ingold, 1965; Li and Kendrick, 1994, 1995). As such, surveys of fungi from indoor air and dust usually demonstrate the presence of phylloplane taxa that are qualitatively similar to outdoor air albeit at lower levels (Abdel-Hafez et al., 1993; Bunnag et al., 1982; Calvo et al., 1980; Dillon et al., 1996; Ebner et al., 1992).

Fungal propagules in household dust can be divided into two ecological categories according to their origin. Dustborne fungi may be **1)** active inhabitants of dust (autochthonic *sensu* Bronswijk, 1981); or, **2)** they may be imported, as passive entrants from other sources (allochthonic ibid.; *see also* Cohen et al., 1935; Davies, 1960; Gravesen, 1978; Morey, 1990). Davies (1960) reported dust-bound concentrations of viable fungal propagules in excess of 300 CFU/mg. The magnitude of this concentration prompted Bronswijk (1981) to infer that this dust-bound spora could not have been imported and must have been produced within the dust. Even when fungi are not produced within dust proper, an indoor fungal amplification site produces a characteristic pattern of species distribution in indoor air and consequently house dust.

INDOOR SOURCES OF DUST MYCOFLORA

Indoor fungal growth contributes to disproportionately high spore levels in indoor air relative to those observed in outdoor air (Agrawak et al., 1988; Berk et al., 1957; Grant et al., 1989). Furthermore, when a fungal amplifier is local, the composition of the indoor fungal flora usually differs qualitatively, in being dominated by a single or few abundant species which may not be components of the background flora (Giddings, 1986; Miller, 1992; Miller et al., 1988; Moriyama et al., 1992). For instance, *Cladosporium sphaerospermum* is a frequent colonist of indoor finishes as a consequence of excessive indoor relative humidity (Burge and Otten, 1999). This species has a proclivity for many characteristically refractile substrates such as oil-based paints, and polymeric decorative finishes (e.g. vinyl wall coverings) (Domsch et al., 1980). Interestingly, *Cl. sphaerospermum* is a comparatively rare component of outdoor air flora where species such as *Cl. herbarum* and *Cl. cladosporioides* typically dominate (Burge and Otten, 1999). Despite the abundance of *Mycosphaerella* and its *Cladosporium* anamorphs in outdoor epiphyllous habitats and consequently as spora in outdoor air (Farr et al., 1989; Ho et al., 1999), *Cl. sphaerospermum* is comparably rare in these habitats and even low levels of this fungus in indoor air are unusual and strongly indicate active indoor fungal growth.

Indoor plantings can also serve as reservoirs of fungal material (Burge et al., 1982; Summerbell, 1992). Summerbell and co-workers (1989) examined soils from potted plants in hospital wards and found a large number of potential human pathogenic fungi including *Aspergillus fumigatus* and *Scedosporium apiospermum*, an anamorph of *Pseudallescheria boydii*. Although these workers did not investigate airborne concentrations of these fungi related to their presence in soil, based upon the results of Kaitzis (1977) and Smith and co-workers (1988) Summerbell and colleagues theorized that activites such as watering were likely to cause spore release. The recognition and elimination of indoor amplifiers of opportunistic human pathogenic fungi within the hospital environment are important in the reduction of nosocomial infection. *Aspergillus fumigatus* and *A. flavus* are of particular concern because these fungi are frequent agents of pulmonary aspergillosis especially in immunocompromised patients such as organ recipients and HIV patients (Summerbell, 1998).

PENICILLIUM IN INDOOR ENVIRONMENTS

Perhaps the most famous of all indoor fungi was made so in a 10 page paper written in 1929 by Alexander Fleming, which described the inhibition of several groups of cocciform bacteria by a fungus in the genus *Penicillium*. This fungus, identified for Fleming by St. Mary's Hospital mycologist Charles La Touche as *P. rubrum* Grassberger-Stoll ex. Biourge, was sent by Fleming to Harold Raistrick at the University of London, who in turn sent it to Charles Thom of the US Department of Agriculture in Peoria, Illinois (Fleming, 1929; Gray, 1959; Howard, 1994). Thom (1930) considered Fleming's isolate to be *P. notatum*, a species described by Westling (1911) from the branches of *Hyssopus* L. (Lamiaceae) in Norway. Over a decade after Fleming's discovery, Ernst Chain and Howard Florey isolated the active principal, penicillin, and demonstrated its success in clinical trials, a collective achievement for which the three shared the Nobel Prize for Physiology and Medicine in 1945 (Howard, 1994).

The discovery of penicillin ranks as one of the most significant events in the history of medicine and possibly of human civilization and has been the subject of much discussion (Hare, 1970;

MacFarlane, 1979, 1984; Williams, 1984). Fleming's pivotal role in the penicillin story has been described as a most remarkable case of serendipity, since the vast majority of Penicillia produce metabolites with profound mammalian toxicity (Gray, 1959; Samson et al., 1996). Others have alleged that this discovery was inevitable. From knowledge of the substrate of Westling's (1911) species *P. notatum*, Selwyn (1980) and later Lowe and Elander (1983) inferred the naïve use of penicillin from the following passage of the Old Testament Book of Psalms:

> "Purge me with hyssop, and I shall be clean, wash me, and I shall be whiter than snow.
>
> (Psalms 51:7)

Similarly, a passage from the Third Book of Moses describes a treatment for leprosy[2]:

> "This is the law of the leper in the day of his cleansing… He shall take… the cedarwood, and the scarlet and the hyssop, and shall dip them… in the blood of the bird… And he shall sprinkle upon him that is to be cleansed from the leprosy…
>
> (Lev. 14:2-7)

Certainly the habitat of *P. chrysogenum* is not restricted to *Hyssopus*, as this fungus is known from a vast range of outdoor substrates (Domsch et al., 1980; Pitt and Hocking, 1999). Despite the ubiquitous nature of *P. chrysogenum* outdoors, however, it remains poorly represented in samples of outdoor air where typical phylloplane fungi such as *Alternaria, Aureobasidium, Cladosporium, Epicoccum* and *Ulocladium* dominate (Dillon et al., 1996; Scott et al., 1999b; Tobin et al., 1987). Indoors, *P. chrysogenum* is typically the most commonly occurring airborne and dustborne species of this genus (Abdel-Hafez et al., 1986; Mallea et al., 1982; Summerbell et al., 1992). Certainly an important factor in the establishment of high indoor levels of *P. chrysogenum* is its role as an agent of food spoilage. Pitt and Hocking (1999) indicated that *P. chrysogenum* was the most common species of this genus associated with food contamination, known from numerous fruits, vegetables, cereals, meats and dairy products (Domsch et al., 1980; Pitt and Hocking, 1999;

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[2] In biblical translations and allusions, leprosy refers to any disfiguring skin disease, whose cause is not necessarily limited to Hansen's bacillus, *Mycobacterium leprae* (Brown, 1993).

Samson et al., 1996). Indeed, most high penicillin-producing strains of this species were derived from a single isolate obtained from cantaloupe (Gray, 1956; Lowe and Elander, 1983; Raper and Thom, 1949). The growth of *P. chrysogenum* on wooden food-shipping crates has also been responsible for the tainting of foodstuffs by the release of chloroanisole produced during the breakdown of phenolic wood preservatives (Pitt and Hocking, 1999; Hill et al., 1995). Frisvad and Gravesen (1994) speculated that the indoor abundance of this species could not be explained by its occurrence on foodstuffs alone, and suggested that the somewhat xerophilic nature of both *P. chrysogenum* and *P. brevicompactum* may facilitate their colonization of other indoor substrates such as wood and paint. Adan and Samson (1994) listed *P. chrysogenum* as a common colonist of acrylic-based paint finishes, noting that this species exhibited growth at relative humidities as low as 79 %. This species is also known from wallpaper, textiles, broadloom, visual art and optical lenses (Samson et al., 1994). Similarly, *P. brevicompactum* is known from a wide range of indoor substrates including foods, building materials and decorative finishes (Adan and Samson, 1994; Domsch et al., 1981; Scott et al., 1999a).

Many of the microfungi that are routinely observed as colonists on indoor finishes and construction materials, such as *Aspergillus*, *Paecilomyces*, *Penicillium* and *Scopulariopsis* species tend to grow at relatively low water activity often on refractile substrates (Samson et al., 1996). These genera form the core of the group commonly referred to as "domicile fungi" owing to their inordinate abundance in the air and dust of residential interiors. While these fungi are common agents of structural deterioration in North America, the dry rot fungus *Serpula lacrimans* remains the principal agent of structural decay in Britain and Northern Europe (Singh, 1994). Similarly, the importance of indoor exposure to fungal spores indoors in the development of allergic asthma is greater in North America than in Europe, where dust mite and dander exposures are the primary exposure risk factors for this disease (Beaumont et al., 1985; Flannigan and Miller, 1994).

HEALTH EFFECTS OF EXPOSURE TO INDOOR FUNGI

Although environmental fungal reservoirs have rarely been implicated in human infection (Miller, 1992; Summerbell et al., 1992), their presence has long been accepted as an important risk factor to respiratory morbidity (Dillon et al., 1996). Human exposure to indoor fungi has been implicated in the etiology of a multiplicity of health problems that ranges from allergies and respiratory diseases to toxicoses and neoplastic diseases. To the extent that fungi are involved in these processes, the inhalation or ingestion of fungal cellular debris is thought to be the principal route of exposure. Ancillary products of mould growth such as volatile organic metabolites (e.g. alcohols) or volatile breakdown products from extracellular processes (e.g. formaldehyde) may contribute to symptoms of illness or discomfort independent of exposure to fungal biomass (Miller, 1992). The diversity in clinical scope of building-related illnesses makes their diagnosis difficult. Similarly, the identification and localization of agents that may contribute to decreased indoor air quality (IAQ) is often problematic. Over the past 30 years, "Sick Building Syndrome", in which the air quality in a building is compromised as a result of biological or chemical pollutants, has been recognized as a serious threat to modern public health (Mishra et al., 1992; Su et al., 1992; Tobin et al., 1987).

Despite the ubiquity of fungi in indoor air and dust, indoor fungal exposures are rarely implicated in the etiology of human infection (Burge, 1989; Summerbell et al., 1992). However, their involvement in irritative disorders (i.e. primarily non-infective diseases such as allergy and asthma) has long been recognised (Al-Doory, 1984; Cohen et al., 1935; Flannigan et al., 1991;

Gravesen, 1979; Reymann and Schwartz, 1946). Bioaerosols of fungal origin, consisting of spores and hyphal fragments are readily respirable, and are potent elicitors of bronchial irritation and allergy (Brunekreef et al., 1989; Burge, 1990a; Dales et al., 1991a, 1991b; Platt et al., 1989; Sakamoto et al., 1989; Samet et al., 1988; Sherman and Merksamer, 1964; Strachan et al., 1990).

ALLERGIC RHINITIS AND SINUSITIS

Type I allergic syndromes

Concern regarding human exposure to mould aerosols in indoor environments is mainly related to direct mucosal irritation and elicitation of an IgE-mediated hypersensitivity response that precipitates rhinitis and upper airways irritation, eye irritation and frequently sinusitis that characterize allergic syndromes (Pope et al., 1993). The symptoms of allergy are not manifested until sensitisation in which an individual incurs repeated exposures to the antagonistic agent. During this process, antigen-specific IgE is produced that attaches to receptors on mast cells that are concentrated on gastric and respiratory mucosa. In a sensitised individual, the IgE on mast cells binds to antigen following exposure, mediating mast cell rupture, histamine release and the ensuant hypersensitivity response (Guyton, 1982). The principal fungal allergens are either high molecular weight carbohydrates (e.g. beta 1-3 glucans) or water soluble glycoproteins (such as enzymes) (ibid.). Typically, these compounds are sequestered within fungal spores or secreted into fungus-contaminated debris. These allergens become airborne which when these materials are aerosolized. A link between respiratory exposure to fungal material and seasonal allergy was first proposed in 1873 by Blackley who demonstrated the provocation of allergic respiratory symptoms by exposure to *Penicillium* spores (*fide* Nilsby, 1949). Latgé and Paris (1991) listed 106 fungal genera with members documented to elicit allergy, although it is likely that the true number is actually much larger (Li, 1994). Although the principal allergenic vehicles of fungal allergies are spores and other cellular debris, the culprit allergens are not always constitutively present in these materials. Savolainen and co-workers (1990) suggested that certain allergenic enzymes may only be produced upon germination. Exposure to these compounds requires inhalation of germinable propagules, followed by germination on upper respiratory tract mucosa.

Dust mites and allergy

Other notable biological elicitors of similar allergic cascades include plant pollen (particularly *Ambrosia* spp. in northern temperate North America *fide* Jelks, 1994), and so-called "dust mites", typically of the genus *Dermatophagiodes* (especially *D. pteronyssinus* and *D. farinae*, Bronswijk, 1981). Considerable research has examined the relationship of dust mite allergen exposure to clinical allergy. Bronswijk (1981) provides an excellent review of this work. Dust mite sensitisation in domestic settings appears to be influenced by additional biotic agents. Miyamoto and colleagues (1969) showed allergenic cross-reactivity between domestic dust mites and other biological sensitizers including dust and fungi. It is likely that this cross-reactivity is a consequence of correlated exposures because mites often occur together with fungi on water-damaged indoor materials (Bronswijk, 1981)[3]. The feces of dust mites are considerably allergenic because of the large content of partially digested food materials and intact digestive enzymes (Tovey et al., 1981). In addition, mite fecal pellets often contain large numbers of intact and partially degraded fungal spores because these materials are a preferred food of many dustborne mite taxa (Samson and Lustgraaf, 1978).

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[3] It is common to observe dense mite colonization on superficial fungal growth on wall surfaces, especially where *Cl. sphaerospermum* has disfigured the finished sides of exterior walls pursuant to excessive indoor relative humidity during the winter months. In such cases, elevated mite populations are a predictable consequence. Indeed, by gauging the level of mite activity on a fungus-contaminated surface it is often possible to determine the time-course of contamination, since mite populations do not generally develop until 3-6 months after the emergence of fungal growth (data not presented).

Hypersensitivity syndromes

Extrinsic allergic alveolitis, or hypersensitivity pneumonitis (HP) is an acute inflammatory reaction of the lower airways upon exposure to an agent to which a sensitivity has developed from prior exposure. Hypersensitivity pneumonitis involves cell-mediated immunity (Type IV allergic response), in contrast to Type I allergic syndromes that are IgE-mediated, and thus may exist independently of the latter. Numerous environmental antigens have been implicated as elicitors of HP, including fungal aerosols. The majority of case literature on fungus-mediated HP involves occupational exposures where exposures to mould aerosol exceed background by several orders of magnitude. Furthermore, these exposures often involve a stable, low species diversity related to a particular substrate or process. Although the clinical presentation of these disorders is relatively uniform, a florid nomenclature has developed based primarily on the particular occupation or the sensitising agent implicated (*see* Table 1-1). In non-industrial, non-agricultural settings, some case reports suggest that sufficiently high airborne levels of otherwise innocuous fungal particulates have caused HP where patients exhibited pneumonia-like symptoms following even low exposures to irritant agents (Jacob et al., 1989; Pepys, 1969; Samet et al., 1988; Weissman and Schuyler, 1991). Four of the hypersensitivity pneumonitides in Table 1-1 have been reported from indoor environments: Humidifier Lung (fungal etiologic agents include *Penicillium* spp. and *Cephalosporium* [=*Acremonium*] spp.), Cephalosporium HP (*Cephalosporium* spp.) and Japanese Summer-Type HP (probable etiologic agent *Trichosporon cutaneum*) (Pope et al., 1993).

Asthma

Asthma is a disease characterized by reversible airway obstruction triggered by any of a number of provocation agents, including allergens, cold and exercise stress, and relieved by the inhalation of aerosolised beta-adrenergic antagonists (Hunninghake and Richardson, 1998; Pope et al., 1993). Asthmatic conditions are loosely categorized as **1)** allergic asthma, with typical onset at an early age in patients with positive skin tests to common allergens or a family history of allergy; and, **2)** idiosyncratic asthma, where onset is usually later in life, in the absence of immunological allergic predisposition, family history indicators or comorbid stimuli such as smoking. Asthma symptoms include wheezing, usually accompanied by dyspnea (shortness of breath) and cough, often in an episodic pattern with intermittent or extended periods of remission. For over a decade, it has been quite clear that the presence of moulds (as indicated by dampness) in housing exerts an adverse effect on the respiratory health of children (Martin et al., 1987; Platt et al., 1989). Strachan and co-workers (1988; 1990) showed an increase in symptoms of wheezing in children living in mouldy homes in Edinburgh, Scotland; however, these workers found little quantitative difference in the airborne mycoflora of households in which asthmatic children lived, as measured by viable sampling. These workers postulated that the disagreement between objective measurement of airborne mould levels and subjective assessment of housing conditions by occupants indicated a reporting bias in which asthmatics were more likely to report mould conditions than non-asthmatics. A Canadian cross-sectional study of over 13,000 children by Dales and colleagues (1991a) also showed a significant increase in respiratory symptoms according to reported mould or damp conditions in housing. These workers suggested that short-term indoor air samples ("grab samples") such as those employed by Strachan and co-workers (1988; 1990) were not necessarily reflective of longer-term conditions, due to the periodic nature of spore release. An earlier US-based cross-sectional study ("The Harvard Six-Cities Study", Brunekreef et al., 1989) showed a significantly lower prevalence of wheeze than the Edinburgh study, yet demonstrated a comparable odds ratio between this symptom and mouldy housing conditions, suggesting that wheeze may have been over-reported

TABLE 1-1: Selected hypersensitivity pneumonitides with probable microbial etiologies

DISEASE	SOURCE	PROBABLE ALLERGEN
Bagassosis	Mouldy bagasse (sugar cane)	Thermophilic actinomycetes
Cephalosporium HP	Basement sewage contamination	*Cephalosporium* spp. (=*Acremonium*)
Cheese washer's lung	Mouldy cheese	*Penicillium casei* (=*P. roquefortii*)
Compost lung	Compost	*Aspergillus* spp.
Familial HP	Contaminated wood dust in walls	*Bacillus subtilis*
Farmer's lung	Mouldy hay, grain or silage	*Aspergillus fumigatus* and thermophilic actinomycetes
Hot tub lung	Mould on ceiling	*Cladosporium* spp.
Housewife's lung	Moldy wooden flooring	*Penicillium expansum* and other moulds
Humidifier/ Air-conditioner lung	Contaminated water or coils in humidifiers and air-conditioners	*Aureobasidium pullulans*, *Cephalosporium* spp., *Penicillium* spp. and thermophilic actinomycetes
Japanese summer house HP	Bird droppings, house dust	*Trichosporon cutaneum*
Lycoperdonosis	Puffballs	*Lycoperdon* spp.
Malt worker's lung	Mouldy barley	*Aspergillus fumigatus* or *As. clavatus*
Maple bark disease	Maple bark	*Cryptostroma corticale*
Mushroom worker's lung	Mushroom compost	Thermophilic actinomycetes and other microorganisms
Potato riddler's lung	Mouldy hay around potatoes	*Aspergillus* spp. and thermophilic actinomycetes
Sauna taker's lung	Contaminated sauna water	*Cladosporium* spp. and others
Suberosis	Mouldy cork dust	unknown
Tap water lung	Contaminated tap water	unknown
Thatched roof disease	Dried grasses and other leaves	*Sacchoromonospora viridis*
Tobacco worker's disease	Mouldy tobacco	*Aspergillus* spp.
Winegrower's lung	Mouldy grapes	*Botrytis cinerea*
Wood trimmer's disease	Contaminated wood trimmings	*Rhizopus* spp. and *Mucor* spp.
Woodman's disease	Oak and maple trees	*Penicillium* spp.
Woodworker's lung	Oak, cedar and mahogany dusts, pine and spruce pulp	*Alternaria* spp. and wood dust

SOURCES: Hunninghake and Richardson (1998); Park et al. (1994); Pope et al. (1993)

in the study by Strachan and co-workers (1988). In their review of asthma trends, Pope and co-workers (1993) noted that the magnitude of allergen exposure increased the potential for allergic sensitisation, and was both a risk factor for lowered age of asthma onset as well as increased disease severity. Furthermore, these workers proposed a recent increase in asthma morbidity and mortality as reflected by hospital admission statistics.

MYCOTOXINS

In addition to their roles as irritants and allergens, many fungi produce toxic chemical constituents (Kendrick, 1992; Miller, 1992; Wyllie and Morehouse, 1977). Samson and co-workers (1996) defined mycotoxins as "fungal secondary metabolites that in small concentrations are toxic to vertebrates and other animals when introduced via a natural route". These compounds are non-volatile and may be sequestered in spores and vegetative mycelium or secreted into the growth substrate. The mechanism of toxicity of many mycotoxins involves interference with various aspects of cell metabolism, producing neurotoxic, carcinogenic or teratogenic effects (Rylander, 1999). Other toxic fungal metabolites such as the cyclosporins exert potent and specific toxicity on the cellular immune system (Hawksworth et al., 1995); however, most mycotoxins are known to possess immunosuppressant properties that vary according to the compound (Flannigan and Miller, 1994). Indeed, the toxicity of certain fungal metabolites such as aflatoxin, ranks them among the most potently toxic, immunosuppressive and carcinogenic substances known (ibid.). There are unambiguous links between ingestion as well as inhalation exposures to outbreaks of human and animal mycotoxicoses (Abdel-Hafez and Shoreit, 1985; Burg et al., 1982; Croft et al., 1986; Hintikka, 1978; Jarvis, 1986; Norbäck et al., 1990; Sorenson et al., 1987; Schiefer, 1986). Several common mycotoxigenic indoor fungi and their respective toxins are listed in Table 1-2.

TABLE 1-2: Mycotoxins of significance produced by indoor fungi

MYCOTOXIN	PRIMARY HEALTH EFFECT	FUNGAL PRODUCERS
Aflatoxins	Carcinogens, hepatotoxins	*Aspergillus flavus* *As. parasiticus*
Citrinin	Nephrotoxin	*Penicillium citrinum* *Pe. verrucosum*
Cyclosporin	Immunosuppressant	*Tolypocladium inflatum*
Fumonisins	Carcinogens, neurotoxins	*Fusarium moniliforme* (=*F. verticillioides*) *F. proliferatum*
Ochratoxin A	Carcinogen	*As. ochraceus* *Pe. verrucosum*
Patulin	Protein synthesis inhibitor, nephrotoxin	*As. terreus* *Paecilomyces variotii* *Pe. expansum* *Pe. griseofulvum* *Pe. roquefortii*
Sterigmatocystin	Carcinogen, hepatotoxin	*As. nidulans* *As versicolor* *Chaetomium* spp.
Trichothecenes, macrocyclic		
Satratoxins	Protein synthesis inhibitors	*Stachybotrys chartarum* *Myrothecium* spp.
Trichothecenes, non-macrocyclic		
Deoxynivalenol (vomitoxin)	Emetic	*F. cerealis* *F. culmorum* *F. graminearum*
T-2 toxin	Hemorrhagic, emetic, carcinogen	*F. sporotrichioides*
Verrucosidin	Neurotoxin	*Pe. aurantiogriseum* group
Xanthomegnin	Hepatotoxin, nephrotoxin	*As. ochraceus* *Pe. aurantiogriseum* group
Zeralenone	Estrogenic	*Fusarium* spp.

SOURCES: Burge and Ammann (1999); Rodricks et al. (1977); Samson et al. (1996)

VOLATILE FUNGAL METABOLITES

During exponential growth, many fungi release low molecular weight, volatile organic compounds (VOCs) as products of secondary metabolism. These compounds comprise a great diversity of chemical structure, including ketones, aldehydes and alcohols as well as moderately to highly modified aromatics and aliphatics. Cultural studies of some common household moulds suggest that the composition of VOCs remains qualitatively stable over a range of growth media and conditions (Sunesson et al., 1995). Furthermore, the presence of certain marker compounds common to multiple species, such as 3-methylfuran, may be monitored as a proxy for the presence of a fungal amplifier (Sunesson et al., 1995). This method has been suggested as a means of monitoring fungal contamination in grain storage facilities (Börjesson et al., 1989; 1990; 1992; 1993). Limited evidence suggests that exposure to low concentrations of VOCs may induce respiratory irritation independent of exposure to allergenic particulate (Koren et al., 1992). Volatile organic compounds may also arise through indirect metabolic effects. A well-known example of this is the fungal degradation of urea formaldehyde foam insulation. Fungal colonization of this material results in the cleavage of urea from the polymer, presumably to serve as a carbon or nitrogen source for primary metabolism. During this process formaldehyde is evolved as a derivative, contributing to a decline in IAQ (Bissett, 1987).

OBJECTIVES OF THE CURRENT STUDY

The present study was conceived with two primary objectives. First, this investigation shall characterize the fungal biodiversity of house dust. This work shall investigate correlations between dustborne fungal species, and examine the ecological similar of positively associated taxa based on the hypothesis that positively associated dustborne fungi are likely to share habitat characteristics. From this, a second hypothesis follows that mechanisms that permit the entry or concentration a given species will tend to facilitate the entry of other positively correlated taxa.

A second objective of this research is to assess the extent of genotypic variability in two dustborne Penicillia, *P. brevicompactum* and *P. chrysogenum*. The goal of this work shall be to examine the extent of clonality within these two species, and to determine if the observed patterns of genotypic variation support the current species concepts.

CHAPTER 2. ANALYSIS OF HOUSE DUST MYCOFLORA

ABSTRACT

Broadloom dust samples were enumerated for culturable fungi from 369 homes in Wallaceburg, Ontario, Canada in winter, 1994. In total, 253 fungal taxa were identified. The taxa observed were consistent with other published reports on the fungal flora of household dust and indoor air. Taxa observed in the present study followed a Raunkiaer-type distribution, where several species accounted for the majority of observations (abundance), and the greater proportion of species documented were observed only rarely. A calculation of sampling efficiency according to Good's Hypothesis suggested high overall sampling efficiency, averaging over 92 % of the total expected biodiversity. Association analysis based on two-way chi-square contingency resolved a number of species assemblages. These assemblages were primarily correlated to ecological specialization. The three main ecological categories that characterized the main assemblages comprised **1)** phylloplane fungi; **2)** soil fungi and **3)** food spoilage/ xerophilic fungi. A number of smaller assemblages contained species known to be active contaminants of water damaged building materials.

INTRODUCTION

It has long been hypothesized that indoor dusts possess allergenic properties (Lucretius, 50 BC). However, the importance of fungal materials as dust-borne allergens, was not demonstrated with fair certainty until early in the 20th century (Flood, 1931; Hopkins et al., 1930). Recently, however, there have been efforts to study household dust as an ecosystem, in an attempt to determine the characteristics of dust-borne fungi that facilitated their diversification into this relatively new habitat (Davies, 1960; Bronswijk, 1981; Bronswijk et al., 1986; Swaebly and

Christensen, 1952; Verhoeff et al., 1994). It is difficult to interpret much of the existing literature in this area for two main reasons: 1) many authors provide only genus-level identifications of fungi, or employ species names that are antiquated or confused; and, 2) the lack of voucher isolates precludes the confirmation of results.

The present study is an examination of the fungal flora of household broadloom dust obtained during the course of a larger research project funded by the Canada Mortgage and Housing Corporation (CMHC) (Ottawa). This project sought to measure various parameters of environmental exposure incurred by housing occupants, and attempted to correlate these findings to objective measures of illness. Within this context, the present study shall (1) determine the numbers and kinds of moulds present in household broadloom dust in a study site in Wallaceburg , and (2) investigate statistical associations between different mould taxa in an attempt to form hypotheses on sources and contamination pathways.

MATERIALS AND METHODS

Field work for this study was conducted by a private company under contract to CMHC over a period of five months starting in January, 1994. Initially, 400 households in Wallaceburg, Ontario agreed to participate in Phase I the study (*see* Figure 2-1).

COLLECTION OF DUST SAMPLES

Vacuum cleaner bag samples of carpet dust were collected from 369 houses. Sample coverage is illustrated on the residential street map shown in Figure 2-2. These samples were supplied in sealed, 10 mL polypropylene vials which were stored at room temperature until analysis.

FIGURE 2-1. Map of Ontario, Canada, indicating the location of Wallaceburg

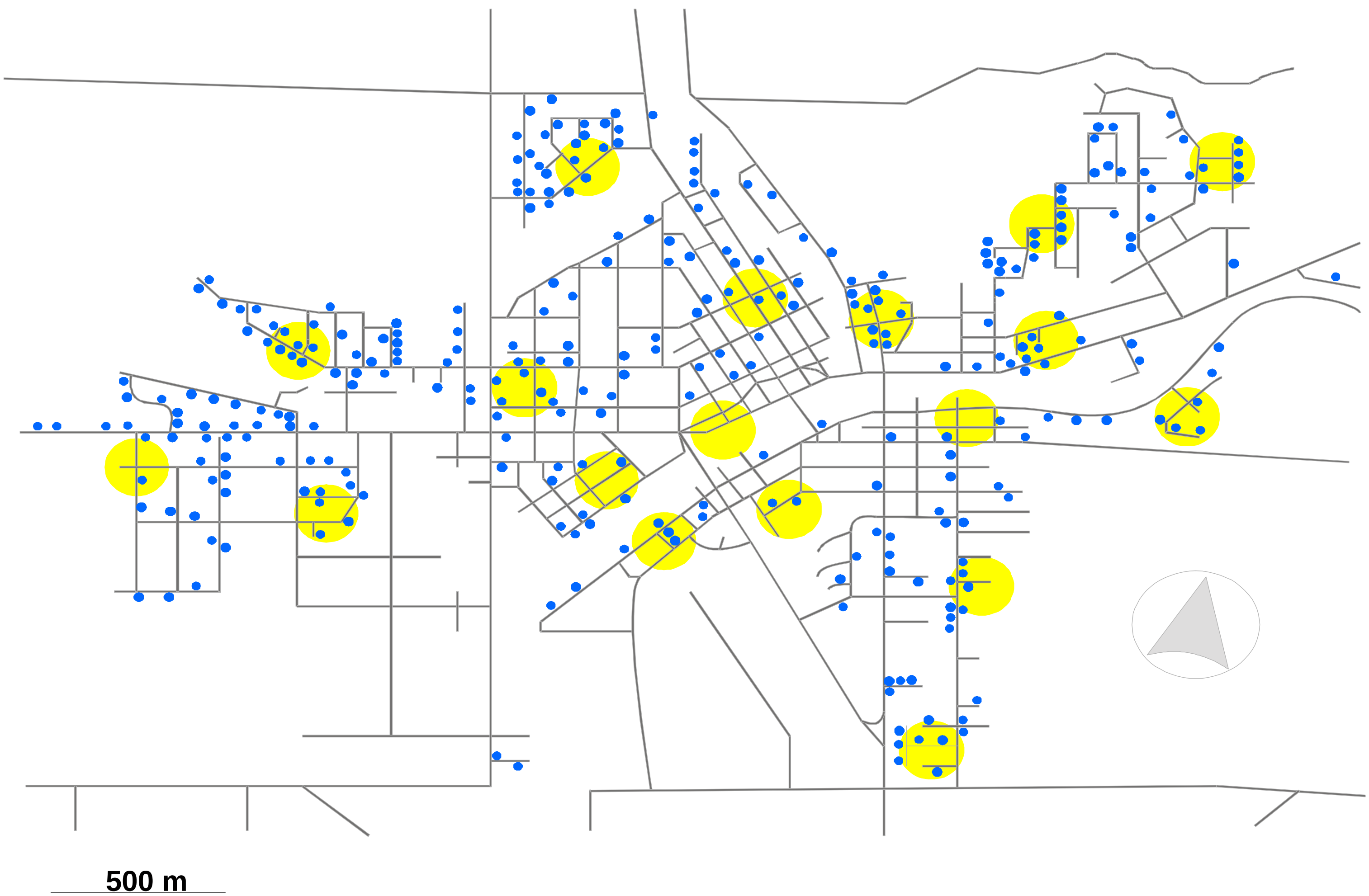


Figure 2-2: Locations of urban houses sampled (small blue dots). Locations of air samples taken during late summer, 1995 using the RCS sampler (each sample tested 80,000 cc of air) are indicated by large yellow circles.

ANALYSIS OF DUST SAMPLES

Two subsamples of approximately 50 mg (the actual mass was recorded) were added individually to 10 mL of sterile 2% peptone broth and suspended by vortexing at medium speed. Two serial dilutions of these stock suspensions were made subsequently using an adaptation of the standard technique reviewed by Malloch (1981); the first was made by diluting 1 mL of stock suspension in 9 mL of 2% peptone broth and the second was made by diluting 1 mL of the first serial dilution in 9 mL of 2% peptone broth. Four aliquots of 1 mL each were taken from each of the two sets of dilutions and dispensed individually into polystyrene 100 mm Petri dishes (Fisher). Two Petri plates were set up in this manner for each of the two stock suspensions. Molten sterile Rose Bengal agar (RBA) (Malloch, 1981) and RBA containing 25 % glycerol (RBGA) as an osmoticant. Both media were amended with 60 ppm of chlortetracycline hydrochloride (Sigma), streptomycin sulphate (Sigma) and benzylpenicillin (penicillin-G, Sigma), were cooled to 45 °C and aseptically dispensed each into half of the Petri plate replicates at a volume of 25 mL per plate using a Pour-o-matic Petri plate filling machine (New Brunswick Scientific, New Jersey). The medium was mixed with the dilution aliquot by gently swirling the Petri plates prior to solidification. A schematic of the plating regime is provided in Figure 2-3.

After 12 to 18 hr the plates were removed from the machine, wrapped with Parafilm (Alcan) and inverted in stacks of 20 plates each. The plates were incubated under 12 hr artificial daylight at room temperature (ca. 24 °C) for 7 days. One of the three sets of dilutions averaging between 15 and 60 colonies per plate was selected for identification and enumeration. Except where one of the media used could not be enumerated at the dilution selected (due to excessively high- or low numbers of colonies or contamination) the same dilution set was enumerated for both media. This method was refined by multiple preliminary experiments.

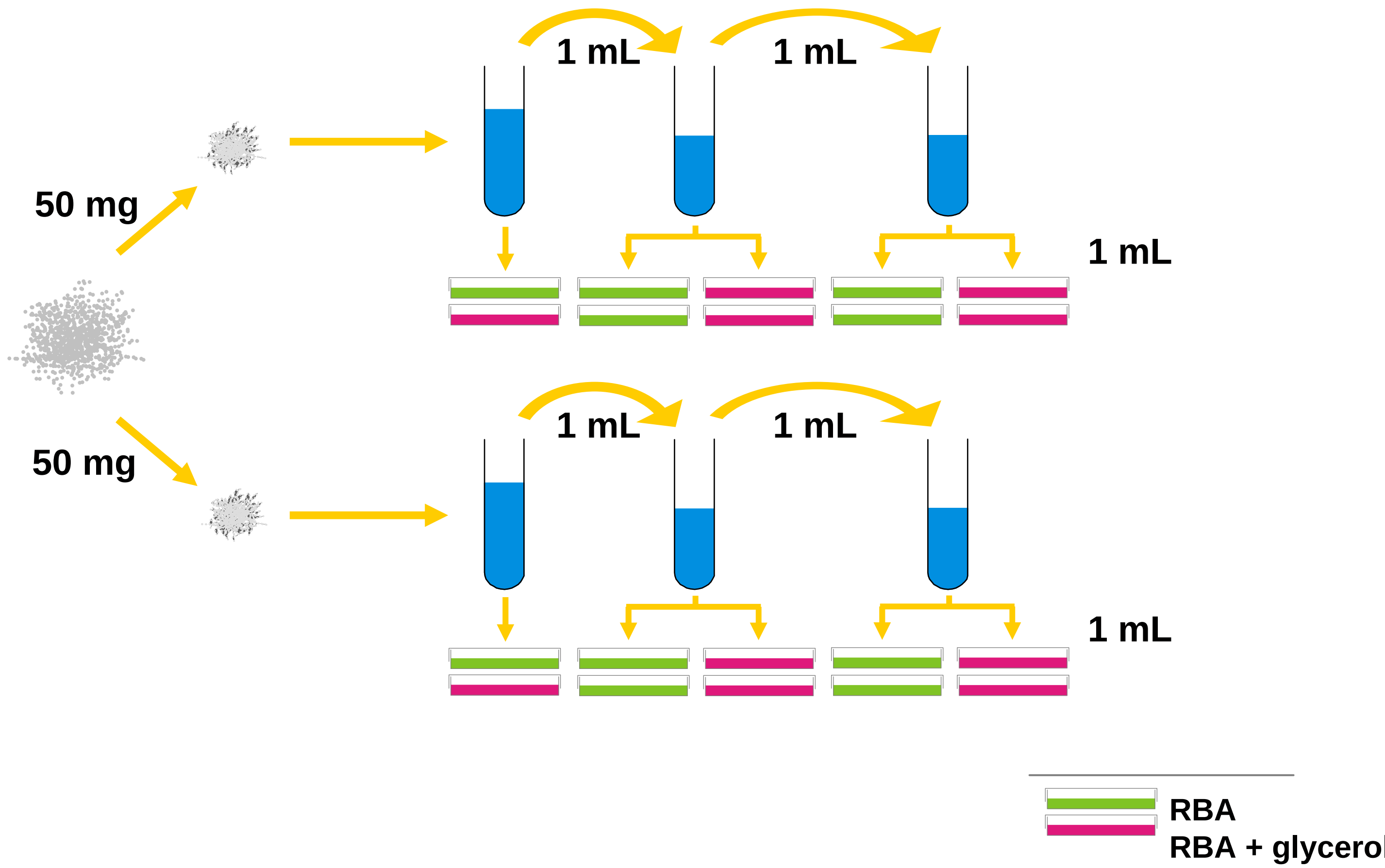


Figure 2-3. Plating regimen for dust samples.

Microscopic mounts were made in either distilled water with Photoflo (Kodak) or lacto-fuchsin (Carmichael, 1955). All culture media and stock solutions were autoclaved for 20 min at 15 psi prior to use. Sterile glass- and plasticware were used for all aseptic procedures.

IDENTIFICATION AND ISOLATION OF CULTURES

Where possible, fungi were identified to the genus level directly from colonies on the Rose Bengal isolation media using well-established techniques of macroscopic and microscopic examination and standard reference works for the identification of moulds (e.g. Arx, 1970; Barnett and Hunter, 1986; Barron, 1968; Carmichael et al., 1980; Domsch et al. 1980; Ellis, 1971, 1976; Hanlin, 1990; Malloch, 1981). Many isolates were further identified to species level using appropriate monographs.

Species of *Penicillium* were grouped according to macroscopic and microscopic similarity, averaging five groups per house. Representatives of each of the groups with similar penicillia were subcultured on four diagnostic media for further identification using a central-point inoculation technique modified from Pitt (1979). The Petri plates were wrapped with Parafilm, and incubated inverted under 12 hr artificial daylight at room temperature for 7 to 14 days prior to examination. The following media were employed in the identification of cultures of *Penicillium* to species level: Czapek's yeast-autolysate agar (CYA) (Pitt, 1979), Creatine sucrose agar (CREA) (as modified by Frisvad, 1985), 25% Glycerol-nitrate agar (G25N) (Pitt, 1979) and Modified Leonian's agar (MLA) (Malloch, 1981). Multiple unique isolates of *Penicillium* spp. were retained for subsequent use. Cultures were identified according to colonial and microscopic morphologies produced on these media and compared to the species descriptions given by Pitt (1980, 1988). Other fungi that could not be identified directly on RBA and RBGA plates were subcultured on a range of other growth media (including CYA, MLA, 2% water agar, Weitzman-Silva Hutner's agar and Sabouraud's glucose agar (Malloch, 1981)) and incubated in a manner similar to that used for the species identification of *Penicillium* cultures.

RELIABILITY OF IDENTIFICATIONS

This study involved the examination and identification of over 200,000 individual fungal colonies. Over half of these identifications were performed by the author; the balance were carried out by B.M. Koster, D. Malloch and L.J. Hutchison in addition to several contracted student assistants (*see* Acknowledgements, p. iv). Discussions between the author and other project workers during the plating/ isolation phase suggested that the rate of misidentifications was relatively low, and typically restricted to rare or difficult taxa (e.g. *Pencillium aurantiogriseum* group). This speculation has been supported by retrospective examination of many retained cultures. For the purposes of the analyses presented in this chapter, all identifications were accepted as accurate and comparable; however, the reader is cautioned that the reliability of identifications may vary to some extent according to the skill of the investigator and the condition of the particular isolate examined.

STORAGE OF CULTURES

Each representative isolate of *Penicillium* was subcultured in duplicate into 2 mL screw cap (with rubber “O”-ring) flat-bottom microcentrifuge (microculture) tubes (Sarstedt) containing 1 mL per tube of 2 % MLA. Additional representatives of *Penicillium* and other genera were subcultured in a similar manner pending future need. The tubes were capped and incubated under 12 hr artificial daylight at room temperature for 7 to 10 days prior to transfer to 5 °C for short-term storage. Cultures requiring long-term preservation (e.g. for use in fingerprinting) were subcultured subsequently and checked for purity. Axenic cultures were subcultured in triplicate in microculture tubes and incubated as outlined above. After colonies had grown out, cultures were aseptically overlaid with 1 mL sterile 20 % glycerol combined with 17 % skim milk as a cryoprotectant and stored at -70 °C (McGinnis and Pasarell, 1992).

ORGANIZATION AND ANALYSIS OF DATA

Data were compiled using the Borland Paradox database (ver. 3.0, Borland Corp.). The database consisted of one record for each occurrence of a species on each plate examined (for both RBA and RBGA). Each record comprised 6 fields: House number; Plate identifier; Species name; Number of colonies counted; Mass of dust used in subsample (mg); and, Total number of plates of each medium (RBA or RBGA) that were examined for that house. Subsequent manipulations of the data including statistical analyses were carried out by means of specific software routines programmed and compiled by the author using QuickBasic (ver. 4.5, Microsoft Corp.).

An index of sampling efficiency (*I*) was calculated using Good's Hypothesis as modified by Moore and Holdeman (Good, 1953; Moore and Holdeman, 1974), such that;

$$I = (1 - N_1 / N_T) \times 100 \qquad (1)$$

where,

N_1 = number of species observed once
N_T = total number of observations of all species

Presence-absence (occurrence) data for taxa present in 2 % or more of samples were analysed using chi-square association analysis with Yate's correction factor for small datasets (Greig-Smith, 1964; Kent and Coker, 1992), such that:

$$\chi^2 = \frac{n(ad-bc-n/2)^2}{(a+b)\cdot(c+d)\cdot(a+c)\cdot(b+d)} \tag{2}$$

where,

a = observed number of relevés containing "a & b"
b = observed number of relevés containing "a" only
c = observed number of relevés containing "b" only
d = observed number of relevés lacking "a & b"
n = total number of relevés examined

The relative degree of association was summarized graphically for all combinations of taxa involved in one or more significant associations based on negative inverse logarithms of chi-square values. These values were compiled into an artificial "distance matrix" in which closely-associated pairs of taxa had smaller interposing distances relative to those with lesser associations, which were separated by greater distance. A cluster analysis of this matrix was conducted using the UPGMA method in the PAUP* software package (PAUP* version 4.0b4a for 32 bit Microsoft Windows, Sinauer Associates, Inc., Sunderland, Massachusetts). It is acknowledged that as test statistics, chi-square values calculated from pair-wise contingency of nominal data such as those in the present study represent multiple non-independent comparisons, and thus should not properly be analysed in un-corrected combination. It is important to note, however, that the use of chi-square values in the present application is soley a measure of the degree of association and not an assessment of the statistical significance of correlation (*see* Causton, 1988). Following UPGMA cluster analysis, terminal clusters of three or more closely-associated taxa were pruned from the dendrogram and re-examined graphically as 2-way matrices upon which the level of significance and polarity of association of individual chi-square statistics were encoded.

RESULTS

SPECIES DIVERSITY AND DISTRIBUTION

Two hundred and fifty-three fungal taxa were isolated from the 369 dust samples analysed. The proportion of house dust samples containing each taxon are summarized in Figure 2-4. A complete list of abbreviations used is given in the front matter. The distribution of fungal taxa in the study site was of a Raunkiaer-type, whereby species were distributed unevenly in abundance. In this model, most species were observed only rarely, and the majority of individuals in the population comprised relatively few species (Daubenmire, 1968; Raunkiaer, 1934).

Thirty-three taxa were observed in 10 % or more of samples; six of these taxa, *Alternaria alternata*, *Aureobasidium pullulans*, *Eurotium herbariorum*, *Epicoccum nigrum*, *Aspergillus versicolor* and *Penicillium chrysogenum* were present in 50 % or more of the samples analysed. Forty-three taxa were observed in 2 to 10 % of samples, while an additional 177 taxa were present in fewer than 2 % of samples. Interestingly, unidentified yeasts were observed in 85 % of samples analysed while the most commonly encountered filamentous fungus, *Alternaria alternata*, was observed in 89 % of samples. The most commonly occurring species of *Penicillium* were: *P. chrysogenum* (52 % of samples), *P. spinulosum* (39 %), *P. corylophilum* (29 %), *P. commune* (26 %) and *P. brevicompactum* (23 %). Most taxa observed were anamorphic species; however, a few sexual species were encountered (e.g. *Eurotium herbariorum*, *Sordaria* spp., and *Eupenicillium ochrosalmonium*).

EFFICIENCY OF SAMPLING

According to Moore and Holdeman's modification of Good's hypothesis (Good, 1953; Moore and Holdeman, 1974), the species that were observed comprised, on average, 92.1 % (8.8 %,

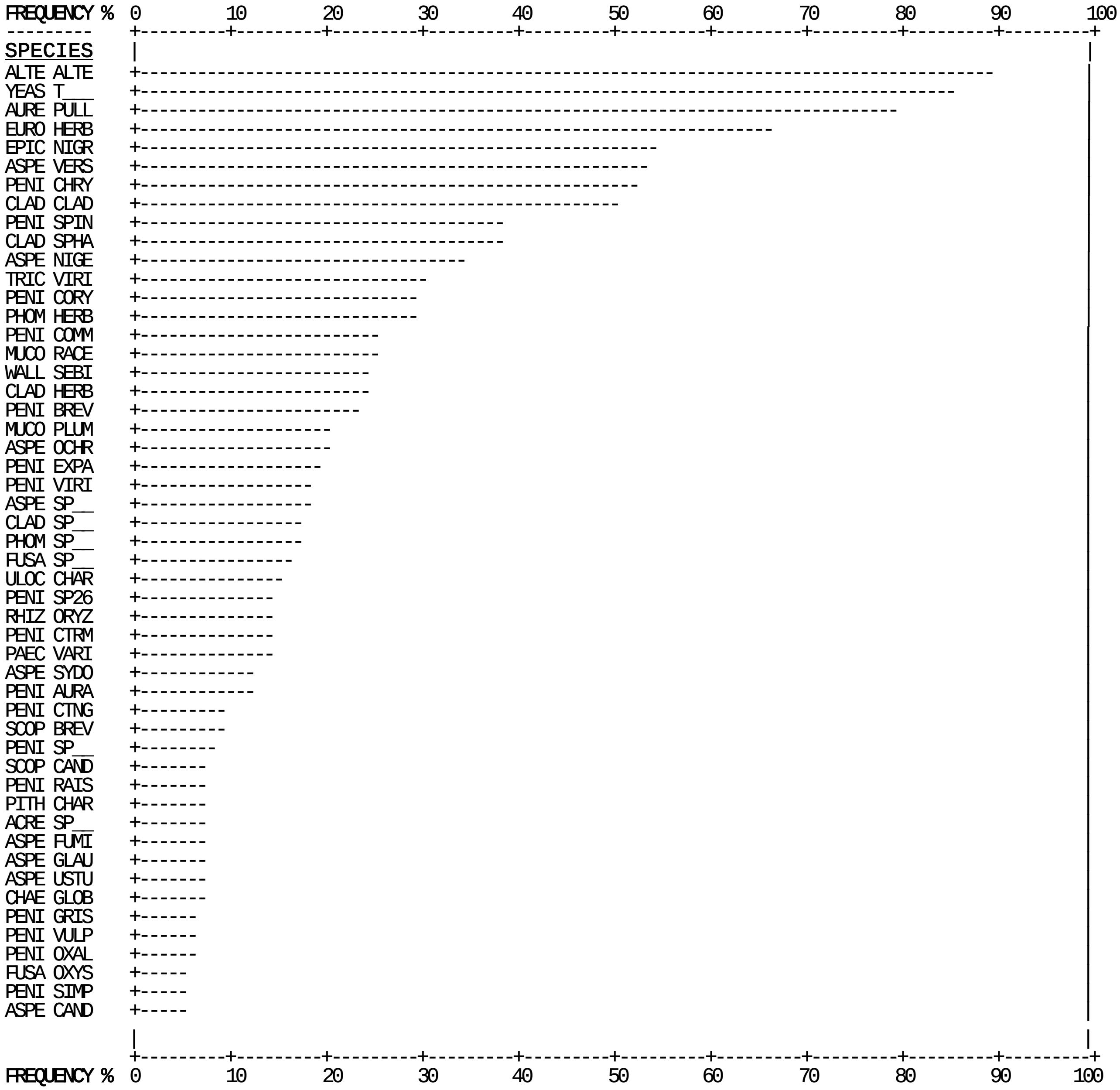


FIGURE 2-4. Frequency of dustborne fungi observed in broadloom dust samples from Wallaceburg, Ontario.

```
FREQUENCY %  0         10        20        30        40        50        60        70        80        90        100
---------    +---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
SPECIES      |                                                                                                   |
PENI DECU    +-----                                                                                              |
PENI IMPL    +-----                                                                                              |
PENI ECHI    +-----                                                                                              |
ALTE SP__    +----                                                                                               |
CHRS PMSP    +----                                                                                               |
PENI CRUS    +----                                                                                               |
PENI MICZ    +----                                                                                               |
PENI GLAN    +----                                                                                               |
SPHA SP__    +----                                                                                               |
STAC CHAR    +----                                                                                               |
GEOM PANN    +---                                                                                                |
PENI VARI    +---                                                                                                |
PENI ISLA    +---                                                                                                |
PENI ITAL    +---                                                                                                |
CONI SP__    +---                                                                                                |
EMER NIDU    +---                                                                                                |
PENI COPR    +---                                                                                                |
PENI DIGI    +---                                                                                                |
PENI SP64    +---                                                                                                |
ASPE ORYZ    +--                                                                                                 |
PENI ATRA    +--                                                                                                 |
PENI PURP    +--                                                                                                 |
PENI REST    +--                                                                                                 |
PENI SP01    +--                                                                                                 |
PENI VERR    +--                                                                                                 |
PAEC SP__    +--                                                                                                 |
TRIC SP__    +--                                                                                                 |
ALTE TENU    +--                                                                                                 |
ASPE REST    +--                                                                                                 |
MICR OLIV    +--                                                                                                 |
PENI ROQU    +--                                                                                                 |
PEST SP__    +--                                                                                                 |
SPOR BLMY    +--                                                                                                 |
STEM SP__    +--                                                                                                 |
CLAD MACR    +-                                                                                                  |
EURO SP__    +-                                                                                                  |
MYRO OLIV    +-                                                                                                  |
OIDI SP__    +-                                                                                                  |
PENI SP87    +-                                                                                                  |
PITH SP__    +-                                                                                                  |
TRIC HARZ    +-                                                                                                  |
ASPE CERV    +-                                                                                                  |
ASPE CLAV    +-                                                                                                  |
ASPE FLAV    +-                                                                                                  |
ASPE TERR    +-                                                                                                  |
CHAE COCH    +-                                                                                                  |
CONI FUCK    +-                                                                                                  |
EXOP JEAN    +-                                                                                                  |
GEOM SP__    +-                                                                                                  |
GEOT CAND    +-                                                                                                  |
GLIO SP__    +-                                                                                                  |
             |                                                                                                   |
             +---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
FREQUENCY %  0         10        20        30        40        50        60        70        80        90        100
```

FIGURE 2-4. Frequency of dustborne fungi observed in broadloom dust samples from Wallaceburg, Ontario.

```
FREQUENCY %  0         10        20        30        40        50        60        70        80        90       100
---------    +---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
SPECIES      |                                                                                                   |
HORT WERN    +-                                                                                                  |
HUMI FUSC    +-                                                                                                  |
MUCO MUCE    +-                                                                                                  |
PAEC INFL    +-                                                                                                  |
PENI JANT    +-                                                                                                  |
SCOP SP__    +-                                                                                                  |
ULOC SP__    +-                                                                                                  |
ASPE ORNA    +-                                                                                                  |
BOTR SP__    +-                                                                                                  |
CHAE SP__    +-                                                                                                  |
COCH GENI    +-                                                                                                  |
COCH SATI    +-                                                                                                  |
EXOP SP__    +-                                                                                                  |
MICR SP__    +-                                                                                                  |
MUCO SP__    +-                                                                                                  |
MYRO SP__    +-                                                                                                  |
PENI HIRS    +-                                                                                                  |
PENI WAKS    +-                                                                                                  |
PHIA FAST    +-                                                                                                  |
PHOM CHRY    +-                                                                                                  |
PHOM EUPY    +-                                                                                                  |
PHOM EXIG    +-                                                                                                  |
PHOM MEDI    +-                                                                                                  |
SCOP CHAR    +-                                                                                                  |
SYNC RACE    +-                                                                                                  |
TRIC KONI    +-                                                                                                  |
VERT SP__    +-                                                                                                  |
ABSI CORY    +-                                                                                                  |
ACRE RUTI    +-                                                                                                  |
ACRE SCLE    +-                                                                                                  |
ACRE STRI    +-                                                                                                  |
ASPE PARX    +-                                                                                                  |
ASPE TAMA    +-                                                                                                  |
BOTR CINE    +-                                                                                                  |
CAND SP__    +-                                                                                                  |
CHAE FUNI    +-                                                                                                  |
CHRY SITO    +-                                                                                                  |
CHRY NLSP    +-                                                                                                  |
CLAD CHLO    +-                                                                                                  |
CURV PRAS    +-                                                                                                  |
DREC SP__    +-                                                                                                  |
EMER SP__    +-                                                                                                  |
EMER VARI    +-                                                                                                  |
EPIC SP__    +-                                                                                                  |
EURO AMST    +-                                                                                                  |
EURO RUBR    +-                                                                                                  |
GRAP SP__    +-                                                                                                  |
HORM DEMA    +-                                                                                                  |
LECY HOFF    +-                                                                                                  |
LEPT AUST    +-                                                                                                  |
MONA RUBE    +-                                                                                                  |
             |                                                                                                   |
             +---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
FREQUENCY %  0         10        20        30        40        50        60        70        80        90       100
```

FIGURE 2-4. Frequency of dustborne fungi observed in broadloom dust samples from Wallaceburg, Ontario.

```
FREQUENCY %  0         10        20        30        40        50        60        70        80        90        100
---------    +---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
SPECIES      |                                                                                                   |
MUCO CIRC    +-                                                                                                  |
MYRO CINC    +-                                                                                                  |
NIGR SPHA    +-                                                                                                  |
PENI FUNI    +-                                                                                                  |
PENI MELI    +-                                                                                                  |
PEST PALU    +-                                                                                                  |
PHIA SP__    +-                                                                                                  |
PHOM FIME    +-                                                                                                  |
PHOM GLOM    +-                                                                                                  |
PHOM LEVE    +-                                                                                                  |
RHIZ STOL    +-                                                                                                  |
RHOD SP__    +-                                                                                                  |
SCOP BRUM    +-                                                                                                  |
SCOP FUSC    +-                                                                                                  |
SORD SP__    +-                                                                                                  |
STEM SOLA    +-                                                                                                  |
SYNC SP__    +-                                                                                                  |
TALA FLAV    +-                                                                                                  |
TORU HERB    +-                                                                                                  |
TRIC ASPE    +-                                                                                                  |
ABSI SP__    +                                                                                                   |
ACRE BUTY    +                                                                                                   |
ACRE FURC    +                                                                                                   |
ACRE KILI    +                                                                                                   |
ACRE MURO    +                                                                                                   |
ALTE CITR    +                                                                                                   |
APIO MONT    +                                                                                                   |
APIO SP__    +                                                                                                   |
ASPE FLAP    +                                                                                                   |
ASPE NIVE    +                                                                                                   |
ASPE PARS    +                                                                                                   |
ASPE PENI    +                                                                                                   |
ASPE SCLE    +                                                                                                   |
ASPE WENT    +                                                                                                   |
BASI DIOM    +                                                                                                   |
BLAS SP__    +                                                                                                   |
BOTR PILU    +                                                                                                   |
BOTR ALLI    +                                                                                                   |
CHAE AURE    +                                                                                                   |
CHAE CIRC    +                                                                                                   |
CHAE NOZD    +                                                                                                   |
CHAE SUBS    +                                                                                                   |
CONI SPOR    +                                                                                                   |
CUNN SP__    +                                                                                                   |
CURV PROT    +                                                                                                   |
CURV SENE    +                                                                                                   |
CYLI SP__    +                                                                                                   |
DIPL SPIC    +                                                                                                   |
DORA MICR    +                                                                                                   |
DOTH CZSP    +                                                                                                   |
DOTH LASP    +                                                                                                   |
             |                                                                                                   |
             +---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
FREQUENCY %  0         10        20        30        40        50        60        70        80        90        100
```

FIGURE 2-4. Frequency of dustborne fungi observed in broadloom dust samples from Wallaceburg, Ontario.

```
FREQUENCY %  0         10        20        30        40        50        60        70        80        90        100
---------    +---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
SPECIES      |                                                                                                   |
DREC BISE    +                                                                                                   |
EUPE OCHR    +                                                                                                   |
EURO CHEV    +                                                                                                   |
FUSA EQUI    +                                                                                                   |
FUSA FLOC    +                                                                                                   |
GILM HUMI    +                                                                                                   |
GLIO ROSE    +                                                                                                   |
GLIO VIRE    +                                                                                                   |
GLIO MURO    +                                                                                                   |
GLIO MUFE    +                                                                                                   |
GLIO MUMU    +                                                                                                   |
HAIN LYTH    +                                                                                                   |
HYAL SP__    +                                                                                                   |
LECY SP__    +                                                                                                   |
MONI SP__    +                                                                                                   |
MRTR AMAT    +                                                                                                   |
MUCO HIEM    +                                                                                                   |
MYRO RORI    +                                                                                                   |
NEOS SP__    +                                                                                                   |
OIDI RHOD    +                                                                                                   |
OPHI SP__    +                                                                                                   |
OPHI TENE    +                                                                                                   |
PAEC FULV    +                                                                                                   |
PAEC FUMO    +                                                                                                   |
PENI CANE    +                                                                                                   |
PENI SP13    +                                                                                                   |
PENI SP35    +                                                                                                   |
PENI SP38    +                                                                                                   |
PENI SP44    +                                                                                                   |
PENI SP52    +                                                                                                   |
PENI SP84    +                                                                                                   |
PYRE SP__    +                                                                                                   |
PYTH SP__    +                                                                                                   |
SCOL CONS    +                                                                                                   |
SCYT SP__    +                                                                                                   |
SPOR THSP    +                                                                                                   |
SPOR PRUI    +                                                                                                   |
STAC PARV    +                                                                                                   |
STEM BOTR    +                                                                                                   |
SYNC VERR    +                                                                                                   |
TALA TRAC    +                                                                                                   |
THAM ELEG    +                                                                                                   |
TOLY SP__    +                                                                                                   |
TRIC POLY    +                                                                                                   |
TRIC TONS    +                                                                                                   |
TRIC ROSE    +                                                                                                   |
TRUN ANGU    +                                                                                                   |
ULOC ATRU    +                                                                                                   |
WARD HUMI    +                                                                                                   |
ZETI HETE    +                                                                                                   |
             |                                                                                                   |
             |                                                                                                   |
             +---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
FREQUENCY %  0         10        20        30        40        50        60        70        80        90        100
```

FIGURE 2-4. Frequency of dustborne fungi observed in broadloom dust samples from Wallaceburg, Ontario.

SD) of the total expected biodiversity in the study site. This result, in combination with the Raunkiaer-type distribution of taxa within the sample set, suggests that an increase in the number of sample sites would have only contributed to an increase in the number of rare species observed (*see* Figure 2-5).

SPECIES ABUNDANCE

The calculated abundance data (not presented here) showed numbers of colony-forming units (CFUs) per gram of dust that ranged, on average, from 2 to 10 CFUs/mg; but, species abundance occasionally was observed as high as 500 CFUs/mg. Generally, yeasts and yeast-like fungi (e.g. *Aureobasidium pullulans*) tended to occur at greater abundances than strictly filamentous species. Due to the relatively low number of replications per sample (i.e. the number of plates examined) which varied from 4 to 8, the standard deviations of average species abundances tended to be excessive, often in excess of calculated means. For this reason, excessive outlying data would not permit trends of species associations to be resolved using canonical correspondence analysis (Braak, 1992). Species that occurred at a low frequency (i.e. in fewer than 2 % of samples) tended to skew the chi-statistic artifactually towards significance. For this reason, rare species were eliminated from this analysis. The results of significant chi-square associations are shown in trellis-diagram format in Figure 2-6. The 52 pairings of species represent the significant associations (α = .05, df = 1) that resulted from the inspection of 3,003 pairings (*see* Appendix B). The first 21 couplets were highly significant (α=.001, *see* Appendix B).

ASSOCIATION ANALYSIS

The 52 associations of significance involved forty-seven taxa (including a category of unidentified yeasts); forty-three of these associations were positive correlations while the

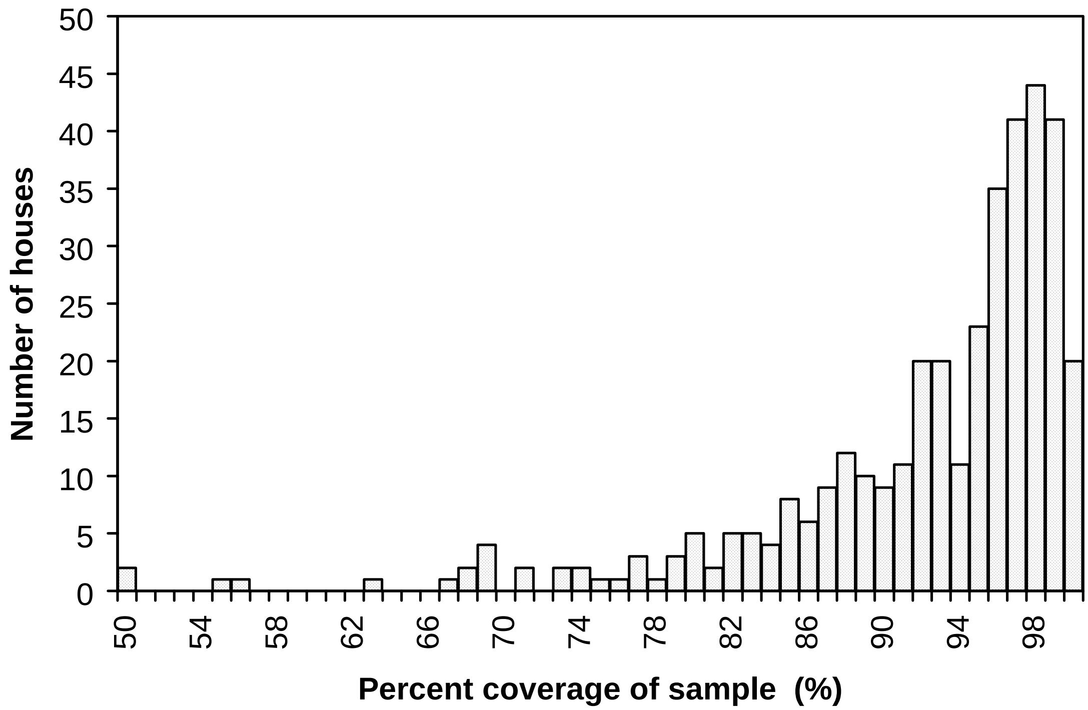
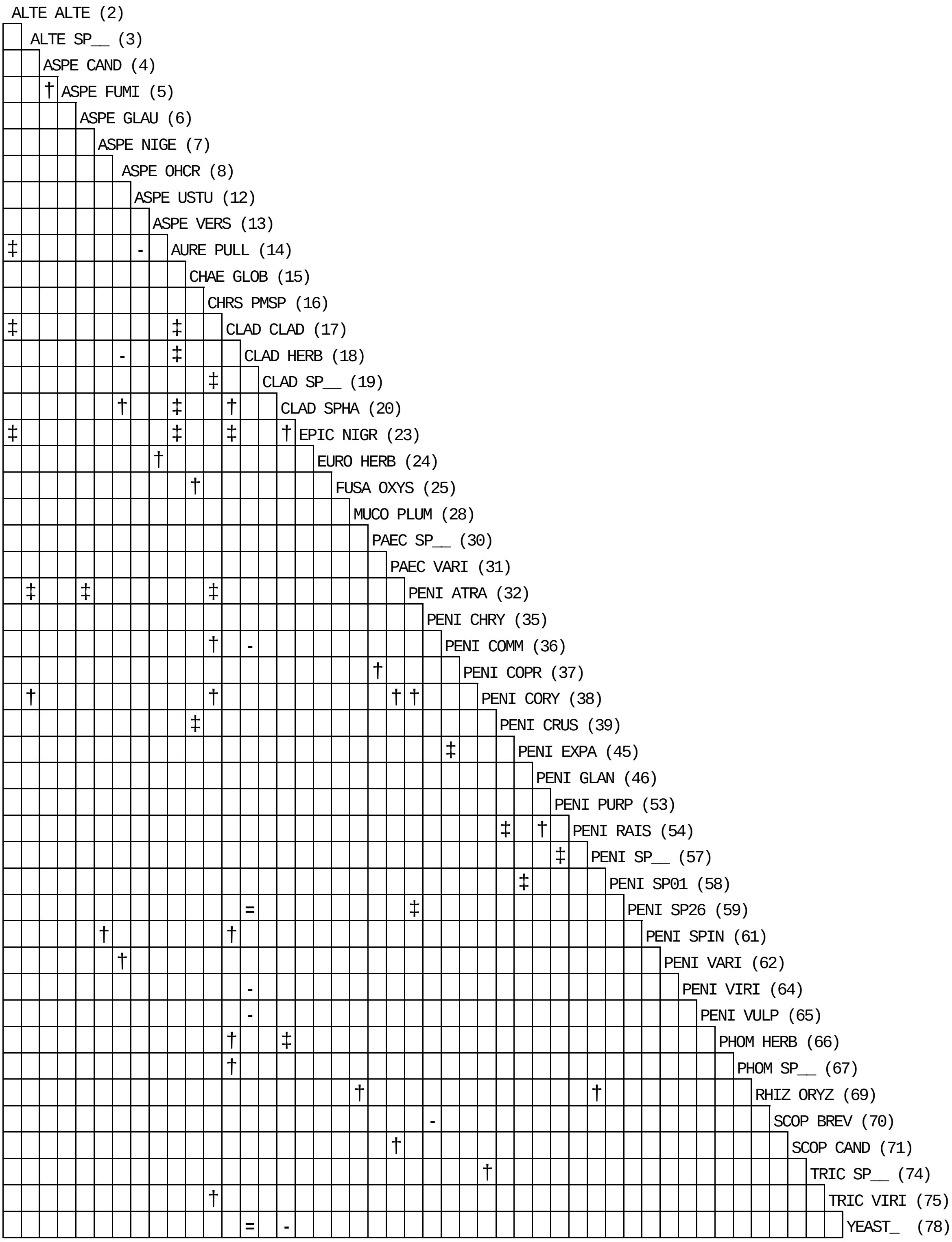


FIGURE 2-5. Sampling efficiency for house dust mycoflora as estimated based on Good's Hypothesis.



LEGEND: Positive association significant at α = .05 (†) and α = .001 (‡)
Negative association significant at α = .05 (-) and α = .001 (=)

FIGURE 2-6. Trellis diagram summarizing significant associations of dustborne taxa. Positive associations are indicated by **†** (α=0.05) **‡** (α=0.001). Negative associations are indicated by **-**(α=0.05) and **=** (α=0.001).

remainder (9) were negatively associated. Interestingly, *Cladosporium herbarum* was a partner in two thirds of the negative associations.

The results of this association analysis are presented as a dendrogram based on average distance by an inverse logarithmic transformation of the χ^2 value. Overall, 14 clusters of more than two taxa were observed (*see* Figure 2-7). These terminal clusters of 3 or more taxa are shown in Figure 2-8, and their polarity is indicated. Each terminal branch is shown as a matrix, in which the positive or negative nature of the correlation is shown by a shaded circle at each node. Following is a summary of these terminal clusters:

Cluster a) An unidentified species of *Paecilomyces* was positively correlated to *Penicillium coprophilum* (*see* Figure 2-8a). This pair was negatively correlated to *Trichoderma* sp. and *Penicillium italicum* (the latter pair also showed a negative correlation).

Cluster b) A similar arrangement was observed in Figure 2-8 cluster b, in which *Coniothyrium* sp. was positively correlated to *Penicillium vulpinum* yet this pair showed negative correlation to *Emericella nidulans* and *Penicillium restrictum* (the latter two also showed negative correlation).

Cluster c) *Stachybotrys chartarum* was negatively correlated to the positively-associated pair *Penicillium implicatum* and *Penicillium miczynskii* (*see* Figure 2-8c).

Cluster d) Cluster d (Figure 2-8d) showed positive associations between *Penicillium atramentosum*, *Penicillium* sp. #26, *Aspergillus glaucus*, *Alternaria* sp. and *Penicillium corylophilum*. Within this

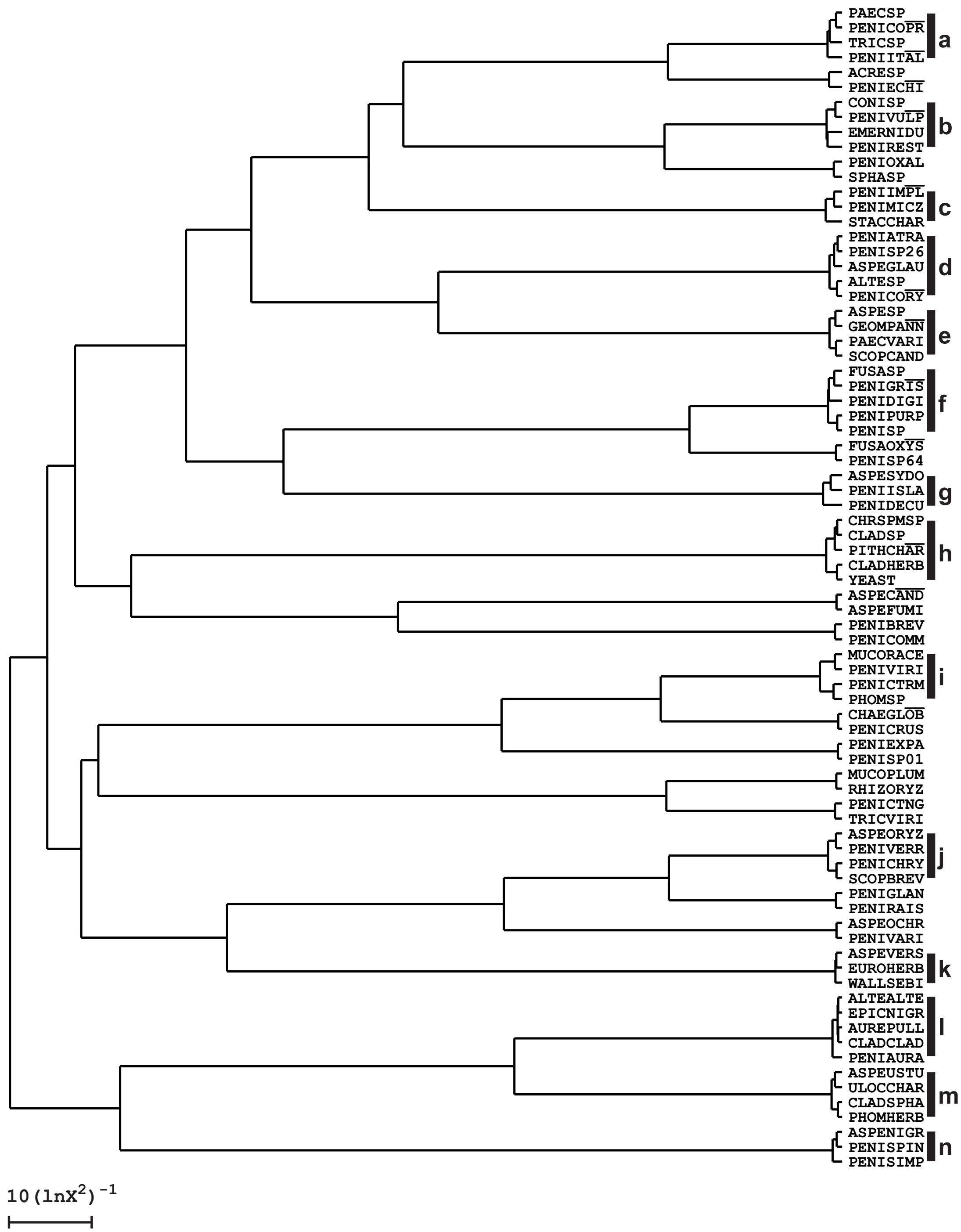


FIGURE 2-7. Cluster analysis based on associations between dustborne fungi determine by pair-wise Chi-square contingency.

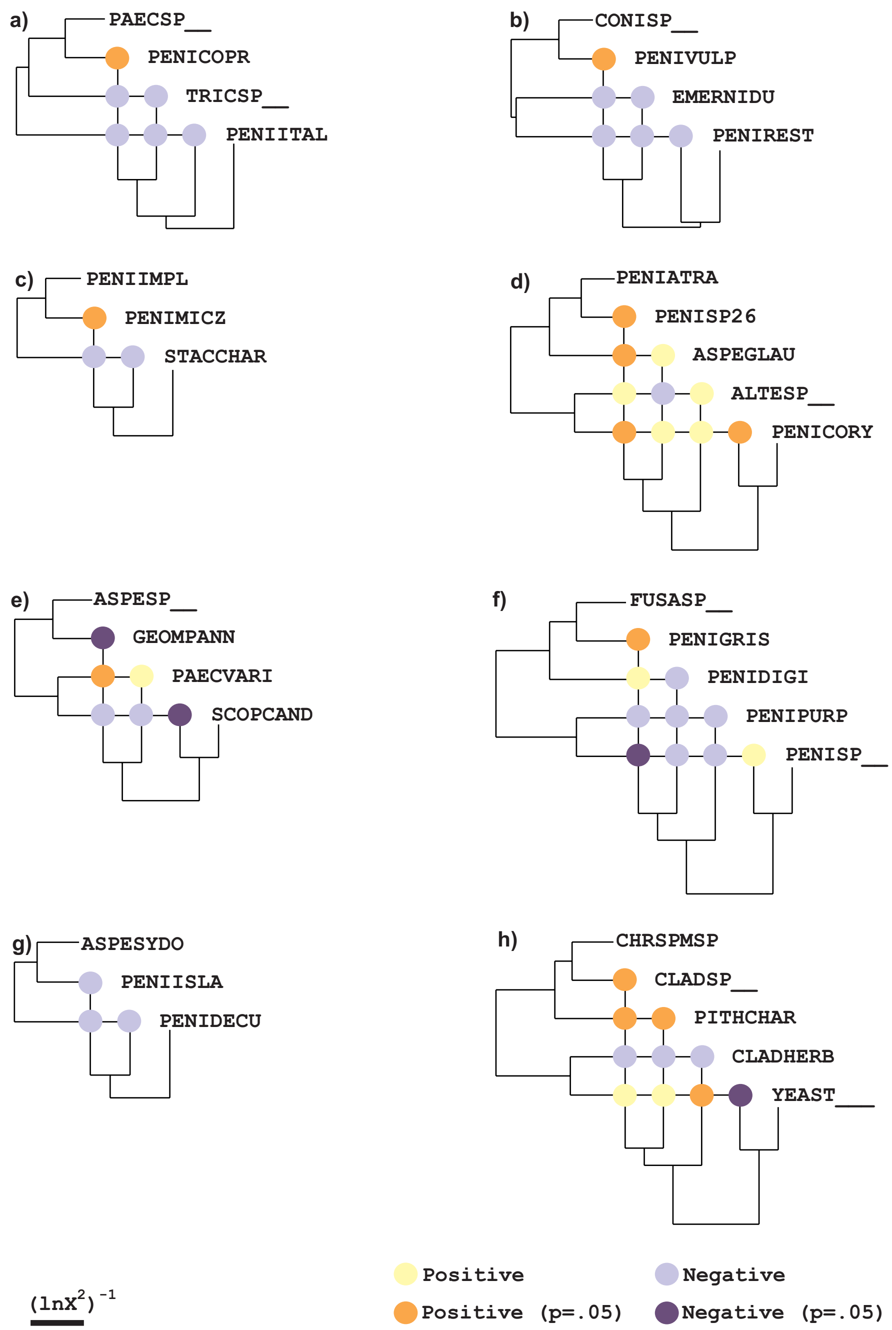


FIGURE 2-8. Significant associations between taxa in significant clusters (> 2 taxa).

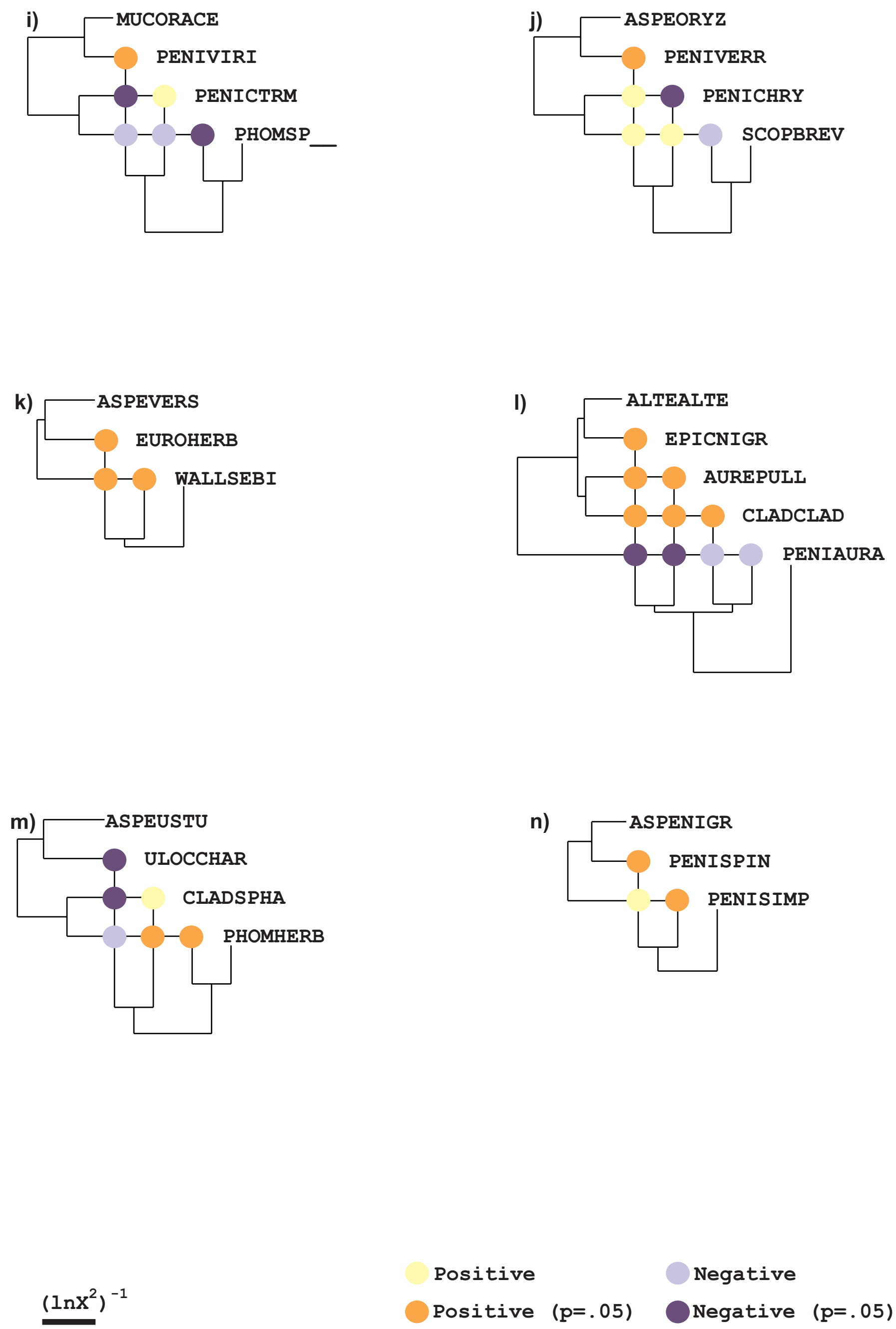


FIGURE 2-8 (cont'd). Significant associations between taxa in significant clusters (> 2 taxa).

assemblage, however, a negative association was observed between *Alternaria* sp. and *Penicillium* sp. #26.

Cluster e) *Geomyces pannorus* was positively associated with *Paecilomyces variotii* (*see* Figure 2-8e). An unidentified species of *Aspergillus* showed a negative correlation to the former, and a positive correlation to the latter. Collectively, this group was negatively associated with *Scopulariopsis candida*.

Cluster f) *Fusarium* sp. in cluster f (Figure 2-8f) was positively allied with *Penicillium griseofulvum* and *Penicillium digitatum* (the latter two were negatively associated). This group was negatively associated with the positively correlated pair of *Penicillium purpurogenum* and an un-named *Penicillium* species.

Cluster g) The species negatively-associated assemblage in cluster g (Figure 2-8g) comprised *Aspergillus sydowii*, *Penicillium islandicum* and *Penicillium decumbens*.

Cluster h) The three taxa *Chrysosporium* sp., *Cladosporium* sp., *Pithomyces chartarum* and uncategorized yeast were positively associated in cluster h (Figure 2-8h). This group was negatively correlated to *Cladosporium herbarum*.

Cluster i) *Mucor racemosus* was positively correlated with *Penicillium viridicatum*, which was further positively correlated to *Penicillium citrinum* (*see* Figure 2-8i). However, *Penicillium citrinum* showed a strongly negative correlation to *Mucor racemosus*. As well, an unidentified species of *Phoma* showed negative correlations to all taxa in this cluster (Figure 2-8i).

Cluster j) *Penicillium chrysogenum* was negatively correlated with *Penicillium brevicompactum*, yet these two taxa were positively correlated with *Aspergillus oryzae* (*see* Figure 2-8j). Within this assemblage, *Penicillium verrucosum* showed a positive association with *Aspergillus oryzae* and *Penicillium brevicompactum* and a strongly negative association with *Penicillium chrysogenum*.

Cluster k) The xerophilic fungi *Aspergillus versicolor, Eurotium herbariorum* and *Wallemia sebi* formed a positively correlated assemblage (*see* Figure 2-8k).

Cluster l) There were positive associations between the typical phylloplane fungi, *A. alternata*, *Aureobasidium pullulans*, *C. cladosporioides*, and *Epicoccum nigrum* (*see* Figure 2-8l). This assemblage tended to be negatively associated with *Penicillium aurantiogriseum*.

Cluster m) The phylloplane taxon *Ulocladium chartarum* was positively associated with *Cladosporium sphaerospermum* and *Phoma herbarum*. This assemblage was collectively negatively associated with the xerophilic fungus *Aspergillus ustus* (*see* Figure 2-8m).

Cluster n) Similar to Cluster k (*As. versicolor, Eu. herbariorum* and *W. sebi*), *Aspergillus niger* was positively associated with *Penicillium spinulosum* and *Penicillium simplicissimum* (*see* Figure 2-8n).

The remaining couplet assemblages are summarized in Table 2-1. Ten of these associations were positive and one was negative (*Acremonium* sp. with *Penicillium echinulatum*). Of the positive associations, several are of interest. In particular, the soil fungi *Aspergillus candidus* and *Aspergillus fumigatus* were associated. *Aspergillus ochraceus* was positively associated with *Penicillium variabile*. Both of these taxa are common indoor contaminants on damp building materials (Adan and

Table 2-1: Couplets of associated dustborne taxa

Polarity	Taxon #1	Taxon #2	p-value
Positive	*Aspergillus candidus*	*Aspergillus fumigatus*	0.003
	Aspergillus ochraceus	*Penicillium variabile*	0.002
	Chaetomium globosum	*Penicillium crustosum*	< 0.001
	Fusarium oxysporum	*Penicillium* sp. #64	0.006
	Mucor plumbeus	*Rhizopus oryzae*	0.003
	Penicillium brevicompactum	*Penicillium commune*	0.015
	Penicillium citreonigrum	*Trichoderma viride*	0.014
	Penicillium expansum	*Penicillium* sp. #1	< 0.001
	Penicillium glandicola	*Penicillium raistrickii*	0.004
	Penicillium oxalicum	*Sphaeropsis* sp.	0.032
Negative	*Acremonium* sp.	*Penicillium echinulatum*	0.103

Samson, 1994). Similarly, *Chaetomium globosum* showed an association with *Penicillium crustosum*. These taxa are common colonists of very wet gypsum wall board. *Mucor plumbeus* was correlated with *Rhizopus oryzae*. Both of these taxa are rapid colonists of substrates under high disturbance, particularly in the presence of simple carbohydrates (e.g. such as decaying fruits) (Samson and Reenen-Hoekstra, 1988). *Penicillium brevicompactum* showed a positive association with *Penicillium commune*. These Penicillia occur frequently on indoor finishes, particularly wall paper or drywall which incurs intermittent wetting. The soil fungi *Penicillium citreonigrum* and *Trichoderma viride* were positively associated. For comparative purposes, the houses which were observed to have active mould growth on indoor surfaces are summarized in Table 2-2.

DISCUSSION

The most commonly occurring species found in the present study are consistent with reports on the species composition of household dust by other authors (Bronswijk, 1981; Calvo et al., 1982; Davies, 1960; Gravesen, 1978; Hamada and Yamada, 1991; Ishii et al., 1979; Lustgraaf and Bronswijk, 1977; Mallea et al., 1982; Saad and El-Gindy, 1990; Schober, 1991; Swaebly and Christensen, 1952; Wickman et al., 1992). The species assemblages of dust microfungi observed in this study comprised a mixture of ecologically homogeneous groups:

1) Phylloplane (leaf surface) moulds (e.g. *Alternaria alternata*, *Aureobasidium pullulans*, *Cladosporium cladosporioides* and *Epicoccum nigrum*), all of which were negatively correlated to *Penicillium aurantiogriseum*, a typical xerophilic food spoilage fungus.

2) Xerophilic moulds typically associated with food spoilage such as *Aspergillus versicolor* group, *Eurotium herbariorum* and *Wallemia sebi* (*see* Pitt and Hocking, 1985; Samson and Reenen-Hoekstra, 1988)

Table 2-2: Houses with visible mould growth observed

House Number	Number of isolates recovered	
	P. brevicompactum	*P. chrysogenum*
10		
24		
28		
30		
31		
34		2
43		
45	2	5
48		5
55		
86		
96		
100	1	
102		1
111		1
115		
117		
122		
132	2	1
134		
136	1	
150		
154		2
157		
167		
177		3
190		
197		
201	1	
206		1
216		1
235		
247		1
250		
276		1
332		
377		
395		
396		

3) Soilborne fungi such as *Trichoderma viride* and *Penicillium citreonigrum* (*see* Barron, 1968; Domsch et al., 1980). The existence of these distinct species assemblages was corroborated by chi-square association analysis.

Besides the groups with obvious ecological similarity, several species assemblages were noted that contained taxa notable as contaminants of water-damaged building materials or finishes (e.g. *Aspergillus versicolor, As. ustus, Chaetomium globosum, Penicillium aurantiogriseum, Pe. brevicompactum, Pe. chrysogenum* and *Stachybotrys chartarum*). Often these taxa (e.g. *As ustus*, *Pe. aurantiogriseum*, etc.) were negatively correlated to clusters of taxa from defined ecological groups discussed above. It is likely that these taxa are true household residents, as agents of structural contamination or growing in dust following episodic wetting.

The results of this study showed disproportionately high viable levels of small-spored fungi, such as *Aspergillus* or *Penicillium* (data presented in Appendix A). This observation is consistent with those of other workers (e.g. Flannigan and Miller, 1994), who have suggested that additional factors besides proliferation *in situ* may lead to accumulation of these spores in dust in homes absent of indicators of mould problems (e.g. in good repair, clean and free from water damage) and objective measurements demonstrate a high standard of IAQ (Flannigan and Miller, 1994; Scott et al., 1999a). Scott and co-workers (1999a) postulated that dilute levels of spores of these taxa from outdoors might enter houses passively and accumulate in dust, either because of differentially long viability period of spores of these species or through mechanical means. The large component of phylloplane fungi in house dust suggests that, although these fungi may in some cases become resident in homes, their collective occurrence in dust is a function of their abundance in outdoor air; thus, in house dust, the accumulation of propagules of these fungi likely results from the settling of spores from ambient air. The fact that many small spored taxa are often well-represented in carpet dust may relate to the tendency of these spore types to be produced by phialidic species, many of which produce spores prolifically on compound conidiophores with the number of spores per conidiophore greatly in excess of many common, non-phialidic phylloplane moulds (e.g. *Alternaria*, *Cladosporium*). Differences in viability over time between these two spore types may also be important. For instance, the relatively thick-walled nature of these typically phylloplane spores intuitively suggests an adaptation to increased spore viability; however, Sussman (1968) documented the disproportionate longevity of small, thin-walled globose spores such as *Aspergillus* and *Penicillium*, relative to larger, thicker walled spores of phylloplane moulds. Despite the lack of input of xerophilic species into the indoor environment from outdoors during winter months while windows remain closed to conserve heat, a stable reservoir of propagules of phylloplane moulds remains in the biological "memory" of the carpet. Flannigan and Miller (1994) recognized the longevity of *Aspergillus* and *Penicillium* spores in household dust, and suggested that this property may permit the use of dust as a long-term spore trap which, by analysis, could reveal transient bursts of airborne spores of these taxa over time. However, Verhoeff and co-workers (1994) found only a weak correlation between houses that had objectively demonstrable mould problems and a substantial change in the dust mycoflora, suggesting that dust analysis may not be a reliable predictor of indoor contamination.

The viability of the mycoflora was followed over three years for dust samples from selected Wallaceburg stored under dry conditions. Fifteen dust samples (indicated in bold in Table 2-2) in follow-up testing showed the complete dying off of all taxa except *Aureobasidium pullulans* and *Penicillium* spp. These results confirmed the observation of Sussman (1968) that spores of species of *Aspergillus* and *Penicillium* remain viable for a much longer period of time compared to most phylloplane fungi under our storage conditions (e.g. *Alternaria*, *Cladosporium*, *Epicoccum* and *Ulocladium* and support the hypothesis that the culture-presence of high numbers of *Aspergillus* and *Penicillium* relative to phylloplane taxa from household dust may be an artifact of the longer period of spore viability of the former group. Davies (1960) proposed that mould colonization of house dust required at least one of several conditions to be met: **1)** the direct observation of conidiophores in the dust; **2)** the ability to culture particular fungi from dust-borne mycelial fragments; and, **3)** an abundance of a particular fungus in dilution plates that significantly exceeds the representation of that same species in control samples. These principles are supported by the present study.

I hypothesize that various routine mechanical processes within houses permit the accumulation of fungal spores. Since spores of *Aspergillus* and *Penicillium* are typically in the size range of 2-5 μm in diameter it is possible that these particles may penetrate inefficient filters, such as dust bags in portable vacuum cleaners or filters in forced-air heating systems, and thus, not be efficiently removed from the indoor environment by these processes (Stetzenbach et al., 1999). This being the case, a properly installed, externally-vented central vacuum cleaner may help to reduce the accumulation of indoor mould spores.

The negative correlation of *C. herbarum* with a number of other, presumably resident carpet dust fungi may result from its particular abundance in outdoor air during early spring (Abdel-Hafez et al., 1986, 1993; Ripe, 1962). Additional examinations of outdoor air samples by the author have shown that *C. herbarum* is typically the most abundant species of *Cladosporium* isolated from outdoor air from early spring through summer in Toronto. This species remained relatively uncommon in dust samples until late spring, at which point, the colony counts of *C. herbarum* became sufficiently high that higher orders of dilution were used in order to maintain overall counting efficiency (data not shown). As such, the occurrences of other species that remained present at roughly constant background levels were displaced by the high input of *C. herbarum* and proportionally were observed to decrease.

Soilborne fungi occur only at very low levels in indoor air, and their presence in indoor environments is mostly limited to the soil of indoor, potted ornamental plants (Summerbell et al., 1992). The results of the present study indicate that many common soilborne taxa occur frequently in carpet dust as well. This may result from the commonplace North American practice of wearing footwear in the house, a custom uncommon in most parts of Europe and Asia.

The indices of coverage that were calculated using Good's hypothesis showed that in all but a few cases (e.g. house numbers 137, 288 and 291) the sampling technique employed was adequate to detect close to the total number of species expected in each dust sample (see Appendix C). Nevertheless, the number of replications that would be required to establish statistical confidence in abundance data is prohibitively large in a study of this magnitude. Even so, the interpretation of abundance data is complicated by the tendency of heavily sporulating fungi such as *Aspergillus*, *Penicillium* and fungi exhibiting yeast-like growth forms to be over-represented in surveys employing serial dilution techniques.

CONCLUSIONS

The fungal flora of broadloom-bound house dust consists of a mixture of active and passive residents. The passive occupants of carpet substrates are mainly allochthonous, and arise from ecologically diverse habitats, mostly outside of the indoor environment. The main sources of allochthonous indoor moulds are 1) the phylloplane; 2) soil and 3) xerophilic fungal food-spoilage. The accumulation of spores of these fungi within broadloom dust is a result of multiple mechanical processes operating within the indoor environment. These processes may include the propagation of phylloplane spores indoors on air currents and clothing and the movement of soil-borne fungi indoor on footwear and by pets.

The small-spored nature of many xerophilic food spoilage fungi may favor their passage through inefficient filters, such as on vacuum cleaners and forced air furnaces. This likelihood, coupled with the differentially greater longevity relative to phylloplane taxa may facilitate their artifactual accumulation within broadloom over time. Many of the taxa common to any of these groupings may undergo active growth in the indoor environment under suitable conditions, however, the primary sources of inoculum for these fungi are allochthonous. The active residents of broadloom dust are mostly restricted to a small subset of the total fungal biodiversity contained within this substrate. These species proliferate within broadloom dust (autochthonous), and are similarly often responsible for fungal disfigurement of other indoor finishes and building elements under conditions of water accumulation (e.g. *As versicolor, W. sebi*).

CHAPTER 3. A REVIEW OF TECHNIQUES FOR THE ASSESSMENT OF GENOTYPIC DIVERSITY[4]

INTRODUCTION

The development of the polymerase chain reaction (PCR) in the mid 1980s precipitated a series of rapid technological advancements in DNA-based diagnostics as well as DNA sequencing technology. Many such improvements have lead to the widespread acceptance and, indeed, routine use of DNA sequencing as a tool for addressing a myriad of previously untenable biological hypotheses. In particular, DNA sequencing has permitted the inferential elucidation of phylogeny in many difficult taxonomic groups, such as the Trichocomaceae.

As problems of relatedness and species concept among the anamorphs of the Trichocomaceae are resolved, questions of population biology or genetic variation below the species level become germane. To date, many molecular genetic techniques have been devised to discriminate 'individuals'. These methods include the classical hybridisation approach of Restriction Fragment Length Polymorphism (RFLP) as well as several PCR-based approaches such as Random Amplified Polymorphic DNA (RAPD), Amplified Fragment Length Polymorphism (AFLP), RFLP of PCR products (PCR-RFLP), Single-Strand Conformation Polymorphism (SSCP), Microsatellite Single-Locus Fingerprinting and Heteroduplex Mobility Assay (HMA).

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[4] This chapter is reprinted with the kind consent of the copyright owners, Overseas Publishers Association (OPA) N.V., with permission from Gordon and Breach Publishers, from Scott, J.A. and Straus, N.A. 2000. A review of current methods in DNA fingerprinting. pp. 209-224. *In* Integration of Modern Taxonomic Methods for *Penicillium* and *Aspergillus* Classification. R.A. Samson and J.I. Pitt (eds). Amsterdam: Harwood Academic Publishers. This work was a contribution to the Third International Workshop on *Penicillium* and *Aspergillus*, held in Baarn, The Netherlands, from 26-29 May 1997, and is presented here as justification for the use of heteroduplex mobility assay as a method of genotypic comparison in this dissertation. For up-to-date discussion of DNA fingerprinting techniques, the reader is referred to Blears et al. (1998), Ryskov (1999), Savelkoul et al. (1999), Smouse and Chevillon (1998) and Soll (2000).

This chapter presents a critical assessment of these techniques and comments upon their appropriate uses.

THE DETECTION OF GENETIC VARIATION

The ability to analyse and characterize genetic variation between individuals of the same species with both accuracy and precision has been a technological grail of biological science since Gregor Mendel's pioneering work on heredity in the mid-nineteenth century. Traditionally, morphological and later physiological characteristics of phenotype served as proxy measurements of genotypic variation. However, most phenotypic traits do not behave as strict Mendelian determinants and instead are regulated by multifactorial genetic expression (i.e. polygenetic inheritance) coupled with complex environmental influences. Thus, while useful as taxonomic and ecological indicators, these markers pose problems in population genetic studies. In more recent time, molecular approaches have attempted to solve these shortcomings, first with studies on protein variation and later, following the emergence of recombinant DNA technology, by analyses of the genetic material itself. The recent introduction of the polymerase chain reaction (PCR) (Mullis, 1990; Saiki et al., 1985, 1988) represents a quantum technological advance in applied molecular genetics, and has driven the development of a great diversity of ancillary methodologies (White et al., 1989).

THE USE OF PROTEINS TO DISTINGUISH VARIATION

Early approaches to the assessment of genetic diversity exploited polymorphisms in a variety of well characterized enzymes. Extracted proteins were separated by gel electrophoresis and allozymes (allelic variants of the same enzyme) were detected by reacting the gel with an appropriate substrate and dye. Allozymes with differing amino acid sequences appeared as bands with unique electrophoretic mobilities in native gels. With the development of allozyme analysis in the mid 1960s, it at once became possible to address questions about spatial and temporal distribution of genetic variability within and between populations and to investigate fundamental aspects of mating systems, recombination, gene flow and genetic drift. This early form of molecular genetic analysis remained prominent until the mid 1980s.

HYBRIDIZATION-BASED MARKERS

In the early 1970s, DNA-based technologies began to replace protein analyses. Initially, DNA-DNA reassociation kinetics coupled with DNA hybrid stability was used to analyse phylogenetic relationships of single-copy DNA in eukaryotic organisms (e.g. Shields and Straus, 1975; Sohn et al., 1975). These pioneering techniques of the 1970s rapidly gave way to the more powerful methodologies of genetic engineering. Unlike allozyme assays, the still-widespread analysis of restriction fragment length polymorphisms (RFLP) had the advantage of examining DNA variability directly. In RFLP, genomic DNA is digested with a restriction endonuclease. The resulting DNA fragments are separated by gel electrophoresis, chemically denatured and transferred by Southern blotting to a DNA-binding membrane. The membrane is incubated in a solution containing a labelled nucleic acid probe and the hybridising fragment bands are visualized by autoradiographic or chemiluminescent techniques. The resulting patterns may represent polymorphic forms of a structural gene with implication for breeding strategies or may be the result of more complex patterns arising from repeated elements of cryptic function.

Variable number tandem repeats (VNTRs) range from short, interspersed repeats of short nucleotide sequences to long stretches of recurrent, tandem sequence motifs. Families of VNTR sequences are known variously as "satellite" DNAs, appropriately prefixed to indicate the relative size category of the repeated element and its extent of dispersion within the genome (e.g. microsatellite, minisatellite). Variable minisatellite DNA was first investigated for DNA fingerprinting by Jefferies and co-workers (1985a, 1985b), and is discussed in detail by Jefferies (1987). RFLP technology has been widely exploited for mycological analysis. This method has been reviewed in depth by Weising and colleagues (1995).

Although RFLP methodologies have been powerful analytical tools, they require large amounts of genomic DNA, are difficult to automate and require substantial time to complete. The discovery of the polymerase chain reaction (PCR) (Saiki et al., 1985, 1988) provided an opportunity to alleviate all of these constraints and in addition, offered new strategies of exploiting sequence variation.

LOW-STRINGENCY PCR

Randomly amplified polymorphic DNA (RAPD)

Perhaps the most widespread PCR-based fingerprinting techniques currently in use are based on random-primed PCR. The use of single oligonucleotide primers of arbitrary sequence was introduced simultaneously by the independent groups of Williams and co-workers (1990) and Welsh and McClelland (1990). Williams et al. (1990) systematically studied single primer PCR using a set of randomly designed decamers as well as sequentially truncated versions of a selected primer. In their methodology, known as random amplified polymorphic DNA (RAPD), amplified fragments were separated using agarose gel electrophoresis and visualized by ethidium bromide staining. In contrast, Welsh and McClelland (1990) described a similar method, where single primers of arbitrary sequence of various lengths (optimally 20 bp) were used in PCR of candidate template DNAs, into which α-^{32}P dCTP was incorporated as a radiolabel. The fingerprint generated consists of a unique profile of fragment sizes separated by denaturing polyacrylamide gel electrophoresis and visualized by autoradiography. A third variation was proposed by Caetano-Anollés and colleagues (1992) where even shorter oligonucleotide primers (5 bp) were used in a single-primer PCR. Fragment profiles were separated using denaturing polyacrylamide gel electrophoresis and visualized by silver staining. Of these three related methods, RAPD (*sensu* Williams et al., 1990) has enjoyed the greatest acceptance to date (Hedrick, 1992; Weising et al., 1995). These techniques offer a cheaper and less time-consuming alternative to RFLPs. In addition, markers may be developed rapidly by screening a panel of candidate arbitrary-sequence oligonucleotide primers without *a priori* knowledge of target sequence (Williams et al., 1990). Also, polymorphisms that are inaccessible by RFLP analysis may be accessed by these methods (Williams et al., 1990). However, marker dominance is not a complication for the analysis of true fungi since with few exceptions, their vegetative mycelia are haploid (Weising et al., 1995; Williams et al., 1990).

With time, numerous authors have advanced general modifications and application-specific refinements to the basic concept behind RAPD technology, such as varying the concentrations of reactants (Tommerup et al., 1995), thermal cycling set-up protocols and profiles (Bielawski et al., 1995; Kelly et al., 1994; Yu and Pauls, 1992) and using paired primers (Micheli et al., 1993; Welsh and McClelland, 1991). However, many investigators have found random primer fingerprinting methods to be hampered by problems relating to reproducibility and consequently have questioned RAPD reliability for certain types of analyses. These problems largely stem from a critical dependence of the fragment profile and relative yield on all of the basic parameters of PCR (Bielawski et al., 1995), such as annealing temperature and extension time (Ellsworth et al., 1993; Penner et al., 1993), primer concentration (Ellsworth et al., 1993;

MacPherson et al., 1993; Muralidharan and Wakeland, 1993), template quality (Micheli et al., 1993) and concentration (Davin-Regli et al., 1995; Micheli et al., 1993; Muralidharan and Wakeland, 1993), reactant concentration (Ellsworth et al., 1993), the particular commercial brand of DNA polymerase (Meunier and Grimont, 1993; Schierwater and Ender, 1993; Tommerup et al., 1995) and the make and model of thermocycler (He et al., 1994; MacPherson et al., 1993; Meunier and Grimont, 1993). Penner and co-workers (1993) noted problems with RAPD reproducibility between seven laboratories utilizing the same primers and templates with some varied reaction conditions. Also, several workers have described the presence of non-parental bands resulting from PCR artifacts such as heteroduplexes (Ayliffe et al., 1994) or other interference (Hallden et al., 1996; Micheli et al., 1993; Riedy et al., 1992). The observation of heteroduplexed DNAs as RAPD bands, however, has been suggested as a means of identifying codominant RAPD markers (Davis et al., 1995). While useful as initial screens for polymorphic loci which subsequently may be cloned and sequenced to construct site-specific primers (e.g. Groppe et al., 1995), PCR-based fingerprinting techniques relying on random primers are not robust and generally unsuitable for use as population markers, particularly in critical or demanding situations such as human diagnostics or courtroom evidence (Riedy et al., 1992).

Amplified fragment length polymorphism (AFLP)

A fingerprinting method that combines elements of both RFLP and random primer PCR was described by Zabeau and Vos (1993) and Vos and co-workers (1995). The authors called this technique amplification fragment length polymorphism (AFLP[5], Vos et al., 1995), a clearly intentional allusion to the acronym "RFLP". Although RFLPs originally examined

[5] "AFLP" as "amplification fragment length polymorphism" had been applied previously by Caetano-Anollés and co-workers (1992) as a general term referring to PCR fingerprinting methods directed by single primers of arbitrary sequence.

polymorphisms at identified loci by hybridisation, AFLP compares polymorphic patterns in fragments generated from the selected amplification of a subset of restriction fragments. In the first stage of this method, a template DNA is digested with restriction endonucleases. Concomitantly, one or two "adapter" molecules, consisting of 18-20 bp duplexed oligomers synthesized with 5'- and 3' sequence homology to the respective "sticky" ends produced by restriction digestion of the template DNA are ligated such that the original restriction sites are not restored. A panel of single primers (Mueller et al., 1996) or primer pairs (Vos et al., 1995; Zabeau and Vos, 1993) designed with homology to core sequences in the adaptor molecules, but with the addition of two arbitrary bases at the 3' termini were used in high stringency, "touchdown" PCR (Don et al., 1991). In the seminal paper by Vos and colleagues (1995), primers were end-labelled using T4 polynucleotide kinase with either γ-^{32}P- or γ-^{33}P-dATP to facilitate detection of the amplified fragments by autoradiography following separation by denaturing polyacrylamide gel electrophoresis. Curiously, this paper specifically stated that "adapters were not phosphorylated", in which case it is apparent that the template strand of the adapters could not ligate to the 3'-OH terminus of the cleaved genomic DNA. As such, it is not clear how the primers initiate the first round of PCR.

To date, several studies have demonstrated the use of a practical variation of this methodology in resolving relatedness within bacterial (Lin et al., 1996) and fungal populations (Majer et al., 1996; Mueller et al., 1996). Mueller and co-workers (1996) used a single adapter, and the double-stranded PCR products were resolved by agarose gel electrophoresis and visualized with ethidium bromide staining. However, the study by Majer and colleagues (1996) followed more closely the original AFLP technique (Vos et al., 1995). They suggest that AFLP appears to be more robust than RAPD and related methods because the longer primers and known target sequence permit a higher stringency of hybridisation during the amplification procedure (Majer et al., 1996). High stringency hybridisations in PCR inherently produce fewer artifactual bands due to spurious priming events (Cha and Thilly, 1993; Dieffenbach et al., 1993).

HIGH-STRINGENCY PCR -- SITE-SPECIFIC POLYMORPHISMS

The identification of specific, polymorphic loci circumvents the problem of irreproducibility common to random-primer fingerprinting methods. However, unlike random primer techniques, locus-specific methods often require a substantial initial effort to identify and characterize suitable loci.

One category of site-specific polymorphisms exploits microsatellite DNA. Microsatellite regions are PCR-amplified using primers either based on adjacent, conserved sequences (Groppe et al., 1995) or consisting of a short, repeated sequence known to be present in the test organism from probe hybridisation data (Buscot, 1996; Meyer et al., 1992; Morgante and Olivieri, 1993; Schönian et al., 1993). Polymorphisms in microsatellite DNA consist of variation in the number of repeated elements and are detected as relative length polymorphisms following electrophoretic separation. Due to the high degree of variation in these sequences, however, individual loci may be quite taxon-specific, restricting their use as general markers. Several current reviews discuss applications of microsatellite single-locus fingerprinting (Bruford and Wayne, 1993; Weising et al., 1995).

Another source of site-specific genetic variability can be found in the sequences of introns (short stretches of non-coding sequences which punctuate many genes) of single copy metabolic and structural genes. Although these loci, like microsatellite markers, are difficult to develop, they are particularly useful when fingerprint data from multiple loci are needed to study patterns of genetic variability (e.g. clonality vs. mating and recombination) (Anderson and Kohn, 1995). Primers designed using highly conserved sequences flanking introns have been described in a number of genes for filamentous fungi and yeasts (Glass and Donaldson, 1995). The variability of intron sequences, however, may not necessarily involve length polymorphism and may result solely from alterations in base sequence between fragments of identical size, necessitating a more sophisticated method of detection than that used for microsatellite typing. Several of the more commonly used methods are discussed below. These techniques and others have been reviewed by Prosser (1993) and Cotton (1993).

Unquestionably the most widely used locus for genetic discrimination to date is the subrepeat of the nuclear and mitochondrial ribosomal RNA (rRNA) genes (Gargas and DePriest, 1996; White et al., 1990). These genes provide a wide range of useful polymorphism, with highly variable regions suitable for fingerprinting (e.g. internal transcribed- and intergenic, non-transcribed spacer regions) as well as more conserved domains appropriate for several levels of phylogenetic study (e.g. small and large ribosomal subunit genes). Numerous primer sequences have been described for PCR mediated amplification of specific regions of rDNA from filamentous fungi and yeasts (Gargas and DePriest, 1996; White et al., 1990). Like intron loci, polymorphisms in rRNA may be cryptic and not necessarily reflected by length polymorphism of PCR-amplified fragments, requiring a sensitive detection method.

DETECTION OF LOW-LEVEL SEQUENCE VARIABILITY

The determination of base sequence is the ultimate, definitive method for the discrimination of occult genetic differences and the defining of mutations. However, despite recent extraordinary technological advancements in DNA sequencing technologies since the introduction of these methods (Maxam and Gilbert, 1980; Sanger et al., 1977), the resources required for large-scale sequencing projects remain untenable for most laboratories (Chowdhury et al., 1993; Cotton, 1993). Therefore, a number of techniques have been described which permit the inferential comparison of base sequence, each aspiring to offer a high degree of sensitivity and reliability with low cost and ease of use.

Restriction endonuclease digestion of PCR products

The simplest method for screening sequence variability in PCR products is digestion by restriction endonucleases (PCR-RFLP) in which subject PCR products are digested individually with a set of restriction enzymes. Typically, restriction endonucleases that cleave at quadrameric recognition sequences are chosen because the occurrence of the shorter recognition motif statistically occurs with greater frequency. Polymorphisms are recognized by different fragment profiles following electrophoretic separation. Variation detected by this method is limited to either fragment length differences or changes in base sequence that result in the loss or gain of a restriction enzyme recognition site. Several studies of fungal populations have used this method with some success (Buscot et al., 1996; Donaldson et al., 1995; Gardes et al., 1991; Glass and Donaldson, 1995). As well, PCR-RFLP has been used as a means of taxonomic positioning (Vilgalys and Hester, 1990). However, relatively little sequence information can be inferred from PCR-RFLP analysis since the probability of encountering a change in a specific site of four nucleotides is quite low. Although the inclusion of additional restriction enzymes improves the analysis, very little base sequence can be compared using this method.

Denaturing-gradient gel electrophoresis (DGGE)

Denaturing-gradient gel electrophoresis (DGGE) is a method that has long been used to identify single base mutations in DNA fragments (Fisher and Lerman, 1983). This technique relies upon the alteration of melting domains between DNA fragments differing in base composition when separated electrophoretically on gels containing an ascending gradient of chemical denaturant. Partially annealed DNA duplexes migrate differentially, modulated by the degree and relative location of melted domains. Thus, the resolution of the technique is dependent upon at least partial association of the DNA strands, and ceases to provide further useful separation upon complete denaturation. Myers and co-workers (1985) attached a segment of G/C-rich sequence (a "GC-clamp") to one end of the DNA fragment prior to DGGE, to maintain partial duplex association at higher concentrations of denaturant in order to achieve better resolution. Sheffield and colleagues (1989, 1992) described the inclusion of similar G/C-rich sequences using PCR. Several reviews discuss applications of DGGE (Cotton, 1993; Prosser, 1993).

Single-strand conformation polymorphism (SSCP)

A popular method for studying low-level sequence variability in PCR products known as single-strand conformation polymorphism (SSCP) was described by Orita and co-workers (1989a, 1989b). In this technique, radiolabelled PCR products are chemically denatured, separated by electrophoresis in native polyacrylamide gels and visualized by autoradiography. The electrophoretic migration of single strands is a function of secondary structure formed due to spontaneous self-annealing upon entry into the non-denaturing gel matrix. Single base substitutions may alter this secondary structure, hence changing the relative electrophoretic mobility of the molecule.

SSCP analysis has been used widely to identify deleterious mutations relating to human genetic diseases such as color vision defects (Zhang and Minoda, 1996), cystic fibrosis (Ravnikglavac et al., 1994), Tay-Sachs disease (Ainsworth et al., 1991), phenylketonuria (Dockhorn-Dworniczak et al., 1991), and a number of p53-associated carcinomas including lung cancer (Suzuki et al., 1990), lymphoblastic leukemia and non-Hodgkin lymphoma (Gaidano et al., 1991), breast- and colon cancer (Soto and Sukumar, 1992) and resistance to thyroid hormone (Grace et al., 1995). As well, SSCP has been employed in numerous investigations of organismal variability such as human papilloma virus (HPV) (Spinardi et al., 1991), major histocompatibility complex in Swedish moose (Ellegren et al., 1996), and differentiation of species of *Aspergillus* section *Flavi* (Kumeda and Asao, 1996).

Sheffield and co-workers (1993) studied the sensitivity of SSCP analysis for the detection of single base substitutions using an assortment of 64 characterized mutations (e.g. murine globulin promoter, p53 and rhodopsin). Using SSCP, they were able to detect roughly 80 % of these single base mutations. This detection rate is consistent with results from other studies (Hayashi, 1992; Spinardi et al., 1991). Hayashi (1991, 1992) and Sheffield and colleagues (1993) found that fragment size[6] as well as location of the substituted base are the major factors governing the sensitivity and thus the success of this technique. Dideoxy-fingerprinting (ddF) is a hybrid variant of SSCP (Orita et al., 1989a, 1989b) and dideoxy sequencing (Sanger et al., 1977) in which a typical Sanger reaction with one dideoxynucleotide is followed by chemical denaturation and electrophoresis on a non-denaturing polyacrylamide gel (Blaszyk et al., 1995). This technique has been used to detect single base mutations with an astonishingly high level of

[6] The ability to discriminate mutations diminishes with increased fragment size, e.g. > 200 bp.

sensitivity (Blaszyk et al., 1995; Ellison et al., 1994; Felmlee et al., 1995; Fox et al., 1995; Stratakis et al., 1996).

A number of procedural modifications have been proposed to enhance the sensitivity and reproducibility of SSCP, including concentrating a single strand using asymmetric PCR (Ainsworth et al., 1991); decreasing dNTP concentration in initial PCR to increase incorporation of radiolabel (Dean and Gerrard, 1991); using non-isotopic detection systems including silver staining (Ainsworth et al., 1991; Dockhorn-Dworniczak et al., 1991; Mohabeer et al., 1991); fluorescence-based methods (Makino et al., 1992), and ethidium bromide staining (Grace et al., 1995); modifying the gel substrate (Dean and Gerrard, 1991; Spinardi et al., 1991); altering electrophoresis conditions such as temperature (Dean and Gerrard, 1991; Spinardi et al., 1991), ionic strength of the electrophoresis buffer and gel matrix (Spinardi et al., 1991) and various changes to facilitate large-scale screening (Mashiyama et al., 1990). Liu and Sommer (1995) performed multiple restriction enzyme digests on large PCR-amplified fragments and combined the products prior to SSCP, permitting this technique to be used effectively on larger amplicons. Several authors however have noted that results of SSCP analyses vary considerably between experiments under identical conditions (Dean and Gerrard, 1991; Soto and Sukumar, 1992).

Heteroduplex mobility assay (HMA)

Heteroduplex mobility assay (HMA) (Delwart et al., 1993; Keen et al, 1991) is a relatively new technique which is comparable in sensitivity to SSCP, but not so widely used (Cotton, 1993). In HMA, the PCR amplification products of a pair of isolates are combined in equimolar proportion, heat denatured and reannealed at lower temperature. The resulting mixture comprises duplexed molecules of all possible combinations of compatible DNAs including two populations of homoduplexes identical to the fragments of each original amplification product, as well as two hybrid DNAs (heteroduplexes) created by the cross-annealing of compatible strands originating from different "parent" duplexes. Differences in base sequence such as substitutions, insertions or deletions between the two strands of heteroduplexed DNAs produce local "bubbles" or "kinks" in these hybrid molecules. Indeed, Wang and co-workers (1992) confirmed the bent physical conformation of heteroduplexed DNA fragments by visualizing fragments containing deletional kinks using electron microscopy. These structural instabilities result in the slower migration of the heteroduplex molecules to duplexes with total base complementarity when separated by electrophoresis in native polyacrylamide gels. The rate of detection of single base mutations by this technique is comparable to that observed in SSCP (Ganguly et al., 1993; Ravnikglavac et al., 1994; White et al., 1992). Other authors have suggested significantly better discrimination of small mutations using HMA relative to SSCP (Offermans et al., 1996). However, a number of studies using heteroduplexed DNA employ excessively long annealing times, or inappropriate annealing temperatures which unintentionally favour the reannealing of homoduplexes (e.g. Bachmann et al., 1994; Cheng et al., 1994; D'Amato and Sorrentino, 1994; Delwart et al., 1993, 1994; El-Borai et al., 1994; Gross and Nilsson, 1995; Soto and Sukumar, 1992; Wilson et al., 1995; Winter et al., 1985).

While DNA heteroduplexes were first noted as artifacts of PCR (Jensen and Straus, 1993; Nagamine et al., 1989), the differential mobility of deliberate DNA heteroduplexes has since been used in the recognition of various human genetic mutations including human p53-related tumours (Soto and Sukumar, 1992), *ras* oncogenes (Winter et al., 1985;), type 1 antithrombin (Chowdhury et al., 1993), cystic fibrosis (Dodson and Kant, 1991; Ravnikglavac et al., 1994), endometrial adenocarcinoma (Doherty et al., 1995), sickle cell anaemia (Wood et al., 1993) and β-thalassaemia (Cai et al., 1991; Hatcher et al., 1993; Law et al., 1994; Savage et al., 1995). As well, heteroduplex technology has been proposed as a means of human leukocyte antigen typing (HLA typing) (D'Amato and Sorrentino, 1994; El-Borai et al., 1994; Martinelli et al., 1996). HMA has also been used to study genetic variation in viruses such as human immunodeficiency virus (HIV) (Bachmann et al., 1994; Delwart et al., 1993, 1994; Louwagie et al., 1994) and hepatitis C virus (Gretch et al., 1996; Wilson et al., 1995), as well as eukaryotes such as European populations of the basidiomycete plant pathogen *Heterobasidion annosum* (Cheng et al., 1994), Swedish populations of brown trout (Gross and Nilsson, 1995) and eastern Australian rabbit populations (Fuller et al., 1996).

Since the introduction of HMA as a diagnostic tool, a number of modifications have been proposed including the use of ethidium bromide staining (Bachmann et al., 1994; Chowdhury et al., 1993; D'Amato and Sorrentino, 1994; Delwart et al., 1994; Dodson and Kant, 1991; El-Borai et al., 1994; Hatcher et al., 1993; Pulyaeva et al., 1994; Soto and Sukumar, 1992; Wood et al., 1993) or silver staining (Gross and Nilsson, 1995) for visualization, lower ionic strength of electrophoresis buffer (Chowdhury et al., 1993; Soto and Sukumar, 1992), the use of buffering system other than TBE (D'Amato and Sorrentino, 1994; Ganguly et al., 1993), detection of heteroduplexed fragments by capillary electrophoresis (Cheng et al., 1994), electrophoresis on temperature gradient gels (Campbell et al., 1995) and the use of heteroduplex generators or universal comparative DNAs (D'Amato and Sorrentino, 1995; Doherty et al., 1995; El-Borai et al., 1994; Gross and Nilsson, 1995; Law et al., 1994; Louwagie et al., 1994; Martinelli et al., 1996; Savage et al., 1995; Wack et al., 1996; Wood et al., 1993).

Much of the earlier work using DNA heteroduplex analysis used Hydrolink MDE, which forms a vinyl polymer as an electrophoresis medium (Soto and Sukumar, 1992). Zakharov and Chrambach (1994) demonstrated increased resolution of DNA heteroduplexes by electrophoresis in low-crosslinked polyacrylamide gels, noting however that the gel matrix is more prone to swelling when synthesized with lower concentrations of N,N'-methylenebisacrylamide (Bis) due to less reproducible fibre properties (Zakharov and Chrambach, 1994). Pulyaeva and co-workers (1994) used uncrosslinked polyacrylamide gels with similar success. However, they noted that uncrosslinked polyacrylamide media lacked the mechanical strength of low, or standard crosslinked gels and thus were not suitable for many applications (Pulyaeva et al., 1994). Xing and colleagues (1996) amended 12 % polyacrylamide gels with 10 % glycerol and 2 % agarose for resolving DNA heteroduplexes. Several investigators have incorporated chemical denaturants such as ethylene glycol, formamide (Ganguly et al., 1993) and urea (White et al., 1992) into polyacrylamide gels as a means of destabilizing small heteroduplexes to facilitate their detection.

A number of related techniques have developed from HMA including the enzymatic cleavage of mismatched bases in RNA/RNA or RNA/DNA heteroduplexes using RNase A as a way of facilitating the detection of heteroduplexed molecules by gel electrophoresis (Winter et al., 1985), and the use of bacteriophage resolvases to cleave mismatched bases in DNA/DNA heteroduplexes (Marshal et al., 1995). Gross and Nilsson (1995) performed a restriction digest of PCR-amplified growth hormone 2 (GH2) gene from brown trout prior to heteroduplex generation as a means reducing fragment size and thus enhancing electrophoretic resolution of heteroduplexes.

Oka and co-workers (1994) demonstrated that a carefully controlled thermal annealing gradient can be used to cause the preferential formation of DNA homoduplexes relative to heteroduplexes. Using double-labelled DNA fragments (one strand labelled with biotin, the other strand labelled with dinitrophenyl (DNP)) they performed a temperature-gradient annealing with a test DNA, following which the duplexes bearing a biotin-labelled strand were captured onto a streptavidin-coated microtitre plate. The treatment of these fragments with an anti-DNP conjugated alkaline phosphatase followed by the introduction of a chromogenic substrate permitted the quantification of original double-labelled homoduplexes by spectrophotometry. The population of regenerated double-labelled homoduplexes was inversely proportional to the degree of homology of the double-labelled DNA to the tester DNA. Using this method, which they named PCR-dependent preferential homoduplex formation assay (PCR-PHFA), Oka and colleagues (1994) were able to detect differences of as little as a single nucleotide substitution between the double-labelled fragment and the tester. Although proposed as an alternative to HLA typing, PCR-PHFA may hold promise for other automated diagnostic applications.

Like SSCP, HMA is a rapid technique that takes into account the entirety of the sequence variability of a PCR-amplified DNA fragment, rather than the limited amount of sequence information available from PCR-RFLP. Both SSCP and HMA require less sample manipulation than PCR-RFLP and fewer gel runs. However, SSCP requires the ability to compare lanes both within and between gel runs to assess similarity or difference between different products. This necessitates a high degree of quality control and thus is demanding of hardware technology capable of precisely duplicating run conditions on an ongoing basis. On the other hand, because

HMA compares two individual products in the same gel lane, there is little need for comparison of migration distances between different gels.

SUMMARY

A review of various commonly-used approaches to assessing fungal genotypic diversity shows that methods based on site specific polymorphisms offer a more robust approach than RAPD or other non-specific methods. For the identification of different strains heteroduplex mobility analysis (HMA) may be superior to single-strand conformation polymorphism (SSCP) because two strains/isolates are compared in the same gel lane, eliminating difficulties in gel-to-gel comparison due to mobility variations from differences in running conditions inherent to SSCP analysis.

CHAPTER 4. DEVELOPMENT OF METHODS FOR THE ASSESSMENT OF GENOTYPIC DIVERSITY OF PENICILLIA[7]

ABSTRACT

Techniques for 1) small-scale isolation of high molecular weight total DNA; 2) heteroduplex mobility assay for screening genotypic diversity; and, 3) identification of polymorphic genetic loci in *P. brevicompactum* and *P. chrysogenum* are described.

ISOLATE SELECTION

Isolates of *Penicillium* for genetic studies were collected and stored according to the methods presented in Chapter 2. Two species of *Penicillium* were selected for intensive study based on the strong representation in the culture collection and their good representation across the set of houses studied. *Penicillium chrysogenum* was selected because this was the most commonly occurring species of the genus in broadloom dust (*see* Figure 2-4) and was represented by 700 isolates in the accumulated collection. *Penicillium brevicompactum* was also chosen for further investigation. Although this species was outnumbered in the dataset and culture collection by isolates of *P. spinulosum*, *P. corylophilum*, and *P. commune*, its species circumscription seemed to be more stable and its identification less prone to confusion.

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[7] Parts of this chapter are reprinted with the kind permission of: 1) Eastern New York Occupational and Environmental Health Centre (ENYOEHC), Albany, New York, USA, from Scott, J.A., Straus, N.A. and Wong, B. 1999. Heteroduples DNA fingerprinting of *Penicillium brevicompactum* from house dust. pp. 335-342, *In* Bioaerosols, fungi and mycotoxins: health effects, assessment, prevention and control. E. Johanning (ed). Albany, New York: ENYOEHC. 638 pp.; and 2) Overseas Publishers Association (OPA) N.V., with permission from Gordon and Breach Publishers, from Scott, J.A., D. Malloch, B. Wong, T. Sawa and Straus, N.A. 2000. DNA heteroduplex fingerprinting in *Penicillium*. pp. 225-236, *In* Integration of Modern Taxonomic Methods for *Penicillium* and *Aspergillus* Classification. R.A. Samson and J.I. Pitt (eds). Amsterdam: Harwood Academic Publishers, as a contribution to the Third International Workshop on *Penicillium* and *Aspergillus*, held in Baarn, The Netherlands, from 26-29 May 1997.

All isolates of *P. brevicompactum* and *P. chrysogenum* that had been catalogued during the collection phase of this project were subcultured on several diagnostic media including modified Leonian's agar (MLA), Czapek's yeast autolysate agar (CYA) and modified Creatine-sucrose agar (CSA). Cultures were incubated at room temperature and rated for colony characteristics at 1, 2 and 3-week intervals. Microscopic preparations were made after 1 wk from cultures on MLA. Subcultures on MLA were also rated for growth after 1 wk at 5 °C and 37 °C. Based on the results of these tests, a subset of isolates that demonstrated high phenotypic homogeneity were selected for each species for further study (data not shown).

ISOLATION OF DNA FROM *PENICILLIUM* CONIDIA

Many of the existing techniques for isolating fungal DNA were designed for methods requiring milligram amounts of total DNA (Weising et al., 1995). These methods typically involve the preparation of broth cultures, followed by mycelial harvest and grinding. On a small-scale, these procedures are practical; however, the labour-intensive nature of these techniques makes them ill-suited to projects requiring DNA isolations from large numbers of samples. Furthermore, the potential for aerosol generation posed by such large-scale grinding risks potential biological hazards as well as sample cross-contamination. For the purposes of the current project, a modified technique was developed which permits rapid small-scale preparation of total DNA which facilitates the processing of large numbers of samples.

Materials and methods, DNA isolation

Fungal isolates were inoculated centrally on a Petri plate of Weitzman and Silva-Hutner's agar (WSHA) (Weitzman and Silva Hutner, 1967), and grown for 7 days at room temperature under 12 hr artificial daylight. The plates were flooded with 2 mL of 95 % ethanol and the conidia and mycelium were suspended by gently scraping the surface of the colonies with a sterile bent glass rod. The conidial suspensions were collected in microcentrifuge tubes, centrifuged at 12 Krpm and the supernatant ethanol was discarded. The pellets were dried for 30 min in a vacuum concentrator centrifuge. This protocol yielded approximately 15 mg of pelleted conidia per vial. Each vial was sufficient for a single DNA isolation.

Approximately 15 mg of sterile, acid-cleaned Dicalite 1400 (diatomaceous earth-based swimming pool filter, Grefco Inc., Torrance, California), was added to a tube containing a roughly equal volume of dry, pelleted, ethanol-killed conidia. Following the addition of 10 μL of 70 % EtOH, the mixture was ground with a sterile glass rod for 1 min and suspended in 600 μL of lysis buffer containing 1.4 M NaCl, 2 % w/v CTAB, 200 mM Tris·HCl pH 8.0 and 20 mM EDTA (adapted from Weising et al., 1995). Tubes were incubated at 65 °C for 1 hr, during which they were mixed by inversion at 30 min intervals.

After extraction, the tubes were cooled to room temperature and centrifuged at 10 K rpm for 1 min to pellet the Dicalite and cellular debris. The supernatant liquid was extracted twice with chloroform:isoamyl alcohol (24:1) and the DNA was precipitated with 100 % isopropanol for 10 min at -80 °C. The pellets were rinsed with 70 % ethanol and dried. The DNA was resuspended in 200 μL Tris-EDTA (10 mM and 1 mM, respectively) (TE) pH 8.0 (Sambrook et al., 1989). Ribonuclease A was added to the DNA at a final concentration of 0.2 μg/μL, and incubated for 30 min at 37 °C. The DNA was subsequently extracted with chloroform:isoamyl alcohol as above, and following the addition of sodium acetate to a concentration of 0.3 M, the DNA was precipitated with 250 μL of 100 % ethanol at -80 °C. The DNA solution was pelleted and pellets were rinsed with 70 % ethanol, dried and resuspended in 100 μL TE pH 8.0. The concentration of DNA in solution was determined spectrophotometrically.

Results and discussion, DNA isolation

Dicalite was selected as a grinding agent because it is commercially available and inexpensive. It acts both as an abrasive to disrupt conidial walls, and as a bulking agent to ensure surface contact between the abrasive and the biological material. Although tight binding between DNA and glass powder in the presence of high concentrations of chaotropic salts (e.g. sodium iodide) forms the basis of several proprietary technologies for DNA purification (e.g. Geneclean® II, Bio 100 Inc.; Qiagen purification spin-columns), controlled experiments using herring sperm DNA indicated that negligible DNA bound to the Dicalite under the conditions used in this procedure (data not shown). Typically, a single Petri plate of *P. brevicompactum* grown for 14 days yielded 10 to 100 mg, dry weight, of harvestable conidia. From this, 10 to 100 μg of high molecular weight DNA was isolated.

Many of the currently used methods for the isolation of DNA from harvested cellular material involve grinding procedures that risk generating aerosols. In cases where the fungi submitted to these procedures are either pathogenic, opportunistic or heavily sporulating, a potential biological hazard exists from the generation of viable fungal aerosols. Other risks independent of the viability of conidial or cellular aerosols, such as mycotoxins and allergenic beta-glucans, are greater with large mycelial isolations. In the procedure presented, ethanol serves as the initial harvesting medium. Ethanol is an efficient wetting agent for hydrophobic conidia, which prevents conidial aerosolization during the early stages of preparation. In addition, ethanol treatment kills *Penicillium* conidia, thereby eliminating the potential of cross culture contamination during the DNA isolation procedures. The small scale of the preparations, and the limited use of grinding due to the inclusion of diatomaceous earth further reduce the potential for the generation of cellular aerosols which could cross-contaminate sample preparations.

HETERODUPLEX MOBILITY ASSAY

This section describes a PCR-based heteroduplex analysis to screen for variability between homologous amplification products from different isolates of *P. brevicompactum* (Jensen and Straus, 1993). In this method, the PCR-amplified products of a pair of isolates are combined in equal proportion, denatured at 94 °C for 3 min and reannealed at 65 °C for 5 min. The resulting mixture comprises all possible combinations of compatible DNA strands including two homoduplexes identical to each original amplification product, along with two hybrid DNAs (heteroduplexes) created from the cross-annealing of compatible strands originating from different "parents". Any sequence differences, including base substitutions, insertions or deletions produce local "bubbles" or "kinks" in the hybrid molecules. These anomalies result in differential electrophoretic migration of these structures relative to duplexed strands 100 % base complimentarity. Thus, small dissimilarities in sequence between two isolates at a given locus can be detected readily.

Materials and methods, HMA

DNA amplification

An identified polymorphic region near the 5'-end of the beta-tubulin gene benA was amplified using primer sequences Bt2a and Bt2b described by Glass and Donaldson (1995). PCRs consisted of 1 unit of Taq DNA polymerase (Boeringher Mannheim), 50 mM KCl, 2.0 mM

$MgCl_2$, 250 μM each of dATP, dTTP, dCTP and dGTP, 0.2 mM of each primer and approximately 60 ng high molecular weight template DNA in a total reaction volume of 50 μL overlaid with a drop of sterile mineral oil to prevent evaporation. A template-free reaction was included in each set of reactions. Reactions were carried out in a PTC-100 thermocycler (MJ Research). The typical PCR profile used consisted of 94 °C for 30 s to denature, 58 °C for 30 s to anneal primers and 72 °C for 30 s to extend. This profile was repeated for 30 cycles, followed by a final extension at 72 °C for 2 min. PCR yield was roughly quantified based on ethidium bromide staining and UV visualization following electrophoresis on 1.2% agarose gels.

Cloning and sequencing of PCR products

Initial work on the heteroduplex screening method used cloned homologous fragments from a polymorphic region at the 5' end of the beta tubulin gene, benA. During the initial investigations into the use of the heteroduplex technique, cloned products were used to eliminate the influence of potential PCR artifacts.

Products for cloning were amplified directly from genomic template DNA using 5'-phosphorylated primers. Primers were phosphorylated in 0.2 μL 10 mM ATP, 1 μL 10x polynucleotide kinase buffer (Promega) and 0.5 μL T4 polynucleotide kinase (Promega), 7.3 μL sterile distilled deionized water and 1 μL of 500 μM oligonucleotide primer, incubated at 37 °C for 30 min and the enzyme was inactivated by incubation at 65 °C for 20 min.

Following amplification and soft gel purification of products (Sambrook et al., 1989), 42 μL aliquots of products were blunt-ended with 5 μL 10x T4 DNA polymerase buffer, 0.25 μL acetylated bovine serum albumin, 100 μM deoxynucleotide triphosphates (dNTPs) and 0.25 μL T4 DNA polymerase (New England Biologicals). The resulting products were extracted once with phenol:chloroform (1:1) and once with chloroform and precipitated at -80 °C by the addition of 0.1 M NaCl and two volumes of cold 100 % ethanol. Prior to ligation, plasmid vector was digested to completion with *Hinc*II and treated with shrimp alkaline phosphatase according to suppliers instructions (US Biochemical). Ligation was performed using 45 ng of linearized pUC19 vector, 45 ng insert DNA, 2.4% polyethylene glycol 8000, 2 μL 5x DNA ligase buffer and 0.6 μL DNA ligase (BRL) in a reaction volume made to 10 μL with sterile distilled deionized water and incubated at room temperature for 3-4 hr. Following ligation, reactions were diluted to 40 μL total volume with 1x DNA ligase buffer and transformed into *E. coli* strains DH5α and JM109 using the method described by Hanahan (1985). Cells were plated in 3 replicates of 100 μL aliquots of transformation reaction onto LB agar containing 60 μg/mL ampicillin. Isopropylthio-β-D-galactoside (IPTG) (80 μg/mL) and 5-bromo-4-chloro-3-indolyl-β-D-galactoside (XGAL) (20 ng/mL) were incorporated to permit blue/white selection. Recombinant plasmids were isolated by alkaline lysis (Sambrook et al., 1989). Cloned DNA fragments were sequenced by the method of Sanger and co-workers (1977), using universal and reverse primers for pUC19.

Preparation and analysis of DNA heteroduplexes

Preliminary experiments used cloned, sequenced DNA fragments which were PCR-amplified as described above using the Bt2 primer set. Products were amplified directly from total DNA. For each locus examined, PCRs were diluted to 50 % of the original concentration, with 4 mM EDTA and 50 mM KCl and combined in equimolar proportion in a total volume of 10 μL, and overlaid with a drop of sterile mineral oil. PCRs of sequentially numbered isolates were combined in an pair-wise manner such that each numerically adjacent pair were combined with each-other, and the first and last isolate of each series were combined. Reactions were heated to boiling for 4 min and immediately annealed at 65°C for 6 min. Based upon the results of this first pass, all adjacent "like" isolates were reduced to a single representative strain by transitive property. Subsequent rounds of HMA compared non- numerically juxtaposed "proxy" isolates ultimately reducing the entire population to a set of genotypically distinct alleles represented by a minimum number of proxy isolates for each locus tested.

ELECTROPHORESIS AND IMAGING

Prior to use in heteroduplexing reactions, the quality and yield of PCRs was assessed by electrophoresis on 1.5 % agarose gels in 1 x TAE. Agarose and proprietary gels were stained in 250 ng/mL ethidium bromide for 5-30 min and destained in distilled water for 10-30 min. Polyacrylamide gels were stained in 250 ng/mL ethidium bromide for 2-4 hr and destained in distilled water for 2 hr to overnight. All gels were visualized on an ultraviolet light transilluminator at 300 nm (Fotodyne).

Resolution of heteroduplexed DNAs on Phast system

Initial experiments to resolve heteroduplexed DNAs were conducted using the Phast gel electrophoresis system (Pharmacia, New Jersey). The Phast gel depicted in Figure 4-1 shows slow-migrating heteroduplexed DNA bands in lanes 2-5 and 7-8. The homoduplex band front is shown by the migration of native PCR product in lane 6. Despite that the Phast system provided good resolution of heteroduplexed DNAs, this system was not amenable to scale-up use given the 12 lane capacity of Phast gels.

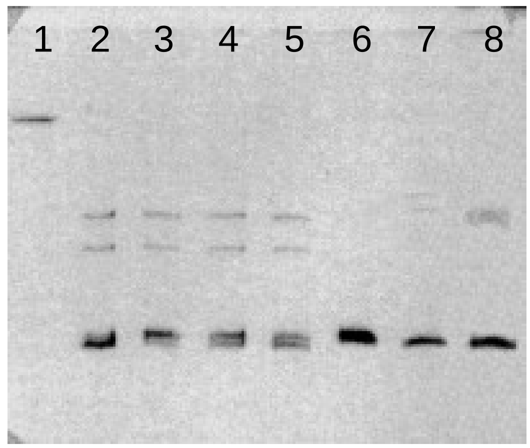


FIGURE 4-1. Demonstration of DNA heteroduplexes using the Phast gel system. Lanes contain (*from left to right*) **1)** 1 ug HindIII-digested λ-DNA; lanes 2-8 contain heteroduplexed PCR products for the following pairs of *P. brevicompactum* isolates: **2)** B91 + B119; **3)** B119 + B132; **4)** B 132 + B166; **5)** B166 + ALG1; **6)** ALG1 + DAOM 214776; **7)** DAOM 214776 + DAOM 214783 (deposited as *P. chrysogenum*, but appears to be misidentified); and **8)** DAOM 214783 + B36.

Horizontal gel electrophoresis (HGE) in HMA

A technique of horizontal gel electrophoresis (HGE) was investigated for use in resolving heteroduplexed DNAs. In this method, agarose gel casting trays (BioRad minisubmarine) were modified by gluing a spacer strip of 6 mm square extruded poly(methyl-methacrylate) (PMMA) rod (General Electric), equal in length to the casting tray, into each corner of the tray using a glue that consisted of 1 % (w/v) PMMA and 1 % (v/v) acetic acid in dichloromethane. The volume of the gel tray was recalculated based on the decreased width. A removable cover plate designed to rest on top of the square rods was cut from 1/8" thick PMMA (Plexiglass, General Electric). The cover plate was cut to approximately 1 cm shorter than the total length of the gel tray to accommodate insertion of the comb. The use of a cover plate ensured a uniform thickness for the gel. In addition, the cover plate prevented contact with air during polymerization. The ends of the tray were sealed with masking tape (3M). The cover plate and comb were put in place prior to pouring. A solution of 7.7 % acrylamide, 0.3 % bisacrylamide and 0.04 % ammonium persulfate was prepared in 1 x TAE (Sambrook et al., 1989), to which 0.2 % N,N,N',N'-tetramethylethylenediamine (TEMED) was added immediately prior to casting after degassing of the solution.

Preliminary experiments using this method were conducted in which running buffer was in contact with the upper surface of the gel. In this configuration, it was found that a vertical ionic gradient was established during electrophoresis. This ionic gradient caused the differential migration of the lower portion of bands relative to the upper portion, producing an appearance of bending in cross-section (Figure 4-2). Visualization of these gels in face view showed smeared bands (not shown).

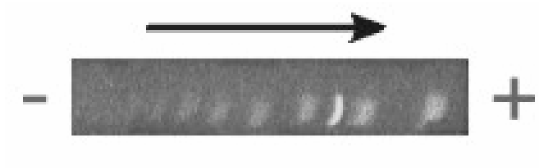


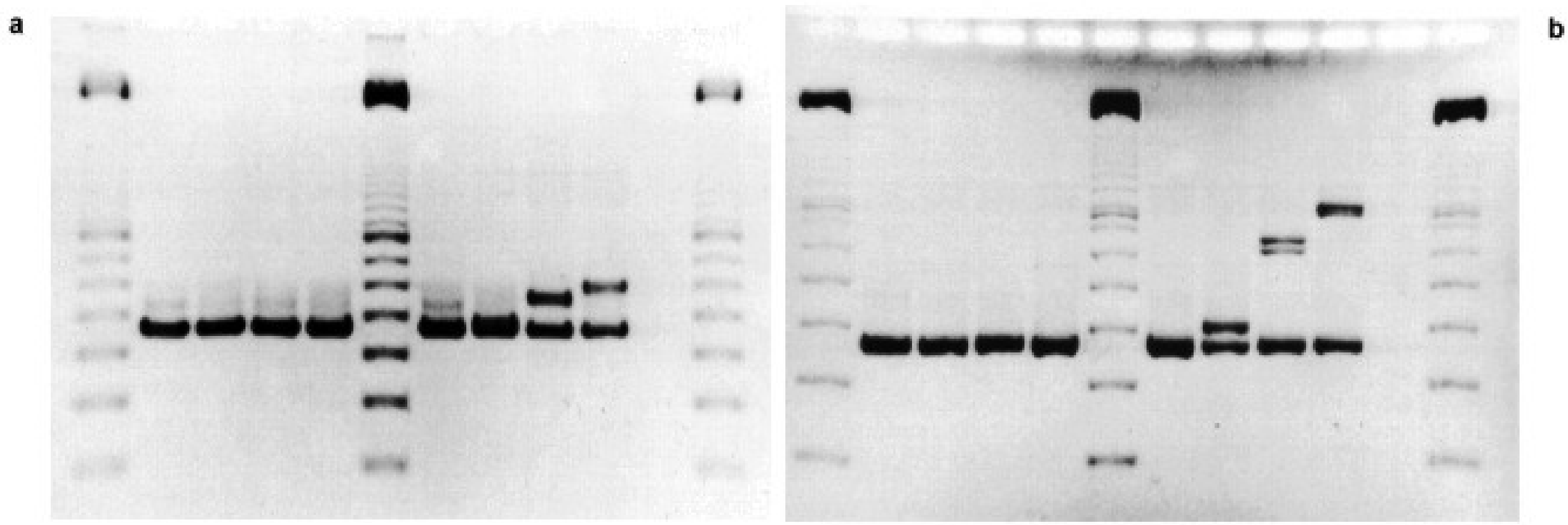
FIGURE 4-2 Cross-section of band fronts of Promega 100 bp marker run on horizontal PAG cast and run without top-plate. Arrow indicates direction of electrophoretic migration. Note the convex configuration of band fronts in direction of anode (+). This bent morphology produced considerable blurring of bands in face view (not shown).

To address this problem, a cover plate was kept in position on the upper surface of the gel during electrophoresis to prevent contact with the running buffer. Exclusion of the running buffer from contacting the upper surface of the gel prevented ionic migration across the gel-buffer interface, thus preventing the formation of a vertical, ionic gradient in the gel matrix. This modification tended to sharpen the appearance of bands greatly.

Comparative sets of samples were electrophoresed in 1.5 % agarose (BioRad) as well as the proprietary media, Clearose®, a modified agarose (Elchrom), and 9 % Poly-NAT® (poly N-acryloyltris-(hydroxymethylaminomethane)) (Elchrom). Proprietary gel media electrophoresed in 0.75 x TAE (30 mM tris-acetate, 0.75 mM EDTA adjusted to pH 8.0) (Sambrook, 1989) using a temperature controlled, buffer-recirculating electrophoresis system (SEA 2000, Elchrom) running at 40 °C with a field strength of 5 Vcm^{-1}. Polyacrylamide and poly-NAT gels were stained for 1 hr in 250 ng/mL ethidium bromide and destained in distilled water for 3-4 hr. Concentrations of amplification products were standardized based on band intensity as compared to a quantitative standard.

Results and discussion, HGE

Preliminary investigations for appropriate electrophoresis methods used a set of morphologically and physiologically indistinguishable isolates of *P. brevicompactum*, notably three isolates, 114, 132 and 244 which were shown to differ in the Bt2 locus by sequencing on cloned PCR-amplified products (Figure 4-3). Different allelic forms of Bt2 were observed for each of these isolates using heteroduplex techniques. An additional isolate, 112, which did not form a heteroduplex with 114, was selected as a control. Aligned sequences of the cloned fragments for the Bt2 locus of isolates 114, 132 and 244 are shown in Appendix F-1. Isolates 114 and 244 have the greatest



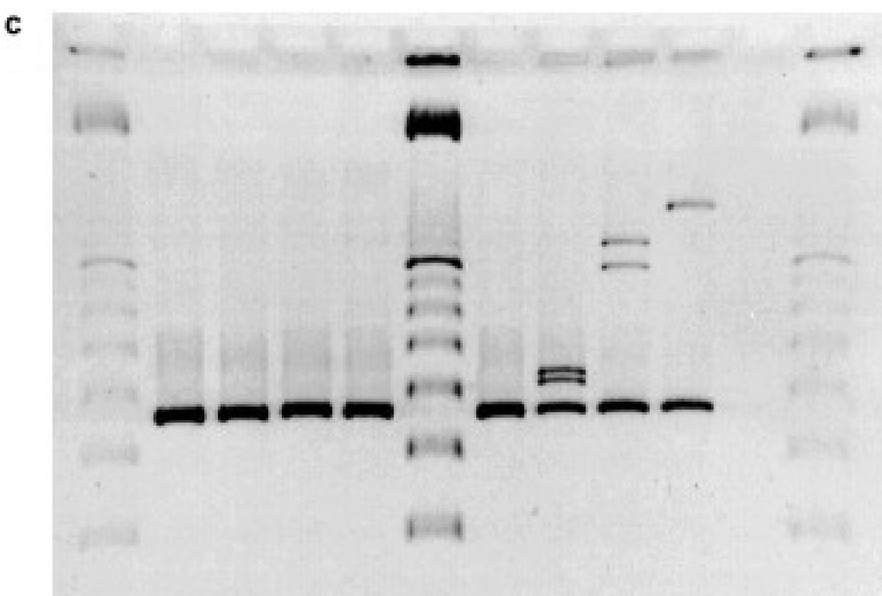


FIGURE 4-3. Comparison of media in HGE for the resolution of DNA HDXs. **Gel 1** shows a Clearose BG © gel run in 0.75 x TAE at 40 °C for 60 min under a field strength of 5 V/cm; **Gel 2** shows a 9% poly-NAT gel run as above for 225 min; **Gel 3** shows an 8% acrylamide, 0.2 % bisacrylamide gel run as above for 75 min. Lanes of all gels contain cloned PCR products of Bt2 primer pair (*from left to right*) **1, 6** and **12)** Promega 100 bp marker; 2) B112; 3) B114; 4) B132.1; 5) B244. Lanes 7-10 contained heteroduplexed cloned products in the following combinations; **7)** B112 + B114; **8)** B114 + B244; **9)** B114 + B132.1; **10)** B132.1 + B244.

sequence similarity (15 base substitutions and two non-contiguous insertions/ deletions). Isolates 114 and 132 differ by 42 base substitutions, 9 non-contiguous insertions/deletions and a four-base contiguous insertion/deletion. Isolates 132 and 244 differ by 44 base substitutions, 8 non-contiguous insertions/deletions, and the same four-base contiguous insertion/deletion. Sequence obtained for the Bt2 amplicon from isolate 112 was identical to that of isolate 114 (data not shown).

Each of these clones was amplified by PCR and heteroduplexed as described in Materials and Methods. The resulting reassociated structures were compared under three different conditions of electrophoresis (Figure 4-3). These conditions included Clearose BG (Elchrom) (Figure 4-3a), 9 % poly-NAT (Elchrom) (Figure 4-3b) and 8 % polyacrylamide (crosslinked with 0.2 % bisacrylamide) (Fig. 4-3c). These gels show that the low-crosslinked polyacrylamide provided the greatest level discriminate of heteroduplexed structures. Of the pre-cast gels, 9 % poly-NAT provide an acceptable degree of resolution for situations where the volume of analyses precludes in-house gel preparation. All of these analyses were completed on a temperature-regulated horizontal gel apparatus that is amenable to polyacrylamide or other polymeric gel substrates (SEA 2000, Elchrom). Horizontal gel electrophoresis system gels have the advantages of rapid loading, and easy gel casting and manipulation inherent to this configuration (Bellomy and Record, 1989).

The heteroduplex patterns that appeared in the poly-NAT and polyacrylamide electrophoretic gels (Figs. 4-3b &-c, respectively) corresponded to the mobilities expected based on the differences in sequence of the fragments such that the order of retardation of heteroduplex mobility corresponds to the degree of sequence dissimilarity. However, as pointed out by White et al. (1992) and Ganguly et al. (1993), the actual gel mobility retardation in heteroduplex structures is related in a complex manner both to the type and distribution of sequence differences. Clustered base sequence changes that are centrally located produce local destabilization domains and have a much larger effect on mobility than non-contiguous differences dispersed throughout the molecule. However, the most pronounced heteroduplex mobility shifts result from molecular kinks caused by insertions or deletions between paired strands (Ganguly et al., 1993; Wang et al., 1992). This is seen in the substantial difference between the heteroduplex mobilities of the 114/132 and 132/244 heteroduplexes. Although the structures produced from 114/132 and 132/244 pairings show substantial difference in electrophoretic mobilities, the cumulative dissimilarities are only 55 and 56, respectively. The differences between these mobilities relative to both the homoduplexed DNAs and the 114/244 heteroduplexes seem unduly large because this total cumulative sequence difference between the 114/132 and 132/244 heteroduplexes is only one additional single base insertion/deletion in the latter.

Vertical gel electrophoresis (VGE) in HMA

The low level of sequence variation between PCR fragments necessitated a greater running distance to achieve adequate resolution of DNA heteroduplexes. To address this need, the method of vertical gel electrophoresis (VGE) described by Xing and colleagues (1996) was used, in which a hybrid low crosslinked polyacrylamide / agarose gel was cast between large glass plates using a vertically-oriented protein-type electrophoresis apparatus (e.g. Protean II, BioRad, La Jolla, CA). The gel matrix was made to be weakly denaturing by the addition of glycerol prior to casting. This weakly denaturing gel matrix destabilized small heteroduplexes and facilitated their detection. This system was used for scaled-up evaluation of PCR-amplified polymorphic loci from numerous fungal isolates since the system permitted the simultaneous electrophoresis of 100 products per run.

Similar to the horizontal method, a solution of 12.0 % acrylamide, 0.2 % bisacrylamide and 0.04 % ammonium persulfate was prepared in 1 x TBE to which 1.2 % agarose and 0.2 % N,N,N',N'-tetramethyl-ethylenediamine (TEMED) were added after degassing of the solution and immediately prior to casting. Gels were cast in a BioRad Protean electrophoresis apparatus at 1 mm thick, and allowed to polymerise for 4-5 hours prior to use. For electrophoresis, gels were cooled to 12 °C using a constant temperature refrigerated water bath and electrophoresed at 10 V/cm for up to 20 hr. Following electrophoresis, gels were stained in 250 ng/mL ethidium bromide for 2 hr, destained in distilled water for 3-4 hr prior to imaging. The large size of the gels and their relative fragility made their handling difficult. Custom plexiglass staining trays were constructed to accommodate these large gels. The trays were assembled using walls of PMMA plexiglass (General Electric) glued with 1 % (w/v) PMMA and 1 % (v/v) acetic acid in dichloromethane to a bottom plate of Acrylite OP-4 (General Electric), an ultraviolet transparent plastic sheet. The use of these trays allowed the gels to be stained, destained and visualized in a manner that limited their direct handling.

HMA Screening approaches

For scale-up comparison of PCR products, two general screening approaches were used.

Overlapped pairs

In the first method, all isolates were screened in overlapping pairs. In this technique, PCR products of all isolates were arranged in fixed, arbitrary sequence. For the initial round of HMA, all adjacent pairs were compared. For example, the hypothetical set A, B, C & D, would be compared in the pairs A+B, B+C, C+D and D+A. Following this initial round of HMA, all like-isolates were collapsed to a single representative by transitive property. A smaller second round of HMA compared alternating combinations of the remaining representative isolates. Often, with four rounds of reductive HMA, it was possible to determine haplotype for the entire set of 198 isolates of *P. chrysogenum* and 75 isolates of *P. brevicompactum*. An example of this approach is shown in Figure 4-4.

Universal heteroduplex generator

A second screening approach used for HMA involved the selection of a single isolate as a "universal heteroduplex generator". This isolate was selected on the basis of it being relatively distant from the panel of test isolates, typically from a closely related species. For example, *P. polonicum* was used as a universal heteroduplex generator for *P. chrysogenum* test panel. In this approach, each isolate was paired with the universal heteroduplex generator and submitted to electrophoresis (as above) under identical conditions. An example gel run using this approach is shown in Figure 4-5.

Results and discussion, VGE

Overall, the use of the vertical electrophoresis method increased the resolution of small differences by HMA due to the greater length of the gels. As well, the larger format of the BioRad system allowed the electrophoresis of 25 lanes per gel. Gels were run back-to-back in the configuration recommended by the manufacturer. Thus, the operation of two electrophoresis apparatuses in this configuration permitted the simultaneous screening of 100 isolates.

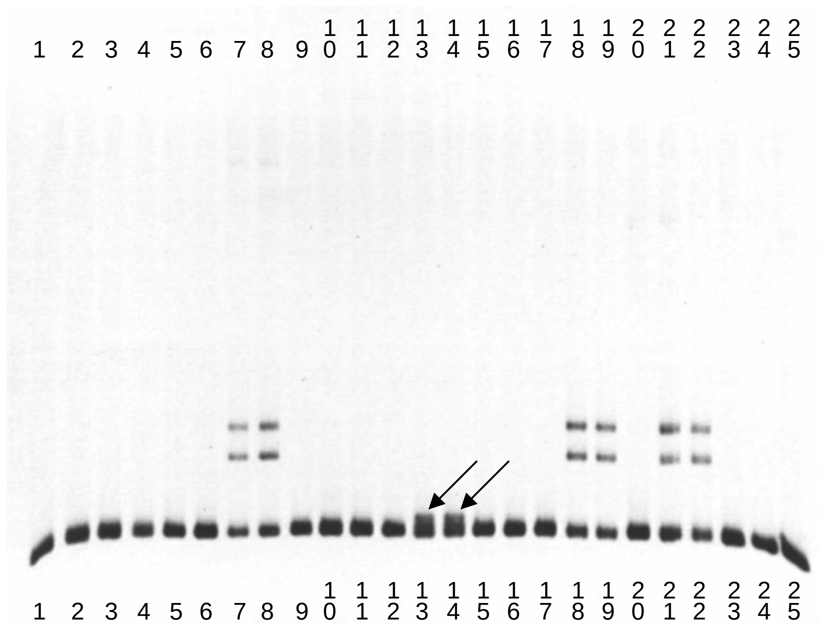


FIGURE 4-4. Vertical 12% PAG run in 1 x TBE at 5 °C under a field strength of 10 V/cm using the "Overlapping Pairs" screening method for HMA. Lanes contain heteroduplexed pairs of *P. chrysogenum* isolates as follows (*from left to right*): **1)** C52.2 + C53; **2)** C53 + C56.3; **3)** C56.3 + C56.4; **4)** C56.4 + C56.5; **5)** C56.5 + C58.3; **6)** C58.3 + C58.4; **7)** C58.4 + C58.7; **8)** C58.7 + C58.8; **9)** C58.8 + C58.11; **10)** C58.11 + C58.12; **11)** C58.12 + C58.13; **12)** C58.13 + C58.14; **13)** C58.14 + C58.15; **14)** C58.15 + C58.16; **15)** C58.16 + C59.2; **16)** C59.2 + 64.1; **17)** C64.1 + 64.2; **18)** C64.2 + C67.3; **19)** C67.3 + C70; **20)** C70 + C70.1; **21)** C70.1 + C70.3; **22)** C70.3 + C70.5; **23)** C70.5 + C70.6; **24)** C70.6 + C70.7; **25)** C70.7 + C71.2. Note the large heteroduplex band shifts in lanes 7-8, 18-19 and 21-22. Small heteroduplex band shifts are indicated by the arrows in lanes 13-14.

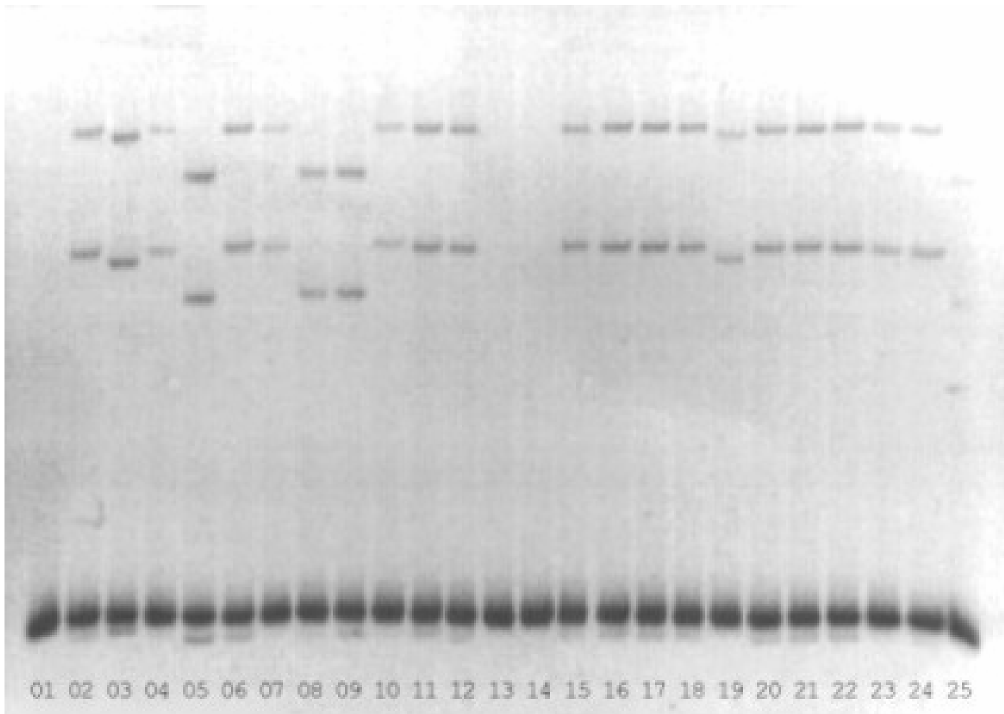


FIGURE 4-5. Vertical 12% PAG run in 1 x TBE at 5 °C under a field strength of 10 V/cm using the "Universal Heteroduplex Generator" screening method for HMA. Lanes contain PCR products amplified using the Bt2 primer set of *P. brevicompactum* isolates heteroduplexed against isolate B91, as follows (*from left to right*): **1)** B91 (negative control); **2)** B98; **3)** B99; **4)** B100.2; **5)** B109.1; **6)** B109.2; **7)** B65.4 (positive control) **8)** B112; **9)** B114; **10)** B117; **11)** B119.1; **12)** B119.2; **13)** 132.1; **14)** B132.2; **15)** B136; **16)** B165; **17)** B166; **18)** B170.1; **19)** 183; **20)** 185; **21)** 189; **22)** 192.1; **23)** 192.2; **24)** 201; and **25)** B204. Lanes 1, 13 and 14 did not show heteroduplex bands. Note the large distinctive heteroduplex band shifts in lanes 5, 8, 9 and 25, and the minor shifts in lanes 3 and 19, relative to the heteroduplex migrations in remaining lanes.

The overlapping pairs screening method was used to assess haplotype for all loci in both *P. brevicompactum* and *P. chrysogenum*. This technique performed well for both test panels which in both cases were dominated by a single genotype. Using this method it was possible to reduce the test panel by an average of approximately 80 % in all cases following the first round of HMA. This screening approach was also convenient since it did not require the inclusion of external lane standards to account for slight variation in electrophoretic conditions or the separation of gel runs in time. Rather, each lane compared two contiguously accessioned isolates directly, eliminating the need for relative assessment of band migration in different lanes. Figure 4-4 shows a gel in which *P. chrysogenum* isolates were compared at the Bt2 locus employing the overlapping pairs screening approach. Note that heteroduplex bands are absent in lanes 1-6, 9-12, 15-17, 20 and 23-25, indicating that these lanes contain isolate pairs with indistinguishable sequences at this locus. In contrast, the isolate common to lanes 7-8, 18-19 and 21-22 differs from its paired isolates in these two lanes by a total of 4 non-contiguous base substitutions at positions 127 (A/G), 267 (A/G) and 351 (T/C) (total product length of 433 bp) and a deletion of 2 contiguous bases at position 242-243 (*see* Appendix G). The small heteroduplex shift indicated by arrows in lanes 13-14 differed from its paired isolates in these two lanes by a total of 7 non-contiguous base substitutions at positions 134 (C/T), 195 (G/A), 198 (T/C), 233 (A/G), 246 (G/A), 267 (A/G) and 351 (T/C). The smallest difference revealed using this technique was a single base substitution between isolates C8.12 and C8.24 at position 363 (T/G) in the 548 bp ITS fragment amplified from *P. chrysogenum* isolates (gel not shown) (*see* Appendix G).

For loci that demonstrated greater frequency of allelic differences, a screening method employing a universal heteroduplex generator method was used in addition to the overlapping pairs method. The use of a divergent universal heteroduplex generator increased the separation between heteroduplex and homoduplex band fronts, reducing interference of the latter in evaluating band shifts. Figure 4-5 shows an HDX gel of *P. brevicompactum* using the Bt2 locus using a universal heteroduplex generator (in this case the same locus amplified from a distant isolate of *P. brevicompactum*, B91 (=B132.1, *see* Chapter 5, Table 5-3)). A small shift in mobility can be seen in the heteroduplex bands in lanes 3 and 19, relative to lanes 2, 4, 6, 7, 10-12, 15-18 and 20-24. This shift between these two groups was correlated to a difference of 4 non-contiguous base substitutions at positions 55 (G/A), 75 (A/T), 258 (T/G) and 420 (G/A), along with a single, contiguous 2-base substitution at position 71-71 (AT/GC) in a total product length of 438 bp (*see* Appendix F). Similarly, a larger shift between the latter group and lanes 5, 8 and 9 was correlated to 5 non-contiguous base substitutions at positions 60 (T/A), 148 (C/T), 158 (T/G), 259 (G/T) and 420 (A/G), with a contiguous 2-base substitution at position 74-75 (CT/TA) in a product of 438 bp in length. Lanes 13 an 14 contained control of isolate B91.

IDENTIFICATION OF POLYMORPHIC GENETIC LOCI

Preliminary investigation to determine polymorphic loci for use in the characterization of isolates of *P. brevicompactum* and *P. chrysogenum* used a randomly selected test panel of 10 isolates for each of these species. Primer pairs that amplified intron regions in conserved metabolic and structural proteins as well as the internal transcribed spacer regions (ITS1-2) of nuclear ribosomal DNA were assessed for their ability to discriminate strains using HMA. Tables 4-1 and 4-2 summarize the loci investigated for the screening of *P. brevicompactum* and *P. chrysogenum* isolates, respectively. For *P. brevicompactum* 7 loci were investigated, three of which, benA, his4 and ITS, showed readily observable polymorphisms with HMA (*see* Table 4-1). Similarly, four informative loci (acuA, benA, ITS and trxB) were identified from preliminary studies of a *P. chrysogenum* test panel that investigated 13 candidate loci (*see* Table 4-2).

PHYLOGENETIC ANALYSIS OF *PENICILLIUM* SENSU STRICTO

An analysis of phylogeny within the genus *Penicillium* was conducted in an effort to determine 1) the placement of *P. brevicompactum* and *P. chrysogenum* within the genus, and 2) to assist in the selection of appropriate outgroup taxa for later use in this study. Subgenus *Biverticillium* was not included in the present analysis because this group consists of anamorphs of the genus *Talaromyces*, which is only distantly related to *Eupenicillium* (Lobuglio et al., 1993).

Sequence data for the internal transcribed spacer and partial 28S regions of nuclear ribosomal DNA collected by Dr. Steve Peterson (United States Department of Agriculture, Northern Regional Research Laboratories in Peoria, Illinois) were obtained from GenBank for a set of 85 species of *Penicillium* including representatives of all accepted subgenera comprising the genus in the strict sense (e.g. subgen. *Aspergilloides*, *Exilicaulis*, *Divaricatum*, *Furcatum* and *Penicillium*) (*see* Table 4-3). A similar analysis of this dataset by parsimony methods is presented by Peterson (2000). Most of these sequences originated from authentic isolates from the NRRL culture collection. Sequences were aligned using Clustal X (version 1.8) (*see* Jeannmougin et al., 1998; Thompson et al., 1997) and a distance tree was generated using Neighbor-Joining. Alignment of the dataset is provided in Appendix D. Tree branch support was determined by 1000 bootstrap replications. Trees were generated using version 1.5.2 of TreeView for Microsoft Windows 32 bit (Roderick Page, Oxford University), and formatted using Corel Draw version 8.232 (Corel Corporation, Ottawa). *Penicilliopsis clavariiformis* was used as an outgroup taxon. The absence of partial 28S sequence prohibited the inclusion of *P. brevicompactum* in this analysis.

A Neighbor-Joining tree rooted using *Penicilliopsis clavariiformis* is shown in Figure 4-6. An unrooted version of this tree is presented for comparison in Figure 4-7. Branches for which

Table 4-1: Candidate loci examined for polymorphisms in *P. brevicompactum*

Gene	Source of primers	No. primer pairs tested	No. with polymorphisms
anonymous locus (A1)	Glass & Donaldson, 1995	1	
Beta-tubulin (benA)	Glass & Donaldson, 1995	2	1
Histone 3 (his3)	Glass & Donaldson, 1995	1	
Histone 4 (his4)	Glass & Donaldson, 1995	1	1
Phosphoglycerate kinase (pgk)	Glass & Donaldson, 1995	1	
rDNA Intergenic spacer region (IGS)	this study*	2	
rDNA Internal transcribed spacer region (ITS1-5.8S-ITS2)	White et al., 1989	1	1

* Primer pairs developed in this study were based on gene sequences available in GenBank

Table 4-2 Candidate loci examined for polymorphisms in *P. chrysogenum*

Gene	Source of primers	No. primer pairs tested	No. with polymorphisms
Acid phosphatase (phoG)	this study*	1	
Antifungal protein PAF (paf)	this study	1	
Acetyl co-enzyme A synthase (acuA)	this study	2	2
Beta-tubulin (benA)	Glass & Donaldson, 1995	2	1
Histone 3 (his3)	Glass & Donaldson, 1995	1	
Histone 4 (his4)	Glass & Donaldson, 1995	1	
Nitrogen regulation protein (areA)	this study	1	
Orotidine-5'-phosphate decarboxylase (pyrG)	this study	1	
Phosphoglycerate kinase (pgk)	Glass & Donaldson, 1995 & this study	2	
rDNA Intergenic spacer region (IGS)	this study	2	
rDNA Internal transcribed spacer region (ITS1-5.8S-ITS2)	White et al., 1989	1	1
Thioredoxin reductase (trxB)	this study	1	1
Xylanase (xyl)	this study	3	

* Primer pairs developed in this study were based on gene sequences from *P. chrysogenum* deposited in GenBank

Table 4-3: Sources of nuclear ribosomal ITS and partial 28S sequences used in this study

Identification	Strains number	Status	GenBank accession
Eupenicillium cinnamopurpureum DB Scott & Stolk	NRRL 3326	ex-type	AF033414
Eu. crustaceum F Ludw.	NRRL 3332	ex-type	AF033466
Eu. egyptiacum Beyma	NRRL 2090	ex-type	AF033467
Eu. lapidosum DB Scott & Stolk	NRRL 718	ex-type	AF033409
Eu. shearii Stolk & DB Scott	NRRL 715	ex-type	AF033420
Hemicarpenteles paradoxus AK Sarbhoy & Elphick	NRRL 2162	ex-type	AF033484
Penicilliopsis clavariiformis Solms	NRRL 2482	ex-type	AF033391
Penicillium adametzii Zalesky	NRRL 736		AF034459
P. adametzii	NRRL 737	ex-type	AF033401
*P. adametzioides** Abe *ex* G Smith	NRRL 3405	ex-type	AF033403
P. asperosporum G Smith	NRRL 3411	ex-type	AF033412
P. atramentosum Thom	NRRL 795	ex-type	AF033483
P. atrovenetum G Smith	NRRL 2571	ex-type	AF033492
P. aurantiogriseum Dierckx	NRRL 971	ex-type	AF033476
P. bilaii Chalab.	NRRL 3391	ex-type	AF033402
P. camemberti Thom	NRRL 874	ex-type	AF034453
P. camemberti	NRRL 875		AF033474
P. canescens Sopp	NRRL 2147		AF034463
P. canescens	NRRL 910	ex-type	AF033493
*P. charlesii** G Smith	NRRL 778	ex-type	AF033400
P. chermesinum Biourge	NRRL 735	ex-type	AF033413
P. chrysogenum Thom	NRRL 807	ex-type	AF033465
P. chrysogenum	NRRL 824	Fleming	AF034450
P. cinerascens Biourge	NRRL 748		AF033455
P. citreonigrum Dierckx	NRRL 761	ex-type	AF033456
P. citrinum Thom	NRRL 1841	ex-type	AF033422
*P. coprophilum** (Berk. & Curtis) Siefert & Samson	NRRL 13627	ex-type	AF033469
P. corylophilum (Berk. & Curtis) Siefert & Samson	NRRL 793		AF034456
P. corylophilum	NRRL 802	ex-type	AF033450
P. corylophilum	NRRL 803		AF034457
P. crustosum Thom	NRRL 968		AF033472
P. daleae Zalesky	NRRL 922	ex-type	AF033442
P. decumbens Thom	NRRL 741	ex-type	AF033453
P. decumbens	NRRL 742		AF034458
P. digitatum (Pers.:Fr.) Sacc.	NRRL 786	ex-type	AF033471
P. donkii Stolk	NRRL 5562	ex-type	AF033445
P. echinulatum Raper & Thom	NRRL 1151	ex-type	AF033473
P. expansum Link	NRRL 974		AF033479
P. fellutanum Biourge	NRRL 746	ex-type	AF033399
*P. fuscum** (Sopp) Biourge	NRRL 721	ex-type	AF033443
P. glabrum (Wehmer) Westling	NRRL 766	ex-type	AF033407
P. griseofulvum Dierckx	NRRL 2300	ex-type	AF033468
P. griseofulvum	NRRL 734		AF034452
P. griseoroseum Dierckx	NRRL 820		AF034857
P. griseoroseum	NRRL 832		AF034449
P. herquei Bainier & Sartory	NRRL 1040	ex-type	AF033405
P. janthinellum Biourge	NRRL 2016	ex-type	AF033434
*P. kojigenum** G Smith	NRRL 3442	ex-type	AF033489
P. lividum Westling	NRRL 754	ex-type	AF033406
P. melinii Thom	NRRL 2041	ex-type	AF033449

*names not accepted by Pitt and Samson (1993), NCU-2

Table 4-3: Sources of nuclear ribosomal ITS and partial 28S sequences used in this study

Identification	Strains number	Status	GenBank accession
P. miczynskii Zalesky	NRRL 1077	ex-type	AF033416
*P. notatum** Westling	NRRL 821	ex-type	AF034451
P. ochrochloron Biourge	NRRL 926	ex-type	AF178516
P. oxalicum Currie & Thom	NRRL 787	ex-type	AF033438
P. oxalicum	NRRL 790		AF034455
P. paxilli Bainier	NRRL 2008	ex-type	AF033426
*P. polonicum** Zalesky	NRRL 995	ex-type	AF033475
P. purpurescens (Sopp) Biourge	NRRL 720	ex-type	AF033408
*P. raciborskii** Zalesky	NRRL 2150	ex-type	AF033447
P. raistrickii G Smith	NRRL 2039	ex-type	AF033491
P. raperi G Smith	NRRL 2674	ex-type	AF033433
P. restrictum Gilman & Abbott	NRRL 1748	ex-type	AF033457
P. restrictum	NRRL 25744		AF033459
P. rolfsii Thom	NRRL 1078	ex-type	AF033439
*P. roseopurpureum** Dierckx	NRRL 2064	ex-type	AF033415
*P. roseopurpureum**	NRRL 733		AF034462
P. sartoryi Thom	NRRL 783	ex-type	AF033421
P. sclerotigenum W Yamam.	NRRL 3461		AF033470
P. sclerotiorum Beyma	NRRL 2074	ex-type	AF033404
P. simplicissimum HZ Kong & ZT Qi	NRRL 1075	ex-type	AF033440
P. soppii Zalesky	NRRL 2023	ex-type	AF033488
P. spinulosum Thom	NRRL 1750	ex-type	AF033410
P. spinulosum	NRRL 728		AF034461
*P. sumatrense** v. Szilvinyi	NRRL 779	ex-type	AF033424
*P. swiecickii** Zalesky	NRRL 918	ex-type	AF033490
P. thomii Maire	NRRL 2077	ex-type	AF034448
P. thomii	NRRL 760		AF034460
P. turbatum Westling	NRRL 757	ex-type	AF034454
P. turbatum	NRRL 759		AF033452
P. velutinum Beyma	NRRL 2069	ex-type	AF033448
P. vinaceum Gilman & Abbott	NRRL 739	ex-type	AF033461
P. viridicatum Westling	NRRL 958	ex-type	AF033477
P. viridicatum	NRRL 961		AF033478
P. waksmanii Zalesky	NRRL 777	ex-type	AF033417
P. westlingii Zalesky	NRRL 800	ex-type	AF033423

*names not accepted by Pitt and Samson (1993), NCU-2

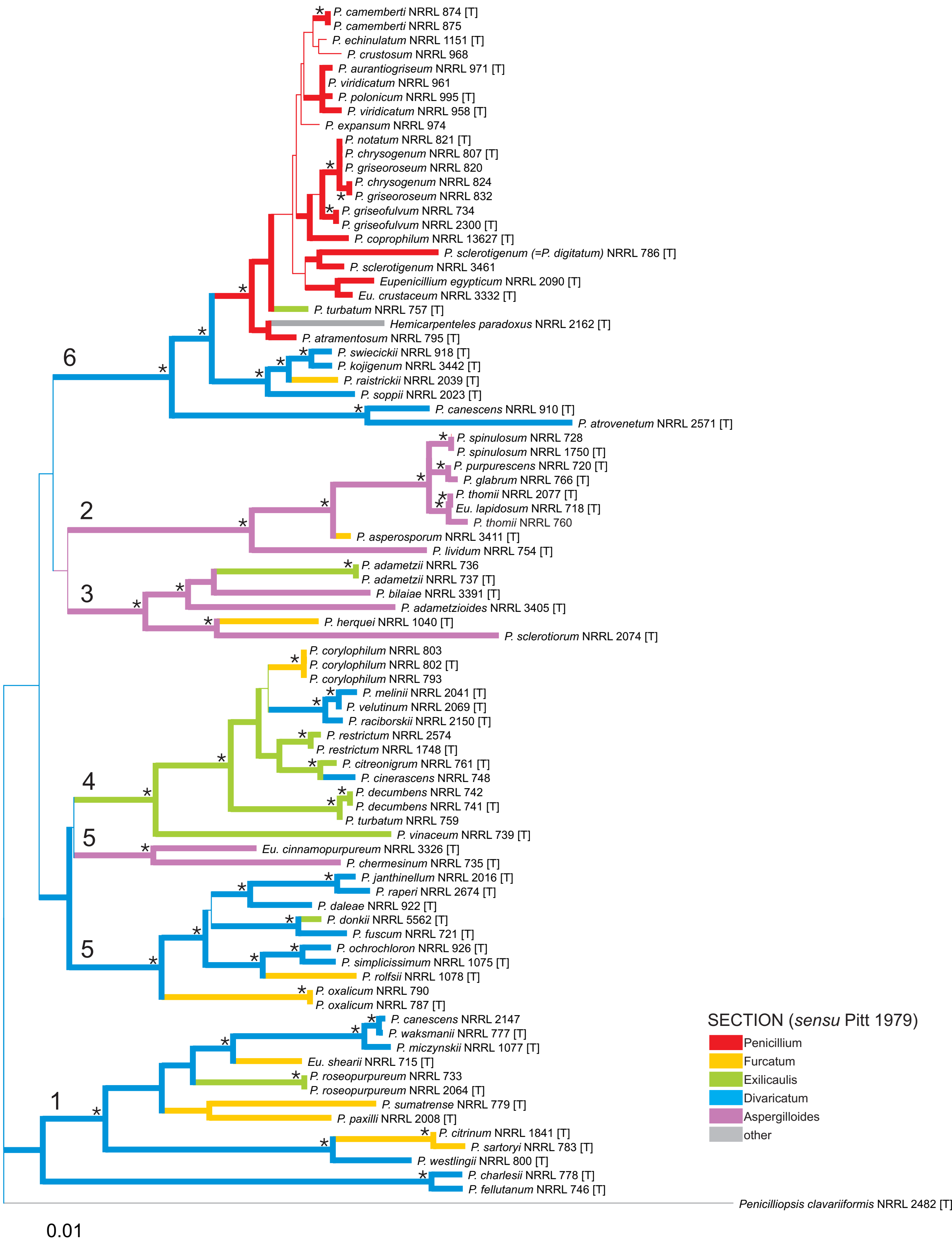


FIGURE 4-6. Neighbor-Joining tree depicting phylogenetic relationships within *Penicillium sensu stricto* inferred from nuclear ribosomal ITS1-5.8S-ITS2 and partial 28S sequences rooted using *Penicilliopsis clavariiformis*. Thick branches demonstrated over 50% bootstrap support, and branches marked with an asterisk showed over 80% bootstrap support in 1000 replications. Branch colour indicates taxonomic affiliation (*sensu* Pitt 1979). Numbered branches correspond to the clades identified by Peterson (2000).

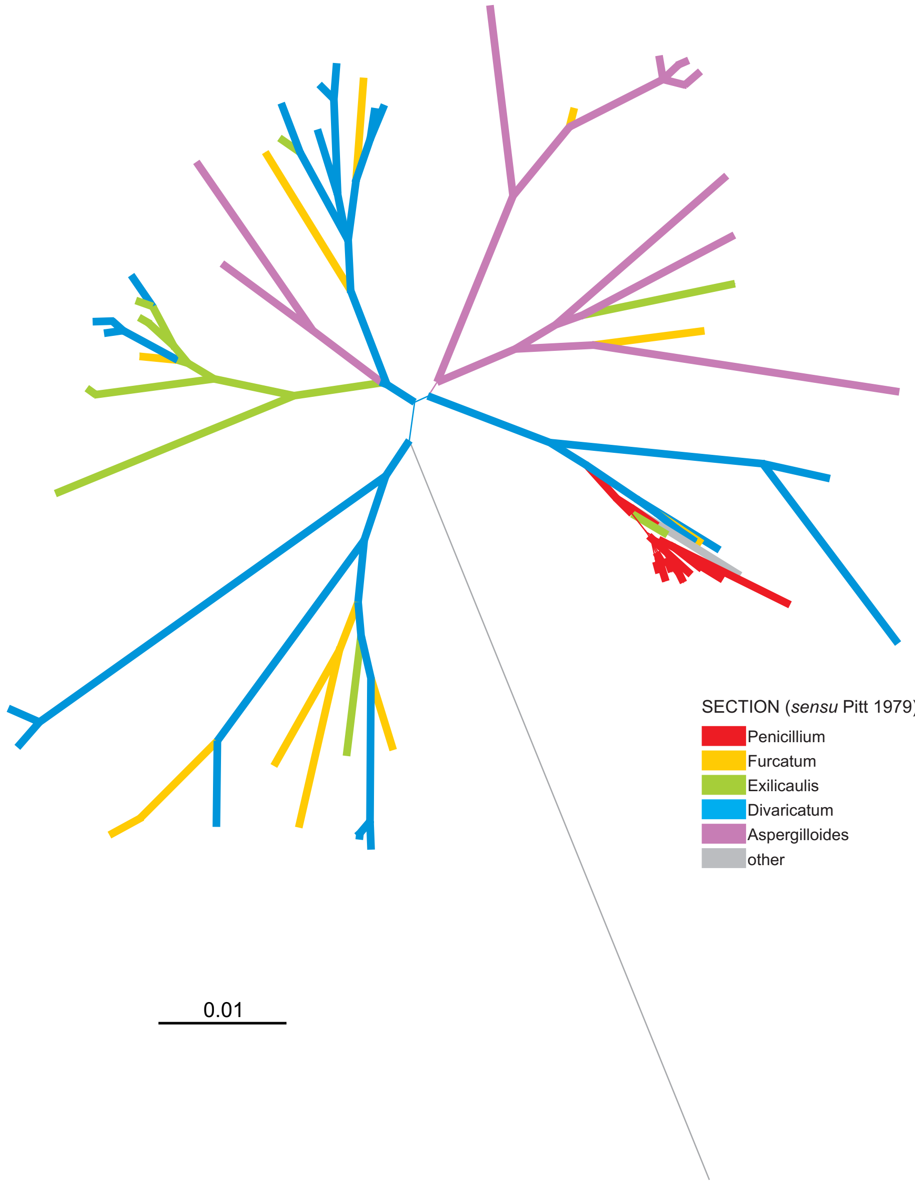


FIGURE 4-7. Unrooted Neighbor-Joining tree depicting phylogenetic relationships within *Penicillium sensu stricto* inferred from nuclear ribosomal ITS1-5.8S-ITS2 and partial 28S sequences rooted using *Penicilliopsis clavariiformis*. Thick branches demonstrated over 50% bootstrap support, and branches marked with an asterisk showed over 80% bootstrap support in 1000 replications. Branch colour indicates taxonomic affiliation (*sensu* Pitt 1979).

bootstrap values were greater than 50 % are indicated as thick lines. Bootstrap support at greater than 80 % is indicated by an asterisk. Ex-type strains are indicated by "[T]", and subgeneric classification following Pitt (1979) is indicated by color-coded branches.

The terverticillate taxa classified in *Penicillium* subgen. *Penicillium* formed a well-supported monophyletic clade at the top of the tree (indicated in red). *Penicillium chrysogenum* isolates grouped centrally within this clade, and were sister to *P. griseofulvum*. Isolates of *Penicillium* subgen. *Aspergilloides* formed a clade (bootstrap support less than 50 %) that was sister to the subgenus *Penicillium* clade. Several extraneous taxa, including *P. adametzii, P. herquei* and *P. asperosporum* (subgen. *Furcatum sensu* Pitt, 1980) were also found within this group. Representatives of subgenus *Furcatum* (indicated in yellow) were interspersed throughout the tree, indicating the multiple origin of the furcate conidiophore form characteristic of this group. Similarly, isolates of subgenus *Divaricatum* (indicated in blue) appeared throughout the tree. Divaricate conidiophore morphology appears to be the ancestral branching state, as it forms the backbone of the phylogeny. A multiple origin for the furcate form and an ancestral divaricate morphology for the genus provide the best interpretation of the internal branching topology of this tree. The principal clades identified in this analysis corresponded well to those observed by Peterson (2000) in a parsimony-based analysis of this dataset. The numbered groups observed by Peterson (2000) are indicated on the dendrogram in Figure 4-6 on the corresponding branches. Peterson's results concur that penicillius complexity is not a reliable phylogenetic predictor, and that this feature is likely influenced by aspects of life history and dispersal of the species (or lineage) in question. The exception is the terverticillate Penicillia, which in both analyses formed a well-supported monophyletic group. Within this group, however, species were poorly separated. The employment of faster-evolving genes may better resolve these taxa.

PENICILLIUM CHRYSOGENUM

A subset of the above dataset limited to ITS1-5.8S-ITS2 region of GenBank sequences of 36 taxa in Penicillium *sensu stricto* collected by Dr. Steve Peterson (USDA, Peoria) were reanalyzed as above. Other sequences included in this dataset were representatives of Wallaceburg isolates of *P. brevicompactum*, *P. chrysogenum* and *P. polonicum*, as well as ex-type strains of species considered to be closely related to these taxa (e.g. *P. aethiopicum* CBS 484.84; *P. olsonii* CBS 232.32, *P. stoloniferum* ATCC 10111 and *P. brevicompactum* DAOM 193712). Sequences were analyzed and a distance tree was generated, as described above. The Neighbor-Joining tree shown in Figure 4-8 was rooted using *Eupenicillium lapidosum* and *Penicillium biliae* (subgenus *Aspergilloides*). Isolates representing the *P. chrysogenum* complex group together in a weakly supported clade centrally within subgenus *Penicillium* (indicated as clade **a**, Figure 4-8). Within this group, two voucher strains deposited as *P. notatum* (NRRL 824 from Fleming and NRRL 832 from Biourge), the Wallaceburg strains represented by C8.12 (179 isolates in total) and *P. nalgiovense* (ex-type strain NRRL 911) formed a well-supported clade.

PENICILLIUM BREVICOMPACTUM

Isolates of *P. brevicompactum* formed a well-supported clade sister to the terverticillates (indicated as clade **b**, Figure 4-8). Within the *P. brevicompactum* clade, two well-defined groups were observed. The first of these contained the ex-type strains of *P. brevicompactum* (DAOM 193712) and *P. stoloniferum* (ATCC 10111) along with 60 isolates from the Wallaceburg collection represented by B65.4 (46 isolates) and B251 (15 isolate). The second group consisted of 10 Wallaceburg isolates represented by B132.1.

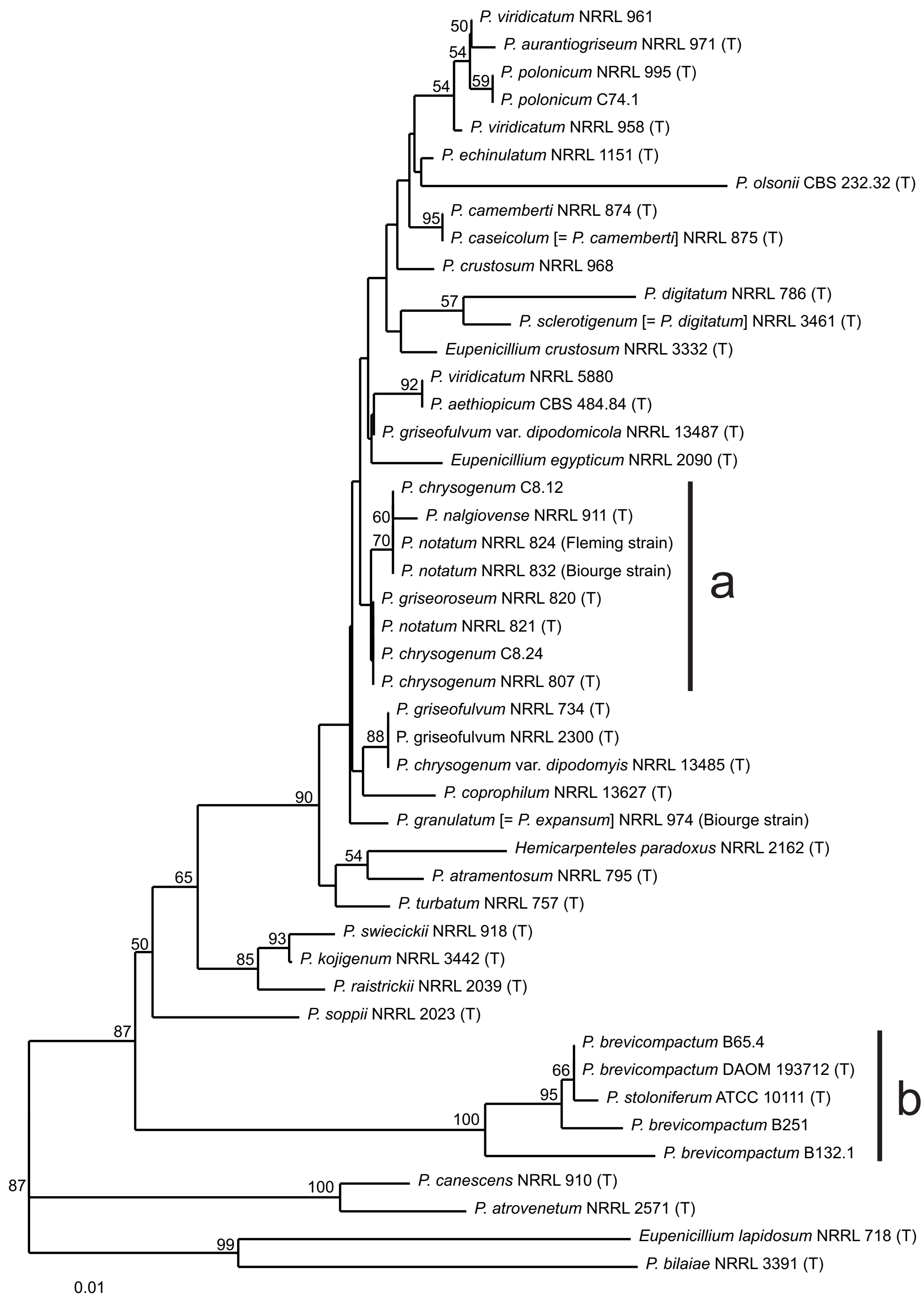


FIGURE 4-8. Distance tree of *Penicillium* subgen. *Penicillium* inferred from ITS1-5.8S-ITS2 rDNA data outgroup-rooted using *Eupenicillium lapidosum* and *P. bilaiae*.

CHAPTER 5. ASSESSMENT OF GENETIC VARIATION IN INDOOR ISOLATES OF *PENICILLIUM BREVICOMPACTUM*[8]

ABSTRACT

Penicillium brevicompactum is a commonly occurring putatively asexual soilborne fungus and inhabitant of the decaying fruit bodies of fleshy fungi. This species is also known as a frequent contaminant of water-damaged building materials such as gypsum wallboard (Scott, 1999a). The present study examined the distribution of genotypic diversity based on sequences of two genes between indoor and outdoor populations of this fungus. The primary objective of this study was to test the current species concept applied to *P. brevicompactum*.

Seventy-five morphologically and physiologically uniform isolates of *P. brevicompactum* were obtained from 54 houses in Wallaceburg, Ontario, Canada. Three polymorphic genetic loci, beta-tubulin (benA), internal transcribed spacer regions of ribosomal DNA (ITS1-2) and histone 4 (his4) were amplified using PCR and compared by heteroduplex mobility assay (HMA). Nine unique multilocus haplotypes were observed in which alleles showed strong association indicating predominantly clonal reproduction. Two major genotypes were observed, which dominated the houses sampled, accounting for 88.6 % and 5.4 % of the sample, respectively. Other haplotypes were observed at low frequency in several of the houses from which multiple isolates were obtained.

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[8] Parts of this chapter are reprinted with the kind permission of Eastern New York Occupational and Environmental Health Centre (ENYOEHC), Albany, New York, USA, from Scott, J.A., Straus, N.A. and Wong, B. 1999. Heteroduples DNA fingerprinting of *Penicillium brevicompactum* from house dust. pp. 335-342, *In* Bioaerosols, fungi and mycotoxins: health effects, assessment, prevention and control. E. Johanning (ed). Albany, New York: ENYOEHC. 638 pp.

DNA sequence analysis of the beta-tubulin and rDNA loci for all alleles confirmed two genetically divergent groups within *P. brevicompactum* as currently circumscribed. Authentic strains of *P. brevicompactum* and *P. stoloniferum* clustered together in the predominant indoor clade which accounted for 86 % of the Wallaceburg isolates. The second lineage contained 14 % of the Wallaceburg isolates, and clustered with voucher collections obtained from the rotting fruit bodies of macrofungi.

INTRODUCTION

There is widespread agreement that the outdoor environment contributes substantially to the burden of biological particulate present in building interiors (Miller, 1992). Although airborne fungal spores of outdoor origin are accepted to be amongst the principal allergenic mediators of seasonal allergic rhinitis, the presence of amplifiers of fungi within the building envelope presents a more serious concern. This is so for two main reasons: 1) In contrast to most outdoor surfaces, building materials of organic origin remain devoid of active growth until they become water damaged, at which point the absence of microbial competition facilitates the unbridled growth of primary fungal colonists; and 2) the indoor environment contains a finite dilution volume of air, permitting the establishment of airborne concentrations of these contaminants which may profoundly exceed outdoor levels. In the case of persistently wet drywall, the species most often observed are *Aspergillus nidulans* group, *As. versicolor, Chaetomium* spp., *Penicillium brevicompactum* and *Stachybotrys chartarum*. Curiously however, certain species, notably *As. versicolor, P. brevicompactum* and *P. chrysogenum* may be observed in abundance even in building environments lacking conspicuous amplifiers (Scott et al., 1999a, b). Investigations of both outdoor air and organic substrata fail to a demonstrate sufficient presence of propagules of these fungi to account for their predominance in the indoor spora relative to other typical background taxa, such as phylloplane moulds (Scott et al., 1999a). Thus, the culture-presence of these taxa from dust isolations, many of which range from xerotolerant to xerophilic, has been interpreted as evidence for the proliferation of these species in the dust substrate under "normal" conditions (e.g. low water activity) (e.g. Davies, 1960; Bronswijk, 1981). Despite considerable observation and documentation of these species from household dust and indoor air, there is scant empirical evidence to support this widespread hypothesis of generalized cryptic indoor proliferation under normal circumstances. Furthermore, the phylogenetic placement of *P. brevicompactum* within *Penicillium* has not been tested using molecular methods.

The present study was undertaken in cooperation with the Canada Mortgage and Housing Corporation (CMHC) in which multiple isolates of *P. brevicompactum* were obtained from houses in Wallaceburg, Ontario (*see* Figure 2-1). The amount of genotypic variability in PCR-amplified polymorphic genetic loci was assessed using a heteroduplex mobility assay. This method has been used previously in the screening of human genes for mutations of clinical diagnostic significance (e.g. White et al., 1992), and in the epidemiological investigation of human viral populations (Delwart et al., 1993; 1994). Chapters 3 and 4 present a more detailed discussion of this method.

MATERIALS AND METHODS

COLLECTION AND CHARACTERIZATION OF ISOLATES

Vacuum cleaner bag samples of carpet dust were collected from 369 houses in Wallaceburg, Ontario, Canada by a private company under contract to the Canada Mortgage and Housing Corporation over a period of five months starting in January, 1994. The distribution of house locations sampled is shown on the street map in Figure 5-1. Fungal isolates were obtained using

FIGURE 5-1. Street map of Wallaceburg, Ontario, indicating collection sites for *P. brevicompactum* isolates used in this study.

a standard dilution plating technique (Malloch, 1981). Isolates of *Penicillium* were identified using conventional methods (e.g. Pitt, 1980). Isolates selected for genetic screening were indistinguishable based upon microscopic morphology and physiological profiles on standard growth media (Pitt, 1979). Chapter 4 contains detailed information on these procedures. A set of isolates of *P. brevicompactum* from other locations was included for comparison (*see* Table 5-1).

DNA isolation and PCRs were performed according to the methods described in Chapter 4. Three polymorphic loci consisting of introns in the genes encoding beta-tubulin (BenA), histone 4 (H4) and the region spanning the internal transcribed spacers (ITS1 to ITS2) of nuclear ribosomal DNA (rDNA) were PCR-amplified using the primer sequences given in Table 5-2. The position of these primers is shown in Figure 5-2. Methods used for heteroduplex analysis of PCR products are given in Chapter 4.

SEQUENCE ANALYSIS

PCR templates were purified using QIAquick PCR purification kit (Qiagen, Inc., Valencia, Calif.). PCR templates were sequenced using the Taq DyeDeoxy cycle sequencing kit(Applied Biosystems, Inc., Foster City, Calif.) and extension products were analysed on an ABI-50 fluorescent automated sequencer (Applied Biosystems, Inc.). Sequences were determined on both sense and anti-sense strands using the same primers that were used for amplification (*see* Table 5-2).

Alignments of sequences were performed using Clustal X software package (version 1.8) (*see* Jeannmougin et al., 1998; Thompson et al., 1997) and adjusted by visual inspection using a text editor. Sequences were combined for analysis based on congruence as determined by the

Table 5-1: List of comparative strains used in this study

Strain number	Identification	Status	Substratum
ALG1	*P. brevicompactum*		decaying agaric, Algonquin Prov. Pk., Ontario, Canada
ALG2	*P. brevicompactum*		decaying agaric, Algonquin Prov. Pk., Ontario, Canada
ATCC 10111	*P. stoloniferum* Thom	ex-type	decaying bolete, Connecticut, USA
CBS 232.60	*P. olsonii*	ex-type	root of *Picea*,
DAOM 147648	*P. brevicompactum* Dierckx		mushroom, Ottawa, Ontario
DAOM 191327	*P. brevicompactum* Dierckx		*Cytospora* sp. on *Prunus persica*, Harrow, Ontario
DAOM 192262	*P. brevicompactum* Dierckx		urea formaldehyde foam insulation, Ottawa Ontario
DAOM 193710	*P. chrysogenum*	ex-type	cheese, Connecticut, USA
DAOM 193712	*P. brevicompactum* Dierckx	ex-type	*substr. incertum*, ?Belgium
DAOM 193713	*P. stoloniferum* Thom	ex-type	decaying bolete, Connecticut, USA
DAOM 214776	*P. brevicompactum* Dierckx		decaying mushroom, Denmark
DAOM 215331	*P. brevicompactum* Dierckx		spruce lumber, Quebec
DAOM 215332	*P. brevicompactum* Dierckx		on *Picea*, Quebec
DAOM 215335	*P. brevicompactum* Dierckx		spruce lumber, Quebec

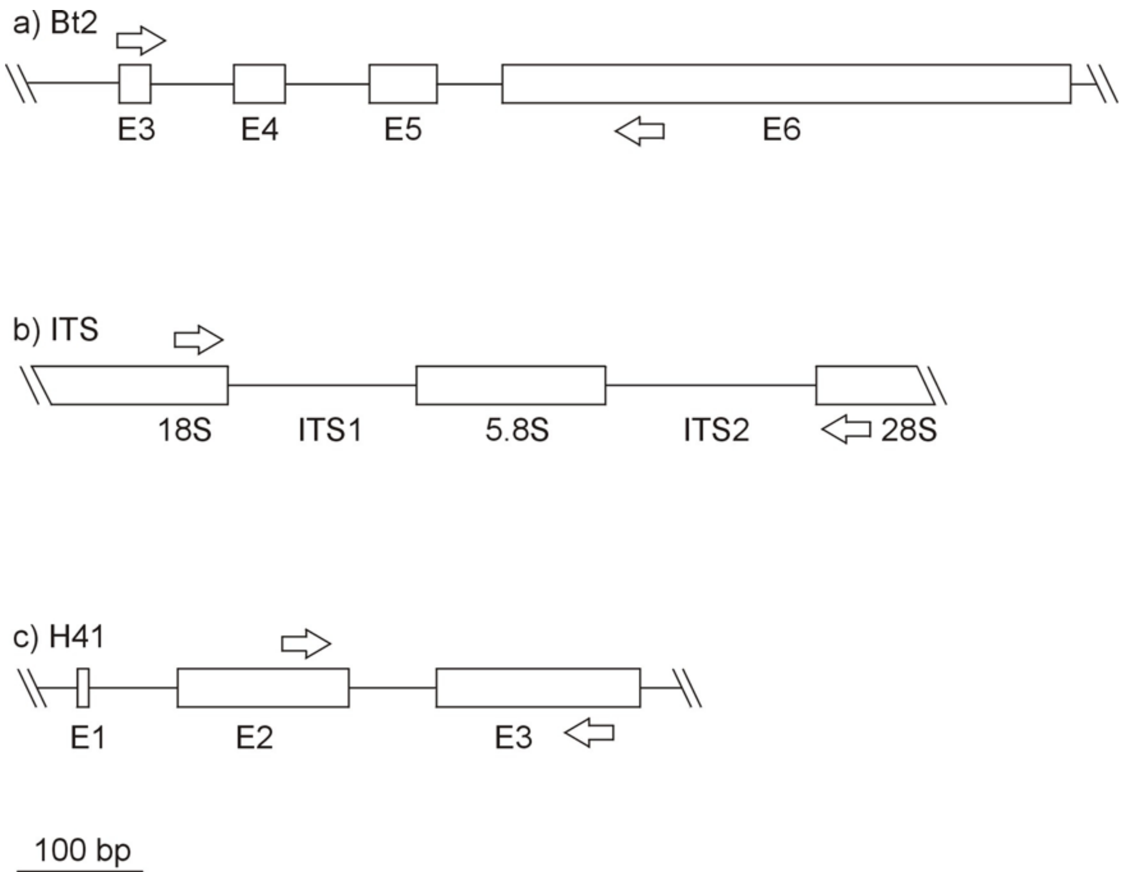

FIGURE 5-2. Locations of primers used to amplify polymorphic regions in *P. brevicompactum*.

Table 5-2: Primers sequences employed in this study

Beta-tubulin (benA)			
	Source:	Glass & Donaldson, 1995	
	Fwd primer 5'-3':	GGT AAC CAA ATC GGT GCT GCT TTC	(Bt2a)
	Rvs primer 5'-3':	ACC CTC AGT GTA GTG ACC CTT GGC	(Bt2b)
Nuclear rDNA ITS regions			
	Source:	White et al., 1990, fwd; Untereiner et al., 1995, rvs	
	Fwd primer 5'-3':	GGA AGT AAA AGT CGT AAC AAG G	(ITS5)
	Rvs primer 5'-3':	TAT GCT TAA GTT CAG CGG	(WNL1)
Histone 4 (H41)			
	Source:	Glass & Donaldson, 1995	
	Fwd primer 5'-3':	GCT ATC CGC CGT CTC GCT	(H41a)
	Rvs primer 5'-3':	GGT ACG GCC CTG GCG CTT	(H41b)

Partition Homogeneity Test (PHT). The PHT has been subject to recent criticism for its performance in determining sequence congruence (Barker and Lutzoni, 2000). Certain datasets which have been demonstrably congruent have not been reported so using this test. As such, the PHT should only be used as a guideline and not an absolute determinant of congruence; however, it remains widely used for this purpose and is offered as a best available assessment of congruence in the present study. These problems are considered in greater detail in the discussion section of this chapter.

Phylogenetic analyses were carried out using the Clustal X and PAUP* software packages (PAUP* version 4.0b4a for 32 bit Microsoft Windows, Sinauer Associates, Inc., Sunderland, Massachusetts) using the Neighbor-Joining method. The data were re-sampled by 1000 bootstrap replicates, and the proportion of Neighbor-Joining trees possessing each particular internal branch is indicated to express its level of support. Phylogenetic trees were generated using the TreeView software package, version 1.5.2 for Microsoft Windows 32 bit (Roderick Page, Oxford University), and formatted using Corel Draw version 8.232 (Corel Corporation, Ottawa).

RESULTS

Collection locations of house dust isolates are shown in Figure 5-1. Isolates of *P. brevicompactum* were obtained from 54 of the 369 houses examined (15 %). Six of these houses were in rural locations (i.e. outside the town limits). In total, 72 isolates were examined, 54 of which originated from urban locations and the remainder (18) from rural locations.

HETERODUPLEX MOBILITY ASSAY

The genotypes of house dust *P. brevicompactum* isolates are summarized in Table 5-3. The lowest degree of allelic variation was observed in the histone 4 locus (2 alleles) whereas the highest variation (6 alleles) was seen in the beta-tubulin locus (*see* Table 5-4). The three most commonly observed haplotypes were present in 57 %, 17 % and 16 % of isolates. The remaining minor haplotypes occurred in 4 % or fewer isolates. Mixed populations of two-or more genotypes were observed in two thirds of houses from which multiple isolates of *P. brevicompactum* were obtained suggesting the stable co-existence of multiple genotypes within individual houses.

DNA SEQUENCE ANALYSIS

DNA sequences were obtained for representatives of each allele for the benA and ITS loci. Difficulties were encountered in obtaining unambiguous sequence for the histone 4 locus in house dust isolates and voucher strains. Further attempts to resolve these difficulties were not made due to the low allelic variation in this locus, and it was excluded from sequence analyses.

Sequence alignments of partial beta-tubulin and ITS sequences are give in Appendix F. Figure 5-3 shows the results of a Partition Homogeneity Test (PHT) conducted on a combined alignment of beta-tubulin and ITS sequences including representative isolates of all house dust genotypes and voucher strains (listed in Table 5-1). The PHT produced a p-value = 0.0943, indicating that sequence data from these two genetic loci were congruent and could be combined. A distance tree produced from the combined benA-ITS dataset with PAUP* using the Neighbor-Joining method and rooted to *P. chrysogenum* (DAOM 193710 T) is shown in Figure 5-4c. Branch support is given as the percentage of 1000 bootstrap replications. Two well supported clades were observed. Clade 1 contained authentic strains of *P. brevicompactum* and *P.*

Table 5-3: Summary of haplotypes of *P. brevicompactum isolates*

Isolate #	LOCUS			Isolate #	LOCUS		
	benA	his4	ITS		benA	his4	ITS
42.1	A	A	A	132.2	B	B	C
45.1	B	B	C	136	A	A	A
45.2	B	B	C	165	A	A	A
62	A	A	A	166	A	A	A
65.1	A	A	A	170.1	A	A	A
65.3	A	A	A	183	D	A	A
65.4	A	A	A	185	A	A	A
65.5	B	B	C	189	A	A	A
65.6	C	A	B	192.1	A	A	A
67.2	A	A	A	192.2	A	A	A
67.3	A	A	A	201	A	A	A
67.4	A	A	A	204	C	A	B
67.5	C	A	B	217.2	A	A	A
67.6	B	B	C	228.1	C	A	B
67.7	A	A	A	233.1	B	B	C
70.4	A	A	A	233.2	C	A	B
72	A	A	A	240	A	A	A
74.1	A	A	A	244.1	F	A	B
75.1	A	A	A	244.3	A	A	A
75.2	C	A	B	245.2	E	A	A
75.3	C	A	D	251	A	A	B
79	A	A	A	259	A	A	A
81.1	A	A	A	263.1	A	A	A
87	C	A	B	264	D	A	A
91	B	B	C	266	A	A	A
98	A	A	A	273	A	A	A
99	D	A	A	274	A	A	A
100.2	A	A	A	280	A	A	A
109.1	C	A	B	306.2	E	A	B
109.2	A	A	A	319	A	A	A
112	C	A	B	322	A	A	A
114	C	A	B	325	C	A	B
117	E	A	A	340	B	B	C
119.1	A	A	A	353.1	B	B	C
119.2	A	A	A	373	A	A	A
132.1	B	B	C	374	C	A	B

Table 5-4: Haplotype frequencies for *P. brevicompactum* isolates

Representative Isolate	**LOCUS** Bt2	H41	ITS	**Frequency**
B65.4	A	A	A	0.569
B65.6	C	A	B	0.167
B132.1	B	B	C	0.139
B99	D	A	A	0.042
B117	E	A	A	0.028
B251	A	A	B	0.014
B75.3	C	A	D	0.014
B306.2	E	A	B	0.014
B244	F	A	B	0.014

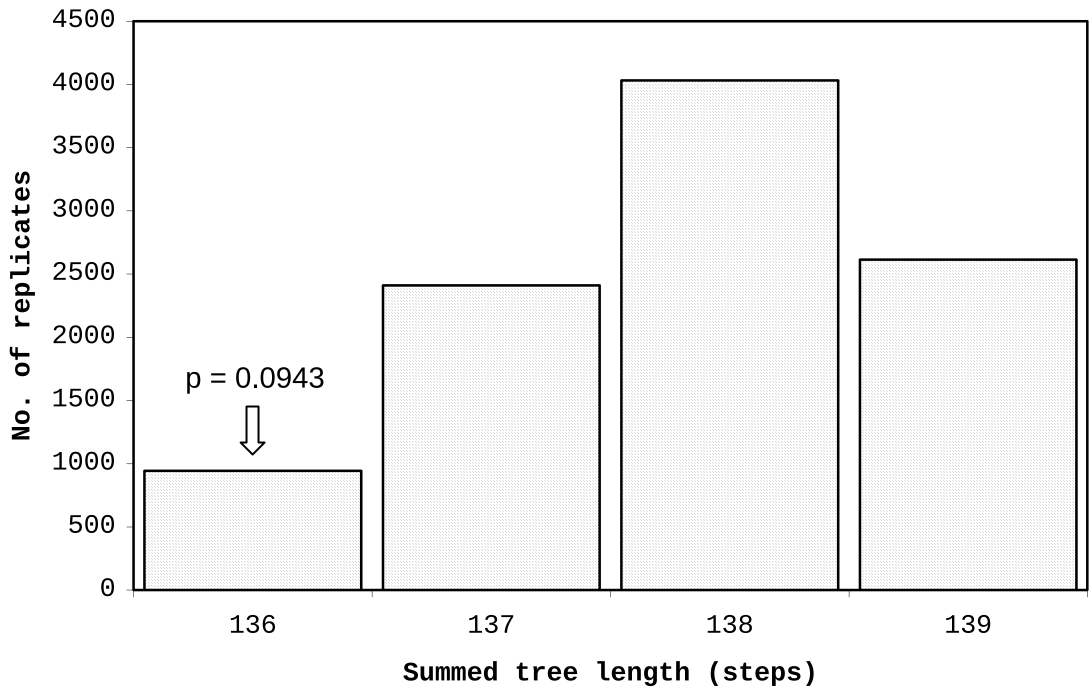

FIGURE 5-3. Results of Partition Homogeneity Test for combined benA and ITS sequence data for *P. brevicompactum*. Bars show the distribution of the total summed branch lengths of 10,000 trees generated from data sampled randomly across partitioned gene sequences (benA and ITS) using PAUP* 4.0b4a (Swofford, 1999). Summed branch length for the observed MPT is indicated by the arrow.

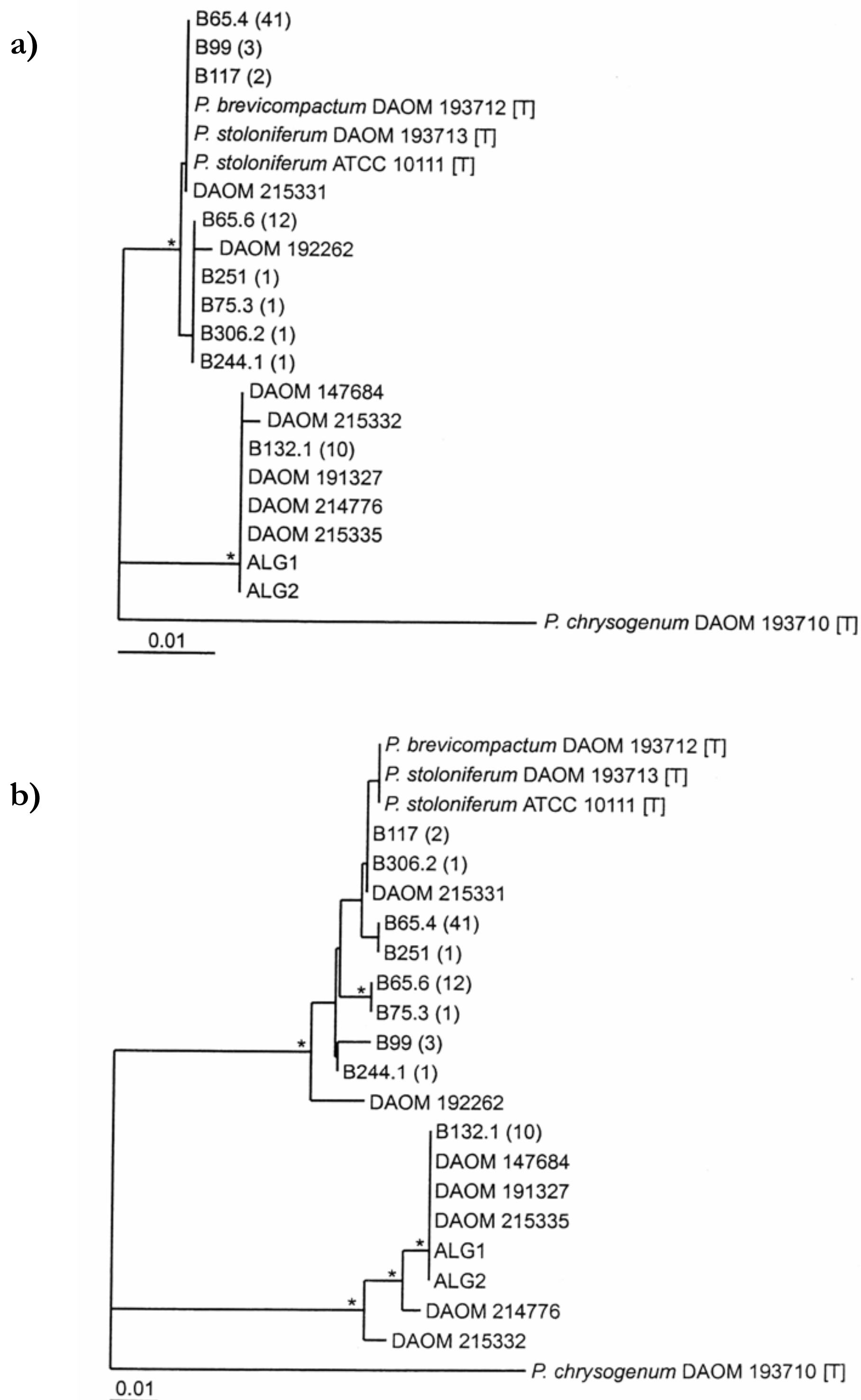

FIGURE 5-4A, B: Neighbour-Joining trees of *Penicillium brevicompactum* isolates based on a) ITS dataset, and b) Bt2 dataset, rooted to the authentic strain of *P. chrysogenum* (DAOM 193710 T). Asterisks indicate bootstrap support greater than 90% based on 1000 replications.

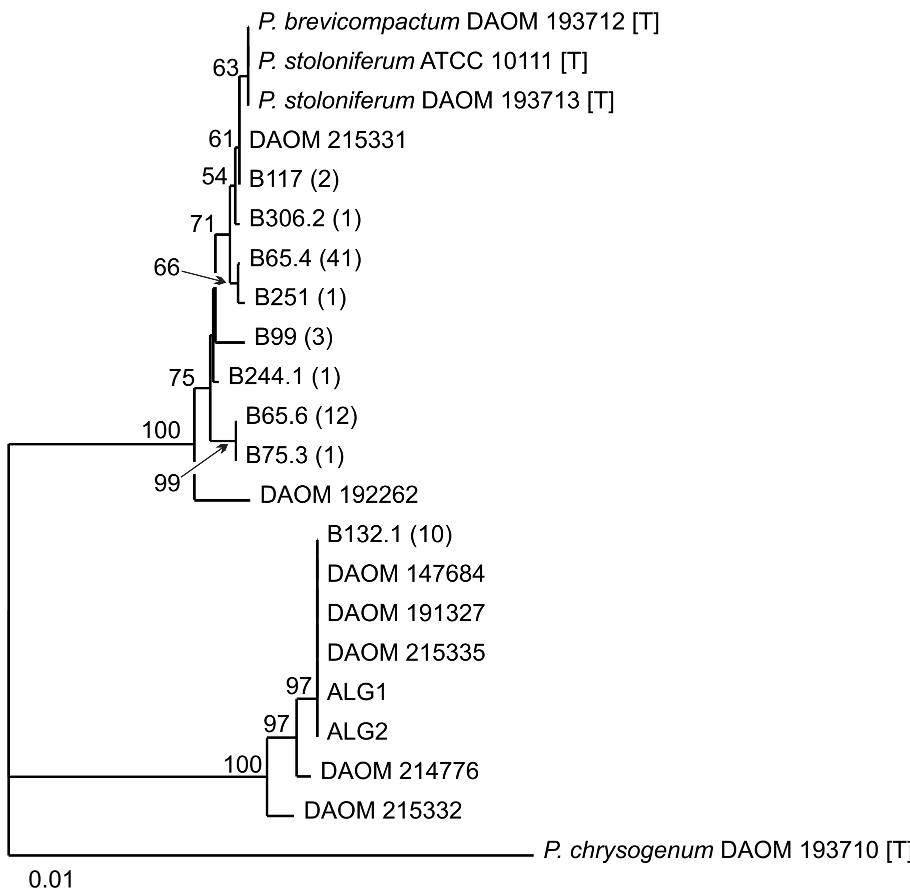

FIGURE 5-4C. Neighbour-Joining tree to *Penicillium brevicompactum* isolates based on combined ITS-benA data rooted to the authentic strain of *P. chrysogenum* (DAOM 193710 T). Asterisks indicate bootstrap support greater than 90% based on 1000 replications.

stoloniferum as well as 62 of the Wallaceburg house dust isolates and two DAOM strains (DAOM 192262 from urea formaldehyde foam insulation in Ottawa and DAOM 215331 from spruce lumber in Quebec). The synonymy of the *P. stoloniferum* with *P. brevicompactum* proposed initially by Pitt (1979) is supported. Within this clade, the house dust isolates clustered centrally, showing less than 1 % genetic distance between any pair of isolates. Isolate DAOM 215331 (*ex Picea* lumber, Quebec) was closest to B117, B306.2, B65.4, B251, B99 and B244.1, respectively, comprising 68 % of the isolates obtained from Wallaceburg. Sister to this group was a well supported clade containing 18 % of Wallaceburg strains represented by B65.6 and B75.3. Isolate DAOM 192262 (*ex* UFFI, Ottawa) was at the base of Clade 1 on a well-supported branch.

Clade 2 contained the remaining Wallaceburg house dust isolates (14 %) represented by B132.1 that clustered on a well-supported branch with 5 voucher collections (DAOM 147684, DAOM 191327, DAOM 215335, AlG1 and ALG2), 4 of which were obtained from decaying macrofungi. Sister to this cluster was DAOM 214776, an isolate obtained from a decaying mushroom in Denmark. Isolate DAOM 215332 from spruce lumber in Quebec was at the base of clade 2 on a well-supported branch.

Following the elimination of sequences of voucher strains from the combined gene dataset, a parsimony analysis was conducted using PAUP*. Sequences of authentic strains were retained in this analysis. This reduced dataset yielded 29 parsimony informative characters and produced 20 MTPs of 139 steps in length. A strict consensus tree produced from the 20 MPTs is shown in Figure 5-5 (L = 141 ,CI = 0.9433, RI = 0.8182, RC = 0.7718). Branch support is shown as the percentage of trees showing a particular branch in 1000 bootstrap replications. The branching

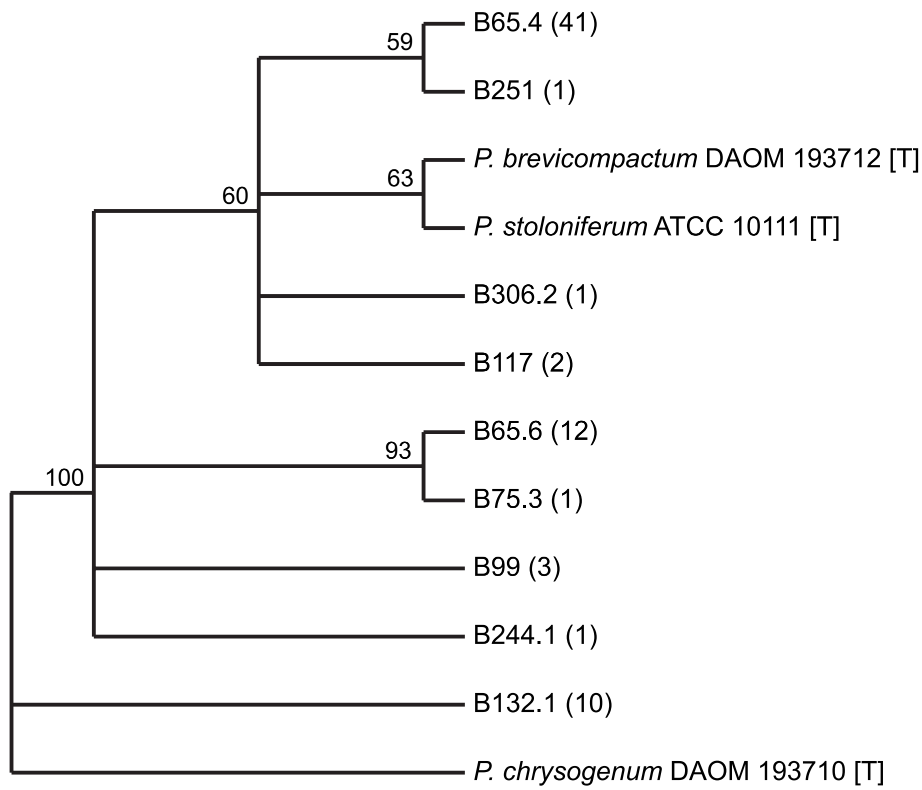

FIGURE 5-5. Strict consensus tree of 20 MPTs for *Penicillium brevicompactum* isolates based on combined ITS-benA data rooted to the authentic strain of *P. chrysogenum* (DAOM 193710 T). Bootstrap values based on 1000 replications are indicated for branches that demonstrated over 50% bootstrap support.

topology of this tree is not in conflict with the distance tree shown in Figure 5-4 and shows strong support for the same clades of indoor isolates resolved by the latter.

SPATIAL DISTRIBUTION

A graphical summary of the distribution of isolate genotypes according to the proximity of source houses is shown in Figure 5-6. The only trend that is clearly evident is the disproportionate observation of clade 2-type isolates from rural locations (constrained at the base of the dendrogram). Eight percent of the houses sampled were from rural locations and accounted for one quarter of all isolates of the species examined. However, rural isolations provided half of all clade 2 genotypes. Overall, isolates with this genotype accounted for 9 % of urban isolates and 28 % of rural isolates.

DISCUSSION

As methods of DNA sequencing improve and associated costs decrease, there has been a growing trend to infer phylogenies based on the analysis of multiple rather than single molecular datasets. Thus, approaches to analysing multiple datasets have received much recent discussion. Huelsenbeck and co-workers (1996) summarized and compared three fundamental strategies for dealing with multiple datasets: 1) Total evidence approach; 2) Separate Analysis and 3) Conditional Combination. The Total Evidence approach follows the assertion of Kluge (1989) that the inclusion of all available taxa (including both extant and extinct taxa) and all available characters favours convergence on the correct phylogenetic tree. Critics have argued that the demonstration of conditions under which parsimony fails to yield the correct branch topology given every informative character (*viz* Bull et al., 1993) counterindicates this approach (Huelsenbeck and Hillis, 1993). Miyamoto and Fitch (1995) advocated Separate Analysis of

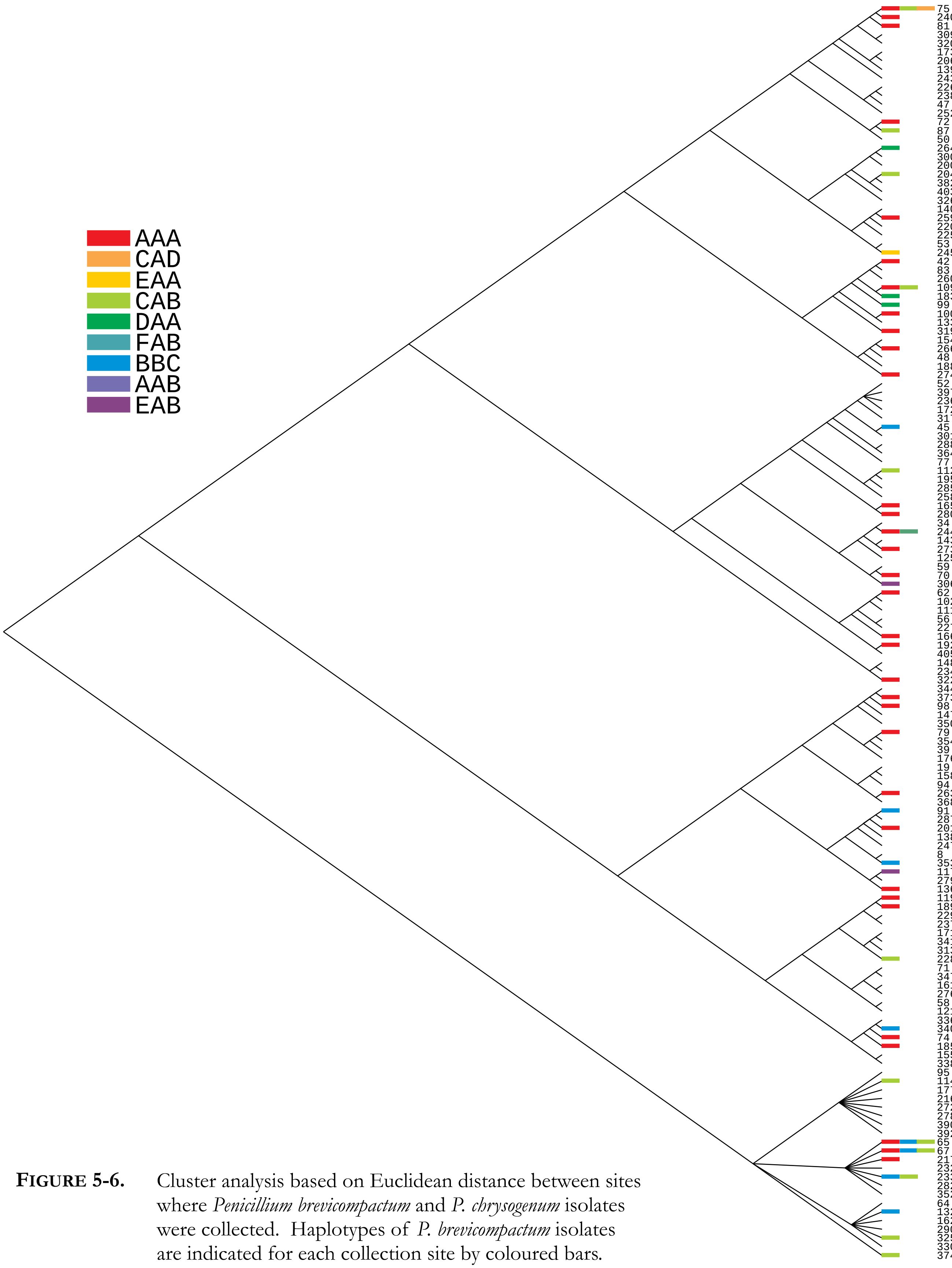

FIGURE 5-6. Cluster analysis based on Euclidean distance between sites where *Penicillium brevicompactum* and *P. chrysogenum* isolates were collected. Haplotypes of *P. brevicompactum* isolates are indicated for each collection site by coloured bars.

multiple datasets, citing that the loss of independence of characters resulting from the combined analysis of multiple datasets weakens statistical support for phylogenetic inference. In contrast, these authors favoured multiple independent confirmation of phylogeny based upon the analysis of data partitions separately as a means to enhance accuracy and lend statistical support to the inferred pattern of descent. Several authors have proposed a middle-ground compromise to these conflicting viewpoints, offering that independent datsets may by analysed in combination when the data partitions can be shown to be congruent (Bull et al., 1993; Huelsenbeck et al., 1996; de Queiroz, 1993; Rodrigo et al., 1993). This approach of "Conditional Combination" mandates the prior demonstration of homogeneity of partitions. One favoured method to test sequence congruence has been the Partition Homogeneity test (PHT) (*viz* PAUP* software package by Swofford) also known as the Incongruence Length Difference (ILD) (*viz* Farris et al., 1995) test, whereby separate datasets are randomly resampled across partitions without replacement, and these resampled data are used to generate trees by parsimony analysis. The sum of the branch lengths of the "best" tree obtained without resampling is then compared to the distribution of the sums of branch lengths taken from a set of trees inferred from randomly resampled data. These sums should be similar where datasets are congruent (the null hypothesis), and differ under incongruence (*see* Farris et al., 1995). This test is used widely to test congruence of partitioned datasets and has shown superior performance relative to other statistical tests used for this purpose (Cunningham, 1997). Barker and Lutzoni (2000), however, noted that the ILD test was susceptible to rejecting the null hypothesis of congruence erroneously when data partitions showed differing levels of homoplasy. This problem was similarly noted by Carbone and co-workers (1999). The PHT has been employed in the present study as a test of congruence of sequence data prior to combined analysis. However, the reader is cautioned that spurious rejection of partition homogeneity may be an issue.

The present study concerns *Penicillium brevicompactum*, which is a common colonist of water damaged indoor substrates, particularly drywall (Scott et al., 1999a; *also see* pg. 194). This species is also known from a number of outdoor substrates including decomposing fruiting bodies of macrofungi and other decaying organic matter (Pitt, 1979). However *P. brevicompactum* is poorly represented in outdoor air. Scott and colleagues (1999a) proposed that the differential removal of larger-spored fungi by mechanical and filtration effects (e.g. vacuum cleaning and elutriation in air conveyance systems), and the lengthy spore viabilities characteristic of anamorphs of the Trichocomaceae play a significant role in the artifactual concentration of propagules of these microfungi in indoor environments.

The present study identified two distinct lineages within *P. brevicompactum* (clades 1 & 2). Isolates from Clade 1 were distributed throughout the set of houses sampled, whereas Clade 2 isolates showed an increased prevalence in rural localities. Voucher isolates included in sequencing studies that clustered in Clade 2 demonstrated a substrate preference for decaying fungal fruit bodies. It is clear that the name *P. brevicompactum* applies to taxa included in Clade 1; however, based on the authentic isolates included in this study, there does not appear to be an available name for taxa in Clade 2. Seifert and Frisvad (2000) studied *Penicillium* species on solid wood products and reported two discrete micromorphologies for isolates of *P. brevicompactum*. In particular, certain *P. brevicompactum* isolates showed predominantly biverticillate branching and strongly apically inflated metulae in fresh cultures. These authors suggested that these cultural variants may represent distinct taxa. It is of interest to assess the use of these characters in separating the genetic lineages revealed in the present study. Furthermore, the genotypic markers employed in this study may help to elucidate Seifert and Frisvad's (2000) observation.

PENICILLIUM STOLONIFERUM

Thom (1910) described *Penicillium stoloniferum* based on an isolate obtained from a decaying mushroom in Connecticut. This species was reduced to synonymy with *P. brevicompactum* by Thom (1930) but later included in the *P. brevicompactum* series by Raper and Thom (1949), which included *P. brevicompactum*, *P. stoloniferum* and *P. paxilli*. Pitt (1979) suggested that isolates *P. stoloniferum* and *P. brevicompactum* showed a continuum of variation, and once again reduced *P. stoloniferum* to synonymy with *P. brevicompactum*. This synonymy is supported by the present study.

PENICILLIUM PAXILLI

The third species included by Raper and Thom (1949) in the *P. brevicompactum* series, *P. paxilli*, was described by Bainier (1907) from an isolate obtained from banana cultivated in the Paris Botanical Garden. This species was accepted by Thom (1930) and further characterized by Raper and Thom (1949) based on an isolate obtained from optical glass in Panama (NRRL 2008) due to the unavailability of authentic material. Pitt (1979) neotypified *P. paxilli* using this isolate (as Herb. IMI 40226), and noted morphological similarity of *P. paxilli* to isolates of *P. brevicompactum* in the production of apically inflated metulae. However, he justified the placement of *P. paxilli* in subgenus *Furcatum* based on the absence of rami in this taxon (Pitt, 1979), later noting that branching variation present in some isolates of *P. paxilli* might indicate the existence of two distinct species (Pitt, 1985). It is likely that the current concept of *P. paxilli* is inconsistent with *P. paxilli sensu* Bainier (1907) based on the dissimilarity of the habitat from which the neotype was obtained. In the present study, *P. paxilli* (NRRL 2008 T) clustered with the type strain of *P. sumatrense* (NRRL 779 T) on a well-supported branch that was sister to the clade that included ex-type strains of the divaricate taxa *P. canescens* (NRRL 2147 T), *P. waksmanii*

(NRRL 777 T) and *P. miczynskii* (NRRL 1077 T), the furcated taxon *Eu. shearii* (NRRL 715 T) and the monoverticillate taxon *P. roseopurpureum* (NRRL 2064 T) (*see* Chapter 4, Figure 4-6). This clade was distantly separated from the clade that included terverticillate taxa, the closest relatives of the *P. brevicompactum* group (*see* Figure 4-8). Despite some similarity in appearance of *P. paxilli* to the *P. brevicompactum* group, the former taxon is only distantly related. Nevertheless, it is possible that the recognition of a second species within the current circumscription of *P. paxilli* as suggested by Pitt (1985) may redistribute some isolates currently treated under this name to the *P. brevicompactum* group. However, the elucidation of this problem awaits the molecular characterization of multiple isolates of *P. paxilli*, including representatives from the originally described habitat (i.e. cultivated bananas).

AFFILIATIONS OF *P. BREVICOMPACTUM*

During the First International *Penicillium* and *Aspergillus* Workshop (PAW-I) Williams and colleagues (1985) postulated that *P. brevicompactum* was derived from *P. aurantiogriseum* and that it represented a central evolutionarily lineage in the terverticillates. These authors depicted *P. brevicompactum* as a penultimate evolutionary step between *P. aurantiogriseum* (basal) and *P. olsonii* (derived) in a "nested trumpet" diagram (Williams et al., 1985). In discussion that followed the presentation of this paper, Samson (1985) further suggested that the immediate ancestor of *P. brevicompactum* may be *P. chrysogenum*. Neither of these hypotheses is supported by the present study. As shown in the ITS-based phylogeny presented in Chapter 4, isolates of *P. brevicompactum* including the ex-type of this species formed a basal clade that was sister to the terverticillate Penicillia (Figure 4-8), although bootstrap support for this branch was weak.

Ironically, the placement of *P. olsonii* by Williams and co-workers (1985) is in agreement with the position of this taxon inferred from the present molecular phylogeny based on ITS sequence (*see* Chapter 4, Figure 4-8). The type strain of *Penicillium olsonii* Bainier and Sartory (CBS 232.32 T) was situated on a long, weakly-supported branch that was sister to the type strain of *P. echinulatum* (NRRL 1151 T). In turn, this clade was basal to the clade that included the type strains of *P. aurantiogriseum* (NRRL 971 T), *P. polonicum* (NRRL 995 T) and *P. viridicatum* (NRRL 958 T). This inferred phylogeny suggests that *P. brevicompactum* (= *P. stoloniferum*) and *P. olsonii* represent distantly-related lineages which show convergent evolution of characters such as variously apically inflated metulae and compact, fan-shaped penicilli. Similarly, the elongated stipes reported from *P. stoloniferum* are reminiscent of those produced by *P. olsonii*. At present, however, I cannot exclude the possibility that the type strain of *P. olsonii* (CBS 232.32) included in this phylogeny was a specious isolate. As such, confirmation of this sequence using collections of the type strain from other culture collections is required to establish the proper phylogenetic position of *P. olsonii*.

CONCLUSIONS

Penicillium brevicompactum as presently circumscribed consists of at least two lineages which may represent distinct species. One of these lineages, *P. brevicompactum* sensu stricto occurred commonly in broadloom dust in houses in southern Ontario. Members of the second lineage tended to occur predominantly as saprotrophs on the decaying fruit bodies of fleshy fungi, and were isolated rarely from indoor dust samples.

CHAPTER 6. ASSESSMENT OF GENETIC VARIATION IN INDOOR ISOLATES OF *PENICILLIUM CHRYSOGENUM*[9]

ABSTRACT

Isolates of *Penicillium chrysogenum* were examined from 369 houses in Wallaceburg, Ontario, Canada. In total, approximately 700 isolates of *P. chrysogenum* were obtained by serial dilution plating of broadloom dust samples, and identified based on standard criteria. From this collection, a subset of 198 isolates representing 109 houses was selected for genetic characterization based upon micromorphological and physiological uniformity on several carbon and nitrogen sources.

Multiple genetic loci spanning introns in structural and metabolic genes such as thioredoxin reductase (trxB), beta-tubulin (benA) and acetyl co-enzyme A synthase (acuA), as well as the internal transcribed spacer regions of the non-coding nuclear ribosomal sub-repeat (rDNA, ITS1-2) were compared using heteroduplex mobility assay. In this method, homologous PCR amplicons were pooled pairwise in equimolar proportion, thermally denatured and reannealed. Dissimilar amplicon pairs were resolved by the slower electrophoretic migration of heteroduplexed dsDNAs relative to homoduplexes on low-crosslinked polyacrylamide-agarose hybrid gels into which glycerol was incorporated as a mild denaturant.

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[9] Parts of this work were presented as an invited symposium contribution at the IX International Congress of Mycology in Sydney, Australia, August 1999, as Scott, J.A., Straus, N. and Malloch, D. 1999. Molecular genetic characterization of variability in *Penicillium chrysogenum* from indoor environments. MOS5.6, IX International Union of Microbiological Societies (IUMS) Abstracts Book, p. 185.

Five unique multilocus haplotypes were revealed with no evidence of recombination, indicating clonal propagation. Two major genotypes were observed, which dominated the houses sampled, accounting for 88.6 % and 5.4 % of the sample, respectively. Three other multilocus motifs were observed at low frequency in several houses from which multiple isolates were obtained. Base sequencing of representatives of all groupings, including ex-type strains of *P. chrysogenum* and *P. notatum*, suggested that *P. chrysogenum* as currently circumscribed comprises three strongly supported lineages. Both ex-type strains clustered with the secondary genotype (7% of dust isolates), while the un-named, primary genotype (90%) included the notable laboratory contaminant isolated by Alexander Fleming in 1929. No nomenclatural types included in the present study clustered within the minor clade (4%).

The groups defined using the heteroduplex method were supported by three separate DNA fingerprinting methods: Two randomly amplified polymorphic DNA-type (RAPD) techniques using either the M13 core sequence or $(GACA)_4$ as a single primer; and a third method employing a primer pair of arbitrary sequence.

Extensive sampling of outdoor air in the study locality during the late summer 1995 failed to reveal *P. chrysogenum*. Outdoor air samples taken throughout the year at other localities in southern Ontario, Canada, have confirmed the rarity of this species complex in outdoor air.

INTRODUCTION

Viable fungal spores occur in great numbers in household dust and indoor air. A large proportion of these spores typically arise outdoors in the phylloplane and are propagated indoors by mechanical means (e.g. upon air currents and contaminated footwear). In contrast, the genera *Aspergillus* and *Penicillium* are among the most common indoor fungi, yet these moulds are relatively poorly represented in outdoor air. Thus, it is widely believed that they proliferate indoors, often cryptically, on various substrates including dust itself under conditions of low water activity.

Penicillium chrysogenum Thom is perhaps the most common of all Penicillia (Pitt, 1980; Raper and Thom, 1949), occurring as an agent of food spoilage (Samson et al., 1996) as well as a resident of household dust (Davies, 1960) and indoor air. *Penicillium chrysogenum* is also a well-known contaminant of damp building materials (Chang et al., 1995; Gravesen, 1999; Hunter and Lea, 1995) and indoor finishes (Adan and Samson, 1994). This species is one of the few terverticillate Penicillia that typically does not produce mycotoxins with significant mammalian toxicity (Dillon et al., 1996; Nielsen and Gravesen, 1999; Pitt and Cruikshank, 1990). However, *P. chrysogenum* has been identified as a significant allergen in the indoor environment (Cooley, 1999; Cooley et al., 1999; Fergusson et al., 1984) and as a rare causative agent of opportunistic human mycosis (Eschete et al., 1981; Hoffman et al., 1992).

Little is known about the distribution and variability of the *P. chrysogenum* group. Samson and co-workers (1977) applied a broad taxonomic interpretation of the variability they observed in this group, and elected to synonymize a number of later names with *P. chrysogenum*. *Penicillium chrysogenum* is thought to be a strictly asexual species, since no teleomorph has been identified. The putatively clonal nature of *P. chrysogenum* as well as its circumscription and the validity of proposed synonyms remains to be tested using modern molecular means. The present study will examine the extent of clonality within a core group of isolates from the *P. chrysogenum* group including representative authentic isolates, and test the suitability of current species concepts.

MATERIALS AND METHODS

ISOLATION AND IDENTIFICATION OF STRAINS

Over seven hundred isolates of *P. chrysogenum* were collected from 376 houses in Wallaceburg, Ontario, as described in Chapter 4. These isolates were grown for 14 days at room temperature on modified Leonian's agar (Malloch, 1981) and modified Creatine-Sucrose agar medium (Frisvad, 1993). A duplicate plate of each isolate was incubated at 37°C for 7 days. Based on the results of this preliminary examination, a subset of 198 micromorphologically and physiologically uniform isolates was selected for genetic characterization. Air sampling was conducted at 18 outdoor locations distributed evenly throughout the Wallaceburg study site during late summer, 1995, using a Reuter Centrifugal sampler (RCS) on Rose Bengal agar medium with a sampling volume of 80 L per sample. Colonies were incubated and identified as above.

The spatial relationship of participant houses is shown in Figure 6-1, in which houses are identified by arbitrary "house numbers" to protect occupant privacy. Sources of house dust isolates are summarized in Table 6-1, including houses from which multiple isolates were obtained. The observed condition of the house with respect to obvious mould damage at the time of site inspection is indicated. The number assigned to each fungal isolate is unique, and consists of the "house number" coupled with an incremental accession number reflective of the total number of isolates of *P. chrysogenum* obtained from that house.

Additional isolates included in sequencing studies consisted of authentic strains as well as a geographical range of voucher material (*see* Table 6-2).

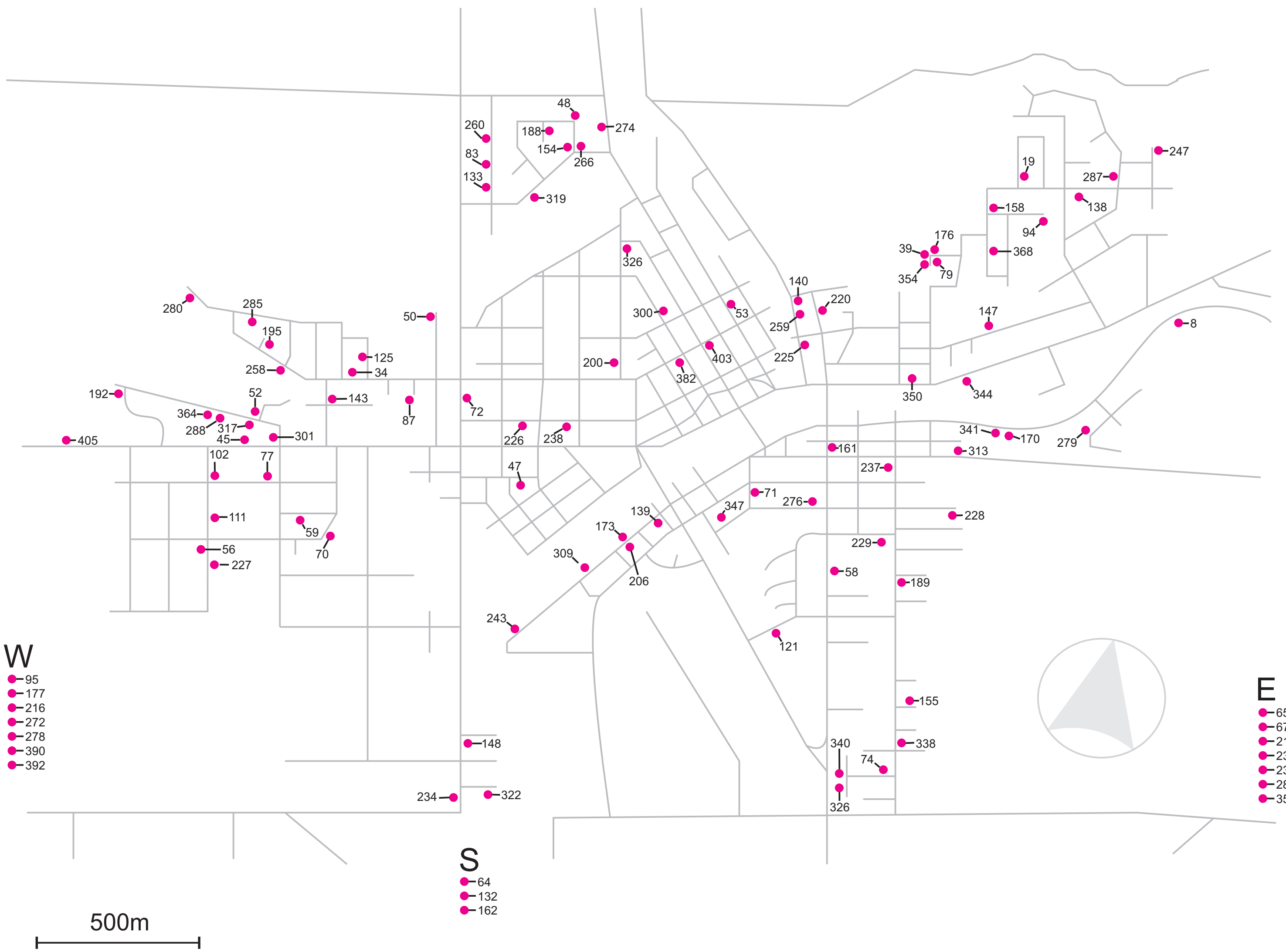

FIGURE 6-1. Street map of Wallaceburg, Ontario, indicating collection sites for *Penicillium chrysogenum* isolates used in this study.

Table 6-1: Sources of house dust isolates used in this study

House No.	No. of isolates	House No.	No. of isolates	House No.	No. of isolates
8	9	*** 154**	**2**	278	1
19	2	155	1	279	1
*** 34**	**2**	158	1	280	1
39	2	161	1	282	1
*** 45**	**5**	162	1	285	1
47	1	172	1	287	1
*** 48**	**5**	173	1	288	1
50	5	176	1	290	1
52	2	*** 177**	**3**	300	1
53	1	188	1	301	1
56	3	189	1	309	1
58	10	192	1	313	2
59	1	195	1	317	2
64	2	200	1	319	1
67	1	*** 206**	**1**	320	1
70	6	*** 216**	**1**	322	1
71	2	217	1	326	3
72	3	220	1	330	1
74	2	225	23	336	1
77	2	226	1	338	1
79	1	227	2	340	1
83	1	228	2	341	1
87	7	229	1	344	1
94	1	232	2	347	1
95	1	234	1	350	1
*** 102**	**1**	237	1	352	1
*** 111**	**1**	238	1	354	2
121	1	239	1	364	1
125	1	243	1	368	1
*** 132**	**1**	*** 247**	**1**	382	1
133	1	258	2	390	1
138	1	259	1	392	1
139	3	260	1	397	1
140	1	266	1	403	1
143	1	272	1	405	2
147	1	274	1		
148	1	*** 276**	**1**		

*****Houses showed visible mould growth on interior surfaces

Table 6-2: List of culture collection strains used in this study

Strain number	Identification	Status	Substratum
ATCC 10108	*Penicillium notatum* Westling	ex-type	branches of *Hyssopus* sp., Norway
CBS 484.84	*P. aethiopicum* Frisvad	ex-type	grains of *Hordeum vulgare*, Ethiopia
DAOM 155627	*P. chrysogenum* Thom		paper, Ottawa, Ontario
DAOM 155628	*P. chrysogenum* Thom		paper, Ottawa, Ontario
DAOM 155631	*P. chrysogenum* Thom		paper, Ottawa, Ontario
DAOM 167036	*P. chrysogenum* Thom		*Picea* forest soil, Quebec
DAOM 171025	*P. chrysogenum* Thom		salami, Ottawa, Ontario
DAOM 175157	*P. chrysogenum* Thom		walls of mouldy house, Niagara Falls, Ontario
DAOM 175176	*P. chrysogenum* Thom		*Lycopersicum esculentum* leaves, Prince Edward Island
DAOM 175758	*P. chrysogenum* Thom		office building, Quebec
DAOM 178623	*P. chrysogenum* Thom		*substr. et loc. incerta*
DAOM 190864	*P. chrysogenum* Thom		grains of *Hordeum*, Manitoba
DAOM 193710	*P. chrysogenum* Thom	ex-type	cheese, Connecticut, USA
DAOM 212031	*P. chrysogenum* Thom		wooden wall studs, Alberta
DAOM 215336	*P. chrysogenum* Thom		wooden wall studs, Alberta
DAOM 215337	*P. chrysogenum* Thom		hemlock lumber, British Columbia
DAOM 216700	*P. chrysogenum* Thom		grains of *Hordeum*, Canada
DAOM 216701	*P. chrysogenum* Thom		*Sesamum indicum*, Korea
DAOM 59494C	*P. chrysogenum* Thom		*substr. incert.*, Honduras
NRRL 13485	*P. dipodomyis* (Frisvad, Filtenborg & Wicklow) Banke, Frisvad & Rosendahl	ex-type	cheek pouch of *Dipodomyis spectabilis*, Arizona, USA
NRRL 13487	*P. dipodomyicola* (Frisvad, Filtenborg & Wicklow) Frisvad	ex-type	cheek pouch of *Dipodomyis spectabilis*, Arizona, USA
NRRL 824	*P. chrysogenum* Thom	Fleming strain	laboratory contaminant, London, England
NRRL 911	*P. nalgiovense* Laxa	ex-type	cheese, Nalzovy, Czech Republic

DNA PREPARATION AND HETERODUPLEX ANALYSIS

DNA isolation, PCR and preparation of DNA heteroduplexes were performed according to the methods described in Chapter 4. Four polymorphic loci consisting of partial regions spanning introns in the genes encoding acetyl co-enzyme A synthase (acuA), beta-tubulin (benA), thioredoxin reductase (trxB) and the region spanning the internal transcribed spacers (ITS1 to ITS2) of nuclear ribosomal DNA (rDNA) were PCR-amplified using the primer sequences given in Table 6-3, employing the methods described in Chapter 4. Figure 6-2 shows the locations of primers used for PCR amplification and sequencing. Heteroduplexing reactions were set up in the manner described in Chapter 4, whereby isolates with adjacent numbers were pooled, pairwise in overlapped combinations, so as to encompass the entire set. Subsequent rounds of heteroduplexing were performed in which distinctive isolates were compared until the entire collection was completely characterized.

Electrophoresis and imaging of HMA reactions was conducted using the vertical method of electrophoresis described in Chapter 4.

PCR FINGERPRINTING[10]

A subset of 40 isolates including representation of all observed multilocus haplotypes was selected for fingerprinting analysis. All minor multilocus haplotypes were included, and representative major haplotypes were randomly selected for inclusion. Two oligonucleotides, $(GACA)_4$, and the core sequence of the wild-type phage M13 (5'-GAG GGT GGC GGT TTG T-3'), both minisatellite-specific primers were used as single primers in a PCR containing 25 ng

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[10] This work was conducted as a collaboration with Dr. Wieland Meyer, Department of Medicine, University of Sydney, Australia

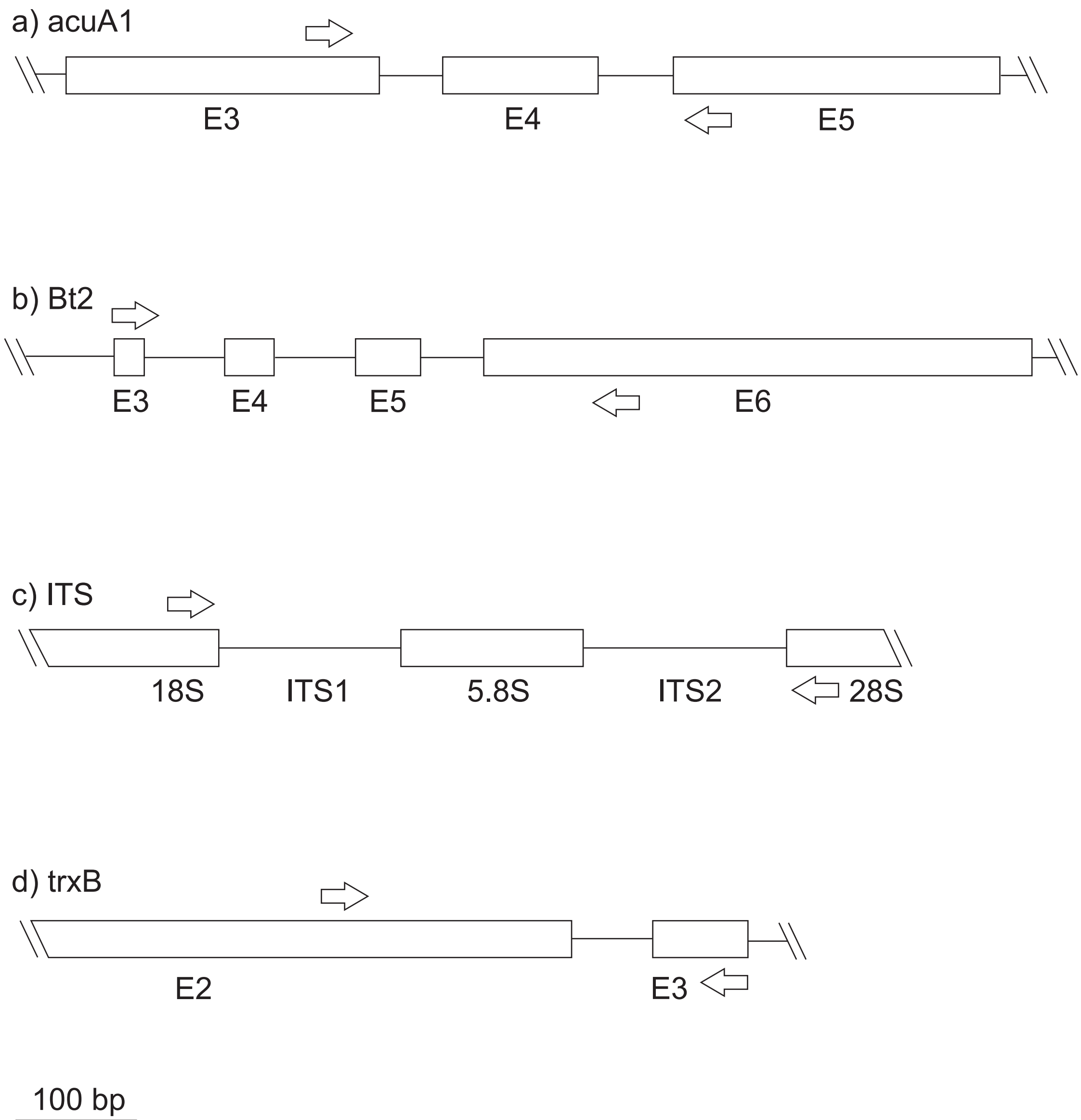

FIGURE 6-2. Locations of primers used to amplify polymorphic regions in *P. chrysogenum* in this study.

Table 6-3: Primers sequences employed in this study

Acetyl-CoA synthetase (acuA)		
Source:	Genbank L09598, +2102 - 2452, spanning introns 3 & 4	
Fwd primer 5'-3':	ACC GTG TGG GGT GCC CAC AAG CGT TAC ATG	(acuA-2F)
Rvs primer 5'-3':	GGT CAG CTC GTC GGC AAT ACC AAC GAC AGC	(acuA-1R)
Beta-tubulin (benA)		
Source:	Glass & Donaldson, 1995	
Fwd primer 5'-3':	GGT AAC CAA ATC GGT GCT GCT TTC	(Bt2a)
Rvs primer 5'-3':	ACC CTC AGT GTA GTG ACC CTT GGC	(Bt2b)
Nuclear rDNA ITS regions		
Source:	White et al., 1990, fwd; Untereiner et al., 1995, rvs	
Fwd primer 5'-3':	GGA AGT AAA AGT CGT AAC AAG G	(ITS5)
Rvs primer 5'-3':	TAT GCT TAA GTT CAG CGG	(WNL1)
Thioredoxin reductase (trxB)		
Source:	EMBL X76119, +801 - 1153, spanning intron 2	
Fwd primer 5'-3':	AAC GCG GAG GAG GTC GTT GAG GCT AAC GGT	(trxB-1F)
Rvs primer 5'-3':	TTA GAG CAC AGG CTT TGC CTC CTG GTG AGT	(trxB-1R)

template, 250 μM each of dATP, dCTP, dGTP, dTTP, 300 μM magnesium acetate, 150 μM magnesium chloride, 5 mM potassium chloride, 1mM Tris-HCl pH 8.3, 200 μM primer and 1 unit of AmpliTaq (Perkin Elmer Corp.), brought to a total volume of 50 μL with sterile deionized water, overlaid with one drop of sterile, light mineral oil. Reactions were submitted to 35 cycles of the following thermal incubation: 94 °C for 20 sec denaturation, 50 °C for 1 min annealing, 72 °C for 20 sec extension, with a final extension of 6 min at 72 °C.

Products of PCR were electrophoresed on a 1.4 % agarose gel (containing 1x TBE [10.8 g/L Tris-base, 5.5 g/L boric acid, 2mM EDTA pH 8.0] with 200 μg/L ethidium bromide), in 1x TBE at a field strength of 2 V/cm, and visualized by ultraviolet light transillumination at 302 nm. A 1 kbp DNA ladder (Pharmacia) was loaded in several lanes for reference. This method follows the protocol described by Weising and co-workers (1995).

RANDOM PRIMER-PAIR FINGERPRINTING[11]

The random-sequence oligonucleotides 5SOR (5'-ATG GGA ATA CGA CGT GCT GTA A-3') and MYC1 (5'-GAG GAA GGT GGG GAT GAC GT-3') were used as a primer pair in a PCR containing 10 ng template, 200 μM each of dATP, dCTP, dGTP, dTTP, 200 mM ammonium sulphate, 15 mM magnesium chloride, 5 mM potassium chloride, 750mM Tris-HCl pH 8.8, 5 pM of each primer and 1 unit of Taq DNA polymerase (Advanced Biotechnology, Surrey, UK), 0.1 % Tween 20 brought to a total volume of 25 μL with sterile deionized water, and overlaid with one drop of sterile, light mineral oil. Following an initial denaturation of 3 min at 93 °C, reactions were submitted to 10 initial cycles of the following low-stringency thermal incubation:

[11] This work was conducted as a collaboration with Dr. Wieland Meyer, Department of Medicine, University of Sydney, Australia

93 °C for 1 min denaturation, 35 °C for 1 min annealing, 72 °C for 1 min extension, with a final extension of 6 min at 72 °C; this profile was followed by 20 cycles of high stringency thermal incubation: 1 min denaturation at 93 °C, 1 min annealing at 55 °C and an extension of 1 min at 72 °C.

Following PCR, products were electrophoresed on a 10 % polyacrylamide gel (1x TBE [10.8 g/L Tris-base, 5.5 g/L boric acid, 2mM EDTA pH 8.0] polymerised by free-radical method by the addition of 0.7 % ammonium persulfate and catalysed by the addition of 6.6 mM TEMED) at a field strength of 10 V/cm in 1x TBE until the bromophenol dye from was 3 cm from the bottom of the gel. A *Hae*III restriction digest of the plasmid ΦX174 was used as a size marker. Gels were silver stained using a method modified from Bassam and Caetano-Anollés (*see* Weising et al., 1995) in a solution of 0.1 % silver nitrate and 0.07 % (w/w) formaldehyde for 30 min at room temperature. Following staining, gels were rinsed twice in distilled water and developed in a solution of 3 % sodium carbonate, 0.003 % sodium thiosulphate and 1.5 % formaldehyde. Development was stopped by the addition of 10 % acetic acid, prior to the drying of gels at 80 °C for 30 min on 3M Whatman paper. Gel bands were scored using the Gelcompar II software package (Applied Maths).

CLUSTER ANALYSIS

Cluster analyses of all fingerprinting data were analysed using the Neighbor-Joining method and outgrouped using *P. polonicum* and *P. thomii* (Wallaceburg isolates no. 170 and 236, respectively) (*see* Weising et al., 1995).

DNA SEQUENCING

PCR templates were purified using QIAquick PCR purification kit (Qiagen, Inc., Valencia, Calif.). PCR templates were sequenced using the Taq DyeDeoxy cycle sequencing kit (Applied Biosystems, Inc., Foster City, Calif.) and extension products were analysed on an ABI50 fluorescent automated sequencer (Applied Biosystems, Inc.). Sequences were determined on both sense and anti-sense strands using the same primers that were used for amplification (*see* Table 6-3).

SEQUENCE ANALYSIS

Alignments of all sequences were performed using Clustal X software package version 1.8 (*see* Jeannmougin et al., 1998; Thompson et al., 1997) and adjusted by visual inspection using a text editor. Phylogenetic analyses were carried out by the Neighbor-Joining method using Clustal X and PAUP* (PAUP* version 4.0b4a for 32 bit Microsoft Windows, Sinauer Associates, Inc., Sunderland, Massachusetts). In all cases, the data were re-sampled by 1000 bootstrap replicates and the proportion of Neighbor-Joining trees possessing each internal branch was indicated to express its level of support. *Penicillium dipodomyis* was selected as an outgroup taxon on the basis of the ITS phylogeny presented in Chapter 4, Figure 4-9.

Data for trxB were further analysed using the maximum parsimony method in PAUP*. Most-parsimonious trees (MPTs) were identified by exhaustive heuristic searches, upon which strict consensus tree were constructed.

Prior to combining sequence datasets, sequence alignments were analysed using the PHT within PAUP* to determine the congruence of sequences. Results of the PHT were reproduced graphically using Microsoft Excel, of the Microsoft Office 2000 software package (Microsoft Corp.). The limitations of the PHT are discussed in Chapter 5.

SPATIAL ANALYSIS

Euclidean distances between all possible pairs of participating Wallaceburg houses were calculated from transformed x-y coordinates of all properties as plotted on a scale street map, and compiled in a distance matrix. The Neighbor-Joining method was used to cluster the house numbers according to the Euclidean distances between locations using the "Neighbor" module of PHYLIP.

DENDROGRAM CONSTRUCTION

Dendrograms were generated using the TreeView software package, version 1.5.2 for 32 bit Microsoft Windows (Roderick Page, University of Glasgow), and formatted using Corel Draw version 8.232 (Corel Corporation).

RESULTS

Isolates of *P. chrysogenum* were obtained from 109 of the 369 houses examined (30 %). Seventeen of these houses were in rural locations (i.e. outside the town limits). No isolates of *Penicillium* were obtained from the 18 outdoor air samples taken in Wallaceburg.

HETERODUPLEX ANALYSIS

Multilocus genotypes identified by heteroduplex analysis for all loci are listed for all isolates in Table 6-4, and summarized in Table 6-5. The multilocus haplotype AAAA (acuA, bt2, ITS and trxB, respectively), represented by the isolate C8.12, was the most commonly observed

Table 6-4: Summary of haplotypes of *P. chrysogenum* isolates

Isolate	acuA	benA	ITS	trxB	**Isolate**	acuA	benA	ITS	trxB
8.1	A	A	A	A	**58.13**	A	A	A	A
8.4	A	A	A	A	**58.14**	A	A	A	A
8.8	A	A	A	A	**58.15**	A	C	B	C
8.12	A	A	A	A	**58.16**	A	A	A	A
8.14	A	A	A	A	**59.2**	A	A	A	A
8.16	A	A	A	A	**64.1**	A	A	A	A
8.18	A	C	B	C	**64.2**	A	A	A	A
8.19	A	A	A	A	**67.3**	B	B	B	B
8.24	B	B	B	B	**70.1**	A	A	A	A
19.2	A	A	A	A	**70.3**	B	B	B	B
19.3	A	A	A	A	**70.5**	A	A	A	A
34.4	B	B	B	B	**70.6**	A	A	A	A
34.10	A	A	A	A	**70.7**	A	A	A	A
39.1	A	A	A	A	**70**	A	A	A	A
39.4	A	A	A	A	**71.1**	C	B	B	B
45.2	A	A	A	A	**71.2**	A	A	A	A
45.3	A	A	A	A	**72.1**	B	B	B	B
45.5	A	A	A	A	**72.2**	B	B	B	B
45.6	A	A	A	A	**72.3**	A	A	A	A
45.7	A	A	A	A	**74.1***	D	D	D	D
47	B	B	B	B	**74.2**	A	A	A	A
48.2	A	A	A	A	**74.3**	A	A	A	A
48.3	A	A	A	A	**77.1**	A	A	A	A
48.8	A	A	A	A	**77.2**	A	C	B	C
48.11	A	A	A	A	**79**	A	A	A	A
48.12	A	A	A	A	**83**	A	A	A	A
50.3	A	A	A	A	**87.1**	A	A	A	A
50.5	A	A	A	A	**87.2**	A	A	A	A
50.7	A	A	A	A	**87.3**	A	A	A	A
50.9	A	A	A	A	**87.4**	A	A	A	A
50.10	A	A	A	A	**87.5**	A	A	A	A
52.1	A	A	A	A	**87.6**	A	A	A	A
52.2	A	A	A	A	**87.7**	A	A	A	A
53	A	A	A	A	**94**	B	B	B	B
56.3	A	A	A	A	**95**	A	A	A	A
56.4	A	A	A	A	**102**	A	A	A	A
56.5	A	A	A	A	**111**	A	A	A	A
58.3	A	A	A	A	**121.4**	A	A	A	A
58.4	A	A	A	A	**125**	A	A	A	A
58.7	B	B	B	B	**132**	A	A	A	A
58.8	A	A	A	A	**133**	A	A	A	A
58.11	A	A	A	A	**138**	A	A	A	A
58.12	A	A	A	A	**139.1**	A	A	A	A

Table 6-4: Summary of haplotypes of *P. chrysogenum* isolates

Isolate	acuA	benA	ITS	trxB	Isolate	acuA	benA	ITS	trxB
139.2	A	A	A	A	**225.19**	A	A	A	A
139.3	A	A	A	A	**225.20**	A	A	A	A
140.1	A	A	A	A	**225.22**	A	A	A	A
143	A	A	A	A	**225.23**	A	A	A	A
147	A	A	A	A	**225.25**	A	A	A	A
148	A	A	A	A	**225.26**	A	A	A	A
154.1	A	A	A	A	**225.30**	A	A	A	A
154.2	A	A	A	A	**225.31**	A	A	A	A
155	A	A	A	A	**226**	A	A	A	A
158.2	A	A	A	A	**227.1**	A	A	A	A
161	A	A	A	A	**227.2**	A	A	A	A
162	A	A	A	A	**228.2**	A	A	A	A
170*	D	D	D	D	**228.3**	A	A	A	A
172	A	A	A	A	**229.2**	A	A	A	A
173	A	A	A	A	**232.1**	B	B	B	B
176	A	A	A	A	**232.2**	B	B	B	B
177.1	A	A	A	A	**234**	A	A	A	A
177.2	A	A	A	A	**237.2**	A	A	A	A
177.3	A	A	A	A	**238**	C	B	B	B
188	A	A	A	A	**239**	A	A	A	A
189	A	A	A	A	**243**	A	A	A	A
192	A	A	A	A	**247**	A	A	A	A
195	A	A	A	A	**258.1**	A	A	A	A
200	A	C	C	C	**258.2**	A	A	A	A
206	A	A	A	A	**259**	A	A	A	A
216	A	A	A	A	**260**	A	A	A	A
217	A	A	A	A	**266**	A	A	A	A
220	A	A	A	A	**272**	A	A	A	A
225.2	A	A	A	A	**274**	A	A	A	A
225.3	A	A	A	A	**276.1**	A	A	A	A
225.4	A	A	A	A	**278**	A	A	A	A
225.5	A	A	A	A	**279.1**	A	A	A	A
225.6	A	A	A	A	**280.2**	A	A	A	A
225.7	A	A	A	A	**282**	A	A	A	A
225.8	A	A	A	A	**285**	A	A	A	A
225.9	A	A	A	A	**287**	A	A	A	A
225.10	A	A	A	A	**288**	A	A	A	A
225.12	A	A	A	A	**290**	A	A	A	A
225.13	A	A	A	A	**300**	A	A	A	A
225.14	A	A	A	A	**301.1**	A	A	A	A
225.15	A	A	A	A	**309**	A	A	A	A
225.16	A	A	A	A	**313.1**	A	A	A	A
225.18	A	A	A	A	**313.2**	A	A	A	A

Table 6-4: Summary of haplotypes of *P. chrysogenum* isolates

Isolate	acuA	benA	ITS	trxB	**Isolate**	acuA	benA	ITS	trxB
317.1	A	C	B	C	**347.1**	A	A	A	A
317.2	A	C	B	C	**350**	A	A	A	A
319	A	A	A	A	**352**	A	A	A	A
320	A	A	A	A	**354.1**	A	A	A	A
322	A	A	A	A	**354.2**	A	A	A	A
326.1	A	A	A	A	**364.1**	A	A	A	A
326.2	A	A	A	A	**368**	A	A	A	A
326.4	A	A	A	A	**382**	A	A	A	A
330.1	A	A	A	A	**390**	A	A	A	A
336.1	A	A	A	A	**392**	A	A	A	A
338	A	A	A	A	**397**	A	A	A	A
340	A	A	A	A	**403**	A	A	A	A
341	A	A	A	A	**405.1**	A	A	A	A
344.1	A	A	A	A	**405.2**	A	A	A	A

*isolates of *P. polonicum* included as reference

Table 6-5: Haplotype frequencies of *P. chrysogenum* isolates

Representative Isolate	LOCUS acuA	Bt2	ITS	trxB	Frequency
C8.12	A	A	A	A	0.904
C317.1	A	C	B	C	0.025
C8.24	B	B	B	B	0.056
C238	C	B	B	B	0.010
C200	A	C	C	C	0.005

multilocus haplotype in the population and comprised over 90 % of all isolates. The second most common multilocus haplotype, BBBB, accounted for 5.6 % of the isolates studied and is represented by isolate C8.24 (the same house as the representative isolate used for AAAA, above). Three other minor multilocus haplotypes (ACBC, ACCC & CBBB) comprised the remainder of the isolate set. One or more characteristic isolates for each multilocus haplotype were sequenced for phylogenetic analysis.

INDIVIDUAL DATA SETS

Distance trees for each of the four genetic loci, acuA, benA, ITS and trxB, are presented in Figures 6-3 to 6-6, respectively. Due to the lower degree of resolution in the ITS tree, it will be discussed separately. In the acuA, benA and trxB distance trees, the isolates were divided into two main groups. The first clade contained 179 or more of the 198 Wallaceburg isolates along with the strain of *P. chrysogenum* (as *P. notatum*) isolated in 1929 by Alexander Fleming (NRRL 824), and 11 DAOM voucher strains. This clade was supported by bootstrap values of 99 % or greater, and was dominated by the AAAA multilocus haplotype.

The second major clade was characterized by 13 Wallaceburg strains (11 with the multilocus genotype BBBB as determined by heteroduplex analyses, *see* Table 6-5), as well as the ex-type strains of *P. chrysogenum* (DAOM 193710) and *P. notatum* (ATCC 10108).

Several isolates showed re-assortment between acuA, benA and trxB trees. Notably, 6 isolates represented by C200 and C317.1 clustered in the first clade in the acuA tree, but were sister to the second clade in the benA and trxB trees (*see* Figures 6-3, 6-4 and 6-6). In addition, two

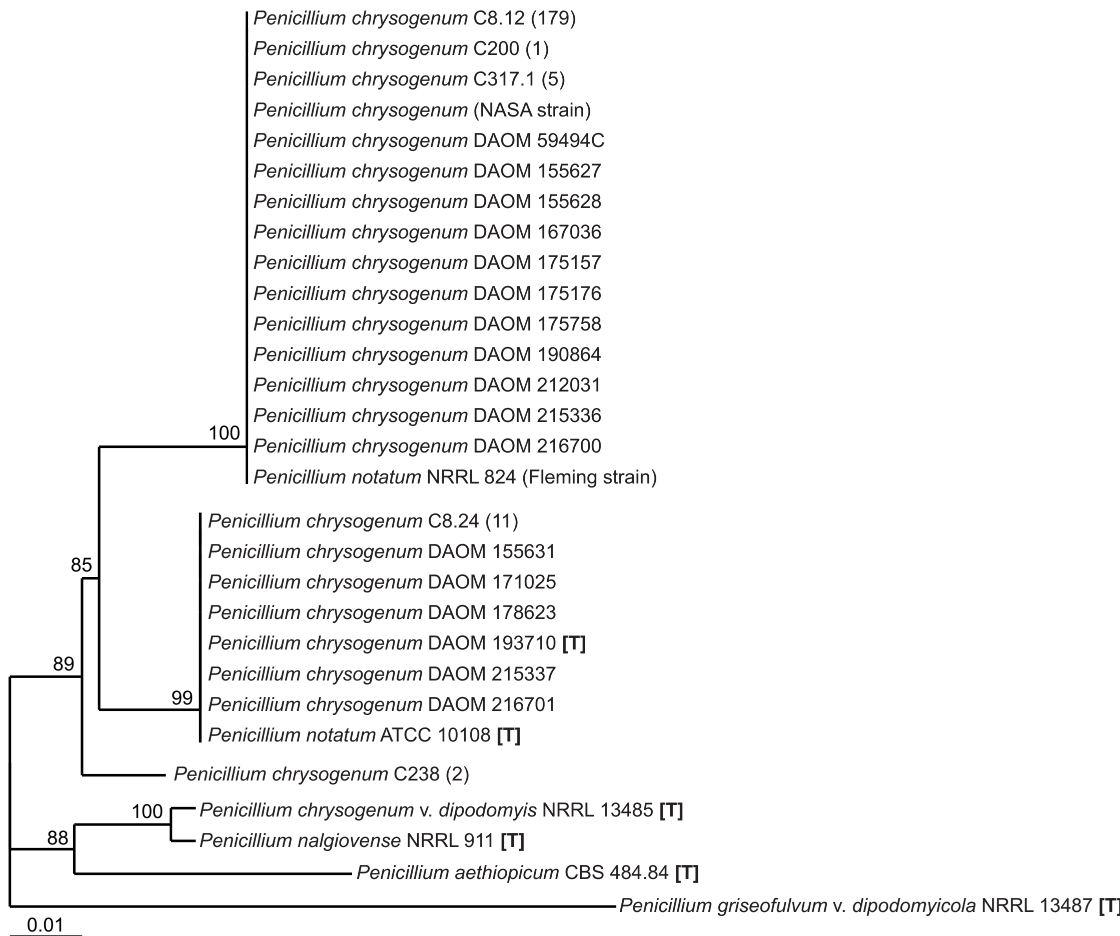

FIGURE 6-3. Neighbor-Joining tree of *P. chrysogenum* isolates based on partial acuA gene rooted to the authentic strain of *P. griseofulvum* var. *dipodomyicola* (NRRL 13487 T). Bootstrap values based on 1000 replicates are indicated for branches which demonstrated over 50% bootstrap support.

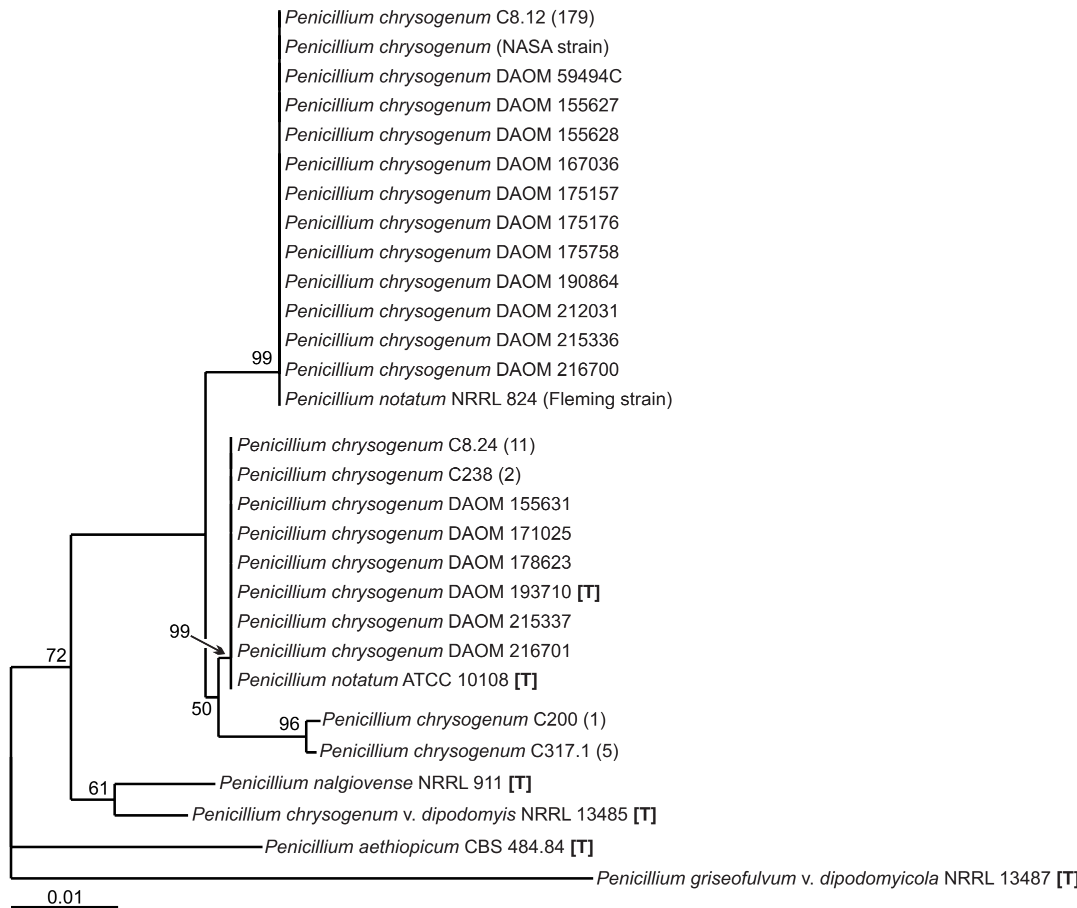

FIGURE 6-4. Neighbor-Joining tree of *P. chrysogenum* isolates based on partial benA gene rooted to the authentic strain of *P. griseofulvum* var. *dipodomyicola* (NRRL 13487 T). Bootstrap values based on 1000 replicates are indicated for branches which demonstrated over 50% bootstrap support.

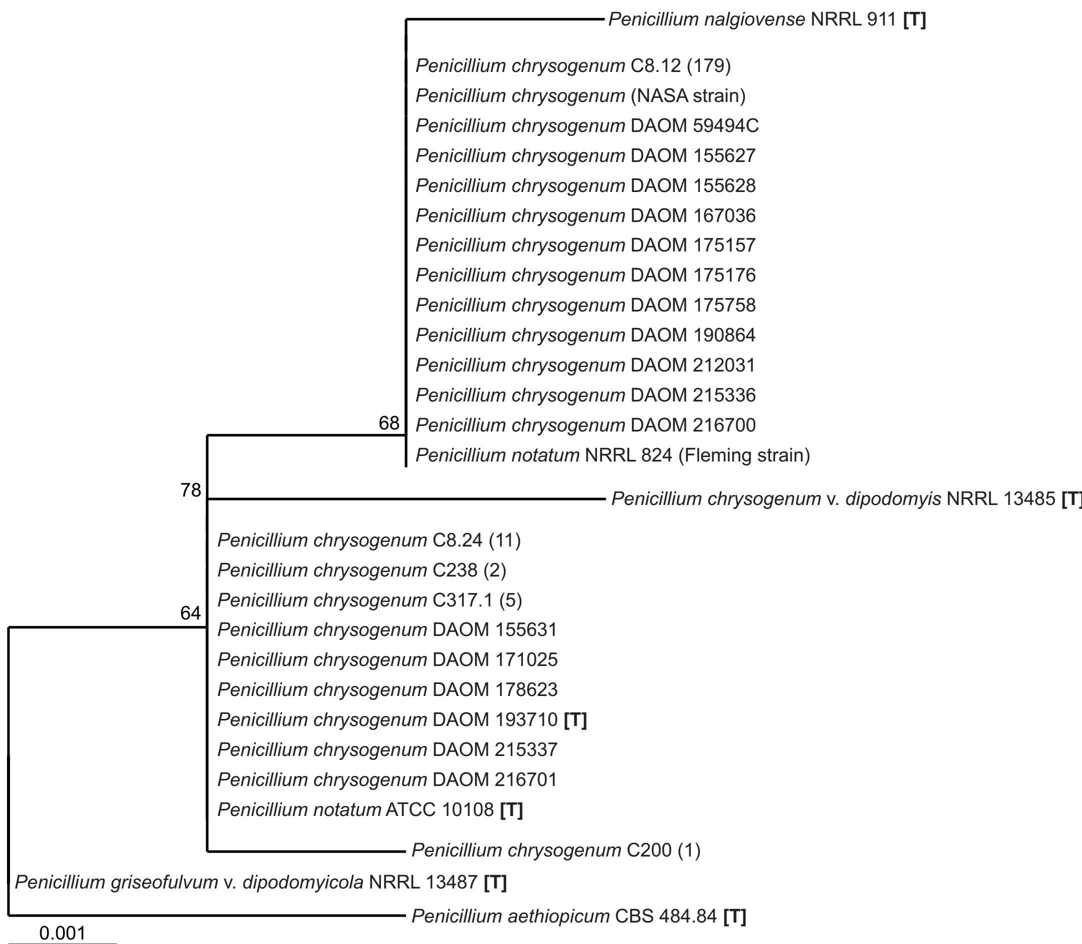

FIGURE 6-5. Neighbor-Joining tree of *P. chrysogenum* isolates based on ITS1-5.8S-ITS2 data rooted to the authentic strain of *P. griseofulvum* var. *dipodomyicola* (NRRL 13487 T). Bootstrap values based on 1000 replicates are indicated for branches which demonstrated over 50% bootstrap support.

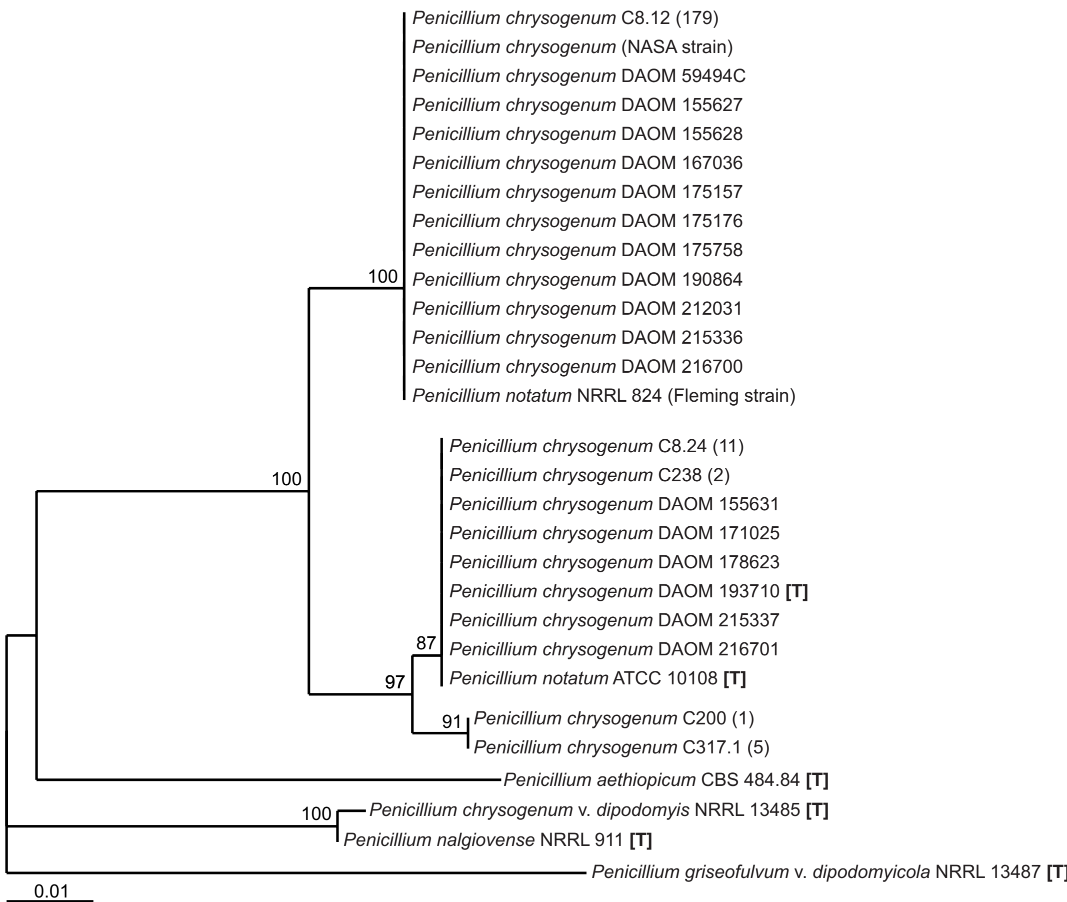

FIGURE 6-6. Neighbor-Joining tree of *P. chrysogenum* isolates based on partial trxB gene rooted to the authentic strain of *P. griseofulvum* var. *dipodomyicola* (NRRL 13487 T). Bootstrap values based on 1000 replicates are indicated for branches which demonstrated over 50% bootstrap support.

isolates represented by C238 clustered within the second clade in the benA and trxB trees, but formed a group that was sister to the two major *P. chrysogenum* clades in the acuA tree.

A distance tree based on ITS sequences (Figure 6-5) was similar in topology to the trees inferred from the other three loci; but, it resolved the two major clades of *P. chrysogenum* at a lower level of support.

Parsimony analysis of the trxB dataset consisted of 306 bases of which 35 were parsimony-informative. An exhaustive search of this dataset yielded produced two MPTs 79 steps in length (L) with a consistency index (CI) of 0.8734, a retention index (RI) of 0.8305, and a re-scaled consistency index (RC) of 0.7354 (*see* Figure 6-7). The topology of this tree was similar to the tree produced by distance methods using this locus (Figure 6-6), as well as to those based on the other loci (Figures 6-3, 6-4 & 6-5). This analysis yielded a well-supported clade (bootstrap support of 99 %) that included representative isolates of the major groups of *P. chrysogenum*. The topology of this tree was similar to that produced by distance methods using this locus, and also to distance trees produced using other loci.

COMBINED SEQUENCE DATA

Sequence data from all genetic loci from representative Wallaceburg isolates, as well as culture collection strains (as summarized in Table 6-2) were pooled and subjected to PHT. Ten thousand trees were generated from this dataset and the summed branch lengths of these trees were depicted as a histogram (Figure 6-8). In this histogram the sum of branch lengths for the actual MPT (L = 210), is indicated by an arrow, and showed significance at p = 0.0161. This p-value indicates that the data sets produce significantly different topologies and therefore cannot

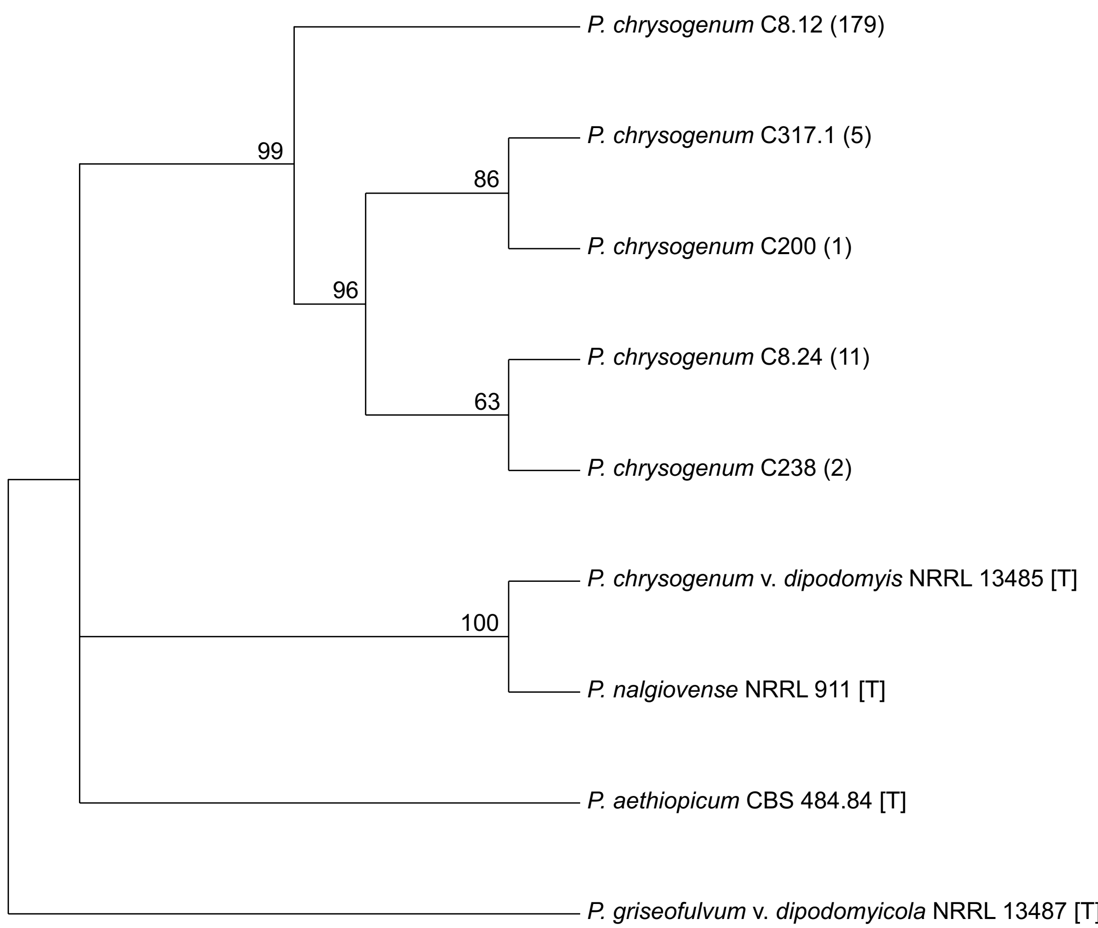

FIGURE 6-7. Strict consensus of two MPTs produced from partial trxB sequence rooted to the authentic strain of *P. griseofulvum* var. *dipodomyicola* (NRRL 13487 T). Bootstrap values based on 1000 replicates are indicated for branches which demonstrated over 50% bootstrap support.

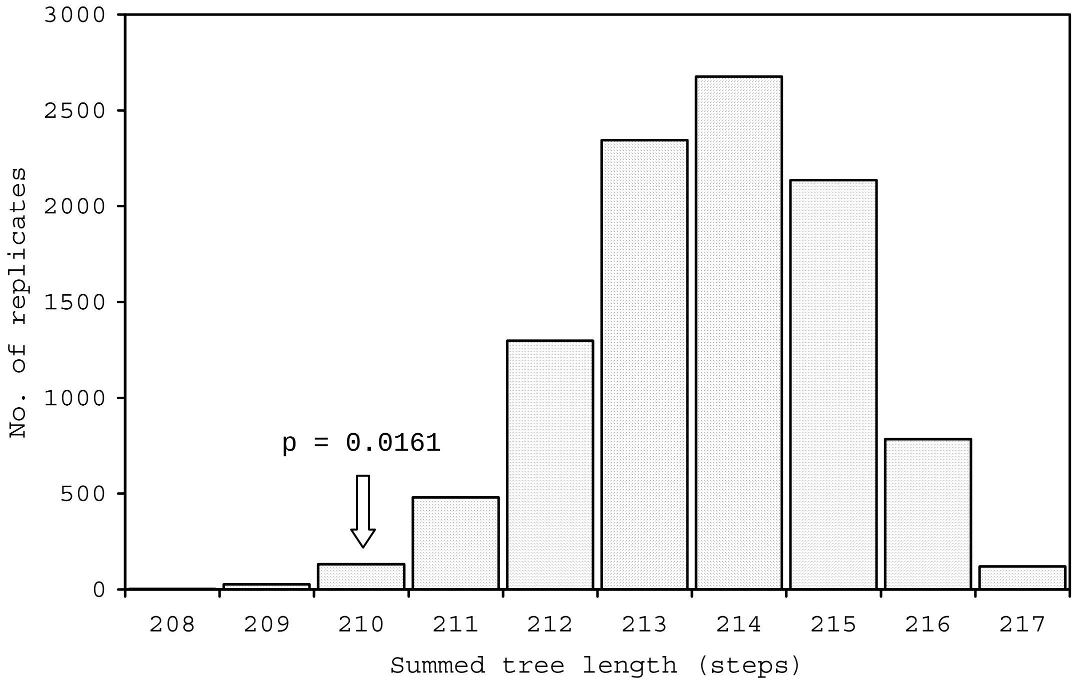

FIGURE 6-8. Results of partition homogeneity test. Bars show the distribution of the total summed branch lengths of 10,000 trees generated from data sampled randomly across partitioned gene sequences (acuA, benA, ITS & trxB) using PAUP* 4.0b4a (Swofford, 1999). Summed branch length for the observed single most parsimonious tree is indicated by the arrow.

be combined. One possible explanation for the incongruence of this data set is the inclusion in it of more than one biological species.

A second PHT was conducted on a subsample of isolates that included representatives of the Wallaceburg multilocus haplotypes as well as authentic material of *P. chrysogenum* (DAOM 193710), *P. notatum* (ATCC 10108), and the Alexander Fleming strain (NRRL 824) deposited under the latter name. The ITS data were eliminated from the partitioned dataset since no parsimony-informative characters were provided by this locus in the reduced panel of isolates (*see* Table 6-6). Furthermore, as shown in Table 6-6, elimination of the ITS data from this dataset reduced by two steps the total length of the MPT, from 35 to 33 steps. Results of this PHT are shown in Figure 6-9. The total branch length of the actual MPT fell within the 90th percentile of all tree lengths (L = 33, p = 1) based on random subsampling across partitions. The position of the actual MPT is indicated by an arrow in Figure 6-9. This result demonstrates that the three loci examined (acuA, benA and trxB) produce congruent topologies and that these sequence data may be combined. Furthermore, this result suggests that the isolates sampled have been propagated by strictly clonal means, in absence of recombination.

Analysis of the dataset that included sequences for the acuA, benA and trxB loci produced a single MPT (L = 33, CI = 0.9333, RI = 0.9286, RC = 0.9004) (Figure 6-10). The Wallaceburg *P. chrysogenum* isolates were divided among three well-supported clades and this tree showed essentially the same topology as the distance trees derived from analysis of individual genes. The first of these clades contained ex-type strains of *P. chrysogenum* and *P. notatum* along with 13 of the Wallaceburg isolates. The second clade was limited to 6 Wallaceburg isolates and the third clade contains 179 of 198 Wallaceburg isolates along with the Fleming strain (NRRL 824).

Table 6-6: Summary of MPTs produced from each of 4 loci examined

Locus	No. of MPTs	No. of steps	CI*	PI** chars	Total chars	Constant chars
acuA	3	14	1.0000	6	291	277
benA	3	9	0.8333	5	431	423
ITS	15	2	0/0	0	546	544
trxB	1	10	1.0000	3	306	296
all 4 loci	1	35	0.9333	14	1,580	1,546
all (w/o ITS)	1	33	0.9333	14	1,028	996

*CI = Consistency index
**PI = Parsimony-informative

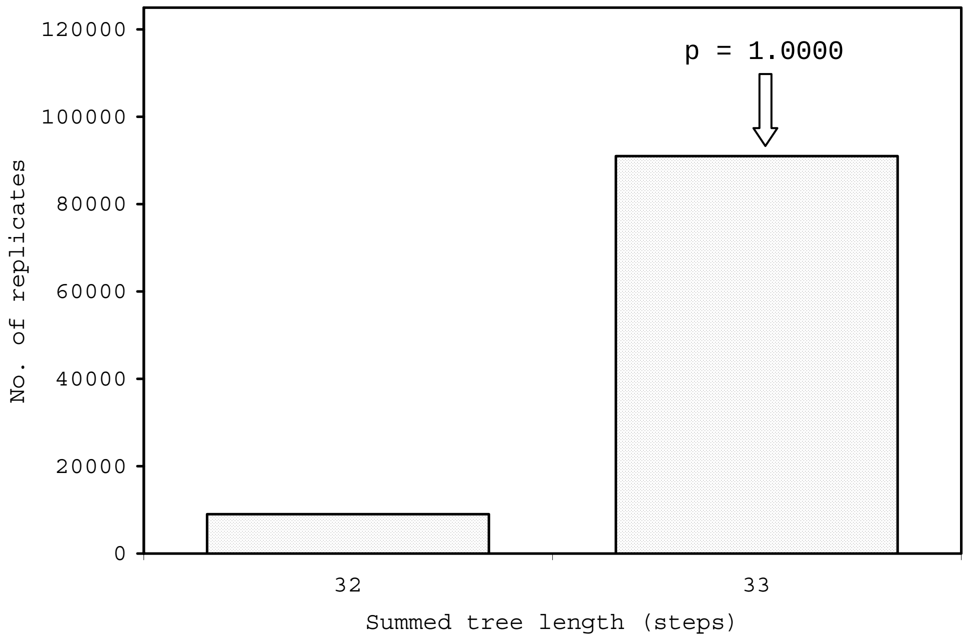

FIGURE 6-9. Results of partition homogeneity test of acuA, benA & trxB sequence data for Wallaceburg dust isolates, including authentic material for *P. chrysogenum* (DAOM 193710), *P. notatum* (ATCC 10108) and the Fleming strain (NRRL 824). Bars show the distribution of the total summed branch lengths of 100,000 trees generated from data sampled randomly across partitioned gene sequences using PAUP* 4.0b4a (Swofford, 1999). Summed branch length for the observed single most parsimonious tree is indicated by the arrow.

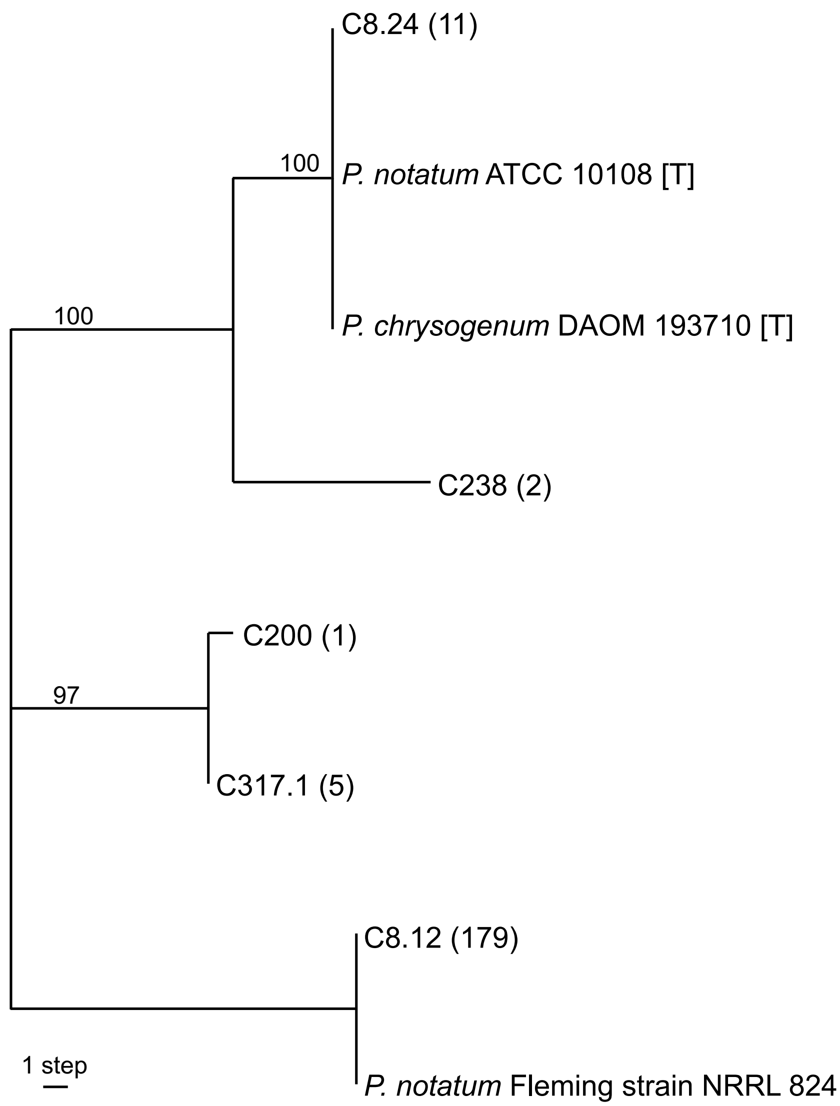

FIGURE 6-10. Unrooted MPT produced from combined acuA, benA and trxB sequences, including representative dust isolates and authentic strains (L=33, CI=0.9333, RI=0.9286, RC=0.9004).

Spatial analysis

Figure 6-11 shows a dendrogram of Wallaceburg house numbers used in this study that have been clustered by UPGMA analysis of geographic proximity. The array of multilocus haplotypes obtained from each house is mapped on this dendrogram. Visual inspection of these graphical data fail to reveal any obvious pattern of geographic distribution of genotypes. This may be due mainly to the strong dominance of a single genotype throughout the study site, as well as to the relatively low number of sites from which multiple isolates were obtained (*see* Table 6-1).

PCR fingerprinting

Photographs of electrophoresis gels based on M13-primed PCR amplifications are shown in Figures 12a & b. The isolates shown were arranged according to similarity following preliminary electrophoresis of the PCR products. Used as a single primer, the core M13 primer generated DNA products ranging in size from 0.9 to 4.1 kbp. Cluster analysis of M13 PCR fingerprint data separated the *P. chrysogenum* complex isolates into three distinct groups (Figure 6-13) that corresponded to the major clades revealed by parsimony analysis of the combined acuA-benA-trxB dataset shown in Figure 6-10.

Products of PCR generated using $(GACA)_4$ as a single primer are shown in Figures 6-14a & b and are arranged based on a preliminary assessment of similarity. The PCR products generated by this primer ranged in size from approximately 1.2 to 3.8 kbp. Cluster analysis of band variation demonstrated the same major clades observed using the M13 and $(GACA)_4$ primers; but, minor variation in branch topology was observed in the dendrograms based on analyses of these primers (Figure 6-15).

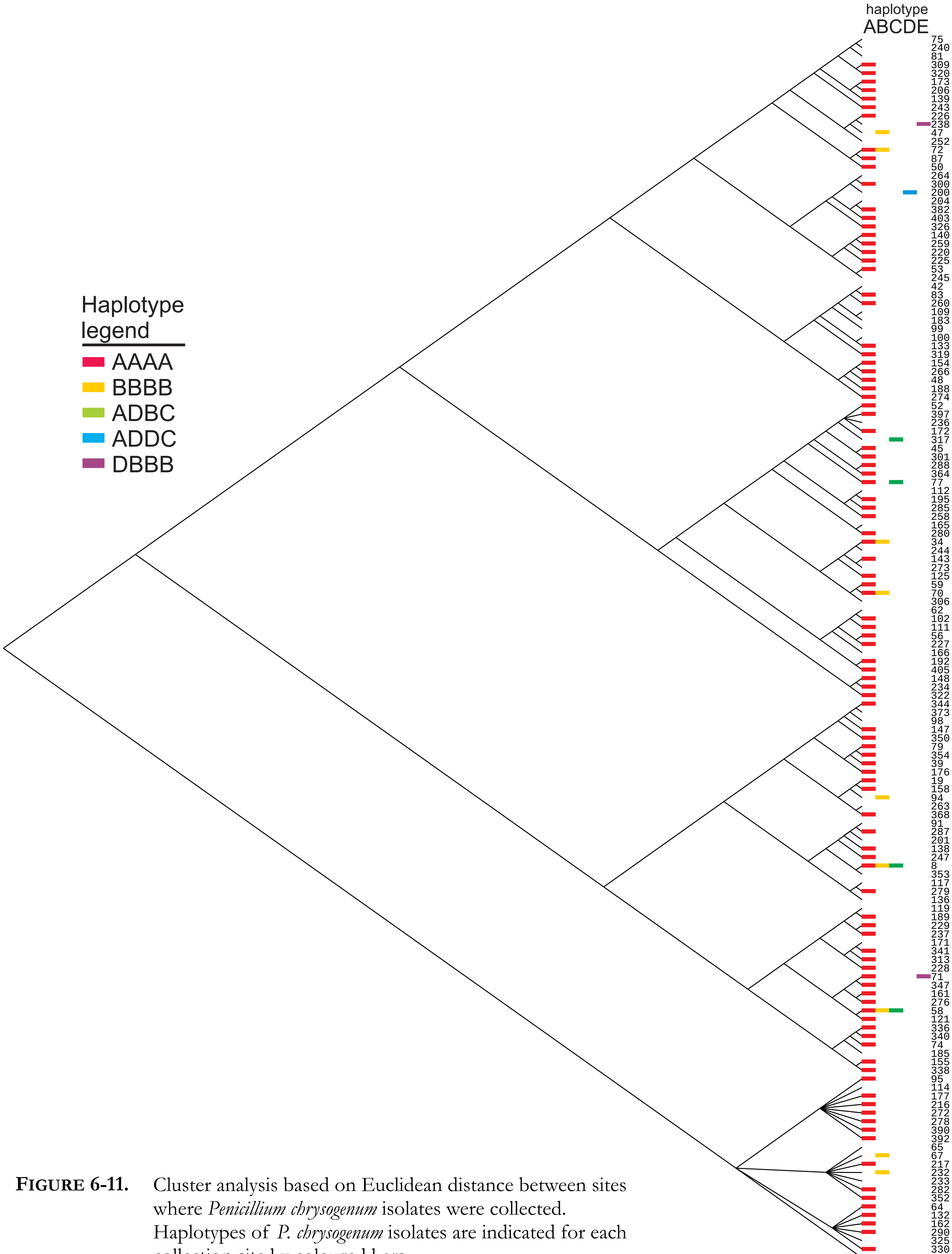

FIGURE 6-11. Cluster analysis based on Euclidean distance between sites where *Penicillium chrysogenum* isolates were collected. Haplotypes of *P. chrysogenum* isolates are indicated for each collection site by coloured bars.

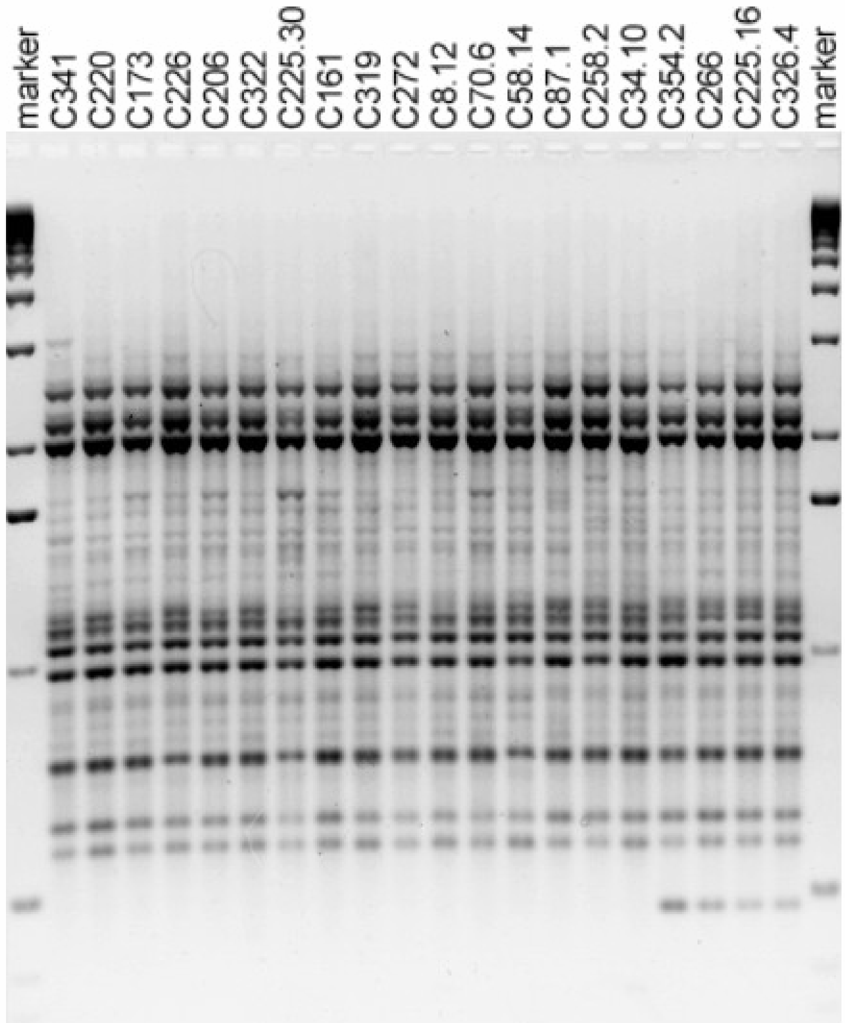

FIGURE 6-12a. DNA fingerprinting gel based on single-primer PCR using the M13 core sequence. Isolate numbers indicated above respective gel lanes.

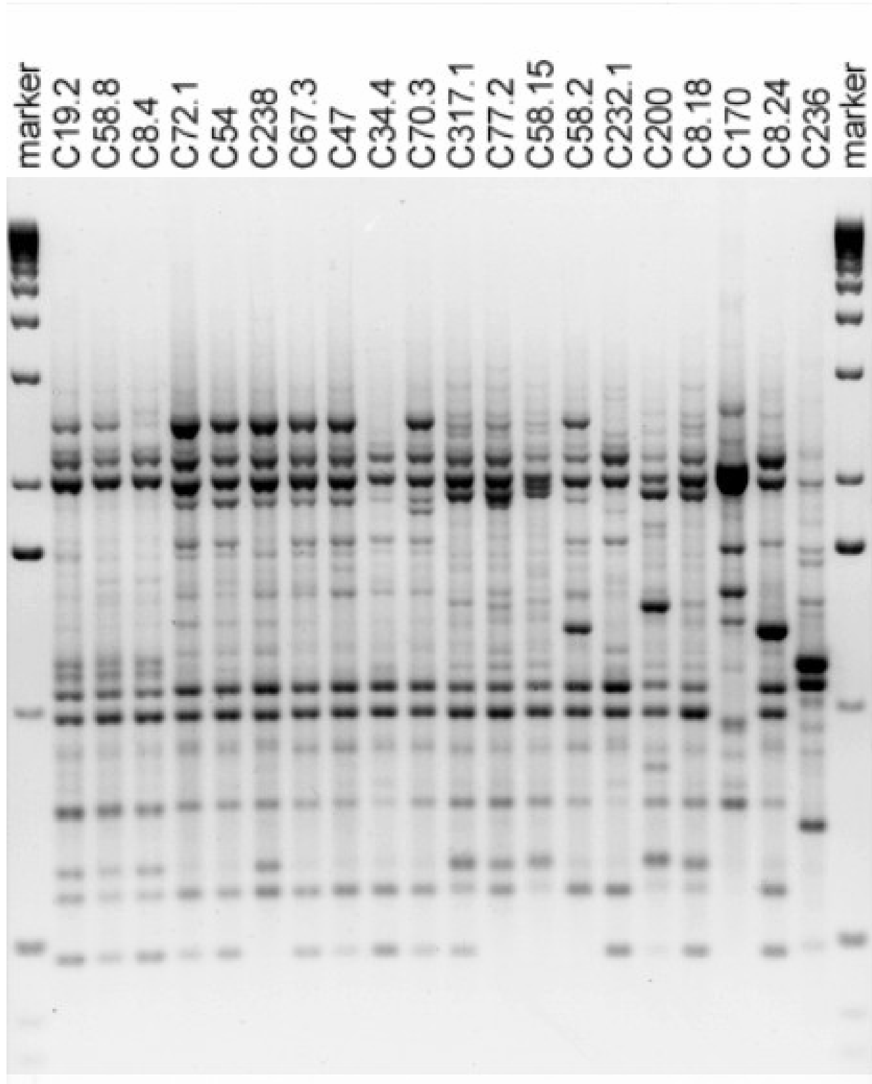

FIGURE 6-12b. DNA fingerprinting gel based on single-primer PCR using the M13 core sequence. Isolate numbers indicated above respective gel lanes

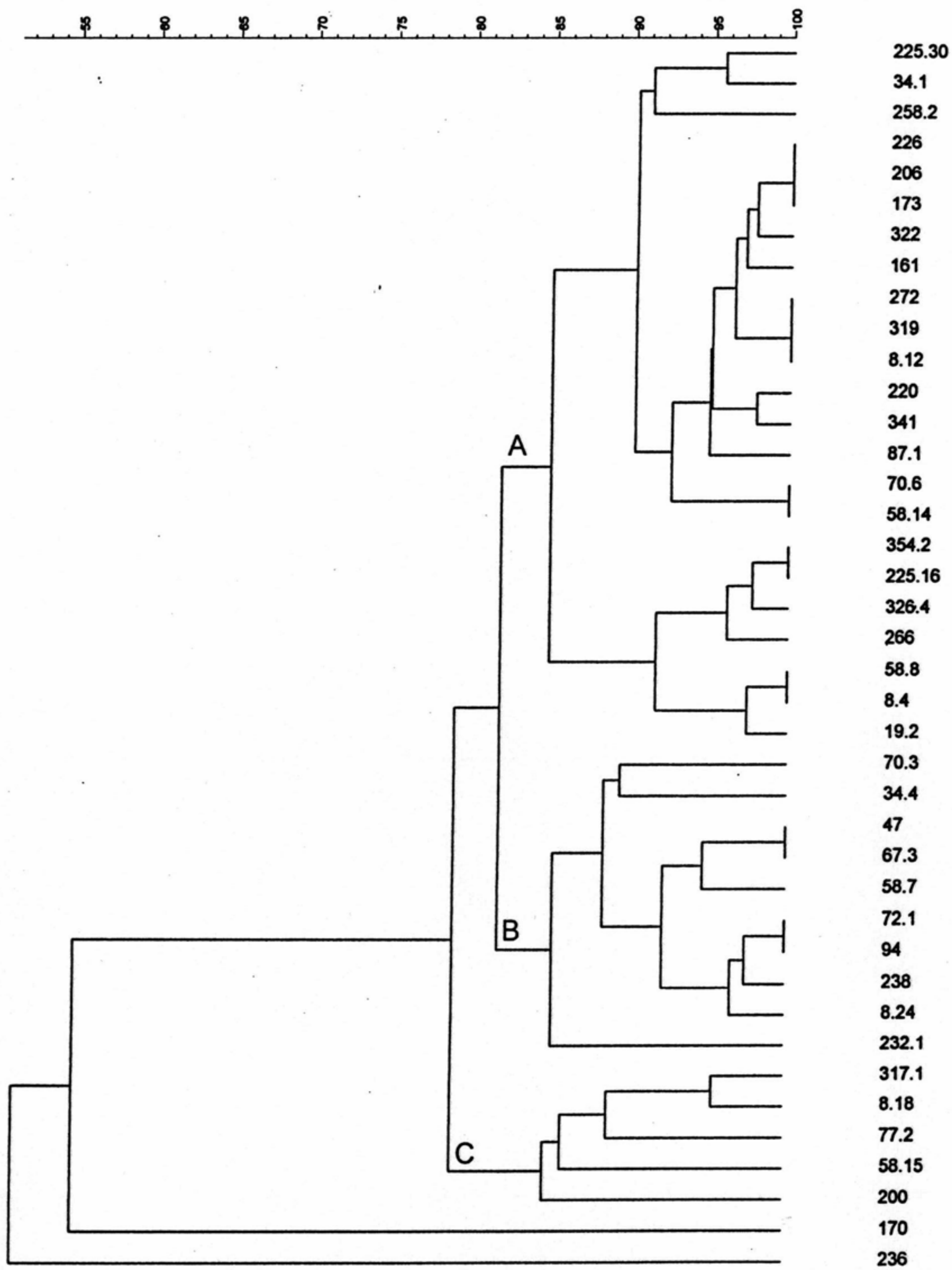

FIGURE 6-13. Neighbour-Joining cluster analysis based on band similarity of single-primer PCR products using M13 core sequence. Letters (A-C) indicate branches that correspond to major clades revealed in sequencing studies (*see* Fig. 6-10, p. 154).

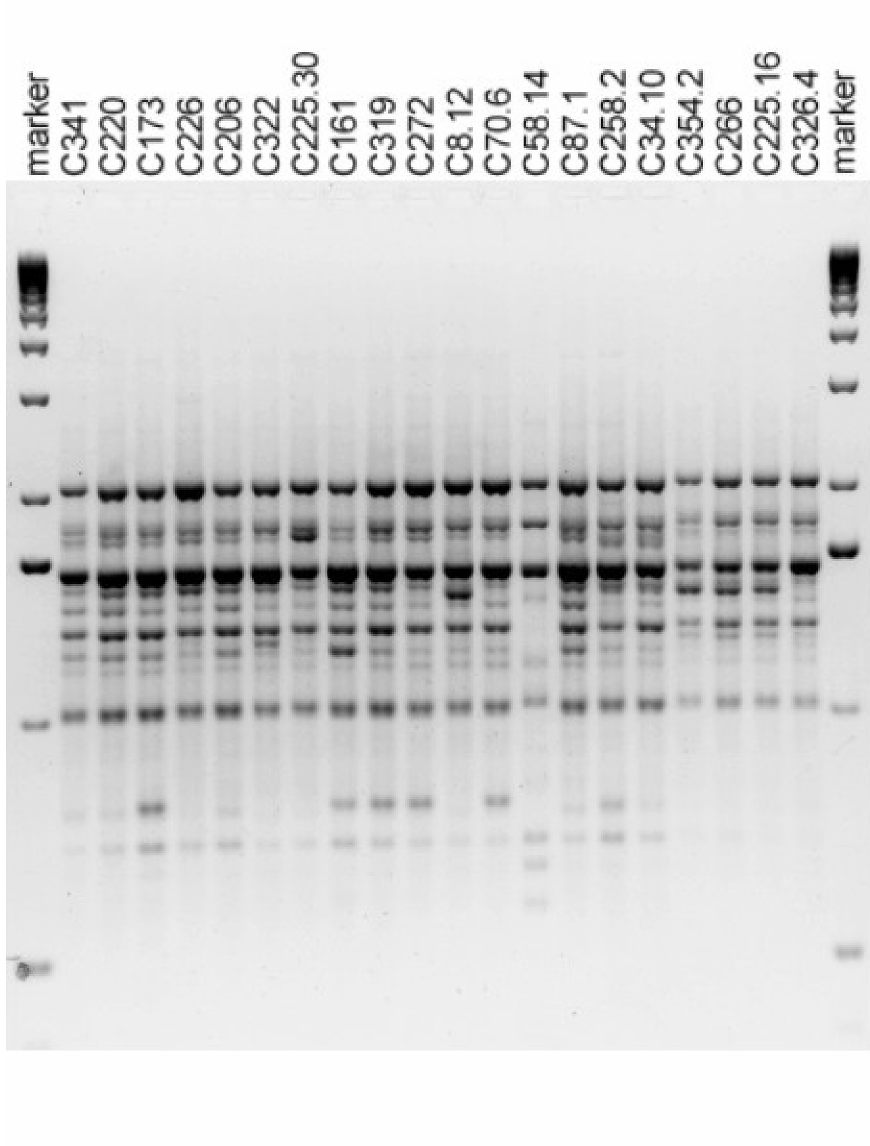

FIGURE 6-14a. Electrophoresis gel of PCR products amplified using the oligonucleotide $(GACA)_4$ in single-primer PCR. Isolate numbers indicated above respective lanes.

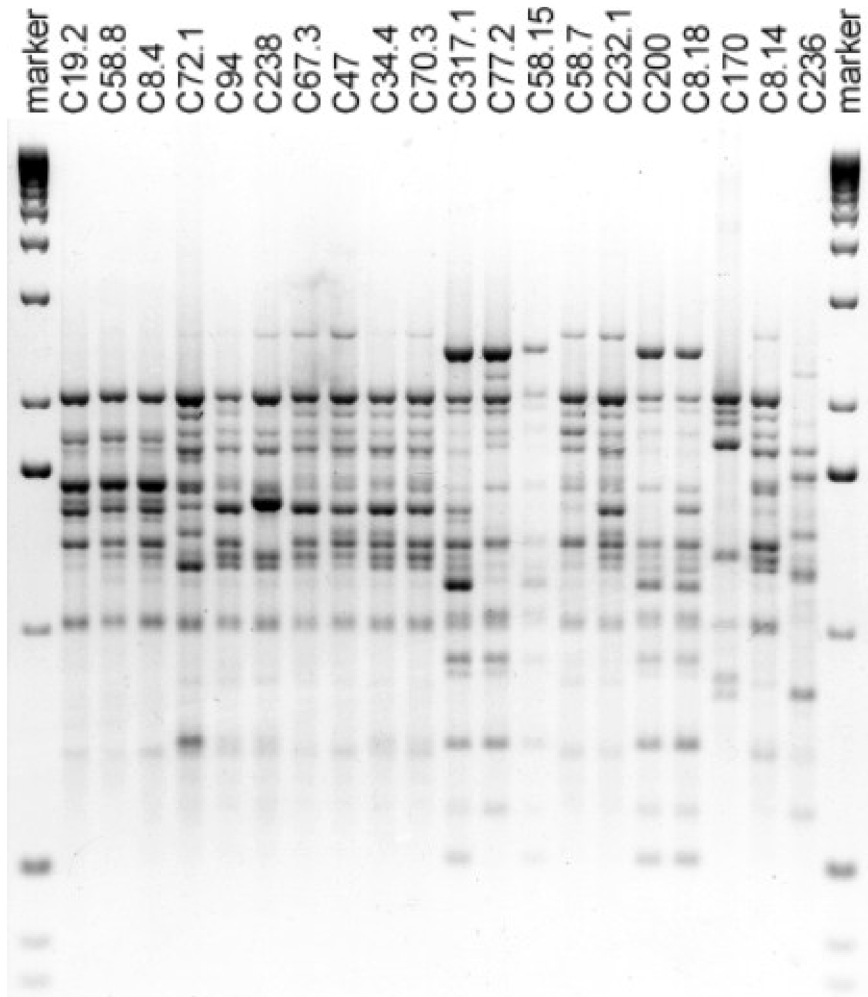

FIGURE 6-14B. Electrophoresis gel of PCR products amplified using the oligonucleotide $(GACA)_4$ in single-primer PCR. Isolate numbers indicated above respective lanes.

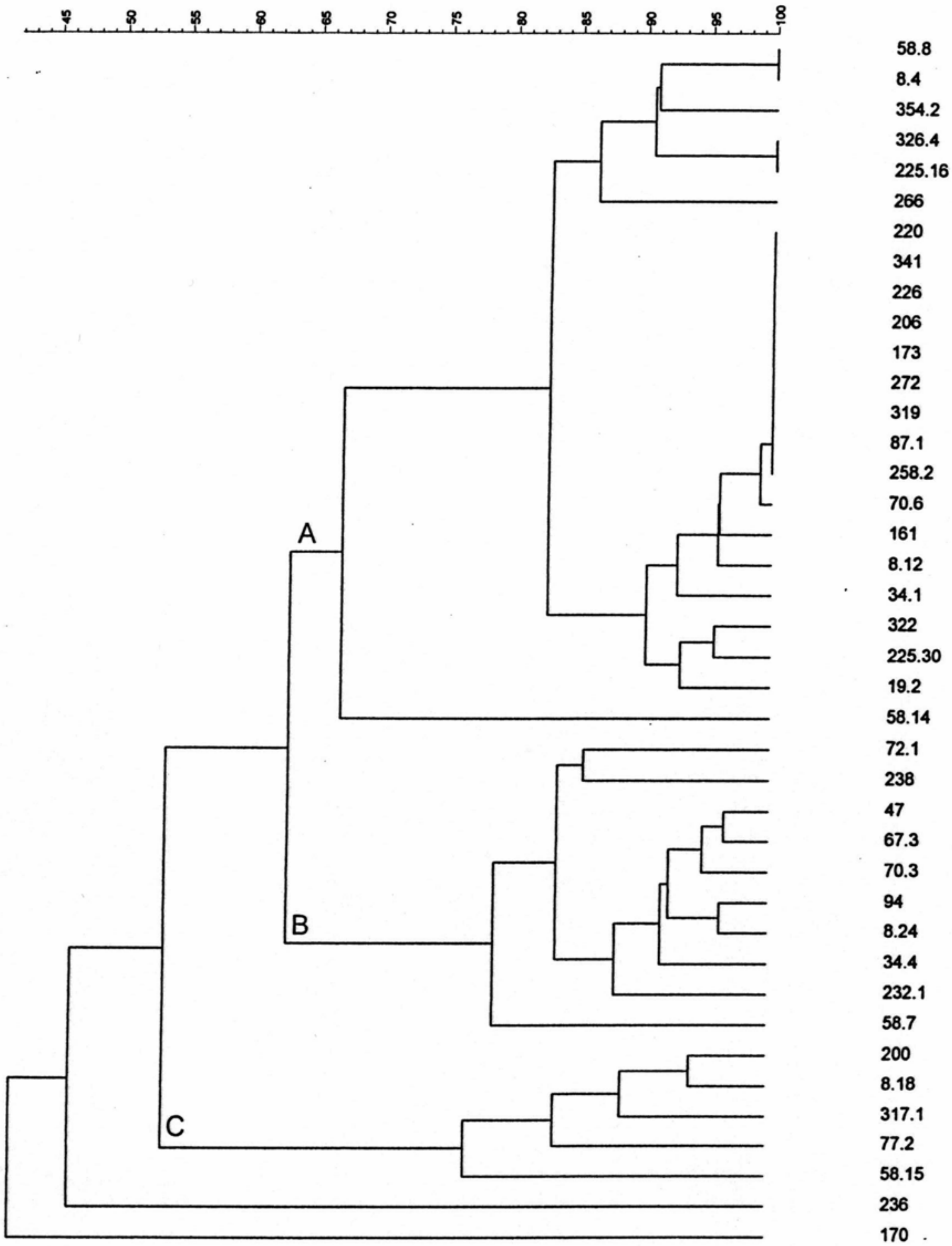

FIGURE 6-15. Neighbour-Joining cluster analysis based on band similarity of single-primer PCR products using the oligonucleotide $(GACA)_4$. Letters (A-C) indicate branches that correspond to major clades revealed in sequencing studies (*see* Fig. 6-10, p. 154).

RANDOM PRIMER FINGERPRINTING

Photographs of silver-stained polyacrylamide gels showing PCR products of the random-primer pair 5SOR & MYC1 are reproduced in Figures 6-16a & b. Amplified DNA products ranged in size from 80 to 1,300 bp and showed 30-40 discrete bands per isolate. Cluster analysis of the banding patterns is shown in Figure 6-17. Overall variation observed using the 5SOR and MYC1 primer pair was greater than for the single primer loci. While the three principal clades observed in this analysis corresponded to those inferred from the single-primer datasets, the pattern of terminal branching within the clades differed.

A cluster analysis of the combined fingerprinting data (M13 + $GACA_4$ + 5SOR/MYC1) is shown in Figure 6-18. Again, the major branches corresponded to principal clades identified in the sequence-based phylogeny. The branches supporting the principal clades were reinforced in the combined dataset relative to individual datasets (*see* Table 6-6). As well, the boundary similarity (minimum level of similarity shared by all members of a clade) of Clade A increased in the combined dataset (*see* Table 6-6).

Figure 6-19 shows a comparison between the combined fingerprint data tree (left) and the unrooted MPT based on combined acuA, benA and trxB sequence data (*viz* Figure 6-10) (right). Overall, the fingerprinting methods revealed the same strongly supported clades observed in the sequence-based phylogenies. The shared clades (A-C) are highlighted by colored rectangles.

Although ex-type isolates were not included in the fingerprinting studies, the exact agreement of these data with sequence data suggests that the ex-type of *P. chrysogenum* and *P. notatum* should be situated in clade B whereas the Fleming strain should be found in clade A.

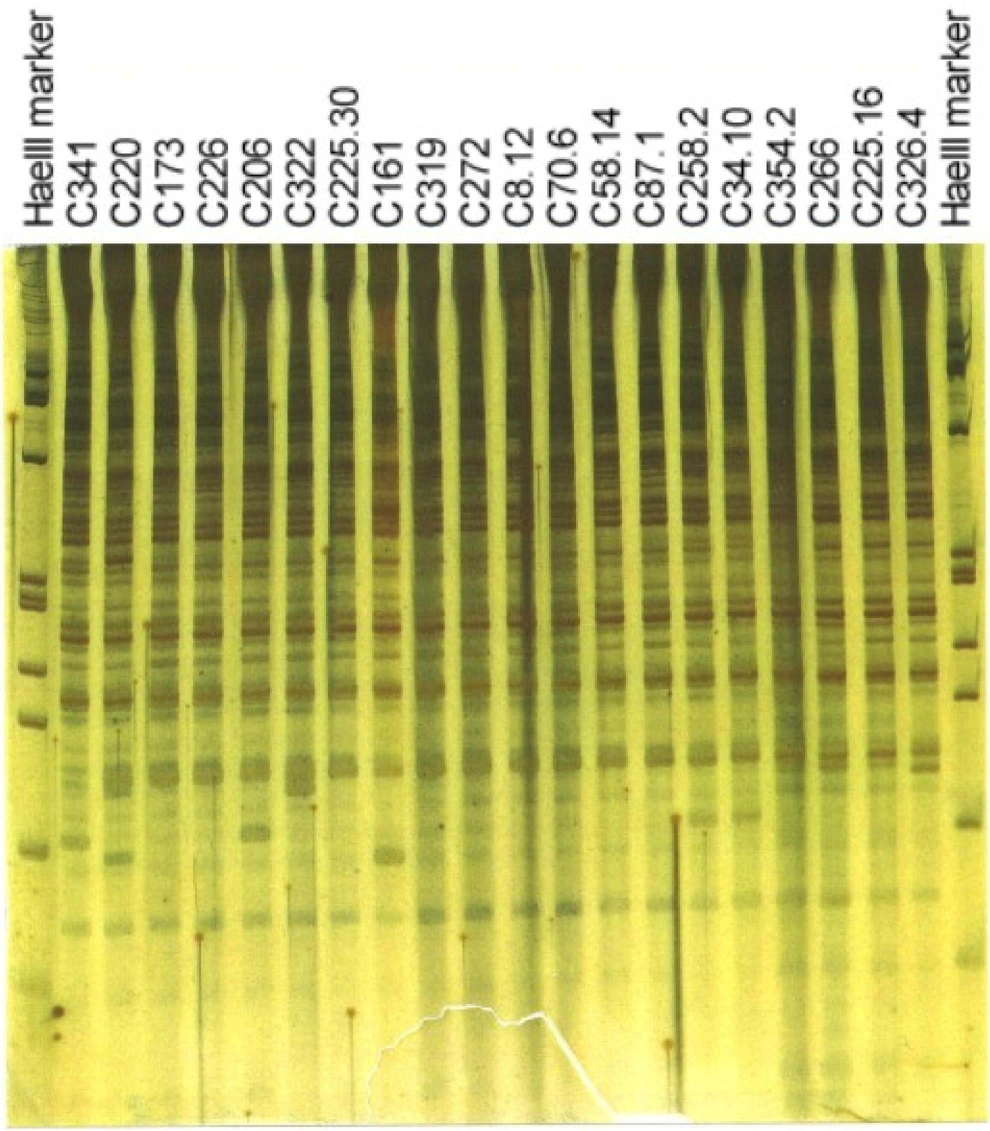

FIGURE 6-16a. Electrophoresis gel of PCR products amplified using the oligonucleotide primer pair 5SOR/MYC1. Isolate numbers indicated above respective lanes.

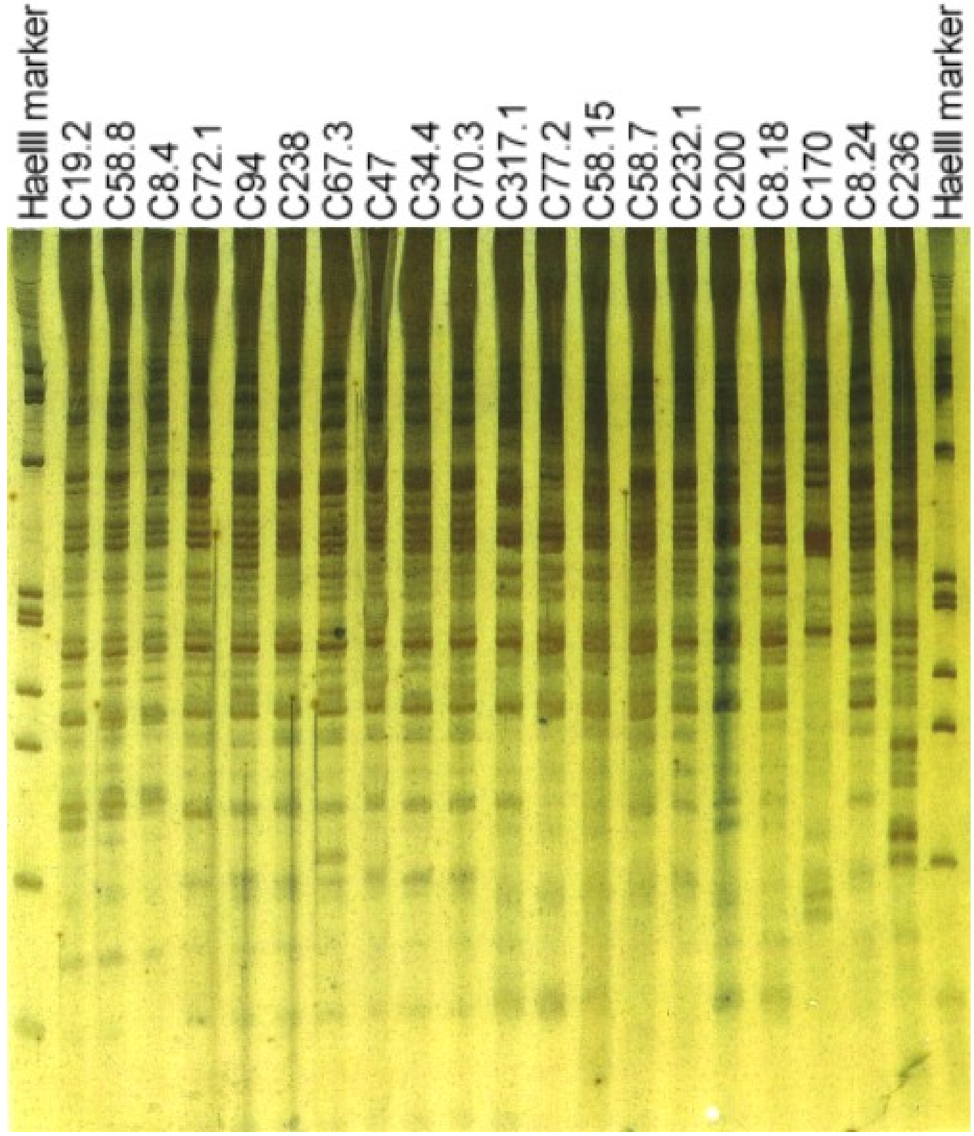

FIGURE 6-16B. Electrophoresis gel of PCR products amplified using the oligonucleotide primer pair 5SOR/MYC1. Isolate numbers indicated above respective lanes.

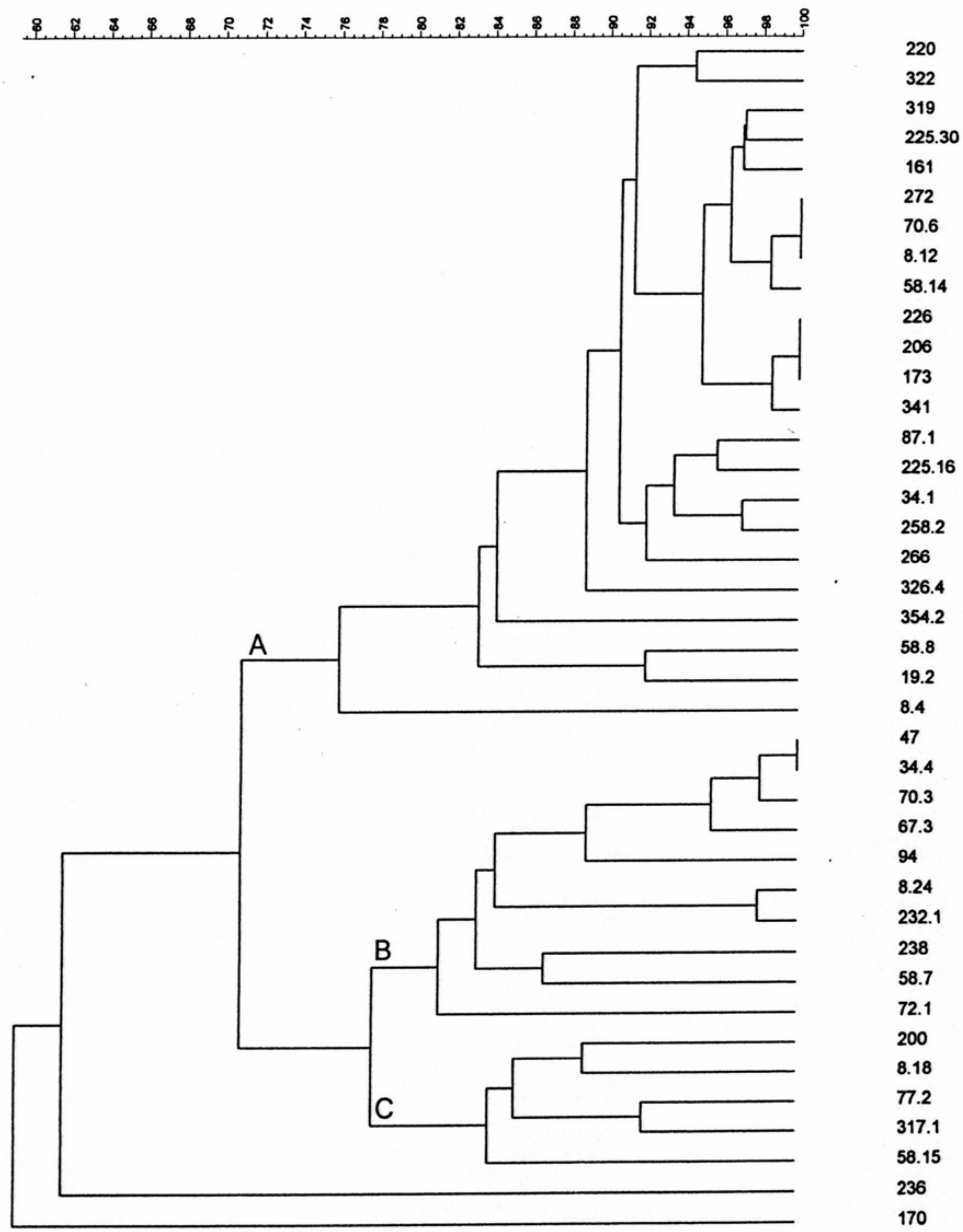

FIGURE 6-17. Neighbour-Joining cluster analysis based on band similarity of banding patterns of PCR products of the oligonucleotide primer pair 5SOR/ MYC1. . Letters (A-C) indicate branches that correspond to major clades revealed in sequencing studies (*see* Fig. 6-10, p. 154).

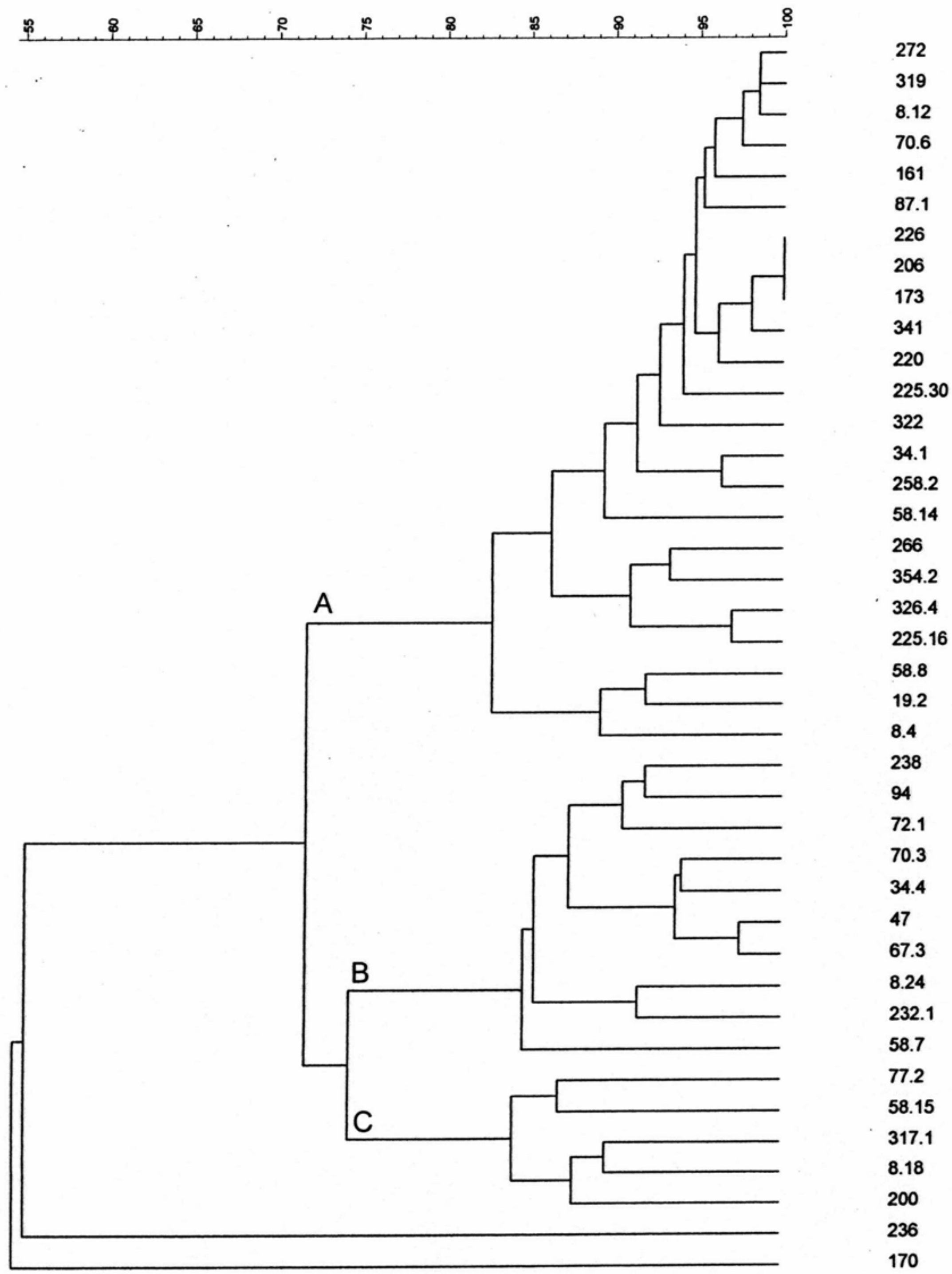

FIGURE 6-18. Neighbour-Joining cluster analysis based on band similarity of combined banding patterns of PCR products from three independent loci: the single primers M13 and $(GACA)_4$ and the oligonucleotide primer pair 5SOR/ MYC1. Letters (A-C) indicate branches that correspond to major clades revealed in sequencing studies (*see* Fig. 6-10, p. 154).

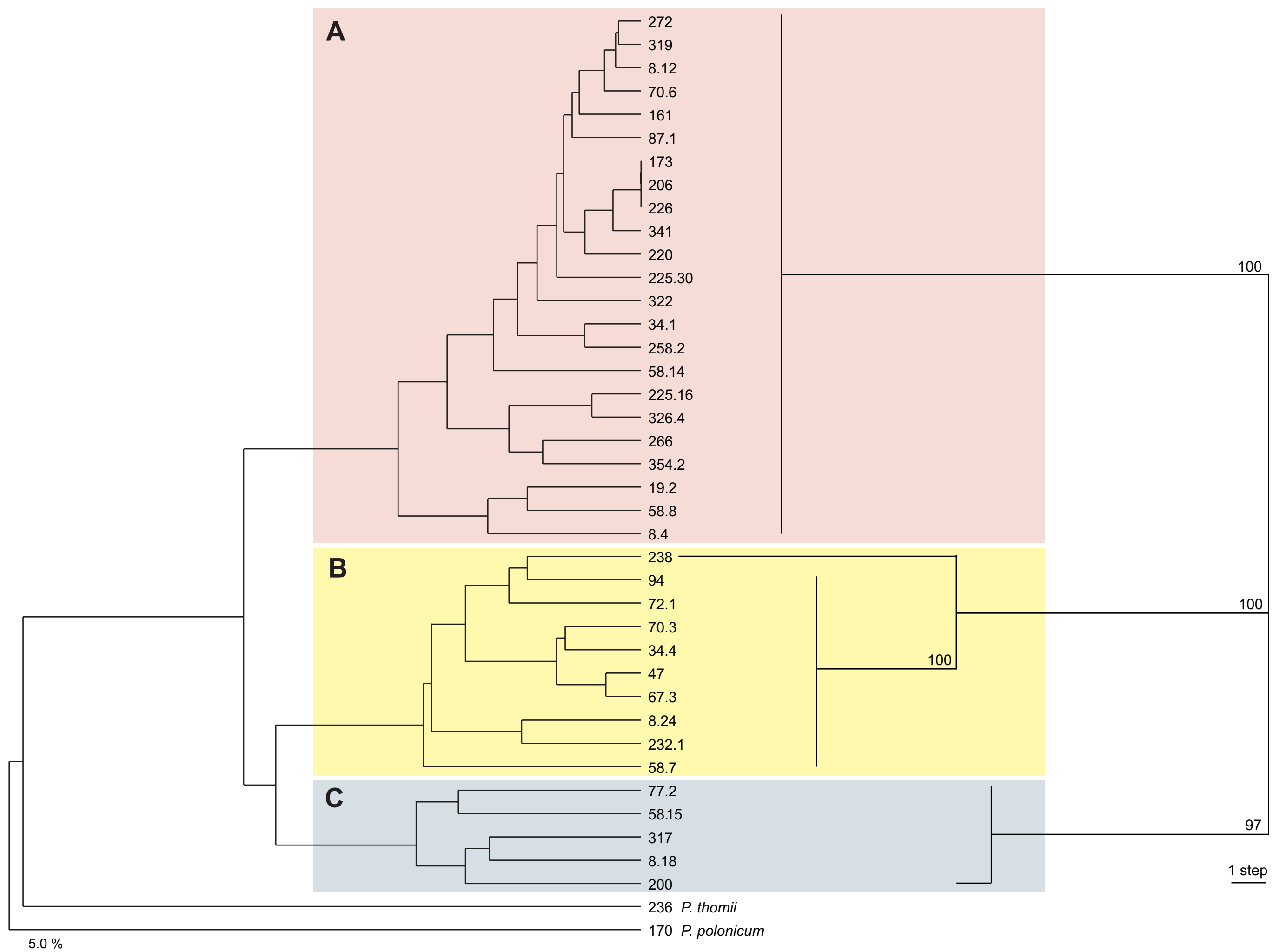

FIGURE 6-19. Comparison of combined fingerprint data (*left*) and the single MPT produced from combined gene sequences of acuA, benA and trxB genes (*from* FIG. 6-10) (*right*).

Figure 6-20 shows the correlation between genotype, as revealed by comparing clade A of combined fingerprinting method (from Figure 6-18) (left), geographic proximity of the houses from which isolates were obtained (right). The house numbers in clade A were 34 and 258. Similarly, the houses in clade B were 173, 206 and 226. The physical locations of these houses are shown in Figure 6-1.

DISCUSSION

The combined sequence-based phylogeny revealed three strongly supported groups within the *P. chrysogenum* complex. The same major groups were revealed by three, independent DNA fingerprint datasets. A PHT of the sequence data for the core isolates comprising the *P. chrysogenum* clade showed that the independent loci were highly congruent, suggesting an absence of recombinatory signal in the present dataset (Geiser et al., 1998). This conclusion is in contrast to work by Rosendahl (1999) who reported recombination in a local population of *P. chrysogenum* using 50 isolates obtained from within and outside a single building on the campus of the University of Copenhagen (Rosendahl, pers. comm.). Their study examined a total of 6 polymorphic markers using SSCP (number of identified alleles shown in parentheses), including acetyl co-enzyme A synthase (acuA) (3), gamma-actin (act) (3), glutamine amido transferase (trpC) (4), orotidine-5'-phosphate decarboxylase (pyrG) (4), phosphoglycerate kinase (pgk) (7), and xylanase (xyl) (3) (Rosendahl, pers. comm.).

FINGERPRINT DATA

Despite the strong correlation of the three principal clades by all fingerprinting methods, little consistency was observed in terminal branching of the trees obtained using these different methods. Inspection of the gel photographs (Figures 6-12a,b; 6-14a,b; & 6-16a,b) suggests that

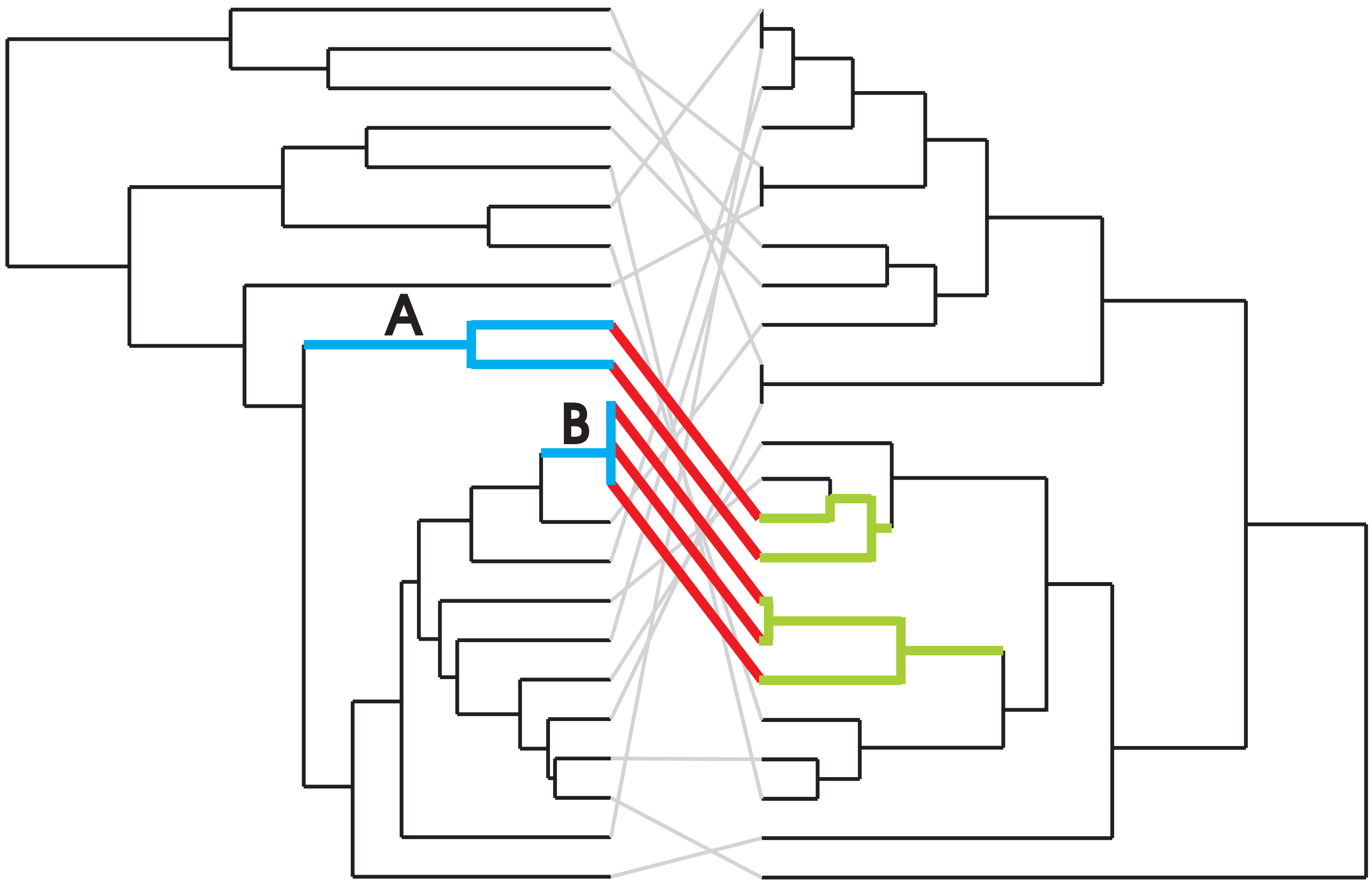

FIGURE 6-20. Comparison of combined fingerprint data (*left*) and collection location (*right*) based on Neighbor-Joining cluster analysis of distance matrix of linear distances between collection sites.

the contribution of densely staining bands to the datasets may account for the deep branches which form the backbone of the dendrograms, while the less intensely staining banding may produce the fine branches. Thus, a likely explanation for the poor correlation of fine branch topology between loci is the ambiguous nature of faint bands, and the unreliability of their scoring due to lack of intensity. If this is the case, a comparison of terminal branching topology between clades should produce relative incongruence. In graphical terms, this incongruence is reflected in a loss of a robust dichotomous resolution, producing instead a stepped branching topology. This shift in branching topology is correlated to an increase in singlet terminal taxa, as well as an increase in the number of intermediate nodes along the longest path from root to terminal OTU. In other words, the number of intermediate nodes in the path from the root of a clade to a tip of the longest branch increases when such datasets are combined. This trend was observed in the present data, whereby the number of nodes in the longest path to a terminal OTU in Clade #1 was 8, 7, 9 and 11 for M13, $GACA_4$, 5SOR/MYC1 and the combined data, respectively (*see* Table 6-7). As well, the relative number of singlet terminal OTUs increased in the combined dataset (*see* Table 6-7).

MORPHOLOGICAL AND PHYSIOLOGICAL VARIATION

Thom (1930) reported color variation during 22 years of cultivation of the type strain of *P. chrysogenum*. However, the authentic strain of *P. chrysogenum* used in the present study was robust and produced growth patterns and physiological responses that were highly comparable to descriptions provided by Raper and Thom (1949) and Pitt (1979). The variation in colony coloration reported by Thom (1930) may have been related to variations in copper and zinc content of the culture media. Copper and zinc co-factors facilitate melanin biosynthesis via the pentaketide pathway (Hughes and Poole, 1989; Williamson, 1997). Deficiency of these metals in

Table 6-7: Comparison of "Clade A" in all fingerprinting cluster analyses

Comparative Parameter	Fingerprint primer(s)			
	M13	**$GACA_4$**	**5SOR/MYC1**	**Combined**
Similarity	85 %	67 %	76 %	83 %
N*	0.38 (8/21)	0.38 (7/21)	0.43 (9/21)	0.52 (11/21)
OTUR	0.30 (7/23)	0.35 (8/23)	0.30 (7/23)	0.44 (10/23)

N* = ratio of number of nodes in longest branch (n) to total number of hypothetical internal nodes in the clade (N_T = number of taxa - 2).

OUTR = ratio of terminal unpaired OTUs (t') to the total number of taxa (t_T).

growth media was first suggested by Frisvad (published from a round table discussion *In* PAW-I, p. 101) to produce unusual colony pigmentation. Frisvad's observation has since served as justification for the supplementation of growth media with these metals to ensure consistency in colonial appearance (Samson et al., 1996). Similar variation has been noted in secondary metabolite profiles according to trace metal availability (Filtenborg et al., 1990). Indeed, much earlier Knight and Frazier (1945) hypothesized that the presence of trace minerals in corn steep liquor was partly responsible for the stimulatory effect of this compound on penicillin production in early industrial production of the antibiotic.

HISTORY OF *P. CHRYSOGENUM*

Charles Thom (1910) described *P. chrysogenum* as a contaminant from cheese. The authentic strain of this taxon is deposited as NRRL 807 (from Thom #26), ATCC 10107, DAOM 193710 and CBS 306.48. This species was characterized by loosely branched smooth terverticillate conidiophores and smooth ellipsoidal conidia. The original description considered radially furrowed, velvety colonies with heavy sporulation, the production of yellow guttation and a yellow reverse pigment to be definitive characters (Thom, 1910). Raper and Thom (1949) concluded that the taxa described by Dierckx (1901) and Biourge (1923) were allied with their "*P. chrysogenum* Series" (*sensu* Raper & Thom, 1949 p.355. *nom. inval. Arts 21 & 36* = Series *Chrysogena* Raper & Thom *ex* Stolk & Samson, PAW-I, p. 180) and that they represented variant isolates along a continuum of variation. They proposed that the compliment of this variation could be better accommodated within 4 species: *P. chrysogenum* Thom, *P. meleagrinum* Biourge*, P. notatum* Westling and *P. cyaneo-fulvum* Biourge.

Samson and co-workers (1977) regarded *P. citreoroseum* and *P. brunneorubrum* as uncertain since Biourge's redescriptions of these taxa were based solely upon the drawings and unpublished notes of Dierckx and authentic material was unavailable for these species (Hennebert, 1985; Samson et al., 1977). These authors also considered *P. griseoroseum* as doubtful despite the availability of an authentic strain (as Dierckx Culture No. 3). Pitt (1979) "lectotypified" *P. chrysogenum* with a dried culture of IMI 24314 (as Herb. IMI 24314). However, this specimen must correctly be considered a neotype since the use of a living ex-type that has been maintained in culture cannot be assumed to have remained consistent with the original collection despite its heritage. Furthermore, the original author did not examine the specimen designated. In his examination of this strain and various voucher collections, Pitt (1979) noted that these isolates appeared to be floccose variants of *P. chrysogenum* that produced biverticillate to irregularly terverticillate penicillia, and classified *P. griseoroseum* in subgenus *Furcatum*. However, Cruickshank and Pitt (1987) showed support for the conspecificity of *P. chrysogenum* and *P. griseoroseum* on the basis of isozyme electrophoretic patterns. Although the stability of these markers in *Penicillium* taxonomy was later questioned by Samson (1991), empirical studies have demonstrated that isozyme methods can provide robust taxonomic separation within subgenus *Penicillium* under a range of experimental conditions (Paterson, 1993). Frisvad and Filtenborg (1989) similarly grouped *P. griseoroseum* with *P. chrysogenum* on the basis of mycotoxin profiles.

NOMENCLATURAL STABILITY OF *P. CHRYSOGENUM*

Samson and co-workers (1977) considered the three Dierckxian species (*P. citreoroseum*, *P. brunneorubrum* and *P. griseoroseum*) as doubtful and placed them in synonymy with *P. chrysogenum*. They based this decision on their inability to locate authentic material (*fide* Hennebert, 1985) and the inadequacy of the descriptions provided by Biourge (1923). Furthermore, Samson and co-workers (1977) noted that an authentic strain of *P. griseoroseum* had been examined by Raper and Thom (1949), who considered it a synonym of *P. notatum*. Pitt (1979) similarly examined an extant culture of *P. griseoroseum* (as IMI 92220, *fide* Hennebert, 1985) and lectotypifed [sic] (a neotypification, see above discussion) the taxon based on a dried culture of Dierckx' original isolate (Pitt, 1980; Hennebert, 1985). The pedigree of this isolate of *P. griseoroseum* selected by Pitt (1979) (IMI 92220) was seven transfers removed from the original collection (e.g. Dierckx #3 (original) > Inst. Pasteur 85 > Biourge 29 > Thom 4733.70 > LSHB P39-1930 > CMI 1962 > IMI 92220). Pitt's decision to retain this taxon which he clearly considered to be close to *P. chrysogenum* was doubtlessly sentimental, since this Dierckx isolate is the oldest laboratory-maintained culture of the genus known (Pitt, 1979). Subsequent examinations of *P. griseoroseum* have suggested that it is conspecific with *P. chrysogenum* (Cruickshank and Pitt, 1987; Bridge et al., 1989). Interestingly, numerical analysis of morphological and physiological data by Bridge et al. (1989) excluded Thom's strain of *P. chrysogenum* (Cluster 7) from the core of isolates of this species, which included the authentic culture of *P. griseoroseum* (Clusters 7 and 14, respectively). These authors rationalized the position of the ex-type culture of *P. chrysogenum* (IMI 24314) by suggesting that it was an attenuated strain (Bridge et al., 1989). However, investigations of the *P. chrysogenum* type strain by other authors have not demonstrated any significant cultural deterioration (Pitt, 1980; Pitt and Samson, 1993). Indeed, Raper and Thom (1949) noted that during 40 years of continuous cultivation, the ex-type strain of *P. chrysogenum* remained stable.

Conspecificity of *P. griseoroseum* and *P. chrysogenum* is supported in the present study, in which isolate NRRL 820 clustered with the type cultures of *P. chrysogenum* (NRRL 807) and *P. notatum* (NRRL 821) (*see* Chapter 4, Figure 4-9, clade A). As such, *P. chrysogenum* is a later synonym, since *P. griseoroseum* has priority based on earlier publication.

The nomenclatural instability of *P. chrysogenum* and the clear industrial importance of this fungus prompted a recommendation for conservation of the name (Frisvad et al., 1990a, b). In fact, Frisvad and colleagues (1990a) went so far as to recommend broad conservation of *P. chrysogenum* as "the species name for the principal producer of penicillin". This recommendation was advanced on the basis that the association between the name "*Penicillium chrysogenum*" and the biochemical characteristic of penicillin biosynthesis was of paramount industrial importance (Lowe and Elander, 1983), despite that this metabolite is known from other filamentous fungi (Abraham and Newton, 1967; Samson et al., 1996). Frisvad (PAW-I, p. 159) reported that he obtained identical secondary metabolite profiles for 150 isolates of *P. chrysogenum* that he examined. Frisvad and colleagues (1990a) included Westling's (1911) species, *P. notatum*, as a synonym in their conservation recommendation despite that *P. chrysogenum* has nomenclatural priority in this case. A textual refinement of this article was advanced later as a formal proposal to conserve the name *P. chrysogenum* against earlier names (Kozakiewicz et al., 1992), stating that the conspecificity of *P. griseoroseum* and *P. chrysogenum* was "firmly established" by Bridge and co-workers (1989).

The present study suggests that the current concept of *P. chrysogenum* comprises three lineages which likely represent distinct species. There do not appear to be any available names which can be applied to the un-named clades. The erection of new species to accommodate these lineages is not in conflict with the nomenclatural conservation of *P. chrysogenum* (Frisvad et al., 1990a; Kozakiewicz et al., 1992). However, since it is clear that Frisvad and colleagues (1990a) intended to conservation *P. chrysogenum* upon biochemical- rather than taxonomic grounds, the erection of segregate species within the *P. chrysogenum* group might be an unpopular undertaking. At present, the delineation of sibling species from *P. chrysogenum* awaits the identification of stable, readily observable morphological and/or physiological characters that reliably separate the members of these lineages.

SYNONYMS OF P. CHRYSOGENUM

The following synonymy of *P. chrysogenum* is based on an examination of existing taxonomic literature in addition to several authentic strains included in the present study.

Penicillium chrysogenum Thom in U.S. Dept. Agr. Bur. Anim. Ind., Bul. 118, 1910. pp. 58-60, fig. 20. NT: Herb. IMI 24314 Pitt Gen. *Penicillium* 1980, Pitt & Samson, Reg. Veg. **128**: 41. 1993., *nom. cons. prop.* Kozakiewicz et al., Taxon **41**: 109-110, 1992.

= *Penicillium citreoroseum* Dierckx, Annls. Soc. Scient. Brux. **25**: 86. 1901, *syn. fide* Samson et al., 1977., *prop. nom. rej.* Kozakiewicz et al., Taxon **41**: 109-110, 1992.

= *P. brunneorubrum* Dierckx, Annls. Soc. Scient. Brux. **25**: 88. 1901, *syn. fide* Samson et al., 1977., *prop. nom. rej.* Kozariewicz et al., Taxon **41**: 109-110, 1992.

= *P. griseoroseum* Dierckx, Annls. Soc. Scient. Brux. **25**: 89. 1901, *syn. fide* Samson et al., 1977., LT: IMI 92220i *ex* CMI 1962 Pitt, 1980, *prop. nom. rej.* Kozariewicz et al., Taxon **41**: 109-110, 1992.

= *P. baculatum* Westling, Svensk Botanisk Tidskrift **4**: 139-145, figs. 1-3. 1910, *syn. fide* Raper & Thom 1949.

= *P. notatum* Westling, Ark. Bot. **11**: 55. 1911, *syn. fide* Samson et al., 1977; Pitt, 1980.

= *P. chlorophaeum* Biourge, Monogr., La Cellule **33**: fasc. 1, pp. 271-273. Pls. VIII & XIII, fig. 78. 1923, *syn. fide* Raper & Thom 1949.

= *P. rubens* Biourge, Monogr. La Cellule **33**: fasc. 1, p. 265. Pls. XI & XIX, fig. 111. 1923, *syn. fide* Raper & Thom 1949.

= *P. flavidomarginatum* Biourge, Monogr., La Cellule **33**: fasc. 1, p. 150. 1923, *syn. fide* Pitt 1980.

= *P. fluorescens* Laxa, Zentbl. f. Bakt. &c. (II) **86**: 164-165. 1932, *nom. nud. fide* Raper & Thom 1949.

= *P. roseocitreum* Biourge Monogr., La Cellule **33**: fasc. 1, pp. 184-186. Pls. IV & VII, fig. 39. 1923, *syn. fide* Raper & Thom 1949.

= P. *meleagrinum* Biourge, Monogr. La Cellule **33**: fasc. 1, p. 184. 1923 *syn. fide* Samson et al., 1977.

= P. *cyaneofulvum* Biourge, Monogr. La Cellule **33**: fasc. 1, p. 171. 1923 *syn. fide* Samson et al., 1977.

= P. *camerunense* Heim, Nouvel & Saccas, Bull. Acad. Belg. Cl. Sci., Ser 5, **35**: 52. 1949, *syn. fide* Samson et al., 1977.

= P. *chrysogenum* Thom var. *brevisterigma* Forster, Brit. Pat. 691: 242. 1953, *nom. nud. fide* Samson et al., 1977.

= P. *aromaticum* Sopp forma *microsporum* Romankova (Zap. Lenin. Univ. Zhdanov **191**: 102. 1955) *fide* Samson et al., 1977.

= P. *harmonense* Baghdadi, Nov. Sist. niz. Rast. **5**: 102. 1968, *syn. fide* Pitt 1980.

= P. *verrucosum* var. *cyclopium* strain *ananas-olens* Ramírez, Man. & Atl. Penicillia. 1982, *syn. fide* Stolk et al., in Modern concepts in *Penicillium* and *Aspergillus* classification. 1990. p. 126.

Recently, Banke and co-workers (1997) described *P. flavigenum*, a segregate species of *P. chrysogenum*, based on isozyme profiles. These workers examined 17 isolates which they assigned to this species. Two of these isolates were obtained from *Hordeum* grain from Canada. It is not clear if these isolates were obtained from the DAOM collection. At present the DAOM on-line catalogue lists two isolates of *P. chrysogenum* from *Hordeum* from Canada both of which were examined in the present study and clustered with the Fleming isolate of *P. notatum*. If these isolates represent *P. flavigenum sensu* Banke and co-workers (1997), then this name may be available for the clade containing the Fleming isolate. Examination of authentic material of *P. flavigenum* is necessary to make this determination.

PENICILLIUM CHRYSOGENUM AND THE INDOOR ENVIRONMENT

Raper and Thom (1949) observed that contamination of foods with *P. chrysogenum* resulted in sufficient content of penicillin to prevent the growth of *Clostridium*. Indeed, it is interesting to note that *P. chrysogenum* is one of only a few species in subgenus *Penicillium* not known to produce metabolites of significant toxicity to animals (Dillon et al., 1996; Samson et al., 1996). Similar attenutated toxicity has been noted for mycotoxin-producing species of *Aspergillus* associated with the seed caches of burrowing rodents (D. Wicklow, pers. comm.). It is conceivable that the reduced mycotoxicity of *P. chrysogenum* coupled with its predominance relative to other Penicillia in human-associated habitats reflect a similar adaptation to the human environment. This being the case, the production of penicillin, a potent antibacterial metabolite with negligible mammalian toxicity, would clearly be an adaptive advantage, particularly given that the fungus in question is a frequent contaminant of foodstuffs. Similarly, the ubiquity of *P. chrysogenum* in indoor environments has led to speculation that exposure to this penicillin-producing species may be a factor in the development of allergy to this antibiotic, however, such a link so far has not been demonstrated (Gravesen, 1979).

CONCLUSIONS

Penicillium chrysogenum is one of the most prevalent species in the indoor environment. Spores of this mould occur commonly in indoor dusts often at considerably high CFU per gram-mass concentration. To date, there has been little investigation into the level of genotypic diversity within this species. The present study supports the existence of a *P. chrysogenum* complex which consists of as many as three species propagated clonally in absence of recombination. *Penicillium notatum* is a valid synonym of *P. chrysogenum*. Formal description of the two un-named clades as separate species awaits the identification of defining phenotypic characters (e.g. micro-morphology and/or physiology).

Mycologia, 96(5), 2004, pp. 1095–1105.

Genotypic variation in *Penicillium chysogenum* from indoor environments

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Abstract: We examined 198 isolates of *P. chysogenum* recovered from 109 houses in Wallaceburg, Ontario, and 25 culture collection isolates including seven ex-type strains. Multilocus genotypes were determined by heteroduplex mobility assay of regions spanning introns in acetyl co-enzyme A synthase, beta-tubulin, thioredoxin reductase and the internal transcribed spacer regions of the nuclear ribosomal subrepeat. Five unique multilocus haplotypes were revealed without evidence of recombination, indicating strictly clonal population structures. Phylogenetic analysis of allele sequences using maximum parsimony resolved three strongly supported lineages. The dominant clade included more than 90% of house isolates in addition to the notable laboratory contaminant isolated by Alexander Fleming in 1929 in Britain. A second clade contained more than 5% of house isolates clustered with the ex-type strains of *P. chysogenum* and *P. notatum.* Follow-up sampling of outdoor air in the locality failed to reveal *P. chysogenum,* confirming the rarity of this fungus in outdoor air.

Key words: DNA sequence analysis, dust biology, fungal population genetics, heteroduplex mobility assay, indoor air quality, indoor molds

INTRODUCTION

Viable fungal spores occur in great numbers in household dust and indoor air. Many of these spores typically arise outdoors in the phylloplane and are carried indoors on air currents and contaminated footwear. Other genera, such as *Aspergillus* Fr. : Fr. and *Penicillium* Link, are poorly represented in outdoor air in contrast to their indoor frequency. Thus, it is widely believed that these molds proliferate indoors, often cryptically, on various substrates including dust itself under dry conditions.

Penicillium chysogenum Thom is perhaps the most common of all Penicillia (Pitt 1980, Raper and Thom 1949), occurring as an agent of food spoilage (Samson et al 1996) as well as a resident of household dust (Davies 1960) and indoor air. *Penicillium chysogenum* is also a well-known contaminant of damp building materials (Chang et al 1995, Gravesen 1999, Hunter and Lea 1995) and indoor finishes (Adan and Samson 1994). This species is one of the few terverticillate Penicillia that typically does not produce mycotoxins of significant mammalian toxicity (Dillon et al 1996, Nielsen and Gravesen 1999, Pitt and Cruikshank 1990). However, *P. chysogenum* has been identified as an important allergen in the indoor environment (Cooley 1999, Cooley et al 1999, Fergusson et al 1984) and as a rare causative agent of opportunistic mycosis in humans (Eschete et al 1981, Hoffman et al 1992).

Charles Thom (1910) described *P. chysogenum* as a contaminant from cheese. The authentic strain of this taxon is deposited as NRRL 807 (Thom's culture No. 26 = ATCC 10107, CBS 306.48 and DAOM 193710). Thom named *P. chysogenum* fundamentally based on the production of yellow guttation droplets on the colony surface, a characteristic he observed consistently during cultivation on a range of growth media. Thom discussed several strains that produced yellow guttation but varied in colony morphology to some degree, and he interpreted *P. chysogenum* in a broad sense to include these variant ''races'' (Thom 1910). Raper and Thom (1949) later expanded this already broad concept to include several taxa described by Dierckx (1901) and Biourge (1923), noting that these authors described taxa based largely on the examination of single strains that represented contrasting forms of *P. chysogenum.* However, they chose to maintain *P. cyaneo-fulvum* Biourge, *P. meleagrinum* Biourge and *P. notatum* Westling to accommodate the variation they observed in examinations

Accepted for publication March 17, 2004.
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of hundreds of isolates of the *P. chysogenum* ''series''. Raper and Thom (1949) considered *P. griseoroseum* Dierckx to be a synonym of *P. notatum.* Samson and co-workers (1977) reinforced the broad concept of *P. chysogenum* by further reducing *P. cyaneofulvum, P. meleagrinum* and *P. notatum* to synonymy with *P. chysogenum.*

Pitt (1980) neotypified *P. chysogenum* with a dried culture of IMI 24314 (as Herb. IMI 24314). Although, in his designation, Pitt referred to the specimen as a lectotype, it formally must be considered a neotype because the designated specimen was not examined by the original author (Article 9.2, ICBN) and the use of a living ex-type that has been maintained in culture cannot be assumed to have remained consistent with the original collection despite its pedigree. In his examination of authentic isolates from the *P. chysogenum* group, Pitt (1980) noted that *P. griseoroseum* produced a floccose colony morphology and biverticillate to irregularly terverticillate penicillia. On this basis, Pitt (1980) reclassified *P. griseoroseum* in *Penicillium* subgenus *Furcatum* and neotypified it with a dried culture at least seven transfers removed from the original isolate (Dierckx 3 > Inst. Pasteur 85 > Biourge 29 > Thom 4733.70 > LSHB P39-1930 > CMI 1962 > IMI 92220) (Hennebert 1985). Despite this subgeneric separation, Pitt (1980) considered *P. griseoroseum* to be close to *P. chysogenum.* In part, his decision to retain the former taxon might have been influenced by the historical significance of the strain in question, which is the oldest laboratory-maintained culture of the genus known (Pitt 1980, p. 7). Cruickshank and Pitt (1987) later supported the conspecificity of *P. chysogenum* and *P. griseoroseum* on the basis of isozyme electrophoretic patterns and reduced *P. griseoroseum* into synonymy with the former. Frisvad and Filtenborg (1989) further supported this conclusion by the comparison of mycotoxin profiles. In contrast, the numerical analysis of morphological and physiological data by Bridge et al (1989) excluded Thom's strain of *P. chysogenum* (Cluster 7) from the core of isolates of this species, which included the authentic culture of *P. griseoroseum* (Cluster 14). These authors rationalized the position of the ex-type culture of *P. chysogenum* (IMI 24314) by suggesting that it was an attenuated strain (Bridge et al 1989). However, investigations of *P. chysogenum* ex-type strains by other authors have not demonstrated any significant cultural deterioration (Pitt 1980, Pitt and Samson 1993). Indeed, Raper and Thom (1949) noted that during 40 years of continuous cultivation, the ex-type strain of *P. chysogenum* remained stable.

The modern concept of *P. chysogenum* includes rapidly growing isolates with loosely branched smooth terverticillate conidiophores and smooth ellipsoidal conidia. The production of yellow guttation and yellow diffusible pigment is also characteristic but varies from isolate to isolate. *Penicillium chysogenum* generally is thought to be strictly asexual because no teleomorph has been identified for this species. However, the clonal nature of *P. chysogenum* has not been tested systematically using a modern molecular genetic approach. Several additional taxa recently have been described that appear to be allied with *P. chysogenum,* specifically *P. aethiopicum* Frisvad, *P. dipodomyis* Frisvad, Filtenborg & Wicklow, *P. flavigenum* Frisvad & Sampson. The placement of these taxa relative to *P. chysogenum* similarly has not been investigated using molecular phylogenetic methods.

In the present study, we examined the extent of clonality within a core group of isolates from the *P. chysogenum* group and representative authentic isolates of related taxa and tested the phylogenetic validity of the current species concept of *P. chysogenum* based on the analysis of multilocus haplotype and DNA sequence data.

MATERIALS AND METHODS

Isolation and identification of strains.—More than 700 isolates of *P. chysogenum* were collected from 376 houses in Wallaceburg, Ontario, in 1994. These isolates were grown 14 d at room temperature on modified Leonian's agar (Malloch 1981) and modified Creatine-Sucrose agar medium (CSA) (Frisvad 1993). A duplicate plate of each isolate was incubated 7 d at 37 C. A subset of 198 micromorphologically and physiologically uniform isolates was selected for genetic characterization based on the hypothesis that these isolates represented a single phylogenetic species. Air sampling was conducted at 18 outdoor locations distributed evenly throughout Wallaceburg during late summer 1995, using a Reuter Centrifugal sampler (RCS) (Biotest, Dreieich, Germany) on Rose Bengal agar medium (Malloch 1981) with a sampling volume of 80 L per sample. Growth media were incubated and colonies analyzed as above.

The number assigned to each fungal isolate is unique and consists of an arbitrary ''house number'' coupled with an incremental accession number reflective of the total number of isolates of *P. chysogenum* obtained from that house. Additional isolates included in sequencing studies consisted of authentic strains as well as a geographical range of voucher isolates (TABLE I).

DNA isolation.—Fungal isolates were inoculated centrally on a Petri plate of Weitzman and Silva-Hutner's agar (WSHA) (Weitzman and Silva-Hutner 1967), and grown 7 d at room temperature under 12 h artificial daylight. The plates were flooded with 2 mL of 95% ethanol, and the conidia and mycelium were suspended by gently scraping the surface of the colonies with a sterile bent glass rod. Conidial suspensions were collected in microcentrifuge tubes, centrifuged at 12 000 rpm, and the supernatant was

TABLE I. Strains examined in this study

Species	Strain no.	Status	Substratum and locality
Penicillium aethiopicum Frisvad	CBS 484.84	ex-type	grains of *Hordeum vulgare,* Ethiopia
P. chrysogenum Thom	C8.12		house dust, Wallaceburg, ON, Canada
P. chrysogenum	C8.24		house dust, Wallaceburg, ON, Canada
P. chrysogenum	C200		house dust, Wallaceburg, ON, Canada
P. chrysogenum	C238		house dust, Wallaceburg, ON, Canada
P. chrysogenum	C317.1		house dust, Wallaceburg, ON, Canada
P. chrysogenum	DAOM 155627		paper, Ottawa, ON, Canada
P. chrysogenum	DAOM 155628		paper, Ottawa, ON, Canada
P. chrysogenum	DAOM 155631		paper, Ottawa, ON, Canada
P. chrysogenum	DAOM 167036		*Picea* forest soil, QC, Canada
P. chrysogenum	DAOM 171025		salami, Ottawa, ON, Canada
P. chrysogenum	DAOM 175157		walls of mouldy house, Niagara Falls, ON, Canada
P. chrysogenum	DAOM 175176		*Lycopersicum esculentum* leaves, PEI, Canada
P. chrysogenum	DAOM 175758		office building, OC, Canada
P. chrysogenum	DAOM 178623		*substr. et loc. incert.*
P. chrysogenum	DAOM 190864		grains of *Hordeum,* MB, Canada
P. chrysogenum	DAOM 193710	ex-type	cheese, CT, USA
P. chrysogenum	DAOM 212031		wooden wall studs, AB, Canada
P. chrysogenum	DAOM 215336		wooden wall studs, AB, Canada
P. chrysogenum	DAOM 215337		hemlock lumber, BC, Canada
P. chrysogenum	DAOM 216700		grains of *Hordeum,* Canada
P. chrysogenum	DAOM 216701		*Sesamum indicum,* Korea
P. chrysogenum	DAOM 59494C		*substr. incert.,* Honduras
P. chrysogenum	NRRL 824		laboratory contaminant, London, England
P. dipodomyis (Frisvad et al) Banke et al	NRRL 1485	ex-type	cheek pouch of *Dipodomyis spectabilis,* AZ, USA
P. flavigenum Frisvad & Samson	CBS 419.89	ex-type	flour, Lyngby, Denmark
P. flavigenum	IMI 321909		*substr. et loc. incert.*
P. nalgiovense Laxa	NRRL 911	ex-type	cheese, Nalzovy, Czech Republic
P. notatum Westling	ATCC 10108	ex-type	branches of *Hyssopus* sp., Norway

discarded. The pellets were dried 30 min in a vacuum concentrator centrifuge. This protocol yielded approximately 15 mg of pelleted conidia per vial. Each vial was sufficient for a single DNA isolation.

Approximately 15 mg of sterile, acid-cleaned Dicalite 1400 (diatomaceous earth-based swimming pool filter, Grefco Inc., Torrance, California) was added to each tube of dry, pelleted, ethanol-killed conidia (Scott et al 1999). After the addition of 10 μL of 70% EtOH, the mixture was ground with a sterile glass rod 1 min and suspended in 600 μL of lysis buffer containing 1.4 M NaCl, 2% w/v CTAB, 200 mM Tris·HCl (pH 8.0) and 20 mM EDTA (Weising et al 1995). Tubes were incubated at 65 C for 1 h and were mixed by inversion at 30 min intervals.

After extraction, the tubes were cooled to room temperature and centrifuged at 10 000 rpm for 1 min. The supernatant liquid was extracted twice with chloroform : isoamyl alcohol (24:1), and the DNA was precipitated with 100% isopropanol at −80 C for 10 min. The pellets were rinsed with 70% ethanol, air-dried and resuspended in 200 μL TE (pH 8.0) (Sambrook et al 1989). Ribonuclease A was added to the DNA at a final concentration of 0.2 μg/μL and incubated at 37 C for 30 min. The DNA was extracted with chloroform : isoamyl alcohol and precipitated with 0.3 M sodium acetate and an equal volume of 100% ethanol at −80 C. DNA pellets were rinsed with 70% ethanol, air-dried and resuspended in 100 μL TE (pH 8.0). DNA concentration was adjusted to 60 ng/μL based on spectrophotometry.

DNA preparation and heteroduplex mobility assay (HMA).— Four polymorphic loci consisting of partial regions spanning introns in the genes encoding acetyl co-enzyme A synthase (acuA), beta-tubulin (benA), thioredoxin reductase (trxB) and the region spanning the internal transcribed spacer (ITS1-5.8S-ITS2) of the nuclear ribosomal RNA gene (rDNA) were PCR-amplified using the primers listed in TABLE II. PCR mixtures consisted of 1 unit of *Taq* DNA polymerase (Boehinger Mannheim, Laval, QC), 50 mM KCl, 2.0 mM $MgCl_2$, 250 μM of each dNTP, 0.2 mM of each primer and 60 ng of template DNA in a total reaction volume of 50 μL overlaid with a drop of sterile mineral oil. Reactions were carried out in a PTC-100 thermocycler (MJ Research, Reno, Nevada). Cycling conditions consisted of 30 cycles of 94 C for 30 s, 58 C for 30 s and 72 C for 30 s with a final extension at 72 C for 2 min. Yield was quantified based on ethidium bromide staining and UV visualization after electrophoresis on 1.2% agarose gels.

Heteroduplexing reactions pooled homologous PCR products pairwise in overlapped combinations (pairs comprised numerically adjacent isolates in a sequentially numbered series of PCRs and the first and last isolate of each series) to encompass the entire set. For each locus exam-

TABLE II. Primers sequences employed in this study

Acetyl-CoA synthetase (acuA)	
Source: this study, Genbank L09598, +2102-2452, spanning introns 3 and 4	
acuA-2F (fwd)	5′-ACC GTG TGG GGT GCC CAC AAG CGT TAC ATG-3′
acuA-1R (rvs)	5′-GGT CAG CTC GTC GGC AAT ACC AAC GAC AGC-3′
Beta-tubulin (benA)	
Source: Glass and Donaldson (1995)	
Bt2A (fwd)	5′-GGT AAC CAA ATC GGT GCT GCT TTC-3′
Bt2b (rvs)	5′-ACC CTC AGT GTA GTG ACC CTT GGC-3′
Nuclear ribosomal DNA ITS1, 5.8S and ITS2 region (ITS)	
Source: White et al (1990), fwd; Untereiner et al (1995), rvs	
ITS5 (fwd)	5′-GGA AGT AAA AGT CGT AAC AAG G-3′
WNL1 (rvs)	5′-TAT GCT TAA GTT CAG CGG-3′
Thioredoxin reductase (trxB)	
Source: this study, EMBL X76119, +801-1153, spanning intron 2	
trxB-1F (fwd)	5′-AAC GCG GAG GAG GTC GTT GAG GCT AAC GGT-3′
trxB-1R (rvs)	5′-TTA GAG CAC AGG CTT TGC CTC CTG GTG AGT-3′

ined, PCRs were diluted to 50% of the original concentration with 4 mM EDTA and 50 mM KCl, combined in equimolar proportion in a total volume of 10 μL and overlaid with a drop of sterile mineral oil. Reactions were heated to boiling for 4 min and immediately annealed at 65 C for 6 min. Products of HMA reactions were separated by electrophoresis in gels consisting of 12% acrylamide, 0.2% bisacrylamide and 0.04% ammonium persulfate in 1 × TBE. Immediately before casting, 0.5% agarose and 0.2% TEMED were added to the degassed solution. Gels were cast in a BioRad Protean electrophoresis apparatus (La Jolla, California) at 1 mm thick, allowed to polymerize 4–5 h and run on a vertical electrophoresis apparatus (Protean II, BioRad) at 10 V/cm, 12 C for up to 20 h. Gels were stained for 2 h in ethidium bromide (250 ng/mL) and destained in dH_2O 3–4 h before imaging.

Using HMA, like pairs of isolates were reduced to a single "proxy" strain by transitive property of equality (Scott et al 1999, Scott et al 2000). Subsequent rounds of HMA compared proxy isolates ultimately reducing the entire population to a set of genotypically distinct alleles represented by a minimum number of proxy isolates for each locus tested. One or more isolates for each multilocus genotype identified by heteroduplex analysis were sequenced for phylogenetic analysis.

DNA sequencing and analysis.—PCR templates were purified using QIAquick PCR purification kit (Qiagen Inc., Valencia, California) and sequenced using a *Taq* DyeDeoxy cycle sequencing kit (Applied Biosystems Inc., Foster City, California) and the same primers employed for amplification. Extension products were run on an ABI50 fluorescent automated sequencer (Applied Biosystems Inc.).

Alignments of sequences were performed using Clustal X software version 1.64b (Thompson et al 1997) and adjusted by visual inspection. Phylogenetic relationships were inferred from aligned sequences using the maximum parsimony (MP) method found in PAUP* (beta version 4.0b10) (Swofford 2003).

An heuristic search of the benA dataset (29 taxa, 434 bp, gaps treated as missing) was performed employing tree bisection-reconstruction (TBR) branch swapping with MulTrees and steepest descent options activated. We also performed exhaustive searches of individual datasets consisting of sequences of *P. chysogenum* (DAOM 193710 ex-type, NRRL 824 Fleming strain), *P. notatum* (ATCC 10108 ex-type) and representatives of the Wallaceburg multilocus haplotypes (*P. chysogenum* C8.24, C8.12, C200, C238, C317.1) for each of the four genetic loci (acuA 291 bp, benA 430 bp, ITS 546 bp, trxB 306 bp). In addition, the ITS dataset was expanded to include the sequence of the ex-type strain of *P. griseoroseum* (NRRL 820). Phylogenies of the eight-taxon dataset also were generated from exhaustive searches of a combined three-locus (acuA, benA, trxB) and four-locus datasets. A single multibase indel in the benA dataset was rescored as a single gap, and gaps were treated as a fifth character in analyses of the pruned datasets that included sequences for this locus. Taxa use as outgroups included *P. nalgiovense* NRRL 911 and *P. dipodomyis* NRRL 13485 (29-taxon benA dataset) and *P. chysogenum* NRRL 824 (eight-taxon dataset).

Bootstrap support (Felsenstein 1985) for internal branches was evaluated from 1000 heuristic searches, and groups with a frequency of greater than 50% were retained in the bootstrap consensus trees. Congruence between the three (acuA, benA, trxB) and four loci for eight taxa was measured based on 10 000 heuristic searches (TBR branch swapping with MulTrees and steepest descent options activated) using the partition-homogeneity test (PHT) included in PAUP*.

RESULTS

Penicillium chysogenum was observed in 52% of houses investigated. Isolates of *P. chysogenum* were re-

TABLE III. Haplotype frequencies of indoor *P. chrysogenum* isolates

Proxy isolate	Locus				No. of isolates	Frequency
	acuA	benA	ITS	trxB		
C8.12	A	A	A	A	179	0.904
C317.1	A	C	B	C	5	0.025
C8.24	B	B	B	B	11	0.056
C238	C	B	B	B	2	0.010
C200	A	C	C	C	1	0.005

tained from a subset of houses investigated (109/369 houses), yielding a total of 198 isolates. Multiple isolates were obtained from 30 houses. *Penicillium chysogenum* was not observed in the 18 outdoor air samples taken throughout Wallaceburg during August 1995.

Haplotypes of house dust isolates identified by heteroduplex analysis are given in TABLE III. The multilocus haplotype AAAA (acuA, benA, ITS and trxB, respectively), represented by the isolate C8.12, was the most commonly observed haplotype in the population and represented more than 90% of all isolates. The second most common multilocus haplotype, BBBB, accounted for 5.6% of the isolates studied and is represented by isolate C8.24 (the same house as the representative isolate used for AAAA, above). Thee minor multilocus haplotypes (ACBC, ACCC and CBBB) accommodated the remainder of the isolates. Multiple genotypes were recovered from 27% of houses where multiple isolates were obtained. Allele identities were confirmed by the sequencing of proxy isolates. Genbank accession numbers for these and other sequences used in this study are given in TABLE IV.

Phylogenetic relationships of species in the *P. chysogenum* group were inferred from an heuristic analysis of partial sequences of the beta-tubulin (benA) gene. This dataset included 29 taxa and consisted of a 434 bp region spanning introns 3–5. MP analysis yielded four MPTs 48 steps in length (L) with a con-

TABLE IV. Sequences used or developed in this study

Identification	Strain no.	GenBank accession numbers			
		acuA	benA	ITS	trxB
P. aethiopicum	CBS 484.84	AY371577	AY371605	AY371635	AY371663
P. chrysogenum	C8.12	AY371550	AY371578	AY371608	AY371637
P. chrysogenum	C8.24	AY371552	AY371579	AY371610	AY371640
P. chrysogenum	C200	AY371555	AY371580	AY371614	AY371639
P. chrysogenum	C238	AY371556	AY371581	AY371613	AY371642
P. chrysogenum	C317.1	AY371554	AY371582	AY371612	AY371638
P. chrysogenum	DAOM 155627	AY371561	AY371584	AY371619	AY371647
P. chrysogenum	DAOM 155628	AY371562	AY371585	AY371620	AY371648
P. chrysogenum	DAOM 155631	AY371563	AY371586	AY371629	AY371657
P. chrysogenum	DAOM 167036	AY371564	AY371587	AY371621	AY371649
P. chrysogenum	DAOM 171025	AY371565	AY371588	AY371630	AY371658
P. chrysogenum	DAOM 175157	AY371566	AY371589	AY371622	AY371650
P. chrysogenum	DAOM 175176	AY371567	AY371590	AY371623	AY371651
P. chrysogenum	DAOM 175758	AY371568	AY371591	AY371624	AY371652
P. chrysogenum	DAOM 178623	AY371569	AY371592	AY371631	AY371659
P. chrysogenum	DAOM 190864	AY371570	—	AY371625	AY371653
P. chrysogenum	DAOM 193710	AY371553	AY371594	AY371611	AY371641
P. chrysogenum	DAOM 212031	AY371571	AY371595	AY371626	AY371654
P. chrysogenum	DAOM 215336	AY371572	AY371596	AY371627	AY371655
P. chrysogenum	DAOM 215337	AY371573	AY371597	AY371632	AY371660
P. chrysogenum	DAOM 216700	AY371574	AY371598	AY371628	AY371656
P. chrysogenum	DAOM 216701	AY371575	AY371599	AY371633	AY371661
P. chrysogenum	DAOM 59494C	AY371560	AY371583	AY371618	AY371646
P. chrysogenum	NRRL 824	AY371551	AY371600	AY371609	AY371636
P. dipodomyis	NRRL 13485	AY371557	AY371602	AY371615	AY371644
P. flavigenum	CBS 419.89	—	AY371607	—	—
P. flavigenum	IMI 321909	—	AY371606	—	—
P. griseoroseum	NRRL 820	—	—	AF034857	—
P. nalgiovense	NRRL 911	AY371559	AY371601	AY371617	AY371645
P. notatum	ATCC 10108	AY371576	AY371604	AY371634	AY371662

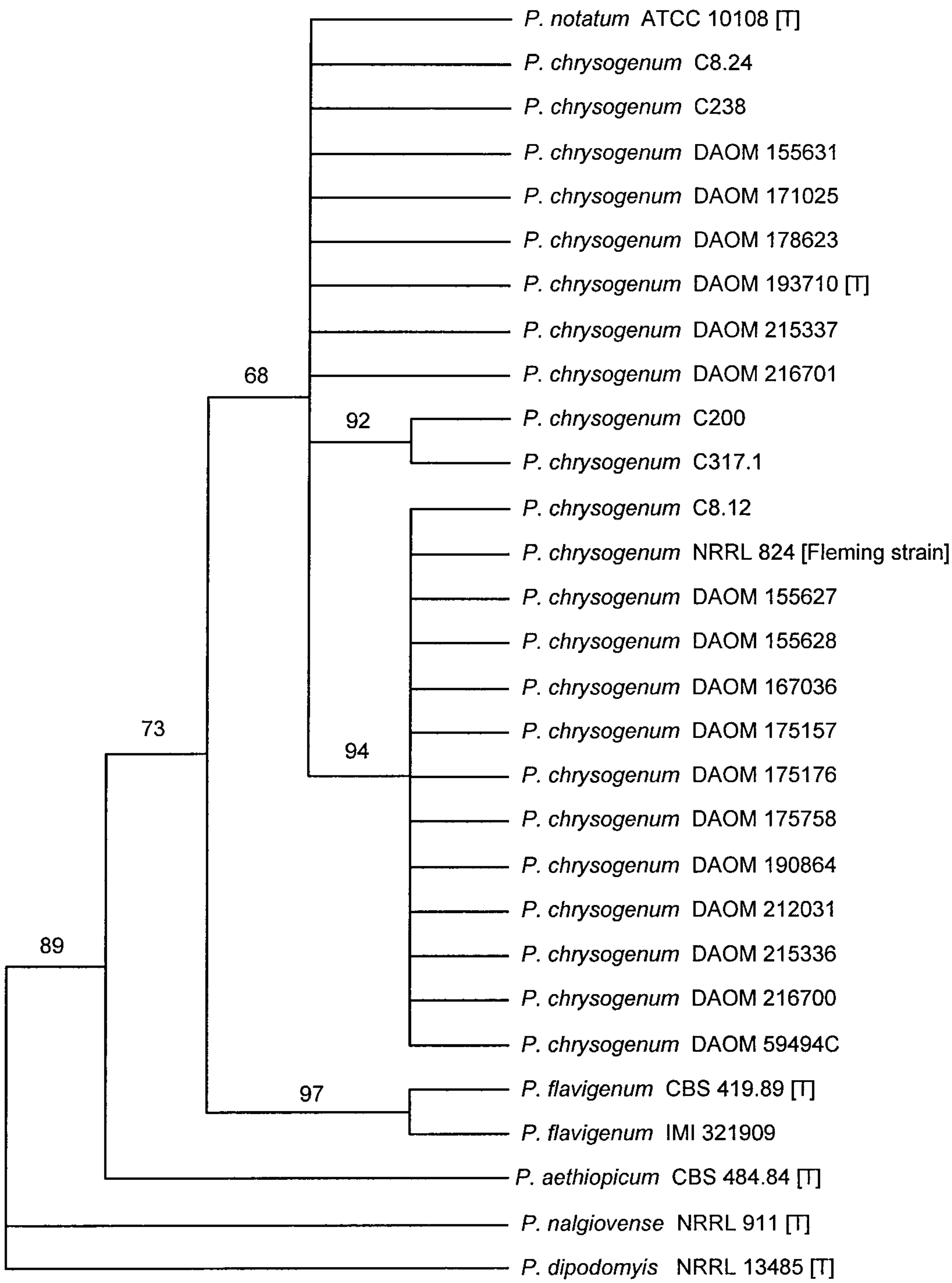

FIG. 1. Phylogenetic relationships of members of the *P. chrysogenum* group inferred from partial beta-tubulin gene sequences. This is a strict consensus of 4 MPTs (L = 48, CI = 0.878, RI = 0.918) generated from a heuristic analysis of 434 bp for 29 taxa. Bootstrap values greater than 50% calculated from 1000 replicates are indicated above the branches. The outgroup taxon are *P. dipodomyis* NRRL 13485 and *P. nalgiovense* NRRL 911.

sistency index (CI) and a retention index (RI) of 0.878 and 0.918, respectively. The strict consensus of these trees (FIG. 1) shows a large well supported lineage (bootstrap support of 73% in 1000 replicates) that corresponds to the *P. chysogenum-P. flavigenum* clade (TreeBase SN1793-5703). In this phylogeny, *P. chysogenum sensu lato* (bootstrap support of 68%) comprised two well supported lineages as well as representative isolates from Canada (British Columbia and Ontario), Norway (ATCC 10108), South Korea

TABLE V. Summary of MPTs produced from each of 4 loci examined

Locus	Number of MPTs	Length (steps)	CI	RI	Total chrs	PI chrs
acuA	1	14	1.000	1.000	291	10
benA	1	12	0.833	0.846	432	10
ITS	1	2	1.000	1.000	546	1
trxB	1	10	1.000	1.000	306	10
4 loci	1	38	0.947	0.962	1575	31
3 loci (w/o ITS)	1	36	0.944	0.961	1029	30

(DAOM 216701) and the United States (DAOM 178623, DAOM 193710). The larger of these clades (bootstrap support of 94%) contained isolates from Canada (including Alberta, Manitoba, Ontario, Prince Edward Island and Quebec), Honduras (DAOM 59494C) and the United Kingdom (NRRL 824). The smaller clade (bootstrap support of 94%) included six isolates obtained from Wallaceburg house dust.

Analysis of individual data from partial acuA, benA and trxB sequences resulted in 10 parsimony-informative characters for each locus (TABLE V). Analysis of ITS data yielded only a single parsimony-informative character (TABLE V). MPTs generated from individual locus datasets showed identical or compatible topologies, supporting the analysis of these datasets in combination (data not shown). Results of 10 000 heuristic searches implementing the PHT ($P = 1.0$) also demonstrated that these topologies are congruent and that sequences from the four different loci may be combined.

Combined analysis of data from partial acuA, benA, ITS and trxB sequences included eight taxa comprising the core of the *P. chysogenum* group. An exhaustive search of the combined dataset (1575 bp, 31 parsimony-informative characters) produced a single MPT (L = 38, CI = 0.947, RI = 962) dividing *P. chysogenum sensu lato* into four well-supported clades (bootstraps 98% or higher) (FIG. 2) (TreeBase SN1793-5704). Clade 1 included the ex-type strains of *P. chysogenum* (DAOM 193710), *P. notatum* (ATCC 10108) and 11 (5.6%) isolates from Wallaceburg house dust (represented in FIG. 2 by C8.24). This lineage was sister of Clade 2, a group that contained two Wallaceburg isolates (1.0% of isolates). Clade 3 consisted of six Wallaceburg isolates (3.0%). The majority of Wallaceburg *P. chysogenum* isolates (179/198, 90.4%) clustered in Clade 4 with the British strain isolated by Alexander Fleming (NRRL 824).

The single dataset MPT based on ITS sequences divided *P. chysogenum sensu lato* into two lineages corresponding to Clades 1/2/3 and Clade 4 from the combined analysis (data not shown) (TreeBase SN1793-5705). The ex-type strain of *P. griseoroseum* (NRRL 820, GenBank AF034857) grouped with the ex-type strains of *P. chysogenum* and *P. notatum,* but this clade was not strongly supported (data not shown).

DISCUSSION

Five unique multilocus haplotypes were revealed without evidence of recombination, indicating strictly clonal population structures in these lineages. Our results support the conclusions of Banke et al (1997) that *P. chysogenum, P. flavigenum, P. nalgiovense* and *P. dipodomyis* are distinct species and that the former two taxa are sister groups. Banke et al (1997) noted a high degree of infraspecific variability in *P. flavigenum* and suggested that this species might consist of several subgroups. Our analysis showed two strains of *P. flavigenum* to be closely related, however these isolates did not share complete sequence homology for the region of beta-tubulin gene examined. Further work is necessary to resolve the phylogenetic structure of this species.

The phylogeny based on partial beta-tubulin sequence showed lineages in *P. chysogenum sensu lato* to be represented across Canada and from a broad geographic range extending to localities in North and Central America, Europe/Scandinavia and Asia (FIG. 1). Our analysis of four gene regions yielded thee topologically compatible trees revealing thee well supported clonal lineages within *P. chysogenum sensu lato.* Applying the phylogenetic species concept advocated by Taylor et al (2000) on the basis of concordance of multiple gene genealogies, these lineages represent distinct phylogenetic species. These lineages collectively may be called the *P. chysogenum* species complex. Our study showed *P. chysogenum sensu stricto* (Clade 1) to be uncommon in the indoor dust mycobiota relative to isolates of Clade 4. Culture collection strains positioned within Clade 1 were isolated as contaminants from raw wood, paper and proteinaceous foods (e.g., sausage, cheese). In contrast, strains clustering with Clade 4 isolates originated from cereals, paper, soil, construction materials and indoor environments, and included the strain isolat-

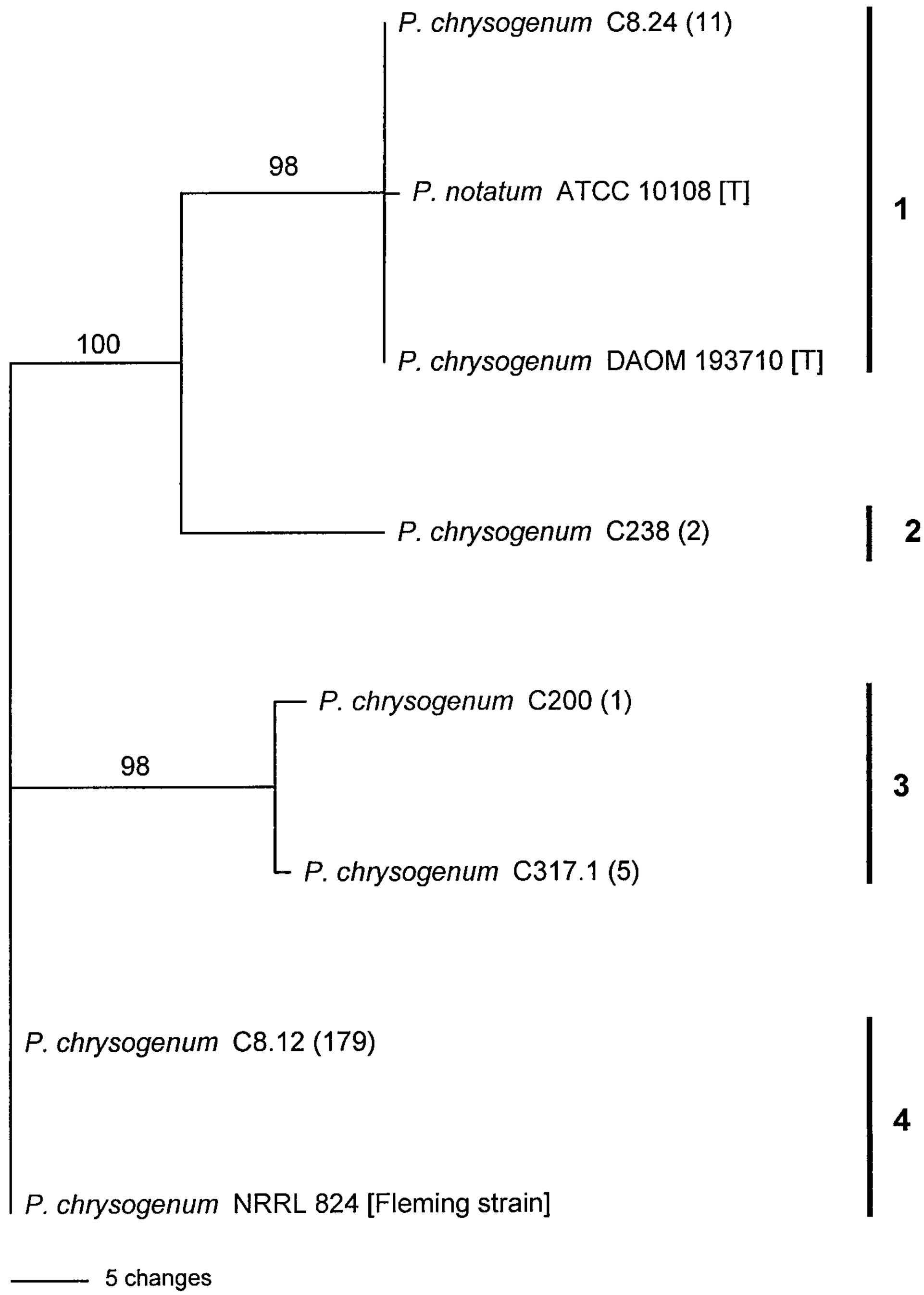

FIG 2. Single MPT inferred from an exhaustive search of the combined acuA, benA, ITS and trxB sequences of authentic or type strains of *P. chrysogenum* strains and Wallaceburg house dust isolates (1575 bp, L = 38, CI = 0.947, RI = 962; 1537 characters are constant, five variable characters are parsimony-uninformative, 31 characters are parsimony-informative). Bootstrap values greater than 50% calculated from 1000 replicates are indicated above the branches. The numbers of Wallaceburg isolates of identical multilocus haplotype are indicated in parentheses.

ed by Alexander Fleming in 1929 as a laboratory plate contaminant (Fleming 1929). The abundance of isolates assigned to Clade 4 suggests that this lineage may have a competitive advantage over other lineages to exploit human-associated indoor niches, although support for this hypothesis would require the investigation of distribution patterns of members of this group in other geographic regions.

The absence of members of the *P. chysogenum* species complex in outdoor air in comparison to the abundance of this group in indoor dust is intriguing. Two competing hypotheses could explain this observation:

(i) Members of the *P. chysogenum* complex form autochthonous populations (i.e., true populations) in household dust and/or on other indoor materials in the presence of superfluous moisture. Consequently, growth and sporulation (amplification) of these fungi indoors over time leads to their quantitative predominance in the dust mycoflora (Bronswijk 1981).

(ii) Viable indoor spores of the *P. chysogenum* complex originate from few airborne members of these taxa in the phyloplane and simply accumulate indoors faster than spores of other taxa as a consequence of their disproportionately longer viability and relatively inefficient removal. It is known that the asexual spores of members of the Trichocomaceae retain viability for a long time under dry conditions (Sussman 1968). Indeed, reculture of dust samples used in this project after a period of 5 yr in dry storage yielded only members of the Trichocomaceae and *Aureobasidium pullulans* (data not shown). In this manner, the number of *P. chysogenum* complex in indoor dust might relate in part to the ''removal'' of other taxa due to attenuated viability. Mechanical factors relating to size distribution also might be important. The spores of members of the *P. chysogenum* complex and related trichocomaceous anamorphs are small in relation to the majority of mitosporic taxa that quantiatively dominate dust in building interiors (e.g., *Cladosporium, Alternaria, Ulocladium*). These small-spored species might be inefficiently removed from the indoor environment by filtration systems in vacuum cleaners and forced-air heating systems. Stetzenbach et al (1999) reported this effect in relation to consumer market vacuum-cleaning devices. Combined, these effects or longer viability and less efficient removal might result in the emergence of an indoor allochthonous population (i.e., pseudo populations) whose constituent elements arise episodically in the phylloplane.

The conspecificity of *P. griseoroseum* and *P. chysogenum* is supported in the present study, in which the ex-type isolate (NRRL 820) clustered with the ex-type cultures of *P. chysogenum* (NRRL 807) and *P. notatum* (NRRL 821) based on the analysis of ITS sequences (data not shown). *Penicillium chysogenum* is thus a later synonym of *P. griseoroseum* based on priority of publication. This conclusion is not surprising because Banke et al (1997) obtained highly similar secondary metabolite profiles for 18 isolates of *P. chysogenum* including the ex-type strain of *P. griseoroseum.* Their proposed conspecificity of *P. chysogenum* with *P. griseoroseum* led Frisvad and co-workers (1990) to recommend conservation of the name due to the industrial importance of this species. They recommended the conservation of *P. chysogenum* as ''the species name for the principal producer of penicillin'' on the basis that the association between the name ''*Penicillium chysogenum*'' and the biochemical characteristic of penicillin biosynthesis was of paramount industrial importance (Frisvad et al 1990a, Lowe and Elander 1983). However, penicillin is known from a range of filamentous fungi (Abraham and Newton 1967, Samson et al 1996) and is speculated to have originated in fungi by horizontal gene transfer from a penicillin-producing actinomycete (Rosewich and Kistler 2000). Kozakiewicz et al (1992) later made a formal proposal to conserve the name *P. chysogenum.* From a nomenclatural standpoint, there do not appear to be existing species or varietal names that can be applied to our clades 3 and 4. Moreover, the erection of new taxa to accommodate these lineages would not conflict with the nomenclatural conservation of *P. chysogenum* and should be pursued. The phylogenetic positions of the major penicillin-producing strains of *P. chysogenum sensu lato* in relation to these new species have not been investigated.

ACKNOWLEDGMENTS

We are grateful to Carolyn Babcock (CCFC, Agriculture Canada, Ottawa) and Dr Stephen W. Peterson (ARS Culture Collection, USDA, Peoria Illinois) for providing isolates used in this study. Financial support for this work was provided by an NSERC Doctoral Postgraduate Scholarship (PGS-B) to JS, an NSERC Strategic grant to DM and NAS, and an NSERC Discovery Grant to WAU.

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DAOM accession numbers for *Penicillium chrysogenum* group cultures*

CLADE 1

Penicillium chrysogenum
DAOM 238886 (C8.24)
DAOM 238887 (C34.4)
DAOM 238888 (C47)
DAOM 238889 (C58.7)
DAOM 238893 (C67.3)
DAOM 238895 (C72.1)
DAOM 238896 (C72.2)
DAOM 238898 (C94)
DAOM 238902 (C232.1)

CLADE 2

Penicillium sp. nov. 1
DAOM 238894 (C71.1)
DAOM 238903 (C238)

CLADE 3

Penicillium sp. nov. 2
DAOM 238885 (C8.18)
DAOM 238892 (C58.15)
DAOM 238897 (C77.2)
DAOM 238900 (C200)
DAOM 238904 (C317.1)

CLADE 4

Penicillium sp. nov. 3
DAOM 238883 (C8.4)
DAOM 238884 (C8.12)
DAOM 238890 (C58.8)
DAOM 238891 (C58.14)
DAOM 238899 (C161)
DAOM 238901 (C225.30)
DAOM 238905 (C326.4)
DAOM 238906 (C354.2)

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*Clades after Scott et al (2004) [updated April 3, 2007]

CHAPTER 7. CONCLUSIONS AND GENERAL SUMMARY

The impact of indoor fungal contamination on human health has received ever-increasing attention since the early 1970s. Despite evidence that such problems have existed throughout recorded history, the present involvement of fungi as agents of declining IAQ and structural compromise is comparably recent and lacks historical precedent. I propose that the occurrence of three protracted events during the last century have collectively precipitated the present fungal epinostic in North America. These include:

1. The shift from a mainly industrial- to a white collar labor force
2. The development of an economy dependent upon access to Middle-Eastern reserves of fossil fuels
3. The movement to design and construct energy efficient buildings following the 1973 oil crisis

This hypothesis supports the view that the exploitation of indoor niches formed by water incursion on structural elements or indoor finishes by the ecological group of fungi collectively known as "domicile fungi" is a contemporary phenomenon. Despite that various of the fungal taxa involved in the contamination of human environments may to some extent have been pre-adapted to these habitats, principally as agents of food spoilage, I shall briefly outline a course of events in recent social history that refutes an hypothesis that these fungi have co-evolved with humans principally as contaminants of domestic structures.

The construction of houses for human habitation is thought to have coincided with the Agricultural Revolution 8,000 to 10,000 years ago, which was marked by a gradual shift from a primarily nomadic, hunter-gather lifestyle to a more sedentary life of agriculture (Childe, 1950; Grigg, 1974). The first observation of airborne spores may be credited to the Roman philosopher Lucretius of the first century BC, who remarked on the shimmering clouds of fine particles made visible by the passage of rays of sunlight through the air (Lucretius, *ca.* 50 BC). Although Lucretius incorrectly interpreted these particles as evidence of "thin images" that he hypothesized were perpetually radiated by all objects permitting their perception, the fact that he was able to visualize particles whose minute size rendered them otherwise imperceptible to the unaided eye was because of the "Tyndall effect" which was not elucidated until nearly two millennia later by Faraday (Considine, 1976).

FUNGAL DECAY IN EARLY STRUCTURES

Perhaps the earliest clearly attributable description of indoor fungal contamination comes from the Old Testament book of Leviticus, which provided a convincing account of the timber dry-rot fungi, *Serpula lacrimans* (Wulfen: Fr.) Schröeter and *S. incrassata* (Berk. & M.A. Curtis) Donk. This passage cautioned against structural rot in which the walls of a house develop "hollow strakes, greenish or reddish" (Lev. 14:37) or manifest as "a bright spot" (Lev. 14:56). Leviticus instructed that an affected house shall be sealed up for seven days after which it shall be examined to determine if the growth is active, in which case a series of remedies were proposed of increasing fervour. The goal of these procedures was the ultimate removal and disposal of affected materials with care not to risk contaminating other houses.

> "…take away the stones in which the plague is, and… cast them into an unclean place without the city… cause the house to be scraped within round about, and… pour out the dust… without the city and into an unclean place.
>
> (Lev. 14:40-41)

If remedial efforts failed, destruction of the house was recommended.

> "…break down the house, the stones of it, and the timber thereof, and all the mortar of the house; and… carry them forth out of the city into an unclean place.
> (Lev. 14:45)

In his seminal work on wood decay fungi, Bondartsev (1953) characterized dry rot of timber by the production of "…slightly noticeable discolorations… followed later by white spots and depressions". Dolenko and colleagues (1981) similarly noted that dry rot infections begins as:

> "thin, silky-gray mycelium with patches of yellow, or as a fan-shaped, lilac-colored mycelial mat. Characteristic thick strands, which are brown to black, may develop on the wood… In time the conk becomes rusty red as a result of myriads of spores produced.

The mycelium of *Serpula* produces aggressive rhizomorphs that can penetrate masonry and stone walls, often travelling long distances over concrete surfaces or plumbing to colonize more wood (Ellis and Ellis, 1990; Singh, 1994). Ginns (1986) reported this fungus as a frequent agent of brown rot of timbers in Canada, but noted that it was unknown from natural habitats. Similarly, the occurrence of this fungus in Europe appears limited to woods in service (Buczacki, 1989; Gray, 1956; Singh, 1994). Indeed the most natural habitat for this fungus worldwide is perhaps best described by its Swedish common name, *hussvamp*, literally house-mushroom (Ryman and Holmåsen, 1998). Dry rot is undeniably the most common agent of decay of wooden structure worldwide (Singh, 1994) and there is little doubt that this is the organism described in Leviticus.

VENTILATION

Aurora (1986) suggested that the practice of occluding exterior house vents in Europe during WWII contributed to the extent of problems posed to British housing by dry rot. Indeed, archaeological evidence indicates that the ancients deliberately included structural features in their buildings to promote ventilation and prevent the build-up of indoor contaminants, including dampness (Janssen, 1999). The goal of most early ventilation was the removal of smoke from heating and cooking fires (Spengler and Samet, 1991); however, ventilation was also used for disease prevention in ancient Egypt following the observation that stone carvers who worked in tightly enclosed buildings experienced a greater incidence of lung disease than those working in tents or outdoors (Woods, 1988). Later, in the Middle Ages, overcrowding of indoor environments and poor ventilation were recognized as factors for the transmission of communicable diseases (Janssen, 1999).

EARLY HOUSING AND URBANIZATION

During the vast stretch of time from the Neolithic to the 13th century AD, few improvements were made to the construction of basic European housing (Bronswijk, 1981). Typical human dwellings consisted of elongate structures of wooden poles bound with twigs and thatched with reeds and loam, in which the interior space was generally divided up with the central third used for habitation while the front and back thirds provided grain storage and shelter for livestock (ibid.). This practice, and the widespread use of straw as a flooring material almost certainly contributed to IAQ-related problems, particularly dander allergies and contagious diseases (Pope et al., 1993).

In the late 17th century, the amateur Dutch optics experimenter Antonie van Leeuwenhoek was first to observe microscopic arthropods in dust collected from his home (Bronswijk, 1981). By this time, European urbanization had reached a sufficient density to cause significant levels of outdoor air pollution resulting from the consumption of coal and wood for fuel (Spengler and Samet, 1991). The British diarist John Evelyn wrote of its effects:

> "It is this horrid smoke, which obscures our churches and makes our palaces look old, which fouls our clothes and corrupts the water so that the very rain and refreshing dews which fall in the several seasons precipitate this impure vapour,

> which with its black and tenacious quality, spots and contaminates whatever is exposed to it.
>
> (Evelyn, 1661 *fide* Spengler and Samet, 1991)

At the arrival of the Industrial Revolution in the middle of the 18th century, there was already widespread acknowledgement that declining outdoor air quality negatively influenced human respiratory health (Spengler and Samet, 1991). The dramatic shift in the workforce from agriculture to industry had the further effect of redistributing large segments of the population throughout Europe. In the period from the beginning to the end of the 19th century, the proportion of the world population who lived in towns of 20,000 or more inhabitants rose from 2.5 to 10 % (Davis, 1965). Matossian (1989) suggested that advances in agricultural practices, notably the introduction of the potato into Europe by the Spanish (Simpson and Ogorzaly, 1986), facilitated this population explosion. Her argument centred on the fact that the potato offered more caloric value than grain as a function of cultivated acreage, and that the potato was healthier, being less prone to the insidious mycotoxin contamination that so plagued stored cereals, particularly rye (Matossian, 1989). Nevertheless, increased urbanization meant a sharp increase in the proportion of the world's population that relied on food provided through commercial agriculture (Schlebeker, 1960). The gradual movement away from an agriculture-centred society marked by the Industrial Revolution was similarly correlated to the rapid build-up of urban centres at pivotal points along burgeoning trade routes by a large influx of working class population (Engels, 1845). Living conditions were grim, buildings were "badly planned, badly built, and kept in the worst condition, badly ventilated, damp, and unwholesome" (ibid.).

MODERN ERA

The formal study of airborne fungi began with the work of the French microbiologist Louis Pasteur. In his landmark work which ultimately razed the Theory of Spontaneous Generation, Pasteur collected microscopic airborne fungi in broth medium contained in swan-necked flasks from the air at numerous sites in and around Paris (Pasteur, 1861). Pasteur's work demonstrated that minute fungal propagules are carried upon air currents. It was this invisible microbial burden of air, he proposed, and not spontaneous generation that was responsible for microbial problems ranging from the spoilage of foods to human infections (Drouhet, 1999). Pierre Miquel, a student of Pasteur, documented in his 1883 dissertation the fungal content of air in homes and hospitals. He was first to propose an airborne route of exposure to fungal spores as an important factor in the establishment of nosocomial and opportunistic pulmonary mycotic infections (Drouhet, 1999).

Legislation of formalized building codes in Europe during the late 19th and early 20th centuries brought about an end to 6 millennia of *ad hoc* residential construction using sod, branches and clay (Bronswijk, 1981); although the concept of a standardized building practice was not new and examples of such directives are known from ancient Babylonia ca. 2000 BC (DeGrace, 1960) and the Bible. Canada however did not formalize a national building code until 1941 (Payne, 1981).

The large-scale emergence of health complaints due to IAQ problems began in the early 1970s and continues to the present day (Marbury and Woods, 1991). One factor contributing to the current problem is the increased exposure potential from the tendency of modern society to spend more and more of its time indoors (Singh, 1994). In addition, continued efforts have been made to improve building engineering and design to maximize thermal energy retention, thereby reducing heating costs. These same design improvements have brought about drastic reductions in dilution ventilation, and facilitated the build-up of indoor airborne contaminants

(Pope et al., 1993). This stringent concern about cost of heating fuel is a new phenomenon, since much of western civilization developed in an economic climate where fuel was relatively inexpensive and the inefficient use of fuel was tolerated. Prior to this time, the fungus-related building problem was structural, with the primary agent being *Serpula*, the dry rot fungus. The move to build tighter buildings and the awareness of IAQ problems that it precipitated was influenced by a number of social and technological developments.

THE CHANGING URBAN LANDSCAPE

Following the Second World War, the western world experienced an unprecedented boom in economic prosperity. The arrival of the information age was marked in 1956 when, for the first time in US history, the majority of jobs were non-labor (Bloom, 1995). The shift away from a primarily industrial economy had a further effect of changing the urban landscape. Because a greater proportion of wage-earners were office-based, rather than factory workers, proximity to shipping and rail ports dwindled in importance. Workspace and residential accommodation necessary for a growing white-collar labor force were at a premium in growing urban centres during this post-war boom (Fishman, 1987). The skyscraper began as a novelty experiment by Massachusetts engineer William Le Baron Jenny in the late 19th century to optimise space by building on a primarily vertical, rather than horizontal axis (Fargis and Bykofsky, 1989). During the first 50 years of the 20th century this architectural form had been greatly developed in urban centres across North America. The continuing construction of high-rise structures was instrumental in providing office and commercial space in the growing post-war economy.

SUBURBAN LIFE

Addressing of the post-war housing shortage required innovation, since the North American cultural preference was for detached homes (Warner, 1995). In part, the automobile which had become an ubiquitous symbol of freedom and status was crucial to the resolution of this problem since widespread automobile ownership permitted the decentralization of urban populations by dividing work and home between the city and suburb, respectively (ibid.). Indeed over the 20 years from 1950 to 1970, population growth in suburban America exceeded inner-city growth by nearly a factor of ten, and accounted for over three-quarters of new jobs in the manufacturing and retail sectors (Fishman, 1987). By 1970 the proportion of the US population living in suburbs had exceeded that in city cores or rural areas (37.6 %, 31.4% and 31.0%, respectively) (ibid.). The shortage of residential and institutional buildings was also partly addressed by the adoption of industrialized building techniques which involved the large-scale production and installation of pre-fabricated buildings with cost as the primary optimisation criterion (Payne, 1981; Testa, 1990).

NORTH AMERICAN DEPENDENCE ON PETROLEUM

Along with changing architecture, transportation underwent a gradual yet profound transformation. The railway system that had figured so prominently in the settlement of North America steadily yielded to overland trucking as a means of freight transport, and the light gauge railways of urban streetcar systems slowly gave way to diesel buses (Bothwell, 1986). One theory on the impetus for this change was advanced in 1974 by US anti-trust attorney Bradford Snell (Slater, 1997). Snell's theory held that the American industrial giant, General Motors Corporation, had repeatedly allied with oil and rubber interests collectively fronted by shell companies operating as local public transit competitors in order to acquire control of local streetcar transit systems, dismantle them and replace them with diesel buses (ibid.). Although Snell's ideas have been widely criticized (e.g. Bottles, 1987), the fact remains that GM and others had prospered on defence contracts during the First- and Second World Wars and when faced with post-war uncertainty in the defence sector, sought to exploit other markets.

At the same time, there was a shift to petroleum as a fuel for residential heating. Until the early 1950s, home heating had relied mostly on coal or wood to fuel central stoves or recirculated hot water systems. The use of oil as a home heating fuel became increasingly popular because of its ease of use, as well as its greater availability and comparative low cost (Nash, 1968).

THE ENERGY CRISIS AND THE SICK BUILDING

The rapid expansion of North American oil markets over the 30 years following WWII approximated a mounting gluttony for petroleum driven by favourable economics and insatiable consumer appetite for the automobile. The so-called "oil crisis" of the 1970's began during a protracted period of political uncertainty in key Middle East oil-producing nations. The alliance of the United States with Israel during the "Yom Kippur War" of 1973 brought about a temporary embargo on US oil exports by Arab oil-producers. Shortly afterwards, a general strike in the Iranian oil fields preceded the eruption of full-scale political revolution in the Middle East, bringing a temporary halt to crude oil production and export. Dwindling reserves and uncertainty about future availability prompted the Organization of Petroleum Exporting Countries (OPEC) to implement a sharp increase in the minimum reference price of crude oil to protect remaining reserves (Nash, 1968). Within a few years, the base price of crude oil surged from its century-long average of around $2 USD per barrel to over $40 USD (*see* Figure 7-1. The dependence of North America on petroleum that had grown gradually in the years following WWII (*see* Figure 7-2) posed economically disastrous consequences if means could not be found to stem consumption.

HEATING AND VENTILATION

Klauss and colleagues (1970) credited Cornish mining engineer Thomas Tredgold with the first formal calculation of a minimal ventilation requirement, in this case 4 CFM per person, based on the physiological needs of miners. Workers at the beginning of the 20^{th} century adopted ventilation rates of 30 CFM per person for workplace environments including hospitals to reduce the potential for disease spread and comfort issues such as minimizing odour generation (Janssen, 1999). Based on considerable empirical data regarding perception thresholds for body odour, Yaglou (1938) reduced the minimum ventilation requirement to 10 CFM per person. Subsequent standards published by the American Standards Association (ASA) and the American Society for Heating and Refrigeration Engineers (ASHRAE) maintained the minimum ventilation requirement at this level, where it remained until 1981 when unabating financial constraints on fuel use prompted ASHRAE to reduce the requirement further to 5 CFM per person (Janssen, 1999). ASHRAE Standard 62-1989 increased this to 15 CFM per person where it remains today based on confirmation of Yaglou's work (Berg-Munch et al., 1984; Cain, 1983). Although not formally included as a rationale for increasing the minimum ventilation rate, the groundswell of IAQ related complaints following ASHRAE 62-1981 undoubtedly played a role in this decision. Figure 7-3 shows a graphical history of changes in recommended minimum indoor ventilation rates. A decrease in the minimum ventilation level in the early 1980s coincided closely with a sharp surge in oil prices (*see* Figure 7-1), marking the beginning of the modern era of sick building syndrome.

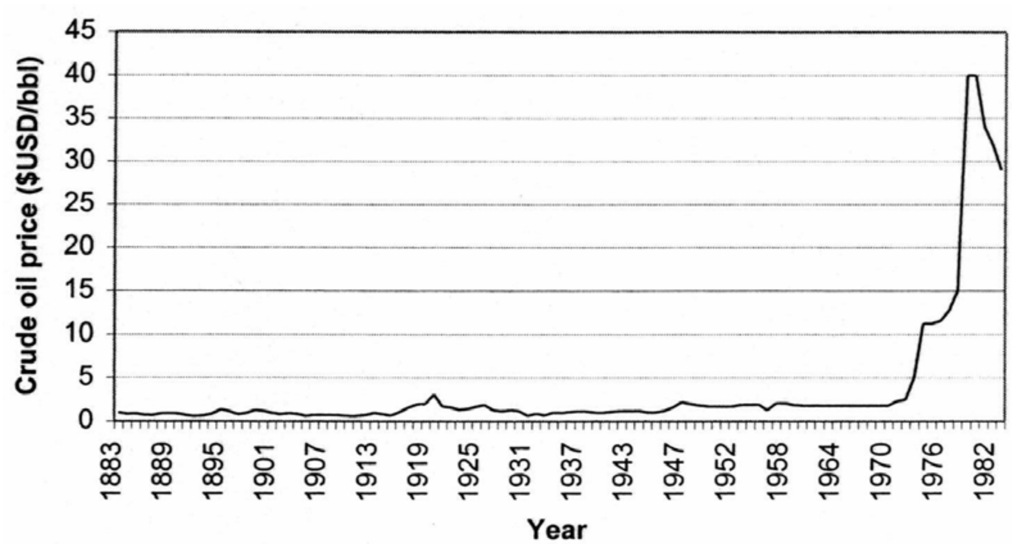

FIGURE 7-1. Year-end reference price per barrel of crude oil from 1883 to 1981 (in 1981 USD). Source: Jenkins, G. 1983. Oil Economists' Handbook. New York: Applied Science Publishers. pp. 19, 50, 51 & 94.

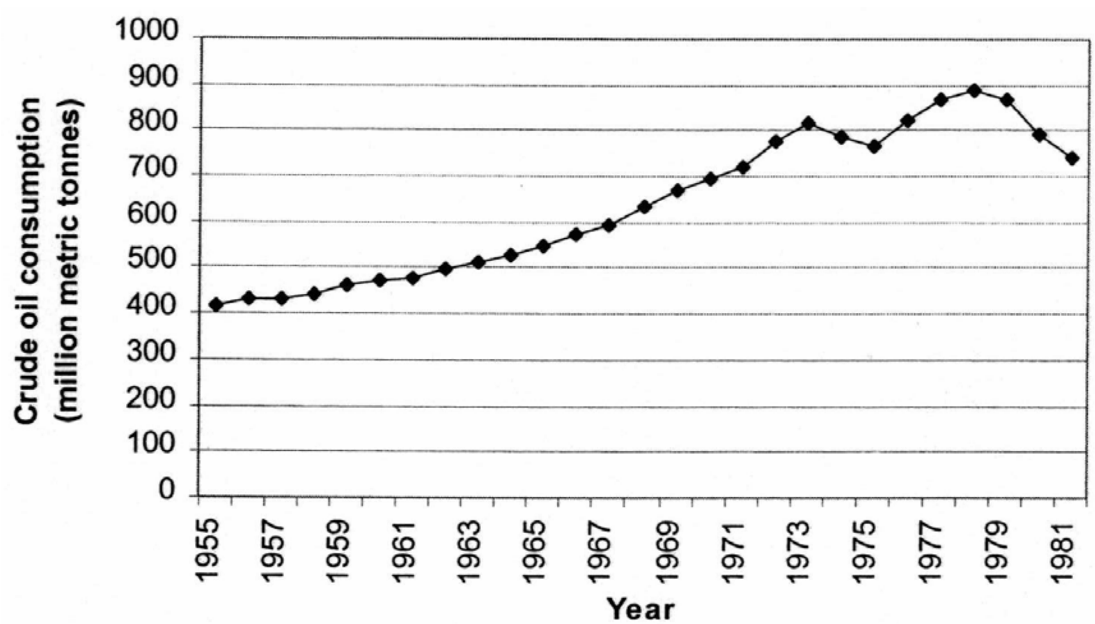

FIGURE 7-2. Break-down of crude oil consumption from to 1955 to 1981. SOURCE: Jenkins, G. 1983. Oil Economists' Handbook. New York: Applied Science Publishers. pp. 19, 50, 51 & 94.

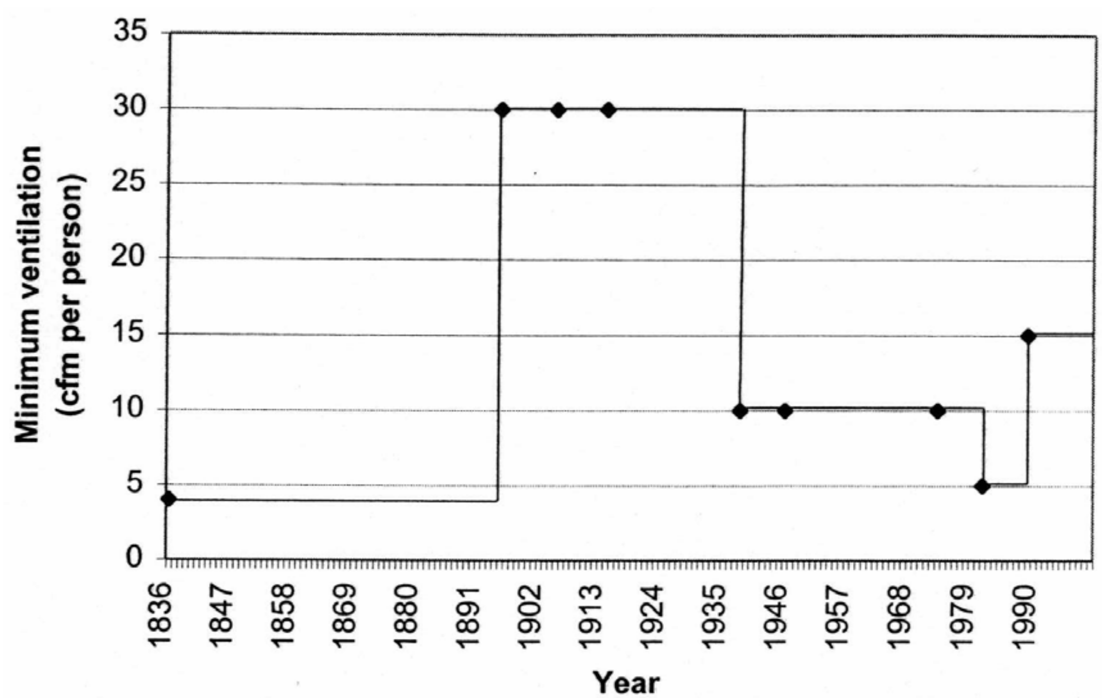

FIGURE 7-3. Minimum prescribed ventilation rates from 1836 to the present.
SOURCE: Janssen (1999)

CONSTRUCTION PRACTICES[12]

Besides influencing prescribed ventilation rates, rising fuel costs also drove changes in construction practices. Modern residential construction employs a tightly sealed building envelope design, with a vapour retardant membrane on the warm side- and an air barrier membrane on the cold side of a highly insulated wall assembly (Kesik et al., 1997). This wall construction deliberately restricts the infiltration of outdoor air, often permitting the accumulation of indoor pollutants including emission products from building products or furnishings, moisture and moulds (Flannigan and Morey, 1996).

Fungal contamination by dry rot fungi tends to dominate in buildings constructed prior to the 1920s (Koch, 1994). The introduction of many new building materials has both increased the potential for water damage and the biodiversity of ensuant fungal growth. In particular, many contemporary materials used for exterior sheathing are composites of wood or paper products bound together using a variety of resins, especially phenol-formaldehyde compounds (Mullins and McKnight, 1981). In Ontario, these products commonly include oriented strand boards (OSBs) and wafer boards, mostly made from chipped poplar. Composite products are lighter and less expensive to produce than solid wood or laminated wood products (such as plywood); however, they exhibit a greater potential for water absorption according to the vast, effective surface areas of these products (i.e. the total additive surface areas of individual chips). This tendency leads to greater susceptibility to fungal contamination.

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[12] The following two sections contain considerable information of an anecdotal nature that draws upon personal experience studying fungal contamination within buildings. These observations remain largely subjective and have not been substantiated by systematic research. However, they are presented as a context for the work done in the thesis, and as a basis to determine logical directions for future research.

GYPSUM-BASED WALLBOARD PRODUCTS

Perhaps the most common fungal problem affecting modern buildings results from the use of another highly susceptible building material, "drywall" or "gypsum board", a wallboard panel made of gypsum plaster with a covering of paper (CMHC, 1982). *Stachybotrys chartarum* is a principal colonist of this material following water damage (Straus et al., 1999; Tsai et al., 1999). Leaks resulting from building envelope failures are the most common factors that cause water damage and lead to contamination. Drywall is used commonly as an interior finishing board, but may occasionally be used on the exterior side of a wall assembly as a fire retardant or an air barrier (Kesik and Lio, 1997) where it is susceptible to water damage and mould growth[13]. Mould damage on gypsum drywall is often limited to exterior walls and frequently occurs **1)** following water infiltration through exterior walls, beneath windows or mechanical penetrations in exterior walls, especially basements; **2)** in the interior of wall assemblies as a result of condensation on cold cavity elements of the wall assembly following exfiltration of humid room air (especially on leeward walls in wintertime); **3)** due to pipe leaks (often sanitary returns) or dripping condensation from uninsulated cold water pipes; and, **4)** at wall base behind baseboard due to saturation by mop water. Conversely, fungal disfigurement of the interior finished surfaces of exterior walls is often due to condensation, in which case *Stachybotrys* is rarely involved. The fungi most frequently encountered as agents of surface disfigurement are: *Cladosporium cladosporioides* and *Cl. sphaerospermum*, *Alternaria*, *Ulocladium*, *Aspergillus versicolor,*

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[13] Recurrent water penetration often establishes a vertical moisture gradient whereby the lower extent of a wall remains saturated and the water diminishes at increasing vertical distance from the sill plate. *Stachybotrys chartarum* is both hydrophilic and strongly cellulolytic, and tends to proliferate on the lower extent of gypsum wallboard where the surface is buffered to intermittent drying (e.g. interior of the wall cavity, beneath baseboards, etc.). Micro-arthropods, primarily mites, are common in this region as active grazers of *Stachybotrys* conidia, as evidenced by the often exclusive content of these spores in their fecal pellets. *Acremonium* (resembling of *A. butyri*) frequently co-occurs in this region, and in addition is a common colonist of mite fecal pellets. At increasing distance from the water-damaged area hydrophilic species give way to mesophilic and xerophilic moulds such as *Aspergillus ustus*, *A. versicolor* and several species of *Penicillium* including *P. brevicompactum*.

Penicillium chrysogenum, P. griseofulvum and *P. spinulosum* (Adan and Samson, 1994). These problems are common where furnishings are placed directly against cool exterior walls, producing static air pockets which result in condensation on wall surfaces and fungal growth which often affects a dramatically large area, reciprocal in outline to the furnishing, and thus resembles a "shadow".

THE DAWN OF "SICK BUILDING SYNDROME"

The disease that heralded current awareness of IAQ as an influence on health was of bacterial etiology, namely Legionnaire's Disease, and it's eponymous causative agent, *Legionella pneumophila*. Legionellosis was first recognized in 1976 during a convention of the American Legion in Cincinnati, Ohio, at which several hundred participants presented with symptoms of pneumonia. After an exhaustive search to attempt to identify the infectious agent and route of exposure, investigators identified the HVAC system of the host complex. Humidification units were found to contain stagnant water containing the disease causing agent, which was aspirated into the ventilation system and inhaled by the building occupants. In all, 34 deaths were recorded in this initial outbreak (Yu, 2000). To date, the earliest recorded outbreak of Legionella pneumonia determine by retrospective studies occurred in 1957 in meat-packing plant in Austin, Minnesota, 78 people were hospitalised (Mulazimoglu and Yu, 1998; Yu, 2000). The elucidation of Legionnaire's Disease began a continuing awareness of buildings as sources for potentially harmful biological aerosols.

ECOLOGY OF DUST-BORNE FUNGI

Household dust is host to a great variety of microfungi that originate from diverse sources. Principally, dust functions as an accumulator of biological particles that settle out from the ambient air. Much of this spora originates from outdoor sources, such as the phylloplane, and enters the indoor environment passively through open doors and windows. Another common contributor to the indoor airborne spore-load comes from indoor substrates manifesting fungal spoiling, including construction materials, furnishings and foodstuffs. The influx of spores from these sources into house dust effectively builds a microfungal “seed-bank”, in which fungal propagules accumulate over time, remaining dormant unless suitable conditions permit germination and growth. Many common house-cleaning practices do less to remove dust than they do to aerosolize and redistribute it. As such, asthmatic children typically show an increase in respiratory symptom prevalence following house-cleaning procedures (Clark et al., 1976). This disruption of dust-bound spores by housekeeping practices is particularly true for the vacuum-cleaning of broadloom (Stetzenbach et al., 1999). Association analysis of the mycoflora of broadloom dust shown in Chapter 2 of this study identified three distinct ecological assemblages which correspond well to the hypothesized primary sources of indoor mycoflora that ultimately contribute to dust formation.

ASSOCIATION ANALYSIS OF DUST-BORNE FUNGI

The first and most obvious dust-borne fungal assemblage consists of phylloplane fungi. Species identified in the present study that belonged to this ecological group included *Alternaria alternata*, *Aureobasidium pullulans*, *Cladosporium cladosporioides* and *Epicoccum nigrum*. All of these taxa are well-known from outdoor habitats, particularly on decaying vegetation during the growing season in northern temperate climates (*see* Domsch et al., 1980). However, it cannot be assumed that the growth of these fungi is necessarily limited to the phylloplane and that their presence in building interiors is exclusively from extralimital sources. Clearly the majority of construction materials employed in small-scale residential construction are based on plant fibre products, including dimensional lumber, laminates, oriented strand boards and paper products (Kesik and Lio, 1997;

Mullins and McKnight, 1981). Thus, it is not unexpected that in the event of water damage, these same fungi are common colonists of wood-based construction materials, which serve as intrinsic sources of fungal propagules in indoor air and subsequently in dust. Species of *Cladosporium* are of particular interest in this regard, since they are frequent colonists of indoor surfaces incurring intermittent wetting, such as winter-time condensation on exterior walls (*see* Chapter 2). Similarly *Alternaria* occurs commonly on wooden window sills, and *Aureobasidium pullulans* may be found on bathroom surfaces such as shower curtains, bath mats and tile grout (Domsch et al., 1980; Samson et al., 1996; Singh, 1994). Hence, the interpretation of typical "phylloplane" species as such depends upon the exclusion of significant indoor amplifiers of these taxa.

A second important contributor to the dust mycobiota indicated in the present study arises from the importation of soil fungi into indoor environments on soiled footwear. Based on these data, putative "indicator species" of this group include *Trichoderma viride*, *Penicillium citreonigrum*, and possibly *Rhizopus oryzae* and *Mucor plumbeus*. In my experience, these taxa are less prone to colonize indoor substrates under conditions of water damage than phylloplane taxa, but all are known as occasional foodborne contaminants (Domsch et al., 1980; Samson et al., 1996). Pitt and Hocking (1999) questioned the identification of foodborne *Trichoderma* isolates, and suggested that most isolates referred in the literature to *T. viride* are likely misidentified isolates of *T. harzianum*. Indoors, species of *Trichoderma* have been reported from urea formaldehyde foam insulation (Bissett, 1987); however, use of this material has been banned in Canada due to adverse health effects from formaldehyde release during deterioration of the product. The presence of *Trichoderma* and other typical soil fungi in household dust is most likely from passive entry on footwear and from implements contaminated by soil fomites.

A third source of allochthonous dust mycobiota likely arises from the growth of fungi on food materials indoors. Many typical food spoilage fungi are tolerant of low water activity and some species, such as *Aspergillus versicolor* and *Wallemia sebi* are highly xerophilic (Pitt and Hocking, 1999). The principal indicator species from this ecological group observed in the present study were *As. versicolor*, *Eurotium herbariorum* and *W. sebi*. As well, the most common species of *Penicillium* observed in Wallaceburg dust samples were *P. aurantiogriseum-viridicatum* group, *P. brevicompactum*, *P. chrysogenum*, *P. commune*, *P. corylophilum*, *P. expansum* and *P. spinulosum*. All of these species, particularly the first three, are well-known food contaminants and spoilage agents (Pitt and Hocking, 1999; Samson et al., 1996). Although their principal indoor niche may be foodstuffs, many of these species are also known as contaminants of building materials, interior finishes and furnishings following water damage (Domsch et al., 1980; Adan and Samson, 1994). This trend is not limited to the Penicillia. As discussed in Chapter 2, many fungi that are adventitious colonists of foodstuffs appear similarly to have diversified into other indoor niches, given suitable conditions (e.g. *As. versicolor*, *As. ustus*, *Chaetomium globosum*, *P. aurantiogriseum*, *P. brevicompactum*, *P. chrysogenum* and *Stachybotrys chartarum*). Within the group of indoor fungi characterized by this ecological group, there are considerable taxonomic difficulties, especially in the genus *Penicillium*. A second aspect of this thesis involved the examination of the taxonomy of two commonly occurring dust-borne Penicillia, *P. brevicompactum* and *P. chrysogenum*, presented in Chapters 5 and 6, respectively, using molecular genetic characters derived from multiple genetic loci.

PENICILLIUM BREVICOMPACTUM

The heteroduplex mobility assay (HMA) was used to identify alleles in PCR-amplified regions of the beta-tubulin-encoding gene, benA, the gene encoding histone 4 (his4) and the internal transcribed spacer region of nuclear ribosomal RNA including the 5.8S region (rDNA ITS1-5.8S-ITS2). Nine multilocus haplotypes were observed in 75 isolates of *P. brevicompactum* collected from 50 houses. These haplotypes showed a strong association of alleles, suggesting clonal propagation in absence of recombination in the set of isolates examined. Representative alleles were sequenced for the benA and ITS loci (the histone locus was not included in sequencing studies due to difficulties in obtaining clean sequence). Sequence data from these two loci were combined for phylogenetic analyses based on the congruence of these data sets as demonstrated by the Partition Homogeneity Test (PHT). Two well-supported, highly divergent clades were resolved. The principal clade contained 86% of the isolates obtained from house dust samples. This clade included the type strains of *P. brevicompactum* and *P. stoloniferum*. As such, *P. brevicompactum* is the correct name for this taxon, since *P. stoloniferum* is a later epithet, and phylogenetic analyses presented in Chapter 5 supported the synonymy of the two taxa. The second clade contained 14% of house dust isolates, and was sufficiently divergent from the principal clade to warrant recognition as a distinct species. Several voucher collections deposited in the DAOM under the name *P. brevicompactum* clustered within this clade. Interestingly, the habitats for these voucher isolates tended to be the decomposing fruit bodies of fleshy fungi. The majority of house dust isolates from this clade were obtained from houses at rural addresses (extralimital to the municipal boarder of the Town of Wallaceburg), further suggesting that this presently unrecognized species is affiliated with more natural conditions, such as forested areas or other localities where macrofungi fruit in high density. No isolates of nomenclatural standing that were included in the present study clustered within this clade. The microscopic morphology of this taxon appears indistinguishable from *P. brevicompactum* in which metulae show considerable apical swelling, producing a characteristically aspergilloid conidiophore appearance. It is unlikely that this taxon can be accommodated in any currently recognized taxa, given that this morphology is of limited distribution within subgenus *Penicillium*. A review of existing taxonomic literature on *Penicillium* failed to yield morphologically similar taxa described from fungicolous habitats. A future goal of research shall be the evaluation of multiple phenotypic characters such as carbon and nitrogen utilization patterns as well as morphometric analyses in an attempt to identify reliable characters upon which this new species may be based.

Inclusion of ITS sequences of these taxa within a larger sample of terverticillate Penicillia indicated that the clade containing members of the *P. brevicompactum* complex formed a monophyletic group situated on a long branch that was sister to the core of the terverticillate Penicillia, in the basal position (*see* Chapter 4, FIG. 4-8). In their phylogeny of the terverticillate Penicillia, Skouboe and colleagues (1999) did not include representatives of *P. brevicompactum*, and rDNA sequences are presently not available for this taxon on GenBank. Thus, the current study appears to be the first investigation of the phylogenetic placement of *P. brevicompactum* using modern phylogenetic methods.

PENICILLIUM CHRYSOGENUM

An investigation of genotypic diversity in 198 isolates of *P. chrysogenum* obtained from broadloom dust from 109 houses was presented in Chapter 6. This study employed HMA to determine the allelic diversity of 4 polymorphic genetic loci amplified by PCR from genes encoding acetyl coenzyme-A synthase gene (acuA), beta-tubulin (benA), and thioredoxin reductase (trxB), as well as the non-coding internal transcribed spacer regions of nuclear ribosomal DNA encompassing the 5.8S region (ITS1-5.8S-ITS2), as above. Two of these loci (acuA and trxB) were developed during the course of the present investigation. Three unique alleles were observed for each locus examined, grouping the isolates into five multilocus haplotypes in which a strictly clonal pattern of inheritance was observed, indicating the absence of recombination in the isolates tested.

Representative isolates of all alleles for each locus were sequenced, and the sequence data were combined for analysis based on congruence of the data as demonstrated by the PHT. Sequence data for ITS regions of rDNA were excluded from final analyses due to the absence of parsimony-informative characters at this locus (*see* Table 6-6). Parsimony analysis of the combined acuA-benA-trxB dataset divided the set of 198 dust isolates of *P. chrysogenum* into three well-supported lineages, containing 90%, 7% and 3% of Wallaceburg isolates, respectively. These principal lineages were in agreement with the major groups resolved by cluster analyses of electrophoretic banding patterns obtained from PCR amplification products primed using the core sequence of M13 phage DNA, the repeated sequence $(GACA)_4$, as well as the arbitrary primer pair 5SOR/ MYC1 (*see* Chapter 6, Table 6-3). Considerably greater fine resolution was observed in terminal branches of cluster analyses of fingerprint data. However, this fine resolution may be the result of difficulties in scoring low intensity bands, and may be uninformative.

The primary well-supported lineage of dust-borne isolates included the original penicillin-producing strain collected by Alexander Fleming in 1929 (identified as *P. rubrum*). No isolates of nomenclatural standing clustered within this clade, suggesting that it may represent a distinct species within the *P. chrysogenum* species complex. The recognition of this species awaits the identification of stable phenotypic characters by which it can be separated from *P. chrysogenum* sensu stricto. A preliminary plate assay for penicillin production examining the inhibition of a penicillin-sensitive strain of *Staphylococcus aureus* demonstrated a general inhibitory effect of *P.*

chrysogenum on *S. aureus*, but failed to reveal patterns of antibiosis that correlated to the genetic groupings observed (data not presented). Future investigations shall assess patterns of carbon and nitrogen utilization, growth rates at different temperature regimens and tolerance to low water activity in an effort to identify distinguishing phenotypic characters. A third well-supported clade contained 6 house dust isolates. None of the isolates of nomenclatural status clustered within this clade, and it may represent a second undescribed taxon within the *P. chrysogenum* species complex. Preliminary investigations of isolates from this clade show increased sporulation and generally more robust growth relative to members of the other two clades when grown on Creatine-sucrose agar. This medium may prove useful in the delimitation of this species.

Type isolates of other closely related taxa including *P. aethiopicum*, *P. chrysogenum* v. *dipodomyis*, *P. griseofulvum* v. *dipodomyis* and *P. nalgiovense* were sequenced for all loci, facilitating the examination of species concepts within this broader group of smooth-stiped terverticillate Penicillia. These results supported the synonymy between *P. notatum* and *P. chrysogenum*, in which the latter name has nomenclatural priority (and has been proposed as *nomen conservandum* by Kozakiewicz and colleagues, 1992). *Penicillium chrysogenum* v. *dipodomyis* clustered as sister to *P. nalgiovense*, outside of the *P. chrysogenum* clade, and warrants transfer to avoid paraphylly in *P. chrysogenum*.

SUMMARY

For millennia, fungi have occurred commonly in the indoor environments within which humans live and work. Their presence has influenced both human disease and structural decay. Until the early 20th century, the principal agent of structural decay worldwide has been dry rot caused mainly by species of the basidiomycete, *Serpula*. The construction of tighter buildings due to higher constraints on thermal energy retention, and the greater use of processed wood products in place of solid wood has brought about an increase in problems related to indoor fungal contamination, and simultaneously a shift in the fungal taxa responsible. Presently, many of the fungi responsible for structural contamination originate as dustborne moulds or food spoilage agents. Relative to *Serpula*, contamination by these fungi may pose less structural risk; however, many of the taxa involved produce mycotoxins, and may present a relatively greater hazard to building occupants.

The present study examined fungi in house dust from 369 houses in Wallaceburg, Ontario, Canada. A total of 256 fungal taxa were observed, which followed a Raunkaier-type distribution. Three distinct ecological assemblages were observed in dust-borne species: phylloplane fungi, soil fungi and food-spoilage/ xerophilic fungi. It is likely that these habitats serve as the major sources of the culturable fungal propagules that accumulate in house dust where indoor amplifiers are absent.

Allelic variability was assessed for multiple PCR-amplified polymorphic regions in conserved structural and metabolic genes from isolates of *P. brevicompactum* and *P. chrysogenum* using heteroduplex mobility assay. Allele identities were confirmed by sequencing and phylogenetic analyses were conducted on representative sequences of all alleles. Both *P. brevicompactum* and *P. chrysogenum* as currently circumscribed appear to consist of species complexes containing multiple cryptic species.

Penicillium stoloniferum is recognized as a synonym of *P. brevicompactum*. This lineage is a common inhabitant of house dust and indoor air. A second related lineage occurs occasionally in household dust but is primarily associated with the decaying fruit bodies of fleshy fungi outdoors. At present, this lineage lacks an available name.

Penicillium notatum is recognized as a synonym of *P. chrysogenum*. This lineage is an occasional inhabitant of household dust. A second more commonly occurring dust-borne lineage includes the original penicillin-producing isolate obtained by Alexander Fleming in 1929. There is presently no available name for this lineage.

Further investigation is necessary to determine the taxonomic level at which the un-named lineages in *P. brevicompactum* and *P. chrysogenum* should be recognized, and suitable phenotypic characters by which they may be defined.

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APPENDICES

APPENDIX A

SUMMARY OF RESULTS OF BROADLOOM DUST CULTURES
FROM WALLACEBURG HOUSES

HN indicates "house number"
G+/- indicates the presence/ absence of 10% glycerol in the isolation medium
Viable fungal levels are expressed as CFU/g dust

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
1	Alternaria alternata	2830		3	Penicillium citrinum	1415	
1	Alternaria tenuissima	1603	+	3	Penicillium corylophilum	471	
1	Alternaria tenuissima	471		3	Penicillium spinulosum	471	
1	Aspergillus niger	47	+	3	Phoma herbarum	943	
1	Aspergillus sydowii	471		3	Phoma sp.	943	
1	Aureobasidium pullulans	1886		3	Trichoderma viride	1415	
1	Chaetomium globosum	471		3	Ulocladium chartarum	943	+
1	Epicoccum nigrum	6603		3	unknown	9905	
1	Epicoccum nigrum	2358	+	3	unknown	5660	+
1	Mucor racemosus	235	+	3	yeast	147169	
1	Penicillium corylophilum	471	+	4	Alternaria alternata	50471	
1	Penicillium expansum	1462	+	4	Alternaria alternata	471	+
1	Penicillium sp. #1	2358		4	Aspergillus candidus	471	
1	Penicillium sp. #13	47	+	4	Aspergillus flavus	943	+
1	Penicillium spinulosum	1509	+	4	Aspergillus flavus	471	
1	Penicillium spinulosum	471		4	Aspergillus glaucus	471	+
1	Penicillium viridicatum	518	+	4	Aspergillus niger	4245	+
1	Penicillium viridicatum	471		4	Aspergillus niger	3301	
1	Pithomyces chartarum	471		4	Epicoccum nigrum	1886	
1	Pithomyces chartarum	471	+	4	Epicoccum nigrum	943	+
1	unknown	4716		4	Eurotium herbariorum	3301	+
1	unknown	3301	+	4	Eurotium sp.	471	+
1	yeast	9433		4	Fusarium sp.	471	
2	Alternaria alternata	7075		4	Fusarium sp.	471	+
2	Alternaria alternata	141	+	4	Mucor circinelloides	471	
2	Alternaria sp.	1415		4	Mucor hiemalis	471	
2	Alternaria tenuissima	3537	+	4	Mucor plumbeus	471	
2	Aspergillus glaucus	1179	+	4	Mucor racemosus	471	
2	Aureobasidium pullulans	2830		4	Penicillium chrysogenum	2830	+
2	Aureobasidium pullulans	566	+	4	Penicillium citrinum	471	
2	Curvularia protuberata	471	+	4	Penicillium expansum	471	+
2	Epicoccum nigrum	1886		4	Penicillium sp. #1	471	
2	Penicillium atramentosum	94	+	4	Penicillium sp. #26	471	
2	Penicillium chrysogenum	1037	+	4	Penicillium spinulosum	10377	+
2	Penicillium chrysogenum	471		4	Penicillium spinulosum	6132	
2	Penicillium citrinum	471		4	Phoma herbarum	471	
2	Phoma herbarum	1415		4	Rhizopus oryzae	943	
2	Ulocladium chartarum	566	+	4	Stemphylium solani	943	+
2	unknown	7547		4	unknown	2358	
2	unknown	2783	+	4	unknown	471	+
2	yeast	3773		4	yeast	15094	
3	Alternaria alternata	1415		5	Alternaria alternata	1415	
3	Alternaria alternata	943	+	5	Alternaria sp.	943	
3	Alternaria sp.	1415		5	Alternaria tenuissima	1886	+
3	Aspergillus candidus	471	+	5	Aspergillus glaucus	471	+
3	Aspergillus flavus	943		5	Aspergillus niger	1415	
3	Aspergillus fumigatus	8962	+	5	Aspergillus sydowii	943	+
3	Aspergillus fumigatus	3301		5	Aureobasidium pullulans	18396	
3	Aspergillus glaucus	471	+	5	Aureobasidium pullulans	8018	+
3	Aspergillus ochraceus	943	+	5	Chrysosporium sp.	2358	+
3	Aspergillus terreus	2358	+	5	Cladosporium cladosporioides	471	
3	Aspergillus terreus	943		5	Cladosporium sp.	943	
3	Aureobasidium pullulans	3773		5	Epicoccum nigrum	471	
3	Aureobasidium pullulans	2358	+	5	Eurotium herbariorum	471	
3	Chrysosporium sp.	3773		5	Eurotium herbariorum	471	+
3	Chrysosporium sp.	471	+	5	Eurotium sp.	471	+
3	Cladosporium cladosporioides	471		5	Mucor plumbeus	471	
3	Mucor racemosus	471	+	5	Penicillium atramentosum	471	
3	Penicillium atramentosum	471	+	5	Penicillium atramentosum	471	+
3	Penicillium chrysogenum	1415	+	5	Penicillium citrinum	471	
3	Penicillium chrysogenum	471		5	Penicillium commune	1415	

HN	Identification	AVG CFU/g	G
5	Penicillium corylophilum	1415	+
5	Penicillium expansum	3773	+
5	Penicillium expansum	943	
5	Penicillium sp. #26	943	
5	Penicillium sp. #26	471	+
5	Penicillium spinulosum	1886	+
5	Penicillium spinulosum	943	
5	Phoma herbarum	471	
5	Pithomyces chartarum	471	+
5	Scopulariopsis brevicaulis	471	+
5	unknown	4245	+
5	unknown	1415	
5	yeast	8962	
6	Alternaria alternata	4725	+
6	Aspergillus fumigatus	4672	+
6	Aspergillus versicolor	4672	+
6	Aureobasidium pullulans	9345	+
6	Cladosporium chlorocephalum	9345	+
6	Cladosporium macrocarpum	7556	
6	Cladosporium sp.	4672	+
6	Cladosporium sphaerospermum	51931	+
6	Epicoccum nigrum	4725	
6	Epicoccum nigrum	4725	+
6	Eurotium herbariorum	9398	+
6	Paecilomyces variotii	14018	
6	Penicillium expansum	9345	+
6	Phoma herbarum	4672	+
6	unknown	79704	+
6	unknown	18797	
6	Wallemia sebi	4672	+
6	yeast	37701	
7	Alternaria alternata	52228	
7	Alternaria alternata	458	+
7	Aspergillus niger	458	
7	Aspergillus versicolor	2752	
7	Cladosporium herbarum	910	+
7	Eurotium herbariorum	6860	+
7	Eurotium herbariorum	455	
7	Penicillium aurantiogriseum	458	+
7	Penicillium brevicompactum	455	
7	Penicillium chrysogenum	3663	+
7	Penicillium chrysogenum	1369	
7	Penicillium commune	1376	+
7	Penicillium commune	455	
7	Penicillium expansum	3642	+
7	Penicillium expansum	2286	
7	Penicillium simplicissimum	458	+
7	Penicillium sp. #1	458	
7	unknown	1831	
7	unknown	458	+
7	Verticillium sp.	914	+
7	yeast	35291	
8	Aspergillus niveus	4743	+
8	Aspergillus ochraceus	10104	
8	Aspergillus paradoxus	1897	
8	Aspergillus sp.	4743	+
8	Aspergillus versicolor	2851	
8	Eurotium chevalieri	474	
8	Eurotium herbariorum	38041	+
8	Hormonema dematioides	18975	+
8	Myrothecium cinctum	474	
8	Penicillium aurantiogriseum	4743	+
8	Penicillium chrysogenum	15685	
8	Penicillium chrysogenum	9505	+
8	Penicillium decumbens	9523	+
8	Penicillium decumbens	3796	
8	Penicillium spinulosum	476	
8	Phoma herbarum	474	
8	unknown	28553	+
8	yeast	6185	
10	Acremonium sp.	4901	
10	Alternaria alternata	4970	
10	Alternaria tenuissima	4901	+
10	Aspergillus sp.	4901	
10	Aspergillus versicolor	4901	
10	Aureobasidium pullulans	4901	
10	Aureobasidium pullulans	4901	+
10	basidiomycete	24509	+
10	basidiomycete	4970	
10	Chrysosporium sp.	14774	+
10	Chrysosporium sp.	4970	
10	Cladosporium sphaerospermum	19812	+
10	Diplococcium spicatum	24850	
10	Epicoccum nigrum	24850	
10	Epicoccum nigrum	19744	+
10	Exophiala jeanselmei	49701	+
10	Exophiala jeanselmei	14910	
10	Fusarium sp.	9872	
10	Geomyces pannorum	14910	+
10	Geomyces pannorum	9803	
10	Hortaea werneckii	14910	
10	Monascus ruber	9803	
10	Penicillium chrysogenum	19676	
10	Penicillium citreonigrum	24646	
10	Penicillium citreonigrum	19880	+
10	Penicillium commune	4901	
10	Penicillium corylophilum	4970	
10	Penicillium expansum	54330	+
10	Penicillium implicatum	4970	
10	Penicillium miczynskii	4901	+
10	Penicillium spinulosum	14705	+
10	Phoma herbarum	19812	
10	Phoma herbarum	9940	+
10	Pyrenochaeta sp.	24850	
10	Stemphylium solani	9940	+
10	Trichoderma harzianum	4901	
10	Trichoderma viride	24850	
10	Trichoderma viride	24782	+
10	unknown	74279	+
10	unknown	34723	
10	yeast	84015	
11	Acremonium butyri	15387	
11	Alternaria alternata	2418	+
11	Aspergillus versicolor	1456	+
11	Aspergillus versicolor	485	
11	Aureobasidium pullulans	14940	+
11	Chaetomium globosum	954	
11	Cladosporium cladosporioides	1916	+
11	Cladosporium sp.	477	+
11	Cladosporium sphaerospermum	1933	+
11	Epicoccum nigrum	3373	+
11	Eurotium herbariorum	962	+

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
11	Fusarium oxysporum	962		15	Cladosporium chlorocephalum	2369	+
11	Fusarium oxysporum	954	+	15	Cladosporium cladosporioides	3431	+
11	Penicillium chrysogenum	970	+	15	Cladosporium sp.	1470	
11	Penicillium commune	1908		15	Cladosporium sp.	960	+
11	Penicillium expansum	3373	+	15	Cladosporium sphaerospermum	939	+
11	Penicillium expansum	1456		15	Epicoccum nigrum	3390	+
11	Penicillium sp. #26	18773		15	Epicoccum nigrum	490	
11	Penicillium sp. #26	8646	+	15	Eurotium herbariorum	8150	+
11	Penicillium viridicatum	1916	+	15	Eurotium herbariorum	1470	
11	Phoma herbarum	485	+	15	Humicola fuscoatra	980	
11	Pithomyces chartarum	485	+	15	Oidiodendron sp.	469	
11	unknown	4318		15	Paecilomyces variotii	939	
11	unknown	1941	+	15	Penicillium brevicompactum	490	
11	yeast	6746		15	Penicillium brevicompactum	490	+
12	Aspergillus sp.	13368	+	15	Penicillium chrysogenum	3350	+
12	Aspergillus sydowii	17825	+	15	Penicillium chrysogenum	2390	
12	Aspergillus versicolor	8912	+	15	Penicillium corylophilum	980	+
12	Aureobasidium pullulans	36816	+	15	Penicillium purpurogenum	939	
12	Epicoccum nigrum	4844		15	Penicillium sp.	469	+
12	Epicoccum nigrum	4456	+	15	Penicillium spinulosum	1920	+
12	Fusarium sp.	4844		15	Penicillium spinulosum	469	
12	Mucor racemosus	18602		15	Phoma herbarum	469	+
12	Mucor racemosus	4844	+	15	Scopulariopsis candida	3431	
12	Penicillium commune	9301		15	Trichoderma viride	939	
12	Penicillium expansum	70342	+	15	Trichoderma viride	469	+
12	Penicillium expansum	37982		15	unknown	5189	
12	Penicillium sp. #26	13368	+	15	unknown	2880	+
12	Phialophora fastigiata	4844		15	yeast	939	
12	Pithomyces sp.	4456		16	Aspergillus candidus	495741	
12	Rhizopus oryzae	4844	+	16	Aspergillus candidus	184177	+
12	Scopulariopsis brevicaulis	4844		16	Aspergillus sp.	56818	+
12	Trichoderma viride	8912		16	Aspergillus ustus	4708	
12	unknown	23447		16	Aspergillus versicolor	94161	+
12	unknown	4456	+	16	Aspergillus versicolor	56711	
12	Wallemia sebi	66274	+	16	Aureobasidium pullulans	4734	+
12	yeast	53294		16	Cladosporium sp.	4734	+
13	Alternaria alternata	972	+	16	Cladosporium sphaerospermum	9442	+
13	Aspergillus sp.	499	+	16	Epicoccum nigrum	4708	
13	Aspergillus versicolor	11135		16	Eurotium herbariorum	37771	+
13	Aureobasidium pullulans	3441	+	16	Mucor racemosus	23540	+
13	Cladosporium cladosporioides	2917	+	16	Mucor racemosus	4734	
13	Eurotium herbariorum	1970	+	16	Penicillium aurantiogriseum	42372	
13	Eurotium sp.	499	+	16	Penicillium chrysogenum	94161	+
13	Penicillium brevicompactum	473	+	16	Penicillium chrysogenum	84933	
13	Penicillium chrysogenum	2891	+	16	Penicillium echinulatum	4708	
13	Penicillium citrinum	473	+	16	Penicillium expansum	123106	+
13	Penicillium corylophilum	998	+	16	Penicillium sp. #1	4708	
13	Penicillium spinulosum	972		16	Penicillium sp. #26	4708	
13	Scopulariopsis brevicaulis	499		16	Penicillium sp. #26	4708	+
13	unknown	972	+	16	Penicillium spinulosum	4734	
13	unknown	499		16	unknown	9469	
13	yeast	18990		17	Alternaria alternata	2341	+
15	Alternaria alternata	3330	+	17	Alternaria alternata	462	
15	Aspergillus candidus	40843		17	Alternaria sp.	489	+
15	Aspergillus candidus	469	+	17	Alternaria tenuissima	952	
15	Aspergillus fumigatus	3431		17	Aspergillus versicolor	1851	
15	Aspergillus niger	490	+	17	Aspergillus versicolor	1388	+
15	Aspergillus versicolor	490		17	Aureobasidium pullulans	8054	+
15	Aureobasidium pullulans	10601	+	17	Aureobasidium pullulans	489	
15	Aureobasidium pullulans	2839		17	Cladosporium cladosporioides	2935	+
15	Botrytis sp.	469	+	17	Cladosporium macrocarpum	1388	+

HN	Identification	AVG CFU/g	G
17	Cladosporium macrocarpum	952	
17	Epicoccum nigrum	978	+
17	Eurotium herbariorum	952	+
17	Geotrichum candidum	2419	
17	Mucor plumbeus	489	
17	Penicillium commune	489	+
17	Penicillium expansum	462	
17	Penicillium verrucosum	462	
17	Rhizopus oryzae	462	
17	unknown	462	+
17	yeast	10037	
18	Alternaria alternata	5303	
18	Alternaria alternata	294	+
18	Aspergillus niger	98	
18	Aureobasidium pullulans	3331	+
18	Aureobasidium pullulans	581	
18	Cladosporium cladosporioides	757	+
18	Coniothyrium sp.	884	+
18	Penicillium chrysogenum	98	
18	Penicillium commune	286	
18	Penicillium corylophilum	98	
18	Penicillium expansum	769	
18	Penicillium expansum	577	+
18	Penicillium sp. #35	98	+
18	Penicillium viridicatum	470	+
18	Phoma herbarum	491	
18	Rhizopus oryzae	98	+
18	unknown	98	
18	unknown	94	+
18	yeast	1047	
19	Alternaria alternata	1351	+
19	Alternaria alternata	1297	
19	Aureobasidium pullulans	7207	+
19	Aureobasidium pullulans	900	
19	Cochliobolus sativus	1801	+
19	Epicoccum nigrum	450	
19	Epicoccum nigrum	450	+
19	Mucor plumbeus	450	
19	Penicillium chrysogenum	2252	+
19	Penicillium citrinum	450	+
19	Penicillium expansum	1801	
19	Penicillium expansum	1351	+
19	Phoma herbarum	12612	+
19	Phoma herbarum	900	
19	unknown	1351	+
19	unknown	900	
19	yeast	3153	
20	Alternaria alternata	9400	
20	Alternaria alternata	4761	+
20	Aspergillus ochraceus	9523	+
20	Aspergillus ochraceus	4761	
20	Aureobasidium pullulans	75200	
20	Aureobasidium pullulans	66171	+
20	Cladosporium sphaerospermum	28076	+
20	Epicoccum nigrum	9523	+
20	Epicoccum nigrum	9276	
20	Eurotium herbariorum	4638	+
20	Hortaea werneckii	9523	
20	Penicillium citrinum	4638	+
20	Penicillium commune	4761	
20	Penicillium corylophilum	174582	
20	Penicillium corylophilum	160791	+
20	Penicillium purpurogenum	28324	
20	Penicillium raistrickii	4761	+
20	Phoma herbarum	4761	+
20	Trichoderma viride	4761	
20	unknown	37724	
22	Alternaria alternata	2882	
22	Alternaria alternata	1926	+
22	Aspergillus candidus	2879	
22	Aspergillus fumigatus	2406	
22	Aspergillus fumigatus	961	+
22	Aspergillus niger	481	
22	Aspergillus ochraceus	963	
22	Aspergillus versicolor	39428	+
22	Aspergillus versicolor	26456	
22	Aureobasidium pullulans	25972	+
22	Aureobasidium pullulans	4804	
22	Cladosporium cladosporioides	481	+
22	Cladosporium sphaerospermum	2404	+
22	Epicoccum nigrum	1445	
22	Epicoccum nigrum	961	+
22	Eurotium herbariorum	3846	+
22	Penicillium chrysogenum	1923	
22	Penicillium chrysogenum	1443	+
22	Penicillium commune	1924	
22	Penicillium expansum	7206	+
22	Penicillium purpurogenum	4804	
22	Penicillium spinulosum	481	+
22	Penicillium viridicatum	1923	+
22	Penicillium viridicatum	959	
22	unknown	10076	
22	unknown	3358	+
22	Wallemia sebi	1443	
22	Wallemia sebi	479	+
22	yeast	42311	
24	Alternaria alternata	34929	
24	Alternaria alternata	34212	+
24	Alternaria tenuissima	3409	
24	Aspergillus ochraceus	1072	
24	Aspergillus sp.	3218	+
24	Aureobasidium pullulans	10037	+
24	Aureobasidium pullulans	9090	
24	Cladosporium cladosporioides	5681	+
24	Cladosporium sp.	4545	
24	Cladosporium sp.	1136	+
24	Epicoccum nigrum	9027	
24	Epicoccum nigrum	3282	+
24	Eurotium herbariorum	4418	+
24	Geomyces sp.	1136	
24	Penicillium restrictum	1072	
24	Penicillium sp. #38	2272	+
24	Penicillium spinulosum	3218	+
24	Penicillium variabile	1072	+
24	Penicillium viridicatum	1072	
24	Phoma herbarum	5555	+
24	Scopulariopsis brevicaulis	1136	
24	Trichoderma viride	1136	
24	Trichothecium roseum	1136	
24	Ulocladium chartarum	2272	
24	unknown	4291	
24	yeast	2209	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
25	Alternaria alternata	5684		27	Eurotium herbariorum	464	+
25	Alternaria alternata	1438	+	27	Mucor racemosus	464	+
25	Aspergillus candidus	475	+	27	Paecilomyces variotii	942	
25	Aspergillus niger	481	+	27	Penicillium commune	478	+
25	Aspergillus ochraceus	475	+	27	Penicillium commune	464	
25	Aspergillus versicolor	481	+	27	Penicillium corylophilum	464	+
25	Aureobasidium pullulans	44361		27	Penicillium expansum	464	+
25	Aureobasidium pullulans	34001	+	27	Penicillium sp.	464	+
25	Cladosporium cladosporioides	481	+	27	Penicillium viridicatum	478	
25	Cladosporium sp.	11445	+	27	Phoma herbarum	464	+
25	Cladosporium sp.	481		27	Rhizopus oryzae	464	+
25	Cladosporium sphaerospermum	475	+	27	Ulocladium chartarum	464	+
25	Epicoccum nigrum	1425	+	27	yeast	13184	
25	Epicoccum nigrum	963		28	Alternaria alternata	13865	
25	Penicillium citrinum	475	+	28	Alternaria alternata	13751	+
25	Penicillium digitatum	2376	+	28	Aspergillus niger	1467	
25	Penicillium digitatum	1438		28	Aspergillus niger	1467	+
25	Penicillium implicatum	481	+	28	Aureobasidium pullulans	4927	+
25	Penicillium sp. #44	475	+	28	Aureobasidium pullulans	3957	
25	Penicillium sp. #87	1901		28	Cladosporium cladosporioides	489	+
25	Penicillium sp. #87	1432	+	28	Cladosporium sp.	498	+
25	Penicillium spinulosum	3821		28	Cladosporium sphaerospermum	498	+
25	Penicillium spinulosum	1920	+	28	Epicoccum nigrum	987	+
25	Rhizopus oryzae	8079	+	28	Epicoccum nigrum	489	
25	Rhizopus oryzae	2851		28	Penicillium chrysogenum	1485	+
25	Trichoderma viride	1438		28	Penicillium commune	489	
25	unknown	13905	+	28	Penicillium oxalicum	4438	+
25	unknown	2402		28	Penicillium simplicissimum	489	+
26	Alternaria alternata	945	+	28	Penicillium variabile	489	
26	Aspergillus ochraceus	474		28	Penicillium viridicatum	1467	
26	Aspergillus versicolor	5692	+	28	Penicillium vulpinum	489	
26	Aspergillus versicolor	3313		28	unknown	978	
26	Aureobasidium pullulans	34001		28	yeast	997483	
26	Aureobasidium pullulans	19816	+	29	Alternaria alternata	475	+
26	Chaetomium globosum	474	+	29	Aspergillus niger	947	+
26	Chaetomium globosum	470		29	Aspergillus versicolor	4258	+
26	Cladosporium cladosporioides	3309	+	29	Aspergillus versicolor	475	
26	Cladosporium sp.	474		29	Aureobasidium pullulans	6159	+
26	Cladosporium sphaerospermum	474	+	29	Aureobasidium pullulans	2840	
26	Epicoccum nigrum	2368		29	Cladosporium herbarum	475	+
26	Eurotium herbariorum	5667	+	29	Eurotium herbariorum	1423	+
26	Geotrichum candidum	470		29	Penicillium chrysogenum	2368	+
26	Penicillium aurantiogriseum	941		29	Penicillium chrysogenum	1423	
26	Penicillium aurantiogriseum	941	+	29	Penicillium spinulosum	475	+
26	Penicillium brevicompactum	474	+	29	Scopulariopsis chartarum	950	
26	Penicillium commune	1419		29	Scopulariopsis fusca	475	+
26	Penicillium variabile	474	+	29	Scopulariopsis sp.	472	
26	Penicillium viridicatum	941		29	Ulocladium chartarum	475	
26	Phoma herbarum	1419	+	29	Ulocladium chartarum	475	+
26	unknown	7590		29	unknown	1895	
26	unknown	470	+	29	unknown	947	+
26	yeast	1423		29	yeast	104508	
27	Alternaria alternata	6626		30	Alternaria alternata	20000	
27	Alternaria alternata	1885	+	30	Alternaria alternata	482	+
27	Alternaria sp.	929	+	30	Aspergillus niger	98	+
27	Aspergillus sydowii	478		30	Aspergillus niger	94	
27	Aspergillus versicolor	464		30	Aspergillus ochraceus	470	+
27	Aureobasidium pullulans	9851	+	30	Aspergillus ochraceus	282	
27	Aureobasidium pullulans	929		30	Aspergillus sp.	98	+
27	Cladosporium cladosporioides	2363	+	30	Aureobasidium pullulans	1529	+
27	Epicoccum nigrum	464	+	30	Aureobasidium pullulans	772	

HN	Identification	AVG CFU/g	G
30	Cladosporium cladosporioides	196	+
30	Cladosporium cladosporioides	98	
30	Epicoccum nigrum	94	+
30	Fusarium oxysporum	294	+
30	Penicillium atramentosum	94	
30	Penicillium aurantiogriseum	384	+
30	Penicillium aurantiogriseum	98	
30	Penicillium brevicompactum	376	
30	Penicillium brevicompactum	94	+
30	Penicillium citrinum	98	
30	Penicillium commune	94	+
30	Penicillium roquefortii	98	
30	Penicillium sp.	294	
30	Penicillium sp. #26	98	
30	Penicillium sp. #52	282	+
30	Penicillium spinulosum	192	
30	Penicillium verrucosum	384	+
30	Penicillium verrucosum	98	
30	Penicillium vulpinum	196	+
30	Scopulariopsis brevicaulis	98	
30	Trichoderma viride	94	
30	Ulocladium chartarum	98	
30	unknown	388	
30	unknown	196	+
30	yeast	19220	
31	Alternaria alternata	1177	
31	Alternaria alternata	1084	+
31	Aspergillus fumigatus	97	
31	Aspergillus niger	97	+
31	Aspergillus sp.	197	+
31	Aspergillus versicolor	97	
31	Aureobasidium pullulans	589	+
31	Cladosporium cladosporioides	97	+
31	Drechslera sp.	97	+
31	Emericella sp.	97	+
31	Epicoccum nigrum	592	
31	Epicoccum nigrum	97	+
31	Monascus ruber	97	+
31	Mucor plumbeus	197	+
31	Penicillium chrysogenum	296	+
31	Penicillium chrysogenum	198	
31	Penicillium corylophilum	99	+
31	Pithomyces chartarum	97	+
31	unknown	589	
31	yeast	1287	
33	Aureobasidium pullulans	8474	
33	Aureobasidium pullulans	1878	+
33	Cladosporium cladosporioides	939	+
33	Cladosporium sp.	465	+
33	Eurotium herbariorum	12231	+
33	Penicillium expansum	931	+
33	Penicillium spinulosum	946	+
33	Penicillium spinulosum	465	
33	Phoma herbarum	473	+
33	Trichoderma viride	473	
33	Ulocladium chartarum	465	+
33	unknown	6099	
33	yeast	237673	
34	Alternaria alternata	4242	
34	Alternaria alternata	3771	+
34	Aspergillus fumigatus	466	
34	Aspergillus versicolor	466	
34	Aureobasidium pullulans	2858	+
34	Aureobasidium pullulans	952	
34	Chaetomium globosum	466	
34	Cladosporium cladosporioides	486	+
34	Cladosporium sphaerospermum	486	
34	Cladosporium sphaerospermum	466	+
34	Epicoccum nigrum	2818	+
34	Epicoccum nigrum	466	
34	Eurotium herbariorum	19362	+
34	Paecilomyces variotii	486	
34	Penicillium chrysogenum	1945	
34	Penicillium commune	2878	+
34	Penicillium commune	1439	
34	Penicillium corylophilum	4724	
34	Penicillium corylophilum	3751	+
34	Penicillium crustosum	486	
34	Penicillium expansum	952	+
34	Penicillium sp. #1	1419	
34	Penicillium sp. #1	486	+
34	Penicillium spinulosum	1905	
34	Penicillium spinulosum	952	+
34	Scopulariopsis brevicaulis	486	
34	Ulocladium chartarum	486	+
34	Ulocladium sp.	466	
34	unknown	3791	+
34	unknown	466	
34	yeast	17457	
35	Alternaria alternata	7138	
35	Alternaria alternata	2380	+
35	Aspergillus versicolor	471	+
35	Aureobasidium pullulans	50568	
35	Aureobasidium pullulans	46312	+
35	Cladosporium cladosporioides	471	+
35	Cladosporium sp.	3356	+
35	Cladosporium sphaerospermum	482	+
35	Epicoccum nigrum	1436	+
35	Epicoccum nigrum	943	
35	Eurotium herbariorum	7612	+
35	Eurotium herbariorum	954	
35	Mucor racemosus	482	+
35	Penicillium chrysogenum	471	
35	Penicillium chrysogenum	471	+
35	Penicillium corylophilum	954	+
35	Penicillium sp. #1	1919	
35	Penicillium spinulosum	943	+
35	Penicillium variabile	471	
35	Phoma herbarum	1415	+
35	Ulocladium chartarum	1426	
35	unknown	1930	+
35	unknown	1886	
35	yeast	2358	
36	Alternaria alternata	5254	
36	Alternaria alternata	1431	+
36	Aspergillus niger	469	+
36	Aspergillus ochraceus	947	+
36	Aspergillus ochraceus	477	
36	Aureobasidium pullulans	68619	
36	Aureobasidium pullulans	23220	+
36	Cladosporium cladosporioides	1416	+
36	Cladosporium sp.	954	+

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
36	Cladosporium sphaerospermum	469	+	40	Aureobasidium pullulans	470	
36	Epicoccum nigrum	1424		40	Coniothyrium sp.	468	+
36	Epicoccum nigrum	469	+	40	Epicoccum nigrum	1883	+
36	Eurotium herbariorum	469	+	40	Eurotium herbariorum	1407	+
36	Mucor plumbeus	477		40	Mucor racemosus	1877	+
36	Mucor racemosus	477		40	Penicillium miczynskii	2343	+
36	Penicillium brevicompactum	469		40	Penicillium sp. #26	7993	+
36	Penicillium citrinum	939	+	40	Penicillium sp. #26	5165	
36	Penicillium coprophilum	469		40	Penicillium viridicatum	4702	+
36	Penicillium corylophilum	469	+	40	Penicillium viridicatum	468	
36	Penicillium expansum	13749	+	40	Penicillium vulpinum	468	+
36	Penicillium expansum	947		40	Phialophora sp.	470	
36	Penicillium purpurogenum	1409		40	Rhizopus oryzae	470	
36	Penicillium simplicissimum	7113	+	40	Sphaeropsis sp.	1404	
36	Penicillium simplicissimum	3339		40	Sphaeropsis sp.	468	+
36	Penicillium sp. #26	1431		40	Trichoderma viride	5636	
36	Penicillium spinulosum	21767	+	40	Trichoderma viride	4221	+
36	Penicillium spinulosum	17089		40	unknown	22556	
36	Phoma herbarum	477	+	40	unknown	6580	+
36	unknown	3303		40	yeast	1883	
36	unknown	1879	+	41	Alternaria alternata	196	+
36	yeast	14653		41	Aspergillus sydowii	1084	+
39	Alternaria alternata	4726		41	Aspergillus versicolor	4698	
39	Alternaria alternata	1420	+	41	Aspergillus versicolor	196	+
39	Aspergillus niger	476	+	41	Aureobasidium pullulans	1475	
39	Aspergillus sp.	949		41	Aureobasidium pullulans	983	+
39	Aspergillus sp.	476	+	41	Eurotium herbariorum	98	+
39	Aspergillus sydowii	476	+	41	Exophiala sp.	1572	
39	Aspergillus versicolor	473	+	41	Exophiala sp.	392	+
39	Aureobasidium pullulans	1896	+	41	Penicillium aurantiogriseum	2262	+
39	Aureobasidium pullulans	946		41	Penicillium aurantiogriseum	393	
39	Cladosporium cladosporioides	476	+	41	Penicillium coprophilum	98	
39	Cladosporium sp.	946	+	41	Penicillium miczynskii	98	
39	Cladosporium sp.	476		41	Penicillium simplicissimum	98	+
39	Cladosporium sphaerospermum	946		41	Penicillium spinulosum	294	
39	Cladosporium sphaerospermum	476	+	41	Penicillium spinulosum	196	+
39	Epicoccum nigrum	1420		41	unknown	98	+
39	Epicoccum nigrum	473	+	41	yeast	2267	
39	Eurotium herbariorum	476		42	Alternaria alternata	14775	
39	Eurotium herbariorum	473	+	42	Alternaria alternata	4854	+
39	Penicillium chrysogenum	1423	+	42	Aspergillus ochraceus	24443	+
39	Penicillium chrysogenum	473		42	Aspergillus restrictus	9765	
39	Penicillium corylophilum	476		42	Aspergillus restrictus	4911	+
39	Penicillium echinulatum	476	+	42	Aspergillus sp.	4854	+
39	Penicillium spinulosum	6639	+	42	Aspergillus tamarii	4854	+
39	Penicillium spinulosum	5224		42	Aspergillus versicolor	4911	
39	Penicillium vulpinum	2375	+	42	Aureobasidium pullulans	82810	+
39	Penicillium vulpinum	473		42	Aureobasidium pullulans	19417	
39	Scopulariopsis candida	476	+	42	Chaetomium globosum	4854	
39	Scopulariopsis sp.	476	+	42	Cladosporium cladosporioides	9708	+
39	Ulocladium chartarum	473		42	Cladosporium cladosporioides	9708	
39	unknown	3325		42	Cladosporium sphaerospermum	39063	+
39	unknown	949	+	42	Epicoccum nigrum	4911	+
39	yeast	2370		42	Eurotium herbariorum	9765	+
40	Acremonium sp.	48842	+	42	Penicillium brevicompactum	9765	+
40	Acremonium sp.	8945		42	Penicillium chrysogenum	4854	+
40	Alternaria alternata	1409	+	42	Penicillium citrinum	4911	
40	Alternaria alternata	470		42	Penicillium citrinum	4911	+
40	Aspergillus fumigatus	470		42	Penicillium commune	9765	+
40	Aspergillus versicolor	941	+	42	Penicillium commune	4911	
40	Aspergillus versicolor	468		42	Penicillium echinulatum	4854	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
42	Penicillium expansum	4854	+	45	Wallemia sebi	47787	+
42	Penicillium vulpinum	14677	+	45	yeast	33508	
42	Trichoderma viride	4854		47	Alternaria alternata	318458	
42	unknown	73044	+	47	Alternaria alternata	2429	+
42	unknown	4854		47	Aspergillus niger	485	
42	Wallemia sebi	4854	+	47	Aspergillus sp.	1457	+
42	yeast	359738		47	Aureobasidium pullulans	10690	+
43	Alternaria alternata	135869		47	Aureobasidium pullulans	7288	
43	Alternaria alternata	23228	+	47	Cladosporium sphaerospermum	2430	+
43	Aspergillus penicilloides	4708	+	47	Cladosporium sphaerospermum	486	
43	Aureobasidium pullulans	18416		47	Coniothyrium sp.	2914	
43	Aureobasidium pullulans	14124	+	47	Coniothyrium sp.	2427	+
43	Chrysosporium sp.	9416		47	Epicoccum nigrum	970	
43	Cladosporium cladosporioides	9208	+	47	Fusarium oxysporum	1458	+
43	Cladosporium sp.	13812	+	47	Mucor racemosus	485	
43	Cladosporium sphaerospermum	9416	+	47	Penicillium brevicompactum	1458	
43	Epicoccum nigrum	4708	+	47	Penicillium chrysogenum	485	+
43	Penicillium aurantiogriseum	4708	+	47	Penicillium citreonigrum	486	+
43	Penicillium brevicompactum	4708		47	Penicillium corylophilum	971	+
43	Penicillium citreonigrum	4708		47	Penicillium corylophilum	486	
43	Penicillium commune	14020		47	Penicillium vulpinum	485	
43	Penicillium corylophilum	4708		47	Pithomyces chartarum	485	
43	Penicillium spinulosum	9416		47	Trichoderma viride	485	
43	Penicillium spinulosum	4604	+	47	unknown	4859	+
43	Phoma herbarum	4708		47	unknown	2913	
43	Pithomyces chartarum	27728		47	yeast	6798	
43	Syncephalastrum verruculosum	4604		48	Aspergillus sp.	1949	+
43	Trichoderma harzianum	9416	+	48	Aureobasidium pullulans	4377	
43	Trichoderma viride	4708		48	Aureobasidium pullulans	2916	+
43	unknown	1146721		48	Cladosporium sp.	974	
43	unknown	879686	+	48	Cladosporium sphaerospermum	974	+
43	yeast	9208		48	Epicoccum nigrum	483	+
45	Alternaria alternata	9372		48	Eurotium herbariorum	483	+
45	Alternaria alternata	9328	+	48	Fusarium oxysporum	982	+
45	Aspergillus fumigatus	77490	+	48	Fusarium oxysporum	483	
45	Aspergillus fumigatus	4664		48	Geomyces pannorum	483	+
45	Aureobasidium pullulans	43695		48	Humicola fuscoatra	491	
45	Aureobasidium pullulans	13992	+	48	Penicillium chrysogenum	5372	+
45	Cladosporium cladosporioides	4664	+	48	Penicillium chrysogenum	2924	
45	Cladosporium sp.	4664		48	Penicillium citreonigrum	483	
45	Cladosporium sphaerospermum	9614	+	48	Penicillium citrinum	483	+
45	Epicoccum nigrum	9614	+	48	Penicillium coprophilum	483	+
45	Eurotium herbariorum	4950	+	48	Penicillium corylophilum	491	
45	Penicillium brevicompactum	9328	+	48	Penicillium sp. #64	491	
45	Penicillium chrysogenum	38745	+	48	Penicillium spinulosum	491	+
45	Penicillium chrysogenum	19229		48	Penicillium vulpinum	483	
45	Penicillium citreonigrum	4664		48	Trichoderma viride	491	
45	Penicillium commune	38745	+	48	unknown	5372	+
45	Penicillium corylophilum	9614		48	unknown	2924	
45	Penicillium echinulatum	4950		48	yeast	3891	
45	Penicillium expansum	4664	+	49	Alternaria alternata	6300	
45	Penicillium viridicatum	9328		49	Alternaria alternata	1992	+
45	Penicillium viridicatum	4664	+	49	Aureobasidium pullulans	996	+
45	Pestalotiopsis sp.	4664	+	49	Botrytis sp.	978	
45	Phoma herbarum	27985		49	Cladosporium cladosporioides	1494	+
45	Rhizopus oryzae	4950	+	49	Cladosporium sphaerospermum	498	+
45	Trichoderma viride	28844		49	Epicoccum nigrum	498	
45	Ulocladium chartarum	9614	+	49	Epicoccum nigrum	498	+
45	Ulocladium chartarum	9328		49	Penicillium brevicompactum	480	
45	unknown	139842	+	49	Penicillium chrysogenum	498	
45	unknown	67302		49	Penicillium decumbens	498	+

HN	Identification	AVG CFU/g	G
49	Penicillium raistrickii	1442	
49	Penicillium raistrickii	978	+
49	Penicillium spinulosum	2953	+
49	Penicillium spinulosum	1940	
49	unknown	1940	+
49	unknown	1494	
49	yeast	28815	
50	Alternaria alternata	11791	
50	Alternaria alternata	6334	+
50	Alternaria sp.	488	+
50	Aspergillus niger	488	
50	Aspergillus versicolor	1461	+
50	Aureobasidium pullulans	19016	
50	Aureobasidium pullulans	15596	+
50	Botrytis cinerea	488	
50	Cladosporium cladosporioides	486	
50	Cladosporium cladosporioides	486	+
50	Cladosporium sp.	486	+
50	Cladosporium sphaerospermum	1461	+
50	Epicoccum nigrum	1949	
50	Eurotium herbariorum	486	+
50	Mucor racemosus	6332	
50	Mucor racemosus	3410	+
50	Penicillium chrysogenum	5840	+
50	Penicillium chrysogenum	3896	
50	Penicillium citrinum	976	+
50	Penicillium corylophilum	1459	+
50	Penicillium expansum	974	+
50	Penicillium sp. #1	488	+
50	Phoma herbarum	488	+
50	Trichoderma sp.	488	+
50	Ulocladium chartarum	488	
50	unknown	4379	
50	unknown	2920	+
50	yeast	1461	
51	Alternaria alternata	1450	+
51	Alternaria alternata	483	
51	Aureobasidium pullulans	39046	
51	Aureobasidium pullulans	10537	+
51	Cladosporium cladosporioides	948	
51	Cladosporium sphaerospermum	967	+
51	Eurotium herbariorum	1450	+
51	Mucor plumbeus	9998	
51	Mucor plumbeus	9059	+
51	Mucor racemosus	483	
51	Paecilomyces variotii	967	+
51	Penicillium aurantiogriseum	4306	+
51	Penicillium aurantiogriseum	1925	
51	Penicillium citrinum	957	
51	Penicillium citrinum	474	+
51	Penicillium expansum	12425	
51	Penicillium expansum	10537	+
51	Penicillium spinulosum	483	+
51	Penicillium spinulosum	474	
51	Phoma herbarum	1897	+
51	Rhizopus oryzae	474	
51	Rhodotorula sp.	5264	
51	unknown	6723	
51	unknown	2371	+
51	Wallemia sebi	474	+
51	yeast	19825	
52	Alternaria alternata	4752	+
52	Aspergillus sydowii	4770	+
52	Aureobasidium pullulans	114345	
52	Cladosporium cladosporioides	9523	+
52	Cladosporium sphaerospermum	4752	+
52	Geotrichum candidum	4752	+
52	Mucor racemosus	4770	+
52	Paecilomyces variotii	9505	+
52	Penicillium chrysogenum	9523	
52	Penicillium commune	47619	
52	Penicillium digitatum	19029	
52	Penicillium digitatum	4770	+
52	Penicillium expansum	28589	+
52	Penicillium spinulosum	4752	+
52	Penicillium viridicatum	52335	+
52	Penicillium viridicatum	42848	
52	Phoma herbarum	4752	+
52	unknown	14312	+
52	unknown	9523	
52	yeast	9505	
53	Alternaria alternata	171918	
53	Alternaria alternata	951	+
53	Aspergillus niger	941	+
53	Aspergillus niger	480	
53	Aspergillus ochraceus	480	
53	Aspergillus sp.	470	+
53	Aspergillus sydowii	951	+
53	Aureobasidium pullulans	1432	+
53	Chrysosporium sp.	480	
53	Eurotium herbariorum	470	+
53	Mucor plumbeus	470	
53	Mucor racemosus	3335	
53	Mucor racemosus	2354	+
53	Penicillium aurantiogriseum	3816	
53	Penicillium aurantiogriseum	1412	+
53	Penicillium chrysogenum	470	
53	Penicillium commune	1893	
53	Penicillium commune	1412	+
53	Penicillium expansum	480	
53	Penicillium sp.	1923	+
53	Penicillium spinulosum	951	
53	Penicillium viridicatum	6160	+
53	Penicillium vulpinum	2844	+
53	Penicillium vulpinum	1903	
53	Rhizopus oryzae	1923	+
53	unknown	951	
53	unknown	941	+
53	yeast	10958	
54	Alternaria alternata	14793	+
54	Aureobasidium pullulans	34246	+
54	Aureobasidium pullulans	5373	
54	Cladosporium cladosporioides	24461	+
54	Cladosporium sp.	9900	+
54	Penicillium citrinum	4892	
54	Penicillium corylophilum	19627	+
54	Penicillium corylophilum	4950	
54	Penicillium islandicum	4892	
54	Penicillium sp. #26	4950	
54	Penicillium spinulosum	24752	+
54	Penicillium spinulosum	4892	
54	Penicillium verrucosum	4950	+

HN	Identification	AVG CFU/g	G
54	Trichoderma harzianum	4950	
54	Trichoderma viride	98370	+
54	Trichoderma viride	44438	
54	Ulocladium chartarum	9784	
54	unknown	29412	+
54	yeast	14677	
55	Aspergillus niger	492	+
55	Aspergillus niger	481	
55	Aspergillus parasiticus	492	
55	Aspergillus sp.	984	+
55	Aspergillus versicolor	492	+
55	Aureobasidium pullulans	12136	
55	Cladosporium sp.	28167	+
55	Cladosporium sphaerospermum	17560	+
55	Cladosporium sphaerospermum	492	
55	Eurotium herbariorum	9727	+
55	Geomyces pannorum	2952	
55	Paecilomyces sp.	984	
55	Penicillium chrysogenum	973	
55	Penicillium citrinum	973	
55	Penicillium commune	3434	+
55	Penicillium coprophilum	1947	+
55	Rhodotorula sp.	1926	+
55	Rhodotorula sp.	963	
55	Scopulariopsis candida	492	
55	unknown	492	
55	Wallemia sebi	133261	
56	Acremonium sclerotigenum	440283	
56	Alternaria alternata	1960	+
56	Alternaria alternata	998	
56	Aspergillus niger	487	
56	Aureobasidium pullulans	1960	+
56	Cladosporium cladosporioides	986	+
56	Cladosporium sphaerospermum	974	+
56	Epicoccum nigrum	499	+
56	Eurotium herbariorum	487	+
56	Mucor plumbeus	487	
56	Penicillium brevicompactum	2483	+
56	Penicillium brevicompactum	986	
56	Penicillium chrysogenum	2935	+
56	Penicillium chrysogenum	986	
56	Penicillium citrinum	3956	+
56	Penicillium citrinum	499	
56	Penicillium commune	499	+
56	Penicillium expansum	974	
56	Penicillium miczynskii	499	
56	Penicillium sp. #26	986	+
56	Penicillium spinulosum	2471	+
56	Penicillium spinulosum	499	
56	Penicillium viridicatum	499	+
56	Scopulariopsis brevicaulis	499	+
56	Scopulariopsis brevicaulis	487	
56	Trichoderma viride	974	
56	Ulocladium chartarum	2958	+
56	Ulocladium chartarum	986	
56	unknown	2947	+
56	unknown	998	
56	Wallemia sebi	986	+
56	yeast	10826	
57	Acremonium sp.	24432	
57	Alternaria alternata	4752	+
57	Aureobasidium pullulans	43069	
57	Cladosporium cladosporioides	4826	+
57	Eurotium herbariorum	23837	+
57	Ophiostoma tenellum	9505	
57	Paecilomyces variotii	14405	
57	Paecilomyces variotii	4752	+
57	Penicillium brevicompactum	4752	
57	Penicillium citreonigrum	4752	+
57	Penicillium corylophilum	4752	
57	Penicillium restrictum	4826	
57	Penicillium sp. #26	9505	
57	Penicillium spinulosum	143539	+
57	Penicillium spinulosum	62227	
57	Scopulariopsis candida	4826	
57	Trichoderma sp.	14405	+
57	Trichoderma viride	14258	
57	unknown	47968	
58	Alternaria alternata	38380	
58	Aspergillus sp.	4743	+
58	Aspergillus sydowii	4743	+
58	Chaetomium funicola	4743	+
58	Cladosporium sphaerospermum	4743	
58	Penicillium chrysogenum	42749	
58	Penicillium chrysogenum	38169	+
58	Scopulariopsis candida	4798	
58	unknown	33316	+
58	unknown	23719	
58	yeast	42694	
59	Alternaria alternata	490	+
59	Aspergillus versicolor	491	+
59	Aureobasidium pullulans	1472	
59	Chrysosporium sp.	491	
59	Penicillium chrysogenum	1960	
59	Penicillium commune	2451	+
59	Penicillium expansum	2942	
59	Penicillium viridicatum	9321	+
59	Penicillium viridicatum	4906	
59	Ulocladium chartarum	490	+
59	unknown	2451	+
59	unknown	1472	
59	yeast	7847	
61	Aspergillus sp.	25474	
61	Coniothyrium fuckelii	478	+
61	Fusarium sp.	473	
61	Mucor racemosus	946	
61	Mucor racemosus	946	+
61	Penicillium corylophilum	473	
61	Penicillium corylophilum	473	+
61	Penicillium expansum	473	
61	Penicillium viridicatum	1424	
61	Penicillium viridicatum	951	+
61	Trichoderma viride	478	+
61	unknown	5240	+
61	unknown	1898	
61	yeast	956	
62	Aureobasidium pullulans	20651	
62	Aureobasidium pullulans	4807	+
62	Eurotium herbariorum	92676	+
62	Eurotium herbariorum	4807	
62	Mucor racemosus	43269	
62	Mucor racemosus	24038	+

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
62	Oidiodendron sp.	4807		65	Penicillium sp. #26	489	
62	Penicillium brevicompactum	19629		65	Penicillium sp. #26	481	+
62	Penicillium brevicompactum	9881	+	65	Penicillium spinulosum	4372	+
62	Penicillium corylophilum	4940		65	Penicillium spinulosum	2927	
62	Penicillium corylophilum	4807	+	65	Phialophora fastigiata	481	
62	Penicillium restrictum	4940		65	Trichoderma viride	1460	+
62	Penicillium spinulosum	9881	+	65	Trichoderma viride	978	
62	Penicillium spinulosum	4940		65	unknown	130811	
62	Penicillium viridicatum	9881	+	65	unknown	124589	+
62	Penicillium viridicatum	4807		65	yeast	12667	
62	Phoma herbarum	1976284		67	Alternaria alternata	48288	+
62	Phoma herbarum	1976284	+	67	Aureobasidium pullulans	23808	+
62	Trichoderma viride	24171		67	Aureobasidium pullulans	20207	
62	unknown	135945		67	Cladosporium cladosporioides	14374	+
62	yeast	264271		67	Cladosporium macrocarpum	4716	+
64	Alternaria alternata	3324	+	67	Cladosporium sp.	4940	+
64	Aspergillus niger	14893		67	Cladosporium sphaerospermum	9657	+
64	Aspergillus sp.	4781	+	67	Eurotium herbariorum	4940	
64	Aspergillus sp.	941		67	Eurotium herbariorum	4940	+
64	Aspergillus versicolor	485		67	Penicillium brevicompactum	33466	+
64	Aureobasidium pullulans	3324	+	67	Penicillium brevicompactum	4940	
64	Aureobasidium pullulans	1456		67	Penicillium chrysogenum	9657	+
64	Cladosporium herbarum	470	+	67	Penicillium chrysogenum	9433	
64	Cladosporium sphaerospermum	970	+	67	Penicillium spinulosum	24032	+
64	Epicoccum nigrum	970	+	67	Penicillium spinulosum	9657	
64	Epicoccum nigrum	470		67	Trichoderma harzianum	63334	+
64	Eurotium amstelodami	2427		67	Trichoderma harzianum	24032	
64	Eurotium herbariorum	5266	+	67	Trichoderma koningii	9433	
64	Mucor plumbeus	470	+	67	Trichoderma viride	102188	
64	Penicillium atramentosum	970	+	67	unknown	58393	+
64	Penicillium atramentosum	485		67	unknown	19315	
64	Penicillium chrysogenum	1897	+	67	yeast	9433	
64	Penicillium corylophilum	6722		70	Alternaria alternata	64044	
64	Penicillium corylophilum	3810	+	70	Alternaria alternata	1980	+
64	Penicillium echinulatum	485	+	70	Aspergillus sp.	1459	
64	Penicillium sp. #26	1897		70	Aspergillus versicolor	9345	+
64	Pestalotiopsis sp.	470		70	Aspergillus versicolor	1968	
64	Phoma chrysanthemicola	5339	+	70	Aureobasidium pullulans	8373	+
64	Phoma herbarum	470		70	Aureobasidium pullulans	2466	
64	unknown	956		70	Epicoccum nigrum	972	
64	unknown	470	+	70	Epicoccum nigrum	498	+
64	yeast	956		70	Eurotium herbariorum	2478	+
65	Alternaria alternata	3386	+	70	Geomyces pannorum	486	
65	Aspergillus sp.	489	+	70	Mucor plumbeus	486	+
65	Aspergillus versicolor	489	+	70	Penicillium brevicompactum	5419	+
65	Aureobasidium pullulans	12617		70	Penicillium chrysogenum	996	
65	Aureobasidium pullulans	970	+	70	Penicillium citrinum	498	+
65	Epicoccum nigrum	2423	+	70	Penicillium corylophilum	984	+
65	Epicoccum nigrum	481		70	Penicillium expansum	5431	
65	Eurotium herbariorum	481	+	70	Penicillium viridicatum	498	+
65	Mucor racemosus	1445	+	70	Rhizopus oryzae	498	
65	Paecilomyces sp.	978	+	70	Scopulariopsis candida	486	+
65	Paecilomyces sp.	481		70	unknown	7377	
65	Penicillium brevicompactum	3402	+	70	unknown	3462	+
65	Penicillium citreonigrum	489		70	yeast	11835	
65	Penicillium coprophilum	481		71	Alternaria alternata	8287	
65	Penicillium decumbens	481		71	Alternaria alternata	1431	+
65	Penicillium implicatum	963		71	Aspergillus ochraceus	23359	+
65	Penicillium implicatum	489	+	71	Aspergillus ochraceus	15744	
65	Penicillium miczynskii	2920	+	71	Aspergillus versicolor	950	+
65	Penicillium miczynskii	1941		71	Aureobasidium pullulans	25752	+

HN	Identification	AVG CFU/g	G
71	Cladosporium sp.	478	+
71	Cladosporium sphaerospermum	478	+
71	Eurotium herbariorum	956	+
71	Mucor racemosus	475	+
71	Mucor sp.	478	
71	Penicillium chrysogenum	2387	+
71	Penicillium chrysogenum	953	
71	Penicillium citrinum	1431	
71	Penicillium citrinum	475	+
71	Penicillium corylophilum	478	+
71	Penicillium islandicum	5719	
71	Penicillium islandicum	953	+
71	Penicillium spinulosum	478	+
71	Penicillium spinulosum	475	
71	Phoma herbarum	475	
71	unknown	27719	+
71	unknown	1903	
71	Wallemia sebi	3340	+
71	yeast	98403	
72	Alternaria alternata	11915	
72	Alternaria alternata	478	+
72	Aspergillus niger	1467	
72	Aspergillus niger	489	+
72	Aspergillus ochraceus	489	
72	Aspergillus versicolor	957	+
72	Aureobasidium pullulans	957	+
72	Cladosporium cladosporioides	478	+
72	Cladosporium sphaerospermum	1467	+
72	Epicoccum nigrum	1447	+
72	Eurotium herbariorum	13075	+
72	Penicillium brevicompactum	489	+
72	Penicillium chrysogenum	2914	+
72	Penicillium chrysogenum	2904	
72	Penicillium coprophilum	489	+
72	Penicillium spinulosum	489	
72	Penicillium variabile	478	
72	Penicillium viridicatum	2435	+
72	Penicillium viridicatum	978	
72	Phoma herbarum	478	
72	Phoma herbarum	478	+
72	Trichoderma viride	478	
72	unknown	2904	+
72	unknown	2415	
72	yeast	11077	
73	Alternaria alternata	9588	+
73	Alternaria alternata	7679	
73	Aspergillus candidus	4844	
73	Aureobasidium pullulans	14332	
73	Aureobasidium pullulans	9588	+
73	Chrysosporium sp.	4743	+
73	Cladosporium sp.	23921	+
73	Cladosporium sphaerospermum	4743	+
73	Eurotium herbariorum	9588	+
73	Penicillium chrysogenum	19278	
73	Penicillium commune	28867	+
73	Penicillium commune	23820	
73	Penicillium sp. #26	24022	+
73	Penicillium sp. #26	14534	
73	Penicillium spinulosum	4743	
73	Penicillium vulpinum	24123	+
73	Trichoderma viride	14332	+
73	Trichoderma viride	9689	
73	yeast	47438	
74	Alternaria alternata	31870	
74	Alternaria alternata	4874	+
74	Aspergillus versicolor	8255	+
74	Aspergillus versicolor	5897	
74	Aureobasidium pullulans	3486	+
74	Cladosporium cladosporioides	1939	+
74	Cladosporium sp.	2988	+
74	Cladosporium sphaerospermum	471	+
74	Eurotium herbariorum	2490	+
74	Penicillium brevicompactum	943	
74	Penicillium brevicompactum	471	+
74	Penicillium chrysogenum	12318	+
74	Penicillium chrysogenum	3852	
74	Penicillium digitatum	498	
74	Penicillium viridicatum	498	+
74	Phoma herbarum	471	+
74	unknown	5976	
74	unknown	5870	+
74	yeast	62953	
75	Alternaria alternata	23140	
75	Aspergillus ochraceus	485	
75	Aspergillus versicolor	5354	+
75	Aspergillus versicolor	485	
75	Aureobasidium pullulans	20416	+
75	Candida sp.	1460	
75	Cladosporium cladosporioides	6813	+
75	Cladosporium sphaerospermum	487	
75	Cladosporium sphaerospermum	485	+
75	Epicoccum nigrum	974	+
75	Eurotium herbariorum	3403	+
75	Mucor plumbeus	487	
75	Penicillium brevicompactum	3889	+
75	Penicillium brevicompactum	485	
75	Penicillium chrysogenum	1458	+
75	Penicillium chrysogenum	974	
75	Penicillium coprophilum	487	+
75	Penicillium coprophilum	485	
75	Penicillium expansum	2434	+
75	Penicillium raistrickii	4378	+
75	Penicillium sp. #26	487	+
75	Penicillium spinulosum	1460	
75	Penicillium spinulosum	974	+
75	Penicillium viridicatum	485	
75	Phoma herbarum	970	
75	Phoma leveillei	45234	+
75	unknown	19972	+
75	unknown	5347	
75	yeast	159465	
76	Alternaria alternata	73569	
76	Aspergillus niger	469	
76	Aspergillus ochraceus	469	+
76	Aspergillus sp.	482	+
76	Aspergillus versicolor	482	+
76	Aureobasidium pullulans	2870	
76	Aureobasidium pullulans	952	+
76	Botrytis sp.	482	+
76	Cladosporium sp.	965	+
76	Penicillium citreonigrum	1879	
76	Penicillium citreonigrum	1409	+

HN	Identification	AVG CFU/g	G
76	Penicillium commune	12383	+
76	Penicillium commune	9563	
76	Penicillium crustosum	469	+
76	Penicillium echinulatum	4280	+
76	Penicillium raistrickii	3314	+
76	Penicillium raistrickii	469	
76	Penicillium sp.	1905	+
76	Penicillium sp. #26	939	
76	Penicillium sp. #26	469	+
76	Penicillium sp. #64	3810	
76	Penicillium spinulosum	3810	+
76	Penicillium spinulosum	939	
76	Pithomyces chartarum	482	+
76	yeast	4280	
77	Alternaria alternata	1424	
77	Alternaria alternata	1418	+
77	Aureobasidium pullulans	1895	+
77	Aureobasidium pullulans	1425	
77	Chrysosporium sp.	470	
77	Cladosporium cladosporioides	477	
77	Epicoccum nigrum	477	+
77	Epicoccum nigrum	470	
77	Eurotium herbariorum	477	+
77	Exophiala jeanselmei	470	
77	Hortaea werneckii	477	
77	Penicillium chrysogenum	1425	+
77	Penicillium commune	3320	
77	Penicillium commune	2354	+
77	Penicillium corylophilum	2850	+
77	Penicillium corylophilum	941	
77	Penicillium glandicola	470	+
77	Penicillium islandicum	947	
77	Pithomyces chartarum	1412	+
77	Sphaeropsis sp.	470	+
77	Trichoderma viride	954	
77	Ulocladium chartarum	477	
77	unknown	17621	+
77	unknown	7112	
77	yeast	18945	
78	Alternaria alternata	18593	
78	Alternaria alternata	3924	+
78	Aspergillus candidus	497	+
78	Aspergillus niger	479	+
78	Aspergillus ochraceus	497	+
78	Aureobasidium pullulans	8243	+
78	Aureobasidium pullulans	3838	
78	Chrysosporium sp.	497	
78	Cladosporium sp.	479	+
78	Cladosporium sphaerospermum	1473	+
78	Epicoccum nigrum	976	
78	Hortaea werneckii	497	
78	Mucor racemosus	1439	+
78	Rhizopus oryzae	959	
78	Scopulariopsis brevicaulis	497	+
78	Sporotrichum pruinosum	497	
78	Trichoderma viride	1491	
78	unknown	1936	
78	yeast	57962	
79	Alternaria alternata	495	+
79	Aspergillus flavipes	7364	
79	Aspergillus sp.	2475	+
79	Aspergillus ustus	1467	+
79	Aspergillus ustus	990	
79	Aspergillus versicolor	30518	+
79	Aspergillus versicolor	6424	
79	Penicillium brevicompactum	984	
79	Penicillium chrysogenum	2463	
79	Penicillium citreonigrum	978	+
79	Penicillium commune	2958	
79	Penicillium commune	1467	+
79	Penicillium digitatum	6895	
79	Penicillium digitatum	4950	+
79	Penicillium oxalicum	984	
79	Penicillium sp. #84	3942	+
79	Penicillium sp. #84	3453	
79	unknown	27094	
80	Alternaria alternata	959	+
80	Aspergillus versicolor	5878	
80	Aspergillus versicolor	479	+
80	Aureobasidium pullulans	7153	+
80	Aureobasidium pullulans	1900	
80	Cladosporium sphaerospermum	3333	+
80	Cladosporium sphaerospermum	479	
80	Eurotium herbariorum	473	+
80	Mucor plumbeus	1433	+
80	Mucor plumbeus	473	
80	Penicillium citrinum	2386	+
80	Penicillium commune	953	
80	Penicillium commune	479	+
80	Penicillium corylophilum	479	+
80	Penicillium expansum	479	+
80	Phoma herbarum	479	
80	unknown	16756	+
80	unknown	3358	
80	Wallemia sebi	47984	+
80	yeast	121088	
81	Alternaria alternata	1449	+
81	Aspergillus niger	99589	
81	Aspergillus niger	94	+
81	Aureobasidium pullulans	377	+
81	Cochliobolus sativus	94	+
81	Eurotium herbariorum	289	+
81	Mucor plumbeus	194	
81	Mucor plumbeus	194	+
81	Penicillium brevicompactum	477	+
81	Penicillium brevicompactum	94	
81	Penicillium chrysogenum	1427	+
81	Penicillium chrysogenum	286	
81	Penicillium corylophilum	383	+
81	Rhizopus oryzae	94	
81	Trichoderma viride	97	
81	unknown	383	
81	unknown	383	+
81	yeast	377	
82	Aspergillus sp.	24460	
82	Aspergillus sp.	19305	+
82	Aspergillus versicolor	189930	+
82	Aspergillus versicolor	175025	
82	Aureobasidium pullulans	4911	+
82	Cladosporium cladosporioides	4826	+
82	Eurotium herbariorum	4911	+
82	Penicillium brevicompactum	4826	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
82	Penicillium chrysogenum	24472		86	Aureobasidium pullulans	4578	
82	Penicillium chrysogenum	19475	+	86	Chrysonilia sp.	14258	+
82	Penicillium coprophilum	14478	+	86	Chrysosporium sp.	4752	+
82	Penicillium corylophilum	24301	+	86	Cladosporium sp.	13910	+
82	Penicillium decumbens	19475		86	Cladosporium sp.	4578	
82	Penicillium decumbens	19305	+	86	Cladosporium sphaerospermum	88215	+
82	Penicillium sp. #26	9652		86	Cladosporium sphaerospermum	4578	
82	Penicillium sp. #87	4826	+	86	Eurotium herbariorum	60916	+
82	Trichoderma viride	24301		86	Eurotium herbariorum	4578	
82	Trichoderma viride	4826	+	86	Penicillium citrinum	4578	
82	unknown	130735		86	Penicillium corylophilum	9331	
82	Wallemia sebi	9652		86	Penicillium griseofulvum	9157	+
83	Alternaria alternata	952	+	86	Penicillium raistrickii	4752	+
83	Aureobasidium pullulans	3330	+	86	Penicillium sp.	4752	+
83	Cladosporium sp.	475	+	86	Penicillium viridicatum	9157	
83	Gilmaniella humicola	146542		86	Rhizopus oryzae	4752	
83	Mucor plumbeus	5229		86	Talaromyces flavus	4578	
83	Mucor racemosus	10474	+	86	Trichoderma viride	4752	+
83	Mucor racemosus	4758		86	unknown	4578	+
83	Paecilomyces variotii	952		86	Wallemia sebi	13910	+
83	Penicillium chrysogenum	10479		86	yeast	125715	
83	Penicillium citrinum	1427	+	87	Alternaria alternata	5455	+
83	Penicillium citrinum	475		87	Aspergillus niger	422116	
83	Penicillium commune	2857		87	Aspergillus niger	1379	+
83	Penicillium commune	2380	+	87	Aspergillus sp.	452	+
83	Penicillium sp. #64	1902		87	Aspergillus versicolor	3232	+
83	Penicillium viridicatum	2858	+	87	Aspergillus versicolor	1811	
83	Penicillium viridicatum	477		87	Aureobasidium pullulans	1379	
83	Trichoderma viride	477		87	Aureobasidium pullulans	452	+
83	unknown	952		87	Chaetomium sp.	946	
83	yeast	13826		87	Cladosporium sphaerospermum	19309	+
85	Alternaria alternata	1899		87	Epicoccum nigrum	905	+
85	Alternaria alternata	480	+	87	Eurotium herbariorum	1852	+
85	Aspergillus niger	471	+	87	Mucor plumbeus	473	+
85	Aureobasidium pullulans	17144	+	87	Mucor racemosus	473	
85	Aureobasidium pullulans	480		87	Penicillium brevicompactum	946	+
85	Cladosporium sp.	943	+	87	Penicillium chrysogenum	2779	
85	Cladosporium sphaerospermum	471	+	87	Penicillium chrysogenum	452	+
85	Emericella nidulans	471	+	87	Penicillium corylophilum	452	
85	Mucor plumbeus	480		87	Penicillium crustosum	3643	+
85	Mucor racemosus	471		87	Penicillium crustosum	3623	
85	Mucor racemosus	471	+	87	Penicillium griseofulvum	8296	+
85	Penicillium corylophilum	1415	+	87	Penicillium griseofulvum	1811	
85	Penicillium corylophilum	480		87	Penicillium raistrickii	1358	+
85	Penicillium sp. #26	943		87	Penicillium sp. #26	946	+
85	Penicillium spinulosum	2376	+	87	Penicillium sp. #26	905	
85	Penicillium viridicatum	3800	+	87	Rhizopus oryzae	452	
85	Penicillium viridicatum	2358		87	Scopulariopsis sp.	9799	
85	Pithomyces chartarum	471		87	Scopulariopsis sp.	1832	+
85	Rhizopus oryzae	471		87	Sphaeropsis sp.	452	+
85	Trichoderma viride	1442		87	Ulocladium chartarum	473	+
85	unknown	2385		87	unknown	38269	+
85	unknown	943	+	87	unknown	10540	
85	yeast	23149		87	Wallemia sebi	13175	+
86	Acremonium kiliense	34583		87	yeast	7925	
86	Acremonium kiliense	4752	+	88	Alternaria alternata	936	+
86	Acremonium sp.	9157	+	88	Aspergillus ochraceus	472	+
86	Alternaria alternata	4752	+	88	Aspergillus sclerotiorum	4111	
86	Aspergillus ochraceus	9505	+	88	Aureobasidium pullulans	2826	+
86	Aspergillus ochraceus	4752		88	Aureobasidium pullulans	940	
86	Aureobasidium pullulans	18489	+	88	Chaetomium globosum	468	

HN	Identification	AVG CFU/g	G
88	Cladosporium sp.	472	+
88	Cladosporium sphaerospermum	936	+
88	Eurotium herbariorum	2349	+
88	Penicillium commune	468	
88	Penicillium expansum	6594	+
88	Penicillium expansum	1413	
88	Penicillium sp. #26	1881	
88	Penicillium sp. #26	945	+
88	Penicillium waksmanii	945	
88	Scopulariopsis brevicaulis	472	
88	Scopulariopsis brumptii	472	+
88	Ulocladium chartarum	472	+
88	unknown	940	
88	unknown	940	+
88	yeast	4712	
89	Alternaria alternata	3772	
89	Alternaria alternata	1926	+
89	Aspergillus niger	481	+
89	Aspergillus ochraceus	481	+
89	Aspergillus sp.	481	+
89	Aureobasidium pullulans	5780	+
89	Aureobasidium pullulans	1926	
89	Chrysosporium sp.	963	
89	Cladosporium cladosporioides	963	+
89	Cladosporium herbarum	963	+
89	Cladosporium sp.	963	+
89	Cladosporium sphaerospermum	1445	+
89	Epicoccum nigrum	1445	
89	Epicoccum nigrum	481	+
89	Eurotium herbariorum	963	+
89	Penicillium brevicompactum	3371	+
89	Penicillium citrinum	7707	+
89	Penicillium corylophilum	1445	
89	Penicillium echinulatum	481	+
89	Penicillium spinulosum	2408	+
89	Penicillium spinulosum	1926	
89	Penicillium variabile	481	+
89	Trichoderma viride	481	
89	unknown	1445	
89	unknown	1445	+
89	Wallemia sebi	481	+
89	yeast	96339	
90	Alternaria alternata	18298	
90	Alternaria sp.	927	
90	Aureobasidium pullulans	4223	+
90	Eurotium herbariorum	2807	+
90	Fusarium oxysporum	476	
90	Penicillium commune	3283	+
90	Penicillium commune	1391	
90	Penicillium raistrickii	476	+
90	unknown	463	+
90	Wallemia sebi	61539	+
90	yeast	168194	
91	Absidia sp.	18150	
91	Alternaria alternata	4621	+
91	Aspergillus niger	4816	+
91	Aureobasidium pullulans	38339	+
91	Aureobasidium pullulans	9633	
91	Cladosporium sp.	4621	+
91	Penicillium brevicompactum	4621	+
91	Penicillium commune	4816	+
91	Penicillium commune	4621	
91	Penicillium expansum	9438	+
91	Penicillium sp.	9438	
91	Penicillium sp. #26	4621	+
91	Penicillium sp. #87	4816	+
91	Penicillium verrucosum	4816	+
91	Penicillium viridicatum	4621	+
91	Phoma leveillei	4816	
91	Trichoderma viride	23497	
91	Trichoderma viride	4621	+
91	unknown	9438	+
91	yeast	19267	
92	Alternaria alternata	478	+
92	Aspergillus sp.	478	+
92	Aureobasidium pullulans	956	+
92	Epicoccum nigrum	478	+
92	Fusarium sp.	478	
92	Penicillium aurantiogriseum	3346	
92	Penicillium aurantiogriseum	957	+
92	Penicillium expansum	1912	
92	Penicillium hirsutum	3830	
92	Penicillium hirsutum	478	+
92	Penicillium miczynskii	478	
92	Penicillium miczynskii	478	+
92	Penicillium viridicatum	2391	
92	unknown	956	+
92	unknown	478	
92	yeast	191387	
94	Alternaria alternata	464	+
94	Alternaria sp.	467	+
94	Aspergillus fumigatus	21959	
94	Aspergillus fumigatus	2798	+
94	Aspergillus niger	1396	+
94	Aspergillus ochraceus	2333	
94	Aureobasidium pullulans	931	
94	Chrysosporium sp.	464	
94	Cladosporium sp.	464	+
94	Cladosporium sphaerospermum	931	+
94	Epicoccum nigrum	934	
94	Eurotium herbariorum	2795	+
94	Mucor plumbeus	934	+
94	Mucor racemosus	464	
94	Paecilomyces variotii	21892	+
94	Paecilomyces variotii	467	
94	Penicillium chrysogenum	934	+
94	Penicillium commune	464	
94	Penicillium corylophilum	467	
94	Trichoderma harzianum	467	
94	Trichoderma viride	931	
94	Trichoderma viride	467	+
94	unknown	931	
94	yeast	101822	
95	Acremonium sp.	154440	
95	Alternaria alternata	14204	+
95	Alternaria alternata	4612	
95	Aspergillus glaucus	18450	+
95	Aspergillus niger	14204	+
95	Aspergillus niger	9347	
95	Aspergillus ochraceus	4734	+
95	Aspergillus ochraceus	4612	
95	Aspergillus ustus	23185	+

HN	Identification	AVG CFU/g	G
95	Aspergillus ustus	9225	
95	Aspergillus versicolor	18450	
95	Aspergillus versicolor	4734	+
95	Aspergillus wentii	14082	
95	Aureobasidium pullulans	65920	+
95	Aureobasidium pullulans	9225	
95	Cladosporium macrocarpum	18572	+
95	Cladosporium sp.	27675	+
95	Cladosporium sphaerospermum	79147	+
95	Coniothyrium fuckelii	4734	
95	Epicoccum nigrum	13959	
95	Eurotium herbariorum	37389	+
95	Moniliella sp.	9347	
95	Penicillium chrysogenum	37267	
95	Penicillium chrysogenum	13837	+
95	Penicillium citrinum	4612	+
95	Penicillium corylophilum	14082	+
95	Penicillium crustosum	4734	
95	Penicillium crustosum	4612	+
95	Penicillium decumbens	18817	+
95	Penicillium decumbens	13959	
95	Trichoderma viride	4612	
95	unknown	305319	+
95	unknown	37022	
95	Wallemia sebi	112413	+
95	Wardomyces humicola	4734	
95	yeast	145068	
96	Alternaria alternata	2814	+
96	Aspergillus fumigatus	117739	
96	Aspergillus fumigatus	474	+
96	Aspergillus niger	474	
96	Aspergillus sp.	1423	+
96	Aspergillus versicolor	1423	+
96	Aureobasidium pullulans	77946	+
96	Aureobasidium pullulans	943	
96	Cladosporium cladosporioides	469	+
96	Drechslera sp.	469	+
96	Epicoccum nigrum	943	+
96	Mucor plumbeus	943	
96	Mucor racemosus	7094	+
96	Mucor racemosus	7083	
96	Penicillium citreonigrum	948	+
96	Penicillium citrinum	943	+
96	Penicillium sp.	474	
96	Penicillium spinulosum	4743	+
96	Penicillium spinulosum	938	
96	Penicillium viridicatum	9930	+
96	Penicillium viridicatum	4253	
96	Trichoderma viride	2830	
96	unknown	2361	+
96	unknown	469	
96	yeast	63614	
98	Acremonium sp.	48397	
98	Alternaria alternata	143280	+
98	Alternaria alternata	9881	
98	Aspergillus ochraceus	154755	
98	Aspergillus ochraceus	68185	+
98	Aspergillus sp.	4743	
98	Aspergillus versicolor	288961	
98	Aspergillus versicolor	102179	+
98	Aureobasidium pullulans	472339	
98	Aureobasidium pullulans	44466	+
98	Cladosporium cladosporioides	339174	+
98	Cladosporium cladosporioides	4940	
98	Cladosporium sphaerospermum	923594	+
98	Cladosporium sphaerospermum	779704	
98	Epicoccum nigrum	4743	
98	Eurotium herbariorum	57910	+
98	Penicillium brevicompactum	44269	
98	Penicillium brevicompactum	14822	+
98	Penicillium commune	48619	+
98	Penicillium commune	9684	
98	Phoma sp.	4743	
98	Scopulariopsis candida	4940	
98	unknown	24703	
98	Wallemia sebi	974145	+
99	Alternaria alternata	79949	
99	Alternaria alternata	5517	+
99	Aspergillus oryzae	1121	
99	Aspergillus versicolor	42723	+
99	Aspergillus versicolor	39506	
99	Aureobasidium pullulans	19738	
99	Aureobasidium pullulans	18705	+
99	Epicoccum nigrum	3275	
99	Epicoccum nigrum	1091	+
99	Eurotium herbariorum	17731	+
99	Penicillium brevicompactum	3275	
99	Penicillium chrysogenum	11093	+
99	Penicillium chrysogenum	4484	
99	Penicillium expansum	5517	
99	Penicillium expansum	4425	+
99	Penicillium spinulosum	2183	
99	Penicillium spinulosum	1091	+
99	Phoma sp.	2183	
99	unknown	9854	
100	Alternaria alternata	9076	
100	Alternaria alternata	3340	+
100	Aspergillus niger	495	
100	Aspergillus niger	495	+
100	Aureobasidium pullulans	3835	
100	Aureobasidium pullulans	1948	+
100	Chrysosporium sp.	463	
100	Cladosporium sp.	2845	+
100	Cladosporium sphaerospermum	958	+
100	Epicoccum nigrum	990	
100	Epicoccum nigrum	463	+
100	Penicillium atramentosum	495	+
100	Penicillium brevicompactum	4361	+
100	Penicillium commune	495	
100	Penicillium corylophilum	1886	+
100	Penicillium janthinellum	495	+
100	Penicillium miczynskii	495	
100	Penicillium simplicissimum	8875	
100	Penicillium sp. #26	958	
100	Penicillium sp. #64	927	
100	Penicillium spinulosum	2876	
100	Penicillium spinulosum	1422	+
100	Pithomyces chartarum	990	
100	Trichoderma viride	1948	
100	unknown	5784	+
100	unknown	4825	
100	yeast	11042	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
101	Alternaria alternata	12102		104	Alternaria alternata	4476	
101	Alternaria alternata	9699	+	104	Alternaria alternata	1886	+
101	Aspergillus ochraceus	296474		104	Apiospora montagnei	471	
101	Aspergillus ochraceus	254723	+	104	Apiospora sp.	510	
101	Aspergillus sp.	6578	+	104	Aspergillus sp.	1925	+
101	Aspergillus versicolor	19399	+	104	Aspergillus sp.	471	
101	Aspergillus versicolor	3289		104	Aureobasidium pullulans	510	
101	Cladosporium cladosporioides	488360	+	104	Cladosporium herbarum	510	+
101	Cladosporium cladosporioides	371794		104	Cladosporium herbarum	471	
101	Cladosporium sp.	3289	+	104	Cladosporium sp.	4437	+
101	Cladosporium sphaerospermum	19399	+	104	Cladosporium sp.	2474	
101	Coniothyrium sp.	19230		104	Epicoccum nigrum	2358	+
101	Eurotium herbariorum	9699	+	104	Epicoccum nigrum	1453	
101	Penicillium chrysogenum	6494	+	104	Epicoccum sp.	471	
101	Penicillium chrysogenum	6410		104	Eurotium herbariorum	1453	+
101	Phoma sp.	3205		104	Eurotium sp.	510	+
101	Rhizopus oryzae	3205		104	Microsphaeropsis sp.	1886	
101	Trichoderma viride	6410		104	Penicillium griseofulvum	3022	+
101	unknown	1234817		104	Penicillium griseofulvum	1415	
101	unknown	221406	+	104	Penicillium implicatum	471	+
102	Alternaria alternata	85802		104	Penicillium sp.	510	
102	Aspergillus ochraceus	2873		104	Penicillium sp. #26	471	+
102	Aureobasidium pullulans	148881		104	Penicillium spinulosum	1453	
102	Aureobasidium pullulans	95798	+	104	Penicillium spinulosum	981	+
102	Cladosporium cladosporioides	35997	+	104	Penicillium viridicatum	471	
102	Cladosporium cladosporioides	3378		104	Sphaeropsis sp.	3340	
102	Cladosporium sphaerospermum	12503		104	unknown	2512	
102	Epicoccum nigrum	5747		104	unknown	1925	+
102	Epicoccum nigrum	2873	+	104	yeast	943	
102	Penicillium aurantiogriseum	6251	+	105	Aspergillus versicolor	2258	
102	Penicillium chrysogenum	22639		105	Eurotium herbariorum	1744	+
102	Penicillium chrysogenum	9630	+	105	Humicola fuscoatra	338	
102	Penicillium corylophilum	14367	+	105	Mucor racemosus	371	
102	Penicillium corylophilum	2873		105	Penicillium atramentosum	169	
102	Penicillium spinulosum	2873		105	Penicillium aurantiogriseum	1066	
102	Phoma sp.	174161		105	Penicillium aurantiogriseum	355	+
102	Phoma sp.	161657	+	105	Penicillium chrysogenum	2438	+
102	Trichoderma viride	5747		105	Penicillium chrysogenum	1219	
102	unknown	2873		105	Penicillium commune	557	+
102	unknown	2873	+	105	Penicillium corylophilum	185	
103	Alternaria alternata	684		105	Penicillium raistrickii	1301	+
103	Alternaria alternata	684	+	105	Penicillium raistrickii	169	
103	Aspergillus glaucus	342	+	105	Penicillium simplicissimum	847	+
103	Aspergillus sp.	684	+	105	Penicillium simplicissimum	727	
103	Aureobasidium pullulans	1712	+	105	Penicillium sp. #26	169	
103	Aureobasidium pullulans	342		105	Penicillium spinulosum	1033	+
103	Cladosporium sp.	342		105	Penicillium spinulosum	169	
103	Cladosporium sp.	342	+	105	Scopulariopsis brevicaulis	338	+
103	Epicoccum nigrum	684		105	unknown	355	
103	Epicoccum nigrum	342	+	105	Wallemia sebi	4871	+
103	Eurotium herbariorum	1027	+	105	yeast	28511	
103	Penicillium commune	342		106	Alternaria alternata	63375	+
103	Penicillium commune	342	+	106	Alternaria alternata	28209	
103	Penicillium expansum	1027		106	Aureobasidium pullulans	179081	
103	Penicillium spinulosum	1369		106	Aureobasidium pullulans	126600	+
103	Penicillium spinulosum	684	+	106	Cladosporium cladosporioides	4921	
103	Penicillium viridicatum	342		106	Cladosporium sphaerospermum	34448	+
103	Phoma fimeti	342	+	106	Epicoccum nigrum	57852	+
103	unknown	1369		106	Epicoccum nigrum	33847	
103	unknown	684	+	106	Eurotium herbariorum	19083	+
103	yeast	1369		106	Fusarium sp.	14763	+

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
106	Mucor racemosus	24155	+	109	Pestalotiopsis sp.	946	+
106	Penicillium chrysogenum	76636		109	unknown	1419	
106	Penicillium chrysogenum	43840	+	109	yeast	2366	
106	Penicillium oxalicum	14763		110	Alternaria alternata	5127	+
106	Penicillium oxalicum	9541	+	110	Alternaria alternata	1612	
106	Penicillium vulpinum	19685		110	Aureobasidium pullulans	22207	+
106	Penicillium vulpinum	19384	+	110	Aureobasidium pullulans	15337	
106	Phoma herbarum	9541		110	Cladosporium cladosporioides	2272	+
106	Trichoderma viride	48761		110	Cladosporium herbarum	566	+
106	unknown	9842	+	110	Cladosporium sphaerospermum	572	
106	unknown	4921		110	Eurotium herbariorum	12513	+
106	Wallemia sebi	38167	+	110	Fusarium sp.	572	+
107	Alternaria alternata	2946		110	Paecilomyces sp.	572	+
107	Alternaria alternata	1476	+	110	Penicillium chrysogenum	2272	
107	Aureobasidium pullulans	30482		110	Penicillium chrysogenum	566	+
107	Aureobasidium pullulans	17681	+	110	Penicillium implicatum	1711	
107	Cladosporium cladosporioides	493		110	Penicillium miczynskii	5122	
107	Cladosporium sphaerospermum	493	+	110	Penicillium miczynskii	3416	+
107	Epicoccum nigrum	1963		110	Scopulariopsis brumptii	572	
107	Epicoccum nigrum	1473	+	110	unknown	5694	
107	Eurotium herbariorum	493	+	110	unknown	2277	+
107	Penicillium commune	2946		110	yeast	1133	
107	Penicillium commune	983	+	111	Alternaria alternata	6195	+
107	Penicillium griseofulvum	493		111	Alternaria alternata	3916	
107	Penicillium viridicatum	1476	+	111	Aspergillus niger	478	
107	Penicillium viridicatum	493		111	Aspergillus niger	476	+
107	Stachybotrys chartarum	490		111	Aspergillus ochraceus	2862	+
107	Ulocladium chartarum	490	+	111	Aspergillus ochraceus	2380	
108	Alternaria alternata	982		111	Aspergillus versicolor	2389	
108	Alternaria alternata	490	+	111	Aureobasidium pullulans	9066	
108	Aspergillus versicolor	490		111	Aureobasidium pullulans	8119	+
108	Aureobasidium pullulans	45637		111	Cladosporium cladosporioides	952	+
108	Aureobasidium pullulans	28954	+	111	Cladosporium sphaerospermum	478	+
108	Cladosporium cladosporioides	980	+	111	Cladosporium sphaerospermum	476	
108	Eurotium herbariorum	2945	+	111	Epicoccum nigrum	3820	
108	Fusarium sp.	491		111	Epicoccum nigrum	478	+
108	Paecilomyces variotii	6866		111	Eurotium herbariorum	478	+
108	Paecilomyces variotii	490	+	111	Mucor plumbeus	957	+
108	Penicillium citrinum	1962		111	Penicillium chrysogenum	4302	+
108	Penicillium citrinum	1471	+	111	Penicillium chrysogenum	2862	
108	Penicillium decumbens	3926		111	Penicillium raistrickii	478	
108	Penicillium raistrickii	19626	+	111	Penicillium spinulosum	478	
108	Penicillium raistrickii	12757		111	Penicillium spinulosum	478	+
108	Phoma herbarum	491		111	unknown	3341	
108	Ulocladium chartarum	491	+	112	Alternaria alternata	13301	+
108	unknown	1960		112	Alternaria alternata	9398	
108	yeast	2452		112	Aspergillus niger	550	
109	Alternaria alternata	8756		112	Aureobasidium pullulans	2759	+
109	Alternaria alternata	945	+	112	Cladosporium cladosporioides	7715	+
109	Aspergillus niger	473		112	Cladosporium cladosporioides	2759	
109	Aspergillus niger	472	+	112	Epicoccum nigrum	3322	+
109	Aureobasidium pullulans	1892	+	112	Epicoccum nigrum	2214	
109	Botrytis allii	1420	+	112	Mucor sp.	550	+
109	Cladosporium cladosporioides	473		112	Nigrospora sphaerica	550	
109	Cladosporium cladosporioides	472	+	112	Penicillium brevicompactum	1107	
109	Epicoccum nigrum	473		112	Penicillium sp. #26	550	+
109	Mucor plumbeus	472	+	112	Penicillium spinulosum	556	
109	Paecilomyces variotii	473		112	Penicillium viridicatum	1113	
109	Penicillium brevicompactum	473	+	112	Penicillium viridicatum	556	+
109	Penicillium brevicompactum	472		112	Sphaeropsis sp.	1107	
109	Penicillium spinulosum	472		112	unknown	3310	+

HN	Identification	AVG CFU/g	G
112	unknown	2759	
112	Wallemia sebi	556	+
112	yeast	11625	
114	Alternaria alternata	6858	
114	Alternaria alternata	2914	+
114	Aspergillus niger	969	+
114	Aspergillus versicolor	2426	+
114	Aureobasidium pullulans	20875	+
114	Aureobasidium pullulans	13559	
114	Cladosporium sphaerospermum	2418	+
114	Epicoccum nigrum	976	
114	Epicoccum nigrum	488	+
114	Eurotium herbariorum	488	+
114	Mucor racemosus	488	
114	Penicillium brevicompactum	480	
114	Penicillium citrinum	1953	
114	Penicillium corylophilum	1930	+
114	Penicillium corylophilum	1449	
114	Phoma herbarum	2892	
114	unknown	2907	
114	yeast	1464	
115	Alternaria alternata	5261	+
115	Alternaria alternata	2868	
115	Aspergillus ochraceus	492	+
115	Aureobasidium pullulans	16395	
115	Aureobasidium pullulans	16361	+
115	Cladosporium cladosporioides	2426	+
115	Cladosporium sphaerospermum	984	
115	Epicoccum nigrum	492	
115	Mucor plumbeus	475	
115	Mucor racemosus	475	+
115	Penicillium brevicompactum	475	+
115	Penicillium islandicum	492	
115	Penicillium oxalicum	475	
115	Penicillium spinulosum	37085	+
115	Penicillium spinulosum	32500	
115	Scopulariopsis candida	492	+
115	Ulocladium chartarum	492	
115	unknown	3835	
115	yeast	475	
116	Alternaria alternata	1081	
116	Aspergillus niger	382	
116	Aspergillus niger	285	+
116	Aspergillus ustus	96	
116	Aspergillus versicolor	94	+
116	Cylindrocarpon sp.	94	
116	Eurotium herbariorum	94	+
116	Fusarium sp.	94	+
116	Mucor racemosus	760	
116	Mucor racemosus	668	+
116	Paecilomyces variotii	96	
116	Penicillium chrysogenum	763	+
116	Penicillium citrinum	189	+
116	Penicillium funiculosum	94	
116	unknown	380	
116	yeast	571	
117	Alternaria alternata	189	+
117	Aspergillus niger	94	
117	Aspergillus ochraceus	94	+
117	Aspergillus ochraceus	92	
117	Aspergillus versicolor	379	+
117	Chaetomium nozdrenkoae	94	
117	Penicillium brevicompactum	92	
117	Penicillium commune	185	+
117	Penicillium corylophilum	278	+
117	Penicillium expansum	375	+
117	Penicillium expansum	189	
117	Penicillium implicatum	658	+
117	Penicillium implicatum	189	
117	Penicillium restrictum	94	
117	Penicillium simplicissimum	94	+
117	Penicillium sp.	92	
117	Rhizopus oryzae	94	+
117	Trichoderma viride	282	
117	Trichoderma viride	94	+
118	Alternaria alternata	959	
118	Alternaria alternata	479	+
118	Aureobasidium pullulans	3358	
118	Aureobasidium pullulans	1439	+
118	Chaetomium globosum	478	+
118	Epicoccum nigrum	478	+
118	Eurotium herbariorum	478	+
118	Microsphaeropsis olivaceus	2390	
118	Microsphaeropsis sp.	2869	
118	Microsphaeropsis sp.	957	+
118	Paecilomyces variotii	1435	
118	Paecilomyces variotii	957	+
118	Penicillium echinulatum	1917	+
118	Penicillium echinulatum	479	
118	Penicillium glandicola	478	
118	Penicillium raistrickii	479	
118	Penicillium raistrickii	478	+
118	unknown	5267	
118	unknown	1439	+
118	Wallemia sebi	479	+
118	yeast	6234	
119	Alternaria alternata	24452	+
119	Alternaria alternata	6320	
119	Aspergillus glaucus	9804	+
119	Aspergillus sp.	4921	+
119	Aspergillus versicolor	19608	+
119	Cladosporium cladosporioides	4921	
119	Cladosporium cladosporioides	4921	+
119	Cladosporium sp.	9842	
119	Cladosporium sp.	9842	+
119	Epicoccum nigrum	4882	
119	Epicoccum sp.	4882	
119	Epicoccum sp.	4882	+
119	Eurotium herbariorum	34295	+
119	Penicillium brevicompactum	9765	+
119	Penicillium brevicompactum	4882	
119	Penicillium commune	24529	
119	Penicillium commune	4882	+
119	unknown	568597	+
119	yeast	29527	
120	Alternaria alternata	676	+
120	Aspergillus niger	714212	
120	Aspergillus niger	75	+
120	Aspergillus versicolor	834	+
120	Chaetomium globosum	75	
120	Cladosporium cladosporioides	834	+
120	Cladosporium herbarum	75	+

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
120	Cladosporium sphaerospermum	759	+	122	Eurotium herbariorum	388	+
120	Emericella nidulans	759	+	122	Leptosphaerulina australis	76	
120	Eurotium herbariorum	909	+	122	Penicillium brevicompactum	76	+
120	Fusarium flocciferum	151		122	Penicillium chrysogenum	3398	
120	Fusarium oxysporum	759	+	122	Penicillium chrysogenum	546	+
120	Lecythophora hoffmannii	759	+	122	Penicillium commune	76	+
120	Paecilomyces sp.	227		122	Penicillium oxalicum	79	+
120	Paecilomyces variotii	75		122	Penicillium sp.	229	
120	Penicillium citreonigrum	834	+	122	Penicillium spinulosum	792	
120	Penicillium commune	75		122	Phoma herbarum	79	+
120	Penicillium commune	75	+	122	Ulocladium chartarum	153	
120	Penicillium crustosum	150	+	122	unknown	766	
120	Penicillium crustosum	75		122	unknown	699	+
120	Penicillium expansum	75	+	122	Wallemia sebi	232	+
120	Penicillium raistrickii	759	+	122	yeast	1890	
120	Penicillium simplicissimum	1518	+	123	Alternaria alternata	525	
120	Penicillium sp.	759	+	123	Aspergillus niger	64	
120	Penicillium sp.	150		123	Aspergillus versicolor	2566	+
120	Penicillium spinulosum	75	+	123	Chaetomium globosum	649	+
120	Penicillium variabile	75		123	Cochliobolus sativus	64	
120	Phoma medicaginis	75	+	123	Eurotium herbariorum	2566	+
120	Scopulariopsis brevicaulis	1058		123	Mucor plumbeus	63	
120	Scopulariopsis brevicaulis	984	+	123	Mucor racemosus	633	+
120	Torula herbarum	759	+	123	Penicillium atramentosum	1283	+
120	Trichoderma viride	75		123	Penicillium aurantiogriseum	1949	+
120	Trichoderma viride	75	+	123	Penicillium corylophilum	128	
120	unknown	1668	+	123	Penicillium crustosum	649	+
120	Wallemia sebi	150	+	123	Penicillium crustosum	129	
120	yeast	454		123	Penicillium echinulatum	649	+
121	Alternaria alternata	10725	+	123	Penicillium expansum	649	+
121	Alternaria alternata	682		123	Penicillium expansum	190	
121	Aspergillus niger	8190	+	123	Penicillium sp. #1	63	
121	Aspergillus niger	5832		123	Penicillium viridicatum	1933	+
121	Aspergillus sydowii	494	+	123	Penicillium vulpinum	649	+
121	Aspergillus sydowii	478		123	Rhizopus oryzae	64	
121	Aspergillus versicolor	972	+	123	Scopulariopsis candida	64	
121	Aspergillus versicolor	478		123	Trichoderma koningii	64	
121	Aureobasidium pullulans	19377		123	Trichoderma viride	649	+
121	Aureobasidium pullulans	5370	+	123	Wallemia sebi	1283	+
121	Epicoccum nigrum	494	+	123	yeast	833	
121	Eurotium herbariorum	4908	+	125	Acremonium rutilum	3947	
121	Penicillium aurantiogriseum	478		125	Alternaria alternata	482	+
121	Penicillium chrysogenum	19297	+	125	Aspergillus ochraceus	97	+
121	Penicillium chrysogenum	14946		125	Cladosporium sphaerospermum	96	+
121	Penicillium citreonigrum	494		125	Epicoccum nigrum	193	+
121	Penicillium italicum	5338		125	Eurotium herbariorum	97	+
121	Penicillium italicum	1482	+	125	Paecilomyces sp.	96	+
121	Penicillium spinulosum	2868	+	125	Penicillium chrysogenum	290	+
121	Penicillium spinulosum	2868		125	Penicillium crustosum	97	+
121	unknown	7840		125	Penicillium expansum	97	
121	unknown	1466	+	125	Pestalotiopsis palustris	96	+
121	yeast	8254		125	Pithomyces chartarum	193	+
122	Alternaria alternata	9362		125	Rhizopus oryzae	289	
122	Alternaria alternata	314	+	125	Rhizopus oryzae	96	+
122	Aspergillus niger	792		125	Stachybotrys parvispora	291	
122	Aspergillus versicolor	79	+	125	Torula herbarum	97	+
122	Aspergillus versicolor	76		125	unknown	97	+
122	Aureobasidium pullulans	311	+	125	yeast	872	
122	Chaetomium globosum	536		126	Aspergillus niger	477	+
122	Emericella nidulans	549	+	126	Aspergillus ochraceus	2831	+
122	Emericella sp.	792		126	Aspergillus ochraceus	567	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
126	Aspergillus paradoxus	3339	+	129	Aspergillus fumigatus	477	+
126	Aspergillus paradoxus	470		129	Aspergillus fumigatus	477	
126	Aspergillus versicolor	6139		129	Aspergillus niger	191	
126	Aspergillus versicolor	3791	+	129	Aspergillus ochraceus	96	+
126	Cladosporium sphaerospermum	1908		129	Aspergillus oryzae	96	+
126	Cladosporium sphaerospermum	470	+	129	Aspergillus restrictus	96	+
126	Emericella variecolor	470	+	129	Cochliobolus geniculatus	95	+
126	Eurotium herbariorum	1889	+	129	Drechslera biseptata	95	+
126	Eurotium rubrum	470	+	129	Epicoccum nigrum	96	
126	Gliomastix murorum var. felina	7081		129	Paecilomyces inflatus	670	
126	Penicillium aurantiogriseum	1425		129	Paecilomyces variotii	96	
126	Penicillium commune	947	+	129	Penicillium commune	191	+
126	Penicillium corylophilum	941		129	Penicillium corylophilum	95	
126	Penicillium decumbens	941		129	Penicillium expansum	191	
126	Penicillium decumbens	470	+	129	Penicillium simplicissimum	479	+
126	Penicillium expansum	477	+	129	Penicillium simplicissimum	96	
126	Penicillium variabile	477		129	Penicillium spinulosum	192	
126	Phoma herbarum	470		129	Pithomyces chartarum	95	
126	Scolecobasidium constrictum	470		129	Pithomyces chartarum	95	+
126	Scopulariopsis brevicaulis	470		129	Pythium sp.	96	
126	Scopulariopsis chartarum	1425	+	129	Scopulariopsis brevicaulis	96	+
126	Scopulariopsis chartarum	470		129	Scopulariopsis candida	96	
126	Sporobolomyces sp.	954		129	Ulocladium atrum	96	+
126	Stachybotrys chartarum	2385		129	Ulocladium chartarum	95	+
126	Trichoderma viride	1412		129	unknown	477	+
126	unknown	941	+	129	unknown	384	
126	unknown	470		130	Alternaria alternata	766	
126	Wallemia sebi	941	+	130	Alternaria alternata	377	+
126	yeast	2366		130	Aspergillus niger	384	+
127	Alternaria alternata	485	+	130	Chaetomium globosum	96	
127	Aspergillus niger	978		130	Epicoccum nigrum	93	+
127	Aspergillus niger	485	+	130	Eurotium herbariorum	283	+
127	Fusarium oxysporum	485		130	Fusarium oxysporum	93	
127	Mucor plumbeus	493	+	130	Penicillium chrysogenum	571	+
127	Penicillium sp. #64	3914	+	130	Penicillium chrysogenum	96	
127	Penicillium sp. #64	493		130	Penicillium commune	93	
127	Penicillium spinulosum	2920	+	130	Penicillium viridicatum	384	
127	Penicillium spinulosum	2450		130	Scopulariopsis brevicaulis	387	
127	Pestalotiopsis palustris	485	+	130	Talaromyces trachyspermus var. macrocarpus	96	
128	Alternaria alternata	2946	+	130	yeast	280	
128	Aspergillus niger	3925	+	132	Alternaria alternata	2366	+
128	Aspergillus niger	2455		132	Alternaria alternata	861	
128	Aspergillus versicolor	491		132	Aspergillus fumigatus	463	+
128	Chaetomium circinatum	491		132	Aspergillus ochraceus	1855	
128	Cladosporium cladosporioides	487	+	132	Aspergillus ochraceus	463	+
128	Eurotium herbariorum	491	+	132	Aspergillus terreus	1391	+
128	Mucor racemosus	487	+	132	Aspergillus versicolor	2806	+
128	Penicillium corylophilum	5890	+	132	Aspergillus versicolor	1855	
128	Penicillium corylophilum	4416		132	Aureobasidium pullulans	3851	+
128	Penicillium expansum	487		132	Aureobasidium pullulans	3781	
128	Penicillium expansum	487	+	132	Cunninghamella sp.	10069	
128	Penicillium spinulosum	3426	+	132	Cunninghamella sp.	5683	+
128	Penicillium spinulosum	487		132	Eurotium herbariorum	3851	+
128	Phoma herbarum	982	+	132	Geomyces sp.	1902	
128	Scopulariopsis candida	491	+	132	Penicillium brevicompactum	4779	+
128	Stachybotrys chartarum	487	+	132	Penicillium chrysogenum	2923	
128	unknown	974	+	132	Penicillium chrysogenum	2389	+
128	Wallemia sebi	45048	+	132	Penicillium commune	463	+
128	yeast	6358		132	Penicillium spinulosum	6611	
129	Alternaria alternata	95	+	132	Penicillium spinulosum	4732	+
129	Alternaria sp.	95	+	132	Phoma sp.	1461	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
132	Trichoderma viride	463	+	136	Penicillium viridicatum	478	+
132	unknown	9488		136	Phoma herbarum	470	+
132	unknown	1949	+	136	unknown	2832	+
132	Wallemia sebi	487	+	136	Wallemia sebi	2846	+
132	yeast	9535		136	yeast	10972	
133	Alternaria alternata	465	+	137	Alternaria alternata	467	+
133	Aspergillus niger	4703		137	Alternaria sp.	467	+
133	Aspergillus niger	4668	+	137	Cladosporium cladosporioides	3347	
133	Aspergillus ochraceus	469		137	Cladosporium cladosporioides	2386	+
133	Eurotium herbariorum	4189	+	137	Eurotium herbariorum	467	+
133	Mucor plumbeus	4211	+	137	Mucor racemosus	3838	+
133	Mucor plumbeus	3276		137	Mucor racemosus	2386	
133	Mucor racemosus	11721		137	Penicillium spinulosum	467	
133	Mucor racemosus	5608	+	137	Penicillium viridicatum	3788	+
133	Penicillium aurantiogriseum	3276		137	Penicillium viridicatum	1906	
133	Penicillium aurantiogriseum	469	+	137	Penicillium vulpinum	479	
133	Penicillium chrysogenum	17264	+	137	unknown	2374	
133	Penicillium chrysogenum	4203		137	unknown	1426	+
133	Penicillium janthinellum	469		137	yeast	1894	
133	Penicillium sp.	931		138	Alternaria alternata	391	+
133	Penicillium sp. #26	2349		138	Alternaria sp.	393	
133	Phoma herbarum	3759	+	138	Aspergillus sydowii	98	+
133	yeast	7492		138	Aspergillus versicolor	194	
134	Alternaria alternata	9398		138	Aspergillus versicolor	97	+
134	Alternaria alternata	4621	+	138	Aureobasidium pullulans	1865	
134	Aspergillus restrictus	4621	+	138	Aureobasidium pullulans	1566	+
134	Aureobasidium pullulans	9398		138	Chaetomium globosum	584	
134	Epicoccum nigrum	4621	+	138	Cladosporium sphaerospermum	97	+
134	Eurotium herbariorum	23183	+	138	Eurotium herbariorum	983	+
134	Mucor racemosus	9320	+	138	Fusarium sp.	98	+
134	Penicillium aurantiogriseum	4621	+	138	Fusarium sp.	97	
134	Penicillium citrinum	4621	+	138	Mucor plumbeus	97	+
134	Penicillium commune	18718	+	138	Paecilomyces variotii	97	+
134	Penicillium commune	13941		138	Penicillium aurantiogriseum	196	
134	Wallemia sebi	4206739	+	138	Penicillium chrysogenum	1171	+
134	yeast	23261		138	Penicillium chrysogenum	683	
135	Alternaria alternata	37825		138	Penicillium corylophilum	98	
135	Alternaria alternata	4210	+	138	Penicillium spinulosum	195	
135	Aureobasidium pullulans	2342		138	Penicillium spinulosum	194	+
135	Epicoccum nigrum	2814	+	138	Scopulariopsis candida	393	
135	Penicillium corylophilum	469		138	unknown	881	+
135	Penicillium raistrickii	2809	+	138	unknown	687	
135	Phoma herbarum	938		138	yeast	583	
135	Phoma herbarum	935	+	139	Aspergillus glaucus	641	+
135	Scopulariopsis brevicaulis	469	+	139	Aspergillus niger	627	+
135	unknown	938	+	139	Aspergillus niger	387	
135	Wallemia sebi	7001	+	139	Chaetomium globosum	64	
135	Wallemia sebi	469		139	Eurotium herbariorum	7639	+
135	yeast	1404		139	Fusarium oxysporum	190	
136	Chaetomium funicola	4699		139	Penicillium aurantiogriseum	1208	
136	Cochliobolus geniculatus	478	+	139	Penicillium chrysogenum	2524	+
136	Epicoccum nigrum	470		139	Penicillium chrysogenum	253	
136	Eurotium herbariorum	470	+	139	Penicillium crustosum	62	
136	Mucor mucedo	470		139	Penicillium spinulosum	1909	+
136	Mucor racemosus	478	+	139	Penicillium spinulosum	252	
136	Penicillium brevicompactum	470	+	139	Phoma herbarum	627	+
136	Penicillium canescens	1412		139	Pithomyces chartarum	1883	+
136	Penicillium commune	5207	+	139	Scopulariopsis candida	7639	+
136	Penicillium commune	3795		139	Scopulariopsis candida	2151	
136	Penicillium corylophilum	948	+	139	unknown	62	
136	Penicillium italicum	478	+	140	Mucor plumbeus	10842	

HN	Identification	AVG CFU/g	G
140	Penicillium chrysogenum	108229	+
140	Penicillium chrysogenum	9881	
140	Penicillium commune	19646	+
140	Penicillium corylophilum	4940	
140	Penicillium decumbens	19675	+
140	Penicillium decumbens	9823	
140	Penicillium expansum	4911	
140	Penicillium griseofulvum	88466	
140	Penicillium spinulosum	4940	
140	Trichoderma viride	4940	+
140	unknown	9823	
143	Alternaria alternata	15236	
143	Alternaria alternata	2358	+
143	Aspergillus versicolor	51482	+
143	Aspergillus versicolor	34472	
143	Aureobasidium pullulans	2830	+
143	Aureobasidium pullulans	943	
143	Cladosporium cladosporioides	472	+
143	Eurotium herbariorum	2361	+
143	Penicillium chrysogenum	4251	+
143	Penicillium citreonigrum	471	+
143	Penicillium corylophilum	1415	
143	Penicillium spinulosum	3776	
143	Penicillium spinulosum	945	+
143	Wallemia sebi	2361	+
143	Wallemia sebi	472	
143	yeast	6132	
145	Acremonium sp.	3769	
145	Alternaria alternata	1409	+
145	Aspergillus versicolor	17750	+
145	Aspergillus versicolor	14530	
145	Cladosporium sphaerospermum	473	+
145	Eurotium herbariorum	2335	+
145	Penicillium chrysogenum	925	+
145	unknown	3272	+
145	unknown	1409	
145	yeast	1388	
146	Alternaria alternata	5774	
146	Alternaria alternata	467	+
146	Aspergillus versicolor	276	
146	Aureobasidium pullulans	276	+
146	Chaetomium globosum	98	
146	Cladosporium cladosporioides	92	
146	Epicoccum nigrum	92	
146	Eurotium herbariorum	197	+
146	Fusarium sp.	98	
146	Penicillium brevicompactum	92	+
146	Penicillium commune	369	+
146	Penicillium commune	92	
146	Penicillium corylophilum	197	+
146	Penicillium crustosum	757	
146	Penicillium crustosum	474	+
146	Penicillium decumbens	289	+
146	Penicillium decumbens	191	
146	Penicillium glandicola	197	+
146	Penicillium raistrickii	184	
146	Penicillium raistrickii	92	+
146	Penicillium viridicatum	289	+
146	Penicillium vulpinum	98	+
146	Penicillium vulpinum	92	
146	unknown	184	+
146	yeast	1337	
147	Alternaria alternata	1464	+
147	Alternaria alternata	491	
147	Aspergillus niger	976	+
147	Aspergillus niger	491	
147	Aureobasidium pullulans	2450	+
147	Cladosporium cladosporioides	488	+
147	Epicoccum nigrum	2441	
147	Paecilomyces variotii	976	
147	Penicillium brevicompactum	491	
147	Penicillium chrysogenum	1961	
147	Penicillium commune	2935	
147	Penicillium commune	2450	+
147	Penicillium corylophilum	6362	+
147	Penicillium corylophilum	5385	
147	Penicillium raistrickii	39648	+
147	Penicillium raistrickii	976	
147	Rhizopus oryzae	488	+
147	unknown	3917	
147	unknown	2946	+
147	yeast	2452	
148	Acremonium sp.	2952	
148	Alternaria alternata	2468	+
148	Aspergillus clavatus	487	
148	Aspergillus fumigatus	498	
148	Aspergillus niger	3919	+
148	Aspergillus niger	487	
148	Aspergillus ochraceus	498	+
148	Aspergillus versicolor	974	
148	Aspergillus versicolor	498	+
148	Aureobasidium pullulans	498	+
148	Cladosporium cladosporioides	487	
148	Lecythophora hoffmannii	974	
148	Mucor racemosus	498	
148	Paecilomyces inflatus	498	
148	Penicillium aurantiogriseum	13752	+
148	Penicillium citreonigrum	498	+
148	Penicillium commune	1472	+
148	Penicillium commune	974	
148	Penicillium sp. #26	498	
148	Penicillium spinulosum	1959	+
148	Penicillium viridicatum	498	+
148	unknown	498	
148	yeast	10774	
149	Aspergillus niger	9299	
149	Aspergillus niger	478	+
149	Aspergillus ochraceus	472	
149	Aspergillus versicolor	3318	+
149	Aspergillus versicolor	472	
149	Aureobasidium pullulans	1890	+
149	Chaetomium cochliodes	1423	
149	Cladosporium sphaerospermum	945	+
149	Eurotium herbariorum	2846	+
149	Penicillium chrysogenum	2857	+
149	Penicillium chrysogenum	950	
149	Phoma fimeti	472	
149	Pithomyces chartarum	472	+
149	unknown	956	+
149	yeast	1895	
150	Acremonium sp.	5695	
150	Alternaria alternata	979	+

HN	Identification	AVG CFU/g	G
150	Aspergillus fumigatus	654	
150	Aspergillus niger	125	+
150	Aspergillus ochraceus	128	+
150	Aspergillus restrictus	627	
150	Aspergillus sp.	627	
150	Aspergillus versicolor	17983	
150	Aspergillus versicolor	646	+
150	Aureobasidium pullulans	7532	
150	Chaetomium globosum	627	
150	Epicoccum nigrum	627	
150	Eurotium herbariorum	1470	+
150	Geomyces pannorum	62	+
150	Penicillium citreonigrum	627	
150	Penicillium expansum	4475	
150	Penicillium expansum	578	+
150	Penicillium variabile	627	
150	Penicillium variabile	130	+
150	Phoma herbarum	1255	
150	Scopulariopsis candida	4394	
150	Trichoderma viride	1255	
150	unknown	10970	
150	unknown	2188	+
150	Wallemia sebi	627	
150	Wallemia sebi	62	+
150	yeast	21831	
151	Alternaria alternata	1456	
151	Aspergillus candidus	99	+
151	Aspergillus ochraceus	289	
151	Aspergillus ochraceus	95	+
151	Aspergillus versicolor	190	+
151	Epicoccum nigrum	476	
151	Eurotium herbariorum	289	+
151	Paecilomyces variotii	99	+
151	Penicillium citrinum	95	+
151	Penicillium corylophilum	194	+
151	Penicillium glandicola	95	
151	Penicillium viridicatum	1058	
151	Penicillium viridicatum	289	+
151	Pithomyces chartarum	190	+
151	Pithomyces chartarum	95	
151	yeast	860	
152	Acremonium sp.	93	
152	Alternaria alternata	93	+
152	Aspergillus sydowii	93	
152	Aspergillus ustus	93	
152	Cochliobolus geniculatus	93	
152	Eurotium herbariorum	93	+
152	Fusarium sp.	93	
152	Penicillium viridicatum	751	
152	Penicillium viridicatum	187	+
152	Phoma eupyrena	93	
152	Phoma herbarum	187	
152	Scopulariopsis brevicaulis	93	+
152	Trichoderma koningii	93	
152	unknown	93	+
152	yeast	1970	
153	Alternaria alternata	5882	+
153	Alternaria alternata	3923	
153	Aspergillus fumigatus	491	+
153	Aureobasidium pullulans	7854	
153	Cladosporium cladosporioides	4905	+
153	Cladosporium cladosporioides	4412	
153	Epicoccum nigrum	1962	
153	Epicoccum nigrum	491	+
153	Eurotium herbariorum	489	+
153	Penicillium citrinum	4410	
153	Penicillium citrinum	3430	+
153	Penicillium purpurogenum	2941	+
153	Penicillium purpurogenum	1473	
153	Penicillium sp.	489	+
153	Penicillium verrucosum	980	+
153	Scopulariopsis brevicaulis	2941	
153	Scopulariopsis brevicaulis	489	+
153	Scopulariopsis fusca	489	
153	Trichoderma viride	491	
153	unknown	8340	
153	unknown	3919	+
153	yeast	10788	
154	Alternaria alternata	114	+
154	Aspergillus fumigatus	23647	
154	Aspergillus ochraceus	345	+
154	Aspergillus ochraceus	114	
154	Aspergillus sydowii	115	
154	Aspergillus versicolor	114	
154	Chaetomium cochliodes	115	
154	Eurotium rubrum	230	+
154	Exophiala jeanselmei	115	
154	Mucor mucedo	343	
154	Mucor plumbeus	114	
154	Mucor racemosus	228	+
154	Penicillium chrysogenum	459	+
154	Penicillium chrysogenum	114	
154	Penicillium citrinum	229	
154	Penicillium oxalicum	229	+
154	Trichoderma viride	343	+
154	Trichoderma viride	115	
154	unknown	115	
154	unknown	114	+
154	yeast	1154	
155	Alternaria alternata	515	
155	Alternaria alternata	96	+
155	Aspergillus oryzae	94	
155	Aspergillus versicolor	191	
155	Aureobasidium pullulans	290	
155	Aureobasidium pullulans	288	+
155	Eurotium herbariorum	964	+
155	Mucor plumbeus	96	
155	Penicillium chrysogenum	2109	
155	Penicillium chrysogenum	1057	+
155	Penicillium corylophilum	288	
155	Penicillium corylophilum	191	+
155	Scopulariopsis brevicaulis	667	
155	Trichoderma viride	96	
155	unknown	1627	
155	unknown	484	+
155	Wallemia sebi	288	+
155	yeast	3726	
156	Acremonium strictum	289	
156	Alternaria alternata	96	
156	Aspergillus ochraceus	95	+
156	Aspergillus sydowii	95	+
156	Blastobotrys sp.	289	

HN	Identification	AVG CFU/g	G
156	Epicoccum nigrum	191	
156	Eurotium herbariorum	191	+
156	Penicillium spinulosum	575	
156	Penicillium spinulosum	95	+
156	Penicillium viridicatum	286	+
156	Penicillium viridicatum	95	
156	unknown	95	
156	yeast	1150	
157	Alternaria alternata	1324	+
157	Alternaria alternata	862	
157	Aspergillus niger	1231	+
157	Aspergillus niger	483	
157	Penicillium citreonigrum	96	+
157	Penicillium citrinum	284	
157	Penicillium oxalicum	290	+
157	Penicillium sp. #26	96	
157	Penicillium spinulosum	383	
157	Trichoderma viride	93	
157	Ulocladium chartarum	93	
157	unknown	958	+
157	unknown	93	
157	Wallemia sebi	2403	+
157	yeast	2417	
158	Alternaria alternata	2122	
158	Alternaria alternata	384	+
158	Aureobasidium pullulans	947	+
158	Aureobasidium pullulans	192	
158	Cladosporium cladosporioides	94	
158	Eurotium herbariorum	959	+
158	Geotrichum candidum	94	
158	Mucor plumbeus	1055	
158	Mucor plumbeus	288	+
158	Penicillium chrysogenum	951	+
158	Penicillium chrysogenum	671	
158	Penicillium commune	94	
158	Penicillium commune	94	+
158	Penicillium spinulosum	94	
158	Trichoderma viride	94	
158	unknown	572	
158	yeast	1977	
160	Aspergillus niger	4423	
160	Aspergillus ochraceus	92	+
160	Eurotium herbariorum	92	+
160	Mucor plumbeus	184	
160	Mucor plumbeus	92	+
160	Nigrospora sphaerica	92	
160	Penicillium spinulosum	277	
160	Penicillium spinulosum	92	+
160	Scopulariopsis brevicaulis	184	
160	unknown	92	
160	yeast	2125	
161	Aspergillus cervinus	75	+
161	Aspergillus oryzae	75	+
161	Aspergillus versicolor	519	
161	Chaetomium globosum	79	+
161	Chaetomium globosum	75	
161	Penicillium chrysogenum	79	+
161	Penicillium citrinum	159	+
161	yeast	51034	
162	Alternaria alternata	1464	+
162	Aspergillus niger	14420	
162	Dothiorella sp.	476	
162	Eurotium herbariorum	1953	+
162	Mucor plumbeus	1904	+
162	Mucor plumbeus	476	
162	Penicillium chrysogenum	488	
162	Penicillium commune	488	
162	Penicillium corylophilum	1464	
162	Penicillium corylophilum	488	+
162	Penicillium expansum	488	+
162	Penicillium italicum	976	
162	Penicillium sp. #26	488	
162	Trichoderma viride	964	
162	Trichoderma viride	476	+
162	unknown	1452	+
162	unknown	476	
162	yeast	7739	
163	Alternaria alternata	1328	
163	Alternaria alternata	525	+
163	Aspergillus versicolor	3320	
163	Aspergillus versicolor	592	+
163	Aureobasidium pullulans	259	+
163	Epicoccum nigrum	194	+
163	Eurotium herbariorum	651	+
163	Fusarium sp.	66	+
163	Penicillium chrysogenum	13835	
163	Penicillium chrysogenum	2163	+
163	Penicillium corylophilum	194	+
163	Penicillium vulpinum	585	+
163	Phoma herbarum	664	
163	unknown	15936	
163	unknown	7955	+
163	yeast	6485	
165	Alternaria alternata	2291	+
165	Alternaria alternata	1091	
165	Aspergillus ochraceus	546	
165	Aspergillus ochraceus	545	+
165	Aureobasidium pullulans	1745	+
165	Cladosporium sphaerospermum	54	+
165	Epicoccum nigrum	1745	+
165	Eurotium herbariorum	54	+
165	Fusarium oxysporum	1635	
165	Fusarium oxysporum	545	+
165	Hainesia lythri	546	
165	Mucor racemosus	545	+
165	Paecilomyces inflatus	545	
165	Paecilomyces variotii	545	
165	Penicillium aurantiogriseum	1090	
165	Penicillium aurantiogriseum	654	+
165	Penicillium brevicompactum	54	+
165	Penicillium corylophilum	599	+
165	Penicillium oxalicum	1090	+
165	Penicillium viridicatum	546	
165	Pestalotiopsis sp.	545	
165	Phoma herbarum	1091	
165	Phoma herbarum	545	+
165	Pithomyces chartarum	546	
165	Scopulariopsis candida	545	
165	Sphaeropsis sp.	1254	+
165	Trichoderma viride	163	+
165	Ulocladium chartarum	54	+
165	unknown	1145	+

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
165	unknown	546		169	Penicillium raistrickii	2033	+
165	yeast	7639		169	Penicillium spinulosum	386	+
166	Alternaria alternata	7572	+	169	Penicillium spinulosum	290	
166	Alternaria alternata	2855		169	Rhizopus oryzae	97	+
166	Aureobasidium pullulans	950	+	169	Trichoderma viride	97	
166	Epicoccum nigrum	469		169	unknown	193	+
166	Fusarium oxysporum	1415		169	yeast	289	
166	Mucor racemosus	475	+	170	Alternaria alternata	3853	+
166	Penicillium aurantiogriseum	1420		170	Aspergillus oryzae	64	
166	Penicillium brevicompactum	3770	+	170	Aspergillus sp.	64	
166	Penicillium corylophilum	9489	+	170	Aspergillus versicolor	642	+
166	Penicillium corylophilum	475		170	Cladosporium sp.	660	+
166	Penicillium decumbens	1901		170	Cladosporium sphaerospermum	2640	+
166	Penicillium sp.	475		170	Eurotium herbariorum	72859	+
166	Penicillium spinulosum	3791	+	170	Fusarium sp.	1302	+
166	Penicillium spinulosum	1885		170	Penicillium brevicompactum	1320	+
166	Trichoderma viride	6578	+	170	Penicillium brevicompactum	770	
166	Trichoderma viride	4736		170	Penicillium commune	1284	+
166	unknown	1420		170	Penicillium commune	385	
166	yeast	1890		170	Penicillium verrucosum	2586	+
167	Alternaria alternata	6867		170	Scopulariopsis brevicaulis	132	
167	Alternaria alternata	384	+	170	Talaromyces flavus	132	
167	Cladosporium cladosporioides	388	+	170	unknown	26064	+
167	Fusarium sp.	98	+	170	Wallemia sebi	68149	+
167	Penicillium brevicompactum	784	+	171	Alternaria alternata	1446	+
167	Penicillium brevicompactum	194		171	Aureobasidium pullulans	11508	+
167	Penicillium commune	98	+	171	Aureobasidium pullulans	2394	
167	Penicillium spinulosum	192		171	Chaetomium globosum	478	
167	Penicillium spinulosum	96	+	171	Fusarium sp.	957	+
167	Trichoderma viride	292	+	171	Mucor plumbeus	967	+
167	Trichoderma viride	290		171	Penicillium brevicompactum	1924	+
168	Aspergillus candidus	95		171	Penicillium corylophilum	478	+
168	Aspergillus fumigatus	482		171	Penicillium raistrickii	7685	+
168	Aspergillus niger	1359		171	unknown	5286	+
168	Aspergillus niger	1345	+	171	unknown	1436	
168	Chaetomium globosum	95		171	yeast	1920	
168	Chaetomium subspirale	98		171	Zetiasplozna heteromorpha	957	
168	Eurotium herbariorum	95	+	172	Alternaria alternata	10424	
168	Mucor mucedo	98	+	172	Alternaria alternata	9345	+
168	Mucor mucedo	95		172	Aspergillus niger	4816	+
168	Penicillium aurantiogriseum	383		172	Aspergillus ochraceus	28613	
168	Penicillium oxalicum	98		172	Aspergillus ochraceus	18691	+
168	Penicillium oxalicum	95	+	172	Aspergillus sydowii	4816	+
168	Penicillium sp. #26	95	+	172	Aspergillus versicolor	14306	
168	Penicillium sp. #64	98		172	Aspergillus versicolor	14018	+
168	Penicillium sp. #87	98	+	172	Aureobasidium pullulans	110357	
168	Penicillium spinulosum	390		172	Aureobasidium pullulans	28037	+
168	Penicillium viridicatum	778	+	172	Botrytis cinerea	4816	+
168	unknown	98		172	Chaetomium sp.	247663	
168	yeast	3168		172	Chaetomium sp.	127608	+
169	Alternaria alternata	579	+	172	Cladosporium cladosporioides	70093	+
169	Alternaria alternata	388		172	Cladosporium cladosporioides	14162	
169	Aspergillus glaucus	1061		172	Cladosporium sphaerospermum	4672	+
169	Aspergillus niger	97		172	Eurotium herbariorum	4672	+
169	Aureobasidium pullulans	7439	+	172	Penicillium chrysogenum	14306	
169	Aureobasidium pullulans	582		172	Penicillium chrysogenum	14306	+
169	Cladosporium cladosporioides	290	+	172	Penicillium spinulosum	9489	+
169	Eurotium herbariorum	290	+	172	Penicillium spinulosum	4816	
169	Mucor plumbeus	96	+	172	Penicillium viridicatum	38103	+
169	Penicillium commune	967	+	172	Penicillium viridicatum	33286	
169	Penicillium commune	291		172	Phoma sp.	14450	

HN	Identification	AVG CFU/g	G
172	unknown	23940	
172	unknown	4672	+
173	Alternaria alternata	24529	+
173	Aspergillus niger	4911	+
173	Aspergillus ochraceus	186515	+
173	Aspergillus ochraceus	63698	
173	Aspergillus sp.	14734	+
173	Aspergillus sp.	4901	
173	Aspergillus sydowii	161957	+
173	Aspergillus versicolor	49019	
173	Aureobasidium pullulans	1487220	+
173	Aureobasidium pullulans	63812	
173	Chaetomium globosum	4901	
173	Cladosporium sphaerospermum	1256616	+
173	Penicillium chrysogenum	9823	
173	Penicillium raistrickii	137428	+
173	Penicillium raistrickii	4911	
173	Penicillium sp. #64	107958	+
173	Penicillium spinulosum	9803	+
173	unknown	39215	+
173	unknown	4911	
173	Wallemia sebi	4901	+
173	yeast	29411	
174	Alternaria alternata	4770	+
174	Aspergillus niger	4770	
174	Aspergillus versicolor	28855	+
174	Aspergillus versicolor	14450	
174	Cladosporium herbarum	4816	+
174	Cladosporium sphaerospermum	62344	+
174	Emericella nidulans	4770	+
174	Eurotium herbariorum	19221	+
174	Mucor plumbeus	4770	+
174	Penicillium aurantiogriseum	4816	+
174	Penicillium commune	14404	+
174	Trichoderma viride	62114	+
174	Trichoderma viride	19267	
174	unknown	52802	+
175	Absidia corymbifera	95	
175	Alternaria alternata	97	
175	Chaetomium globosum	95	
175	Mucor plumbeus	288	+
175	Mucor plumbeus	194	
175	Penicillium chrysogenum	772	
175	Penicillium chrysogenum	673	+
175	Penicillium roquefortii	95	+
175	Penicillium spinulosum	95	
175	Penicillium spinulosum	95	+
175	Penicillium viridicatum	194	
175	Rhizopus oryzae	95	+
175	Sporothrix sp.	287	
175	Trichoderma viride	291	
175	unknown	577	
175	unknown	97	+
175	yeast	6271	
176	Aspergillus glaucus	473	+
176	Aspergillus niger	764	
176	Aspergillus niger	473	+
176	Aspergillus versicolor	5202	
176	Aspergillus versicolor	473	+
176	Chaetomium cochliodes	1420	
176	Chaetomium cochliodes	946	+
176	Eurotium herbariorum	2839	+
176	Paecilomyces variotii	472	
176	Penicillium aurantiogriseum	1890	+
176	Penicillium chrysogenum	473	+
176	Penicillium corylophilum	9933	
176	Penicillium purpurogenum	2838	
176	Penicillium sp.	473	
176	Penicillium viridicatum	473	
176	unknown	1417	
176	yeast	473	
177	Aspergillus niger	166	+
177	Chaetomium cochliodes	10298	
177	Eurotium herbariorum	221	+
177	Penicillium chrysogenum	2219	
177	Penicillium chrysogenum	499	+
177	Penicillium corylophilum	1400	+
177	Penicillium sp. #26	554	
177	Penicillium sp. #26	110	+
177	Penicillium spinulosum	1664	
177	Penicillium spinulosum	166	+
177	Penicillium waksmanii	55	+
177	yeast	4905725	
178	Acremonium sclerotigenum	4032186	
178	Acremonium sclerotigenum	78	+
178	Aspergillus niger	77	
178	Aspergillus ochraceus	77	
178	Aspergillus sydowii	9411	
178	Aspergillus sydowii	1013	+
178	Aspergillus versicolor	2587	+
178	Aspergillus versicolor	2508	
178	Eurotium herbariorum	312	+
178	Penicillium aurantiogriseum	784	
178	Penicillium aurantiogriseum	233	+
178	Penicillium citrinum	77	
178	Penicillium commune	233	
178	Penicillium corylophilum	626	+
178	Penicillium glandicola	77	
178	Penicillium miczynskii	78	+
178	Penicillium raistrickii	77	
178	Penicillium sp. #1	78	+
178	Phialophora sp.	77	
178	Phoma herbarum	784	
178	Scopulariopsis chartarum	784	
178	Scopulariopsis chartarum	625	+
178	Scopulariopsis sp.	32941	
178	Scopulariopsis sp.	78	+
178	unknown	2352	
178	yeast	16218	
180	Alternaria alternata	462	+
180	Alternaria alternata	92	
180	Aspergillus niger	92	+
180	Aspergillus ochraceus	92	+
180	Aureobasidium pullulans	5833	+
180	Eurotium herbariorum	92	+
180	Mucor plumbeus	462	+
180	Mucor plumbeus	370	
180	Penicillium commune	3888	+
180	Penicillium commune	1666	
180	unknown	277	+
180	yeast	1296	
182	Alternaria alternata	4752	+

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
182	Aspergillus niger	477810	+	187	Cladosporium herbarum	958	+
182	Aspergillus niger	19531		187	Cladosporium sphaerospermum	1917	+
182	Aspergillus versicolor	81968	+	187	Cladosporium sphaerospermum	483	
182	Aureobasidium pullulans	4752	+	187	Eurotium herbariorum	1442	+
182	Eurotium herbariorum	9635	+	187	Fusarium sp.	950	
182	Penicillium citreonigrum	33789	+	187	Fusarium sp.	475	+
182	Penicillium citreonigrum	33529		187	Paecilomyces variotii	483	
182	Penicillium corylophilum	4752	+	187	Penicillium commune	1434	
182	Trichoderma viride	57684		187	Penicillium commune	475	+
182	Trichoderma viride	28906	+	187	Penicillium spinulosum	1425	
182	unknown	333999		187	Penicillium spinulosum	475	+
183	Alternaria alternata	23789	+	187	Phoma herbarum	483	+
183	Aspergillus versicolor	14222	+	187	Phoma sp.	1442	
183	Aureobasidium pullulans	9567	+	187	unknown	2392	
183	Cladosporium sphaerospermum	4655	+	188	Alternaria alternata	3845	+
183	Fusarium sp.	9823	+	188	Alternaria alternata	2857	
183	Oidiodendron sp.	116826		188	Aspergillus versicolor	4419	
183	Penicillium brevicompactum	4911	+	188	Aspergillus versicolor	3378	+
183	Trichoderma viride	9823		188	Aureobasidium pullulans	12723	
183	Trichoderma viride	4911	+	188	Aureobasidium pullulans	1922	+
183	unknown	38524	+	188	Cladosporium cladosporioides	2470	
183	unknown	24301		188	Cladosporium cladosporioides	467	+
185	Aspergillus niger	287	+	188	Emericella nidulans	988	
185	Aspergillus ochraceus	191	+	188	Epicoccum nigrum	1401	
185	Aureobasidium pullulans	382	+	188	Epicoccum nigrum	467	+
185	Chaetomium globosum	154193		188	Eurotium herbariorum	467	+
185	Eurotium herbariorum	191	+	188	Penicillium chrysogenum	3324	+
185	Penicillium brevicompactum	191	+	188	Penicillium chrysogenum	2857	
185	Penicillium commune	667	+	188	Penicillium commune	494	
185	Penicillium commune	189		188	Penicillium spinulosum	4833	+
185	Penicillium expansum	954	+	188	Penicillium spinulosum	3404	
185	Penicillium expansum	94		188	Phoma herbarum	2803	
185	Scopulariopsis brevicaulis	95		188	Phoma herbarum	467	+
185	Ulocladium chartarum	94	+	188	unknown	5794	+
185	unknown	191		188	unknown	2857	
185	Wallemia sebi	15509	+	188	yeast	5714	
185	yeast	2004		189	Alternaria alternata	10764	
186	Acremonium strictum	387		189	Alternaria alternata	7383	+
186	Acremonium strictum	98	+	189	Aspergillus niger	498	+
186	Aspergillus niger	99	+	189	Aureobasidium pullulans	8790	
186	Aspergillus ustus	99		189	Aureobasidium pullulans	4438	+
186	Aspergillus versicolor	197	+	189	Cladosporium cladosporioides	498	
186	Aspergillus versicolor	98		189	Cladosporium cladosporioides	498	+
186	Eurotium herbariorum	99	+	189	Cladosporium sp.	967	+
186	Fusarium oxysporum	196	+	189	Epicoccum nigrum	1450	
186	Paecilomyces variotii	99		189	Epicoccum nigrum	483	+
186	Penicillium aurantiogriseum	396		189	Eurotium herbariorum	2944	+
186	Penicillium chrysogenum	395		189	Penicillium brevicompactum	498	+
186	Penicillium sp. #64	98		189	Penicillium chrysogenum	3911	+
186	Penicillium spinulosum	98	+	189	Penicillium chrysogenum	3428	
186	unknown	593		189	Penicillium corylophilum	483	
186	yeast	891		189	Penicillium spinulosum	1948	
187	Acremonium sp.	1925		189	Phoma herbarum	498	
187	Alternaria alternata	1450		189	Rhizopus oryzae	483	+
187	Alternaria alternata	967	+	189	Trichoderma viride	4482	
187	Aspergillus niger	483		189	unknown	4864	
187	Aspergillus versicolor	2384	+	189	unknown	2446	+
187	Aspergillus versicolor	967		189	yeast	28393	
187	Aureobasidium pullulans	15858	+	190	Alternaria alternata	8822	
187	Aureobasidium pullulans	13899		190	Alternaria alternata	2346	+
187	Cladosporium cladosporioides	483	+	190	Eurotium herbariorum	1881	+

HN	Identification	AVG CFU/g	G
190	Myrothecium cinctum	1407	
190	Penicillium brevicompactum	941	
190	Penicillium roquefortii	938	+
190	Penicillium spinulosum	6120	+
190	Penicillium spinulosum	2824	
190	Scopulariopsis brevicaulis	938	+
190	unknown	4697	+
190	unknown	2346	
190	Wallemia sebi	938	
190	yeast	2354	
191	Alternaria alternata	2435	+
191	Aspergillus fumigatus	484	+
191	Aspergillus niger	3424	
191	Aspergillus niger	1957	+
191	Aureobasidium pullulans	26289	+
191	Aureobasidium pullulans	2946	
191	Cladosporium cladosporioides	3391	+
191	Cladosporium sphaerospermum	491	+
191	Eurotium herbariorum	491	+
191	Fusarium sp.	2442	+
191	Geomyces pannorum	484	
191	Graphium sp.	982	
191	Microsphaeropsis olivaceus	484	+
191	Paecilomyces sp.	484	
191	Penicillium brevicompactum	1944	+
191	Penicillium brevicompactum	1466	
191	Penicillium commune	484	
191	Penicillium corylophilum	982	+
191	unknown	2422	+
191	unknown	1944	
191	yeast	4858	
192	Alternaria alternata	2409	+
192	Aspergillus versicolor	479	+
192	Aureobasidium pullulans	10221	+
192	Cladosporium cladosporioides	2440	+
192	Epicoccum nigrum	490	+
192	Fusarium oxysporum	12181	
192	Penicillium brevicompactum	2440	
192	Penicillium brevicompactum	980	+
192	Penicillium chrysogenum	970	
192	Penicillium spinulosum	15582	+
192	Penicillium spinulosum	4901	
192	Phoma sp.	490	
192	Rhizopus stolonifer	2910	+
192	unknown	1940	+
192	unknown	1460	
192	Wallemia sebi	490	+
192	yeast	2930	
193	Acremonium murorum var. felina	4807	
193	Alternaria alternata	4911	+
193	Aspergillus sp.	28846	+
193	Botryotrichum piluliferum	24038	+
193	Botryotrichum piluliferum	9823	
193	Chaetomium globosum	14630	
193	Chaetomium globosum	4911	+
193	Cladosporium cladosporioides	24557	+
193	Cladosporium sphaerospermum	34069	+
193	Eurotium herbariorum	9719	+
193	Geomyces pannorum	4807	
193	Humicola fuscoatra	4807	
193	Penicillium chrysogenum	14526	
193	Penicillium chrysogenum	4807	+
193	Phoma herbarum	4807	
193	Stachybotrys chartarum	4807	
193	unknown	39292	+
193	unknown	19334	
193	Wallemia sebi	576998	+
193	yeast	111096	
194	Alternaria alternata	151337	
194	Alternaria alternata	479	+
194	Aspergillus niger	479	
194	Aspergillus sp.	494	
194	Aspergillus sp.	494	+
194	Aspergillus sydowii	44970	
194	Aspergillus sydowii	22993	+
194	Aureobasidium pullulans	6760	
194	Aureobasidium pullulans	2964	+
194	Cladosporium cladosporioides	2879	+
194	Cladosporium cladosporioides	479	
194	Epicoccum nigrum	479	
194	Eurotium herbariorum	3430	+
194	Penicillium chrysogenum	3444	
194	Penicillium chrysogenum	2413	+
194	Penicillium corylophilum	1453	
194	Penicillium corylophilum	494	+
194	Penicillium simplicissimum	959	+
194	Penicillium spinulosum	973	+
194	Penicillium spinulosum	494	
194	Scopulariopsis candida	973	+
194	Scopulariopsis candida	494	
194	unknown	959	
194	yeast	1947	
195	Alternaria alternata	1369	+
195	Aspergillus terreus	769	+
195	Aspergillus versicolor	198570	
195	Aspergillus versicolor	3076	+
195	Aureobasidium pullulans	29430	
195	Aureobasidium pullulans	23097	+
195	Cladosporium cladosporioides	7702	+
195	Cladosporium sphaerospermum	2307	
195	Paecilomyces variotii	2739	
195	Penicillium chrysogenum	769	+
195	Penicillium citrinum	2992	
195	Penicillium commune	2139	
195	Penicillium commune	1369	+
195	Phoma herbarum	4362	
195	Phoma herbarum	684	+
195	Phoma sp.	6849	
195	Trichoderma viride	2992	
195	Trichoderma viride	769	+
195	Ulocladium chartarum	2054	+
195	unknown	11801	+
195	unknown	6417	
195	yeast	11464	
197	Alternaria alternata	2890	+
197	Aspergillus niger	468	+
197	Aureobasidium pullulans	29129	+
197	Aureobasidium pullulans	19890	
197	Cladosporium cladosporioides	2874	+
197	Cladosporium cladosporioides	468	
197	Epicoccum nigrum	468	
197	Mucor plumbeus	3326	

HN	Identification	AVG CFU/g	G
197	Mucor racemosus	2357	+
197	Phoma sp.	1872	+
197	unknown	1420	
197	yeast	4278	
198	Alternaria alternata	4302	
198	Alternaria alternata	3851	+
198	Aspergillus niger	476	+
198	Aspergillus ochraceus	476	
198	Aspergillus sp.	476	
198	Aspergillus versicolor	968	
198	Aureobasidium pullulans	41259	+
198	Aureobasidium pullulans	15872	
198	Cladosporium cladosporioides	1436	+
198	Cladosporium cladosporioides	484	
198	Coniothyrium sp.	3391	
198	Coniothyrium sp.	968	+
198	Epicoccum nigrum	968	+
198	Epicoccum nigrum	968	
198	Eurotium herbariorum	1904	+
198	Fusarium sp.	1921	
198	Fusarium sp.	968	+
198	Hyalodendron sp.	476	
198	Mucor racemosus	484	+
198	Mucor racemosus	476	
198	Penicillium expansum	1445	+
198	Penicillium simplicissimum	968	+
198	Penicillium spinulosum	1436	
198	Penicillium variabile	960	
198	Phoma herbarum	1436	
198	Phoma medicaginis	5238	
198	unknown	4786	
198	unknown	1428	+
198	yeast	5797	
199	Alternaria alternata	6302	+
199	Alternaria alternata	2004	
199	Aspergillus sydowii	477	
199	Aspergillus versicolor	1146	
199	Aureobasidium pullulans	69621	+
199	Aureobasidium pullulans	18904	
199	Cladosporium cladosporioides	5156	+
199	Cladosporium sphaerospermum	954	
199	Cladosporium sphaerospermum	954	+
199	Epicoccum nigrum	477	
199	Geomyces pannorum	1431	
199	Mucor racemosus	1146	
199	Mucor racemosus	573	+
199	Penicillium aurantiogriseum	6014	+
199	Penicillium commune	8592	+
199	Penicillium commune	1720	
199	Penicillium simplicissimum	9839	+
199	Penicillium spinulosum	2674	
199	Phoma sp.	1146	
199	Sporobolomyces sp.	1431	
199	Trichoderma viride	1050	
199	unknown	11069	
199	yeast	3532	
200	Acremonium sp.	169117	
200	Aspergillus sp.	9842	
200	Aureobasidium pullulans	39142	
200	Aureobasidium pullulans	4807	+
200	Cladosporium sphaerospermum	4921	+
200	Eurotium herbariorum	9842	+
200	Penicillium chrysogenum	58487	+
200	Penicillium chrysogenum	29300	
200	Penicillium implicatum	39370	
200	Penicillium implicatum	33880	+
200	Trichoderma viride	19344	
200	Trichoderma viride	14763	+
200	unknown	63749	
200	unknown	34335	+
201	Alternaria alternata	5412	
201	Alternaria alternata	977	+
201	Aureobasidium pullulans	36293	+
201	Aureobasidium pullulans	8797	
201	Cladosporium cladosporioides	486	
201	Eurotium herbariorum	977	+
201	Exophiala sp.	491	
201	Penicillium brevicompactum	491	+
201	Penicillium chrysogenum	2446	
201	Penicillium chrysogenum	977	+
201	Penicillium purpurogenum	2937	
201	Penicillium sp. #26	977	
201	Penicillium sp. #26	491	+
201	Penicillium spinulosum	486	+
201	Phoma sp.	6866	
201	Phoma sp.	982	+
201	Trichophyton tonsurans	972	
201	Ulocladium sp.	972	+
201	unknown	3914	
201	yeast	3929	
202	Alternaria alternata	1428	
202	Alternaria alternata	1428	+
202	Aspergillus ochraceus	952	
202	Aspergillus sydowii	476	+
202	Aspergillus versicolor	957	+
202	Aspergillus versicolor	476	
202	Aureobasidium pullulans	19639	
202	Aureobasidium pullulans	13859	+
202	Cladosporium cladosporioides	1434	+
202	Cladosporium cladosporioides	952	
202	Cladosporium sphaerospermum	476	+
202	Epicoccum nigrum	476	
202	Eurotium herbariorum	1926	+
202	Geomyces sp.	1434	
202	Gliocladium sp.	476	
202	Microsphaeropsis olivaceus	7148	
202	Microsphaeropsis olivaceus	1921	+
202	Mucor plumbeus	963	+
202	Mucor racemosus	476	+
202	Penicillium citreonigrum	952	+
202	Penicillium citreonigrum	476	
202	Penicillium commune	6229	+
202	Penicillium commune	1915	
202	Penicillium expansum	952	+
202	Penicillium verrucosum	1434	
202	Phoma glomerata	481	
202	Phoma herbarum	2890	
202	Thamnidium elegans	963	
202	Thamnidium elegans	952	+
202	Ulocladium chartarum	963	
202	Ulocladium sp.	963	
202	yeast	3853	

HN	Identification	AVG CFU/g	G
204	Alternaria alternata	3924	
204	Alternaria alternata	2467	+
204	Aspergillus candidus	489	+
204	Aspergillus glaucus	500	
204	Aspergillus niger	14349	+
204	Aspergillus niger	6946	
204	Aspergillus ochraceus	489	+
204	Aspergillus sydowii	500	+
204	Aspergillus ustus	1000	
204	Aspergillus versicolor	500	+
204	Aureobasidium pullulans	33440	+
204	Aureobasidium pullulans	11892	
204	Cladosporium cladosporioides	4424	+
204	Cladosporium sphaerospermum	1989	
204	Cladosporium sphaerospermum	500	+
204	Epicoccum nigrum	1000	
204	Eurotium herbariorum	989	+
204	Fusarium sp.	1467	
204	Fusarium sp.	489	+
204	Mucor plumbeus	500	
204	Penicillium brevicompactum	489	
204	Penicillium simplicissimum	3924	+
204	Penicillium simplicissimum	2456	
204	Penicillium spinulosum	978	+
204	Penicillium spinulosum	489	
204	Phoma sp.	3000	+
206	Acremonium sp.	466	
206	Alternaria alternata	6154	
206	Alternaria alternata	4801	+
206	Aspergillus ochraceus	3310	
206	Aspergillus ochraceus	955	+
206	Aspergillus versicolor	3424	
206	Aspergillus versicolor	3424	+
206	Aureobasidium pullulans	16895	+
206	Aureobasidium pullulans	8248	
206	Cladosporium cladosporioides	7064	+
206	Cladosporium cladosporioides	932	
206	Cladosporium sphaerospermum	1865	+
206	Eurotium herbariorum	6780	+
206	Paecilomyces variotii	1422	
206	Paecilomyces variotii	466	+
206	Penicillium chrysogenum	9977	+
206	Penicillium chrysogenum	3333	
206	Penicillium corylophilum	5244	
206	Penicillium corylophilum	978	+
206	Phoma herbarum	1934	
206	Trichoderma viride	978	
206	Ulocladium sp.	3731	+
206	unknown	4311	
206	unknown	2377	+
206	Wallemia sebi	4403	+
206	yeast	3287	
209	Alternaria alternata	4921	
209	Aspergillus versicolor	73731	
209	Aureobasidium pullulans	4911	+
209	Cladosporium sphaerospermum	4921	
209	Cladosporium sphaerospermum	4921	+
209	Epicoccum nigrum	4921	
209	Penicillium chrysogenum	186785	
209	Penicillium chrysogenum	118003	+
209	Penicillium commune	4911	
212	Alternaria alternata	7219	
212	Alternaria alternata	6191	+
212	Aspergillus niger	9630	+
212	Aspergillus niger	8601	
212	Aspergillus ochraceus	472	+
212	Aspergillus sp.	1417	
212	Aspergillus versicolor	484	
212	Aureobasidium pullulans	36158	
212	Aureobasidium pullulans	6250	+
212	Chaetomium globosum	2362	
212	Cladosporium cladosporioides	1429	+
212	Cladosporium cladosporioides	472	
212	Eurotium herbariorum	3804	+
212	Mucor plumbeus	484	+
212	Mucor racemosus	484	
212	Penicillium brevicompactum	472	
212	Penicillium chrysogenum	20984	+
212	Penicillium chrysogenum	17735	
212	Penicillium italicum	3367	
212	Penicillium italicum	1937	+
212	Penicillium sp. #26	1417	
212	Penicillium sp. #26	968	+
212	Phoma herbarum	1890	+
212	Phoma herbarum	945	
212	unknown	945	
212	yeast	4797	
213	Aspergillus niger	530	
213	Aspergillus ustus	3162	
213	Aspergillus ustus	1586	+
213	Mucor plumbeus	2117	+
213	Mucor plumbeus	1050	
213	Mucor racemosus	3162	
213	Paecilomyces variotii	525	+
213	Penicillium chrysogenum	7917	+
213	Penicillium chrysogenum	4229	
213	Penicillium corylophilum	13152	+
213	Penicillium corylophilum	6347	
213	Rhizopus oryzae	1055	+
213	Syncephalastrum racemosum	3162	+
213	Syncephalastrum racemosum	2642	
213	Syncephalastrum sp.	1050	
214	Aspergillus glaucus	948	
214	Aspergillus glaucus	941	+
214	Eurotium herbariorum	5200	+
214	Paecilomyces variotii	478	
214	Paecilomyces variotii	470	+
214	Penicillium corylophilum	3310	
214	Penicillium corylophilum	941	+
214	Penicillium decumbens	1426	+
214	Penicillium glandicola	17607	
214	Penicillium implicatum	948	
214	Penicillium implicatum	948	+
214	Penicillium sp. #26	5200	+
214	Penicillium viridicatum	30861	+
214	Penicillium viridicatum	20403	
214	Rhizopus oryzae	470	
214	unknown	2846	
215	Alternaria alternata	2899	+
215	Aspergillus niger	486	
215	Aspergillus niger	482	+
215	Aspergillus sp.	482	

HN	Identification	AVG CFU/g	G
215	Aspergillus versicolor	2420	+
215	Aureobasidium pullulans	4852	+
215	Aureobasidium pullulans	2413	
215	Cladosporium cladosporioides	486	+
215	Cladosporium sp.	1455	+
215	Eurotium herbariorum	482	+
215	Mucor racemosus	9686	
215	Mucor racemosus	3389	+
215	Penicillium chrysogenum	486	+
215	Penicillium chrysogenum	482	
215	Penicillium commune	969	
215	Penicillium commune	965	+
215	Penicillium sp.	482	
215	Penicillium sp. #26	486	+
215	unknown	486	
216	Acremonium furcatum	1444	
216	Alternaria alternata	9645	+
216	Alternaria alternata	3865	
216	Aspergillus clavatus	478	
216	Aspergillus niger	487	
216	Aspergillus ochraceus	487	
216	Aspergillus ustus	487	
216	Cladosporium cladosporioides	3386	+
216	Cladosporium macrocarpum	6268	+
216	Epicoccum nigrum	974	+
216	Fusarium sp.	1445	
216	Fusarium sp.	478	+
216	Microsphaeropsis olivaceus	22324	+
216	Microsphaeropsis olivaceus	3394	
216	Mucor racemosus	966	+
216	Penicillium chrysogenum	957	
216	Penicillium echinulatum	3377	+
216	Penicillium echinulatum	1436	
216	Penicillium expansum	957	
216	Penicillium implicatum	487	
216	Penicillium italicum	1445	
216	Penicillium spinulosum	4360	
216	Penicillium spinulosum	966	+
216	Phoma eupyrena	14535	
216	Pithomyces sp.	487	+
216	Rhizopus oryzae	487	
216	Trichoderma polysporum	487	
216	unknown	8250	
216	unknown	4335	+
216	yeast	7251	
217	Alternaria alternata	11600	
217	Alternaria alternata	987	+
217	Aspergillus versicolor	1975	+
217	Aureobasidium pullulans	494	
217	Cladosporium cladosporioides	9376	+
217	Cladosporium cladosporioides	1973	
217	Cladosporium sphaerospermum	9881	
217	Cladosporium sphaerospermum	8389	+
217	Emericella variecolor	3946	
217	Emericella variecolor	1972	+
217	Eurotium herbariorum	3453	+
217	Fusarium oxysporum	494	
217	Mucor plumbeus	1482	+
217	Mucor plumbeus	987	
217	Penicillium brevicompactum	1480	
217	Penicillium brevicompactum	986	+
217	Penicillium chrysogenum	6910	+
217	Penicillium corylophilum	2961	+
217	Penicillium griseofulvum	3453	
217	Penicillium simplicissimum	493	+
217	Penicillium sp.	494	+
217	Penicillium sp. #26	2468	+
217	Penicillium sp. #26	1974	
217	Penicillium spinulosum	1480	
217	Pithomyces sp.	987	+
217	Pithomyces sp.	493	
217	unknown	7406	
217	unknown	5923	+
217	Wallemia sebi	2468	+
217	yeast	3944	
220	Aureobasidium pullulans	6100	
220	Eurotium herbariorum	2047	+
220	Gliomastix murorum	194	
220	Paecilomyces variotii	98	
220	Penicillium chrysogenum	687	+
220	Penicillium chrysogenum	195	
220	Penicillium citreonigrum	293	
220	Penicillium citreonigrum	98	+
220	Penicillium spinulosum	195	
220	Penicillium spinulosum	97	+
220	Scopulariopsis candida	97	
220	unknown	196	
220	unknown	195	+
220	yeast	15225	
223	Alternaria alternata	2846	+
223	Aspergillus fumigatus	473	+
223	Aspergillus versicolor	473	+
223	Aureobasidium pullulans	473	+
223	Cladosporium cladosporioides	2851	+
223	Cladosporium herbarum	2484	
223	Cladosporium herbarum	2372	+
223	Cladosporium sp.	3322	+
223	Coniothyrium fuckelii	476	
223	Fusarium sp.	3322	
223	Fusarium sp.	476	+
223	Penicillium implicatum	476	
223	Penicillium oxalicum	476	
223	Penicillium oxalicum	473	+
223	Pithomyces chartarum	473	+
223	unknown	7594	+
223	unknown	6176	
223	yeast	6642	
225	Absidia corymbifera	19150	
225	Alternaria alternata	138	
225	Alternaria alternata	132	+
225	Aspergillus glaucus	404	+
225	Aspergillus niger	132	
225	Aspergillus ornatus	138	+
225	Aspergillus oryzae	132	
225	Aspergillus ustus	138	
225	Aspergillus versicolor	2163	+
225	Aspergillus versicolor	1340	
225	Chaetomium globosum	132	
225	Cladosporium cladosporioides	138	
225	Eurotium herbariorum	542	+
225	Fusarium oxysporum	138	
225	Paecilomyces variotii	265	+

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
225	Penicillium atramentosum	542	+	228	Cladosporium sphaerospermum	29206	+
225	Penicillium atramentosum	271		228	Cladosporium sphaerospermum	4780	
225	Penicillium chrysogenum	3508		228	Eurotium herbariorum	82445	+
225	Penicillium chrysogenum	3498	+	228	Penicillium brevicompactum	24557	
225	Penicillium corylophilum	276		228	Penicillium brevicompactum	14734	+
225	Penicillium implicatum	941		228	Penicillium chrysogenum	144981	+
225	Penicillium sp. #26	537		228	Penicillium chrysogenum	87751	
225	Penicillium spinulosum	265	+	228	Penicillium citrinum	29206	+
225	Penicillium spinulosum	138		228	Penicillium citrinum	4911	
225	Penicillium verrucosum	404		228	Penicillium corylophilum	29206	+
225	Phoma exigua	276		228	Penicillium corylophilum	19251	
225	Phoma herbarum	138		228	Penicillium echinulatum	58018	
225	Syncephalastrum racemosum	132	+	228	Penicillium funiculosum	9823	
225	Trichoderma sp.	271	+	228	Penicillium sp.	33460	
225	Trichoderma viride	132		228	Penicillium sp. #26	19383	
225	unknown	2711		228	Penicillium variabile	4911	
225	unknown	1074	+	228	Rhizopus oryzae	33723	+
225	yeast	956		228	Rhizopus oryzae	14340	
226	Alternaria alternata	196		228	unknown	265930	
226	Aspergillus versicolor	127		228	unknown	86567	+
226	Aureobasidium pullulans	4029	+	228	yeast	23900	
226	Aureobasidium pullulans	253		229	Alternaria alternata	1182	+
226	Chaetomium aureum	255		229	Aspergillus niger	19908	
226	Cladosporium cladosporioides	191	+	229	Aspergillus niger	132	+
226	Eurotium herbariorum	316	+	229	Aspergillus ustus	130	
226	Fusarium sp.	128		229	Aureobasidium pullulans	16983	+
226	Penicillium chrysogenum	127		229	Aureobasidium pullulans	8294	
226	Penicillium commune	446	+	229	Cladosporium cladosporioides	4476	+
226	Penicillium commune	127		229	Eurotium herbariorum	526	+
226	Penicillium sp. #26	256	+	229	Geomyces pannorum	263	
226	Penicillium sp. #26	64		229	Mucor racemosus	394	+
226	Penicillium spinulosum	63	+	229	Penicillium chrysogenum	3680	+
226	Phoma herbarum	63		229	Penicillium chrysogenum	658	
226	Scopulariopsis candida	256	+	229	Penicillium commune	261	
226	Ulocladium chartarum	63	+	229	Penicillium spinulosum	1449	+
226	unknown	63		229	Penicillium spinulosum	655	
226	Wallemia sebi	63	+	229	unknown	919	
226	yeast	3647		229	yeast	264	
227	Acremonium sp.	3858	+	230	Alternaria alternata	1130	
227	Alternaria alternata	467		230	Alternaria alternata	499	+
227	Aspergillus glaucus	467		230	Aspergillus glaucus	1482	+
227	Aspergillus versicolor	1903		230	Aspergillus niger	998	
227	Aspergillus versicolor	934	+	230	Aspergillus niger	499	+
227	Eurotium herbariorum	968		230	Aspergillus sydowii	1497	
227	Penicillium aurantiogriseum	951		230	Aspergillus ustus	484	+
227	Penicillium chrysogenum	1903	+	230	Coniothyrium fuckelii	499	
227	Penicillium chrysogenum	1886		230	Emericella nidulans	499	
227	Penicillium citreonigrum	2855	+	230	Epicoccum nigrum	499	
227	Penicillium citreonigrum	1869		230	Eurotium herbariorum	1482	+
227	Penicillium commune	467	+	230	Fusarium sp.	998	
227	Penicillium corylophilum	1903	+	230	Lecythophora sp.	1497	
227	Penicillium implicatum	484	+	230	Lecythophora sp.	499	+
227	Pestalotiopsis sp.	467		230	Mucor racemosus	1952	
227	unknown	4274	+	230	Paecilomyces variotii	499	
227	unknown	484		230	Penicillium citrinum	499	+
228	Alternaria alternata	8268		230	Penicillium corylophilum	2451	
228	Aspergillus glaucus	4780	+	230	Penicillium griseofulvum	5900	+
228	Aspergillus sydowii	9823		230	Penicillium oxalicum	1467	
228	Aspergillus versicolor	77139	+	230	Penicillium simplicissimum	3405	+
228	Aspergillus versicolor	53633		230	Penicillium sp. #26	968	
228	Aureobasidium pullulans	9823	+	230	Penicillium spinulosum	1482	+

HN	Identification	AVG CFU/g	G
230	unknown	4931	+
230	unknown	3449	
230	yeast	3919	
231	Alternaria alternata	13183	
231	Aspergillus niger	4743	
231	Aspergillus niger	4743	+
231	Aureobasidium pullulans	104671	+
231	Aureobasidium pullulans	4761	
231	Gliocladium sp.	9523	+
231	Penicillium echinulatum	4761	
231	Penicillium spinulosum	4761	+
231	Phoma herbarum	4761	+
231	Trichoderma viride	9505	
231	yeast	14231	
232	Alternaria alternata	32191	
232	Alternaria alternata	2878	+
232	Aspergillus niger	704	+
232	Aspergillus ustus	72	
232	Epicoccum nigrum	70	
232	Penicillium chrysogenum	2134	+
232	Penicillium chrysogenum	72	
232	Pithomyces chartarum	1409	+
232	Pithomyces chartarum	211	
232	Syncephalastrum racemosum	72	
232	yeast	281	
233	Alternaria alternata	10133	+
233	Aspergillus candidus	480	
233	Aspergillus versicolor	2418	
233	Aspergillus versicolor	968	+
233	Aureobasidium pullulans	24612	+
233	Aureobasidium pullulans	9171	
233	Cladosporium cladosporioides	961	+
233	Exophiala sp.	480	
233	Fusarium sp.	480	+
233	Gliocladium virens	480	
233	Mucor racemosus	1934	+
233	Mucor racemosus	968	
233	Penicillium aurantiogriseum	6287	+
233	Penicillium aurantiogriseum	1442	
233	Penicillium brevicompactum	961	+
233	Penicillium chrysogenum	961	
233	Penicillium chrysogenum	484	+
233	Penicillium corylophilum	480	
233	Penicillium echinulatum	2415	
233	Penicillium implicatum	968	+
233	Penicillium roquefortii	7737	+
233	Penicillium roquefortii	1926	
233	Trichoderma viride	3387	
233	Trichoderma viride	2403	+
233	unknown	2906	
233	unknown	1930	+
233	Wallemia sebi	449873	+
234	Alternaria alternata	4794	+
234	Aspergillus versicolor	3386	+
234	Aureobasidium pullulans	42486	+
234	Aureobasidium pullulans	2390	
234	Cladosporium cladosporioides	1917	+
234	Eurotium herbariorum	24991	+
234	Mucor racemosus	946	+
234	Mucor racemosus	485	
234	Penicillium chrysogenum	970	+
234	Penicillium echinulatum	473	
234	Penicillium oxalicum	485	
234	Penicillium sp. #26	958	+
234	Penicillium sp. #26	473	
234	Trichocladium asperum	485	
234	unknown	3835	
234	unknown	970	+
235	Alternaria alternata	3327	
235	Aspergillus niger	486	+
235	Aspergillus oryzae	486	
235	Aspergillus restrictus	2418	+
235	Aspergillus ustus	1931	+
235	Aspergillus versicolor	1931	+
235	Aureobasidium pullulans	958	
235	Aureobasidium pullulans	945	+
235	Cladosporium cladosporioides	486	+
235	Curvularia prasadii	2431	+
235	Eurotium herbariorum	1445	+
235	Fusarium sp.	472	+
235	Penicillium chrysogenum	1445	+
235	Penicillium miczynskii	3363	+
235	Penicillium miczynskii	472	
235	Penicillium restrictum	1945	+
235	Penicillium spinulosum	958	
235	Phoma sp.	7254	
235	Trichoderma viride	9061	
235	Trichoderma viride	2362	+
235	unknown	10131	
235	unknown	7212	+
235	Wallemia sebi	486	+
235	yeast	3822	
236	Aspergillus versicolor	3802	
236	Aspergillus versicolor	1873	+
236	Aureobasidium pullulans	467	+
236	Cladosporium cladosporioides	938	+
236	Cladosporium cladosporioides	467	
236	Epicoccum nigrum	467	
236	Eurotium herbariorum	7053	+
236	Penicillium chrysogenum	25886	
236	Penicillium chrysogenum	22597	+
236	Sporobolomyces sp.	181092	
236	Sporobolomyces sp.	99532	+
236	unknown	1406	+
236	unknown	467	
237	Aspergillus versicolor	4708	+
237	Eurotium herbariorum	9451	+
237	Mortierella ramanniana var. autotrophica	4725	
237	Mucor mucedo	14159	
237	Mucor mucedo	4708	+
237	Mucor plumbeus	28319	+
237	Mucor plumbeus	23611	
237	Mucor racemosus	42461	+
237	Penicillium chrysogenum	47205	+
237	Penicillium chrysogenum	32992	
237	Penicillium citrinum	14177	+
237	Penicillium restrictum	4708	
237	Rhizopus oryzae	66126	
237	Trichoderma viride	4725	+
237	Trichoderma viride	4708	
237	unknown	23576	
237	yeast	51842	

HN	Identification	AVG CFU/g	G
238	Aspergillus niger	954	+
238	Aspergillus ochraceus	9927	
238	Aspergillus versicolor	478	+
238	Aureobasidium pullulans	17636	+
238	Aureobasidium pullulans	13358	
238	Cladosporium cladosporioides	954	+
238	Eurotium herbariorum	950	+
238	Mucor plumbeus	475	+
238	Penicillium chrysogenum	478	+
238	Penicillium chrysogenum	475	
238	Penicillium implicatum	950	
238	Penicillium spinulosum	475	
238	Penicillium viridicatum	3805	+
238	Penicillium viridicatum	950	
238	Ulocladium chartarum	478	+
238	unknown	4277	
238	unknown	2390	+
238	yeast	2873	
239	Alternaria alternata	3359	
239	Alternaria alternata	2884	+
239	Aureobasidium pullulans	47051	
239	Aureobasidium pullulans	16269	+
239	Cladosporium cladosporioides	2852	+
239	Cladosporium cladosporioides	480	
239	Cladosporium sphaerospermum	474	+
239	Epicoccum nigrum	2403	
239	Epicoccum nigrum	1423	+
239	Fusarium sp.	474	
239	Mucor plumbeus	474	
239	Penicillium chrysogenum	8615	
239	Penicillium chrysogenum	6224	+
239	Penicillium corylophilum	2871	+
239	Penicillium restrictum	1442	
239	Penicillium sp. #26	1910	+
239	Phoma herbarum	24519	
239	unknown	2865	
239	yeast	8077	
240	Alternaria alternata	487	+
240	Aspergillus versicolor	965	
240	Aureobasidium pullulans	16006	+
240	Aureobasidium pullulans	13120	
240	Cladosporium cladosporioides	1457	+
240	Epicoccum nigrum	487	+
240	Mucor racemosus	487	
240	Mucor racemosus	487	+
240	Penicillium brevicompactum	3401	+
240	Penicillium commune	9671	
240	Penicillium commune	7262	+
240	Penicillium expansum	1949	
240	Penicillium sp.	487	
240	Penicillium spinulosum	1935	
240	Penicillium vulpinum	6780	
240	unknown	4863	
240	unknown	1939	+
240	yeast	5308	
241	Alternaria alternata	962	+
241	Alternaria alternata	487	
241	Aspergillus fumigatus	475	
241	Aspergillus niger	475	
241	Aspergillus versicolor	1949	
241	Aspergillus versicolor	475	+
241	Aureobasidium pullulans	30256	+
241	Aureobasidium pullulans	6702	
241	Cladosporium cladosporioides	1937	+
241	Epicoccum nigrum	1425	
241	Eurotium herbariorum	950	+
241	Mucor racemosus	475	+
241	Paecilomyces variotii	962	
241	Paecilomyces variotii	475	+
241	Penicillium chrysogenum	2412	+
241	Penicillium corylophilum	8188	
241	Penicillium corylophilum	4837	+
241	Penicillium viridicatum	10053	
241	Penicillium viridicatum	8627	+
241	Phoma herbarum	487	
241	Rhizopus oryzae	487	
241	unknown	3862	
241	yeast	19023	
243	Alternaria alternata	93	+
243	Aspergillus niger	1994	
243	Aureobasidium pullulans	4890	
243	Aureobasidium pullulans	3610	+
243	Cladosporium sphaerospermum	93	+
243	Mucor plumbeus	292	+
243	Mucor racemosus	195	
243	Penicillium aurantiogriseum	390	
243	Penicillium chrysogenum	2291	+
243	Penicillium chrysogenum	186	
243	Penicillium citrinum	190	
243	Penicillium citrinum	97	+
243	Penicillium italicum	279	
243	Penicillium italicum	93	+
243	Scopulariopsis candida	186	+
243	unknown	1047	
244	Alternaria alternata	4689	
244	Alternaria alternata	3652	+
244	Aspergillus niger	524	
244	Aspergillus ustus	1556	
244	Aspergillus versicolor	524	
244	Aureobasidium pullulans	1037	+
244	Cladosporium sp.	2598	+
244	Cladosporium sp.	1037	
244	Cladosporium sphaerospermum	1566	+
244	Cladosporium sphaerospermum	1037	
244	Eurotium herbariorum	1048	+
244	Exophiala jeanselmei	6245	
244	Fusarium equiseti	2090	
244	Fusarium sp.	1042	+
244	Gliocladium roseum	5727	
244	Penicillium brevicompactum	3652	
244	Penicillium brevicompactum	3652	+
244	Penicillium commune	1566	+
244	Penicillium echinulatum	1561	+
244	Phoma herbarum	524	+
244	Pithomyces chartarum	3128	
244	Trichoderma viride	524	
244	Truncatella angustata	3663	
244	unknown	6775	+
244	unknown	4695	
244	Wallemia sebi	1048	+
244	yeast	20402	
245	Alternaria alternata	8955	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
245	Aspergillus niger	485		247	unknown	24331	
245	Aureobasidium pullulans	94747		247	yeast	19646	
245	Aureobasidium pullulans	64706	+	248	Alternaria alternata	961	
245	Cladosporium cladosporioides	24990	+	248	Alternaria alternata	480	+
245	Cladosporium cladosporioides	478		248	Aspergillus niger	482	
245	Cladosporium sphaerospermum	4316		248	Aspergillus sp.	480	
245	Epicoccum nigrum	963		248	Aspergillus versicolor	480	+
245	Eurotium herbariorum	2897	+	248	Aureobasidium pullulans	27422	
245	Mucor racemosus	956	+	248	Aureobasidium pullulans	18781	+
245	Penicillium brevicompactum	3353		248	Cladosporium cladosporioides	2405	+
245	Penicillium brevicompactum	1456	+	248	Cladosporium cladosporioides	1446	
245	Penicillium corylophilum	1441	+	248	Cladosporium herbarum	7239	+
245	Penicillium corylophilum	478		248	Cladosporium sphaerospermum	480	
245	Penicillium vulpinum	3368		248	Mucor plumbeus	480	+
245	Penicillium vulpinum	956	+	248	Penicillium chrysogenum	5778	+
245	Phoma herbarum	7222		248	Penicillium chrysogenum	4815	
245	Trichoderma sp.	1434		248	Penicillium spinulosum	965	+
245	Ulocladium chartarum	485		248	Penicillium spinulosum	482	
245	unknown	1456	+	248	Phoma sp.	3848	
245	unknown	1441		248	Trichoderma viride	480	
245	yeast	2890		248	unknown	2886	+
246	Alternaria alternata	7721		248	unknown	1928	
246	Aspergillus ochraceus	490		248	yeast	965	
246	Aspergillus sp.	487		249	Aspergillus versicolor	968	+
246	Aureobasidium pullulans	11231		249	Aureobasidium pullulans	484	+
246	Aureobasidium pullulans	4403	+	249	Cladosporium cladosporioides	2403	+
246	Cladosporium cladosporioides	1949		249	Cladosporium sp.	479	+
246	Cladosporium cladosporioides	974	+	249	Cladosporium sphaerospermum	4327	+
246	Cladosporium sphaerospermum	980		249	Eurotium herbariorum	2403	+
246	Eurotium herbariorum	1952	+	249	Mucor plumbeus	479	+
246	Penicillium citreonigrum	1957		249	Myrothecium roridum	484	
246	Penicillium commune	1464	+	249	Penicillium implicatum	968	+
246	Penicillium crustosum	6845	+	249	Penicillium implicatum	964	
246	Penicillium crustosum	4403		249	Penicillium variabile	1928	
246	Penicillium raistrickii	2445		249	Penicillium variabile	964	+
246	Penicillium raistrickii	1955	+	249	Penicillium viridicatum	1444	
246	Penicillium vulpinum	977		249	Penicillium viridicatum	1439	+
246	Ulocladium chartarum	487		249	Phoma exigua	968	
246	unknown	3422	+	249	Phoma exigua	484	+
246	unknown	1955		249	Scopulariopsis brevicaulis	484	
246	yeast	974		249	Trichoderma viride	479	
247	Acremonium sp.	4798		249	unknown	484	+
247	Alternaria alternata	4911		249	yeast	2902	
247	Aspergillus sydowii	4798		250	Alternaria alternata	3378	
247	Aspergillus versicolor	14508		250	Alternaria alternata	482	+
247	Aspergillus versicolor	4911	+	250	Aspergillus versicolor	1447	
247	Aureobasidium pullulans	330933	+	250	Aureobasidium pullulans	8687	+
247	Aureobasidium pullulans	110704		250	Aureobasidium pullulans	3861	
247	Cladosporium sphaerospermum	14621		250	Cladosporium cladosporioides	1447	+
247	Cladosporium sphaerospermum	9823	+	250	Eurotium herbariorum	482	+
247	Epicoccum nigrum	4798		250	Mucor racemosus	482	+
247	Fusarium sp.	9823	+	250	Penicillium citreonigrum	3861	
247	Mucor racemosus	9710	+	250	Penicillium citreonigrum	1447	+
247	Penicillium chrysogenum	43525	+	250	Penicillium commune	482	
247	Penicillium chrysogenum	24218		250	Penicillium spinulosum	482	
247	Penicillium expansum	43638	+	250	Ulocladium chartarum	482	+
247	Penicillium expansum	24331		250	unknown	1930	
247	Penicillium spinulosum	24218	+	250	yeast	13996	
247	Penicillium spinulosum	9710		251	Alternaria alternata	4793	
247	Ulocladium chartarum	9823		251	Alternaria alternata	473	+
247	unknown	29017	+	251	Aureobasidium pullulans	36056	+

HN	Identification	AVG CFU/g	G
251	Aureobasidium pullulans	28450	
251	Cladosporium cladosporioides	2374	+
251	Cladosporium cladosporioides	473	
251	Epicoccum nigrum	475	
251	Penicillium brevicompactum	475	
251	Penicillium commune	475	+
251	Penicillium italicum	475	+
251	Phoma herbarum	2369	
251	Sporobolomyces sp.	4277	
251	unknown	946	
251	unknown	473	+
251	Wallemia sebi	1420	+
253	Alternaria alternata	14404	
253	Alternaria alternata	2398	+
253	Aspergillus ochraceus	472	+
253	Aureobasidium pullulans	14816	
253	Aureobasidium pullulans	8589	+
253	Chrysonilia sitophila	957	+
253	Cladosporium cladosporioides	9630	+
253	Cladosporium cladosporioides	968	
253	Epicoccum nigrum	2422	
253	Epicoccum nigrum	472	+
253	Eurotium herbariorum	3355	+
253	Penicillium commune	472	
253	Penicillium hirsutum	1453	
253	Penicillium hirsutum	484	+
253	Penicillium sp. #64	7656	+
253	Penicillium sp. #64	7243	
253	unknown	4336	
256	Alternaria alternata	4854	+
256	Aspergillus ochraceus	21761	
256	Aspergillus ochraceus	19455	+
256	Aspergillus sp.	555906	
256	Aspergillus sp.	414939	+
256	Aspergillus sydowii	73195	+
256	Aspergillus sydowii	73119	
256	Aureobasidium pullulans	199713	+
256	Aureobasidium pullulans	73119	
256	Eurotium herbariorum	4854	+
256	Penicillium oxalicum	24347	
256	Penicillium oxalicum	14639	+
256	unknown	4892	
256	yeast	4854	
257	Alternaria alternata	5328	
257	Alternaria alternata	955	+
257	Aspergillus versicolor	2371	
257	Aspergillus versicolor	474	+
257	Cladosporium cladosporioides	474	+
257	Cladosporium sphaerospermum	474	+
257	Hormonema dematioides	474	
257	Mucor racemosus	5769	+
257	Penicillium corylophilum	955	+
257	Penicillium spinulosum	474	
257	Pithomyces chartarum	474	
257	Rhizopus oryzae	7692	
257	Rhizopus oryzae	474	+
257	unknown	1429	+
257	unknown	474	
257	Wallemia sebi	1423	+
257	yeast	1423	
258	Alternaria alternata	481	+
258	Aureobasidium pullulans	8179	
258	Aureobasidium pullulans	2890	+
258	Cladosporium sphaerospermum	493	
258	Coniothyrium sp.	481	
258	Eurotium herbariorum	974	+
258	Mucor racemosus	493	+
258	Penicillium chrysogenum	7843	
258	Penicillium chrysogenum	3887	+
258	Penicillium crustosum	974	
258	Penicillium crustosum	481	+
258	unknown	481	
258	yeast	481	
259	Alternaria alternata	1879	
259	Alternaria alternata	469	+
259	Aspergillus candidus	961	
259	Aspergillus flavus	480	
259	Aspergillus niger	1431	+
259	Aspergillus niger	469	
259	Aspergillus versicolor	480	+
259	Aspergillus versicolor	469	
259	Cladosporium cladosporioides	469	
259	Cladosporium sphaerospermum	950	
259	Eurotium herbariorum	1420	+
259	Gliocladium sp.	469	
259	Mucor racemosus	939	+
259	Mucor racemosus	469	
259	Paecilomyces variotii	1442	
259	Penicillium brevicompactum	950	
259	Penicillium brevicompactum	469	+
259	Penicillium chrysogenum	1879	
259	Penicillium citreonigrum	480	
259	Penicillium citrinum	1431	
259	Penicillium islandicum	480	
259	Penicillium miczynskii	469	
259	Penicillium restrictum	480	
259	Penicillium viridicatum	9409	
259	Penicillium viridicatum	480	+
259	Phoma herbarum	469	
259	unknown	950	+
259	unknown	469	
259	yeast	93963	
260	Alternaria alternata	21486	
260	Aspergillus glaucus	485	
260	Aspergillus sydowii	21844	
260	Aspergillus versicolor	17541	+
260	Aspergillus versicolor	8774	
260	Aureobasidium pullulans	7789	+
260	Epicoccum nigrum	485	+
260	Eurotium herbariorum	2926	+
260	Mucor sp.	488	
260	Penicillium chrysogenum	15582	
260	Penicillium chrysogenum	13155	+
260	Penicillium glandicola	1461	+
260	Penicillium glandicola	970	
260	Penicillium sp. #26	1456	
260	Penicillium sp. #26	488	+
260	Phoma herbarum	488	
260	Trichoderma viride	485	+
260	unknown	2438	
260	unknown	1953	+
260	yeast	26838	

HN	Identification	AVG CFU/g	G
261	Alternaria alternata	22879	
261	Alternaria alternata	478	+
261	Aureobasidium pullulans	8679	
261	Aureobasidium pullulans	7706	+
261	Cladosporium cladosporioides	478	+
261	Penicillium chrysogenum	478	+
261	Penicillium oxalicum	486	
261	Penicillium purpurogenum	964	
261	Penicillium sp.	1945	
261	Penicillium viridicatum	1450	+
261	Penicillium vulpinum	2398	
261	Phoma herbarum	478	
261	Phoma sp.	486	
261	unknown	478	
261	yeast	964	
262	Alternaria alternata	284	
262	Aureobasidium pullulans	1442	
262	Aureobasidium pullulans	853	+
262	Cladosporium sp.	94	+
262	Eurotium herbariorum	96	+
262	Penicillium citreonigrum	189	+
262	Penicillium commune	191	
262	Penicillium commune	94	+
262	Penicillium raistrickii	287	+
262	Penicillium raistrickii	191	
262	Penicillium vulpinum	289	
262	Scopulariopsis brevicaulis	189	
262	unknown	382	
263	Alternaria alternata	575	
263	Aspergillus ochraceus	96	
263	Aspergillus versicolor	381	
263	Aspergillus versicolor	189	+
263	Aureobasidium pullulans	2094	
263	Aureobasidium pullulans	1244	+
263	Cladosporium cladosporioides	378	+
263	Cladosporium sphaerospermum	192	+
263	Cladosporium sphaerospermum	96	
263	Curvularia senegalensis	94	
263	Epicoccum nigrum	189	
263	Eurotium herbariorum	94	+
263	Mucor racemosus	96	+
263	Penicillium brevicompactum	763	+
263	Penicillium brevicompactum	287	
263	Penicillium raistrickii	671	+
263	Penicillium raistrickii	665	
263	Penicillium spinulosum	94	
263	Penicillium viridicatum	94	
263	Scopulariopsis candida	96	
263	Sordaria sp.	192	
264	Alternaria alternata	2424	
264	Alternaria alternata	1457	+
264	Aspergillus ochraceus	484	
264	Aspergillus versicolor	970	
264	Aureobasidium pullulans	95935	
264	Aureobasidium pullulans	2916	+
264	Eurotium herbariorum	1455	+
264	Mucor racemosus	486	
264	Penicillium brevicompactum	486	+
264	Penicillium spinulosum	486	+
264	Phoma herbarum	486	
264	Trichoderma viride	486	
264	unknown	1945	+
264	unknown	1939	
264	yeast	106191	
265	Aspergillus niger	149594	
265	Aspergillus niger	62659	+
265	Aureobasidium pullulans	72424	
265	Aureobasidium pullulans	38499	+
265	Cladosporium cladosporioides	19305	+
265	Penicillium sp. #26	4854	
265	Phoma sp.	9652	+
265	Stemphylium sp.	4854	+
265	unknown	9596	
266	Aspergillus versicolor	4970	
266	Aureobasidium pullulans	88376	
266	Aureobasidium pullulans	72379	+
266	Cladosporium cladosporioides	33704	
266	Cladosporium cladosporioides	28734	+
266	Cladosporium sphaerospermum	9940	
266	Epicoccum nigrum	4970	
266	Mucor racemosus	4752	
266	Penicillium brevicompactum	4752	
266	Penicillium chrysogenum	14910	+
266	Penicillium chrysogenum	9940	
266	Penicillium sp. #26	4970	
266	Penicillium spinulosum	19446	+
266	Penicillium spinulosum	9940	
266	unknown	19663	+
266	unknown	19011	
267	Alternaria alternata	2869	+
267	Alternaria alternata	2389	
267	Aspergillus niger	477	
267	Aspergillus versicolor	478	
267	Aspergillus versicolor	478	+
267	Aureobasidium pullulans	16263	
267	Aureobasidium pullulans	12912	+
267	Cladosporium cladosporioides	956	
267	Cladosporium cladosporioides	477	+
267	Epicoccum nigrum	1436	
267	Eurotium herbariorum	1910	+
267	Geomyces sp.	477	
267	Penicillium decumbens	954	
267	Penicillium expansum	2392	+
267	Penicillium expansum	478	
267	Penicillium sp. #26	477	+
267	Ulocladium chartarum	478	
267	unknown	477	
267	yeast	2389	
269	Alternaria alternata	1911	+
269	Alternaria alternata	1909	
269	Aureobasidium pullulans	29525	+
269	Aureobasidium pullulans	24252	
269	Cladosporium cladosporioides	3325	+
269	Cladosporium sp.	2846	+
269	Epicoccum nigrum	957	
269	Fusarium sp.	474	
269	Mucor racemosus	474	
269	Penicillium crustosum	30040	
269	Penicillium crustosum	27623	+
269	Penicillium echinulatum	2381	
269	Penicillium griseofulvum	478	
269	Penicillium viridicatum	2394	+

HN	Identification	AVG CFU/g	G
269	Penicillium viridicatum	953	
269	Phoma herbarum	957	
269	Phoma sp.	948	+
269	Phoma sp.	474	
269	Ulocladium chartarum	478	
269	unknown	2855	
270	Alternaria alternata	6713	
270	Alternaria alternata	3838	+
270	Aspergillus niger	479	+
270	Aureobasidium pullulans	15405	+
270	Aureobasidium pullulans	14919	
270	Cladosporium cladosporioides	5303	+
270	Cladosporium sphaerospermum	1442	+
270	Epicoccum nigrum	1442	
270	Eurotium herbariorum	479	+
270	Penicillium aurantiogriseum	482	
270	Penicillium brevicompactum	482	+
270	Penicillium commune	7696	
270	Penicillium commune	7222	+
270	Penicillium miczynskii	479	+
270	Penicillium spinulosum	962	+
270	Penicillium spinulosum	479	
270	Phoma sp.	1447	
270	unknown	1445	
270	yeast	962	
271	Alternaria alternata	11318	+
271	Alternaria alternata	8966	
271	Aureobasidium pullulans	134512	
271	Aureobasidium pullulans	65948	+
271	Cladosporium cladosporioides	1869	+
271	Cladosporium cladosporioides	950	
271	Cladosporium sphaerospermum	934	
271	Cladosporium sphaerospermum	475	+
271	Epicoccum nigrum	5196	
271	Epicoccum nigrum	1885	+
271	Fusarium sp.	3802	
271	Gliocladium sp.	1885	
271	Mucor plumbeus	475	+
271	Mucor racemosus	1417	+
271	Mucor racemosus	475	
271	Penicillium corylophilum	3287	
271	Penicillium oxalicum	2851	
271	Penicillium viridicatum	3794	+
271	Penicillium viridicatum	942	
271	Phoma herbarum	4229	
271	Trichoderma sp.	475	+
271	unknown	2827	+
271	unknown	1869	
271	yeast	3778	
272	Alternaria alternata	4417	+
272	Alternaria alternata	2944	
272	Aspergillus niger	493	+
272	Aspergillus sp.	490	
272	Aspergillus sydowii	493	
272	Aspergillus sydowii	490	+
272	Aspergillus versicolor	986	
272	Aspergillus versicolor	490	+
272	Aureobasidium pullulans	25530	+
272	Aureobasidium pullulans	17194	
272	Cladosporium cladosporioides	3440	+
272	Cladosporium cladosporioides	1470	
272	Cladosporium herbarum	2462	
272	Cladosporium herbarum	493	+
272	Cladosporium sphaerospermum	493	
272	Cladosporium sphaerospermum	493	+
272	Eurotium herbariorum	2450	+
272	Mucor racemosus	490	
272	Penicillium chrysogenum	2952	+
272	Penicillium chrysogenum	493	
272	Penicillium citrinum	983	
272	Penicillium spinulosum	980	
272	Penicillium spinulosum	490	+
272	Phoma sp.	980	+
272	Phoma sp.	493	
272	Stachybotrys chartarum	490	
272	unknown	1969	
273	Alternaria alternata	17974	
273	Alternaria alternata	8544	+
273	Aspergillus niger	951	
273	Aureobasidium pullulans	23318	+
273	Aureobasidium pullulans	15636	
273	Cladosporium cladosporioides	6140	+
273	Cladosporium sphaerospermum	1422	
273	Epicoccum nigrum	961	
273	Eurotium herbariorum	480	+
273	Paecilomyces variotii	470	+
273	Penicillium brevicompactum	470	+
273	Penicillium coprophilum	480	+
273	Penicillium digitatum	2864	
273	Penicillium expansum	6671	
273	Penicillium expansum	4737	+
273	Penicillium spinulosum	1913	
273	Penicillium vulpinum	1893	+
273	Penicillium vulpinum	1432	
273	Phoma herbarum	470	+
273	Phoma sp.	2824	+
273	Scopulariopsis brevicaulis	480	
273	unknown	1432	
274	Alternaria alternata	1466	+
274	Alternaria alternata	976	
274	Aspergillus sp.	489	+
274	Aureobasidium pullulans	2443	+
274	Cladosporium cladosporioides	978	
274	Cladosporium cladosporioides	489	+
274	Emericella nidulans	488	
274	Epicoccum nigrum	977	
274	Mucor plumbeus	1466	
274	Mucor plumbeus	489	+
274	Penicillium brevicompactum	489	+
274	Penicillium chrysogenum	1465	+
274	Rhizopus stolonifer	489	+
274	unknown	2444	
274	unknown	1956	+
274	yeast	8311	
276	Acremonium sp.	21596	
276	Alternaria alternata	9505	
276	Aspergillus versicolor	4798	+
276	Aureobasidium pullulans	807200	+
276	Aureobasidium pullulans	114524	
276	Cladosporium cladosporioides	4752	+
276	Eurotium herbariorum	19057	+
276	Mucor plumbeus	4798	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
276	Mucor plumbeus	4798	+	281	Alternaria alternata	5803	+
276	Penicillium chrysogenum	14304	+	281	Alternaria alternata	4843	
276	Penicillium chrysogenum	9596		281	Aspergillus ochraceus	479	
276	Penicillium restrictum	4752	+	281	Aspergillus versicolor	33401	
276	Penicillium sp. #26	4798		281	Aspergillus versicolor	22327	+
276	yeast	23992		281	Aureobasidium pullulans	27943	+
278	Alternaria alternata	3358	+	281	Aureobasidium pullulans	10638	
278	Alternaria alternata	1921		281	Cladosporium cladosporioides	1949	+
278	Aspergillus niger	478		281	Cladosporium cladosporioides	974	
278	Aureobasidium pullulans	17814	+	281	Cladosporium sphaerospermum	479	+
278	Aureobasidium pullulans	12524		281	Epicoccum nigrum	974	+
278	Cladosporium cladosporioides	957	+	281	Epicoccum nigrum	487	
278	Cladosporium cladosporioides	484		281	Eurotium herbariorum	479	+
278	Cladosporium sphaerospermum	478		281	Microsphaeropsis olivaceus	1919	+
278	Cladosporium sphaerospermum	478	+	281	Mucor plumbeus	487	
278	Epicoccum nigrum	2884		281	Penicillium corylophilum	1941	
278	Penicillium chrysogenum	1442	+	281	Penicillium digitatum	974	+
278	Penicillium chrysogenum	963		281	Penicillium digitatum	479	
278	Penicillium islandicum	957	+	281	Scopulariopsis candida	479	
278	Penicillium islandicum	478		281	Ulocladium chartarum	479	+
278	Penicillium oxalicum	963		281	unknown	959	+
278	Phoma herbarum	11015		281	unknown	479	
278	Phoma sp.	478	+	281	yeast	3891	
278	unknown	963	+	282	Alternaria alternata	23713	
278	unknown	484		282	Alternaria alternata	494	+
278	yeast	1921		282	Aspergillus sydowii	491	
279	Alternaria alternata	14734		282	Aureobasidium pullulans	19684	+
279	Alternaria alternata	4911	+	282	Candida sp.	8399	
279	Aureobasidium pullulans	44204	+	282	Cladosporium cladosporioides	494	+
279	Aureobasidium pullulans	14734		282	Cladosporium cladosporioides	491	
279	Cladosporium cladosporioides	29241	+	282	Cladosporium sphaerospermum	982	
279	Epicoccum nigrum	4911	+	282	Epicoccum nigrum	2467	
279	Epicoccum nigrum	4835		282	Eurotium herbariorum	491	+
279	Penicillium chrysogenum	272161	+	282	Mucor plumbeus	491	+
279	Penicillium chrysogenum	267705		282	Penicillium chrysogenum	5408	+
279	Penicillium glandicola	9671		282	Penicillium glandicola	4423	
279	unknown	24405		282	Penicillium implicatum	988	
280	Alternaria alternata	968		282	Penicillium spinulosum	2952	+
280	Aspergillus sp.	484	+	282	Phoma sp.	988	+
280	Aspergillus versicolor	2862	+	282	unknown	1970	
280	Aspergillus versicolor	2389		282	Wallemia sebi	3929	+
280	Aureobasidium pullulans	2378		282	yeast	191530	
280	Cladosporium cladosporioides	484	+	283	Alternaria alternata	474	+
280	Eurotium herbariorum	3380	+	283	Alternaria citri	183241	
280	Gliomastix murorum var. murorum	8071		283	Aspergillus sp.	1430	+
280	Mucor plumbeus	473	+	283	Aspergillus sp.	481	
280	Paecilomyces variotii	484	+	283	Aureobasidium pullulans	7210	+
280	Paecilomyces variotii	473		283	Cladosporium cladosporioides	2379	+
280	Penicillium aurantiogriseum	2895		283	Cladosporium herbarum	2393	+
280	Penicillium aurantiogriseum	484	+	283	Curvularia prasadii	2408	
280	Penicillium brevicompactum	957	+	283	Epicoccum nigrum	481	
280	Penicillium chrysogenum	1453	+	283	Eurotium herbariorum	2401	+
280	Penicillium chrysogenum	1420		283	Paecilomyces variotii	474	
280	Penicillium citrinum	484		283	Penicillium aurantiogriseum	10502	
280	Penicillium citrinum	484	+	283	Penicillium aurantiogriseum	474	+
280	Penicillium purpurogenum	484		283	Penicillium brevicompactum	948	+
280	Penicillium sp. #26	4294		283	Penicillium brevicompactum	481	
280	Penicillium sp. #26	2884	+	283	Penicillium chrysogenum	4269	
280	unknown	5252	+	283	Penicillium commune	14311	+
280	unknown	4316		283	Penicillium commune	2401	
280	yeast	10119		283	Penicillium corylophilum	956	

HN	Identification	AVG CFU/g	G
283	Penicillium glandicola	1926	
283	Penicillium glandicola	474	+
283	Penicillium hirsutum	4306	+
283	Penicillium hirsutum	4291	
283	Penicillium implicatum	1430	+
283	Penicillium raistrickii	956	+
283	Penicillium simplicissimum	963	
283	Penicillium sp. #87	2379	
283	Phoma sp.	474	
283	Pithomyces sp.	948	+
283	Rhizopus oryzae	481	+
283	unknown	7174	+
283	unknown	3824	
283	yeast	10487	
284	Alternaria alternata	20365	
284	Alternaria alternata	9784	+
284	Aureobasidium pullulans	53392	
284	Aureobasidium pullulans	48584	+
284	Cladosporium cladosporioides	29269	+
284	Cladosporium sphaerospermum	14507	+
284	Epicoccum nigrum	4807	+
284	Paecilomyces variotii	4892	
284	Penicillium commune	9784	
284	Penicillium spinulosum	9615	
284	Penicillium spinulosum	4892	+
284	Phoma medicaginis	14592	
284	Trichoderma viride	4807	
284	unknown	33992	
284	unknown	14592	+
284	Wallemia sebi	44031	+
284	yeast	33738	
285	Alternaria alternata	9655	+
285	Aspergillus versicolor	4743	+
285	Aureobasidium pullulans	48792	
285	Aureobasidium pullulans	14399	+
285	Mucor plumbeus	4743	
285	Penicillium aurantiogriseum	29301	
285	Penicillium aurantiogriseum	4743	+
285	Penicillium chrysogenum	96050	+
285	Penicillium chrysogenum	77578	
285	Penicillium spinulosum	19310	+
285	Penicillium spinulosum	9655	
285	unknown	14567	
285	yeast	4911	
286	Alternaria alternata	5698	
286	Alternaria alternata	1914	+
286	Aspergillus sydowii	479	
286	Aureobasidium pullulans	7641	
286	Aureobasidium pullulans	7129	+
286	Doratomyces microsporus	2399	
286	Epicoccum nigrum	1425	+
286	Eurotium herbariorum	475	+
286	Fusarium sp.	1901	
286	Penicillium glandicola	479	
286	Penicillium griseofulvum	22438	+
286	Penicillium griseofulvum	16703	
286	Penicillium roquefortii	1919	
286	Trichoderma sp.	475	+
286	Trichoderma viride	475	
286	yeast	18152	
287	Alternaria alternata	11041	
287	Aspergillus fumigatus	480	+
287	Aspergillus versicolor	481	+
287	Aureobasidium pullulans	18297	+
287	Aureobasidium pullulans	9625	
287	Cladosporium cladosporioides	481	
287	Cladosporium cladosporioides	481	+
287	Penicillium chrysogenum	14929	+
287	Penicillium chrysogenum	10587	
287	Penicillium sp. #26	1445	
287	Penicillium sp. #26	480	+
287	Penicillium viridicatum	7704	
287	Penicillium viridicatum	5779	+
287	Sporobolomyces sp.	480	
287	unknown	2888	
287	yeast	480	
288	Acremonium sp.	478	
288	Alternaria alternata	3356	
288	Alternaria alternata	966	+
288	Aspergillus sydowii	956	+
288	Aspergillus versicolor	29477	+
288	Aspergillus versicolor	27585	
288	Aureobasidium pullulans	11209	+
288	Aureobasidium pullulans	8696	
288	Cladosporium cladosporioides	1912	+
288	Cladosporium sphaerospermum	478	+
288	Emericella nidulans	478	
288	Emericella nidulans	478	+
288	Epicoccum nigrum	478	
288	Eurotium herbariorum	11574	+
288	Fusarium sp.	4322	
288	Fusarium sp.	1434	+
288	Penicillium chrysogenum	5777	
288	Penicillium chrysogenum	1444	+
288	Penicillium citreonigrum	488	+
288	Penicillium sp. #26	3865	
288	Penicillium sp. #26	478	+
288	Penicillium spinulosum	1464	+
288	Penicillium viridicatum	488	+
288	Phoma sp.	956	
288	yeast	966	
289	Alternaria alternata	3036	+
289	Alternaria alternata	1016	
289	Aspergillus niger	502	
289	Aspergillus niger	502	+
289	Aspergillus ochraceus	514	+
289	Cladosporium cladosporioides	3049	+
289	Fusarium sp.	514	+
289	Leptosphaerulina australis	1016	
289	Leptosphaerulina australis	514	+
289	Paecilomyces fulva	514	+
289	Penicillium citrinum	502	
289	Penicillium echinulatum	1004	+
289	Penicillium implicatum	1016	+
289	Penicillium implicatum	514	
289	Phoma eupyrena	2032	+
289	Phoma glomerata	1028	+
289	Trichoderma viride	514	
289	unknown	5571	+
289	unknown	5559	
289	yeast	1518	
290	Aspergillus versicolor	489	+

HN	Identification	AVG CFU/g	G
290	Emericella nidulans	46661	
290	Emericella nidulans	973	+
290	Eurotium herbariorum	973	+
290	Penicillium chrysogenum	1458	
290	Penicillium chrysogenum	484	+
290	Penicillium citreonigrum	3909	+
290	Penicillium citreonigrum	1467	
290	Trichoderma viride	489	+
290	unknown	2921	+
290	unknown	1458	
290	yeast	5367	
291	Alternaria alternata	1920	
291	Alternaria alternata	976	+
291	Aureobasidium pullulans	18864	+
291	Aureobasidium pullulans	16556	
291	Cladosporium cladosporioides	1431	+
291	Cladosporium herbarum	965	+
291	Cladosporium herbarum	477	
291	Epicoccum nigrum	488	
291	Eurotium herbariorum	1442	+
291	Geomyces pannorum	3350	
291	Mucor racemosus	2929	+
291	Mucor racemosus	2419	
291	Penicillium citrinum	477	
291	Penicillium corylophilum	488	
291	Penicillium corylophilum	488	+
291	Penicillium sp. #64	976	+
291	Penicillium sp. #64	477	
291	Phoma chrysanthemicola	9553	+
291	Phoma chrysanthemicola	954	
291	Phoma herbarum	954	
291	unknown	3373	
291	unknown	477	+
291	yeast	1953	
292	Acremonium sp.	2859	
292	Alternaria alternata	1910	
292	Alternaria alternata	974	+
292	Aspergillus niger	474	
292	Aspergillus ochraceus	2410	+
292	Aspergillus ochraceus	1936	
292	Aspergillus sp.	487	+
292	Aspergillus sp.	474	
292	Aspergillus sydowii	487	
292	Aspergillus sydowii	487	+
292	Aspergillus versicolor	2436	
292	Aspergillus versicolor	474	+
292	Aureobasidium pullulans	41250	
292	Aureobasidium pullulans	40456	+
292	Cladosporium cladosporioides	1436	+
292	Eurotium herbariorum	1423	+
292	Mucor plumbeus	487	
292	Penicillium griseofulvum	18811	+
292	Penicillium griseofulvum	7680	
292	Penicillium sp. #26	1461	
292	Penicillium sp. #26	487	+
292	Penicillium spinulosum	2410	
292	Penicillium spinulosum	1461	+
292	Rhizopus oryzae	474	+
292	unknown	974	+
292	unknown	487	
292	yeast	2885	
294	Aspergillus ochraceus	481	+
294	Aspergillus ustus	969	+
294	Aureobasidium pullulans	487	+
294	Penicillium chrysogenum	487	
294	Penicillium spinulosum	11084	+
294	Penicillium spinulosum	5780	
294	Penicillium viridicatum	1450	+
294	unknown	487	+
294	unknown	481	
294	yeast	29020	
296	Alternaria alternata	1945	
296	Coniothyrium sporulosum	16924	
296	Coniothyrium sporulosum	11121	+
296	Eurotium herbariorum	957	+
296	Fusarium sp.	478	
296	Paecilomyces variotii	483	
296	Penicillium griseofulvum	967	+
296	Pestalotiopsis sp.	483	+
296	Scytalidium sp.	1441	
296	unknown	6760	
296	unknown	962	+
296	Wallemia sebi	483	+
296	yeast	478	
297	Aureobasidium pullulans	52859	
297	Aureobasidium pullulans	4761	+
297	Cladosporium cladosporioides	4761	+
297	Coniothyrium sp.	90476	+
297	Coniothyrium sp.	71428	
297	Penicillium vulpinum	4761	
297	Penicillium vulpinum	4761	+
297	Trichoderma viride	4761	+
297	unknown	423809	+
298	Aspergillus ochraceus	473	
298	Aspergillus ustus	475	+
298	Aureobasidium pullulans	1422	
298	Penicillium chrysogenum	475	
298	Penicillium corylophilum	2371	+
298	Penicillium corylophilum	948	
298	Penicillium sp. #26	473	+
298	Penicillium spinulosum	475	+
298	Phoma herbarum	946	+
298	unknown	473	
298	yeast	147781	
299	Alternaria alternata	14186	+
299	Aspergillus sp.	16620	
299	Aureobasidium pullulans	4716	+
299	Cladosporium sp.	4752	
299	Cladosporium sp.	4752	+
299	Eurotium herbariorum	4752	+
299	Graphium sp.	4752	+
299	Oidiodendron rhodogenum	14258	
299	Ophiostoma sp.	18867	
299	Penicillium aurantiogriseum	9469	
299	Penicillium vulpinum	18939	
299	Penicillium vulpinum	9433	+
299	Phoma chrysanthemicola	4716	
299	unknown	28445	+
299	unknown	18903	
299	yeast	9469	
300	Alternaria alternata	15235	
300	Alternaria alternata	2435	+

HN	Identification	AVG CFU/g	G
300	Aspergillus ustus	488	
300	Aspergillus versicolor	1462	+
300	Aureobasidium pullulans	486	
300	Aureobasidium pullulans	486	+
300	Cladosporium cladosporioides	1949	
300	Cladosporium cladosporioides	1462	+
300	Cladosporium herbarum	972	+
300	Cladosporium sphaerospermum	1945	+
300	Cladosporium sphaerospermum	1459	
300	Epicoccum nigrum	1949	+
300	Oidiodendron sp.	972	
300	Penicillium chrysogenum	976	+
300	Penicillium corylophilum	1951	+
300	Penicillium corylophilum	976	
300	Penicillium sp.	486	
300	Scopulariopsis candida	488	
300	Trichoderma viride	1459	
300	unknown	2437	+
300	unknown	2435	
300	yeast	10706	
301	Alternaria alternata	32180	
301	Alternaria alternata	14832	+
301	Aspergillus glaucus	4970	+
301	Aspergillus versicolor	4892	+
301	Eurotium herbariorum	9862	+
301	Penicillium brevicompactum	4970	
301	Penicillium chrysogenum	4970	+
301	Penicillium chrysogenum	4892	
301	Penicillium spinulosum	9940	+
301	Phoma sp.	4970	
301	Pithomyces chartarum	4892	
301	Rhizopus oryzae	19647	
302	Alternaria alternata	22998	
302	Alternaria alternata	10037	+
302	Aspergillus fumigatus	958	
302	Aspergillus niger	471	
302	Aspergillus ornatus	3331	+
302	Aspergillus ornatus	486	
302	Aspergillus sp.	471	+
302	Aspergillus sydowii	486	
302	Aureobasidium pullulans	29170	
302	Aureobasidium pullulans	16788	+
302	Cladosporium cladosporioides	7178	+
302	Cladosporium cladosporioides	1930	
302	Cladosporium herbarum	471	
302	Cladosporium sphaerospermum	486	
302	Epicoccum nigrum	4289	
302	Epicoccum nigrum	1444	+
302	Eurotium herbariorum	7148	+
302	Penicillium aurantiogriseum	1916	+
302	Penicillium aurantiogriseum	958	
302	Penicillium spinulosum	2844	
302	Penicillium spinulosum	471	+
302	Phoma herbarum	486	
302	Phoma herbarum	486	+
302	unknown	958	
302	yeast	2844	
304	Alternaria alternata	3371	
304	Alternaria alternata	2394	+
304	Aspergillus glaucus	478	
304	Aspergillus ochraceus	481	
304	Aspergillus sp.	478	+
304	Aspergillus versicolor	957	
304	Aureobasidium pullulans	8177	
304	Aureobasidium pullulans	5284	+
304	Cladosporium cladosporioides	3371	+
304	Cladosporium sphaerospermum	1442	+
304	Eurotium herbariorum	3366	+
304	Fusarium sp.	1439	
304	Microsphaeropsis olivaceus	960	
304	Microsphaeropsis olivaceus	481	+
304	Mucor plumbeus	481	
304	Penicillium chrysogenum	963	+
304	Penicillium corylophilum	481	+
304	Penicillium spinulosum	481	+
304	Sordaria sp.	960	
304	Trichoderma viride	963	
304	unknown	1442	+
304	unknown	478	
304	Wallemia sebi	25480	+
304	yeast	21618	
305	Alternaria alternata	15891	
305	Alternaria alternata	14258	+
305	Aspergillus sydowii	9881	+
305	Aspergillus sydowii	4752	
305	Aspergillus versicolor	29268	
305	Aspergillus versicolor	14822	+
305	Cladosporium cladosporioides	4940	
305	Cladosporium sp.	4752	+
305	Phoma sp.	9505	
305	Pithomyces chartarum	4940	
305	unknown	14258	
305	unknown	14258	+
305	yeast	9505	
306	Acremonium rutilum	477	
306	Alternaria alternata	1431	
306	Alternaria alternata	477	+
306	Aspergillus niger	477	+
306	Aspergillus sydowii	959	+
306	Aureobasidium pullulans	1924	+
306	Cladosporium cladosporioides	3350	+
306	Cladosporium sphaerospermum	1436	+
306	Epicoccum nigrum	477	
306	Eurotium herbariorum	1913	+
306	Mucor racemosus	482	
306	Paecilomyces inflatus	954	
306	Penicillium aurantiogriseum	959	+
306	Penicillium brevicompactum	959	+
306	Penicillium brevicompactum	482	
306	Penicillium commune	2879	
306	Penicillium expansum	2402	+
306	Penicillium sp.	482	
306	Penicillium spinulosum	3827	
306	Penicillium spinulosum	959	+
306	Penicillium viridicatum	959	
306	Penicillium viridicatum	477	+
306	Phoma sp.	89762	
306	Phoma sp.	53088	+
306	Trichoderma viride	2402	
306	Trichoderma viride	2402	+
306	unknown	5275	+
306	unknown	2879	

HN	Identification	AVG CFU/g	G
306	Wallemia sebi	965	+
306	yeast	6690	
307	Alternaria alternata	1457	
307	Aspergillus versicolor	490	
307	Aureobasidium pullulans	13739	
307	Aureobasidium pullulans	490	+
307	Cladosporium cladosporioides	1470	
307	Epicoccum nigrum	1470	+
307	Epicoccum nigrum	491	
307	Eurotium herbariorum	981	+
307	Penicillium spinulosum	981	+
307	Phoma herbarum	491	
307	Sphaeropsis sp.	491	
307	unknown	980	
307	unknown	490	+
307	yeast	3436	
309	Alternaria alternata	33358	
309	Alternaria alternata	4743	+
309	Aspergillus niger	4734	
309	Aureobasidium pullulans	9487	+
309	Cladosporium herbarum	4743	
309	Cladosporium herbarum	4734	+
309	Cladosporium sp.	4734	
309	Cladosporium sp.	4734	+
309	Cladosporium sphaerospermum	9469	+
309	Epicoccum nigrum	4743	+
309	Epicoccum nigrum	4734	
309	Fusarium oxysporum	4743	
309	Fusarium oxysporum	4743	+
309	Myrothecium sp.	4743	
309	Penicillium chrysogenum	4743	+
309	Penicillium expansum	4743	
309	Penicillium spinulosum	9469	
309	Penicillium spinulosum	4734	+
309	Phoma sp.	9487	
309	unknown	14231	
309	yeast	56872	
310	Alternaria alternata	56526	
310	Alternaria alternata	4403	+
310	Aspergillus candidus	489	+
310	Aspergillus versicolor	489	+
310	Aureobasidium pullulans	49653	
310	Aureobasidium pullulans	42886	+
310	Cladosporium cladosporioides	2408	+
310	Cladosporium cladosporioides	1445	
310	Cladosporium sphaerospermum	970	+
310	Cladosporium sphaerospermum	963	
310	Fusarium sp.	481	+
310	Penicillium expansum	3409	+
310	Penicillium expansum	489	
310	Rhizopus oryzae	970	
310	unknown	1445	
310	yeast	5374	
311	Alternaria alternata	13114	
311	Alternaria alternata	5339	+
311	Aspergillus cervinus	1957	+
311	Aspergillus ochraceus	1456	
311	Aspergillus terreus	986	
311	Aspergillus versicolor	3891	+
311	Aureobasidium pullulans	89325	
311	Aureobasidium pullulans	34718	+
311	Cladosporium cladosporioides	3405	+
311	Cladosporium cladosporioides	1941	
311	Cladosporium sphaerospermum	986	
311	Cladosporium sphaerospermum	986	+
311	Epicoccum nigrum	493	
311	Eurotium herbariorum	4368	+
311	Fusarium oxysporum	1456	
311	Fusarium sp.	1972	
311	Fusarium sp.	493	+
311	Paecilomyces variotii	485	
311	Penicillium corylophilum	2457	+
311	Penicillium expansum	978	+
311	Phoma sp.	4384	
311	Phoma sp.	1463	+
311	Rhizopus oryzae	493	
311	Scopulariopsis brevicaulis	970	+
311	Ulocladium chartarum	493	+
312	Alternaria alternata	2614	
312	Aspergillus versicolor	1307	
312	Aspergillus versicolor	663	+
312	Aureobasidium pullulans	14494	
312	Aureobasidium pullulans	8489	+
312	Cladosporium herbarum	1989	+
312	Fusarium sp.	663	+
312	Mucor racemosus	1288	
312	Mucor racemosus	663	+
312	Penicillium aurantiogriseum	3922	+
312	Penicillium aurantiogriseum	1951	
312	unknown	1326	
313	Alternaria alternata	496	
313	Aspergillus niger	992	+
313	Aspergillus sp.	497	
313	Aspergillus ustus	992	+
313	Aspergillus ustus	496	
313	Aspergillus versicolor	993	
313	Aspergillus versicolor	497	+
313	Aureobasidium pullulans	496	
313	Cladosporium cladosporioides	496	
313	Eurotium herbariorum	1491	+
313	Mucor plumbeus	2481	
313	Mucor plumbeus	1491	+
313	Penicillium chrysogenum	19365	+
313	Penicillium chrysogenum	11918	
313	Penicillium commune	2483	+
313	Penicillium sp.	496	
313	Penicillium spinulosum	1490	
313	Penicillium spinulosum	992	+
313	unknown	1490	
315	Alternaria alternata	978	
315	Alternaria alternata	484	+
315	Aspergillus candidus	978	+
315	Aspergillus fumigatus	988	+
315	Aspergillus sp.	494	+
315	Aspergillus sydowii	1482	
315	Aspergillus versicolor	1966	+
315	Aureobasidium pullulans	4854	
315	Aureobasidium pullulans	484	+
315	Eurotium herbariorum	494	+
315	unknown	494	
315	unknown	484	+
315	yeast	153767	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
316	Alternaria alternata	478	+	319	Epicoccum nigrum	1915	
316	Aspergillus flavus	2403	+	319	Eurotium herbariorum	962	+
316	Aspergillus fumigatus	92371		319	Mucor plumbeus	478	+
316	Aspergillus sydowii	2884		319	Penicillium brevicompactum	2896	
316	Aspergillus sydowii	480	+	319	Penicillium chrysogenum	8671	
316	Aspergillus versicolor	480	+	319	Penicillium chrysogenum	8188	+
316	Cladosporium cladosporioides	478	+	319	Penicillium islandicum	483	+
316	Epicoccum nigrum	1439		319	Phoma herbarum	967	
316	Eurotium herbariorum	1914	+	319	Phoma herbarum	478	+
316	Mucor racemosus	480	+	319	Trichoderma viride	483	
316	Penicillium chrysogenum	1439	+	319	unknown	1920	
316	Penicillium citreonigrum	1917		320	Acremonium sp.	961	+
316	Penicillium citreonigrum	958	+	320	Alternaria alternata	5329	
316	Penicillium commune	4791	+	320	Alternaria alternata	1459	+
316	Penicillium commune	2398		320	Aspergillus niger	480	
316	Penicillium decumbens	1917	+	320	Aspergillus ochraceus	480	+
316	Pithomyces chartarum	956		320	Aureobasidium pullulans	6370	
316	Pithomyces chartarum	480	+	320	Aureobasidium pullulans	6336	+
316	Trichoderma viride	3829		320	Cladosporium herbarum	1476	
316	Trichoderma viride	1439	+	320	Cladosporium sphaerospermum	498	+
316	unknown	1917		320	Epicoccum nigrum	1476	+
316	yeast	3357		320	Eurotium herbariorum	1940	+
317	Alternaria alternata	4716	+	320	Eurotium herbariorum	498	
317	Aspergillus ustus	14150	+	320	Paecilomyces variotii	978	
317	Aspergillus ustus	9671		320	Penicillium chrysogenum	1459	
317	Aspergillus versicolor	42808	+	320	Phoma herbarum	1923	
317	Aspergillus versicolor	18867		320	Phoma sp.	996	
317	Cladosporium cladosporioides	9433	+	320	unknown	978	
317	Epicoccum nigrum	9433	+	320	yeast	978	
317	Penicillium chrysogenum	19105		322	Alternaria alternata	4801	
317	Penicillium chrysogenum	14269	+	322	Alternaria alternata	3327	+
317	Penicillium expansum	9433		322	Aspergillus sp.	1133	
317	unknown	9433		322	Aspergillus sp.	542	+
318	Alternaria alternata	1391	+	322	Aspergillus ustus	542	
318	Aspergillus versicolor	3561	+	322	Aspergillus versicolor	1651	+
318	Aspergillus versicolor	1002		322	Aureobasidium pullulans	1626	
318	Cladosporium cladosporioides	1391	+	322	Aureobasidium pullulans	542	+
318	Cladosporium sp.	501	+	322	Cladosporium cladosporioides	3327	+
318	Cladosporium sp.	389		322	Cladosporium cladosporioides	566	
318	Cladosporium sphaerospermum	1279	+	322	Cladosporium herbarum	1109	
318	Cladosporium sphaerospermum	501		322	Epicoccum nigrum	1626	
318	Eurotium herbariorum	389	+	322	Epicoccum nigrum	542	+
318	Mucor racemosus	389		322	Fusarium sp.	2169	+
318	Penicillium italicum	389		322	Fusarium sp.	1133	
318	Phoma sp.	389		322	Mucor racemosus	566	+
318	Stemphylium sp.	1168	+	322	Myrothecium sp.	1084	
318	Ulocladium chartarum	501		322	Paecilomyces variotii	2218	+
318	unknown	1669		322	Penicillium brevicompactum	566	+
318	unknown	1503	+	322	Penicillium chrysogenum	1109	
318	yeast	3338		322	Penicillium chrysogenum	1109	+
319	Alternaria alternata	11555		322	Penicillium citrinum	566	+
319	Alternaria alternata	1450	+	322	Scopulariopsis candida	1084	
319	Aspergillus ochraceus	483	+	322	unknown	3352	
319	Aspergillus ochraceus	478		322	unknown	2242	+
319	Aspergillus versicolor	1446		322	yeast	21592	
319	Aureobasidium pullulans	19770		323	Alternaria alternata	19255	
319	Aureobasidium pullulans	7220	+	323	Aspergillus restrictus	73964	+
319	Cladosporium cladosporioides	478	+	323	Aspergillus restrictus	4882	
319	Cladosporium herbarum	478		323	Aureobasidium pullulans	64102	+
319	Cladosporium sphaerospermum	483	+	323	Cladosporium herbarum	4930	+
319	Cladosporium sphaerospermum	478		323	Epicoccum nigrum	19723	+

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
323	Eurotium herbariorum	9861	+	328	Sporobolomyces sp.	490	
323	Penicillium islandicum	4882		328	Ulocladium chartarum	490	+
323	Trichoderma viride	4882		328	unknown	497	
323	unknown	63476		329	Alternaria alternata	23320	
323	unknown	34516	+	329	Alternaria alternata	4835	+
323	Wallemia sebi	14792	+	329	Aspergillus ochraceus	9699	+
323	yeast	659179		329	Aspergillus sp.	4863	
325	Alternaria alternata	420053		329	Aspergillus versicolor	4863	+
325	Alternaria alternata	11730	+	329	Aspergillus versicolor	4835	
325	Aureobasidium pullulans	2912	+	329	Aureobasidium pullulans	160251	
325	Aureobasidium pullulans	1941		329	Aureobasidium pullulans	77567	+
325	Cladosporium cladosporioides	6357		329	Cladosporium cladosporioides	4863	+
325	Cladosporium cladosporioides	4429	+	329	Cladosporium herbarum	14591	+
325	Cladosporium herbarum	10739	+	329	Cladosporium sphaerospermum	4835	
325	Epicoccum nigrum	1948		329	Epicoccum nigrum	4835	+
325	Epicoccum nigrum	977	+	329	Eurotium herbariorum	9699	+
325	Eurotium herbariorum	485	+	329	Fusarium sp.	14506	
325	Fusarium sp.	1948	+	329	Mucor racemosus	4835	+
325	Fusarium sp.	492		329	Penicillium citreonigrum	9699	+
325	Mucor plumbeus	492	+	329	Penicillium citreonigrum	4863	
325	Oidiodendron sp.	492	+	329	Penicillium decumbens	4863	
325	Penicillium aurantiogriseum	977		329	Phoma herbarum	9671	
325	Penicillium brevicompactum	6377	+	329	Phoma sp.	4863	
325	Penicillium brevicompactum	5400		329	Ulocladium chartarum	4863	
325	Penicillium commune	2932	+	329	unknown	4835	
325	Penicillium commune	1948		330	Acremonium sp.	478	
325	Phoma herbarum	984		330	Acremonium sp.	477	+
325	Rhizopus oryzae	492		330	Alternaria alternata	5729	+
325	Trichoderma viride	485		330	Alternaria alternata	4775	
325	unknown	6337		330	Aureobasidium pullulans	52511	
325	unknown	2440	+	330	Aureobasidium pullulans	27691	+
325	yeast	7321		330	Cladosporium herbarum	13846	+
326	Alternaria alternata	7614		330	Cladosporium herbarum	6202	
326	Aspergillus candidus	4681		330	Cladosporium sphaerospermum	3346	
326	Aspergillus versicolor	323033		330	Epicoccum nigrum	1433	
326	Aspergillus versicolor	14044	+	330	Epicoccum nigrum	1433	+
326	Aureobasidium pullulans	135767	+	330	Eurotium herbariorum	2385	
326	Aureobasidium pullulans	117041		330	Eurotium herbariorum	1431	+
326	Cladosporium cladosporioides	224719	+	330	Fusarium sp.	477	
326	Cladosporium cladosporioides	84269		330	Mucor racemosus	478	+
326	Eurotium herbariorum	650749	+	330	Paecilomyces variotii	8595	
326	Penicillium chrysogenum	1413857		330	Paecilomyces variotii	4776	+
326	Penicillium chrysogenum	964419	+	330	Penicillium chrysogenum	3817	+
326	yeast	23408		330	Penicillium chrysogenum	1432	
328	Alternaria alternata	16019		330	Penicillium corylophilum	478	
328	Alternaria alternata	1981	+	330	Penicillium decumbens	478	
328	Aspergillus cervinus	497		330	Penicillium decumbens	477	+
328	Aureobasidium pullulans	70017		330	Penicillium raistrickii	955	
328	Aureobasidium pullulans	46385	+	330	Phoma herbarum	956	
328	Cladosporium cladosporioides	3955		330	Phoma sp.	1431	
328	Cladosporium cladosporioides	497	+	330	Trichocladium asperum	956	
328	Cladosporium sphaerospermum	980	+	330	Ulocladium chartarum	478	
328	Mucor plumbeus	2471	+	330	unknown	2388	+
328	Mucor plumbeus	987		330	unknown	956	
328	Paecilomyces variotii	2485		331	Alternaria alternata	9689	
328	Paecilomyces variotii	2450	+	331	Aureobasidium pullulans	399342	+
328	Penicillium expansum	14283	+	331	Aureobasidium pullulans	317256	
328	Penicillium expansum	9347		331	Cladosporium herbarum	4844	
328	Phoma herbarum	497		331	Cladosporium sphaerospermum	4844	
328	Phoma sp.	2450		331	Penicillium viridicatum	4798	
328	Phoma sp.	994	+	331	Penicillium viridicatum	4798	+

HN	Identification	AVG CFU/g	G
331	Phoma herbarum	33914	
331	Phoma herbarum	19240	+
332	Alternaria alternata	9161	
332	Alternaria alternata	6783	+
332	Aureobasidium pullulans	12120	
332	Aureobasidium pullulans	12114	+
332	Cladosporium cladosporioides	972	+
332	Cladosporium cladosporioides	483	
332	Cladosporium herbarum	969	+
332	Cladosporium herbarum	483	
332	Cladosporium sphaerospermum	483	+
332	Epicoccum nigrum	1456	
332	Epicoccum nigrum	486	+
332	Eurotium herbariorum	967	+
332	Mucor racemosus	1456	+
332	Penicillium commune	38786	+
332	Penicillium commune	30070	
332	Penicillium viridicatum	483	+
332	Phoma herbarum	483	+
332	unknown	969	+
332	yeast	1450	
333	Alternaria alternata	2262	+
333	Aspergillus versicolor	1146	+
333	Aureobasidium pullulans	3348	+
333	Cladosporium herbarum	18225	+
333	Cladosporium herbarum	2718	
333	Epicoccum nigrum	7935	+
333	Epicoccum nigrum	2293	
333	Penicillium commune	5703	
333	Penicillium commune	4525	+
333	Phoma sp.	2262	
333	unknown	2262	+
333	Wallemia sebi	1146	+
333	yeast	15717	
335	Alternaria alternata	7609	
335	Alternaria alternata	4762	+
335	Aspergillus versicolor	484	
335	Aureobasidium pullulans	44467	
335	Aureobasidium pullulans	24461	+
335	Cladosporium cladosporioides	2401	+
335	Cladosporium cladosporioides	484	
335	Cladosporium herbarum	1453	+
335	Cladosporium sphaerospermum	2782	
335	Cladosporium sphaerospermum	1391	+
335	Epicoccum nigrum	1855	
335	Epicoccum nigrum	1391	+
335	Eurotium herbariorum	4195	+
335	Eurotium sp.	1412	
335	Penicillium expansum	1917	+
335	Penicillium expansum	484	
335	Penicillium italicum	968	+
335	unknown	6153	+
335	unknown	3731	
335	yeast	2906	
336	Alternaria alternata	11235	
336	Alternaria alternata	2884	+
336	Aureobasidium pullulans	9202	+
336	Aureobasidium pullulans	8263	
336	Cladosporium cladosporioides	1449	
336	Cladosporium cladosporioides	976	+
336	Cladosporium herbarum	4364	
336	Cladosporium herbarum	4356	+
336	Epicoccum nigrum	488	+
336	Epicoccum nigrum	480	
336	Fusarium sp.	480	+
336	Penicillium chrysogenum	480	+
336	yeast	480	
337	Alternaria alternata	5219	+
337	Alternaria alternata	477	
337	Aspergillus sp.	950	
337	Aspergillus sp.	477	+
337	Aspergillus versicolor	1420	+
337	Aureobasidium pullulans	4763	+
337	Aureobasidium pullulans	1897	
337	Cladosporium cladosporioides	477	+
337	Cladosporium herbarum	2844	+
337	Eurotium herbariorum	473	+
337	Fusarium sp.	473	+
337	Penicillium chrysogenum	3332	+
337	Penicillium chrysogenum	1424	
337	Penicillium citrinum	473	+
337	Penicillium griseofulvum	946	+
337	Trichoderma viride	7633	+
337	Trichoderma viride	1908	
337	unknown	7629	
337	unknown	3325	+
337	Wallemia sebi	950	+
337	yeast	10452	
338	Alternaria alternata	7124	
338	Alternaria alternata	2375	+
338	Aspergillus candidus	2860	+
338	Aspergillus candidus	1903	
338	Aspergillus niger	478	
338	Aspergillus ornatus	478	
338	Aspergillus versicolor	478	
338	Aureobasidium pullulans	3308	
338	Aureobasidium pullulans	2848	+
338	Cladosporium cladosporioides	951	+
338	Epicoccum nigrum	2381	+
338	Fusarium sp.	957	
338	Myrothecium olivaceum	478	
338	Penicillium chrysogenum	2848	+
338	Penicillium chrysogenum	957	
338	Penicillium janthinellum	472	
338	Phoma sp.	4253	
338	Phoma sp.	478	+
338	Rhizopus oryzae	1890	+
338	Rhizopus oryzae	472	
338	unknown	19861	+
338	unknown	4278	
338	yeast	14304	
339	Alternaria alternata	2413	+
339	Alternaria alternata	1446	
339	Aspergillus glaucus	474	+
339	Aspergillus ochraceus	488	
339	Aspergillus ochraceus	474	+
339	Aspergillus sydowii	962	
339	Aspergillus sydowii	488	+
339	Aspergillus versicolor	488	
339	Aureobasidium pullulans	3808	
339	Aureobasidium pullulans	2846	+
339	Cladosporium cladosporioides	1925	+

HN	Identification	AVG CFU/g	G
339	Cladosporium herbarum	7631	+
339	Cladosporium herbarum	976	
339	Epicoccum nigrum	1437	+
339	Epicoccum nigrum	474	
339	Eurotium herbariorum	5859	+
339	Mucor plumbeus	488	
339	Mucor plumbeus	488	+
339	Mucor racemosus	488	
339	Mucor racemosus	474	+
339	Penicillium expansum	4827	+
339	Penicillium expansum	3850	
339	Penicillium oxalicum	488	
339	Penicillium oxalicum	474	+
339	Penicillium waksmanii	1450	
339	Scopulariopsis brevicaulis	474	
339	Sphaeropsis sp.	474	
339	Stachybotrys chartarum	474	
339	Trichoderma viride	1437	
339	unknown	5775	
339	unknown	5748	+
339	Wallemia sebi	976	+
339	yeast	6724	
340	Alternaria alternata	8680	
340	Alternaria alternata	4804	+
340	Alternaria sp.	9223	
340	Aspergillus versicolor	954	
340	Aureobasidium pullulans	40201	+
340	Aureobasidium pullulans	33663	
340	Cladosporium cladosporioides	485	+
340	Cladosporium herbarum	54010	+
340	Cladosporium herbarum	962	
340	Cladosporium sphaerospermum	1916	+
340	Epicoccum nigrum	485	
340	Fusarium sp.	477	
340	Mucor racemosus	485	+
340	Paecilomyces variotii	477	
340	Penicillium brevicompactum	477	
340	Penicillium chrysogenum	962	+
340	Penicillium chrysogenum	477	
340	Penicillium citreonigrum	477	
340	Penicillium corylophilum	1447	+
340	Penicillium corylophilum	962	
340	Penicillium viridicatum	485	
340	Penicillium viridicatum	477	+
340	Phoma herbarum	954	+
340	Phoma herbarum	477	
340	Phoma sp.	970	+
340	unknown	2410	
341	Acremonium sp.	2396	
341	Alternaria alternata	478	
341	Aspergillus niger	478	
341	Aspergillus ochraceus	478	+
341	Aspergillus sp.	478	+
341	Aureobasidium pullulans	4803	+
341	Aureobasidium pullulans	478	
341	Cladosporium sp.	2886	+
341	Epicoccum nigrum	960	+
341	Epicoccum nigrum	478	
341	Mucor plumbeus	478	+
341	Mucor racemosus	478	+
341	Myrothecium sp.	478	
341	Penicillium chrysogenum	478	
341	unknown	482	
341	unknown	482	+
341	yeast	16836	
342	Alternaria alternata	20257	
342	Alternaria alternata	8290	+
342	Aspergillus fumigatus	1467	
342	Aspergillus fumigatus	980	+
342	Aspergillus ustus	980	
342	Aureobasidium pullulans	25358	
342	Aureobasidium pullulans	23434	+
342	Cladosporium cladosporioides	1461	+
342	Cladosporium herbarum	980	+
342	Cladosporium sp.	980	+
342	Penicillium chrysogenum	1957	+
342	Penicillium chrysogenum	487	
342	Penicillium citreonigrum	490	
342	Penicillium spinulosum	490	+
342	Penicillium spinulosum	487	
342	Rhizopus oryzae	490	
342	Tolypocladium sp.	36274	
342	Tolypocladium sp.	977	+
342	Trichoderma viride	1464	
342	unknown	7825	+
342	unknown	5389	
342	yeast	11251	
344	Alternaria alternata	3248	
344	Alternaria alternata	1407	+
344	Aspergillus ustus	115	
344	Aspergillus versicolor	234	
344	Aspergillus versicolor	119	+
344	Aureobasidium pullulans	1280	+
344	Cladosporium herbarum	465	+
344	Cladosporium herbarum	115	
344	Eurotium herbariorum	119	+
344	Penicillium chrysogenum	2695	+
344	Penicillium chrysogenum	2092	
344	Penicillium simplicissimum	234	
344	Penicillium simplicissimum	115	+
344	unknown	699	+
344	unknown	465	
344	yeast	2832	
345	Alternaria alternata	4424	+
345	Aspergillus versicolor	4713	
345	Aspergillus versicolor	4424	+
345	Epicoccum nigrum	4424	+
345	Penicillium sp.	4621	
345	Rhizopus oryzae	4621	
345	unknown	22123	+
345	unknown	18091	
345	yeast	62732	
347	Alternaria alternata	125597	
347	Alternaria alternata	1037	+
347	Aureobasidium pullulans	13935	
347	Aureobasidium pullulans	6724	+
347	Cladosporium cladosporioides	525	+
347	Cladosporium herbarum	1050	+
347	Cladosporium sphaerospermum	525	+
347	Epicoccum nigrum	1037	+
347	Eurotium herbariorum	1037	+
347	Penicillium chrysogenum	44035	+

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
347	Penicillium chrysogenum	32662		351	Penicillium citreonigrum	499	
347	unknown	4713		351	Penicillium oxalicum	2471	
348	Alternaria alternata	4808	+	351	Penicillium oxalicum	1485	+
348	Alternaria alternata	3064		351	Phoma herbarum	7984	
348	Aspergillus sp.	477	+	351	Trichoderma viride	7895	
348	Aureobasidium pullulans	3395	+	351	Trichoderma viride	5424	+
348	Aureobasidium pullulans	1449		351	unknown	499	
348	Cladosporium cladosporioides	477		351	yeast	499	
348	Epicoccum nigrum	2394		352	Alternaria alternata	4878	
348	Eurotium herbariorum	1449	+	352	Alternaria alternata	1409	+
348	Penicillium corylophilum	1431		352	Aspergillus oryzae	490	
348	Penicillium expansum	1440	+	352	Aspergillus versicolor	469	+
348	Penicillium expansum	477		352	Aureobasidium pullulans	10480	
348	Penicillium simplicissimum	1440		352	Aureobasidium pullulans	4330	+
348	Penicillium sp. #26	1440		352	Cladosporium herbarum	490	+
348	Penicillium spinulosum	2899	+	352	Cladosporium sphaerospermum	490	+
348	Penicillium spinulosum	1449		352	Eurotium herbariorum	960	+
348	Phoma sp.	477	+	352	Paecilomyces variotii	490	
348	unknown	9176	+	352	Penicillium chrysogenum	5229	+
348	unknown	963		352	Penicillium chrysogenum	490	
348	yeast	3816		352	Penicillium islandicum	490	
349	Alternaria alternata	9863		352	Penicillium janthinellum	4371	+
349	Aspergillus versicolor	5000	+	352	Penicillium janthinellum	2860	
349	Aureobasidium pullulans	5000		352	Penicillium spinulosum	939	
349	Cladosporium sp.	5000		352	Penicillium spinulosum	490	+
349	Dothichiza sp.	10000		352	Phoma herbarum	2860	
349	Epicoccum nigrum	15000		352	unknown	490	
349	Penicillium citreonigrum	5000		352	yeast	469	
349	yeast	1230000		353	Alternaria alternata	4301	
350	Alternaria alternata	55979		353	Alternaria alternata	4294	+
350	Alternaria alternata	979	+	353	Aspergillus versicolor	471	+
350	Aspergillus niger	482		353	Aureobasidium pullulans	37126	
350	Aureobasidium pullulans	1973		353	Aureobasidium pullulans	35052	+
350	Aureobasidium pullulans	497	+	353	Cladosporium cladosporioides	951	+
350	Cladosporium herbarum	6900	+	353	Cladosporium sphaerospermum	1439	
350	Cladosporium herbarum	497		353	Cladosporium sphaerospermum	479	+
350	Epicoccum nigrum	979	+	353	Epicoccum nigrum	471	
350	Eurotium herbariorum	2485	+	353	Eupenicillium ochrosalmonium	2391	
350	Fusarium oxysporum	1491		353	Eupenicillium ochrosalmonium	1894	+
350	Paecilomyces variotii	482		353	Eurotium herbariorum	2382	+
350	Penicillium chrysogenum	2967	+	353	Myrothecium olivaceum	1415	+
350	Penicillium chrysogenum	979		353	Penicillium brevicompactum	6701	+
350	Penicillium griseofulvum	1959	+	353	Penicillium brevicompactum	3326	
350	Pithomyces sp.	497		353	Penicillium commune	479	+
350	Pithomyces sp.	497	+	353	Penicillium spinulosum	1903	
350	unknown	2953	+	353	Penicillium spinulosum	479	+
350	unknown	994		353	Phoma herbarum	4741	
350	Wallemia sebi	1973	+	353	Phoma sp.	255278	
350	yeast	21155		353	Rhizopus oryzae	471	
351	Alternaria alternata	11689		353	Ulocladium chartarum	471	+
351	Alternaria alternata	2477	+	353	unknown	471	
351	Aspergillus niger	499		354	Alternaria alternata	2890	
351	Aspergillus niger	493	+	354	Alternaria alternata	2410	+
351	Aspergillus sydowii	499	+	354	Aspergillus ochraceus	9520	+
351	Aspergillus versicolor	992	+	354	Aspergillus ochraceus	9111	
351	Aureobasidium pullulans	12368		354	Aureobasidium pullulans	12951	
351	Aureobasidium pullulans	7431	+	354	Aureobasidium pullulans	8519	+
351	Cladosporium sphaerospermum	1497	+	354	Cladosporium cladosporioides	1450	+
351	Epicoccum nigrum	499	+	354	Cladosporium herbarum	939	+
351	Eurotium herbariorum	986	+	354	Epicoccum nigrum	939	
351	Paecilomyces fumosoroseus	499		354	Eurotium herbariorum	2450	+

HN	Identification	AVG CFU/g	G
354	Penicillium chrysogenum	7660	
354	Penicillium chrysogenum	7620	+
354	Penicillium citrinum	960	
354	Penicillium raistrickii	469	
354	Penicillium spinulosum	960	
354	Penicillium spinulosum	960	+
354	Phoma herbarum	490	
354	Phoma herbarum	469	+
354	Scopulariopsis brevicaulis	469	
354	Scopulariopsis brevicaulis	469	+
354	Stachybotrys chartarum	490	
354	unknown	4881	+
354	unknown	1920	
354	yeast	939	
355	Alternaria alternata	13092	+
355	Alternaria alternata	2921	
355	Aspergillus candidus	495	+
355	Aureobasidium pullulans	24602	+
355	Aureobasidium pullulans	24188	
355	Cladosporium cladosporioides	495	+
355	Cladosporium herbarum	1964	+
355	Cladosporium sphaerospermum	478	
355	Cladosporium sphaerospermum	478	+
355	Epicoccum nigrum	3384	
355	Eurotium herbariorum	1452	+
355	Mucor plumbeus	478	
355	Mucor racemosus	1436	
355	Penicillium viridicatum	5381	
355	Penicillium viridicatum	5348	+
355	Phoma herbarum	3847	
355	Phoma herbarum	1436	+
355	Trichoderma viride	478	
355	unknown	1964	
356	Alternaria alternata	6785	
356	Alternaria alternata	2892	+
356	Aspergillus versicolor	1446	
356	Aspergillus versicolor	481	+
356	Aureobasidium pullulans	4820	+
356	Aureobasidium pullulans	1446	
356	Cladosporium cladosporioides	963	
356	Cladosporium herbarum	1446	+
356	Epicoccum nigrum	2892	+
356	Epicoccum nigrum	482	
356	Eurotium herbariorum	482	+
356	Penicillium corylophilum	964	
356	Penicillium corylophilum	964	+
356	Stachybotrys chartarum	963	
356	unknown	4340	+
356	unknown	1928	
356	Verticillium sp.	481	
356	yeast	3861	
357	Alternaria alternata	4330	
357	Alternaria alternata	1917	+
357	Aspergillus versicolor	1459	+
357	Aspergillus versicolor	954	
357	Aureobasidium pullulans	13882	+
357	Aureobasidium pullulans	10616	
357	Cladosporium cladosporioides	3826	+
357	Cladosporium herbarum	1459	+
357	Cladosporium herbarum	477	
357	Cladosporium sphaerospermum	1459	+
357	Epicoccum nigrum	1449	+
357	Paecilomyces variotii	486	
357	Penicillium brevicompactum	2909	
357	Penicillium brevicompactum	477	+
357	Penicillium chrysogenum	1440	+
357	Penicillium citrinum	1449	
357	Penicillium glandicola	486	
357	Phoma herbarum	972	
357	Scopulariopsis candida	486	+
357	unknown	486	
358	Alternaria alternata	5807	
358	Alternaria alternata	2412	+
358	Aspergillus niger	486	+
358	Aspergillus versicolor	2412	+
358	Aspergillus versicolor	959	
358	Aureobasidium pullulans	17878	+
358	Aureobasidium pullulans	14013	
358	Cladosporium cladosporioides	1439	+
358	Cladosporium cladosporioides	959	
358	Cladosporium herbarum	11594	+
358	Cladosporium herbarum	486	
358	Cladosporium sphaerospermum	1925	+
358	Cladosporium sphaerospermum	486	
358	Epicoccum nigrum	8663	+
358	Epicoccum nigrum	7729	
358	Mucor plumbeus	966	
358	Mucor racemosus	486	+
358	Penicillium brevicompactum	966	
358	Penicillium brevicompactum	966	+
358	Penicillium digitatum	4824	+
358	Penicillium digitatum	3398	
358	Phoma herbarum	479	
358	unknown	3851	
358	unknown	3391	+
359	Alternaria alternata	9480	+
359	Aureobasidium pullulans	47517	+
359	Aureobasidium pullulans	28440	
359	Cladosporium herbarum	4681	+
359	Eurotium herbariorum	4798	+
359	Myrothecium olivaceum	151681	
359	unknown	9596	
361	Alternaria alternata	162637	
361	Alternaria alternata	9633	+
361	Aspergillus versicolor	19323	
361	Aspergillus versicolor	9633	+
361	Aureobasidium pullulans	9671	+
361	Aureobasidium pullulans	4816	
361	Cladosporium herbarum	14450	+
361	Cladosporium sphaerospermum	4816	+
361	Coniothyrium sp.	33811	
361	Epicoccum nigrum	9671	+
361	Penicillium chrysogenum	4835	+
361	Penicillium corylophilum	4835	+
361	Phoma sp.	14469	
361	Phoma sp.	4835	+
361	Stachybotrys chartarum	4816	
361	unknown	9652	
361	unknown	9652	+
361	yeast	19323	
362	Alternaria alternata	24574	
362	Alternaria alternata	1901	+

HN	Identification	AVG CFU/g	G
362	Aspergillus niger	475	+
362	Aspergillus versicolor	470	
362	Aspergillus versicolor	470	+
362	Aureobasidium pullulans	16047	
362	Aureobasidium pullulans	7559	+
362	Cladosporium cladosporioides	475	
362	Cladosporium herbarum	470	
362	Coniothyrium sp.	470	+
362	Epicoccum nigrum	470	+
362	Eurotium herbariorum	470	+
362	Fusarium sp.	475	+
362	Penicillium expansum	4268	+
362	Penicillium expansum	941	
362	Penicillium griseofulvum	5689	+
362	Penicillium griseofulvum	4268	
362	Penicillium italicum	14213	+
362	Penicillium italicum	4721	
362	Phoma herbarum	66539	
362	Phoma herbarum	14733	+
362	Sphaeropsis sp.	475	+
362	Trichoderma viride	1421	
362	Trichoderma viride	946	+
362	unknown	470	
363	Alternaria alternata	3309	
363	Aspergillus cervinus	471	+
363	Aspergillus versicolor	943	+
363	Aspergillus versicolor	471	
363	Aureobasidium pullulans	9451	+
363	Aureobasidium pullulans	7075	
363	Cladosporium cladosporioides	471	
363	Cladosporium herbarum	471	
363	Cladosporium herbarum	471	+
363	Fusarium sp.	471	
363	Mucor plumbeus	28355	+
363	Mucor plumbeus	24101	
363	Penicillium expansum	199902	+
363	Penicillium expansum	190451	
363	Penicillium simplicissimum	15121	+
363	Penicillium simplicissimum	471	
363	Trichoderma viride	471	+
363	unknown	5197	+
363	Wallemia sebi	182547	+
364	Alternaria alternata	5420	
364	Alternaria alternata	3943	+
364	Aspergillus ochraceus	1976	
364	Aspergillus ochraceus	489	+
364	Aspergillus versicolor	1976	+
364	Aureobasidium pullulans	15332	
364	Aureobasidium pullulans	11839	+
364	Cladosporium cladosporioides	499	
364	Cladosporium herbarum	14852	+
364	Cladosporium herbarum	6917	
364	Cladosporium sphaerospermum	4451	+
364	Cladosporium sphaerospermum	489	
364	Epicoccum nigrum	2495	
364	Epicoccum nigrum	1956	+
364	Eurotium herbariorum	2455	+
364	Geomyces pannorum	489	+
364	Mucor racemosus	489	
364	Penicillium chrysogenum	3453	+
364	Penicillium chrysogenum	2954	
364	Penicillium griseofulvum	499	
364	Penicillium spinulosum	2465	
364	Penicillium spinulosum	978	+
364	Phoma herbarum	499	
364	Phoma herbarum	499	+
364	Scopulariopsis brevicaulis	499	
364	unknown	2935	
364	unknown	1477	+
364	yeast	988	
366	Acremonium sp.	497	
366	Alternaria alternata	3458	
366	Alternaria alternata	1988	+
366	Aspergillus sydowii	994	
366	Aspergillus versicolor	980	
366	Aureobasidium pullulans	16823	
366	Aureobasidium pullulans	5936	+
366	Cladosporium herbarum	5882	+
366	Eurotium herbariorum	3458	+
366	Penicillium chrysogenum	8884	+
366	Penicillium chrysogenum	5426	
366	Penicillium citrinum	5453	
366	Penicillium citrinum	2471	+
366	Phoma herbarum	1960	
366	Phoma herbarum	497	+
366	unknown	3438	
368	Alternaria alternata	3907	
368	Aspergillus versicolor	490	
368	Aureobasidium pullulans	40514	
368	Aureobasidium pullulans	18074	+
368	Cladosporium herbarum	2932	+
368	Cladosporium sphaerospermum	490	
368	Cladosporium sphaerospermum	490	+
368	Epicoccum nigrum	1470	
368	Epicoccum nigrum	490	+
368	Fusarium sp.	487	
368	Penicillium chrysogenum	11251	
368	Penicillium chrysogenum	9789	+
368	Penicillium spinulosum	6355	
368	Penicillium spinulosum	1461	+
368	Phoma herbarum	2442	
368	Phoma herbarum	490	+
368	unknown	490	
368	yeast	974	
370	Aspergillus versicolor	73275	
370	Aspergillus versicolor	68803	+
370	Aureobasidium pullulans	19647	
370	Aureobasidium pullulans	14716	+
370	Cladosporium herbarum	24578	+
370	Eurotium herbariorum	19647	+
370	Penicillium brevicompactum	4930	
370	Penicillium expansum	24578	+
370	Penicillium expansum	19647	
370	unknown	24348	+
370	unknown	4930	
370	yeast	44225	
372	Alternaria alternata	96249	
372	Aspergillus versicolor	950	
372	Aureobasidium pullulans	23492	
372	Aureobasidium pullulans	12173	+
372	Cladosporium herbarum	7991	+
372	Cladosporium herbarum	1409	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
372	Cladosporium sphaerospermum	942	+	375	Penicillium chrysogenum	3935	
372	Epicoccum nigrum	1885	+	375	Penicillium chrysogenum	1485	+
372	Epicoccum nigrum	1401		375	Penicillium corylophilum	4875	+
372	Paecilomyces variotii	475	+	375	Penicillium corylophilum	1942	
372	Penicillium chrysogenum	20800	+	375	Penicillium miczynskii	2895	
372	Penicillium chrysogenum	7089		375	Phoma herbarum	9826	
372	Penicillium decumbens	934		375	Phoma herbarum	6410	+
372	Penicillium griseofulvum	4213		375	Rhizopus oryzae	482	
372	Penicillium griseofulvum	475	+	375	unknown	1460	
372	Penicillium oxalicum	467		376	Alternaria alternata	4733	
372	Penicillium spinulosum	475	+	376	Alternaria alternata	4262	+
372	Phoma herbarum	2851		376	Aspergillus niger	948	+
372	Rhizopus oryzae	475		376	Aspergillus niger	472	
372	Rhizopus oryzae	467	+	376	Aspergillus sp.	472	+
373	Alternaria alternata	4725	+	376	Aspergillus sydowii	472	
373	Aspergillus versicolor	12294		376	Aspergillus ustus	1897	
373	Aspergillus versicolor	4725	+	376	Aspergillus ustus	472	+
373	Aureobasidium pullulans	18876	+	376	Aspergillus versicolor	474	
373	Aureobasidium pullulans	9451		376	Aureobasidium pullulans	945	+
373	Cladosporium herbarum	18885	+	376	Cladosporium cladosporioides	1893	+
373	Cladosporium herbarum	14177		376	Cladosporium herbarum	472	+
373	Eurotium herbariorum	4725	+	376	Cladosporium sp.	472	+
373	Penicillium brevicompactum	4725		376	Epicoccum nigrum	2362	
373	Penicillium chrysogenum	4725	+	376	Epicoccum nigrum	474	+
373	Penicillium spinulosum	9433		376	Eurotium herbariorum	474	+
373	unknown	23602	+	376	Fusarium oxysporum	2840	
373	yeast	14168		376	Fusarium oxysporum	472	+
374	Alternaria alternata	5494	+	376	Penicillium brevicompactum	2368	+
374	Aspergillus sydowii	14928		376	Penicillium brevicompactum	1892	
374	Aspergillus versicolor	31789		376	Penicillium commune	474	
374	Aspergillus versicolor	5102	+	376	Phoma sp.	474	
374	Aureobasidium pullulans	5102		376	Rhizopus oryzae	472	+
374	Cladosporium cladosporioides	31789	+	376	Stachybotrys chartarum	946	
374	Cladosporium cladosporioides	5494		376	Trichoderma viride	948	+
374	Cladosporium herbarum	15698		376	Trichoderma viride	946	
374	Cladosporium herbarum	5102	+	376	unknown	946	+
374	Epicoccum nigrum	5102	+	376	unknown	472	
374	Eurotium herbariorum	5102	+	376	yeast	48248	
374	Penicillium brevicompactum	5494	+	377	Aspergillus ochraceus	4716	+
374	Penicillium spinulosum	5102	+	377	Aspergillus versicolor	30723	
374	Scopulariopsis brevicaulis	48665	+	377	Aureobasidium pullulans	191238	+
374	Scopulariopsis brevicaulis	10596		377	Aureobasidium pullulans	94339	
374	Trichoderma viride	10989	+	377	Cladosporium herbarum	4716	+
374	unknown	32967	+	377	Cladosporium sphaerospermum	4844	+
374	unknown	5494		377	Eurotium herbariorum	9689	+
374	yeast	41993		377	Penicillium chrysogenum	230510	+
375	Alternaria alternata	15067		377	Penicillium chrysogenum	61320	
375	Alternaria alternata	2413	+	377	Penicillium expansum	4716	
375	Aspergillus niger	1447	+	377	Phoma herbarum	4716	
375	Aspergillus versicolor	482		377	Trichoderma viride	96259	+
375	Aureobasidium pullulans	51657	+	377	unknown	9433	
375	Aureobasidium pullulans	24899		378	Alternaria alternata	10925	
375	Cladosporium cladosporioides	495	+	378	Alternaria alternata	1988	+
375	Cladosporium herbarum	1955	+	378	Aspergillus glaucus	497	+
375	Cladosporium herbarum	990		378	Aspergillus niger	497	
375	Cladosporium sphaerospermum	990	+	378	Aspergillus oryzae	497	
375	Epicoccum nigrum	977		378	Aureobasidium pullulans	16665	
375	Epicoccum nigrum	495	+	378	Aureobasidium pullulans	6958	+
375	Eurotium herbariorum	1460	+	378	Cladosporium cladosporioides	994	+
375	Geomyces pannorum	2462		378	Cladosporium cladosporioides	497	
375	Mucor racemosus	482	+	378	Cladosporium herbarum	497	

HN	Identification	AVG CFU/g	G
378	Cladosporium herbarum	497	+
378	Epicoccum nigrum	4892	
378	Epicoccum nigrum	994	+
378	Penicillium chrysogenum	1491	
378	Penicillium spinulosum	241217	
378	Penicillium spinulosum	201581	+
378	unknown	497	
381	Alternaria alternata	14796	+
381	Aspergillus sydowii	5197	+
381	Aureobasidium pullulans	13204	
381	Cladosporium herbarum	15592	+
381	Cladosporium sp.	5197	+
381	Epicoccum nigrum	14796	
381	Mucor racemosus	4401	+
381	unknown	17605	
381	unknown	15592	+
381	yeast	13204	
382	Alternaria alternata	12731	
382	Alternaria alternata	9357	+
382	Aspergillus sp.	500	+
382	Aspergillus versicolor	10857	
382	Aspergillus versicolor	10214	+
382	Aureobasidium pullulans	6428	+
382	Aureobasidium pullulans	3928	
382	Cladosporium herbarum	11119	+
382	Cladosporium herbarum	2428	
382	Emericella nidulans	1928	
382	Emericella nidulans	500	+
382	Epicoccum nigrum	1476	
382	Epicoccum nigrum	500	+
382	Eurotium herbariorum	476	+
382	Fusarium oxysporum	500	
382	Fusarium sp.	2928	+
382	Fusarium sp.	1452	
382	Penicillium chrysogenum	1452	
382	Penicillium chrysogenum	1428	+
382	Penicillium corylophilum	1952	+
382	Penicillium griseofulvum	476	
382	Phialophora fastigiata	476	
382	Rhizopus oryzae	1904	+
382	Rhizopus oryzae	476	
382	Ulocladium chartarum	2452	+
382	Ulocladium chartarum	500	
382	unknown	7380	+
382	unknown	1928	
382	Wallemia sebi	4833	+
382	yeast	6476	
385	Alternaria alternata	19319	+
385	Alternaria alternata	4894	
385	Alternaria sp.	499	
385	Aspergillus glaucus	499	+
385	Aspergillus niger	982	+
385	Aspergillus versicolor	982	+
385	Aureobasidium pullulans	4443	+
385	Aureobasidium pullulans	499	
385	Cladosporium herbarum	6439	+
385	Cladosporium herbarum	1980	
385	Epicoccum nigrum	982	
385	Eurotium herbariorum	491	+
385	Fusarium sp.	982	
385	Penicillium commune	499	

HN	Identification	AVG CFU/g	G
385	Penicillium corylophilum	1489	
385	Penicillium expansum	998	+
385	Phoma sp.	1489	
385	Phoma sp.	998	+
385	unknown	3461	+
385	unknown	990	
385	Wallemia sebi	2487	+
385	yeast	8966	
386	Alternaria alternata	6944	
386	Alternaria alternata	2958	+
386	Aspergillus versicolor	497	+
386	Aureobasidium pullulans	17825	
386	Aureobasidium pullulans	14843	+
386	Cladosporium cladosporioides	497	+
386	Cladosporium herbarum	6441	+
386	Cladosporium sphaerospermum	497	
386	Epicoccum nigrum	497	+
386	Eurotium herbariorum	1491	+
386	Myrothecium olivaceum	6461	+
386	Myrothecium olivaceum	986	
386	Penicillium citreonigrum	1976	+
386	Penicillium citreonigrum	1972	
386	Penicillium decumbens	3467	
386	Penicillium decumbens	1483	+
386	Phoma herbarum	497	
386	Rhizopus oryzae	990	+
386	Trichoderma viride	497	
386	unknown	1479	+
386	yeast	493	
387	Acremonium sp.	5755	
387	Alternaria alternata	14285	+
387	Aspergillus glaucus	4892	
387	Aspergillus versicolor	4761	
387	Aureobasidium pullulans	219830	
387	Aureobasidium pullulans	71689	+
387	Cladosporium cladosporioides	9784	
387	Cladosporium cladosporioides	4892	+
387	Cladosporium herbarum	43639	+
387	Cladosporium herbarum	19569	
387	Penicillium corylophilum	4761	
387	Penicillium digitatum	9784	
387	Penicillium digitatum	4761	+
387	Phoma herbarum	23809	
387	Phoma sp.	9523	+
387	unknown	68232	
387	yeast	14285	
388	Alternaria alternata	76732	
388	Alternaria alternata	481	+
388	Aspergillus glaucus	481	
388	Aureobasidium pullulans	124050	+
388	Aureobasidium pullulans	65244	
388	Cladosporium herbarum	15693	+
388	Cladosporium herbarum	8138	
388	Epicoccum nigrum	481	
388	Eurotium herbariorum	938	+
388	Mucor racemosus	2345	+
388	Penicillium chrysogenum	13817	
388	Penicillium chrysogenum	11991	+
388	Penicillium digitatum	938	+
388	Phoma herbarum	469	
388	Phoma sp.	30487	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
388	Phoma sp.	22514	+	392	Stachybotrys chartarum	464	
388	Trichoderma viride	7504		392	Trichoderma sp.	464	+
388	Ulocladium chartarum	1926	+	392	Trichoderma viride	464	
388	unknown	481		392	Ulocladium chartarum	8846	
389	Epicoccum nigrum	4385	+	392	Ulocladium chartarum	6524	+
389	Phoma sp.	344339	+	392	unknown	2798	
389	Phoma sp.	344339		392	yeast	466	
389	unknown	23253	+	393	Alternaria alternata	2101	
389	unknown	4385		393	Alternaria alternata	573	+
389	yeast	27308		393	Aureobasidium pullulans	573	+
390	Alternaria alternata	4844	+	393	Cladosporium cladosporioides	595	+
390	Aureobasidium pullulans	111813	+	393	Cladosporium herbarum	1742	+
390	Aureobasidium pullulans	58329		393	Cladosporium herbarum	573	
390	Cladosporium cladosporioides	14629	+	393	Cladosporium sp.	1190	+
390	Cladosporium herbarum	29069	+	393	Cladosporium sp.	595	
390	Cladosporium herbarum	9689		393	Eurotium herbariorum	595	+
390	Epicoccum nigrum	9737		393	Mucor plumbeus	573	
390	Penicillium chrysogenum	4892		393	Penicillium aurantiogriseum	1168	
390	Penicillium chrysogenum	4844	+	393	Penicillium chrysogenum	2359	+
390	Phoma herbarum	29069		393	Penicillium sp.	573	
390	Phoma herbarum	14534	+	393	Penicillium spinulosum	573	
390	Sphaeropsis sp.	4844		393	Phoma sp.	1168	
390	unknown	14582		393	Phoma sp.	1168	+
391	Alternaria alternata	30569		393	Trichoderma viride	573	
391	Alternaria alternata	17582	+	393	unknown	10386	+
391	Aspergillus versicolor	1648	+	393	unknown	9327	
391	Aspergillus versicolor	1098		393	yeast	7055	
391	Eurotium herbariorum	1098	+	394	Alternaria alternata	8224	+
391	Mucor racemosus	8966	+	394	Alternaria alternata	7388	
391	Mucor racemosus	8966		394	Aspergillus versicolor	970	
391	Penicillium corylophilum	549	+	394	Aureobasidium pullulans	21732	
391	Penicillium melinii	1098	+	394	Aureobasidium pullulans	6282	+
391	Penicillium melinii	549		394	Cladosporium herbarum	5797	+
391	Phoma sp.	549		394	Cladosporium herbarum	970	
391	Scopulariopsis brevicaulis	549		394	Eurotium herbariorum	485	+
391	Scopulariopsis candida	1648		394	Penicillium aurantiogriseum	1941	
391	Scopulariopsis candida	549	+	394	Penicillium digitatum	4854	
391	yeast	1098		394	Rhizopus oryzae	1456	+
392	Acremonium sp.	466	+	394	Scopulariopsis brevicaulis	485	
392	Alternaria alternata	5581	+	394	Stemphylium botryosum	970	+
392	Alternaria alternata	4197		394	Trichoderma viride	970	
392	Aspergillus candidus	466	+	394	unknown	76277	
392	Aureobasidium pullulans	37743	+	394	unknown	53574	+
392	Aureobasidium pullulans	20029		394	yeast	162207	
392	Cladosporium cladosporioides	4197		395	Alternaria alternata	178713	
392	Cladosporium cladosporioides	464	+	395	Alternaria alternata	3914	+
392	Cladosporium herbarum	6053	+	395	Aureobasidium pullulans	25017	+
392	Cladosporium herbarum	464		395	Aureobasidium pullulans	12257	
392	Cladosporium sphaerospermum	932	+	395	Cladosporium herbarum	7851	+
392	Cladosporium sphaerospermum	466		395	Cladosporium herbarum	492	
392	Epicoccum nigrum	931		395	Epicoccum nigrum	1470	
392	Epicoccum nigrum	464	+	395	Epicoccum nigrum	1464	+
392	Penicillium aurantiogriseum	932	+	395	Eurotium herbariorum	972	+
392	Penicillium chrysogenum	2323	+	395	Penicillium glandicola	1470	+
392	Penicillium chrysogenum	932		395	Penicillium griseofulvum	3925	
392	Penicillium corylophilum	3729	+	395	Penicillium griseofulvum	2443	+
392	Penicillium corylophilum	1862		395	Phoma herbarum	2460	+
392	Phoma herbarum	3261		395	Phoma herbarum	984	
392	Phoma herbarum	1397	+	395	Trichoderma viride	486	+
392	Pithomyces chartarum	932		395	Ulocladium chartarum	972	+
392	Sphaeropsis sp.	1395		395	unknown	2929	

HN	Identification	AVG CFU/g	G
395	unknown	1962	+
396	Alternaria alternata	19379	
396	Aspergillus sp.	4844	
396	Aureobasidium pullulans	126994	
396	Aureobasidium pullulans	53750	+
396	Cladosporium cladosporioides	9803	+
396	Cladosporium cladosporioides	9689	
396	Cladosporium herbarum	34142	+
396	Cladosporium sphaerospermum	9746	+
396	Epicoccum nigrum	4901	+
396	Penicillium miczynskii	34199	+
396	Penicillium miczynskii	9803	
396	Phoma exigua	9803	+
396	Phoma herbarum	4901	
396	Phoma sp.	14534	+
396	Sphaeropsis sp.	4901	
396	Ulocladium chartarum	4844	+
396	unknown	29297	
396	Wallemia sebi	43604	+
397	Alternaria alternata	14801	+
397	Alternaria alternata	5730	
397	Aureobasidium pullulans	3345	
397	Aureobasidium pullulans	2863	+
397	Cladosporium herbarum	477	+
397	Coniothyrium sp.	1910	
397	Coniothyrium sp.	955	+
397	Epicoccum nigrum	1432	
397	Epicoccum nigrum	955	+
397	Eurotium herbariorum	21967	+
397	Mucor racemosus	477	
397	Penicillium chrysogenum	956	
397	Penicillium islandicum	954	
397	Scopulariopsis brevicaulis	477	
397	unknown	1909	+
397	unknown	955	
397	yeast	32469	
398	Alternaria alternata	15787	
398	Alternaria alternata	2408	+
398	Aspergillus glaucus	487	+
398	Aspergillus niger	487	+
398	Aureobasidium pullulans	117127	+
398	Aureobasidium pullulans	98091	
398	Cladosporium cladosporioides	3369	+
398	Cladosporium herbarum	4330	+
398	Cladosporium herbarum	487	
398	Cladosporium sphaerospermum	974	+
398	Cladosporium sphaerospermum	487	
398	Epicoccum nigrum	1949	
398	Epicoccum nigrum	473	+
398	Penicillium brevicompactum	16126	+
398	Penicillium brevicompactum	11837	
398	Penicillium griseofulvum	7157	
398	Penicillium griseofulvum	2840	+
398	Penicillium spinulosum	2408	
398	Penicillium spinulosum	487	+
398	Phoma herbarum	2408	+
398	Phoma herbarum	946	
398	unknown	946	
399	Alternaria alternata	9487	+
399	Alternaria alternata	4835	
399	Aspergillus niger	4835	+
399	Aspergillus versicolor	14506	
399	Aspergillus versicolor	4743	+
399	Aureobasidium pullulans	4835	+
399	Cladosporium cladosporioides	4835	+
399	Cladosporium herbarum	19250	+
399	Cladosporium herbarum	4743	
399	Epicoccum nigrum	9487	+
399	Epicoccum nigrum	4743	
399	Microsphaeropsis sp.	9671	
399	Myrothecium olivaceum	18975	
399	Myrothecium olivaceum	14415	+
399	Penicillium chrysogenum	4743	
399	Penicillium coprophilum	4743	
399	Phoma sp.	175521	+
399	Phoma sp.	118687	
399	Pithomyces chartarum	9579	+
399	unknown	9487	+
399	yeast	28921	
400	Alternaria alternata	50363	
400	Alternaria alternata	4277	+
400	Aspergillus sp.	2946	+
400	Aspergillus versicolor	5321	
400	Aspergillus versicolor	4359	+
400	Aureobasidium pullulans	1944	
400	Aureobasidium pullulans	941	+
400	Cladosporium cladosporioides	470	+
400	Cladosporium herbarum	1903	
400	Cladosporium herbarum	941	+
400	Cladosporium sphaerospermum	470	
400	Epicoccum nigrum	2845	
400	Epicoccum nigrum	941	+
400	Eurotium herbariorum	2354	+
400	Mucor plumbeus	470	
400	Mucor plumbeus	470	+
400	Mucor racemosus	1473	
400	Mucor racemosus	491	+
400	Penicillium chrysogenum	2354	+
400	Penicillium chrysogenum	1944	
400	Penicillium griseofulvum	2374	+
400	Penicillium griseofulvum	1412	
400	Penicillium sp.	470	+
400	Rhizopus oryzae	941	
400	Rhizopus oryzae	470	+
400	Trichoderma viride	470	
400	unknown	1903	
400	unknown	1903	+
400	Wallemia sebi	4257	
400	Wallemia sebi	941	+
400	yeast	19977	
401	Alternaria alternata	27483	
401	Alternaria alternata	4699	+
401	Aspergillus sydowii	4699	+
401	Aspergillus versicolor	9398	
401	Aspergillus versicolor	4699	+
401	Aureobasidium pullulans	19083	
401	Aureobasidium pullulans	14312	+
401	Cladosporium herbarum	23783	+
401	Cladosporium herbarum	9398	
401	Cladosporium sphaerospermum	4699	+
401	Epicoccum nigrum	9470	+
401	Epicoccum nigrum	4770	

HN	Identification	AVG CFU/g	G
401	Penicillium chrysogenum	28554	
401	Penicillium crustosum	4699	
401	Penicillium griseofulvum	4770	+
401	Penicillium spinulosum	28410	+
401	Penicillium spinulosum	18940	
401	unknown	42580	
402	Alternaria alternata	23558	
402	Alternaria alternata	4761	+
402	Aureobasidium pullulans	200354	+
402	Aureobasidium pullulans	85841	
402	Cladosporium herbarum	9541	
402	Cladosporium herbarum	9523	+
402	Penicillium italicum	14303	
402	Penicillium italicum	14285	+
402	Phoma herbarum	4761	
402	Trichoderma viride	14285	
402	unknown	9532	
402	unknown	4770	+
402	yeast	548664	
403	Alternaria alternata	181788	
403	Alternaria alternata	1964	+
403	Aspergillus niger	478	
403	Aspergillus niger	478	+
403	Aureobasidium pullulans	14096	
403	Aureobasidium pullulans	6802	+
403	Chrysonilia sitophila	491	
403	Cladosporium cladosporioides	478	
403	Cladosporium cladosporioides	478	+
403	Cladosporium herbarum	491	+
403	Epicoccum nigrum	982	
403	Epicoccum nigrum	478	+
403	Eurotium herbariorum	12672	+
403	Mucor racemosus	6704	
403	Mucor racemosus	4310	+
403	Penicillium chrysogenum	4395	+
403	Penicillium chrysogenum	2443	
403	Penicillium commune	1964	+
403	Penicillium commune	491	
403	Penicillium decumbens	3438	
403	Penicillium oxalicum	491	
403	unknown	3389	
405	Aspergillus sp.	4854	+
405	Aureobasidium pullulans	5836	
405	Cladosporium herbarum	9469	+
405	Cladosporium herbarum	4854	
405	Penicillium chrysogenum	392440	+
405	Penicillium chrysogenum	230858	
405	Rhizopus oryzae	4854	+
405	unknown	416473	
405	unknown	43330	+
405	Wallemia sebi	9469	+
405	yeast	57176	
409	Alternaria alternata	46490	
409	Alternaria alternata	3283	+
409	Aspergillus niger	467	
409	Aureobasidium pullulans	11762	
409	Aureobasidium pullulans	9389	+
409	Cladosporium cladosporioides	1881	
409	Cladosporium herbarum	940	
409	Cladosporium sphaerospermum	467	+
409	Epicoccum nigrum	473	
409	Eurotium herbariorum	1887	+
409	Fusarium sp.	473	
409	Penicillium commune	467	
409	Penicillium decumbens	473	
409	Phoma herbarum	946	+
409	unknown	2816	
409	yeast	1414	
411	Alternaria alternata	6612	
411	Alternaria alternata	700	+
411	Aspergillus sp.	101	+
411	Aureobasidium pullulans	98	+
411	Cladosporium sp.	98	+
411	Epicoccum nigrum	399	+
411	Epicoccum nigrum	196	
411	Eurotium herbariorum	602	+
411	Eurotium herbariorum	101	
411	Mucor racemosus	101	
411	Paecilomyces sp.	101	
411	Penicillium citreonigrum	101	
411	Penicillium expansum	893	+
411	Penicillium expansum	504	
411	unknown	497	
411	unknown	203	+
411	yeast	1877	
412	Alternaria alternata	1782	
412	Aspergillus versicolor	482	+
412	Aureobasidium pullulans	453	
412	Chrysosporium sp.	453	+
412	Cladosporium sphaerospermum	482	+
412	Epicoccum nigrum	1361	
412	Eurotium herbariorum	4652	+
412	Paecilomyces variotii	453	
412	Penicillium chrysogenum	2355	+
412	Penicillium chrysogenum	965	
412	Penicillium corylophilum	965	
412	Penicillium corylophilum	453	+
412	Penicillium viridicatum	1447	+
412	unknown	1418	+
412	yeast	91071	
414	Alternaria alternata	4793	+
414	Aspergillus niger	418	+
414	Aspergillus versicolor	42407	
414	Aspergillus versicolor	512	+
414	Cladosporium cladosporioides	2606	+
414	Cladosporium cladosporioides	2374	
414	Epicoccum nigrum	418	+
414	Eurotium herbariorum	1349	+
414	Mucor circinelloides	512	+
414	Penicillium chrysogenum	1024	
414	Penicillium islandicum	1862	+
414	Phoma sp.	418	+
414	unknown	4793	
414	unknown	1349	+
414	yeast	7261	
415	Alternaria alternata	63960	
415	Alternaria alternata	53304	+
415	Aureobasidium pullulans	81580	+
415	Aureobasidium pullulans	33581	
415	Cladosporium cladosporioides	4930	+
415	Cladosporium herbarum	4930	
415	Epicoccum nigrum	4930	

HN	Identification	AVG CFU/g	G
415	Eurotium herbariorum	4930	+
415	Penicillium viridicatum	4743	+
415	Phoma herbarum	18975	+
415	Phoma herbarum	4930	
415	Phoma sp.	28837	
415	unknown	39260	
415	yeast	9674	
416	Alternaria alternata	3666	+
416	Aspergillus versicolor	526	
416	Aureobasidium pullulans	526	
416	Cladosporium cladosporioides	508	
416	Cladosporium sp.	526	+
416	Epicoccum nigrum	2050	
416	Epicoccum nigrum	1542	+
416	Eurotium herbariorum	1034	+
416	Penicillium chrysogenum	508	
416	Penicillium griseofulvum	526	
416	Penicillium griseofulvum	526	+
416	Penicillium spinulosum	3103	+
416	Penicillium spinulosum	1052	
416	Penicillium viridicatum	1542	+
416	Penicillium viridicatum	1016	
416	Stemphylium sp.	1052	+
416	unknown	1016	+
416	unknown	508	
416	yeast	17603	
417	Alternaria alternata	10403	
417	Alternaria alternata	1204	+
417	Aspergillus clavatus	1078	+
417	Aspergillus niger	602	
417	Aspergillus sydowii	476	+
417	Aureobasidium pullulans	2409	+
417	Aureobasidium pullulans	1428	
417	Chaetomium sp.	602	
417	Chaetomium sp.	476	+
417	Cladosporium cladosporioides	476	+
417	Cladosporium herbarum	602	+
417	Epicoccum nigrum	1078	+
417	Eurotium herbariorum	2157	+
417	Penicillium chrysogenum	602	+
417	Penicillium chrysogenum	476	
417	Penicillium implicatum	602	
417	unknown	1078	
417	unknown	602	+
417	yeast	11193	
419	Alternaria alternata	551	
419	Aureobasidium pullulans	1017	+
419	Cladosporium sphaerospermum	551	+
419	Epicoccum nigrum	1569	+
419	Epicoccum nigrum	551	
419	Eurotium herbariorum	551	+
419	Neosartorya sp.	551	
419	Neosartorya sp.	551	+
419	Penicillium chrysogenum	1017	+
419	unknown	1396	+
419	unknown	551	
419	yeast	60543	
420	Alternaria alternata	10855	+
420	Cladosporium herbarum	5592	+
420	unknown	16448	+
420	unknown	14194	
420	yeast	5592	
424	Alternaria alternata	6226	
424	Aspergillus niger	467	+
424	Aspergillus sydowii	963	
424	Aspergillus sydowii	948	+
424	Aspergillus versicolor	481	
424	Epicoccum nigrum	948	+
424	Eurotium herbariorum	948	+
424	Fusarium sp.	467	
424	Penicillium chrysogenum	948	+
424	Penicillium citrinum	1430	
424	Phoma sp.	948	
424	Ulocladium chartarum	948	
424	Ulocladium chartarum	948	+
424	unknown	1897	
424	unknown	467	+
424	Wallemia sebi	481	
424	yeast	3839	
425	Aspergillus versicolor	5163	
425	Aureobasidium pullulans	4595	+
425	Phoma sp.	4681	
425	Phoma sp.	4681	+
425	Trichoderma viride	9277	+
425	Trichoderma viride	4595	
425	yeast	189365	
427	Alternaria alternata	139338	
427	Alternaria alternata	188	+
427	Aureobasidium pullulans	94	
427	Paecilomyces sp.	94	
427	Paecilomyces variotii	188	+
427	Penicillium chrysogenum	1968	+
427	Penicillium chrysogenum	1168	
427	Penicillium corylophilum	258	+
427	Penicillium corylophilum	172	
427	unknown	188	
427	unknown	94	+
427	yeast	23293	
429	Alternaria alternata	5027	
429	Aspergillus versicolor	9225	
429	Aspergillus versicolor	4604	+
429	Chrysonilia sp.	4604	
429	Cladosporium herbarum	9225	
429	Trichoderma viride	4612	+
429	unknown	18424	
429	unknown	9225	+
431	Alternaria alternata	4737	+
431	Alternaria alternata	488	
431	Cladosporium sp.	556	
431	Epicoccum nigrum	1113	
431	Eurotium herbariorum	556	+
431	Penicillium expansum	1533	+
431	Penicillium expansum	488	
431	Penicillium melinii	1045	+
431	Penicillium oxalicum	488	+
431	unknown	1113	
431	yeast	20404	
432	Alternaria alternata	2505	
432	Alternaria alternata	97	+
432	Aspergillus clavatus	194	
432	Aureobasidium pullulans	97	
432	Epicoccum nigrum	203	+

HN	Identification	AVG CFU/g	G
432	Epicoccum nigrum	194	
432	Eurotium herbariorum	203	+
432	Penicillium chrysogenum	106	
432	Penicillium chrysogenum	106	+
432	Stemphylium sp.	97	+
432	Trichoderma viride	106	+
432	unknown	194	
432	unknown	106	+
432	Verticillium sp.	203	+
432	yeast	20328	
433	Alternaria alternata	5613	
433	Alternaria alternata	4192	+
433	Alternaria sp.	511	
433	Alternaria sp.	452	+
433	Aspergillus versicolor	511	
433	Aspergillus versicolor	452	+
433	Aureobasidium pullulans	452	
433	Cladosporium cladosporioides	2044	+
433	Cladosporium herbarum	1928	+
433	Cladosporium sp.	452	+
433	Epicoccum nigrum	4587	+
433	Eurotium herbariorum	5726	+
433	Fusarium sp.	511	+
433	Penicillium corylophilum	452	+
433	Penicillium spinulosum	905	+
433	Phoma sp.	511	
433	Stemphylium sp.	511	+
433	unknown	8327	+
433	unknown	5156	
433	yeast	14170	
434	Alternaria alternata	4919	+
434	Alternaria alternata	3331	
434	Aspergillus niger	487	
434	Aspergillus sydowii	499	
434	Aspergillus versicolor	499	
434	Aureobasidium pullulans	1984	
434	Cladosporium herbarum	2459	+
434	Epicoccum nigrum	4444	+
434	Epicoccum nigrum	1485	
434	Mucor plumbeus	986	
434	Penicillium raistrickii	986	+
434	Penicillium sp.	499	
434	Penicillium spinulosum	487	+
434	Phoma sp.	487	
434	Rhizopus oryzae	487	
434	unknown	1972	
434	unknown	499	+
434	yeast	8377	
435	Alternaria alternata	310	+
435	Aspergillus niger	5101	
435	Aspergillus niger	302	+
435	Aureobasidium pullulans	499	+
435	Eurotium herbariorum	514	+
435	Mucor racemosus	106	+
435	Penicillium commune	711	+
435	Penicillium commune	196	
435	Penicillium spinulosum	212	+
435	Trichoderma viride	1226	
435	unknown	294	
435	unknown	106	+
435	yeast	7305	
436	Alternaria alternata	3012	+
436	Aspergillus versicolor	722	
436	Aureobasidium pullulans	2167	
436	Aureobasidium pullulans	722	+
436	Cladosporium sp.	2890	+
436	Cladosporium sp.	722	
436	Cladosporium sphaerospermum	2228	+
436	Cladosporium sphaerospermum	722	
436	Epicoccum nigrum	2289	
436	Eurotium herbariorum	1506	+
436	Penicillium chrysogenum	783	
436	Penicillium spinulosum	1506	
436	Phoma sp.	783	+
436	unknown	6625	+
436	unknown	783	
436	yeast	6208	
437	Alternaria alternata	1596	
437	Alternaria alternata	444	+
437	Aspergillus versicolor	1318	+
437	Aspergillus versicolor	1304	
437	Eurotium amstelodami	430	
437	Eurotium herbariorum	430	+
437	Fusarium sp.	1318	
437	Fusarium sp.	430	+
437	Penicillium brevicompactum	1721	+
437	Penicillium citrinum	888	
437	Penicillium spinulosum	430	+
437	Trichoderma viride	430	
437	unknown	2165	
437	unknown	2165	+
437	yeast	16374	
438	Alternaria alternata	974	+
438	Aspergillus sp.	28956	
438	Aspergillus sp.	1441	+
438	Aspergillus versicolor	467	
438	Aureobasidium pullulans	20791	+
438	Cladosporium sphaerospermum	1441	+
438	Epicoccum nigrum	2028	+
438	Epicoccum nigrum	1481	
438	Penicillium corylophilum	507	+
438	Penicillium viridicatum	1014	
438	Penicillium viridicatum	507	+
438	Stachybotrys chartarum	467	
438	unknown	467	
438	Wallemia sebi	1869	
438	yeast	19477	
439	Alternaria alternata	2658	+
439	Aspergillus sp.	1046	
439	Aspergillus sp.	523	+
439	Aureobasidium pullulans	544	+
439	Cladosporium herbarum	544	+
439	Epicoccum nigrum	1590	
439	Eurotium herbariorum	6406	+
439	Fusarium sp.	544	
439	Fusarium sp.	523	+
439	Mucor plumbeus	523	+
439	Penicillium brevicompactum	15513	+
439	Penicillium chrysogenum	1569	
439	Penicillium chrysogenum	544	+
439	Penicillium corylophilum	4357	+
439	Penicillium corylophilum	1046	

HN	Identification	AVG CFU/g	G
439	Penicillium expansum	2135	
439	Penicillium viridicatum	3181	
439	Ulocladium chartarum	2680	
439	unknown	7931	
439	yeast	25840	
442	Alternaria alternata	556	+
442	Alternaria alternata	432	
442	Aspergillus niger	556	+
442	Aspergillus tamarii	432	
442	Aspergillus versicolor	989	
442	Aureobasidium pullulans	432	+
442	Cladosporium cladosporioides	1421	
442	Epicoccum nigrum	1421	
442	Epicoccum nigrum	432	+
442	Eurotium herbariorum	2659	
442	Eurotium herbariorum	1546	+
442	Penicillium aurantiogriseum	865	+
442	Penicillium aurantiogriseum	556	
442	Syncephalastrum sp.	556	
442	Syncephalastrum sp.	556	+
442	yeast	432	
443	Alternaria alternata	563	
443	Alternaria alternata	563	+
443	Aspergillus versicolor	1539	+
443	Aspergillus versicolor	488	
443	Cladosporium sp.	488	+
443	Epicoccum nigrum	563	
443	Eurotium herbariorum	1126	+
443	Penicillium chrysogenum	2177	
443	Penicillium chrysogenum	1539	+
443	Stemphylium sp.	488	+
443	yeast	70338	
444	Acremonium sp.	446	+
444	Alternaria alternata	3006	+
444	Alternaria alternata	1448	
444	Aspergillus versicolor	1002	
444	Aspergillus versicolor	892	+
444	Cladosporium herbarum	892	+
444	Cladosporium sp.	1448	
444	Epicoccum nigrum	1393	
444	Epicoccum nigrum	501	+
444	Eurotium herbariorum	2004	+
444	Mucor plumbeus	501	
444	Mucor plumbeus	501	+
444	Paecilomyces variotii	501	
444	Scopulariopsis candida	446	+
444	unknown	7753	
444	unknown	4290	+
444	yeast	4628	
445	Alternaria alternata	318	+
445	Aspergillus versicolor	6890	
445	Epicoccum nigrum	111	+
445	Penicillium corylophilum	189	
445	Phoma sp.	94	+
445	unknown	206	+
445	unknown	94	
445	Wallemia sebi	94	+
445	yeast	6767	
446	Alternaria alternata	1359	+
446	Alternaria alternata	793	
446	Alternaria sp.	414	
446	Aspergillus versicolor	106	+
446	Aureobasidium pullulans	212	+
446	Epicoccum nigrum	712	+
446	Epicoccum nigrum	95	
446	Eurotium herbariorum	95	+
446	Mucor plumbeus	191	
446	Penicillium chrysogenum	298	+
446	Penicillium chrysogenum	95	
446	Penicillium commune	308	
446	Penicillium commune	308	+
446	Penicillium sp.	106	
446	Rhizopus oryzae	106	+
446	Rhizopus oryzae	95	
446	unknown	298	+
446	unknown	212	
446	yeast	13753	
447	Alternaria alternata	89	+
447	Epicoccum nigrum	510	+
447	Epicoccum nigrum	201	
447	Eurotium herbariorum	89	+
447	Penicillium corylophilum	461	+
447	Penicillium corylophilum	356	
447	Penicillium viridicatum	89	+
447	unknown	89	+
447	yeast	5112	
448	Alternaria alternata	1075	+
448	Aspergillus niger	486	+
448	Aspergillus versicolor	1510	+
448	Aureobasidium pullulans	348	
448	Cladosporium sp.	48	
448	Eurotium herbariorum	1459	+
448	Fusarium sp.	53	
448	Penicillium chrysogenum	1024	+
448	Penicillium chrysogenum	53	
448	Penicillium griseofulvum	2688	+
448	yeast	30578	
449	Alternaria alternata	35675	
449	Alternaria alternata	1355	+
449	Alternaria sp.	896	
449	Aureobasidium pullulans	2251	+
449	Cladosporium sphaerospermum	901	+
449	Eurotium herbariorum	1792	+
449	Penicillium corylophilum	6323	+
449	Penicillium corylophilum	2251	
449	Phoma sp.	1803	+
449	Pithomyces chartarum	4928	
449	unknown	901	
449	unknown	448	+
449	yeast	204370	
460	Alternaria alternata	998	+
460	Alternaria alternata	923	
460	Aureobasidium pullulans	939	
460	Epicoccum nigrum	499	
460	Penicillium chrysogenum	499	
460	Penicillium corylophilum	939	+
460	Penicillium verrucosum	499	+
460	Phoma sp.	1879	
460	Phoma sp.	939	+
460	Scopulariopsis candida	1879	+
460	Stachybotrys chartarum	469	
460	Ulocladium chartarum	968	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
460	Ulocladium chartarum	939	+				
460	yeast	4815					
500	Alternaria alternata	833					
500	Alternaria alternata	463	+				
500	Aspergillus sp.	1250	+				
500	Aspergillus versicolor	463	+				
500	Cladosporium sphaerospermum	463	+				
500	Eurotium herbariorum	463	+				
500	Eurotium herbariorum	416					
500	Paecilomyces variotii	463					
500	Penicillium corylophilum	416					
500	Penicillium roquefortii	1391	+				
500	Penicillium roquefortii	463					
500	Penicillium simplicissimum	927	+				
500	Rhizopus oryzae	833					
500	Rhizopus oryzae	416	+				
500	yeast	5699					

APPENDIX B

Chi square statistics for association analysis of dust-borne taxa

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A+B+ indicates relevés in which taxa A & B were both observed
A+B- indicates relevés in which taxon A was present and taxon B was absent
A-B+ indicates relevés in which taxon A was absent and taxon B was present
A-B- indicates relevés in which taxa A & B were both absent

E(A+B+) indicates the expected number of relevés with both taxa present

Correlation (CORR) is indicated as positive (POS) or negative (NEG)

Statistical significance is given by p-value

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
ALTEALTE	2	ACRESP	1	POS	24	303	1	41	22.2	0.77	0.380
ALTESP	3	ACRESP	1	NEG	0	16	25	328	1.1	2.60	0.107
ALTESP	3	ALTEALTE	2	POS	16	0	311	42	14.2	1.13	0.288
ASPECAND	4	ACRESP	1	NEG	1	18	24	326	1.3	0.54	0.462
ASPECAND	4	ALTEALTE	2	POS	17	2	310	40	16.8	0.06	0.806
ASPECAND	4	ALTESP	3	POS	1	18	15	335	0.8	0.14	0.708
ASPEFUMI	5	ACRESP	1	POS	3	22	22	322	1.7	0.44	0.507
ASPEFUMI	5	ALTEALTE	2	POS	24	1	303	41	22.2	0.77	0.380
ASPEFUMI	5	ALTESP	3	POS	3	22	13	331	1.1	2.07	0.150
ASPEFUMI	5	ASPECAND	4	POS	5	20	14	330	1.3	9.07	0.003
ASPEGLAU	6	ACRESP	1	POS	3	22	22	322	1.7	0.44	0.507
ASPEGLAU	6	ALTEALTE	2	NEG	22	3	305	39	22.2	0.18	0.671
ASPEGLAU	6	ALTESP	3	POS	4	21	12	332	1.1	6.04	0.014
ASPEGLAU	6	ASPECAND	4	POS	3	22	16	328	1.3	1.29	0.256
ASPEGLAU	6	ASPEFUMI	5	NEG	1	24	24	320	1.7	0.97	0.325
ASPENIGE	7	ACRESP	1	NEG	7	119	18	225	8.5	0.79	0.374
ASPENIGE	7	ALTEALTE	2	POS	112	14	215	28	111.7	0.00	1.000
ASPENIGE	7	ALTESP	3	NEG	5	121	11	232	5.5	0.27	0.603
ASPENIGE	7	ASPECAND	4	POS	9	117	10	233	6.5	1.00	0.317
ASPENIGE	7	ASPEFUMI	5	POS	12	114	13	230	8.5	1.68	0.195
ASPENIGE	7	ASPEGLAU	6	POS	12	114	13	230	8.5	1.68	0.195
ASPEOCHR	8	ACRESP	1	POS	9	63	16	281	4.9	3.58	0.058
ASPEOCHR	8	ALTEALTE	2	NEG	62	10	265	32	63.8	0.91	0.340
ASPEOCHR	8	ALTESP	3	NEG	3	69	13	284	3.1	0.16	0.689
ASPEOCHR	8	ASPECAND	4	POS	6	66	13	284	3.7	1.14	0.286
ASPEOCHR	8	ASPEFUMI	5	POS	8	64	17	280	4.9	1.88	0.170
ASPEOCHR	8	ASPEGLAU	6	POS	5	67	20	277	4.9	0.04	0.841
ASPEOCHR	8	ASPENIGE	7	POS	34	38	92	205	24.6	6.10	0.014
ASPEORYZ	9	ACRESP	1	NEG	0	9	25	335	0.6	2.22	0.136
ASPEORYZ	9	ALTEALTE	2	POS	8	1	319	41	8.0	0.26	0.610
ASPEORYZ	9	ALTESP	3	POS	1	8	15	345	0.4	0.03	0.862
ASPEORYZ	9	ASPECAND	4	NEG	0	9	19	341	0.5	2.16	0.142
ASPEORYZ	9	ASPEFUMI	5	POS	1	8	24	336	0.6	0.02	0.888
ASPEORYZ	9	ASPEGLAU	6	POS	2	7	23	337	0.6	1.43	0.232
ASPEORYZ	9	ASPENIGE	7	POS	4	5	122	238	3.1	0.09	0.764
ASPEORYZ	9	ASPEOCHR	8	NEG	1	8	71	289	1.8	1.14	0.286
ASPESP	10	ACRESP	1	POS	6	61	19	283	4.5	0.27	0.603
ASPESP	10	ALTEALTE	2	NEG	58	9	269	33	59.4	0.63	0.427
ASPESP	10	ALTESP	3	NEG	0	67	16	286	2.9	5.10	0.024
ASPESP	10	ASPECAND	4	NEG	2	65	17	285	3.5	1.42	0.233
ASPESP	10	ASPEFUMI	5	POS	5	62	20	282	4.5	0.00	1.000
ASPESP	10	ASPEGLAU	6	NEG	3	64	22	280	4.5	1.20	0.273
ASPESP	10	ASPENIGE	7	POS	24	43	102	200	22.9	0.03	0.862
ASPESP	10	ASPEOCHR	8	POS	19	48	53	249	13.1	3.42	0.064
ASPESP	10	ASPEORYZ	9	NEG	1	66	8	294	1.6	0.99	0.320
ASPESYDO	11	ACRESP	1	POS	5	41	20	303	3.1	0.75	0.386
ASPESYDO	11	ALTEALTE	2	POS	44	2	283	40	40.8	1.84	0.175
ASPESYDO	11	ALTESP	3	POS	3	43	13	310	2.0	0.15	0.699
ASPESYDO	11	ASPECAND	4	NEG	2	44	17	306	2.4	0.38	0.538
ASPESYDO	11	ASPEFUMI	5	POS	4	42	21	302	3.1	0.06	0.806
ASPESYDO	11	ASPEGLAU	6	POS	6	40	19	304	3.1	2.23	0.135
ASPESYDO	11	ASPENIGE	7	POS	20	26	106	217	15.7	1.59	0.207
ASPESYDO	11	ASPEOCHR	8	POS	11	35	61	262	9.0	0.37	0.543
ASPESYDO	11	ASPEORYZ	9	NEG	0	46	9	314	1.1	2.75	0.097
ASPESYDO	11	ASPESP	10	POS	12	34	55	268	8.4	1.66	0.198
ASPEUSTU	12	ACRESP	1	POS	2	22	23	322	1.6	0.01	0.920
ASPEUSTU	12	ALTEALTE	2	NEG	19	5	308	37	21.3	3.39	0.066
ASPEUSTU	12	ALTESP	3	NEG	0	24	16	329	1.0	2.55	0.110
ASPEUSTU	12	ASPECAND	4	POS	2	22	17	328	1.2	0.06	0.806
ASPEUSTU	12	ASPEFUMI	5	NEG	1	23	24	321	1.6	0.89	0.345
ASPEUSTU	12	ASPEGLAU	6	POS	4	20	21	324	1.6	2.48	0.115
ASPEUSTU	12	ASPENIGE	7	POS	14	10	112	233	8.2	5.58	0.018

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
ASPEUSTU	12	ASPEOCHR	8	POS	5	19	67	278	4.7	0.01	0.920
ASPEUSTU	12	ASPEORYZ	9	POS	2	22	7	338	0.6	1.57	0.210
ASPEUSTU	12	ASPESP	10	POS	5	19	62	283	4.4	0.01	0.920
ASPEUSTU	12	ASPESYDO	11	POS	4	20	42	303	3.0	0.11	0.740
ASPEVERS	13	ACRESP	1	POS	17	179	8	165	13.3	1.79	0.181
ASPEVERS	13	ALTEALTE	2	POS	175	21	152	21	173.7	0.07	0.791
ASPEVERS	13	ALTESP	3	NEG	8	188	8	165	8.5	0.26	0.610
ASPEVERS	13	ASPECAND	4	POS	12	184	7	166	10.1	0.44	0.507
ASPEVERS	13	ASPEFUMI	5	POS	16	180	9	164	13.3	0.85	0.357
ASPEVERS	13	ASPEGLAU	6	NEG	13	183	12	161	13.3	0.10	0.752
ASPEVERS	13	ASPENIGE	7	NEG	64	132	62	111	66.9	0.57	0.450
ASPEVERS	13	ASPEOCHR	8	POS	41	155	31	142	38.2	0.35	0.554
ASPEVERS	13	ASPEORYZ	9	POS	7	189	2	171	4.8	1.35	0.245
ASPEVERS	13	ASPESP	10	POS	41	155	26	147	35.6	1.77	0.183
ASPEVERS	13	ASPESYDO	11	POS	30	166	16	157	24.4	2.56	0.110
ASPEVERS	13	ASPEUSTU	12	POS	15	181	9	164	12.8	0.55	0.458
AUREPULL	14	ACRESP	1	POS	21	272	4	72	19.9	0.11	0.740
AUREPULL	14	ALTEALTE	2	POS	270	23	57	19	259.7	15.94	0.000
AUREPULL	14	ALTESP	3	POS	14	279	2	74	12.7	0.25	0.617
AUREPULL	14	ASPECAND	4	NEG	15	278	4	72	15.1	0.12	0.729
AUREPULL	14	ASPEFUMI	5	POS	21	272	4	72	19.9	0.11	0.740
AUREPULL	14	ASPEGLAU	6	NEG	16	277	9	67	19.9	4.97	0.026
AUREPULL	14	ASPENIGE	7	NEG	95	198	31	45	100.1	2.27	0.132
AUREPULL	14	ASPEOCHR	8	POS	58	235	14	62	57.2	0.01	0.920
AUREPULL	14	ASPEORYZ	9	NEG	5	288	4	72	7.2	4.88	0.027
AUREPULL	14	ASPESP	10	POS	58	235	9	67	53.2	2.06	0.151
AUREPULL	14	ASPESYDO	11	POS	37	256	9	67	36.5	0.00	1.000
AUREPULL	14	ASPEUSTU	12	NEG	14	279	10	66	19.1	8.41	0.004
AUREPULL	14	ASPEVERS	13	NEG	154	139	42	34	155.6	0.30	0.584
CHAEGLOB	15	ACRESP	1	NEG	1	23	24	321	1.6	0.89	0.345
CHAEGLOB	15	ALTEALTE	2	NEG	20	4	307	38	21.3	1.38	0.240
CHAEGLOB	15	ALTESP	3	NEG	1	23	15	330	1.0	0.31	0.578
CHAEGLOB	15	ASPECAND	4	NEG	1	23	18	327	1.2	0.49	0.484
CHAEGLOB	15	ASPEFUMI	5	POS	3	21	22	323	1.6	0.54	0.462
CHAEGLOB	15	ASPEGLAU	6	POS	2	22	23	322	1.6	0.01	0.920
CHAEGLOB	15	ASPENIGE	7	POS	12	12	114	231	8.2	2.16	0.142
CHAEGLOB	15	ASPEOCHR	8	POS	7	17	65	280	4.7	0.94	0.332
CHAEGLOB	15	ASPEORYZ	9	POS	2	22	7	338	0.6	1.57	0.210
CHAEGLOB	15	ASPESP	10	POS	5	19	62	283	4.4	0.01	0.920
CHAEGLOB	15	ASPESYDO	11	POS	3	21	43	302	3.0	0.10	0.752
CHAEGLOB	15	ASPEUSTU	12	NEG	1	23	23	322	1.6	0.82	0.365
CHAEGLOB	15	ASPEVERS	13	POS	14	10	182	163	12.8	0.10	0.752
CHAEGLOB	15	AUREPULL	14	NEG	15	9	278	67	19.1	5.66	0.017
CHRSPMSP	16	ACRESP	1	POS	2	12	23	332	1.0	0.36	0.549
CHRSPMSP	16	ALTEALTE	2	POS	14	0	313	42	12.4	0.88	0.348
CHRSPMSP	16	ALTESP	3	POS	3	11	13	342	0.6	6.41	0.011
CHRSPMSP	16	ASPECAND	4	POS	3	11	16	339	0.7	4.81	0.028
CHRSPMSP	16	ASPEFUMI	5	POS	2	12	23	332	1.0	0.36	0.549
CHRSPMSP	16	ASPEGLAU	6	POS	2	12	23	332	1.0	0.36	0.549
CHRSPMSP	16	ASPENIGE	7	POS	6	8	120	235	4.8	0.17	0.680
CHRSPMSP	16	ASPEOCHR	8	POS	6	8	66	289	2.7	3.62	0.057
CHRSPMSP	16	ASPEORYZ	9	NEG	0	14	9	346	0.3	2.21	0.137
CHRSPMSP	16	ASPESP	10	POS	3	11	64	291	2.5	0.00	1.000
CHRSPMSP	16	ASPESYDO	11	POS	2	12	44	311	1.8	0.04	0.841
CHRSPMSP	16	ASPEUSTU	12	NEG	0	14	24	331	0.9	2.43	0.119
CHRSPMSP	16	ASPEVERS	13	NEG	3	11	193	162	7.4	7.26	0.007
CHRSPMSP	16	AUREPULL	14	POS	14	0	279	76	11.1	2.58	0.108
CHRSPMSP	16	CHAEGLOB	15	NEG	0	14	24	331	0.9	2.43	0.119
CLADCLAD	17	ACRESP	1	NEG	10	175	15	169	12.5	1.58	0.209
CLADCLAD	17	ALTEALTE	2	POS	177	8	150	34	163.9	16.95	0.000
CLADCLAD	17	ALTESP	3	NEG	8	177	8	176	8.0	0.07	0.791
CLADCLAD	17	ASPECAND	4	POS	12	173	7	177	9.5	0.87	0.351

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
CLADCLAD	17	ASPEFUMI	5	POS	16	169	9	175	12.5	1.51	0.219
CLADCLAD	17	ASPEGLAU	6	NEG	11	174	14	170	12.5	0.71	0.399
CLADCLAD	17	ASPENIGE	7	POS	66	119	60	124	63.2	0.26	0.610
CLADCLAD	17	ASPEOCHR	8	POS	38	147	34	150	36.1	0.14	0.708
CLADCLAD	17	ASPEORYZ	9	NEG	3	182	6	178	4.5	1.84	0.175
CLADCLAD	17	ASPESP	10	POS	34	151	33	151	33.6	0.00	1.000
CLADCLAD	17	ASPESYDO	11	NEG	21	164	25	159	23.1	0.65	0.420
CLADCLAD	17	ASPEUSTU	12	NEG	11	174	13	171	12.0	0.42	0.517
CLADCLAD	17	ASPEVERS	13	POS	104	81	92	92	98.3	1.19	0.275
CLADCLAD	17	AUREPULL	14	POS	168	17	125	59	146.9	28.14	0.000
CLADCLAD	17	CHAEGLOB	15	NEG	9	176	15	169	12.0	2.22	0.136
CLADCLAD	17	CHRSPMSP	16	NEG	5	180	9	175	7.0	1.88	0.170
CLADHERB	18	ACRESP	1	POS	7	80	18	264	5.9	0.09	0.764
CLADHERB	18	ALTEALTE	2	POS	84	3	243	39	77.1	6.11	0.013
CLADHERB	18	ALTESP	3	NEG	3	84	13	269	3.8	0.59	0.442
CLADHERB	18	ASPECAND	4	NEG	2	85	17	265	4.5	2.73	0.098
CLADHERB	18	ASPEFUMI	5	NEG	3	84	22	260	5.9	2.74	0.098
CLADHERB	18	ASPEGLAU	6	POS	6	81	19	263	5.9	0.04	0.841
CLADHERB	18	ASPENIGE	7	NEG	25	62	101	181	29.7	1.81	0.179
CLADHERB	18	ASPEOCHR	8	NEG	8	79	64	218	17.0	8.60	0.003
CLADHERB	18	ASPEORYZ	9	NEG	2	85	7	275	2.1	0.24	0.624
CLADHERB	18	ASPESP	10	POS	16	71	51	231	15.8	0.01	0.920
CLADHERB	18	ASPESYDO	11	NEG	10	77	36	246	10.9	0.25	0.617
CLADHERB	18	ASPEUSTU	12	NEG	5	82	19	263	5.7	0.33	0.566
CLADHERB	18	ASPEVERS	13	POS	49	38	147	135	46.2	0.32	0.572
CLADHERB	18	AUREPULL	14	POS	81	6	212	70	69.1	11.99	0.001
CLADHERB	18	CHAEGLOB	15	NEG	1	86	23	259	5.7	6.58	0.010
CLADHERB	18	CHRSPMSP	16	NEG	1	86	13	269	3.3	3.23	0.072
CLADHERB	18	CLADCLAD	17	POS	49	38	136	146	43.6	1.43	0.232
CLADSP	19	ACRESP	1	NEG	4	60	21	284	4.3	0.21	0.647
CLADSP	19	ALTEALTE	2	POS	59	5	268	37	56.7	0.60	0.439
CLADSP	19	ALTESP	3	POS	4	60	12	293	2.8	0.24	0.624
CLADSP	19	ASPECAND	4	POS	5	59	14	291	3.3	0.56	0.454
CLADSP	19	ASPEFUMI	5	POS	6	58	19	286	4.3	0.41	0.522
CLADSP	19	ASPEGLAU	6	NEG	4	60	21	284	4.3	0.21	0.647
CLADSP	19	ASPENIGE	7	POS	23	41	103	202	21.9	0.04	0.841
CLADSP	19	ASPEOCHR	8	POS	14	50	58	247	12.5	0.12	0.729
CLADSP	19	ASPEORYZ	9	NEG	1	63	8	297	1.6	0.89	0.345
CLADSP	19	ASPESP	10	POS	17	47	50	255	11.6	3.03	0.082
CLADSP	19	ASPESYDO	11	NEG	5	59	41	264	8.0	2.10	0.147
CLADSP	19	ASPEUSTU	12	POS	5	59	19	286	4.2	0.04	0.841
CLADSP	19	ASPEVERS	13	NEG	31	33	165	140	34.0	0.93	0.335
CLADSP	19	AUREPULL	14	POS	56	8	237	68	50.8	2.53	0.112
CLADSP	19	CHAEGLOB	15	NEG	3	61	21	284	4.2	0.86	0.354
CLADSP	19	CHRSPMSP	16	POS	8	56	6	299	2.4	13.32	0.000
CLADSP	19	CLADCLAD	17	NEG	32	32	153	152	32.1	0.03	0.862
CLADSP	19	CLADHERB	18	NEG	10	54	77	228	15.1	3.28	0.070
CLADSPHA	20	ACRESP	1	POS	13	128	12	216	9.6	1.58	0.209
CLADSPHA	20	ALTEALTE	2	POS	132	9	195	33	125.0	4.88	0.027
CLADSPHA	20	ALTESP	3	NEG	5	136	11	217	6.1	0.72	0.396
CLADSPHA	20	ASPECAND	4	POS	11	130	8	220	7.3	2.47	0.116
CLADSPHA	20	ASPEFUMI	5	NEG	8	133	17	211	9.6	0.77	0.380
CLADSPHA	20	ASPEGLAU	6	NEG	5	136	20	208	9.6	4.64	0.031
CLADSPHA	20	ASPENIGE	7	NEG	48	93	78	150	48.2	0.02	0.888
CLADSPHA	20	ASPEOCHR	8	POS	39	102	33	195	27.5	8.82	0.003
CLADSPHA	20	ASPEORYZ	9	NEG	2	139	7	221	3.4	1.81	0.179
CLADSPHA	20	ASPESP	10	POS	27	114	40	188	25.6	0.06	0.806
CLADSPHA	20	ASPESYDO	11	POS	18	123	28	200	17.6	0.00	1.000
CLADSPHA	20	ASPEUSTU	12	NEG	5	136	19	209	9.2	4.12	0.042
CLADSPHA	20	ASPEVERS	13	POS	83	58	113	115	74.9	2.67	0.102
CLADSPHA	20	AUREPULL	14	POS	128	13	165	63	112.0	16.95	0.000
CLADSPHA	20	CHAEGLOB	15	NEG	9	132	15	213	9.2	0.08	0.777

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
CLADSPHA	20	CHRSPMSP	16	POS	9	132	5	223	5.4	3.12	0.077
CLADSPHA	20	CLADCLAD	17	POS	86	55	99	129	70.7	10.07	0.002
CLADSPHA	20	CLADHERB	18	POS	37	104	50	178	33.2	0.68	0.410
CLADSPHA	20	CLADSP	19	POS	34	107	30	198	24.5	6.55	0.010
CONISP	21	ACRESP	1	POS	1	9	24	335	0.7	0.05	0.823
CONISP	21	ALTEALTE	2	POS	9	1	318	41	8.9	0.13	0.718
CONISP	21	ALTESP	3	NEG	0	10	16	343	0.4	2.16	0.142
CONISP	21	ASPECAND	4	NEG	0	10	19	340	0.5	2.17	0.141
CONISP	21	ASPEFUMI	5	POS	1	9	24	335	0.7	0.05	0.823
CONISP	21	ASPEGLAU	6	NEG	0	10	25	334	0.7	2.26	0.133
CONISP	21	ASPENIGE	7	POS	4	6	122	237	3.4	0.00	1.000
CONISP	21	ASPEOCHR	8	POS	2	8	70	289	2.0	0.13	0.718
CONISP	21	ASPEORYZ	9	NEG	0	10	9	350	0.2	2.39	0.122
CONISP	21	ASPESP	10	POS	3	7	64	295	1.8	0.32	0.572
CONISP	21	ASPESYDO	11	NEG	0	10	46	313	1.3	2.87	0.090
CONISP	21	ASPEUSTU	12	NEG	0	10	24	335	0.7	2.24	0.134
CONISP	21	ASPEVERS	13	NEG	5	5	191	168	5.3	0.27	0.603
CONISP	21	AUREPULL	14	POS	9	1	284	75	7.9	0.20	0.655
CONISP	21	CHAEGLOB	15	NEG	0	10	24	335	0.7	2.24	0.134
CONISP	21	CHRSPMSP	16	NEG	0	10	14	345	0.4	2.18	0.140
CONISP	21	CLADCLAD	17	NEG	5	5	180	179	5.0	0.11	0.740
CONISP	21	CLADHERB	18	POS	3	7	84	275	2.4	0.01	0.920
CONISP	21	CLADSP	19	NEG	1	9	63	296	1.7	1.09	0.296
CONISP	21	CLADSPHA	20	POS	4	6	137	222	3.8	0.04	0.841
EMERNIDU	22	ACRESP	1	POS	1	9	24	335	0.7	0.05	0.823
EMERNIDU	22	ALTEALTE	2	POS	9	1	318	41	8.9	0.13	0.718
EMERNIDU	22	ALTESP	3	NEG	0	10	16	343	0.4	2.16	0.142
EMERNIDU	22	ASPECAND	4	NEG	0	10	19	340	0.5	2.17	0.141
EMERNIDU	22	ASPEFUMI	5	NEG	0	10	25	334	0.7	2.26	0.133
EMERNIDU	22	ASPEGLAU	6	POS	1	9	24	335	0.7	0.05	0.823
EMERNIDU	22	ASPENIGE	7	POS	5	5	121	238	3.4	0.54	0.462
EMERNIDU	22	ASPEOCHR	8	NEG	0	10	72	287	2.0	3.93	0.047
EMERNIDU	22	ASPEORYZ	9	NEG	0	10	9	350	0.2	2.39	0.122
EMERNIDU	22	ASPESP	10	POS	2	8	65	294	1.8	0.07	0.791
EMERNIDU	22	ASPESYDO	11	POS	2	8	44	315	1.3	0.06	0.806
EMERNIDU	22	ASPEUSTU	12	POS	1	9	23	336	0.7	0.04	0.841
EMERNIDU	22	ASPEVERS	13	POS	7	3	189	170	5.3	0.58	0.446
EMERNIDU	22	AUREPULL	14	NEG	6	4	287	72	7.9	3.74	0.053
EMERNIDU	22	CHAEGLOB	15	POS	2	8	22	337	0.7	1.22	0.269
EMERNIDU	22	CHRSPMSP	16	NEG	0	10	14	345	0.4	2.18	0.140
EMERNIDU	22	CLADCLAD	17	NEG	4	6	181	178	5.0	0.94	0.332
EMERNIDU	22	CLADHERB	18	POS	3	7	84	275	2.4	0.01	0.920
EMERNIDU	22	CLADSP	19	NEG	1	9	63	296	1.7	1.09	0.296
EMERNIDU	22	CLADSPHA	20	POS	4	6	137	222	3.8	0.04	0.841
EMERNIDU	22	CONISP	21	NEG	0	10	10	349	0.3	2.32	0.128
EPICNIGR	23	ACRESP	1	NEG	12	188	13	156	13.6	0.73	0.393
EPICNIGR	23	ALTEALTE	2	POS	193	7	134	35	177.2	25.22	0.000
EPICNIGR	23	ALTESP	3	POS	11	189	5	164	8.7	0.88	0.348
EPICNIGR	23	ASPECAND	4	POS	11	189	8	161	10.3	0.01	0.920
EPICNIGR	23	ASPEFUMI	5	POS	15	185	10	159	13.6	0.16	0.689
EPICNIGR	23	ASPEGLAU	6	POS	14	186	11	158	13.6	0.00	1.000
EPICNIGR	23	ASPENIGE	7	POS	69	131	57	112	68.3	0.00	1.000
EPICNIGR	23	ASPEOCHR	8	NEG	39	161	33	136	39.0	0.02	0.888
EPICNIGR	23	ASPEORYZ	9	NEG	3	197	6	163	4.9	2.59	0.108
EPICNIGR	23	ASPESP	10	POS	38	162	29	140	36.3	0.10	0.752
EPICNIGR	23	ASPESYDO	11	POS	29	171	17	152	24.9	1.27	0.260
EPICNIGR	23	ASPEUSTU	12	NEG	10	190	14	155	13.0	2.21	0.137
EPICNIGR	23	ASPEVERS	13	NEG	100	100	96	73	106.2	1.99	0.158
EPICNIGR	23	AUREPULL	14	POS	178	22	115	54	158.8	23.32	0.000
EPICNIGR	23	CHAEGLOB	15	NEG	9	191	15	154	13.0	3.65	0.056
EPICNIGR	23	CHRSPMSP	16	POS	9	191	5	164	7.6	0.25	0.617
EPICNIGR	23	CLADCLAD	17	POS	118	82	67	102	100.3	12.96	0.000

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
EPICNIGR	23	CLADHERB	18	POS	59	141	28	141	47.2	7.80	0.005
EPICNIGR	23	CLADSP	19	POS	38	162	26	143	34.7	0.60	0.439
EPICNIGR	23	CLADSPHA	20	POS	91	109	50	119	76.4	9.16	0.002
EPICNIGR	23	CONISP	21	POS	6	194	4	165	5.4	0.00	1.000
EPICNIGR	23	EMERNIDU	22	NEG	5	195	5	164	5.4	0.35	0.554
EUROHERB	24	ACRESP	1	POS	19	226	6	118	16.6	0.70	0.403
EUROHERB	24	ALTEALTE	2	NEG	216	29	111	13	217.1	0.31	0.578
EUROHERB	24	ALTESP	3	POS	12	233	4	120	10.6	0.23	0.632
EUROHERB	24	ASPECAND	4	NEG	12	233	7	117	12.6	0.31	0.578
EUROHERB	24	ASPEFUMI	5	NEG	16	229	9	115	16.6	0.23	0.632
EUROHERB	24	ASPEGLAU	6	POS	20	225	5	119	16.6	1.62	0.203
EUROHERB	24	ASPENIGE	7	POS	86	159	40	84	83.7	0.18	0.671
EUROHERB	24	ASPEOCHR	8	POS	55	190	17	107	47.8	3.47	0.062
EUROHERB	24	ASPEORYZ	9	POS	6	239	3	121	6.0	0.12	0.729
EUROHERB	24	ASPESP	10	POS	48	197	19	105	44.5	0.74	0.390
EUROHERB	24	ASPESYDO	11	POS	34	211	12	112	30.5	0.97	0.325
EUROHERB	24	ASPEUSTU	12	NEG	14	231	10	114	15.9	1.18	0.277
EUROHERB	24	ASPEVERS	13	POS	144	101	52	72	130.1	8.71	0.003
EUROHERB	24	AUREPULL	14	NEG	193	52	100	24	194.5	0.31	0.578
EUROHERB	24	CHAEGLOB	15	POS	19	226	5	119	15.9	1.31	0.252
EUROHERB	24	CHRSPMSP	16	NEG	8	237	6	118	9.3	1.07	0.301
EUROHERB	24	CLADCLAD	17	POS	123	122	62	62	122.8	0.01	0.920
EUROHERB	24	CLADHERB	18	NEG	56	189	31	93	57.8	0.35	0.554
EUROHERB	24	CLADSP	19	POS	46	199	18	106	42.5	0.77	0.380
EUROHERB	24	CLADSPHA	20	POS	98	147	43	81	93.6	0.78	0.377
EUROHERB	24	CONISP	21	NEG	6	239	4	120	6.6	0.60	0.439
EUROHERB	24	EMERNIDU	22	POS	8	237	2	122	6.6	0.34	0.560
EUROHERB	24	EPICNIGR	23	NEG	130	115	70	54	132.8	0.53	0.467
FUSAOXYS	25	ACRESP	1	NEG	0	20	25	324	1.4	2.88	0.090
FUSAOXYS	25	ALTEALTE	2	NEG	17	3	310	39	17.7	0.78	0.377
FUSAOXYS	25	ALTESP	3	POS	1	19	15	334	0.9	0.17	0.680
FUSAOXYS	25	ASPECAND	4	NEG	0	20	19	330	1.0	2.53	0.112
FUSAOXYS	25	ASPEFUMI	5	NEG	0	20	25	324	1.4	2.88	0.090
FUSAOXYS	25	ASPEGLAU	6	POS	2	18	23	326	1.4	0.02	0.888
FUSAOXYS	25	ASPENIGE	7	POS	11	9	115	234	6.8	3.17	0.075
FUSAOXYS	25	ASPEOCHR	8	NEG	3	17	69	280	3.9	0.66	0.417
FUSAOXYS	25	ASPEORYZ	9	POS	1	19	8	341	0.5	0.00	1.000
FUSAOXYS	25	ASPESP	10	POS	5	15	62	287	3.6	0.27	0.603
FUSAOXYS	25	ASPESYDO	11	NEG	1	19	45	304	2.5	1.92	0.166
FUSAOXYS	25	ASPEUSTU	12	POS	3	17	21	328	1.3	1.25	0.264
FUSAOXYS	25	ASPEVERS	13	NEG	9	11	187	162	10.6	0.96	0.327
FUSAOXYS	25	AUREPULL	14	NEG	14	6	279	70	15.9	1.83	0.176
FUSAOXYS	25	CHAEGLOB	15	POS	5	15	19	330	1.3	8.90	0.003
FUSAOXYS	25	CHRSPMSP	16	NEG	0	20	14	335	0.8	2.30	0.129
FUSAOXYS	25	CLADCLAD	17	NEG	8	12	177	172	10.0	1.35	0.245
FUSAOXYS	25	CLADHERB	18	POS	5	15	82	267	4.7	0.01	0.920
FUSAOXYS	25	CLADSP	19	POS	4	16	60	289	3.5	0.00	1.000
FUSAOXYS	25	CLADSPHA	20	POS	8	12	133	216	7.6	0.00	1.000
FUSAOXYS	25	CONISP	21	POS	1	19	9	340	0.5	0.00	1.000
FUSAOXYS	25	EMERNIDU	22	POS	2	18	8	341	0.5	1.84	0.175
FUSAOXYS	25	EPICNIGR	23	POS	13	7	187	162	10.8	0.59	0.442
FUSAOXYS	25	EUROHERB	24	POS	14	6	231	118	13.3	0.01	0.920
FUSASP	26	ACRESP	1	POS	6	53	19	291	4.0	0.72	0.396
FUSASP	26	ALTEALTE	2	POS	57	2	270	40	52.3	3.55	0.060
FUSASP	26	ALTESP	3	POS	4	55	12	298	2.6	0.43	0.512
FUSASP	26	ASPECAND	4	POS	5	54	14	296	3.0	0.88	0.348
FUSASP	26	ASPEFUMI	5	NEG	2	57	23	287	4.0	1.99	0.158
FUSASP	26	ASPEGLAU	6	POS	5	54	20	290	4.0	0.08	0.777
FUSASP	26	ASPENIGE	7	NEG	17	42	109	201	20.2	1.19	0.275
FUSASP	26	ASPEOCHR	8	NEG	7	52	65	245	11.5	3.23	0.072
FUSASP	26	ASPEORYZ	9	POS	2	57	7	303	1.4	0.00	1.000
FUSASP	26	ASPESP	10	POS	12	47	55	255	10.7	0.08	0.777

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
FUSASP	26	ASPESYDO	11	POS	9	50	37	273	7.4	0.24	0.624
FUSASP	26	ASPEUSTU	12	POS	8	51	16	294	3.8	4.45	0.035
FUSASP	26	ASPEVERS	13	POS	37	22	159	151	31.3	2.16	0.142
FUSASP	26	AUREPULL	14	POS	47	12	246	64	46.9	0.01	0.920
FUSASP	26	CHAEGLOB	15	NEG	3	56	21	289	3.8	0.59	0.442
FUSASP	26	CHRSPMSP	16	NEG	1	58	13	297	2.2	1.67	0.196
FUSASP	26	CLADCLAD	17	POS	33	26	152	158	29.6	0.69	0.406
FUSASP	26	CLADHERB	18	POS	19	40	68	242	13.9	2.36	0.124
FUSASP	26	CLADSP	19	NEG	6	53	58	252	10.2	3.15	0.076
FUSASP	26	CLADSPHA	20	NEG	22	37	119	191	22.5	0.09	0.764
FUSASP	26	CONISP	21	POS	2	57	8	302	1.6	0.01	0.920
FUSASP	26	EMERNIDU	22	POS	3	56	7	303	1.6	0.62	0.431
FUSASP	26	EPICNIGR	23	POS	33	26	167	143	32.0	0.02	0.888
FUSASP	26	EUROHERB	24	NEG	36	23	209	101	39.2	1.22	0.269
FUSASP	26	FUSAOXYS	25	NEG	2	57	18	292	3.2	1.13	0.288
GEOMPANN	27	ACRESP	1	POS	2	10	23	334	0.8	0.64	0.424
GEOMPANN	27	ALTEALTE	2	NEG	10	2	317	40	10.6	1.10	0.294
GEOMPANN	27	ALTESP	3	NEG	0	12	16	341	0.5	2.16	0.142
GEOMPANN	27	ASPECAND	4	NEG	0	12	19	338	0.6	2.20	0.138
GEOMPANN	27	ASPEFUMI	5	POS	2	10	23	334	0.8	0.64	0.424
GEOMPANN	27	ASPEGLAU	6	NEG	0	12	25	332	0.8	2.35	0.125
GEOMPANN	27	ASPENIGE	7	POS	5	7	121	236	4.1	0.06	0.806
GEOMPANN	27	ASPEOCHR	8	NEG	2	10	70	287	2.3	0.39	0.532
GEOMPANN	27	ASPEORYZ	9	NEG	0	12	9	348	0.3	2.27	0.132
GEOMPANN	27	ASPESP	10	POS	6	6	61	296	2.2	6.39	0.011
GEOMPANN	27	ASPESYDO	11	NEG	1	11	45	312	1.5	0.78	0.377
GEOMPANN	27	ASPEUSTU	12	POS	1	11	23	334	0.8	0.11	0.740
GEOMPANN	27	ASPEVERS	13	POS	7	5	189	168	6.4	0.01	0.920
GEOMPANN	27	AUREPULL	14	POS	11	1	282	75	9.5	0.50	0.480
GEOMPANN	27	CHAEGLOB	15	POS	2	10	22	335	0.8	0.73	0.393
GEOMPANN	27	CHRSPMSP	16	POS	1	11	13	344	0.5	0.00	1.000
GEOMPANN	27	CLADCLAD	17	POS	7	5	178	179	6.0	0.08	0.777
GEOMPANN	27	CLADHERB	18	POS	3	9	84	273	2.8	0.05	0.823
GEOMPANN	27	CLADSP	19	NEG	2	10	62	295	2.1	0.20	0.655
GEOMPANN	27	CLADSPHA	20	POS	8	4	133	224	4.6	3.10	0.078
GEOMPANN	27	CONISP	21	NEG	0	12	10	347	0.3	2.22	0.136
GEOMPANN	27	EMERNIDU	22	NEG	0	12	10	347	0.3	2.22	0.136
GEOMPANN	27	EPICNIGR	23	POS	8	4	192	165	6.5	0.34	0.560
GEOMPANN	27	EUROHERB	24	POS	10	2	235	122	8.0	0.91	0.340
GEOMPANN	27	FUSAOXYS	25	POS	1	11	19	338	0.7	0.04	0.841
GEOMPANN	27	FUSASP	26	POS	2	10	57	300	1.9	0.11	0.740
MUCOPLUM	28	ACRESP	1	NEG	4	69	21	275	5.0	0.57	0.450
MUCOPLUM	28	ALTEALTE	2	POS	67	6	260	36	64.7	0.55	0.458
MUCOPLUM	28	ALTESP	3	POS	5	68	11	285	3.2	0.73	0.393
MUCOPLUM	28	ASPECAND	4	NEG	3	70	16	280	3.8	0.55	0.458
MUCOPLUM	28	ASPEFUMI	5	NEG	4	69	21	275	5.0	0.57	0.450
MUCOPLUM	28	ASPEGLAU	6	POS	6	67	19	277	5.0	0.08	0.777
MUCOPLUM	28	ASPENIGE	7	POS	34	39	92	204	24.9	5.58	0.018
MUCOPLUM	28	ASPEOCHR	8	POS	20	53	52	244	14.2	3.00	0.083
MUCOPLUM	28	ASPEORYZ	9	NEG	1	72	8	288	1.8	1.18	0.277
MUCOPLUM	28	ASPESP	10	POS	16	57	51	245	13.3	0.58	0.446
MUCOPLUM	28	ASPESYDO	11	POS	10	63	36	260	9.1	0.03	0.862
MUCOPLUM	28	ASPEUSTU	12	NEG	3	70	21	275	4.8	1.42	0.233
MUCOPLUM	28	ASPEVERS	13	NEG	37	36	159	137	38.8	0.35	0.554
MUCOPLUM	28	AUREPULL	14	POS	60	13	233	63	58.0	0.25	0.617
MUCOPLUM	28	CHAEGLOB	15	POS	5	68	19	277	4.8	0.02	0.888
MUCOPLUM	28	CHRSPMSP	16	POS	3	70	11	285	2.8	0.03	0.862
MUCOPLUM	28	CLADCLAD	17	POS	40	33	145	151	36.6	0.57	0.450
MUCOPLUM	28	CLADHERB	18	NEG	14	59	73	223	17.2	1.31	0.252
MUCOPLUM	28	CLADSP	19	NEG	9	64	55	241	12.7	2.06	0.151
MUCOPLUM	28	CLADSPHA	20	POS	29	44	112	184	27.9	0.03	0.862
MUCOPLUM	28	CONISP	21	NEG	0	73	10	286	2.0	3.98	0.046

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
MUCOPLUM	28	EMERNIDU	22	POS	3	70	7	289	2.0	0.18	0.671
MUCOPLUM	28	EPICNIGR	23	NEG	35	38	165	131	39.6	1.77	0.183
MUCOPLUM	28	EUROHERB	24	NEG	48	25	197	99	48.5	0.07	0.791
MUCOPLUM	28	FUSAOXYS	25	NEG	2	71	18	278	4.0	2.01	0.156
MUCOPLUM	28	FUSASP	26	NEG	10	63	49	247	11.7	0.60	0.439
MUCOPLUM	28	GEOMPANN	27	NEG	1	72	11	285	2.4	1.91	0.167
MUCORACE	29	ACRESP	1	NEG	5	86	20	258	6.2	0.64	0.424
MUCORACE	29	ALTEALTE	2	POS	82	9	245	33	80.6	0.11	0.740
MUCORACE	29	ALTESP	3	POS	6	85	10	268	4.0	0.85	0.357
MUCORACE	29	ASPECAND	4	POS	7	84	12	266	4.7	0.98	0.322
MUCORACE	29	ASPEFUMI	5	POS	8	83	17	261	6.2	0.41	0.522
MUCORACE	29	ASPEGLAU	6	NEG	5	86	20	258	6.2	0.64	0.424
MUCORACE	29	ASPENIGE	7	POS	36	55	90	188	31.1	1.27	0.260
MUCORACE	29	ASPEOCHR	8	POS	21	70	51	227	17.8	0.70	0.403
MUCORACE	29	ASPEORYZ	9	NEG	0	91	9	269	2.2	4.53	0.033
MUCORACE	29	ASPESP	10	POS	17	74	50	228	16.5	0.00	1.000
MUCORACE	29	ASPESYDO	11	POS	15	76	31	247	11.3	1.33	0.249
MUCORACE	29	ASPEUSTU	12	POS	7	84	17	261	5.9	0.08	0.777
MUCORACE	29	ASPEVERS	13	NEG	47	44	149	129	48.3	0.20	0.655
MUCORACE	29	AUREPULL	14	NEG	72	19	221	57	72.3	0.05	0.823
MUCORACE	29	CHAEGLOB	15	NEG	3	88	21	257	5.9	2.80	0.094
MUCORACE	29	CHRSPMSP	16	POS	4	87	10	268	3.5	0.00	1.000
MUCORACE	29	CLADCLAD	17	POS	49	42	136	142	45.6	0.48	0.488
MUCORACE	29	CLADHERB	18	NEG	18	73	69	209	21.5	1.27	0.260
MUCORACE	29	CLADSP	19	NEG	15	76	49	229	15.8	0.17	0.680
MUCORACE	29	CLADSPHA	20	POS	39	52	102	176	34.8	0.86	0.354
MUCORACE	29	CONISP	21	POS	5	86	5	273	2.5	2.29	0.130
MUCORACE	29	EMERNIDU	22	NEG	2	89	8	270	2.5	0.52	0.471
MUCORACE	29	EPICNIGR	23	POS	56	35	144	134	49.3	2.24	0.134
MUCORACE	29	EUROHERB	24	NEG	59	32	186	92	60.4	0.24	0.624
MUCORACE	29	FUSAOXYS	25	NEG	3	88	17	261	4.9	1.68	0.195
MUCORACE	29	FUSASP	26	POS	17	74	42	236	14.6	0.41	0.522
MUCORACE	29	GEOMPANN	27	POS	5	86	7	271	3.0	1.10	0.294
MUCORACE	29	MUCOPLUM	28	POS	25	66	48	230	18.0	3.88	0.049
PAECSP	30	ACRESP	1	NEG	0	8	25	336	0.5	2.20	0.138
PAECSP	30	ALTEALTE	2	NEG	7	1	320	41	7.1	0.44	0.507
PAECSP	30	ALTESP	3	NEG	0	8	16	345	0.4	2.21	0.137
PAECSP	30	ASPECAND	4	NEG	0	8	19	342	0.4	2.18	0.140
PAECSP	30	ASPEFUMI	5	POS	1	7	24	337	0.5	0.00	1.000
PAECSP	30	ASPEGLAU	6	NEG	0	8	25	336	0.5	2.20	0.138
PAECSP	30	ASPENIGE	7	POS	3	5	123	238	2.7	0.03	0.862
PAECSP	30	ASPEOCHR	8	NEG	1	7	71	290	1.6	0.92	0.337
PAECSP	30	ASPEORYZ	9	NEG	0	8	9	352	0.2	2.59	0.108
PAECSP	30	ASPESP	10	POS	3	5	64	297	1.5	0.94	0.332
PAECSP	30	ASPESYDO	11	NEG	0	8	46	315	1.0	2.63	0.105
PAECSP	30	ASPEUSTU	12	NEG	0	8	24	337	0.5	2.19	0.139
PAECSP	30	ASPEVERS	13	NEG	3	5	193	168	4.3	1.57	0.210
PAECSP	30	AUREPULL	14	NEG	6	2	287	74	6.4	0.57	0.450
PAECSP	30	CHAEGLOB	15	POS	1	7	23	338	0.5	0.00	1.000
PAECSP	30	CHRSPMSP	16	NEG	0	8	14	347	0.3	2.26	0.133
PAECSP	30	CLADCLAD	17	NEG	3	5	182	179	4.0	1.17	0.279
PAECSP	30	CLADHERB	18	POS	2	6	85	276	1.9	0.11	0.740
PAECSP	30	CLADSP	19	POS	2	6	62	299	1.4	0.01	0.920
PAECSP	30	CLADSPHA	20	POS	5	3	136	225	3.1	1.13	0.288
PAECSP	30	CONISP	21	NEG	0	8	10	351	0.2	2.49	0.115
PAECSP	30	EMERNIDU	22	POS	1	7	9	352	0.2	0.39	0.532
PAECSP	30	EPICNIGR	23	NEG	3	5	197	164	4.3	1.74	0.187
PAECSP	30	EUROHERB	24	POS	7	1	238	123	5.3	0.81	0.368
PAECSP	30	FUSAOXYS	25	POS	1	7	19	342	0.4	0.01	0.920
PAECSP	30	FUSASP	26	POS	2	6	57	304	1.3	0.05	0.823
PAECSP	30	GEOMPANN	27	POS	2	6	10	351	0.3	6.24	0.012
PAECSP	30	MUCOPLUM	28	NEG	0	8	73	288	1.6	3.49	0.062

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PAECSP	30	MUCORACE	29	POS	2	6	89	272	2.0	0.15	0.699
PAECVARI	31	ACRESP	1	POS	6	44	19	300	3.4	1.63	0.202
PAECVARI	31	ALTEALTE	2	POS	45	5	282	37	44.3	0.01	0.920
PAECVARI	31	ALTESP	3	POS	5	45	11	308	2.2	3.03	0.082
PAECVARI	31	ASPECAND	4	POS	3	47	16	303	2.6	0.00	1.000
PAECVARI	31	ASPEFUMI	5	POS	6	44	19	300	3.4	1.63	0.202
PAECVARI	31	ASPEGLAU	6	POS	4	46	21	298	3.4	0.00	1.000
PAECVARI	31	ASPENIGE	7	POS	18	32	108	211	17.1	0.02	0.888
PAECVARI	31	ASPEOCHR	8	NEG	7	43	65	254	9.8	1.56	0.212
PAECVARI	31	ASPEORYZ	9	POS	3	47	6	313	1.2	1.59	0.207
PAECVARI	31	ASPESP	10	NEG	4	46	63	256	9.1	4.84	0.028
PAECVARI	31	ASPESYDO	11	NEG	4	46	42	277	6.2	1.58	0.209
PAECVARI	31	ASPEUSTU	12	POS	6	44	18	301	3.3	1.92	0.166
PAECVARI	31	ASPEVERS	13	POS	27	23	169	150	26.6	0.00	1.000
PAECVARI	31	AUREPULL	14	NEG	36	14	257	62	39.7	2.50	0.114
PAECVARI	31	CHAEGLOB	15	POS	5	45	19	300	3.3	0.59	0.442
PAECVARI	31	CHRSPMSP	16	POS	2	48	12	307	1.9	0.10	0.752
PAECVARI	31	CLADCLAD	17	NEG	25	25	160	159	25.1	0.03	0.862
PAECVARI	31	CLADHERB	18	POS	12	38	75	244	11.8	0.01	0.920
PAECVARI	31	CLADSP	19	NEG	5	45	59	260	8.7	2.81	0.094
PAECVARI	31	CLADSPHA	20	POS	25	25	116	203	19.1	2.85	0.091
PAECVARI	31	CONISP	21	NEG	0	50	10	309	1.4	3.02	0.082
PAECVARI	31	EMERNIDU	22	POS	2	48	8	311	1.4	0.02	0.888
PAECVARI	31	EPICNIGR	23	NEG	26	24	174	145	27.1	0.24	0.624
PAECVARI	31	EUROHERB	24	POS	36	14	209	110	33.2	0.55	0.458
PAECVARI	31	FUSAOXYS	25	POS	6	44	14	305	2.7	3.51	0.061
PAECVARI	31	FUSASP	26	POS	10	40	49	270	8.0	0.39	0.532
PAECVARI	31	GEOMPANN	27	NEG	0	50	12	307	1.6	3.32	0.068
PAECVARI	31	MUCOPLUM	28	NEG	9	41	64	255	9.9	0.28	0.597
PAECVARI	31	MUCORACE	29	POS	14	36	77	242	12.3	0.17	0.680
PAECVARI	31	PAECSP	30	POS	2	48	6	313	1.1	0.19	0.663
PENIATRA	32	ACRESP	1	NEG	0	9	25	335	0.6	2.22	0.136
PENIATRA	32	ALTEALTE	2	POS	8	1	319	41	8.0	0.26	0.610
PENIATRA	32	ALTESP	3	POS	3	6	13	347	0.4	12.22	0.000
PENIATRA	32	ASPECAND	4	POS	1	8	18	342	0.5	0.00	1.000
PENIATRA	32	ASPEFUMI	5	POS	1	8	24	336	0.6	0.02	0.888
PENIATRA	32	ASPEGLAU	6	POS	4	5	21	339	0.6	15.06	0.000
PENIATRA	32	ASPENIGE	7	POS	6	3	120	240	3.1	2.98	0.084
PENIATRA	32	ASPEOCHR	8	POS	2	7	70	290	1.8	0.05	0.823
PENIATRA	32	ASPEORYZ	9	POS	1	8	8	352	0.2	0.38	0.538
PENIATRA	32	ASPESP	10	POS	2	7	65	295	1.6	0.01	0.920
PENIATRA	32	ASPESYDO	11	NEG	1	8	45	315	1.1	0.40	0.527
PENIATRA	32	ASPEUSTU	12	POS	1	8	23	337	0.6	0.01	0.920
PENIATRA	32	ASPEVERS	13	NEG	4	5	192	168	4.8	0.75	0.386
PENIATRA	32	AUREPULL	14	NEG	6	3	287	73	7.2	1.89	0.169
PENIATRA	32	CHAEGLOB	15	POS	2	7	22	338	0.6	1.57	0.210
PENIATRA	32	CHRSPMSP	16	POS	3	6	11	349	0.3	14.54	0.000
PENIATRA	32	CLADCLAD	17	NEG	4	5	181	179	4.5	0.47	0.493
PENIATRA	32	CLADHERB	18	NEG	1	8	86	274	2.1	1.66	0.198
PENIATRA	32	CLADSP	19	POS	2	7	62	298	1.6	0.00	1.000
PENIATRA	32	CLADSPHA	20	NEG	2	7	139	221	3.4	1.81	0.179
PENIATRA	32	CONISP	21	NEG	0	9	10	350	0.2	2.39	0.122
PENIATRA	32	EMERNIDU	22	NEG	0	9	10	350	0.2	2.39	0.122
PENIATRA	32	EPICNIGR	23	POS	5	4	195	165	4.9	0.07	0.791
PENIATRA	32	EUROHERB	24	NEG	5	4	240	120	6.0	1.11	0.292
PENIATRA	32	FUSAOXYS	25	POS	2	7	18	342	0.5	2.28	0.131
PENIATRA	32	FUSASP	26	NEG	0	9	59	301	1.4	3.19	0.074
PENIATRA	32	GEOMPANN	27	NEG	0	9	12	348	0.3	2.27	0.132
PENIATRA	32	MUCOPLUM	28	POS	3	6	70	290	1.8	0.37	0.543
PENIATRA	32	MUCORACE	29	POS	3	6	88	272	2.2	0.05	0.823
PENIATRA	32	PAECSP	30	NEG	0	9	8	352	0.2	2.59	0.108
PENIATRA	32	PAECVARI	31	NEG	1	8	49	311	1.2	0.50	0.480

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENIAURA	33	ACRESP	1	POS	3	41	22	303	3.0	0.09	0.764
PENIAURA	33	ALTEALTE	2	NEG	35	9	292	33	39.0	5.16	0.023
PENIAURA	33	ALTESP	3	NEG	1	43	15	310	1.9	1.23	0.267
PENIAURA	33	ASPECAND	4	POS	4	40	15	310	2.3	0.81	0.368
PENIAURA	33	ASPEFUMI	5	POS	3	41	22	303	3.0	0.09	0.764
PENIAURA	33	ASPEGLAU	6	POS	3	41	22	303	3.0	0.09	0.764
PENIAURA	33	ASPENIGE	7	POS	19	25	107	218	15.0	1.39	0.238
PENIAURA	33	ASPEOCHR	8	POS	10	34	62	263	8.6	0.14	0.708
PENIAURA	33	ASPEORYZ	9	NEG	0	44	9	316	1.1	2.68	0.102
PENIAURA	33	ASPESP	10	POS	9	35	58	267	8.0	0.05	0.823
PENIAURA	33	ASPESYDO	11	POS	8	36	38	287	5.5	0.96	0.327
PENIAURA	33	ASPEUSTU	12	NEG	2	42	22	303	2.9	0.79	0.374
PENIAURA	33	ASPEVERS	13	NEG	23	21	173	152	23.4	0.08	0.777
PENIAURA	33	AUREPULL	14	NEG	31	13	262	63	34.9	3.11	0.078
PENIAURA	33	CHAEGLOB	15	POS	5	39	19	306	2.9	1.14	0.286
PENIAURA	33	CHRSPMSP	16	POS	2	42	12	313	1.7	0.02	0.888
PENIAURA	33	CLADCLAD	17	NEG	17	27	168	157	22.1	3.19	0.074
PENIAURA	33	CLADHERB	18	NEG	9	35	78	247	10.4	0.50	0.480
PENIAURA	33	CLADSP	19	NEG	5	39	59	266	7.6	1.77	0.183
PENIAURA	33	CLADSPHA	20	NEG	15	29	126	199	16.8	0.58	0.446
PENIAURA	33	CONISP	21	NEG	0	44	10	315	1.2	2.80	0.094
PENIAURA	33	EMERNIDU	22	NEG	1	43	9	316	1.2	0.47	0.493
PENIAURA	33	EPICNIGR	23	NEG	18	26	182	143	23.9	4.19	0.041
PENIAURA	33	EUROHERB	24	POS	32	12	213	112	29.2	0.60	0.439
PENIAURA	33	FUSAOXYS	25	POS	5	39	15	310	2.4	2.25	0.134
PENIAURA	33	FUSASP	26	NEG	5	39	54	271	7.0	1.23	0.267
PENIAURA	33	GEOMPANN	27	NEG	1	43	11	314	1.4	0.71	0.399
PENIAURA	33	MUCOPLUM	28	POS	11	33	62	263	8.7	0.52	0.471
PENIAURA	33	MUCORACE	29	POS	15	29	76	249	10.9	1.85	0.174
PENIAURA	33	PAECSP	30	NEG	0	44	8	317	1.0	2.57	0.109
PENIAURA	33	PAECVARI	31	POS	7	37	43	282	6.0	0.06	0.806
PENIAURA	33	PENIATRA	32	POS	3	41	6	319	1.1	2.21	0.137
PENIBREV	34	ACRESP	1	NEG	2	84	23	260	5.8	4.49	0.034
PENIBREV	34	ALTEALTE	2	POS	80	6	247	36	76.2	1.63	0.202
PENIBREV	34	ALTESP	3	NEG	1	85	15	268	3.7	3.81	0.051
PENIBREV	34	ASPECAND	4	NEG	4	82	15	268	4.4	0.27	0.603
PENIBREV	34	ASPEFUMI	5	NEG	4	82	21	262	5.8	1.30	0.254
PENIBREV	34	ASPEGLAU	6	NEG	5	81	20	263	5.8	0.42	0.517
PENIBREV	34	ASPENIGE	7	POS	32	54	94	189	29.4	0.31	0.578
PENIBREV	34	ASPEOCHR	8	POS	18	68	54	229	16.8	0.05	0.823
PENIBREV	34	ASPEORYZ	9	NEG	2	84	7	276	2.1	0.23	0.632
PENIBREV	34	ASPESP	10	POS	20	66	47	236	15.6	1.54	0.215
PENIBREV	34	ASPESYDO	11	NEG	5	81	41	242	10.7	5.38	0.020
PENIBREV	34	ASPEUSTU	12	NEG	5	81	19	264	5.6	0.30	0.584
PENIBREV	34	ASPEVERS	13	POS	48	38	148	135	45.7	0.20	0.655
PENIBREV	34	AUREPULL	14	POS	75	11	218	65	68.3	3.58	0.058
PENIBREV	34	CHAEGLOB	15	POS	7	79	17	266	5.6	0.20	0.655
PENIBREV	34	CHRSPMSP	16	NEG	3	83	11	272	3.3	0.24	0.624
PENIBREV	34	CLADCLAD	17	POS	55	31	130	153	43.1	7.86	0.005
PENIBREV	34	CLADHERB	18	NEG	15	71	72	211	20.3	2.81	0.094
PENIBREV	34	CLADSP	19	POS	15	71	49	234	14.9	0.02	0.888
PENIBREV	34	CLADSPHA	20	POS	40	46	101	182	32.9	2.83	0.093
PENIBREV	34	CONISP	21	NEG	1	85	9	274	2.3	1.93	0.165
PENIBREV	34	EMERNIDU	22	NEG	2	84	8	275	2.3	0.40	0.527
PENIBREV	34	EPICNIGR	23	POS	53	33	147	136	46.6	2.12	0.145
PENIBREV	34	EUROHERB	24	POS	59	27	186	97	57.1	0.13	0.718
PENIBREV	34	FUSAOXYS	25	POS	7	79	13	270	4.7	1.00	0.317
PENIBREV	34	FUSASP	26	POS	14	72	45	238	13.8	0.01	0.920
PENIBREV	34	GEOMPANN	27	NEG	2	84	10	273	2.8	0.81	0.368
PENIBREV	34	MUCOPLUM	28	POS	18	68	55	228	17.0	0.02	0.888
PENIBREV	34	MUCORACE	29	POS	22	64	69	214	21.2	0.01	0.920
PENIBREV	34	PAECSP	30	POS	2	84	6	277	1.9	0.09	0.764

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENIBREV	34	PAECVARI	31	POS	12	74	38	245	11.7	0.00	1.000
PENIBREV	34	PENIATRA	32	NEG	2	84	7	276	2.1	0.23	0.632
PENIBREV	34	PENIAURA	33	POS	12	74	32	251	10.3	0.22	0.639
PENICHRY	35	ACRESP	1	POS	14	177	11	167	12.9	0.05	0.823
PENICHRY	35	ALTEALTE	2	NEG	166	25	161	17	169.3	1.52	0.218
PENICHRY	35	ALTESP	3	NEG	7	184	9	169	8.3	0.83	0.362
PENICHRY	35	ASPECAND	4	POS	11	180	8	170	9.8	0.10	0.752
PENICHRY	35	ASPEFUMI	5	POS	13	178	12	166	12.9	0.03	0.862
PENICHRY	35	ASPEGLAU	6	POS	14	177	11	167	12.9	0.05	0.823
PENICHRY	35	ASPENIGE	7	POS	66	125	60	118	65.2	0.00	1.000
PENICHRY	35	ASPEOCHR	8	NEG	33	158	39	139	37.3	1.57	0.210
PENICHRY	35	ASPEORYZ	9	POS	7	184	2	176	4.7	1.55	0.213
PENICHRY	35	ASPESP	10	POS	38	153	29	149	34.7	0.58	0.446
PENICHRY	35	ASPESYDO	11	NEG	21	170	25	153	23.8	1.09	0.296
PENICHRY	35	ASPEUSTU	12	POS	19	172	5	173	12.4	6.59	0.010
PENICHRY	35	ASPEVERS	13	POS	114	77	82	96	101.5	6.33	0.012
PENICHRY	35	AUREPULL	14	POS	155	36	138	40	151.7	0.53	0.467
PENICHRY	35	CHAEGLOB	15	POS	13	178	11	167	12.4	0.00	1.000
PENICHRY	35	CHRSPMSP	16	POS	8	183	6	172	7.3	0.02	0.888
PENICHRY	35	CLADCLAD	17	POS	96	95	89	89	95.8	0.00	1.000
PENICHRY	35	CLADHERB	18	POS	46	145	41	137	45.0	0.01	0.920
PENICHRY	35	CLADSP	19	NEG	28	163	36	142	33.1	2.40	0.121
PENICHRY	35	CLADSPHA	20	POS	80	111	61	117	73.0	1.95	0.163
PENICHRY	35	CONISP	21	POS	6	185	4	174	5.2	0.04	0.841
PENICHRY	35	EMERNIDU	22	POS	6	185	4	174	5.2	0.04	0.841
PENICHRY	35	EPICNIGR	23	NEG	99	92	101	77	103.5	1.10	0.294
PENICHRY	35	EUROHERB	24	POS	128	63	117	61	126.8	0.02	0.888
PENICHRY	35	FUSAOXYS	25	POS	12	179	8	170	10.4	0.28	0.597
PENICHRY	35	FUSASP	26	NEG	27	164	32	146	30.5	1.32	0.251
PENICHRY	35	GEOMPANN	27	POS	8	183	4	174	6.2	0.57	0.450
PENICHRY	35	MUCOPLUM	28	POS	42	149	31	147	37.8	0.94	0.332
PENICHRY	35	MUCORACE	29	NEG	44	147	47	131	47.1	0.76	0.383
PENICHRY	35	PAECSP	30	NEG	4	187	4	174	4.1	0.21	0.647
PENICHRY	35	PAECVARI	31	POS	29	162	21	157	25.9	0.64	0.424
PENICHRY	35	PENIATRA	32	POS	5	186	4	174	4.7	0.01	0.920
PENICHRY	35	PENIAURA	33	NEG	21	170	23	155	22.8	0.53	0.467
PENICHRY	35	PENIBREV	34	NEG	40	151	46	132	44.5	1.53	0.216
PENICOMM	36	ACRESP	1	NEG	5	89	20	255	6.4	0.79	0.374
PENICOMM	36	ALTEALTE	2	POS	86	8	241	34	83.3	0.68	0.410
PENICOMM	36	ALTESP	3	POS	8	86	8	267	4.1	4.03	0.045
PENICOMM	36	ASPECAND	4	NEG	2	92	17	258	4.8	3.26	0.071
PENICOMM	36	ASPEFUMI	5	POS	9	85	16	259	6.4	1.03	0.310
PENICOMM	36	ASPEGLAU	6	NEG	6	88	19	256	6.4	0.17	0.680
PENICOMM	36	ASPENIGE	7	POS	40	54	86	189	32.1	3.48	0.062
PENICOMM	36	ASPEOCHR	8	POS	21	73	51	224	18.3	0.42	0.517
PENICOMM	36	ASPEORYZ	9	NEG	2	92	7	268	2.3	0.38	0.538
PENICOMM	36	ASPESP	10	NEG	17	77	50	225	17.1	0.03	0.862
PENICOMM	36	ASPESYDO	11	NEG	11	83	35	240	11.7	0.19	0.663
PENICOMM	36	ASPEUSTU	12	NEG	5	89	19	256	6.1	0.61	0.435
PENICOMM	36	ASPEVERS	13	NEG	47	47	149	126	49.9	0.67	0.413
PENICOMM	36	AUREPULL	14	POS	76	18	217	58	74.6	0.06	0.806
PENICOMM	36	CHAEGLOB	15	POS	10	84	14	261	6.1	2.69	0.101
PENICOMM	36	CHRSPMSP	16	POS	9	85	5	270	3.6	9.52	0.002
PENICOMM	36	CLADCLAD	17	POS	52	42	133	142	47.1	1.09	0.296
PENICOMM	36	CLADHERB	18	NEG	12	82	75	200	22.2	9.01	0.003
PENICOMM	36	CLADSP	19	POS	21	73	43	232	16.3	1.75	0.186
PENICOMM	36	CLADSPHA	20	POS	38	56	103	172	35.9	0.15	0.699
PENICOMM	36	CONISP	21	NEG	1	93	9	266	2.6	2.27	0.132
PENICOMM	36	EMERNIDU	22	POS	4	90	6	269	2.6	0.49	0.484
PENICOMM	36	EPICNIGR	23	NEG	50	44	150	125	51.0	0.12	0.729
PENICOMM	36	EUROHERB	24	POS	68	26	177	98	62.4	1.66	0.198
PENICOMM	36	FUSAOXYS	25	POS	6	88	14	261	5.1	0.05	0.823

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENICOMM	36	FUSASP	26	NEG	12	82	47	228	15.0	1.32	0.251
PENICOMM	36	GEOMPANN	27	POS	5	89	7	268	3.1	0.94	0.332
PENICOMM	36	MUCOPLUM	28	NEG	17	77	56	219	18.6	0.40	0.527
PENICOMM	36	MUCORACE	29	NEG	21	73	70	205	23.2	0.55	0.458
PENICOMM	36	PAECSP	30	POS	3	91	5	270	2.0	0.14	0.708
PENICOMM	36	PAECVARI	31	NEG	12	82	38	237	12.7	0.19	0.663
PENICOMM	36	PENIATRA	32	POS	4	90	5	270	2.3	0.87	0.351
PENICOMM	36	PENIAURA	33	POS	17	77	27	248	11.2	3.81	0.051
PENICOMM	36	PENIBREV	34	POS	31	63	55	220	21.9	5.90	0.015
PENICOMM	36	PENICHRY	35	NEG	39	55	152	123	48.7	5.90	0.015
PENICOPR	37	ACRESP	1	NEG	0	10	25	334	0.7	2.26	0.133
PENICOPR	37	ALTEALTE	2	NEG	7	3	320	39	8.9	5.68	0.017
PENICOPR	37	ALTESP	3	NEG	0	10	16	343	0.4	2.16	0.142
PENICOPR	37	ASPECAND	4	NEG	0	10	19	340	0.5	2.17	0.141
PENICOPR	37	ASPEFUMI	5	NEG	0	10	25	334	0.7	2.26	0.133
PENICOPR	37	ASPEGLAU	6	NEG	0	10	25	334	0.7	2.26	0.133
PENICOPR	37	ASPENIGE	7	POS	5	5	121	238	3.4	0.54	0.462
PENICOPR	37	ASPEOCHR	8	POS	3	7	69	290	2.0	0.20	0.655
PENICOPR	37	ASPEORYZ	9	NEG	0	10	9	350	0.2	2.39	0.122
PENICOPR	37	ASPESP	10	POS	4	6	63	296	1.8	1.96	0.162
PENICOPR	37	ASPESYDO	11	NEG	1	9	45	314	1.3	0.53	0.467
PENICOPR	37	ASPEUSTU	12	NEG	0	10	24	335	0.7	2.24	0.134
PENICOPR	37	ASPEVERS	13	POS	7	3	189	170	5.3	0.58	0.446
PENICOPR	37	AUREPULL	14	POS	10	0	283	76	7.9	1.53	0.216
PENICOPR	37	CHAEGLOB	15	NEG	0	10	24	335	0.7	2.24	0.134
PENICOPR	37	CHRSPMSP	16	NEG	0	10	14	345	0.4	2.18	0.140
PENICOPR	37	CLADCLAD	17	POS	6	4	179	180	5.0	0.10	0.752
PENICOPR	37	CLADHERB	18	NEG	1	9	86	273	2.4	1.97	0.160
PENICOPR	37	CLADSP	19	POS	3	7	61	298	1.7	0.42	0.517
PENICOPR	37	CLADSPHA	20	POS	6	4	135	224	3.8	1.23	0.267
PENICOPR	37	CONISP	21	NEG	0	10	10	349	0.3	2.32	0.128
PENICOPR	37	EMERNIDU	22	NEG	0	10	10	349	0.3	2.32	0.128
PENICOPR	37	EPICNIGR	23	POS	7	3	193	166	5.4	0.48	0.488
PENICOPR	37	EUROHERB	24	POS	9	1	236	123	6.6	1.59	0.207
PENICOPR	37	FUSAOXYS	25	POS	1	9	19	340	0.5	0.00	1.000
PENICOPR	37	FUSASP	26	NEG	0	10	59	300	1.6	3.37	0.066
PENICOPR	37	GEOMPANN	27	POS	2	8	10	349	0.3	4.51	0.034
PENICOPR	37	MUCOPLUM	28	POS	2	8	71	288	2.0	0.15	0.699
PENICOPR	37	MUCORACE	29	NEG	2	8	89	270	2.5	0.52	0.471
PENICOPR	37	PAECSP	30	POS	2	8	6	353	0.2	7.98	0.005
PENICOPR	37	PAECVARI	31	NEG	1	9	49	310	1.4	0.64	0.424
PENICOPR	37	PENIATRA	32	NEG	0	10	9	350	0.2	2.39	0.122
PENICOPR	37	PENIAURA	33	NEG	1	9	43	316	1.2	0.47	0.493
PENICOPR	37	PENIBREV	34	POS	6	4	80	279	2.3	5.78	0.016
PENICOPR	37	PENICHRY	35	POS	6	4	185	174	5.2	0.04	0.841
PENICOPR	37	PENICOMM	36	NEG	1	9	93	266	2.6	2.27	0.132
PENICORY	38	ACRESP	1	POS	9	99	16	245	7.3	0.29	0.590
PENICORY	38	ALTEALTE	2	NEG	94	14	233	28	95.7	0.63	0.427
PENICORY	38	ALTESP	3	POS	11	97	5	256	4.7	10.68	0.001
PENICORY	38	ASPECAND	4	NEG	5	103	14	247	5.6	0.30	0.584
PENICORY	38	ASPEFUMI	5	POS	9	99	16	245	7.3	0.29	0.590
PENICORY	38	ASPEGLAU	6	POS	12	96	13	248	7.3	3.63	0.057
PENICORY	38	ASPENIGE	7	POS	39	69	87	174	36.9	0.15	0.699
PENICORY	38	ASPEOCHR	8	NEG	20	88	52	209	21.1	0.21	0.647
PENICORY	38	ASPEORYZ	9	POS	3	105	6	255	2.6	0.01	0.920
PENICORY	38	ASPESP	10	POS	20	88	47	214	19.6	0.00	1.000
PENICORY	38	ASPESYDO	11	NEG	9	99	37	224	13.5	2.96	0.085
PENICORY	38	ASPEUSTU	12	NEG	6	102	18	243	7.0	0.50	0.480
PENICORY	38	ASPEVERS	13	NEG	56	52	140	121	57.4	0.18	0.671
PENICORY	38	AUREPULL	14	NEG	84	24	209	52	85.8	0.41	0.522
PENICORY	38	CHAEGLOB	15	NEG	7	101	17	244	7.0	0.06	0.806
PENICORY	38	CHRSPMSP	16	POS	10	98	4	257	4.1	10.47	0.001

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENICORY	38	CLADCLAD	17	NEG	49	59	136	125	54.2	1.67	0.196
PENICORY	38	CLADHERB	18	NEG	16	92	71	190	25.5	7.21	0.007
PENICORY	38	CLADSP	19	POS	19	89	45	216	18.7	0.00	1.000
PENICORY	38	CLADSPHA	20	POS	48	60	93	168	41.3	2.15	0.143
PENICORY	38	CONISP	21	POS	3	105	7	254	2.9	0.09	0.764
PENICORY	38	EMERNIDU	22	POS	3	105	7	254	2.9	0.09	0.764
PENICORY	38	EPICNIGR	23	POS	63	45	137	124	58.5	0.83	0.362
PENICORY	38	EUROHERB	24	POS	74	34	171	90	71.7	0.19	0.663
PENICORY	38	FUSAOXYS	25	POS	8	100	12	249	5.9	0.69	0.406
PENICORY	38	FUSASP	26	POS	19	89	40	221	17.3	0.15	0.699
PENICORY	38	GEOMPANN	27	POS	6	102	6	255	3.5	1.64	0.200
PENICORY	38	MUCOPLUM	28	POS	23	85	50	211	21.4	0.11	0.740
PENICORY	38	MUCORACE	29	POS	32	76	59	202	26.6	1.67	0.196
PENICORY	38	PAECSP	30	NEG	2	106	6	255	2.3	0.44	0.507
PENICORY	38	PAECVARI	31	POS	24	84	26	235	14.6	8.78	0.003
PENICORY	38	PENIATRA	32	POS	7	101	2	259	2.6	8.22	0.004
PENICORY	38	PENIAURA	33	POS	14	94	30	231	12.9	0.05	0.823
PENICORY	38	PENIBREV	34	POS	31	77	55	206	25.2	2.08	0.149
PENICORY	38	PENICHRY	35	POS	58	50	133	128	55.9	0.13	0.718
PENICORY	38	PENICOMM	36	NEG	26	82	68	193	27.5	0.28	0.597
PENICORY	38	PENICOPR	37	POS	3	105	7	254	2.9	0.09	0.764
PENICRUS	39	ACRESP	1	POS	1	13	24	331	1.0	0.24	0.624
PENICRUS	39	ALTEALTE	2	POS	13	1	314	41	12.4	0.01	0.920
PENICRUS	39	ALTESP	3	NEG	0	14	16	339	0.6	2.19	0.139
PENICRUS	39	ASPECAND	4	NEG	0	14	19	336	0.7	2.27	0.132
PENICRUS	39	ASPEFUMI	5	POS	1	13	24	331	1.0	0.24	0.624
PENICRUS	39	ASPEGLAU	6	POS	2	12	23	332	1.0	0.36	0.549
PENICRUS	39	ASPENIGE	7	POS	7	7	119	236	4.8	0.98	0.322
PENICRUS	39	ASPEOCHR	8	POS	4	10	68	287	2.7	0.28	0.597
PENICRUS	39	ASPEORYZ	9	NEG	0	14	9	346	0.3	2.21	0.137
PENICRUS	39	ASPESP	10	POS	3	11	64	291	2.5	0.00	1.000
PENICRUS	39	ASPESYDO	11	NEG	1	13	45	310	1.8	1.06	0.303
PENICRUS	39	ASPEUSTU	12	POS	1	13	23	332	0.9	0.21	0.647
PENICRUS	39	ASPEVERS	13	POS	8	6	188	167	7.4	0.00	1.000
PENICRUS	39	AUREPULL	14	NEG	9	5	284	71	11.1	3.11	0.078
PENICRUS	39	CHAEGLOB	15	POS	6	8	18	337	0.9	25.72	0.000
PENICRUS	39	CHRSPMSP	16	NEG	0	14	14	341	0.5	2.16	0.142
PENICRUS	39	CLADCLAD	17	NEG	5	9	180	175	7.0	1.88	0.170
PENICRUS	39	CLADHERB	18	NEG	2	12	85	270	3.3	1.34	0.247
PENICRUS	39	CLADSP	19	POS	3	11	61	294	2.4	0.00	1.000
PENICRUS	39	CLADSPHA	20	POS	8	6	133	222	5.4	1.45	0.229
PENICRUS	39	CONISP	21	POS	1	13	9	346	0.4	0.04	0.841
PENICRUS	39	EMERNIDU	22	POS	1	13	9	346	0.4	0.04	0.841
PENICRUS	39	EPICNIGR	23	POS	8	6	192	163	7.6	0.00	1.000
PENICRUS	39	EUROHERB	24	POS	11	3	234	121	9.3	0.48	0.488
PENICRUS	39	FUSAOXYS	25	POS	3	11	17	338	0.8	4.39	0.036
PENICRUS	39	FUSASP	26	NEG	2	12	57	298	2.2	0.30	0.584
PENICRUS	39	GEOMPANN	27	NEG	0	14	12	343	0.5	2.15	0.143
PENICRUS	39	MUCOPLUM	28	NEG	2	12	71	284	2.8	0.75	0.386
PENICRUS	39	MUCORACE	29	POS	4	10	87	268	3.5	0.00	1.000
PENICRUS	39	PAECSP	30	POS	2	12	6	349	0.3	5.01	0.025
PENICRUS	39	PAECVARI	31	POS	2	12	48	307	1.9	0.10	0.752
PENICRUS	39	PENIATRA	32	POS	1	13	8	347	0.3	0.08	0.777
PENICRUS	39	PENIAURA	33	POS	2	12	42	313	1.7	0.02	0.888
PENICRUS	39	PENIBREV	34	NEG	2	12	84	271	3.3	1.29	0.256
PENICRUS	39	PENICHRY	35	POS	8	6	183	172	7.3	0.02	0.888
PENICRUS	39	PENICOMM	36	POS	6	8	88	267	3.6	1.46	0.227
PENICRUS	39	PENICOPR	37	NEG	0	14	10	345	0.4	2.18	0.140
PENICRUS	39	PENICORY	38	POS	5	9	103	252	4.1	0.06	0.806
PENICTNG	40	ACRESP	1	POS	6	28	19	316	2.3	5.24	0.022
PENICTNG	40	ALTEALTE	2	POS	31	3	296	39	30.1	0.04	0.841
PENICTNG	40	ALTESP	3	NEG	1	33	15	320	1.5	0.74	0.390

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENICTNG	40	ASPECAND	4	NEG	1	33	18	317	1.8	1.04	0.308
PENICTNG	40	ASPEFUMI	5	POS	6	28	19	316	2.3	5.24	0.022
PENICTNG	40	ASPEGLAU	6	NEG	1	33	24	311	2.3	1.67	0.196
PENICTNG	40	ASPENIGE	7	NEG	11	23	115	220	11.6	0.18	0.671
PENICTNG	40	ASPEOCHR	8	NEG	6	28	66	269	6.6	0.27	0.603
PENICTNG	40	ASPEORYZ	9	NEG	0	34	9	326	0.8	2.41	0.121
PENICTNG	40	ASPESP	10	POS	11	23	56	279	6.2	4.08	0.043
PENICTNG	40	ASPESYDO	11	POS	5	29	41	294	4.2	0.02	0.888
PENICTNG	40	ASPEUSTU	12	NEG	2	32	22	313	2.2	0.27	0.603
PENICTNG	40	ASPEVERS	13	POS	23	11	173	162	18.1	2.57	0.109
PENICTNG	40	AUREPULL	14	NEG	27	7	266	69	27.0	0.05	0.823
PENICTNG	40	CHAEGLOB	15	NEG	2	32	22	313	2.2	0.27	0.603
PENICTNG	40	CHRSPMSP	16	POS	2	32	12	323	1.3	0.04	0.841
PENICTNG	40	CLADCLAD	17	NEG	17	17	168	167	17.1	0.04	0.841
PENICTNG	40	CLADHERB	18	NEG	5	29	82	253	8.0	2.22	0.136
PENICTNG	40	CLADSP	19	POS	8	26	56	279	5.9	0.58	0.446
PENICTNG	40	CLADSPHA	20	POS	14	20	127	208	13.0	0.04	0.841
PENICTNG	40	CONISP	21	POS	1	33	9	326	0.9	0.22	0.639
PENICTNG	40	EMERNIDU	22	POS	3	31	7	328	0.9	3.06	0.080
PENICTNG	40	EPICNIGR	23	NEG	18	16	182	153	18.4	0.11	0.740
PENICTNG	40	EUROHERB	24	POS	23	11	222	113	22.6	0.00	1.000
PENICTNG	40	FUSAOXYS	25	POS	3	31	17	318	1.8	0.27	0.603
PENICTNG	40	FUSASP	26	NEG	4	30	55	280	5.4	0.90	0.343
PENICTNG	40	GEOMPANN	27	POS	3	31	9	326	1.1	2.00	0.157
PENICTNG	40	MUCOPLUM	28	NEG	2	32	71	264	6.7	5.58	0.018
PENICTNG	40	MUCORACE	29	POS	11	23	80	255	8.4	0.78	0.377
PENICTNG	40	PAECSP	30	POS	3	31	5	330	0.7	4.75	0.029
PENICTNG	40	PAECVARI	31	POS	5	29	45	290	4.6	0.00	1.000
PENICTNG	40	PENIATRA	32	NEG	0	34	9	326	0.8	2.41	0.121
PENICTNG	40	PENIAURA	33	NEG	4	30	40	295	4.1	0.09	0.764
PENICTNG	40	PENIBREV	34	POS	8	26	78	257	7.9	0.03	0.862
PENICTNG	40	PENICHRY	35	NEG	15	19	176	159	17.6	1.25	0.264
PENICTNG	40	PENICOMM	36	POS	13	21	81	254	8.7	2.51	0.113
PENICTNG	40	PENICOPR	37	POS	2	32	8	327	0.9	0.41	0.522
PENICTNG	40	PENICORY	38	POS	10	24	98	237	10.0	0.03	0.862
PENICTNG	40	PENICRUS	39	POS	3	31	11	324	1.3	1.30	0.254
PENICTRM	41	ACRESP	1	NEG	3	49	22	295	3.5	0.37	0.543
PENICTRM	41	ALTEALTE	2	POS	47	5	280	37	46.1	0.04	0.841
PENICTRM	41	ALTESP	3	POS	4	48	12	305	2.3	0.84	0.359
PENICTRM	41	ASPECAND	4	POS	5	47	14	303	2.7	1.52	0.218
PENICTRM	41	ASPEFUMI	5	POS	4	48	21	296	3.5	0.00	1.000
PENICTRM	41	ASPEGLAU	6	POS	7	45	18	299	3.5	3.14	0.076
PENICTRM	41	ASPENIGE	7	POS	21	31	105	212	17.8	0.75	0.386
PENICTRM	41	ASPEOCHR	8	POS	15	37	57	260	10.2	2.70	0.100
PENICTRM	41	ASPEORYZ	9	NEG	1	51	8	309	1.3	0.56	0.454
PENICTRM	41	ASPESP	10	POS	12	40	55	262	9.4	0.64	0.424
PENICTRM	41	ASPESYDO	11	POS	8	44	38	279	6.5	0.21	0.647
PENICTRM	41	ASPEUSTU	12	POS	4	48	20	297	3.4	0.01	0.920
PENICTRM	41	ASPEVERS	13	POS	29	23	167	150	27.6	0.07	0.791
PENICTRM	41	AUREPULL	14	NEG	39	13	254	63	41.3	1.07	0.301
PENICTRM	41	CHAEGLOB	15	NEG	2	50	22	295	3.4	1.30	0.254
PENICTRM	41	CHRSPMSP	16	POS	4	48	10	307	2.0	1.43	0.232
PENICTRM	41	CLADCLAD	17	NEG	25	27	160	157	26.1	0.22	0.639
PENICTRM	41	CLADHERB	18	NEG	8	44	79	238	12.3	2.82	0.093
PENICTRM	41	CLADSP	19	POS	12	40	52	265	9.0	0.96	0.327
PENICTRM	41	CLADSPHA	20	POS	21	31	120	197	19.9	0.04	0.841
PENICTRM	41	CONISP	21	NEG	0	52	10	307	1.4	3.09	0.079
PENICTRM	41	EMERNIDU	22	NEG	1	51	9	308	1.4	0.70	0.403
PENICTRM	41	EPICNIGR	23	NEG	26	26	174	143	28.2	0.65	0.420
PENICTRM	41	EUROHERB	24	POS	36	16	209	108	34.5	0.10	0.752
PENICTRM	41	FUSAOXYS	25	NEG	2	50	18	299	2.8	0.76	0.383
PENICTRM	41	FUSASP	26	POS	9	43	50	267	8.3	0.01	0.920

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENICTRM	41	GEOMPANN	27	POS	4	48	8	309	1.7	2.33	0.127
PENICTRM	41	MUCOPLUM	28	POS	14	38	59	258	10.3	1.46	0.227
PENICTRM	41	MUCORACE	29	POS	19	33	72	245	12.8	3.88	0.049
PENICTRM	41	PAECSP	30	NEG	1	51	7	310	1.1	0.42	0.517
PENICTRM	41	PAECVARI	31	POS	11	41	39	278	7.1	2.28	0.131
PENICTRM	41	PENIATRA	32	POS	4	48	5	312	1.3	4.69	0.030
PENICTRM	41	PENIAURA	33	NEG	6	46	38	279	6.2	0.10	0.752
PENICTRM	41	PENIBREV	34	POS	14	38	72	245	12.1	0.24	0.624
PENICTRM	41	PENICHRY	35	POS	30	22	161	156	26.9	0.60	0.439
PENICTRM	41	PENICOMM	36	NEG	11	41	83	234	13.3	0.89	0.345
PENICTRM	41	PENICOPR	37	POS	3	49	7	310	1.4	1.01	0.315
PENICTRM	41	PENICORY	38	POS	20	32	88	229	15.2	1.98	0.159
PENICTRM	41	PENICRUS	39	NEG	1	51	13	304	2.0	1.33	0.249
PENICTRM	41	PENICTNG	40	NEG	4	48	30	287	4.8	0.45	0.502
PENIDECU	42	ACRESP	1	POS	2	17	23	327	1.3	0.04	0.841
PENIDECU	42	ALTEALTE	2	NEG	14	5	313	37	16.8	6.13	0.013
PENIDECU	42	ALTESP	3	NEG	0	19	16	334	0.8	2.34	0.126
PENIDECU	42	ASPECAND	4	NEG	0	19	19	331	1.0	2.48	0.115
PENIDECU	42	ASPEFUMI	5	NEG	1	18	24	326	1.3	0.54	0.462
PENIDECU	42	ASPEGLAU	6	POS	2	17	23	327	1.3	0.04	0.841
PENIDECU	42	ASPENIGE	7	NEG	5	14	121	229	6.5	0.98	0.322
PENIDECU	42	ASPEOCHR	8	POS	4	15	68	282	3.7	0.02	0.888
PENIDECU	42	ASPEORYZ	9	NEG	0	19	9	341	0.5	2.16	0.142
PENIDECU	42	ASPESP	10	POS	4	15	63	287	3.5	0.00	1.000
PENIDECU	42	ASPESYDO	11	NEG	1	18	45	305	2.4	1.78	0.182
PENIDECU	42	ASPEUSTU	12	NEG	1	18	23	327	1.2	0.49	0.484
PENIDECU	42	ASPEVERS	13	POS	12	7	184	166	10.1	0.44	0.507
PENIDECU	42	AUREPULL	14	NEG	14	5	279	71	15.1	0.85	0.357
PENIDECU	42	CHAEGLOB	15	NEG	1	18	23	327	1.2	0.49	0.484
PENIDECU	42	CHRSPMSP	16	NEG	0	19	14	336	0.7	2.27	0.132
PENIDECU	42	CLADCLAD	17	POS	10	9	175	175	9.5	0.00	1.000
PENIDECU	42	CLADHERB	18	POS	6	13	81	269	4.5	0.32	0.572
PENIDECU	42	CLADSP	19	NEG	1	18	63	287	3.3	3.02	0.082
PENIDECU	42	CLADSPHA	20	POS	8	11	133	217	7.3	0.01	0.920
PENIDECU	42	CONISP	21	NEG	0	19	10	340	0.5	2.17	0.141
PENIDECU	42	EMERNIDU	22	NEG	0	19	10	340	0.5	2.17	0.141
PENIDECU	42	EPICNIGR	23	POS	13	6	187	163	10.3	1.08	0.299
PENIDECU	42	EUROHERB	24	POS	15	4	230	120	12.6	0.88	0.348
PENIDECU	42	FUSAOXYS	25	NEG	1	18	19	331	1.0	0.30	0.584
PENIDECU	42	FUSASP	26	POS	5	14	54	296	3.0	0.88	0.348
PENIDECU	42	GEOMPANN	27	NEG	0	19	12	338	0.6	2.20	0.138
PENIDECU	42	MUCOPLUM	28	NEG	1	18	72	278	3.8	3.71	0.054
PENIDECU	42	MUCORACE	29	POS	6	13	85	265	4.7	0.20	0.655
PENIDECU	42	PAECSP	30	POS	1	18	7	343	0.4	0.02	0.888
PENIDECU	42	PAECVARI	31	POS	4	15	46	304	2.6	0.41	0.522
PENIDECU	42	PENIATRA	32	NEG	0	19	9	341	0.5	2.16	0.142
PENIDECU	42	PENIAURA	33	POS	3	16	41	309	2.3	0.03	0.862
PENIDECU	42	PENIBREV	34	POS	5	14	81	269	4.4	0.00	1.000
PENIDECU	42	PENICHRY	35	NEG	9	10	182	168	9.8	0.40	0.527
PENIDECU	42	PENICOMM	36	POS	6	13	88	262	4.8	0.13	0.718
PENIDECU	42	PENICOPR	37	POS	2	17	8	342	0.5	2.04	0.153
PENIDECU	42	PENICORY	38	POS	8	11	100	250	5.6	1.01	0.315
PENIDECU	42	PENICRUS	39	POS	2	17	12	338	0.7	0.92	0.337
PENIDECU	42	PENICTNG	40	POS	4	15	30	320	1.8	2.03	0.154
PENIDECU	42	PENICTRM	41	NEG	2	17	50	300	2.7	0.64	0.424
PENIDIGI	43	ACRESP	1	POS	1	9	24	335	0.7	0.05	0.823
PENIDIGI	43	ALTEALTE	2	POS	10	0	317	42	8.9	0.42	0.517
PENIDIGI	43	ALTESP	3	NEG	0	10	16	343	0.4	2.16	0.142
PENIDIGI	43	ASPECAND	4	POS	1	9	18	341	0.5	0.00	1.000
PENIDIGI	43	ASPEFUMI	5	NEG	0	10	25	334	0.7	2.26	0.133
PENIDIGI	43	ASPEGLAU	6	POS	2	8	23	336	0.7	1.10	0.294
PENIDIGI	43	ASPENIGE	7	NEG	3	7	123	236	3.4	0.38	0.538

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENIDIGI	43	ASPEOCHR	8	POS	2	8	70	289	2.0	0.13	0.718
PENIDIGI	43	ASPEORYZ	9	NEG	0	10	9	350	0.2	2.39	0.122
PENIDIGI	43	ASPESP	10	NEG	1	9	66	293	1.8	1.20	0.273
PENIDIGI	43	ASPESYDO	11	NEG	1	9	45	314	1.3	0.53	0.467
PENIDIGI	43	ASPEUSTU	12	POS	1	9	23	336	0.7	0.04	0.841
PENIDIGI	43	ASPEVERS	13	POS	7	3	189	170	5.3	0.58	0.446
PENIDIGI	43	AUREPULL	14	POS	9	1	284	75	7.9	0.20	0.655
PENIDIGI	43	CHAEGLOB	15	NEG	0	10	24	335	0.7	2.24	0.134
PENIDIGI	43	CHRSPMSP	16	NEG	0	10	14	345	0.4	2.18	0.140
PENIDIGI	43	CLADCLAD	17	POS	7	3	178	181	5.0	0.91	0.340
PENIDIGI	43	CLADHERB	18	POS	4	6	83	276	2.4	0.74	0.390
PENIDIGI	43	CLADSP	19	POS	2	8	62	297	1.7	0.04	0.841
PENIDIGI	43	CLADSPHA	20	POS	6	4	135	224	3.8	1.23	0.267
PENIDIGI	43	CONISP	21	NEG	0	10	10	349	0.3	2.32	0.128
PENIDIGI	43	EMERNIDU	22	NEG	0	10	10	349	0.3	2.32	0.128
PENIDIGI	43	EPICNIGR	23	NEG	5	5	195	164	5.4	0.35	0.554
PENIDIGI	43	EUROHERB	24	NEG	5	5	240	119	6.6	2.11	0.146
PENIDIGI	43	FUSAOXYS	25	NEG	0	10	20	339	0.5	2.18	0.140
PENIDIGI	43	FUSASP	26	NEG	0	10	59	300	1.6	3.37	0.066
PENIDIGI	43	GEOMPANN	27	NEG	0	10	12	347	0.3	2.22	0.136
PENIDIGI	43	MUCOPLUM	28	POS	2	8	71	288	2.0	0.15	0.699
PENIDIGI	43	MUCORACE	29	POS	3	7	88	271	2.5	0.00	1.000
PENIDIGI	43	PAECSP	30	NEG	0	10	8	351	0.2	2.49	0.115
PENIDIGI	43	PAECVARI	31	POS	2	8	48	311	1.4	0.02	0.888
PENIDIGI	43	PENIATRA	32	NEG	0	10	9	350	0.2	2.39	0.122
PENIDIGI	43	PENIAURA	33	NEG	1	9	43	316	1.2	0.47	0.493
PENIDIGI	43	PENIBREV	34	POS	4	6	82	277	2.3	0.79	0.374
PENIDIGI	43	PENICHRY	35	NEG	4	6	187	172	5.2	1.16	0.281
PENIDIGI	43	PENICOMM	36	NEG	2	8	92	267	2.6	0.59	0.442
PENIDIGI	43	PENICOPR	37	POS	1	9	9	350	0.3	0.20	0.655
PENIDIGI	43	PENICORY	38	NEG	2	8	106	253	2.9	1.01	0.315
PENIDIGI	43	PENICRUS	39	NEG	0	10	14	345	0.4	2.18	0.140
PENIDIGI	43	PENICTNG	40	POS	1	9	33	326	0.9	0.22	0.639
PENIDIGI	43	PENICTRM	41	NEG	1	9	51	308	1.4	0.70	0.403
PENIDIGI	43	PENIDECU	42	NEG	0	10	19	340	0.5	2.17	0.141
PENIECHI	44	ACRESP	1	NEG	0	17	25	327	1.2	2.66	0.103
PENIECHI	44	ALTEALTE	2	POS	16	1	311	41	15.1	0.12	0.729
PENIECHI	44	ALTESP	3	NEG	0	17	16	336	0.7	2.28	0.131
PENIECHI	44	ASPECAND	4	POS	2	15	17	335	0.9	0.49	0.484
PENIECHI	44	ASPEFUMI	5	NEG	1	16	24	328	1.2	0.41	0.522
PENIECHI	44	ASPEGLAU	6	NEG	1	16	24	328	1.2	0.41	0.522
PENIECHI	44	ASPENIGE	7	POS	9	8	117	235	5.8	1.99	0.158
PENIECHI	44	ASPEOCHR	8	POS	5	12	67	285	3.3	0.55	0.458
PENIECHI	44	ASPEORYZ	9	NEG	0	17	9	343	0.4	2.17	0.141
PENIECHI	44	ASPESP	10	POS	6	11	61	291	3.1	2.42	0.120
PENIECHI	44	ASPESYDO	11	NEG	2	15	44	308	2.1	0.22	0.639
PENIECHI	44	ASPEUSTU	12	POS	3	14	21	331	1.1	1.97	0.160
PENIECHI	44	ASPEVERS	13	POS	10	7	186	166	9.0	0.05	0.823
PENIECHI	44	AUREPULL	14	POS	14	3	279	73	13.5	0.00	1.000
PENIECHI	44	CHAEGLOB	15	POS	3	14	21	331	1.1	1.97	0.160
PENIECHI	44	CHRSPMSP	16	POS	1	16	13	339	0.6	0.04	0.841
PENIECHI	44	CLADCLAD	17	POS	9	8	176	176	8.5	0.00	1.000
PENIECHI	44	CLADHERB	18	NEG	2	15	85	267	4.0	2.15	0.143
PENIECHI	44	CLADSP	19	POS	7	10	57	295	3.0	5.43	0.020
PENIECHI	44	CLADSPHA	20	POS	8	9	133	219	6.5	0.26	0.610
PENIECHI	44	CONISP	21	NEG	0	17	10	342	0.5	2.16	0.142
PENIECHI	44	EMERNIDU	22	NEG	0	17	10	342	0.5	2.16	0.142
PENIECHI	44	EPICNIGR	23	NEG	9	8	191	161	9.2	0.13	0.718
PENIECHI	44	EUROHERB	24	NEG	11	6	234	118	11.3	0.17	0.680
PENIECHI	44	FUSAOXYS	25	NEG	0	17	20	332	0.9	2.43	0.119
PENIECHI	44	FUSASP	26	POS	5	12	54	298	2.7	1.46	0.227
PENIECHI	44	GEOMPANN	27	NEG	0	17	12	340	0.6	2.17	0.141

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENIECHI	44	MUCOPLUM	28	NEG	2	15	71	281	3.4	1.35	0.245
PENIECHI	44	MUCORACE	29	POS	6	11	85	267	4.2	0.57	0.450
PENIECHI	44	PAECSP	30	NEG	0	17	8	344	0.4	2.19	0.139
PENIECHI	44	PAECVARI	31	NEG	1	16	49	303	2.3	1.71	0.191
PENIECHI	44	PENIATRA	32	POS	2	15	7	345	0.4	3.05	0.081
PENIECHI	44	PENIAURA	33	POS	3	14	41	311	2.0	0.13	0.718
PENIECHI	44	PENIBREV	34	POS	6	11	80	272	4.0	0.82	0.365
PENIECHI	44	PENICHRY	35	POS	9	8	182	170	8.8	0.02	0.888
PENIECHI	44	PENICOMM	36	NEG	4	13	90	262	4.3	0.22	0.639
PENIECHI	44	PENICOPR	37	NEG	0	17	10	342	0.5	2.16	0.142
PENIECHI	44	PENICORY	38	POS	7	10	101	251	5.0	0.69	0.406
PENIECHI	44	PENICRUS	39	POS	3	14	11	341	0.6	5.81	0.016
PENIECHI	44	PENICTNG	40	POS	2	15	32	320	1.6	0.00	1.000
PENIECHI	44	PENICTRM	41	POS	4	13	48	304	2.4	0.62	0.431
PENIECHI	44	PENIDECU	42	NEG	0	17	19	333	0.9	2.39	0.122
PENIECHI	44	PENIDIGI	43	NEG	0	17	10	342	0.5	2.16	0.142
PENIEXPA	45	ACRESP	1	NEG	3	66	22	278	4.7	1.33	0.249
PENIEXPA	45	ALTEALTE	2	NEG	60	9	267	33	61.2	0.48	0.488
PENIEXPA	45	ALTESP	3	POS	6	63	10	290	3.0	2.70	0.100
PENIEXPA	45	ASPECAND	4	POS	4	65	15	285	3.6	0.00	1.000
PENIEXPA	45	ASPEFUMI	5	POS	6	63	19	281	4.7	0.19	0.663
PENIEXPA	45	ASPEGLAU	6	POS	5	64	20	280	4.7	0.01	0.920
PENIEXPA	45	ASPENIGE	7	POS	28	41	98	202	23.6	1.23	0.267
PENIEXPA	45	ASPEOCHR	8	POS	18	51	54	246	13.5	1.85	0.174
PENIEXPA	45	ASPEORYZ	9	POS	2	67	7	293	1.7	0.03	0.862
PENIEXPA	45	ASPESP	10	POS	14	55	53	247	12.5	0.11	0.740
PENIEXPA	45	ASPESYDO	11	POS	10	59	36	264	8.6	0.13	0.718
PENIEXPA	45	ASPEUSTU	12	NEG	3	66	21	279	4.5	1.16	0.281
PENIEXPA	45	ASPEVERS	13	POS	38	31	158	142	36.7	0.05	0.823
PENIEXPA	45	AUREPULL	14	NEG	54	15	239	61	54.8	0.18	0.671
PENIEXPA	45	CHAEGLOB	15	POS	9	60	15	285	4.5	4.72	0.030
PENIEXPA	45	CHRSPMSP	16	POS	4	65	10	290	2.6	0.38	0.538
PENIEXPA	45	CLADCLAD	17	NEG	34	35	151	149	34.6	0.09	0.764
PENIEXPA	45	CLADHERB	18	NEG	11	58	76	224	16.3	3.29	0.070
PENIEXPA	45	CLADSP	19	POS	14	55	50	250	12.0	0.29	0.590
PENIEXPA	45	CLADSPHA	20	POS	29	40	112	188	26.4	0.34	0.560
PENIEXPA	45	CONISP	21	POS	3	66	7	293	1.9	0.27	0.603
PENIEXPA	45	EMERNIDU	22	NEG	1	68	9	291	1.9	1.27	0.260
PENIEXPA	45	EPICNIGR	23	POS	45	24	155	145	37.4	3.62	0.057
PENIEXPA	45	EUROHERB	24	POS	48	21	197	103	45.8	0.23	0.632
PENIEXPA	45	FUSAOXYS	25	POS	4	65	16	284	3.7	0.02	0.888
PENIEXPA	45	FUSASP	26	POS	14	55	45	255	11.0	0.81	0.368
PENIEXPA	45	GEOMPANN	27	POS	3	66	9	291	2.2	0.04	0.841
PENIEXPA	45	MUCOPLUM	28	POS	19	50	54	246	13.7	2.64	0.104
PENIEXPA	45	MUCORACE	29	POS	21	48	70	230	17.0	1.16	0.281
PENIEXPA	45	PAECSP	30	POS	3	66	5	295	1.5	0.85	0.357
PENIEXPA	45	PAECVARI	31	POS	10	59	40	260	9.4	0.00	1.000
PENIEXPA	45	PENIATRA	32	POS	2	67	7	293	1.7	0.03	0.862
PENIEXPA	45	PENIAURA	33	NEG	8	61	36	264	8.2	0.09	0.764
PENIEXPA	45	PENIBREV	34	NEG	16	53	70	230	16.1	0.03	0.862
PENIEXPA	45	PENICHRY	35	NEG	28	41	163	137	35.8	4.82	0.028
PENIEXPA	45	PENICOMM	36	POS	31	38	63	237	17.6	15.68	0.000
PENIEXPA	45	PENICOPR	37	POS	3	66	7	293	1.9	0.27	0.603
PENIEXPA	45	PENICORY	38	POS	23	46	85	215	20.2	0.46	0.498
PENIEXPA	45	PENICRUS	39	POS	4	65	10	290	2.6	0.38	0.538
PENIEXPA	45	PENICTNG	40	NEG	6	63	28	272	6.4	0.16	0.689
PENIEXPA	45	PENICTRM	41	POS	10	59	42	258	9.7	0.01	0.920
PENIEXPA	45	PENIDECU	42	NEG	3	66	16	284	3.6	0.40	0.527
PENIEXPA	45	PENIDIGI	43	POS	2	67	8	292	1.9	0.09	0.764
PENIEXPA	45	PENIECHI	44	POS	5	64	12	288	3.2	0.71	0.399
PENIGLAN	46	ACRESP	1	NEG	0	13	25	331	0.9	2.41	0.121
PENIGLAN	46	ALTEALTE	2	NEG	11	2	316	40	11.5	0.82	0.365

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENIGLAN	46	ALTESP	3	NEG	0	13	16	340	0.6	2.17	0.141
PENIGLAN	46	ASPECAND	4	POS	1	12	18	338	0.7	0.05	0.823
PENIGLAN	46	ASPEFUMI	5	NEG	0	13	25	331	0.9	2.41	0.121
PENIGLAN	46	ASPEGLAU	6	POS	2	11	23	333	0.9	0.48	0.488
PENIGLAN	46	ASPENIGE	7	NEG	1	12	125	231	4.4	5.50	0.019
PENIGLAN	46	ASPEOCHR	8	NEG	2	11	70	286	2.5	0.55	0.458
PENIGLAN	46	ASPEORYZ	9	NEG	0	13	9	347	0.3	2.24	0.134
PENIGLAN	46	ASPESP	10	NEG	1	12	66	290	2.4	1.86	0.173
PENIGLAN	46	ASPESYDO	11	POS	4	9	42	314	1.6	2.58	0.108
PENIGLAN	46	ASPEUSTU	12	NEG	0	13	24	332	0.9	2.37	0.124
PENIGLAN	46	ASPEVERS	13	NEG	5	8	191	165	6.9	1.85	0.174
PENIGLAN	46	AUREPULL	14	NEG	10	3	283	73	10.3	0.33	0.566
PENIGLAN	46	CHAEGLOB	15	POS	2	11	22	334	0.9	0.56	0.454
PENIGLAN	46	CHRSPMSP	16	POS	1	12	13	343	0.5	0.00	1.000
PENIGLAN	46	CLADCLAD	17	NEG	6	7	179	177	6.5	0.33	0.566
PENIGLAN	46	CLADHERB	18	NEG	3	10	84	272	3.1	0.14	0.708
PENIGLAN	46	CLADSP	19	NEG	0	13	64	292	2.3	4.22	0.040
PENIGLAN	46	CLADSPHA	20	NEG	2	11	139	217	5.0	4.06	0.044
PENIGLAN	46	CONISP	21	NEG	0	13	10	346	0.4	2.20	0.138
PENIGLAN	46	EMERNIDU	22	NEG	0	13	10	346	0.4	2.20	0.138
PENIGLAN	46	EPICNIGR	23	POS	11	2	189	167	7.1	3.83	0.050
PENIGLAN	46	EUROHERB	24	POS	11	2	234	122	8.6	1.25	0.264
PENIGLAN	46	FUSAOXYS	25	NEG	0	13	20	336	0.7	2.26	0.133
PENIGLAN	46	FUSASP	26	NEG	2	11	57	299	2.1	0.20	0.655
PENIGLAN	46	GEOMPANN	27	NEG	0	13	12	344	0.4	2.16	0.142
PENIGLAN	46	MUCOPLUM	28	NEG	1	12	72	284	2.6	2.16	0.142
PENIGLAN	46	MUCORACE	29	NEG	0	13	91	265	3.2	5.89	0.015
PENIGLAN	46	PAECSP	30	NEG	0	13	8	348	0.3	2.30	0.129
PENIGLAN	46	PAECVARI	31	POS	5	8	45	311	1.8	5.10	0.024
PENIGLAN	46	PENIATRA	32	NEG	0	13	9	347	0.3	2.24	0.134
PENIGLAN	46	PENIAURA	33	POS	2	11	42	314	1.6	0.00	1.000
PENIGLAN	46	PENIBREV	34	NEG	3	10	83	273	3.0	0.13	0.718
PENIGLAN	46	PENICHRY	35	NEG	6	7	185	171	6.7	0.48	0.488
PENIGLAN	46	PENICOMM	36	POS	4	9	90	266	3.3	0.01	0.920
PENIGLAN	46	PENICOPR	37	NEG	0	13	10	346	0.4	2.20	0.138
PENIGLAN	46	PENICORY	38	POS	6	7	102	254	3.8	1.11	0.292
PENIGLAN	46	PENICRUS	39	POS	1	12	13	343	0.5	0.00	1.000
PENIGLAN	46	PENICTNG	40	NEG	0	13	34	322	1.2	2.75	0.097
PENIGLAN	46	PENICTRM	41	POS	3	10	49	307	1.8	0.29	0.590
PENIGLAN	46	PENIDECU	42	POS	2	11	17	339	0.7	1.13	0.288
PENIGLAN	46	PENIDIGI	43	NEG	0	13	10	346	0.4	2.20	0.138
PENIGLAN	46	PENIECHI	44	POS	1	12	16	340	0.6	0.02	0.888
PENIGLAN	46	PENIEXPA	45	NEG	0	13	69	287	2.4	4.51	0.034
PENIGRIS	47	ACRESP	1	POS	2	21	23	323	1.6	0.00	1.000
PENIGRIS	47	ALTEALTE	2	POS	22	1	305	41	20.4	0.57	0.450
PENIGRIS	47	ALTESP	3	NEG	0	23	16	330	1.0	2.51	0.113
PENIGRIS	47	ASPECAND	4	NEG	0	23	19	327	1.2	2.69	0.101
PENIGRIS	47	ASPEFUMI	5	NEG	0	23	25	321	1.6	3.11	0.078
PENIGRIS	47	ASPEGLAU	6	POS	2	21	23	323	1.6	0.00	1.000
PENIGRIS	47	ASPENIGE	7	NEG	7	16	119	227	7.9	0.38	0.538
PENIGRIS	47	ASPEOCHR	8	NEG	3	20	69	277	4.5	1.17	0.279
PENIGRIS	47	ASPEORYZ	9	NEG	0	23	9	337	0.6	2.19	0.139
PENIGRIS	47	ASPESP	10	POS	6	17	61	285	4.2	0.55	0.458
PENIGRIS	47	ASPESYDO	11	POS	4	19	42	304	2.9	0.17	0.680
PENIGRIS	47	ASPEUSTU	12	NEG	1	22	23	323	1.5	0.76	0.383
PENIGRIS	47	ASPEVERS	13	NEG	12	11	184	162	12.2	0.10	0.752
PENIGRIS	47	AUREPULL	14	POS	20	3	273	73	18.3	0.43	0.512
PENIGRIS	47	CHAEGLOB	15	NEG	0	23	24	322	1.5	3.04	0.081
PENIGRIS	47	CHRSPMSP	16	POS	1	22	13	333	0.9	0.18	0.671
PENIGRIS	47	CLADCLAD	17	NEG	10	13	175	171	11.5	0.77	0.380
PENIGRIS	47	CLADHERB	18	POS	11	12	76	270	5.4	6.63	0.010
PENIGRIS	47	CLADSP	19	POS	5	18	59	287	4.0	0.08	0.777

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENIGRIS	47	CLADSPHA	20	POS	9	14	132	214	8.8	0.02	0.888
PENIGRIS	47	CONISP	21	POS	1	22	9	337	0.6	0.03	0.862
PENIGRIS	47	EMERNIDU	22	POS	2	21	8	338	0.6	1.35	0.245
PENIGRIS	47	EPICNIGR	23	POS	16	7	184	162	12.5	1.72	0.190
PENIGRIS	47	EUROHERB	24	POS	18	5	227	119	15.3	1.03	0.310
PENIGRIS	47	FUSAOXYS	25	POS	3	20	17	329	1.3	1.42	0.233
PENIGRIS	47	FUSASP	26	POS	8	15	51	295	3.7	5.04	0.025
PENIGRIS	47	GEOMPANN	27	POS	1	22	11	335	0.8	0.09	0.764
PENIGRIS	47	MUCOPLUM	28	POS	5	18	68	278	4.6	0.00	1.000
PENIGRIS	47	MUCORACE	29	NEG	5	18	86	260	5.7	0.34	0.560
PENIGRIS	47	PAECSP	30	NEG	0	23	8	338	0.5	2.18	0.140
PENIGRIS	47	PAECVARI	31	POS	4	19	46	300	3.1	0.06	0.806
PENIGRIS	47	PENIATRA	32	NEG	0	23	9	337	0.6	2.19	0.139
PENIGRIS	47	PENIAURA	33	NEG	0	23	44	302	2.7	4.64	0.031
PENIGRIS	47	PENIBREV	34	NEG	3	20	83	263	5.4	2.12	0.145
PENIGRIS	47	PENICHRY	35	POS	12	11	179	167	11.9	0.03	0.862
PENIGRIS	47	PENICOMM	36	NEG	2	21	92	254	5.9	4.64	0.031
PENIGRIS	47	PENICOPR	37	NEG	0	23	10	336	0.6	2.22	0.136
PENIGRIS	47	PENICORY	38	NEG	6	17	102	244	6.7	0.34	0.560
PENIGRIS	47	PENICRUS	39	POS	3	20	11	335	0.9	3.36	0.067
PENIGRIS	47	PENICTNG	40	NEG	0	23	34	312	2.1	3.80	0.051
PENIGRIS	47	PENICTRM	41	NEG	3	20	49	297	3.2	0.21	0.647
PENIGRIS	47	PENIDECU	42	POS	2	21	17	329	1.2	0.09	0.764
PENIGRIS	47	PENIDIGI	43	NEG	0	23	10	336	0.6	2.22	0.136
PENIGRIS	47	PENIECHI	44	NEG	1	22	16	330	1.1	0.33	0.566
PENIGRIS	47	PENIEXPA	45	NEG	2	21	67	279	4.3	2.39	0.122
PENIGRIS	47	PENIGLAN	46	POS	2	21	11	335	0.8	0.65	0.420
PENIIMPL	48	ACRESP	1	POS	3	16	22	328	1.3	1.29	0.256
PENIIMPL	48	ALTEALTE	2	NEG	15	4	312	38	16.8	3.01	0.083
PENIIMPL	48	ALTESP	3	NEG	0	19	16	334	0.8	2.34	0.126
PENIIMPL	48	ASPECAND	4	POS	2	17	17	333	1.0	0.31	0.578
PENIIMPL	48	ASPEFUMI	5	NEG	1	18	24	326	1.3	0.54	0.462
PENIIMPL	48	ASPEGLAU	6	POS	3	16	22	328	1.3	1.29	0.256
PENIIMPL	48	ASPENIGE	7	POS	7	12	119	231	6.5	0.00	1.000
PENIIMPL	48	ASPEOCHR	8	POS	5	14	67	283	3.7	0.22	0.639
PENIIMPL	48	ASPEORYZ	9	POS	1	18	8	342	0.5	0.00	1.000
PENIIMPL	48	ASPESP	10	POS	5	14	62	288	3.5	0.41	0.522
PENIIMPL	48	ASPESYDO	11	NEG	2	17	44	306	2.4	0.38	0.538
PENIIMPL	48	ASPEUSTU	12	POS	2	17	22	328	1.2	0.06	0.806
PENIIMPL	48	ASPEVERS	13	NEG	10	9	186	164	10.1	0.08	0.777
PENIIMPL	48	AUREPULL	14	NEG	13	6	280	70	15.1	2.27	0.132
PENIIMPL	48	CHAEGLOB	15	NEG	1	18	23	327	1.2	0.49	0.484
PENIIMPL	48	CHRSPMSP	16	POS	1	18	13	337	0.7	0.07	0.791
PENIIMPL	48	CLADCLAD	17	POS	12	7	173	177	9.5	0.87	0.351
PENIIMPL	48	CLADHERB	18	POS	5	14	82	268	4.5	0.00	1.000
PENIIMPL	48	CLADSP	19	POS	4	15	60	290	3.3	0.02	0.888
PENIIMPL	48	CLADSPHA	20	NEG	6	13	135	215	7.3	0.73	0.393
PENIIMPL	48	CONISP	21	NEG	0	19	10	340	0.5	2.17	0.141
PENIIMPL	48	EMERNIDU	22	NEG	0	19	10	340	0.5	2.17	0.141
PENIIMPL	48	EPICNIGR	23	NEG	8	11	192	158	10.3	1.75	0.186
PENIIMPL	48	EUROHERB	24	NEG	12	7	233	117	12.6	0.31	0.578
PENIIMPL	48	FUSAOXYS	25	NEG	1	18	19	331	1.0	0.30	0.584
PENIIMPL	48	FUSASP	26	POS	6	13	53	297	3.0	2.50	0.114
PENIIMPL	48	GEOMPANN	27	POS	1	18	11	339	0.6	0.02	0.888
PENIIMPL	48	MUCOPLUM	28	NEG	3	16	70	280	3.8	0.55	0.458
PENIIMPL	48	MUCORACE	29	NEG	3	16	88	262	4.7	1.43	0.232
PENIIMPL	48	PAECSP	30	POS	2	17	6	344	0.4	3.10	0.078
PENIIMPL	48	PAECVARI	31	POS	3	16	47	303	2.6	0.00	1.000
PENIIMPL	48	PENIATRA	32	POS	1	18	8	342	0.5	0.00	1.000
PENIIMPL	48	PENIAURA	33	POS	3	16	41	309	2.3	0.03	0.862
PENIIMPL	48	PENIBREV	34	NEG	4	15	82	268	4.4	0.27	0.603
PENIIMPL	48	PENICHRY	35	POS	11	8	180	170	9.8	0.10	0.752

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENIIMPL	48	PENICOMM	36	NEG	4	15	90	260	4.8	0.52	0.471
PENIIMPL	48	PENICOPR	37	POS	1	18	9	341	0.5	0.00	1.000
PENIIMPL	48	PENICORY	38	POS	7	12	101	249	5.6	0.24	0.624
PENIIMPL	48	PENICRUS	39	NEG	0	19	14	336	0.7	2.27	0.132
PENIIMPL	48	PENICTNG	40	POS	3	16	31	319	1.8	0.37	0.543
PENIIMPL	48	PENICTRM	41	NEG	2	17	50	300	2.7	0.64	0.424
PENIIMPL	48	PENIDECU	42	POS	2	17	17	333	1.0	0.31	0.578
PENIIMPL	48	PENIDIGI	43	POS	1	18	9	341	0.5	0.00	1.000
PENIIMPL	48	PENIECHI	44	POS	3	16	14	336	0.9	3.33	0.068
PENIIMPL	48	PENIEXPA	45	NEG	3	16	66	284	3.6	0.40	0.527
PENIIMPL	48	PENIGLAN	46	POS	3	16	10	340	0.7	5.47	0.019
PENIIMPL	48	PENIGRIS	47	NEG	1	18	22	328	1.2	0.44	0.507
PENIISLA	49	ACRESP	1	NEG	0	11	25	333	0.8	2.30	0.129
PENIISLA	49	ALTEALTE	2	POS	11	0	316	42	9.8	0.53	0.467
PENIISLA	49	ALTESP	3	NEG	0	11	16	342	0.5	2.16	0.142
PENIISLA	49	ASPECAND	4	POS	1	10	18	340	0.6	0.01	0.920
PENIISLA	49	ASPEFUMI	5	NEG	0	11	25	333	0.8	2.30	0.129
PENIISLA	49	ASPEGLAU	6	NEG	0	11	25	333	0.8	2.30	0.129
PENIISLA	49	ASPENIGE	7	NEG	3	8	123	235	3.8	0.66	0.417
PENIISLA	49	ASPEOCHR	8	POS	3	8	69	289	2.2	0.07	0.791
PENIISLA	49	ASPEORYZ	9	POS	1	10	8	350	0.3	0.21	0.647
PENIISLA	49	ASPESP	10	NEG	0	11	67	291	2.0	3.93	0.047
PENIISLA	49	ASPESYDO	11	NEG	0	11	46	312	1.4	3.01	0.083
PENIISLA	49	ASPEUSTU	12	NEG	0	11	24	334	0.7	2.28	0.131
PENIISLA	49	ASPEVERS	13	NEG	5	6	191	167	5.8	0.68	0.410
PENIISLA	49	AUREPULL	14	POS	9	2	284	74	8.7	0.03	0.862
PENIISLA	49	CHAEGLOB	15	NEG	0	11	24	334	0.7	2.28	0.131
PENIISLA	49	CHRSPMSP	16	POS	1	10	13	345	0.4	0.02	0.888
PENIISLA	49	CLADCLAD	17	POS	7	4	178	180	5.5	0.36	0.549
PENIISLA	49	CLADHERB	18	POS	4	7	83	275	2.6	0.43	0.512
PENIISLA	49	CLADSP	19	POS	2	9	62	296	1.9	0.11	0.740
PENIISLA	49	CLADSPHA	20	POS	6	5	135	223	4.2	0.67	0.413
PENIISLA	49	CONISP	21	POS	1	10	9	349	0.3	0.14	0.708
PENIISLA	49	EMERNIDU	22	NEG	0	11	10	348	0.3	2.26	0.133
PENIISLA	49	EPICNIGR	23	POS	7	4	193	165	6.0	0.11	0.740
PENIISLA	49	EUROHERB	24	POS	8	3	237	121	7.3	0.02	0.888
PENIISLA	49	FUSAOXYS	25	NEG	0	11	20	338	0.6	2.20	0.138
PENIISLA	49	FUSASP	26	NEG	0	11	59	299	1.8	3.56	0.059
PENIISLA	49	GEOMPANN	27	NEG	0	11	12	346	0.4	2.19	0.139
PENIISLA	49	MUCOPLUM	28	NEG	2	9	71	287	2.2	0.27	0.603
PENIISLA	49	MUCORACE	29	POS	4	7	87	271	2.7	0.31	0.578
PENIISLA	49	PAECSP	30	NEG	0	11	8	350	0.2	2.41	0.121
PENIISLA	49	PAECVARI	31	POS	2	9	48	310	1.5	0.00	1.000
PENIISLA	49	PENIATRA	32	NEG	0	11	9	349	0.3	2.32	0.128
PENIISLA	49	PENIAURA	33	NEG	0	11	44	314	1.3	2.93	0.087
PENIISLA	49	PENIBREV	34	POS	3	8	83	275	2.6	0.00	1.000
PENIISLA	49	PENICHRY	35	POS	8	3	183	175	5.7	1.22	0.269
PENIISLA	49	PENICOMM	36	NEG	1	10	93	265	2.8	2.62	0.106
PENIISLA	49	PENICOPR	37	NEG	0	11	10	348	0.3	2.26	0.133
PENIISLA	49	PENICORY	38	NEG	3	8	105	253	3.2	0.23	0.632
PENIISLA	49	PENICRUS	39	NEG	0	11	14	344	0.4	2.16	0.142
PENIISLA	49	PENICTNG	40	NEG	1	10	33	325	1.0	0.30	0.584
PENIISLA	49	PENICTRM	41	POS	3	8	49	309	1.6	0.70	0.403
PENIISLA	49	PENIDECU	42	NEG	0	11	19	339	0.6	2.18	0.140
PENIISLA	49	PENIDIGI	43	NEG	0	11	10	348	0.3	2.26	0.133
PENIISLA	49	PENIECHI	44	NEG	0	11	17	341	0.5	2.16	0.142
PENIISLA	49	PENIEXPA	45	NEG	0	11	69	289	2.1	4.03	0.045
PENIISLA	49	PENIGLAN	46	POS	1	10	12	346	0.4	0.03	0.862
PENIISLA	49	PENIGRIS	47	NEG	0	11	23	335	0.7	2.25	0.134
PENIISLA	49	PENIIMPL	48	NEG	0	11	19	339	0.6	2.18	0.140
PENIITAL	50	ACRESP	1	NEG	0	11	25	333	0.8	2.30	0.129
PENIITAL	50	ALTEALTE	2	POS	10	1	317	41	9.8	0.06	0.806

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENIITAL	50	ALTESP	3	NEG	0	11	16	342	0.5	2.16	0.142
PENIITAL	50	ASPECAND	4	NEG	0	11	19	339	0.6	2.18	0.140
PENIITAL	50	ASPEFUMI	5	NEG	0	11	25	333	0.8	2.30	0.129
PENIITAL	50	ASPEGLAU	6	NEG	0	11	25	333	0.8	2.30	0.129
PENIITAL	50	ASPENIGE	7	POS	6	5	120	238	3.8	1.27	0.260
PENIITAL	50	ASPEOCHR	8	NEG	2	9	70	288	2.2	0.25	0.617
PENIITAL	50	ASPEORYZ	9	NEG	0	11	9	349	0.3	2.32	0.128
PENIITAL	50	ASPESP	10	NEG	1	10	66	292	2.0	1.41	0.235
PENIITAL	50	ASPESYDO	11	NEG	1	10	45	313	1.4	0.65	0.420
PENIITAL	50	ASPEUSTU	12	POS	1	10	23	335	0.7	0.07	0.791
PENIITAL	50	ASPEVERS	13	NEG	5	6	191	167	5.8	0.68	0.410
PENIITAL	50	AUREPULL	14	NEG	7	4	286	72	8.7	2.86	0.091
PENIITAL	50	CHAEGLOB	15	POS	1	10	23	335	0.7	0.07	0.791
PENIITAL	50	CHRSPMSP	16	NEG	0	11	14	344	0.4	2.16	0.142
PENIITAL	50	CLADCLAD	17	POS	6	5	179	179	5.5	0.00	1.000
PENIITAL	50	CLADHERB	18	POS	3	8	84	274	2.6	0.00	1.000
PENIITAL	50	CLADSP	19	NEG	1	10	63	295	1.9	1.30	0.254
PENIITAL	50	CLADSPHA	20	NEG	3	8	138	220	4.2	1.15	0.284
PENIITAL	50	CONISP	21	POS	1	10	9	349	0.3	0.14	0.708
PENIITAL	50	EMERNIDU	22	NEG	0	11	10	348	0.3	2.26	0.133
PENIITAL	50	EPICNIGR	23	POS	6	5	194	164	6.0	0.08	0.777
PENIITAL	50	EUROHERB	24	NEG	7	4	238	120	7.3	0.27	0.603
PENIITAL	50	FUSAOXYS	25	NEG	0	11	20	338	0.6	2.20	0.138
PENIITAL	50	FUSASP	26	POS	2	9	57	301	1.8	0.05	0.823
PENIITAL	50	GEOMPANN	27	NEG	0	11	12	346	0.4	2.19	0.139
PENIITAL	50	MUCOPLUM	28	POS	3	8	70	288	2.2	0.06	0.806
PENIITAL	50	MUCORACE	29	POS	5	6	86	272	2.7	1.61	0.204
PENIITAL	50	PAECSP	30	NEG	0	11	8	350	0.2	2.41	0.121
PENIITAL	50	PAECVARI	31	NEG	0	11	50	308	1.5	3.17	0.075
PENIITAL	50	PENIATRA	32	NEG	0	11	9	349	0.3	2.32	0.128
PENIITAL	50	PENIAURA	33	POS	2	9	42	316	1.3	0.03	0.862
PENIITAL	50	PENIBREV	34	POS	3	8	83	275	2.6	0.00	1.000
PENIITAL	50	PENICHRY	35	NEG	5	6	186	172	5.7	0.53	0.467
PENIITAL	50	PENICOMM	36	POS	3	8	91	267	2.8	0.05	0.823
PENIITAL	50	PENICOPR	37	NEG	0	11	10	348	0.3	2.26	0.133
PENIITAL	50	PENICORY	38	NEG	2	9	106	252	3.2	1.34	0.247
PENIITAL	50	PENICRUS	39	NEG	0	11	14	344	0.4	2.16	0.142
PENIITAL	50	PENICTNG	40	NEG	1	10	33	325	1.0	0.30	0.584
PENIITAL	50	PENICTRM	41	NEG	1	10	51	307	1.6	0.85	0.357
PENIITAL	50	PENIDECU	42	NEG	0	11	19	339	0.6	2.18	0.140
PENIITAL	50	PENIDIGI	43	NEG	0	11	10	348	0.3	2.26	0.133
PENIITAL	50	PENIECHI	44	POS	1	10	16	342	0.5	0.00	1.000
PENIITAL	50	PENIEXPA	45	POS	4	7	65	293	2.1	1.28	0.258
PENIITAL	50	PENIGLAN	46	NEG	0	11	13	345	0.4	2.17	0.141
PENIITAL	50	PENIGRIS	47	POS	1	10	22	336	0.7	0.06	0.806
PENIITAL	50	PENIIMPL	48	POS	1	10	18	340	0.6	0.01	0.920
PENIITAL	50	PENIISLA	49	NEG	0	11	11	347	0.3	2.22	0.136
PENIMICZ	51	ACRESP	1	POS	2	12	23	332	1.0	0.36	0.549
PENIMICZ	51	ALTEALTE	2	POS	13	1	314	41	12.4	0.01	0.920
PENIMICZ	51	ALTESP	3	NEG	0	14	16	339	0.6	2.19	0.139
PENIMICZ	51	ASPECAND	4	POS	1	13	18	337	0.7	0.07	0.791
PENIMICZ	51	ASPEFUMI	5	POS	1	13	24	331	1.0	0.24	0.624
PENIMICZ	51	ASPEGLAU	6	NEG	0	14	25	330	1.0	2.47	0.116
PENIMICZ	51	ASPENIGE	7	POS	7	7	119	236	4.8	0.98	0.322
PENIMICZ	51	ASPEOCHR	8	NEG	1	13	71	284	2.7	2.35	0.125
PENIMICZ	51	ASPEORYZ	9	POS	1	13	8	347	0.3	0.08	0.777
PENIMICZ	51	ASPESP	10	POS	4	10	63	292	2.5	0.46	0.498
PENIMICZ	51	ASPESYDO	11	POS	2	12	44	311	1.8	0.04	0.841
PENIMICZ	51	ASPEUSTU	12	POS	1	13	23	332	0.9	0.21	0.647
PENIMICZ	51	ASPEVERS	13	POS	8	6	188	167	7.4	0.00	1.000
PENIMICZ	51	AUREPULL	14	POS	12	2	281	74	11.1	0.07	0.791
PENIMICZ	51	CHAEGLOB	15	NEG	0	14	24	331	0.9	2.43	0.119

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENIMICZ	51	CHRSPMSP	16	POS	2	12	12	343	0.5	1.91	0.167
PENIMICZ	51	CLADCLAD	17	NEG	7	7	178	177	7.0	0.08	0.777
PENIMICZ	51	CLADHERB	18	NEG	3	11	84	271	3.3	0.26	0.610
PENIMICZ	51	CLADSP	19	NEG	1	13	63	292	2.4	1.93	0.165
PENIMICZ	51	CLADSPHA	20	POS	8	6	133	222	5.4	1.45	0.229
PENIMICZ	51	CONISP	21	POS	1	13	9	346	0.4	0.04	0.841
PENIMICZ	51	EMERNIDU	22	NEG	0	14	10	345	0.4	2.18	0.140
PENIMICZ	51	EPICNIGR	23	POS	9	5	191	164	7.6	0.25	0.617
PENIMICZ	51	EUROHERB	24	POS	10	4	235	120	9.3	0.01	0.920
PENIMICZ	51	FUSAOXYS	25	NEG	0	14	20	335	0.8	2.30	0.129
PENIMICZ	51	FUSASP	26	POS	4	10	55	300	2.2	0.88	0.348
PENIMICZ	51	GEOMPANN	27	POS	2	12	10	345	0.5	2.58	0.108
PENIMICZ	51	MUCOPLUM	28	NEG	1	13	72	283	2.8	2.41	0.121
PENIMICZ	51	MUCORACE	29	POS	4	10	87	268	3.5	0.00	1.000
PENIMICZ	51	PAECSP	30	POS	2	12	6	349	0.3	5.01	0.025
PENIMICZ	51	PAECVARI	31	NEG	1	13	49	306	1.9	1.24	0.265
PENIMICZ	51	PENIATRA	32	POS	1	13	8	347	0.3	0.08	0.777
PENIMICZ	51	PENIAURA	33	POS	4	10	40	315	1.7	2.37	0.124
PENIMICZ	51	PENIBREV	34	POS	5	9	81	274	3.3	0.64	0.424
PENIMICZ	51	PENICHRY	35	NEG	6	8	185	170	7.3	0.91	0.340
PENIMICZ	51	PENICOMM	36	POS	5	9	89	266	3.6	0.34	0.560
PENIMICZ	51	PENICOPR	37	POS	2	12	8	347	0.4	3.54	0.060
PENIMICZ	51	PENICORY	38	NEG	4	10	104	251	4.1	0.13	0.718
PENIMICZ	51	PENICRUS	39	NEG	0	14	14	341	0.5	2.16	0.142
PENIMICZ	51	PENICTNG	40	POS	3	11	31	324	1.3	1.30	0.254
PENIMICZ	51	PENICTRM	41	POS	3	11	49	306	2.0	0.17	0.680
PENIMICZ	51	PENIDECU	42	POS	1	13	18	337	0.7	0.07	0.791
PENIMICZ	51	PENIDIGI	43	NEG	0	14	10	345	0.4	2.18	0.140
PENIMICZ	51	PENIECHI	44	NEG	0	14	17	338	0.6	2.21	0.137
PENIMICZ	51	PENIEXPA	45	POS	3	11	66	289	2.6	0.01	0.920
PENIMICZ	51	PENIGLAN	46	POS	1	13	12	343	0.5	0.00	1.000
PENIMICZ	51	PENIGRIS	47	NEG	0	14	23	332	0.9	2.39	0.122
PENIMICZ	51	PENIIMPL	48	POS	3	11	16	339	0.7	4.81	0.028
PENIMICZ	51	PENIISLA	49	POS	1	13	10	345	0.4	0.02	0.888
PENIMICZ	51	PENIITAL	50	NEG	0	14	11	344	0.4	2.16	0.142
PENIOXAL	52	ACRESP	1	NEG	0	21	25	323	1.4	2.96	0.085
PENIOXAL	52	ALTEALTE	2	POS	20	1	307	41	18.6	0.40	0.527
PENIOXAL	52	ALTESP	3	NEG	0	21	16	332	0.9	2.42	0.120
PENIOXAL	52	ASPECAND	4	NEG	1	20	18	330	1.1	0.35	0.554
PENIOXAL	52	ASPEFUMI	5	POS	3	18	22	326	1.4	0.93	0.335
PENIOXAL	52	ASPEGLAU	6	POS	2	19	23	325	1.4	0.00	1.000
PENIOXAL	52	ASPENIGE	7	POS	8	13	118	230	7.2	0.02	0.888
PENIOXAL	52	ASPEOCHR	8	POS	5	16	67	281	4.1	0.05	0.823
PENIOXAL	52	ASPEORYZ	9	NEG	0	21	9	339	0.5	2.17	0.141
PENIOXAL	52	ASPESP	10	NEG	2	19	65	283	3.8	1.82	0.177
PENIOXAL	52	ASPESYDO	11	POS	5	16	41	307	2.6	1.64	0.200
PENIOXAL	52	ASPEUSTU	12	POS	2	19	22	326	1.4	0.01	0.920
PENIOXAL	52	ASPEVERS	13	NEG	8	13	188	160	11.2	2.71	0.100
PENIOXAL	52	AUREPULL	14	NEG	15	6	278	70	16.7	1.46	0.227
PENIOXAL	52	CHAEGLOB	15	POS	2	19	22	326	1.4	0.01	0.920
PENIOXAL	52	CHRSPMSP	16	NEG	0	21	14	334	0.8	2.33	0.127
PENIOXAL	52	CLADCLAD	17	NEG	10	11	175	173	10.5	0.21	0.647
PENIOXAL	52	CLADHERB	18	NEG	4	17	83	265	5.0	0.59	0.442
PENIOXAL	52	CLADSP	19	NEG	3	18	61	287	3.6	0.46	0.498
PENIOXAL	52	CLADSPHA	20	NEG	8	13	133	215	8.0	0.06	0.806
PENIOXAL	52	CONISP	21	NEG	0	21	10	338	0.6	2.19	0.139
PENIOXAL	52	EMERNIDU	22	POS	2	19	8	340	0.6	1.66	0.198
PENIOXAL	52	EPICNIGR	23	POS	12	9	188	160	11.4	0.00	1.000
PENIOXAL	52	EUROHERB	24	NEG	11	10	234	114	13.9	2.68	0.102
PENIOXAL	52	FUSAOXYS	25	NEG	1	20	19	329	1.1	0.40	0.527
PENIOXAL	52	FUSASP	26	POS	4	17	55	293	3.4	0.01	0.920
PENIOXAL	52	GEOMPANN	27	NEG	0	21	12	336	0.7	2.25	0.134

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENIOXAL	52	MUCOPLUM	28	NEG	4	17	69	279	4.2	0.14	0.708
PENIOXAL	52	MUCORACE	29	POS	9	12	82	266	5.2	3.00	0.083
PENIOXAL	52	PAECSP	30	NEG	0	21	8	340	0.5	2.17	0.141
PENIOXAL	52	PAECVARI	31	POS	3	18	47	301	2.9	0.05	0.823
PENIOXAL	52	PENIATRA	32	NEG	0	21	9	339	0.5	2.17	0.141
PENIOXAL	52	PENIAURA	33	NEG	2	19	42	306	2.5	0.48	0.488
PENIOXAL	52	PENIBREV	34	NEG	4	17	82	266	4.9	0.55	0.458
PENIOXAL	52	PENICHRY	35	NEG	10	11	181	167	10.9	0.38	0.538
PENIOXAL	52	PENICOMM	36	NEG	4	17	90	258	5.4	0.91	0.340
PENIOXAL	52	PENICOPR	37	NEG	0	21	10	338	0.6	2.19	0.139
PENIOXAL	52	PENICORY	38	NEG	3	18	105	243	6.2	3.24	0.072
PENIOXAL	52	PENICRUS	39	NEG	0	21	14	334	0.8	2.33	0.127
PENIOXAL	52	PENICTNG	40	POS	3	18	31	317	1.9	0.19	0.663
PENIOXAL	52	PENICTRM	41	POS	3	18	49	299	3.0	0.09	0.764
PENIOXAL	52	PENIDECU	42	POS	2	19	17	331	1.1	0.18	0.671
PENIOXAL	52	PENIDIGI	43	POS	1	20	9	339	0.6	0.01	0.920
PENIOXAL	52	PENIECHI	44	POS	1	20	16	332	1.0	0.25	0.617
PENIOXAL	52	PENIEXPA	45	NEG	2	19	67	281	3.9	1.96	0.162
PENIOXAL	52	PENIGLAN	46	NEG	0	21	13	335	0.7	2.28	0.131
PENIOXAL	52	PENIGRIS	47	POS	2	19	21	327	1.3	0.03	0.862
PENIOXAL	52	PENIIMPL	48	NEG	1	20	18	330	1.1	0.35	0.554
PENIOXAL	52	PENIISLA	49	POS	2	19	9	339	0.6	1.33	0.249
PENIOXAL	52	PENIITAL	50	NEG	0	21	11	337	0.6	2.21	0.137
PENIOXAL	52	PENIMICZ	51	NEG	0	21	14	334	0.8	2.33	0.127
PENIPURP	53	ACRESP	1	NEG	0	9	25	335	0.6	2.22	0.136
PENIPURP	53	ALTEALTE	2	POS	8	1	319	41	8.0	0.26	0.610
PENIPURP	53	ALTESP	3	NEG	0	9	16	344	0.4	2.18	0.140
PENIPURP	53	ASPECAND	4	POS	2	7	17	343	0.5	2.51	0.113
PENIPURP	53	ASPEFUMI	5	POS	3	6	22	338	0.6	6.44	0.011
PENIPURP	53	ASPEGLAU	6	POS	1	8	24	336	0.6	0.02	0.888
PENIPURP	53	ASPENIGE	7	POS	4	5	122	238	3.1	0.09	0.764
PENIPURP	53	ASPEOCHR	8	POS	3	6	69	291	1.8	0.40	0.527
PENIPURP	53	ASPEORYZ	9	NEG	0	9	9	351	0.2	2.48	0.115
PENIPURP	53	ASPESP	10	NEG	1	8	66	294	1.6	0.99	0.320
PENIPURP	53	ASPESYDO	11	NEG	0	9	46	314	1.1	2.75	0.097
PENIPURP	53	ASPEUSTU	12	NEG	0	9	24	336	0.6	2.21	0.137
PENIPURP	53	ASPEVERS	13	NEG	4	5	192	168	4.8	0.75	0.386
PENIPURP	53	AUREPULL	14	POS	8	1	285	75	7.2	0.09	0.764
PENIPURP	53	CHAEGLOB	15	NEG	0	9	24	336	0.6	2.21	0.137
PENIPURP	53	CHRSPMSP	16	NEG	0	9	14	346	0.3	2.21	0.137
PENIPURP	53	CLADCLAD	17	POS	7	2	178	182	4.5	1.80	0.180
PENIPURP	53	CLADHERB	18	NEG	0	9	87	273	2.1	4.35	0.037
PENIPURP	53	CLADSP	19	POS	2	7	62	298	1.6	0.00	1.000
PENIPURP	53	CLADSPHA	20	POS	4	5	137	223	3.4	0.00	1.000
PENIPURP	53	CONISP	21	NEG	0	9	10	350	0.2	2.39	0.122
PENIPURP	53	EMERNIDU	22	NEG	0	9	10	350	0.2	2.39	0.122
PENIPURP	53	EPICNIGR	23	POS	5	4	195	165	4.9	0.07	0.791
PENIPURP	53	EUROHERB	24	POS	8	1	237	123	6.0	1.19	0.275
PENIPURP	53	FUSAOXYS	25	NEG	0	9	20	340	0.5	2.17	0.141
PENIPURP	53	FUSASP	26	NEG	0	9	59	301	1.4	3.19	0.074
PENIPURP	53	GEOMPANN	27	NEG	0	9	12	348	0.3	2.27	0.132
PENIPURP	53	MUCOPLUM	28	POS	2	7	71	289	1.8	0.06	0.806
PENIPURP	53	MUCORACE	29	NEG	1	8	90	270	2.2	1.81	0.179
PENIPURP	53	PAECSP	30	NEG	0	9	8	352	0.2	2.59	0.108
PENIPURP	53	PAECVARI	31	POS	3	6	47	313	1.2	1.59	0.207
PENIPURP	53	PENIATRA	32	NEG	0	9	9	351	0.2	2.48	0.115
PENIPURP	53	PENIAURA	33	POS	2	7	42	318	1.1	0.20	0.655
PENIPURP	53	PENIBREV	34	POS	4	5	82	278	2.1	1.25	0.264
PENIPURP	53	PENICHRY	35	POS	6	3	185	175	4.7	0.32	0.572
PENIPURP	53	PENICOMM	36	NEG	2	7	92	268	2.3	0.38	0.538
PENIPURP	53	PENICOPR	37	POS	1	8	9	351	0.2	0.28	0.597
PENIPURP	53	PENICORY	38	POS	4	5	104	256	2.6	0.41	0.522

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENIPURP	53	PENICRUS	39	NEG	0	9	14	346	0.3	2.21	0.137
PENIPURP	53	PENICTNG	40	NEG	0	9	34	326	0.8	2.41	0.121
PENIPURP	53	PENICTRM	41	POS	4	5	48	312	1.3	4.69	0.030
PENIPURP	53	PENIDECU	42	NEG	0	9	19	341	0.5	2.16	0.142
PENIPURP	53	PENIDIGI	43	NEG	0	9	10	350	0.2	2.39	0.122
PENIPURP	53	PENIECHI	44	NEG	0	9	17	343	0.4	2.17	0.141
PENIPURP	53	PENIEXPA	45	POS	2	7	67	293	1.7	0.03	0.862
PENIPURP	53	PENIGLAN	46	NEG	0	9	13	347	0.3	2.24	0.134
PENIPURP	53	PENIGRIS	47	NEG	0	9	23	337	0.6	2.19	0.139
PENIPURP	53	PENIIMPL	48	NEG	0	9	19	341	0.5	2.16	0.142
PENIPURP	53	PENIISLA	49	NEG	0	9	11	349	0.3	2.32	0.128
PENIPURP	53	PENIITAL	50	NEG	0	9	11	349	0.3	2.32	0.128
PENIPURP	53	PENIMICZ	51	NEG	0	9	14	346	0.3	2.21	0.137
PENIPURP	53	PENIOXAL	52	POS	1	8	20	340	0.5	0.00	1.000
PENIRAIS	54	ACRESP	1	POS	2	24	23	320	1.8	0.04	0.841
PENIRAIS	54	ALTEALTE	2	POS	24	2	303	40	23.0	0.09	0.764
PENIRAIS	54	ALTESP	3	NEG	1	25	15	328	1.1	0.39	0.532
PENIRAIS	54	ASPECAND	4	NEG	0	26	19	324	1.3	2.86	0.091
PENIRAIS	54	ASPEFUMI	5	NEG	0	26	25	318	1.8	3.35	0.067
PENIRAIS	54	ASPEGLAU	6	NEG	1	25	24	319	1.8	1.04	0.308
PENIRAIS	54	ASPENIGE	7	POS	9	17	117	226	8.9	0.03	0.862
PENIRAIS	54	ASPEOCHR	8	POS	10	16	62	281	5.1	5.16	0.023
PENIRAIS	54	ASPEORYZ	9	NEG	0	26	9	334	0.6	2.24	0.134
PENIRAIS	54	ASPESP	10	POS	5	21	62	281	4.7	0.01	0.920
PENIRAIS	54	ASPESYDO	11	NEG	3	23	43	300	3.2	0.21	0.647
PENIRAIS	54	ASPEUSTU	12	NEG	0	26	24	319	1.7	3.27	0.071
PENIRAIS	54	ASPEVERS	13	NEG	12	14	184	159	13.8	0.89	0.345
PENIRAIS	54	AUREPULL	14	POS	23	3	270	73	20.6	0.87	0.351
PENIRAIS	54	CHAEGLOB	15	POS	5	21	19	324	1.7	5.37	0.020
PENIRAIS	54	CHRSPMSP	16	POS	1	25	13	330	1.0	0.27	0.603
PENIRAIS	54	CLADCLAD	17	NEG	12	14	173	170	13.0	0.39	0.532
PENIRAIS	54	CLADHERB	18	NEG	5	21	82	261	6.1	0.61	0.435
PENIRAIS	54	CLADSP	19	NEG	3	23	61	282	4.5	1.17	0.279
PENIRAIS	54	CLADSPHA	20	POS	11	15	130	213	9.9	0.06	0.806
PENIRAIS	54	CONISP	21	NEG	0	26	10	333	0.7	2.28	0.131
PENIRAIS	54	EMERNIDU	22	POS	1	25	9	334	0.7	0.07	0.791
PENIRAIS	54	EPICNIGR	23	NEG	14	12	186	157	14.1	0.06	0.806
PENIRAIS	54	EUROHERB	24	POS	19	7	226	117	17.3	0.28	0.597
PENIRAIS	54	FUSAOXYS	25	POS	2	24	18	325	1.4	0.01	0.920
PENIRAIS	54	FUSASP	26	NEG	4	22	55	288	4.2	0.13	0.718
PENIRAIS	54	GEOMPANN	27	NEG	0	26	12	331	0.9	2.38	0.123
PENIRAIS	54	MUCOPLUM	28	POS	6	20	67	276	5.1	0.03	0.862
PENIRAIS	54	MUCORACE	29	NEG	4	22	87	256	6.4	1.89	0.169
PENIRAIS	54	PAECSP	30	POS	1	25	7	336	0.6	0.01	0.920
PENIRAIS	54	PAECVARI	31	POS	6	20	44	299	3.5	1.38	0.240
PENIRAIS	54	PENIATRA	32	POS	1	25	8	335	0.6	0.03	0.862
PENIRAIS	54	PENIAURA	33	NEG	3	23	41	302	3.1	0.14	0.708
PENIRAIS	54	PENIBREV	34	POS	8	18	78	265	6.1	0.48	0.488
PENIRAIS	54	PENICHRY	35	NEG	10	16	181	162	13.5	2.60	0.107
PENIRAIS	54	PENICOMM	36	POS	12	14	82	261	6.6	5.18	0.023
PENIRAIS	54	PENICOPR	37	POS	1	25	9	334	0.7	0.07	0.791
PENIRAIS	54	PENICORY	38	POS	11	15	97	246	7.6	1.67	0.196
PENIRAIS	54	PENICRUS	39	POS	5	21	9	334	1.0	13.99	0.000
PENIRAIS	54	PENICTNG	40	POS	4	22	30	313	2.4	0.60	0.439
PENIRAIS	54	PENICTRM	41	POS	5	21	47	296	3.7	0.24	0.624
PENIRAIS	54	PENIDECU	42	POS	4	22	15	328	1.3	3.96	0.047
PENIRAIS	54	PENIDIGI	43	NEG	0	26	10	333	0.7	2.28	0.131
PENIRAIS	54	PENIECHI	44	POS	2	24	15	328	1.2	0.09	0.764
PENIRAIS	54	PENIEXPA	45	NEG	2	24	67	276	4.9	3.08	0.079
PENIRAIS	54	PENIGLAN	46	POS	4	22	9	334	0.9	8.13	0.004
PENIRAIS	54	PENIGRIS	47	POS	2	24	21	322	1.6	0.01	0.920
PENIRAIS	54	PENIIMPL	48	NEG	1	25	18	325	1.3	0.60	0.439

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENIRAIS	54	PENIISLA	49	NEG	0	26	11	332	0.8	2.33	0.127
PENIRAIS	54	PENIITAL	50	NEG	0	26	11	332	0.8	2.33	0.127
PENIRAIS	54	PENIMICZ	51	POS	1	25	13	330	1.0	0.27	0.603
PENIRAIS	54	PENIOXAL	52	NEG	0	26	21	322	1.5	3.02	0.082
PENIRAIS	54	PENIPURP	53	POS	1	25	8	335	0.6	0.03	0.862
PENIREST	55	ACRESP	1	POS	2	7	23	337	0.6	1.43	0.232
PENIREST	55	ALTEALTE	2	NEG	7	2	320	40	8.0	2.46	0.117
PENIREST	55	ALTESP	3	NEG	0	9	16	344	0.4	2.18	0.140
PENIREST	55	ASPECAND	4	POS	1	8	18	342	0.5	0.00	1.000
PENIREST	55	ASPEFUMI	5	NEG	0	9	25	335	0.6	2.22	0.136
PENIREST	55	ASPEGLAU	6	NEG	0	9	25	335	0.6	2.22	0.136
PENIREST	55	ASPENIGE	7	NEG	3	6	123	237	3.1	0.17	0.680
PENIREST	55	ASPEOCHR	8	POS	2	7	70	290	1.8	0.05	0.823
PENIREST	55	ASPEORYZ	9	POS	1	8	8	352	0.2	0.38	0.538
PENIREST	55	ASPESP	10	NEG	1	8	66	294	1.6	0.99	0.320
PENIREST	55	ASPESYDO	11	NEG	0	9	46	314	1.1	2.75	0.097
PENIREST	55	ASPEUSTU	12	POS	1	8	23	337	0.6	0.01	0.920
PENIREST	55	ASPEVERS	13	POS	5	4	191	169	4.8	0.04	0.841
PENIREST	55	AUREPULL	14	NEG	6	3	287	73	7.2	1.89	0.169
PENIREST	55	CHAEGLOB	15	NEG	0	9	24	336	0.6	2.21	0.137
PENIREST	55	CHRSPMSP	16	NEG	0	9	14	346	0.3	2.21	0.137
PENIREST	55	CLADCLAD	17	POS	6	3	179	181	4.5	0.44	0.507
PENIREST	55	CLADHERB	18	NEG	0	9	87	273	2.1	4.35	0.037
PENIREST	55	CLADSP	19	NEG	1	8	63	297	1.6	0.89	0.345
PENIREST	55	CLADSPHA	20	NEG	2	7	139	221	3.4	1.81	0.179
PENIREST	55	CONISP	21	NEG	0	9	10	350	0.2	2.39	0.122
PENIREST	55	EMERNIDU	22	NEG	0	9	10	350	0.2	2.39	0.122
PENIREST	55	EPICNIGR	23	NEG	2	7	198	162	4.9	5.24	0.022
PENIREST	55	EUROHERB	24	POS	7	2	238	122	6.0	0.14	0.708
PENIREST	55	FUSAOXYS	25	NEG	0	9	20	340	0.5	2.17	0.141
PENIREST	55	FUSASP	26	POS	2	7	57	303	1.4	0.00	1.000
PENIREST	55	GEOMPANN	27	NEG	0	9	12	348	0.3	2.27	0.132
PENIREST	55	MUCOPLUM	28	POS	3	6	70	290	1.8	0.37	0.543
PENIREST	55	MUCORACE	29	POS	3	6	88	272	2.2	0.05	0.823
PENIREST	55	PAECSP	30	NEG	0	9	8	352	0.2	2.59	0.108
PENIREST	55	PAECVARI	31	POS	2	7	48	312	1.2	0.08	0.777
PENIREST	55	PENIATRA	32	NEG	0	9	9	351	0.2	2.48	0.115
PENIREST	55	PENIAURA	33	NEG	0	9	44	316	1.1	2.68	0.102
PENIREST	55	PENIBREV	34	POS	4	5	82	278	2.1	1.25	0.264
PENIREST	55	PENICHRY	35	POS	5	4	186	174	4.7	0.01	0.920
PENIREST	55	PENICOMM	36	NEG	1	8	93	267	2.3	1.93	0.165
PENIREST	55	PENICOPR	37	NEG	0	9	10	350	0.2	2.39	0.122
PENIREST	55	PENICORY	38	POS	4	5	104	256	2.6	0.41	0.522
PENIREST	55	PENICRUS	39	NEG	0	9	14	346	0.3	2.21	0.137
PENIREST	55	PENICTNG	40	POS	2	7	32	328	0.8	0.61	0.435
PENIREST	55	PENICTRM	41	POS	2	7	50	310	1.3	0.05	0.823
PENIREST	55	PENIDECU	42	NEG	0	9	19	341	0.5	2.16	0.142
PENIREST	55	PENIDIGI	43	NEG	0	9	10	350	0.2	2.39	0.122
PENIREST	55	PENIECHI	44	NEG	0	9	17	343	0.4	2.17	0.141
PENIREST	55	PENIEXPA	45	NEG	1	8	68	292	1.7	1.05	0.306
PENIREST	55	PENIGLAN	46	NEG	0	9	13	347	0.3	2.24	0.134
PENIREST	55	PENIGRIS	47	NEG	0	9	23	337	0.6	2.19	0.139
PENIREST	55	PENIIMPL	48	POS	1	8	18	342	0.5	0.00	1.000
PENIREST	55	PENIISLA	49	POS	1	8	10	350	0.3	0.21	0.647
PENIREST	55	PENIITAL	50	NEG	0	9	11	349	0.3	2.32	0.128
PENIREST	55	PENIMICZ	51	POS	2	7	12	348	0.3	4.19	0.041
PENIREST	55	PENIOXAL	52	NEG	0	9	21	339	0.5	2.17	0.141
PENIREST	55	PENIPURP	53	NEG	0	9	9	351	0.2	2.48	0.115
PENIREST	55	PENIRAIS	54	NEG	0	9	26	334	0.6	2.24	0.134
PENISIMP	56	ACRESP	1	NEG	0	20	25	324	1.4	2.88	0.090
PENISIMP	56	ALTEALTE	2	POS	19	1	308	41	17.7	0.32	0.572
PENISIMP	56	ALTESP	3	POS	1	19	15	334	0.9	0.17	0.680

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENISIMP	56	ASPECAND	4	NEG	1	19	18	331	1.0	0.30	0.584
PENISIMP	56	ASPEFUMI	5	NEG	1	19	24	325	1.4	0.61	0.435
PENISIMP	56	ASPEGLAU	6	POS	2	18	23	326	1.4	0.02	0.888
PENISIMP	56	ASPENIGE	7	POS	11	9	115	234	6.8	3.17	0.075
PENISIMP	56	ASPEOCHR	8	POS	5	15	67	282	3.9	0.12	0.729
PENISIMP	56	ASPEORYZ	9	POS	1	19	8	341	0.5	0.00	1.000
PENISIMP	56	ASPESP	10	POS	5	15	62	287	3.6	0.27	0.603
PENISIMP	56	ASPESYDO	11	POS	5	15	41	308	2.5	1.95	0.163
PENISIMP	56	ASPEUSTU	12	POS	3	17	21	328	1.3	1.25	0.264
PENISIMP	56	ASPEVERS	13	POS	12	8	184	165	10.6	0.16	0.689
PENISIMP	56	AUREPULL	14	NEG	13	7	280	69	15.9	3.69	0.055
PENISIMP	56	CHAEGLOB	15	NEG	1	19	23	326	1.3	0.56	0.454
PENISIMP	56	CHRSPMSP	16	POS	1	19	13	336	0.8	0.10	0.752
PENISIMP	56	CLADCLAD	17	POS	11	9	174	175	10.0	0.05	0.823
PENISIMP	56	CLADHERB	18	POS	5	15	82	267	4.7	0.01	0.920
PENISIMP	56	CLADSP	19	NEG	3	17	61	288	3.5	0.35	0.554
PENISIMP	56	CLADSPHA	20	POS	8	12	133	216	7.6	0.00	1.000
PENISIMP	56	CONISP	21	POS	1	19	9	340	0.5	0.00	1.000
PENISIMP	56	EMERNIDU	22	POS	2	18	8	341	0.5	1.84	0.175
PENISIMP	56	EPICNIGR	23	POS	11	9	189	160	10.8	0.02	0.888
PENISIMP	56	EUROHERB	24	POS	14	6	231	118	13.3	0.01	0.920
PENISIMP	56	FUSAOXYS	25	POS	2	18	18	331	1.1	0.18	0.671
PENISIMP	56	FUSASP	26	POS	4	16	55	294	3.2	0.04	0.841
PENISIMP	56	GEOMPANN	27	POS	1	19	11	338	0.7	0.04	0.841
PENISIMP	56	MUCOPLUM	28	POS	4	16	69	280	4.0	0.07	0.791
PENISIMP	56	MUCORACE	29	POS	5	15	86	263	4.9	0.05	0.823
PENISIMP	56	PAECSP	30	POS	1	19	7	342	0.4	0.01	0.920
PENISIMP	56	PAECVARI	31	POS	5	15	45	304	2.7	1.45	0.229
PENISIMP	56	PENIATRA	32	POS	2	18	7	342	0.5	2.28	0.131
PENISIMP	56	PENIAURA	33	POS	5	15	39	310	2.4	2.25	0.134
PENISIMP	56	PENIBREV	34	POS	7	13	79	270	4.7	1.00	0.317
PENISIMP	56	PENICHRY	35	NEG	7	13	184	165	10.4	3.14	0.076
PENISIMP	56	PENICOMM	36	POS	9	11	85	264	5.1	3.23	0.072
PENISIMP	56	PENICOPR	37	POS	2	18	8	341	0.5	1.84	0.175
PENISIMP	56	PENICORY	38	POS	11	9	97	252	5.9	5.51	0.019
PENISIMP	56	PENICRUS	39	POS	1	19	13	336	0.8	0.10	0.752
PENISIMP	56	PENICTNG	40	NEG	1	19	33	316	1.8	1.14	0.286
PENISIMP	56	PENICTRM	41	NEG	2	18	50	299	2.8	0.76	0.383
PENISIMP	56	PENIDECU	42	NEG	0	20	19	330	1.0	2.53	0.112
PENISIMP	56	PENIDIGI	43	NEG	0	20	10	339	0.5	2.18	0.140
PENISIMP	56	PENIECHI	44	NEG	0	20	17	332	0.9	2.43	0.119
PENISIMP	56	PENIEXPA	45	POS	8	12	61	288	3.7	4.92	0.027
PENISIMP	56	PENIGLAN	46	POS	1	19	12	337	0.7	0.07	0.791
PENISIMP	56	PENIGRIS	47	POS	2	18	21	328	1.3	0.06	0.806
PENISIMP	56	PENIIMPL	48	POS	2	18	17	332	1.0	0.24	0.624
PENISIMP	56	PENIISLA	49	NEG	0	20	11	338	0.6	2.20	0.138
PENISIMP	56	PENIITAL	50	NEG	0	20	11	338	0.6	2.20	0.138
PENISIMP	56	PENIMICZ	51	POS	2	18	12	337	0.8	0.80	0.371
PENISIMP	56	PENIOXAL	52	POS	2	18	19	330	1.1	0.13	0.718
PENISIMP	56	PENIPURP	53	POS	1	19	8	341	0.5	0.00	1.000
PENISIMP	56	PENIRAIS	54	POS	3	17	23	326	1.4	0.96	0.327
PENISIMP	56	PENIREST	55	POS	1	19	8	341	0.5	0.00	1.000
PENISP	57	ACRESP	1	NEG	1	28	24	316	2.0	1.27	0.260
PENISP	57	ALTEALTE	2	POS	28	1	299	41	25.7	1.20	0.273
PENISP	57	ALTESP	3	POS	2	27	14	326	1.3	0.05	0.823
PENISP	57	ASPECAND	4	NEG	1	28	18	322	1.5	0.76	0.383
PENISP	57	ASPEFUMI	5	POS	3	26	22	318	2.0	0.17	0.680
PENISP	57	ASPEGLAU	6	NEG	2	27	23	317	2.0	0.13	0.718
PENISP	57	ASPENIGE	7	POS	15	14	111	229	9.9	3.52	0.061
PENISP	57	ASPEOCHR	8	POS	6	23	66	274	5.7	0.01	0.920
PENISP	57	ASPEORYZ	9	NEG	0	29	9	331	0.7	2.29	0.130
PENISP	57	ASPESP	10	POS	8	21	59	281	5.3	1.26	0.262

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENISP	57	ASPESYDO	11	POS	5	24	41	299	3.6	0.27	0.603
PENISP	57	ASPEUSTU	12	POS	2	27	22	318	1.9	0.09	0.764
PENISP	57	ASPEVERS	13	POS	18	11	178	162	15.4	0.66	0.417
PENISP	57	AUREPULL	14	POS	24	5	269	71	23.0	0.05	0.823
PENISP	57	CHAEGLOB	15	POS	2	27	22	318	1.9	0.09	0.764
PENISP	57	CHRSPMSP	16	POS	2	27	12	328	1.1	0.16	0.689
PENISP	57	CLADCLAD	17	POS	15	14	170	170	14.5	0.00	1.000
PENISP	57	CLADHERB	18	NEG	6	23	81	259	6.8	0.37	0.543
PENISP	57	CLADSP	19	POS	7	22	57	283	5.0	0.56	0.454
PENISP	57	CLADSPHA	20	NEG	8	21	133	207	11.1	2.03	0.154
PENISP	57	CONISP	21	NEG	0	29	10	330	0.8	2.35	0.125
PENISP	57	EMERNIDU	22	POS	2	27	8	332	0.8	0.72	0.396
PENISP	57	EPICNIGR	23	NEG	14	15	186	154	16.0	0.74	0.390
PENISP	57	EUROHERB	24	NEG	18	11	227	113	19.3	0.52	0.471
PENISP	57	FUSAOXYS	25	POS	4	25	16	324	1.6	2.71	0.100
PENISP	57	FUSASP	26	NEG	0	29	59	281	4.6	7.35	0.007
PENISP	57	GEOMPANN	27	NEG	0	29	12	328	0.9	2.48	0.115
PENISP	57	MUCOPLUM	28	POS	9	20	64	276	5.7	1.80	0.180
PENISP	57	MUCORACE	29	POS	9	20	82	258	7.2	0.37	0.543
PENISP	57	PAECSP	30	POS	1	28	7	333	0.6	0.03	0.862
PENISP	57	PAECVARI	31	POS	4	25	46	294	3.9	0.06	0.806
PENISP	57	PENIATRA	32	POS	1	28	8	332	0.7	0.07	0.791
PENISP	57	PENIAURA	33	POS	7	22	37	303	3.5	3.30	0.069
PENISP	57	PENIBREV	34	POS	10	19	76	264	6.8	1.57	0.210
PENISP	57	PENICHRY	35	NEG	14	15	177	163	15.0	0.34	0.560
PENISP	57	PENICOMM	36	POS	13	16	81	259	7.4	5.15	0.023
PENISP	57	PENICOPR	37	NEG	0	29	10	330	0.8	2.35	0.125
PENISP	57	PENICORY	38	POS	9	20	99	241	8.5	0.00	1.000
PENISP	57	PENICRUS	39	POS	2	27	12	328	1.1	0.16	0.689
PENISP	57	PENICTNG	40	POS	3	26	31	309	2.7	0.01	0.920
PENISP	57	PENICTRM	41	POS	5	24	47	293	4.1	0.05	0.823
PENISP	57	PENIDECU	42	NEG	1	28	18	322	1.5	0.76	0.383
PENISP	57	PENIDIGI	43	NEG	0	29	10	330	0.8	2.35	0.125
PENISP	57	PENIECHI	44	POS	2	27	15	325	1.3	0.02	0.888
PENISP	57	PENIEXPA	45	POS	7	22	62	278	5.4	0.29	0.590
PENISP	57	PENIGLAN	46	NEG	0	29	13	327	1.0	2.55	0.110
PENISP	57	PENIGRIS	47	POS	4	25	19	321	1.8	1.83	0.176
PENISP	57	PENIIMPL	48	POS	2	27	17	323	1.5	0.00	1.000
PENISP	57	PENIISLA	49	NEG	0	29	11	329	0.9	2.41	0.121
PENISP	57	PENIITAL	50	NEG	0	29	11	329	0.9	2.41	0.121
PENISP	57	PENIMICZ	51	NEG	0	29	14	326	1.1	2.63	0.105
PENISP	57	PENIOXAL	52	POS	2	27	19	321	1.7	0.02	0.888
PENISP	57	PENIPURP	53	POS	4	25	5	335	0.7	12.27	0.000
PENISP	57	PENIRAIS	54	POS	4	25	22	318	2.0	1.21	0.271
PENISP	57	PENIREST	55	POS	1	28	8	332	0.7	0.07	0.791
PENISP	57	PENISIMP	56	POS	3	26	17	323	1.6	0.63	0.427
PENISP01	58	ACRESP	1	NEG	0	9	25	335	0.6	2.22	0.136
PENISP01	58	ALTEALTE	2	NEG	7	2	320	40	8.0	2.46	0.117
PENISP01	58	ALTESP	3	POS	1	8	15	345	0.4	0.03	0.862
PENISP01	58	ASPECAND	4	POS	2	7	17	343	0.5	2.51	0.113
PENISP01	58	ASPEFUMI	5	POS	1	8	24	336	0.6	0.02	0.888
PENISP01	58	ASPEGLAU	6	POS	1	8	24	336	0.6	0.02	0.888
PENISP01	58	ASPENIGE	7	POS	6	3	120	240	3.1	2.98	0.084
PENISP01	58	ASPEOCHR	8	NEG	1	8	71	289	1.8	1.14	0.286
PENISP01	58	ASPEORYZ	9	NEG	0	9	9	351	0.2	2.48	0.115
PENISP01	58	ASPESP	10	NEG	1	8	66	294	1.6	0.99	0.320
PENISP01	58	ASPESYDO	11	POS	2	7	44	316	1.1	0.15	0.699
PENISP01	58	ASPEUSTU	12	POS	1	8	23	337	0.6	0.01	0.920
PENISP01	58	ASPEVERS	13	POS	7	2	189	171	4.8	1.35	0.245
PENISP01	58	AUREPULL	14	NEG	5	4	288	72	7.2	4.88	0.027
PENISP01	58	CHAEGLOB	15	POS	3	6	21	339	0.6	6.87	0.009
PENISP01	58	CHRSPMSP	16	NEG	0	9	14	346	0.3	2.21	0.137

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENISP01	58	CLADCLAD	17	NEG	3	6	182	178	4.5	1.84	0.175
PENISP01	58	CLADHERB	18	NEG	1	8	86	274	2.1	1.66	0.198
PENISP01	58	CLADSP	19	POS	3	6	61	299	1.6	0.70	0.403
PENISP01	58	CLADSPHA	20	POS	4	5	137	223	3.4	0.00	1.000
PENISP01	58	CONISP	21	NEG	0	9	10	350	0.2	2.39	0.122
PENISP01	58	EMERNIDU	22	NEG	0	9	10	350	0.2	2.39	0.122
PENISP01	58	EPICNIGR	23	POS	6	3	194	166	4.9	0.18	0.671
PENISP01	58	EUROHERB	24	POS	8	1	237	123	6.0	1.19	0.275
PENISP01	58	FUSAOXYS	25	NEG	0	9	20	340	0.5	2.17	0.141
PENISP01	58	FUSASP	26	NEG	1	8	58	302	1.4	0.75	0.386
PENISP01	58	GEOMPANN	27	NEG	0	9	12	348	0.3	2.27	0.132
PENISP01	58	MUCOPLUM	28	POS	2	7	71	289	1.8	0.06	0.806
PENISP01	58	MUCORACE	29	POS	6	3	85	275	2.2	6.60	0.010
PENISP01	58	PAECSP	30	NEG	0	9	8	352	0.2	2.59	0.108
PENISP01	58	PAECVARI	31	NEG	1	8	49	311	1.2	0.50	0.480
PENISP01	58	PENIATRA	32	POS	1	8	8	352	0.2	0.38	0.538
PENISP01	58	PENIAURA	33	POS	4	5	40	320	1.1	6.39	0.011
PENISP01	58	PENIBREV	34	NEG	1	8	85	275	2.1	1.63	0.202
PENISP01	58	PENICHRY	35	POS	6	3	185	175	4.7	0.32	0.572
PENISP01	58	PENICOMM	36	POS	3	6	91	269	2.3	0.03	0.862
PENISP01	58	PENICOPR	37	NEG	0	9	10	350	0.2	2.39	0.122
PENISP01	58	PENICORY	38	POS	6	3	102	258	2.6	4.52	0.034
PENISP01	58	PENICRUS	39	POS	2	7	12	348	0.3	4.19	0.041
PENISP01	58	PENICTNG	40	NEG	0	9	34	326	0.8	2.41	0.121
PENISP01	58	PENICTRM	41	POS	3	6	49	311	1.3	1.43	0.232
PENISP01	58	PENIDECU	42	NEG	0	9	19	341	0.5	2.16	0.142
PENISP01	58	PENIDIGI	43	NEG	0	9	10	350	0.2	2.39	0.122
PENISP01	58	PENIECHI	44	POS	2	7	15	345	0.4	3.05	0.081
PENISP01	58	PENIEXPA	45	POS	7	2	62	298	1.7	17.38	0.000
PENISP01	58	PENIGLAN	46	POS	1	8	12	348	0.3	0.11	0.740
PENISP01	58	PENIGRIS	47	NEG	0	9	23	337	0.6	2.19	0.139
PENISP01	58	PENIIMPL	48	NEG	0	9	19	341	0.5	2.16	0.142
PENISP01	58	PENIISLA	49	NEG	0	9	11	349	0.3	2.32	0.128
PENISP01	58	PENIITAL	50	NEG	0	9	11	349	0.3	2.32	0.128
PENISP01	58	PENIMICZ	51	POS	1	8	13	347	0.3	0.08	0.777
PENISP01	58	PENIOXAL	52	NEG	0	9	21	339	0.5	2.17	0.141
PENISP01	58	PENIPURP	53	NEG	0	9	9	351	0.2	2.48	0.115
PENISP01	58	PENIRAIS	54	POS	1	8	25	335	0.6	0.03	0.862
PENISP01	58	PENIREST	55	NEG	0	9	9	351	0.2	2.48	0.115
PENISP01	58	PENISIMP	56	POS	1	8	19	341	0.5	0.00	1.000
PENISP01	58	PENISP	57	NEG	0	9	29	331	0.7	2.29	0.130
PENISP26	59	ACRESP	1	POS	6	47	19	297	3.6	1.27	0.260
PENISP26	59	ALTEALTE	2	NEG	43	10	284	32	47.0	4.36	0.037
PENISP26	59	ALTESP	3	NEG	1	52	15	301	2.3	1.72	0.190
PENISP26	59	ASPECAND	4	POS	4	49	15	301	2.7	0.27	0.603
PENISP26	59	ASPEFUMI	5	POS	4	49	21	295	3.6	0.00	1.000
PENISP26	59	ASPEGLAU	6	POS	7	46	18	298	3.6	2.95	0.086
PENISP26	59	ASPENIGE	7	POS	25	28	101	215	18.1	4.02	0.045
PENISP26	59	ASPEOCHR	8	NEG	10	43	62	254	10.3	0.10	0.752
PENISP26	59	ASPEORYZ	9	NEG	1	52	8	308	1.3	0.58	0.446
PENISP26	59	ASPESP	10	POS	14	39	53	263	9.6	2.23	0.135
PENISP26	59	ASPESYDO	11	POS	7	46	39	277	6.6	0.00	1.000
PENISP26	59	ASPEUSTU	12	POS	4	49	20	296	3.5	0.00	1.000
PENISP26	59	ASPEVERS	13	NEG	27	26	169	147	28.2	0.24	0.624
PENISP26	59	AUREPULL	14	POS	43	10	250	66	42.1	0.02	0.888
PENISP26	59	CHAEGLOB	15	POS	5	48	19	297	3.5	0.40	0.527
PENISP26	59	CHRSPMSP	16	POS	3	50	11	305	2.0	0.14	0.708
PENISP26	59	CLADCLAD	17	POS	28	25	157	159	26.6	0.08	0.777
PENISP26	59	CLADHERB	18	NEG	2	51	85	231	12.5	14.78	0.000
PENISP26	59	CLADSP	19	POS	13	40	51	265	9.2	1.68	0.195
PENISP26	59	CLADSPHA	20	NEG	16	37	125	191	20.3	2.11	0.146
PENISP26	59	CONISP	21	NEG	1	52	9	307	1.4	0.73	0.393

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENISP26	59	EMERNIDU	22	POS	3	50	7	309	1.4	0.95	0.330
PENISP26	59	EPICNIGR	23	NEG	23	30	177	139	28.7	3.44	0.064
PENISP26	59	EUROHERB	24	POS	38	15	207	109	35.2	0.53	0.467
PENISP26	59	FUSAOXYS	25	POS	4	49	16	300	2.9	0.17	0.680
PENISP26	59	FUSASP	26	NEG	6	47	53	263	8.5	1.45	0.229
PENISP26	59	GEOMPANN	27	NEG	0	53	12	304	1.7	3.46	0.063
PENISP26	59	MUCOPLUM	28	POS	16	37	57	259	10.5	3.49	0.062
PENISP26	59	MUCORACE	29	POS	16	37	75	241	13.1	0.70	0.403
PENISP26	59	PAECSP	30	NEG	1	52	7	309	1.2	0.44	0.507
PENISP26	59	PAECVARI	31	NEG	5	48	45	271	7.2	1.35	0.245
PENISP26	59	PENIATRA	32	POS	6	47	3	313	1.3	16.39	0.000
PENISP26	59	PENIAURA	33	POS	7	46	37	279	6.3	0.01	0.920
PENISP26	59	PENIBREV	34	POS	17	36	69	247	12.4	2.12	0.145
PENISP26	59	PENICHRY	35	POS	29	24	162	154	27.4	0.10	0.752
PENISP26	59	PENICOMM	36	POS	15	38	79	237	13.5	0.12	0.729
PENISP26	59	PENICOPR	37	POS	4	49	6	310	1.4	3.56	0.059
PENISP26	59	PENICORY	38	POS	20	33	88	228	15.5	1.69	0.194
PENISP26	59	PENICRUS	39	NEG	2	51	12	304	2.0	0.16	0.689
PENISP26	59	PENICTNG	40	POS	6	47	28	288	4.9	0.10	0.752
PENISP26	59	PENICTRM	41	POS	10	43	42	274	7.5	0.75	0.386
PENISP26	59	PENIDECU	42	POS	4	49	15	301	2.7	0.27	0.603
PENISP26	59	PENIDIGI	43	NEG	0	53	10	306	1.4	3.13	0.077
PENISP26	59	PENIECHI	44	POS	5	48	12	304	2.4	2.12	0.145
PENISP26	59	PENIEXPA	45	POS	13	40	56	260	9.9	0.97	0.325
PENISP26	59	PENIGLAN	46	POS	2	51	11	305	1.9	0.09	0.764
PENISP26	59	PENIGRIS	47	POS	5	48	18	298	3.3	0.54	0.462
PENISP26	59	PENIIMPL	48	POS	4	49	15	301	2.7	0.27	0.603
PENISP26	59	PENIISLA	49	NEG	1	52	10	306	1.6	0.89	0.345
PENISP26	59	PENIITAL	50	POS	2	51	9	307	1.6	0.00	1.000
PENISP26	59	PENIMICZ	51	POS	4	49	10	306	2.0	1.34	0.247
PENISP26	59	PENIOXAL	52	POS	4	49	17	299	3.0	0.10	0.752
PENISP26	59	PENIPURP	53	POS	3	50	6	310	1.3	1.35	0.245
PENISP26	59	PENIRAIS	54	POS	4	49	22	294	3.7	0.02	0.888
PENISP26	59	PENIREST	55	POS	3	50	6	310	1.3	1.35	0.245
PENISP26	59	PENISIMP	56	POS	6	47	14	302	2.9	2.97	0.085
PENISP26	59	PENISP	57	POS	8	45	21	295	4.2	3.38	0.066
PENISP26	59	PENISP01	58	POS	2	51	7	309	1.3	0.04	0.841
PENISP64	60	ACRESP	1	NEG	0	10	25	334	0.7	2.26	0.133
PENISP64	60	ALTEALTE	2	NEG	7	3	320	39	8.9	5.68	0.017
PENISP64	60	ALTESP	3	NEG	0	10	16	343	0.4	2.16	0.142
PENISP64	60	ASPECAND	4	POS	1	9	18	341	0.5	0.00	1.000
PENISP64	60	ASPEFUMI	5	POS	1	9	24	335	0.7	0.05	0.823
PENISP64	60	ASPEGLAU	6	NEG	0	10	25	334	0.7	2.26	0.133
PENISP64	60	ASPENIGE	7	POS	6	4	120	239	3.4	1.99	0.158
PENISP64	60	ASPEOCHR	8	POS	3	7	69	290	2.0	0.20	0.655
PENISP64	60	ASPEORYZ	9	NEG	0	10	9	350	0.2	2.39	0.122
PENISP64	60	ASPESP	10	POS	3	7	64	295	1.8	0.32	0.572
PENISP64	60	ASPESYDO	11	NEG	1	9	45	314	1.3	0.53	0.467
PENISP64	60	ASPEUSTU	12	POS	1	9	23	336	0.7	0.04	0.841
PENISP64	60	ASPEVERS	13	NEG	3	7	193	166	5.3	3.26	0.071
PENISP64	60	AUREPULL	14	NEG	7	3	286	73	7.9	1.30	0.254
PENISP64	60	CHAEGLOB	15	POS	2	8	22	337	0.7	1.22	0.269
PENISP64	60	CHRSPMSP	16	POS	1	9	13	346	0.4	0.04	0.841
PENISP64	60	CLADCLAD	17	NEG	2	8	183	176	5.0	5.08	0.024
PENISP64	60	CLADHERB	18	NEG	1	9	86	273	2.4	1.97	0.160
PENISP64	60	CLADSP	19	POS	4	6	60	299	1.7	2.24	0.134
PENISP64	60	CLADSPHA	20	NEG	3	7	138	221	3.8	0.76	0.383
PENISP64	60	CONISP	21	NEG	0	10	10	349	0.3	2.32	0.128
PENISP64	60	EMERNIDU	22	NEG	0	10	10	349	0.3	2.32	0.128
PENISP64	60	EPICNIGR	23	NEG	4	6	196	163	5.4	1.53	0.216
PENISP64	60	EUROHERB	24	NEG	5	5	240	119	6.6	2.11	0.146
PENISP64	60	FUSAOXYS	25	POS	3	7	17	342	0.5	7.69	0.006

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENISP64	60	FUSASP	26	NEG	0	10	59	300	1.6	3.37	0.066
PENISP64	60	GEOMPANN	27	POS	2	8	10	349	0.3	4.51	0.034
PENISP64	60	MUCOPLUM	28	POS	2	8	71	288	2.0	0.15	0.699
PENISP64	60	MUCORACE	29	NEG	2	8	89	270	2.5	0.52	0.471
PENISP64	60	PAECSP	30	NEG	0	10	8	351	0.2	2.49	0.115
PENISP64	60	PAECVARI	31	POS	2	8	48	311	1.4	0.02	0.888
PENISP64	60	PENIATRA	32	POS	1	9	8	351	0.2	0.28	0.597
PENISP64	60	PENIAURA	33	POS	2	8	42	317	1.2	0.09	0.764
PENISP64	60	PENIBREV	34	NEG	1	9	85	274	2.3	1.93	0.165
PENISP64	60	PENICHRY	35	NEG	4	6	187	172	5.2	1.16	0.281
PENISP64	60	PENICOMM	36	POS	4	6	90	269	2.6	0.49	0.484
PENISP64	60	PENICOPR	37	POS	1	9	9	350	0.3	0.20	0.655
PENISP64	60	PENICORY	38	POS	3	7	105	254	2.9	0.09	0.764
PENISP64	60	PENICRUS	39	POS	1	9	13	346	0.4	0.04	0.841
PENISP64	60	PENICTNG	40	POS	2	8	32	327	0.9	0.41	0.522
PENISP64	60	PENICTRM	41	POS	3	7	49	310	1.4	1.01	0.315
PENISP64	60	PENIDECU	42	NEG	0	10	19	340	0.5	2.17	0.141
PENISP64	60	PENIDIGI	43	NEG	0	10	10	349	0.3	2.32	0.128
PENISP64	60	PENIECHI	44	POS	1	9	16	343	0.5	0.00	1.000
PENISP64	60	PENIEXPA	45	NEG	0	10	69	290	1.9	3.80	0.051
PENISP64	60	PENIGLAN	46	NEG	0	10	13	346	0.4	2.20	0.138
PENISP64	60	PENIGRIS	47	NEG	0	10	23	336	0.6	2.22	0.136
PENISP64	60	PENIIMPL	48	NEG	0	10	19	340	0.5	2.17	0.141
PENISP64	60	PENIISLA	49	NEG	0	10	11	348	0.3	2.26	0.133
PENISP64	60	PENIITAL	50	NEG	0	10	11	348	0.3	2.26	0.133
PENISP64	60	PENIMICZ	51	POS	1	9	13	346	0.4	0.04	0.841
PENISP64	60	PENIOXAL	52	POS	1	9	20	339	0.6	0.01	0.920
PENISP64	60	PENIPURP	53	NEG	0	10	9	350	0.2	2.39	0.122
PENISP64	60	PENIRAIS	54	POS	2	8	24	335	0.7	0.99	0.320
PENISP64	60	PENIREST	55	NEG	0	10	9	350	0.2	2.39	0.122
PENISP64	60	PENISIMP	56	POS	1	9	19	340	0.5	0.00	1.000
PENISP64	60	PENISP	57	POS	1	9	28	331	0.8	0.12	0.729
PENISP64	60	PENISP01	58	NEG	0	10	9	350	0.2	2.39	0.122
PENISP64	60	PENISP26	59	POS	3	7	50	309	1.4	0.95	0.330
PENISPIN	61	ACRESP	1	NEG	7	135	18	209	9.6	1.76	0.185
PENISPIN	61	ALTEALTE	2	NEG	125	17	202	25	127.8	0.20	0.655
PENISPIN	61	ALTESP	3	NEG	6	136	10	217	6.2	0.12	0.729
PENISPIN	61	ASPECAND	4	POS	9	133	10	217	7.3	0.33	0.566
PENISPIN	61	ASPEFUMI	5	POS	11	131	14	213	9.6	0.14	0.708
PENISPIN	61	ASPEGLAU	6	POS	13	129	12	215	9.6	1.50	0.221
PENISPIN	61	ASPENIGE	7	POS	63	79	63	164	48.5	10.00	0.002
PENISPIN	61	ASPEOCHR	8	POS	35	107	37	190	27.7	3.36	0.067
PENISPIN	61	ASPEORYZ	9	POS	6	136	3	224	3.5	2.00	0.157
PENISPIN	61	ASPESP	10	POS	26	116	41	186	25.8	0.01	0.920
PENISPIN	61	ASPESYDO	11	POS	25	117	21	206	17.7	4.85	0.028
PENISPIN	61	ASPEUSTU	12	POS	12	130	12	215	9.2	0.97	0.325
PENISPIN	61	ASPEVERS	13	NEG	73	69	123	104	75.4	0.39	0.532
PENISPIN	61	AUREPULL	14	POS	117	25	176	51	112.8	0.98	0.322
PENISPIN	61	CHAEGLOB	15	POS	10	132	14	213	9.2	0.01	0.920
PENISPIN	61	CHRSPMSP	16	POS	8	134	6	221	5.4	1.40	0.237
PENISPIN	61	CLADCLAD	17	POS	85	57	100	127	71.2	8.11	0.004
PENISPIN	61	CLADHERB	18	NEG	23	119	64	163	33.5	7.66	0.006
PENISPIN	61	CLADSP	19	POS	29	113	35	192	24.6	1.20	0.273
PENISPIN	61	CLADSPHA	20	POS	57	85	84	143	54.3	0.24	0.624
PENISPIN	61	CONISP	21	NEG	1	141	9	218	3.9	4.87	0.027
PENISPIN	61	EMERNIDU	22	POS	6	136	4	223	3.9	1.18	0.277
PENISPIN	61	EPICNIGR	23	NEG	72	70	128	99	77.0	1.38	0.240
PENISPIN	61	EUROHERB	24	POS	95	47	150	77	94.3	0.00	1.000
PENISPIN	61	FUSAOXYS	25	POS	11	131	9	218	7.7	1.76	0.185
PENISPIN	61	FUSASP	26	NEG	17	125	42	185	22.7	3.28	0.070
PENISPIN	61	GEOMPANN	27	POS	5	137	7	220	4.6	0.01	0.920
PENISPIN	61	MUCOPLUM	28	POS	30	112	43	184	28.1	0.14	0.708

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENISPIN	61	MUCORACE	29	POS	37	105	54	173	35.0	0.14	0.708
PENISPIN	61	PAECSP	30	NEG	2	140	6	221	3.1	1.34	0.247
PENISPIN	61	PAECVARI	31	NEG	18	124	32	195	19.3	0.30	0.584
PENISPIN	61	PENIATRA	32	POS	6	136	3	224	3.5	2.00	0.157
PENISPIN	61	PENIAURA	33	POS	22	120	22	205	16.9	2.27	0.132
PENISPIN	61	PENIBREV	34	POS	42	100	44	183	33.1	4.52	0.034
PENISPIN	61	PENICHRY	35	POS	78	64	113	114	73.5	0.73	0.393
PENISPIN	61	PENICOMM	36	POS	37	105	57	170	36.2	0.01	0.920
PENISPIN	61	PENICOPR	37	POS	7	135	3	224	3.9	3.05	0.081
PENISPIN	61	PENICORY	38	NEG	38	104	70	157	41.6	0.91	0.340
PENISPIN	61	PENICRUS	39	NEG	5	137	9	218	5.4	0.25	0.617
PENISPIN	61	PENICTNG	40	POS	16	126	18	209	13.1	0.80	0.371
PENISPIN	61	PENICTRM	41	NEG	19	123	33	194	20.0	0.22	0.639
PENISPIN	61	PENIDECU	42	NEG	6	136	13	214	7.3	0.77	0.380
PENISPIN	61	PENIDIGI	43	NEG	3	139	7	220	3.9	0.79	0.374
PENISPIN	61	PENIECHI	44	NEG	6	136	11	216	6.5	0.28	0.597
PENISPIN	61	PENIEXPA	45	POS	28	114	41	186	26.6	0.07	0.791
PENISPIN	61	PENIGLAN	46	NEG	1	141	12	215	5.0	6.83	0.009
PENISPIN	61	PENIGRIS	47	POS	10	132	13	214	8.9	0.08	0.777
PENISPIN	61	PENIIMPL	48	POS	8	134	11	216	7.3	0.01	0.920
PENISPIN	61	PENIISLA	49	NEG	4	138	7	220	4.2	0.21	0.647
PENISPIN	61	PENIITAL	50	NEG	2	140	9	218	4.2	2.96	0.085
PENISPIN	61	PENIMICZ	51	POS	7	135	7	220	5.4	0.39	0.532
PENISPIN	61	PENIOXAL	52	NEG	6	136	15	212	8.1	1.42	0.233
PENISPIN	61	PENIPURP	53	POS	4	138	5	222	3.5	0.00	1.000
PENISPIN	61	PENIRAIS	54	POS	11	131	15	212	10.0	0.04	0.841
PENISPIN	61	PENIREST	55	POS	4	138	5	222	3.5	0.00	1.000
PENISPIN	61	PENISIMP	56	POS	13	129	7	220	7.7	5.15	0.023
PENISPIN	61	PENISP	57	POS	16	126	13	214	11.2	2.98	0.084
PENISPIN	61	PENISP01	58	POS	5	137	4	223	3.5	0.52	0.471
PENISPIN	61	PENISP26	59	POS	32	110	21	206	20.4	11.48	0.001
PENISPIN	61	PENISP64	60	POS	7	135	3	224	3.9	3.05	0.081
PENIVARI	62	ACRESP	1	POS	1	11	24	333	0.8	0.13	0.718
PENIVARI	62	ALTEALTE	2	NEG	10	2	317	40	10.6	1.10	0.294
PENIVARI	62	ALTESP	3	NEG	0	12	16	341	0.5	2.16	0.142
PENIVARI	62	ASPECAND	4	NEG	0	12	19	338	0.6	2.20	0.138
PENIVARI	62	ASPEFUMI	5	POS	1	11	24	333	0.8	0.13	0.718
PENIVARI	62	ASPEGLAU	6	POS	1	11	24	333	0.8	0.13	0.718
PENIVARI	62	ASPENIGE	7	POS	7	5	119	238	4.1	2.21	0.137
PENIVARI	62	ASPEOCHR	8	POS	7	5	65	292	2.3	9.48	0.002
PENIVARI	62	ASPEORYZ	9	NEG	0	12	9	348	0.3	2.27	0.132
PENIVARI	62	ASPESP	10	POS	4	8	63	294	2.2	1.01	0.315
PENIVARI	62	ASPESYDO	11	NEG	1	11	45	312	1.5	0.78	0.377
PENIVARI	62	ASPEUSTU	12	NEG	0	12	24	333	0.8	2.32	0.128
PENIVARI	62	ASPEVERS	13	POS	9	3	187	170	6.4	1.56	0.212
PENIVARI	62	AUREPULL	14	POS	10	2	283	74	9.5	0.00	1.000
PENIVARI	62	CHAEGLOB	15	POS	3	9	21	336	0.8	4.19	0.041
PENIVARI	62	CHRSPMSP	16	POS	1	11	13	344	0.5	0.00	1.000
PENIVARI	62	CLADCLAD	17	POS	9	3	176	181	6.0	2.13	0.144
PENIVARI	62	CLADHERB	18	NEG	2	10	85	272	2.8	0.84	0.359
PENIVARI	62	CLADSP	19	POS	6	6	58	299	2.1	7.02	0.008
PENIVARI	62	CLADSPHA	20	POS	9	3	132	225	4.6	5.59	0.018
PENIVARI	62	CONISP	21	POS	1	11	9	348	0.3	0.10	0.752
PENIVARI	62	EMERNIDU	22	POS	1	11	9	348	0.3	0.10	0.752
PENIVARI	62	EPICNIGR	23	POS	8	4	192	165	6.5	0.34	0.560
PENIVARI	62	EUROHERB	24	POS	11	1	234	123	8.0	2.48	0.115
PENIVARI	62	FUSAOXYS	25	POS	1	11	19	338	0.7	0.04	0.841
PENIVARI	62	FUSASP	26	NEG	1	11	58	299	1.9	1.29	0.256
PENIVARI	62	GEOMPANN	27	POS	1	11	11	346	0.4	0.03	0.862
PENIVARI	62	MUCOPLUM	28	NEG	1	11	72	285	2.4	1.91	0.167
PENIVARI	62	MUCORACE	29	NEG	2	10	89	268	3.0	0.99	0.320
PENIVARI	62	PAECSP	30	POS	1	11	7	350	0.3	0.23	0.632

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENIVARI	62	PAECVARI	31	NEG	1	11	49	308	1.6	0.93	0.335
PENIVARI	62	PENIATRA	32	NEG	0	12	9	348	0.3	2.27	0.132
PENIVARI	62	PENIAURA	33	POS	2	10	42	315	1.4	0.00	1.000
PENIVARI	62	PENIBREV	34	POS	4	8	82	275	2.8	0.24	0.624
PENIVARI	62	PENICHRY	35	NEG	4	8	187	170	6.2	2.54	0.111
PENIVARI	62	PENICOMM	36	POS	4	8	90	267	3.1	0.09	0.764
PENIVARI	62	PENICOPR	37	POS	1	11	9	348	0.3	0.10	0.752
PENIVARI	62	PENICORY	38	POS	4	8	104	253	3.5	0.00	1.000
PENIVARI	62	PENICRUS	39	POS	1	11	13	344	0.5	0.00	1.000
PENIVARI	62	PENICTNG	40	POS	2	10	32	325	1.1	0.16	0.689
PENIVARI	62	PENICTRM	41	POS	2	10	50	307	1.7	0.03	0.862
PENIVARI	62	PENIDECU	42	POS	1	11	18	339	0.6	0.02	0.888
PENIVARI	62	PENIDIGI	43	NEG	0	12	10	347	0.3	2.22	0.136
PENIVARI	62	PENIECHI	44	POS	2	10	15	342	0.6	1.76	0.185
PENIVARI	62	PENIEXPA	45	POS	4	8	65	292	2.2	0.89	0.345
PENIVARI	62	PENIGLAN	46	NEG	0	12	13	344	0.4	2.16	0.142
PENIVARI	62	PENIGRIS	47	NEG	0	12	23	334	0.8	2.30	0.129
PENIVARI	62	PENIIMPL	48	POS	1	11	18	339	0.6	0.02	0.888
PENIVARI	62	PENIISLA	49	NEG	0	12	11	346	0.4	2.19	0.139
PENIVARI	62	PENIITAL	50	NEG	0	12	11	346	0.4	2.19	0.139
PENIVARI	62	PENIMICZ	51	NEG	0	12	14	343	0.5	2.15	0.143
PENIVARI	62	PENIOXAL	52	POS	1	11	20	337	0.7	0.05	0.823
PENIVARI	62	PENIPURP	53	NEG	0	12	9	348	0.3	2.27	0.132
PENIVARI	62	PENIRAIS	54	POS	1	11	25	332	0.9	0.16	0.689
PENIVARI	62	PENIREST	55	POS	1	11	8	349	0.3	0.16	0.689
PENIVARI	62	PENISIMP	56	POS	3	9	17	340	0.7	5.75	0.016
PENIVARI	62	PENISP	57	POS	2	10	27	330	0.9	0.37	0.543
PENIVARI	62	PENISP01	58	POS	1	11	8	349	0.3	0.16	0.689
PENIVARI	62	PENISP26	59	NEG	1	11	52	305	1.7	1.05	0.306
PENIVARI	62	PENISP64	60	NEG	0	12	10	347	0.3	2.22	0.136
PENIVARI	62	PENISPIN	61	POS	6	6	136	221	4.6	0.28	0.597
PENIVERR	63	ACRESP	1	NEG	0	9	25	335	0.6	2.22	0.136
PENIVERR	63	ALTEALTE	2	POS	9	0	318	42	8.0	0.31	0.578
PENIVERR	63	ALTESP	3	POS	1	8	15	345	0.4	0.03	0.862
PENIVERR	63	ASPECAND	4	NEG	0	9	19	341	0.5	2.16	0.142
PENIVERR	63	ASPEFUMI	5	POS	1	8	24	336	0.6	0.02	0.888
PENIVERR	63	ASPEGLAU	6	POS	1	8	24	336	0.6	0.02	0.888
PENIVERR	63	ASPENIGE	7	NEG	3	6	123	237	3.1	0.17	0.680
PENIVERR	63	ASPEOCHR	8	POS	2	7	70	290	1.8	0.05	0.823
PENIVERR	63	ASPEORYZ	9	POS	2	7	7	353	0.2	7.85	0.005
PENIVERR	63	ASPESP	10	POS	2	7	65	295	1.6	0.01	0.920
PENIVERR	63	ASPESYDO	11	NEG	1	8	45	315	1.1	0.40	0.527
PENIVERR	63	ASPEUSTU	12	POS	1	8	23	337	0.6	0.01	0.920
PENIVERR	63	ASPEVERS	13	NEG	4	5	192	168	4.8	0.75	0.386
PENIVERR	63	AUREPULL	14	NEG	7	2	286	74	7.2	0.29	0.590
PENIVERR	63	CHAEGLOB	15	POS	1	8	23	337	0.6	0.01	0.920
PENIVERR	63	CHRSPMSP	16	NEG	0	9	14	346	0.3	2.21	0.137
PENIVERR	63	CLADCLAD	17	POS	6	3	179	181	4.5	0.44	0.507
PENIVERR	63	CLADHERB	18	NEG	0	9	87	273	2.1	4.35	0.037
PENIVERR	63	CLADSP	19	POS	3	6	61	299	1.6	0.70	0.403
PENIVERR	63	CLADSPHA	20	NEG	2	7	139	221	3.4	1.81	0.179
PENIVERR	63	CONISP	21	NEG	0	9	10	350	0.2	2.39	0.122
PENIVERR	63	EMERNIDU	22	NEG	0	9	10	350	0.2	2.39	0.122
PENIVERR	63	EPICNIGR	23	POS	5	4	195	165	4.9	0.07	0.791
PENIVERR	63	EUROHERB	24	NEG	5	4	240	120	6.0	1.11	0.292
PENIVERR	63	FUSAOXYS	25	POS	2	7	18	342	0.5	2.28	0.131
PENIVERR	63	FUSASP	26	NEG	1	8	58	302	1.4	0.75	0.386
PENIVERR	63	GEOMPANN	27	NEG	0	9	12	348	0.3	2.27	0.132
PENIVERR	63	MUCOPLUM	28	POS	2	7	71	289	1.8	0.06	0.806
PENIVERR	63	MUCORACE	29	NEG	1	8	90	270	2.2	1.81	0.179
PENIVERR	63	PAECSP	30	NEG	0	9	8	352	0.2	2.59	0.108
PENIVERR	63	PAECVARI	31	NEG	1	8	49	311	1.2	0.50	0.480

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENIVERR	63	PENIATRA	32	POS	2	7	7	353	0.2	7.85	0.005
PENIVERR	63	PENIAURA	33	NEG	1	8	43	317	1.1	0.36	0.549
PENIVERR	63	PENIBREV	34	POS	3	6	83	277	2.1	0.10	0.752
PENIVERR	63	PENICHRY	35	NEG	2	7	189	171	4.7	4.55	0.033
PENIVERR	63	PENICOMM	36	POS	5	4	89	271	2.3	2.92	0.087
PENIVERR	63	PENICOPR	37	NEG	0	9	10	350	0.2	2.39	0.122
PENIVERR	63	PENICORY	38	POS	3	6	105	255	2.6	0.01	0.920
PENIVERR	63	PENICRUS	39	NEG	0	9	14	346	0.3	2.21	0.137
PENIVERR	63	PENICTNG	40	POS	1	8	33	327	0.8	0.15	0.699
PENIVERR	63	PENICTRM	41	POS	3	6	49	311	1.3	1.43	0.232
PENIVERR	63	PENIDECU	42	NEG	0	9	19	341	0.5	2.16	0.142
PENIVERR	63	PENIDIGI	43	NEG	0	9	10	350	0.2	2.39	0.122
PENIVERR	63	PENIECHI	44	NEG	0	9	17	343	0.4	2.17	0.141
PENIVERR	63	PENIEXPA	45	POS	3	6	66	294	1.7	0.50	0.480
PENIVERR	63	PENIGLAN	46	NEG	0	9	13	347	0.3	2.24	0.134
PENIVERR	63	PENIGRIS	47	NEG	0	9	23	337	0.6	2.19	0.139
PENIVERR	63	PENIIMPL	48	POS	1	8	18	342	0.5	0.00	1.000
PENIVERR	63	PENIISLA	49	POS	1	8	10	350	0.3	0.21	0.647
PENIVERR	63	PENIITAL	50	NEG	0	9	11	349	0.3	2.32	0.128
PENIVERR	63	PENIMICZ	51	NEG	0	9	14	346	0.3	2.21	0.137
PENIVERR	63	PENIOXAL	52	NEG	0	9	21	339	0.5	2.17	0.141
PENIVERR	63	PENIPURP	53	POS	1	8	8	352	0.2	0.38	0.538
PENIVERR	63	PENIRAIS	54	NEG	0	9	26	334	0.6	2.24	0.134
PENIVERR	63	PENIREST	55	NEG	0	9	9	351	0.2	2.48	0.115
PENIVERR	63	PENISIMP	56	NEG	0	9	20	340	0.5	2.17	0.141
PENIVERR	63	PENISP	57	POS	3	6	26	334	0.7	5.05	0.025
PENIVERR	63	PENISP01	58	NEG	0	9	9	351	0.2	2.48	0.115
PENIVERR	63	PENISP26	59	POS	4	5	49	311	1.3	4.51	0.034
PENIVERR	63	PENISP64	60	NEG	0	9	10	350	0.2	2.39	0.122
PENIVERR	63	PENISPIN	61	NEG	3	6	139	221	3.5	0.45	0.502
PENIVERR	63	PENIVARI	62	NEG	0	9	12	348	0.3	2.27	0.132
PENIVIRI	64	ACRESP	1	POS	5	63	20	281	4.6	0.00	1.000
PENIVIRI	64	ALTEALTE	2	NEG	59	9	268	33	60.3	0.55	0.458
PENIVIRI	64	ALTESP	3	POS	3	65	13	288	3.0	0.09	0.764
PENIVIRI	64	ASPECAND	4	POS	5	63	14	287	3.5	0.37	0.543
PENIVIRI	64	ASPEFUMI	5	POS	8	60	17	284	4.6	2.39	0.122
PENIVIRI	64	ASPEGLAU	6	NEG	3	65	22	279	4.6	1.27	0.260
PENIVIRI	64	ASPENIGE	7	NEG	21	47	105	196	23.2	0.59	0.442
PENIVIRI	64	ASPEOCHR	8	POS	15	53	57	244	13.3	0.17	0.680
PENIVIRI	64	ASPEORYZ	9	NEG	0	68	9	292	1.7	3.53	0.060
PENIVIRI	64	ASPESP	10	NEG	10	58	57	244	12.4	0.98	0.322
PENIVIRI	64	ASPESYDO	11	POS	9	59	37	264	8.5	0.00	1.000
PENIVIRI	64	ASPEUSTU	12	NEG	2	66	22	279	4.4	2.53	0.112
PENIVIRI	64	ASPEVERS	13	NEG	28	40	168	133	36.1	5.38	0.020
PENIVIRI	64	AUREPULL	14	POS	54	14	239	62	54.0	0.03	0.862
PENIVIRI	64	CHAEGLOB	15	POS	8	60	16	285	4.4	2.81	0.094
PENIVIRI	64	CHRSPMSP	16	POS	4	64	10	291	2.6	0.42	0.517
PENIVIRI	64	CLADCLAD	17	POS	36	32	149	152	34.1	0.14	0.708
PENIVIRI	64	CLADHERB	18	NEG	7	61	80	221	16.0	9.09	0.003
PENIVIRI	64	CLADSP	19	POS	15	53	49	252	11.8	0.92	0.337
PENIVIRI	64	CLADSPHA	20	POS	28	40	113	188	26.0	0.18	0.671
PENIVIRI	64	CONISP	21	POS	3	65	7	294	1.8	0.30	0.584
PENIVIRI	64	EMERNIDU	22	POS	2	66	8	293	1.8	0.08	0.777
PENIVIRI	64	EPICNIGR	23	POS	40	28	160	141	36.9	0.51	0.475
PENIVIRI	64	EUROHERB	24	POS	46	22	199	102	45.2	0.01	0.920
PENIVIRI	64	FUSAOXYS	25	NEG	3	65	17	284	3.7	0.49	0.484
PENIVIRI	64	FUSASP	26	NEG	9	59	50	251	10.9	0.76	0.383
PENIVIRI	64	GEOMPANN	27	NEG	1	67	11	290	2.2	1.68	0.195
PENIVIRI	64	MUCOPLUM	28	POS	14	54	59	242	13.5	0.00	1.000
PENIVIRI	64	MUCORACE	29	POS	25	43	66	235	16.8	5.80	0.016
PENIVIRI	64	PAECSP	30	NEG	0	68	8	293	1.5	3.31	0.069
PENIVIRI	64	PAECVARI	31	POS	11	57	39	262	9.2	0.25	0.617

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENIVIRI	64	PENIATRA	32	NEG	1	67	8	293	1.7	1.02	0.313
PENIVIRI	64	PENIAURA	33	POS	9	59	35	266	8.1	0.03	0.862
PENIVIRI	64	PENIBREV	34	POS	18	50	68	233	15.9	0.28	0.597
PENIVIRI	64	PENICHRY	35	NEG	30	38	161	140	35.2	2.34	0.126
PENIVIRI	64	PENICOMM	36	POS	21	47	73	228	17.3	0.96	0.327
PENIVIRI	64	PENICOPR	37	POS	2	66	8	293	1.8	0.08	0.777
PENIVIRI	64	PENICORY	38	POS	23	45	85	216	19.9	0.59	0.442
PENIVIRI	64	PENICRUS	39	POS	5	63	9	292	2.6	1.82	0.177
PENIVIRI	64	PENICTNG	40	NEG	6	62	28	273	6.3	0.13	0.718
PENIVIRI	64	PENICTRM	41	NEG	7	61	45	256	9.6	1.42	0.233
PENIVIRI	64	PENIDECU	42	NEG	2	66	17	284	3.5	1.48	0.224
PENIVIRI	64	PENIDIGI	43	POS	2	66	8	293	1.8	0.08	0.777
PENIVIRI	64	PENIECHI	44	NEG	3	65	14	287	3.1	0.16	0.689
PENIVIRI	64	PENIEXPA	45	POS	19	49	50	251	12.7	3.97	0.046
PENIVIRI	64	PENIGLAN	46	POS	3	65	10	291	2.4	0.01	0.920
PENIVIRI	64	PENIGRIS	47	POS	5	63	18	283	4.2	0.02	0.888
PENIVIRI	64	PENIIMPL	48	POS	4	64	15	286	3.5	0.00	1.000
PENIVIRI	64	PENIISLA	49	NEG	1	67	10	291	2.0	1.45	0.229
PENIVIRI	64	PENIITAL	50	NEG	1	67	10	291	2.0	1.45	0.229
PENIVIRI	64	PENIMICZ	51	POS	4	64	10	291	2.6	0.42	0.517
PENIVIRI	64	PENIOXAL	52	POS	5	63	16	285	3.9	0.13	0.718
PENIVIRI	64	PENIPURP	53	POS	3	65	6	295	1.7	0.54	0.462
PENIVIRI	64	PENIRAIS	54	NEG	4	64	22	279	4.8	0.46	0.498
PENIVIRI	64	PENIREST	55	POS	3	65	6	295	1.7	0.54	0.462
PENIVIRI	64	PENISIMP	56	NEG	1	67	19	282	3.7	3.57	0.059
PENIVIRI	64	PENISP	57	POS	9	59	20	281	5.3	2.48	0.115
PENIVIRI	64	PENISP01	58	POS	2	66	7	294	1.7	0.02	0.888
PENIVIRI	64	PENISP26	59	POS	13	55	40	261	9.8	1.09	0.296
PENIVIRI	64	PENISP64	60	POS	2	66	8	293	1.8	0.08	0.777
PENIVIRI	64	PENISPIN	61	NEG	26	42	116	185	26.2	0.03	0.862
PENIVIRI	64	PENIVARI	62	POS	5	63	7	294	2.2	3.00	0.083
PENIVIRI	64	PENIVERR	63	NEG	1	67	8	293	1.7	1.02	0.313
PENIVULP	65	ACRESP	1	NEG	1	21	24	323	1.5	0.75	0.386
PENIVULP	65	ALTEALTE	2	POS	20	2	307	40	19.5	0.00	1.000
PENIVULP	65	ALTESP	3	POS	1	21	15	332	1.0	0.24	0.624
PENIVULP	65	ASPECAND	4	NEG	1	21	18	329	1.1	0.40	0.527
PENIVULP	65	ASPEFUMI	5	NEG	1	21	24	323	1.5	0.75	0.386
PENIVULP	65	ASPEGLAU	6	NEG	0	22	25	322	1.5	3.03	0.082
PENIVULP	65	ASPENIGE	7	POS	8	14	118	229	7.5	0.00	1.000
PENIVULP	65	ASPEOCHR	8	NEG	4	18	68	279	4.3	0.19	0.663
PENIVULP	65	ASPEORYZ	9	NEG	0	22	9	338	0.5	2.18	0.140
PENIVULP	65	ASPESP	10	POS	8	14	59	288	4.0	4.00	0.046
PENIVULP	65	ASPESYDO	11	NEG	2	20	44	303	2.7	0.68	0.410
PENIVULP	65	ASPEUSTU	12	NEG	0	22	24	323	1.4	2.96	0.085
PENIVULP	65	ASPEVERS	13	NEG	7	15	189	158	11.7	5.22	0.022
PENIVULP	65	AUREPULL	14	POS	20	2	273	74	17.5	1.22	0.269
PENIVULP	65	CHAEGLOB	15	POS	3	19	21	326	1.4	0.91	0.340
PENIVULP	65	CHRSPMSP	16	POS	2	20	12	335	0.8	0.59	0.442
PENIVULP	65	CLADCLAD	17	POS	13	9	172	175	11.0	0.42	0.517
PENIVULP	65	CLADHERB	18	NEG	0	22	87	260	5.2	8.68	0.003
PENIVULP	65	CLADSP	19	POS	6	16	58	289	3.8	0.96	0.327
PENIVULP	65	CLADSPHA	20	POS	10	12	131	216	8.4	0.24	0.624
PENIVULP	65	CONISP	21	POS	3	19	7	340	0.6	6.64	0.010
PENIVULP	65	EMERNIDU	22	NEG	0	22	10	337	0.6	2.20	0.138
PENIVULP	65	EPICNIGR	23	POS	13	9	187	160	11.9	0.06	0.806
PENIVULP	65	EUROHERB	24	POS	16	6	229	118	14.6	0.17	0.680
PENIVULP	65	FUSAOXYS	25	POS	3	19	17	330	1.2	1.61	0.204
PENIVULP	65	FUSASP	26	NEG	3	19	56	291	3.5	0.37	0.543
PENIVULP	65	GEOMPANN	27	POS	1	21	11	336	0.7	0.07	0.791
PENIVULP	65	MUCOPLUM	28	NEG	2	20	71	276	4.4	2.48	0.115
PENIVULP	65	MUCORACE	29	POS	8	14	83	264	5.4	1.12	0.290
PENIVULP	65	PAECSP	30	NEG	0	22	8	339	0.5	2.18	0.140

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PENIVULP	65	PAECVARI	31	NEG	1	21	49	298	3.0	2.54	0.111
PENIVULP	65	PENIATRA	32	POS	2	20	7	340	0.5	1.89	0.169
PENIVULP	65	PENIAURA	33	POS	4	18	40	307	2.6	0.35	0.554
PENIVULP	65	PENIBREV	34	POS	7	15	79	268	5.1	0.51	0.475
PENIVULP	65	PENICHRY	35	NEG	10	12	181	166	11.4	0.69	0.406
PENIVULP	65	PENICOMM	36	POS	9	13	85	262	5.6	2.13	0.144
PENIVULP	65	PENICOPR	37	POS	2	20	8	339	0.6	1.50	0.221
PENIVULP	65	PENICORY	38	POS	7	15	101	246	6.4	0.00	1.000
PENIVULP	65	PENICRUS	39	POS	3	19	11	336	0.8	3.67	0.055
PENIVULP	65	PENICTNG	40	POS	4	18	30	317	2.0	1.25	0.264
PENIVULP	65	PENICTRM	41	NEG	3	19	49	298	3.1	0.14	0.708
PENIVULP	65	PENIDECU	42	NEG	1	21	18	329	1.1	0.40	0.527
PENIVULP	65	PENIDIGI	43	POS	1	21	9	338	0.6	0.02	0.888
PENIVULP	65	PENIECHI	44	POS	3	19	14	333	1.0	2.43	0.119
PENIVULP	65	PENIEXPA	45	POS	5	17	64	283	4.1	0.05	0.823
PENIVULP	65	PENIGLAN	46	POS	1	21	12	335	0.8	0.11	0.740
PENIVULP	65	PENIGRIS	47	NEG	0	22	23	324	1.4	2.90	0.089
PENIVULP	65	PENIIMPL	48	NEG	0	22	19	328	1.1	2.64	0.104
PENIVULP	65	PENIISLA	49	NEG	0	22	11	336	0.7	2.23	0.135
PENIVULP	65	PENIITAL	50	NEG	0	22	11	336	0.7	2.23	0.135
PENIVULP	65	PENIMICZ	51	POS	1	21	13	334	0.8	0.15	0.699
PENIVULP	65	PENIOXAL	52	POS	3	19	18	329	1.3	1.40	0.237
PENIVULP	65	PENIPURP	53	POS	1	21	8	339	0.5	0.00	1.000
PENIVULP	65	PENIRAIS	54	POS	3	19	23	324	1.6	0.67	0.413
PENIVULP	65	PENIREST	55	NEG	0	22	9	338	0.5	2.18	0.140
PENIVULP	65	PENISIMP	56	NEG	1	21	19	328	1.2	0.45	0.502
PENIVULP	65	PENISP	57	POS	4	18	25	322	1.7	2.09	0.148
PENIVULP	65	PENISP01	58	POS	1	21	8	339	0.5	0.00	1.000
PENIVULP	65	PENISP26	59	NEG	3	19	50	297	3.2	0.17	0.680
PENIVULP	65	PENISP64	60	POS	1	21	9	338	0.6	0.02	0.888
PENIVULP	65	PENISPIN	61	NEG	8	14	134	213	8.5	0.19	0.663
PENIVULP	65	PENIVARI	62	POS	1	21	11	336	0.7	0.07	0.791
PENIVULP	65	PENIVERR	63	POS	1	21	8	339	0.5	0.00	1.000
PENIVULP	65	PENIVIRI	64	POS	7	15	61	286	4.1	1.92	0.166
PHOMHERB	66	ACRESP	1	POS	10	98	15	246	7.3	0.99	0.320
PHOMHERB	66	ALTEALTE	2	POS	99	9	228	33	95.7	1.01	0.315
PHOMHERB	66	ALTESP	3	POS	6	102	10	251	4.7	0.21	0.647
PHOMHERB	66	ASPECAND	4	POS	6	102	13	248	5.6	0.00	1.000
PHOMHERB	66	ASPEFUMI	5	NEG	7	101	18	243	7.3	0.14	0.708
PHOMHERB	66	ASPEGLAU	6	POS	10	98	15	246	7.3	0.99	0.320
PHOMHERB	66	ASPENIGE	7	NEG	36	72	90	171	36.9	0.11	0.740
PHOMHERB	66	ASPEOCHR	8	POS	26	82	46	215	21.1	1.63	0.202
PHOMHERB	66	ASPEORYZ	9	NEG	2	106	7	254	2.6	0.71	0.399
PHOMHERB	66	ASPESP	10	NEG	11	97	56	205	19.6	7.31	0.007
PHOMHERB	66	ASPESYDO	11	NEG	10	98	36	225	13.5	1.88	0.170
PHOMHERB	66	ASPEUSTU	12	NEG	4	104	20	241	7.0	2.67	0.102
PHOMHERB	66	ASPEVERS	13	NEG	55	53	141	120	57.4	0.43	0.512
PHOMHERB	66	AUREPULL	14	POS	96	12	197	64	85.8	7.60	0.006
PHOMHERB	66	CHAEGLOB	15	POS	8	100	16	245	7.0	0.05	0.823
PHOMHERB	66	CHRSPMSP	16	NEG	4	104	10	251	4.1	0.13	0.718
PHOMHERB	66	CLADCLAD	17	POS	68	40	117	144	54.2	9.34	0.002
PHOMHERB	66	CLADHERB	18	POS	35	73	52	209	25.5	5.93	0.015
PHOMHERB	66	CLADSP	19	NEG	17	91	47	214	18.8	0.45	0.502
PHOMHERB	66	CLADSPHA	20	POS	60	48	81	180	41.3	18.43	0.000
PHOMHERB	66	CONISP	21	POS	3	105	7	254	2.9	0.09	0.764
PHOMHERB	66	EMERNIDU	22	NEG	2	106	8	253	2.9	1.01	0.315
PHOMHERB	66	EPICNIGR	23	POS	70	38	130	131	58.5	6.34	0.012
PHOMHERB	66	EUROHERB	24	POS	78	30	167	94	71.7	1.97	0.160
PHOMHERB	66	FUSAOXYS	25	NEG	4	104	16	245	5.9	1.41	0.235
PHOMHERB	66	FUSASP	26	POS	20	88	39	222	17.3	0.49	0.484
PHOMHERB	66	GEOMPANN	27	POS	6	102	6	255	3.5	1.64	0.200
PHOMHERB	66	MUCOPLUM	28	NEG	18	90	55	206	21.4	1.23	0.267

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PHOMHERB	66	MUCORACE	29	POS	35	73	56	205	26.6	4.36	0.037
PHOMHERB	66	PAECSP	30	NEG	0	108	8	253	2.3	4.98	0.026
PHOMHERB	66	PAECVARI	31	POS	21	87	29	232	14.6	3.85	0.050
PHOMHERB	66	PENIATRA	32	POS	5	103	4	257	2.6	1.92	0.166
PHOMHERB	66	PENIAURA	33	NEG	12	96	32	229	12.9	0.24	0.624
PHOMHERB	66	PENIBREV	34	POS	28	80	58	203	25.2	0.40	0.527
PHOMHERB	66	PENICHRY	35	NEG	54	54	137	124	55.9	0.30	0.584
PHOMHERB	66	PENICOMM	36	NEG	26	82	68	193	27.5	0.28	0.597
PHOMHERB	66	PENICOPR	37	POS	4	104	6	255	2.9	0.16	0.689
PHOMHERB	66	PENICORY	38	POS	38	70	70	191	31.6	2.19	0.139
PHOMHERB	66	PENICRUS	39	NEG	2	106	12	249	4.1	2.42	0.120
PHOMHERB	66	PENICTNG	40	POS	10	98	24	237	10.0	0.03	0.862
PHOMHERB	66	PENICTRM	41	POS	20	88	32	229	15.2	1.98	0.159
PHOMHERB	66	PENIDECU	42	POS	8	100	11	250	5.6	1.01	0.315
PHOMHERB	66	PENIDIGI	43	POS	6	102	4	257	2.9	3.29	0.070
PHOMHERB	66	PENIECHI	44	POS	5	103	12	249	5.0	0.07	0.791
PHOMHERB	66	PENIEXPA	45	POS	25	83	44	217	20.2	1.60	0.206
PHOMHERB	66	PENIGLAN	46	POS	4	104	9	252	3.8	0.04	0.841
PHOMHERB	66	PENIGRIS	47	NEG	6	102	17	244	6.7	0.34	0.560
PHOMHERB	66	PENIIMPL	48	NEG	2	106	17	244	5.6	4.42	0.036
PHOMHERB	66	PENIISLA	49	POS	5	103	6	255	3.2	0.74	0.390
PHOMHERB	66	PENIITAL	50	POS	5	103	6	255	3.2	0.74	0.390
PHOMHERB	66	PENIMICZ	51	POS	5	103	9	252	4.1	0.06	0.806
PHOMHERB	66	PENIOXAL	52	POS	8	100	13	248	6.2	0.45	0.502
PHOMHERB	66	PENIPURP	53	POS	4	104	5	256	2.6	0.41	0.522
PHOMHERB	66	PENIRAIS	54	NEG	7	101	19	242	7.6	0.25	0.617
PHOMHERB	66	PENIREST	55	POS	4	104	5	256	2.6	0.41	0.522
PHOMHERB	66	PENISIMP	56	NEG	2	106	18	243	5.9	4.84	0.028
PHOMHERB	66	PENISP	57	NEG	5	103	24	237	8.5	2.87	0.090
PHOMHERB	66	PENISP01	58	POS	4	104	5	256	2.6	0.41	0.522
PHOMHERB	66	PENISP26	59	NEG	13	95	40	221	15.5	0.97	0.325
PHOMHERB	66	PENISP64	60	NEG	1	107	9	252	2.9	2.92	0.087
PHOMHERB	66	PENISPIN	61	NEG	39	69	103	158	41.6	0.52	0.471
PHOMHERB	66	PENIVARI	62	POS	7	101	5	256	3.5	3.71	0.054
PHOMHERB	66	PENIVERR	63	NEG	2	106	7	254	2.6	0.71	0.399
PHOMHERB	66	PENIVIRI	64	POS	24	84	44	217	19.9	1.13	0.288
PHOMHERB	66	PENIVULP	65	NEG	5	103	17	244	6.4	0.88	0.348
PHOMSP	67	ACRESP	1	POS	6	56	19	288	4.2	0.52	0.471
PHOMSP	67	ALTEALTE	2	POS	59	3	268	39	54.9	2.43	0.119
PHOMSP	67	ALTESP	3	POS	5	57	11	296	2.7	1.53	0.216
PHOMSP	67	ASPECAND	4	POS	4	58	15	292	3.2	0.04	0.841
PHOMSP	67	ASPEFUMI	5	NEG	2	60	23	284	4.2	2.24	0.134
PHOMSP	67	ASPEGLAU	6	POS	6	56	19	288	4.2	0.52	0.471
PHOMSP	67	ASPENIGE	7	NEG	21	41	105	202	21.2	0.04	0.841
PHOMSP	67	ASPEOCHR	8	NEG	10	52	62	245	12.1	0.83	0.362
PHOMSP	67	ASPEORYZ	9	POS	2	60	7	300	1.5	0.00	1.000
PHOMSP	67	ASPESP	10	NEG	9	53	58	249	11.3	0.99	0.320
PHOMSP	67	ASPESYDO	11	POS	11	51	35	272	7.7	1.36	0.244
PHOMSP	67	ASPEUSTU	12	NEG	3	59	21	286	4.0	0.75	0.386
PHOMSP	67	ASPEVERS	13	POS	37	25	159	148	32.9	0.99	0.320
PHOMSP	67	AUREPULL	14	POS	53	9	240	67	49.2	1.27	0.260
PHOMSP	67	CHAEGLOB	15	NEG	0	62	24	283	4.0	6.55	0.010
PHOMSP	67	CHRSPMSP	16	NEG	1	61	13	294	2.4	1.82	0.177
PHOMSP	67	CLADCLAD	17	POS	43	19	142	165	31.1	10.11	0.001
PHOMSP	67	CLADHERB	18	POS	21	41	66	241	14.6	3.72	0.054
PHOMSP	67	CLADSP	19	NEG	9	53	55	252	10.8	0.69	0.406
PHOMSP	67	CLADSPHA	20	POS	30	32	111	196	23.7	2.77	0.096
PHOMSP	67	CONISP	21	POS	2	60	8	299	1.7	0.02	0.888
PHOMSP	67	EMERNIDU	22	NEG	1	61	9	298	1.7	1.02	0.313
PHOMSP	67	EPICNIGR	23	POS	40	22	160	147	33.6	2.71	0.100
PHOMSP	67	EUROHERB	24	NEG	35	27	210	97	41.2	3.86	0.049
PHOMSP	67	FUSAOXYS	25	POS	4	58	16	291	3.4	0.01	0.920

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PHOMSP	67	FUSASP	26	POS	14	48	45	262	9.9	1.86	0.173
PHOMSP	67	GEOMPANN	27	NEG	1	61	11	296	2.0	1.42	0.233
PHOMSP	67	MUCOPLUM	28	NEG	7	55	66	241	12.3	4.06	0.044
PHOMSP	67	MUCORACE	29	NEG	12	50	79	228	15.3	1.50	0.221
PHOMSP	67	PAECSP	30	NEG	0	62	8	299	1.3	3.11	0.078
PHOMSP	67	PAECVARI	31	POS	9	53	41	266	8.4	0.00	1.000
PHOMSP	67	PENIATRA	32	NEG	1	61	8	299	1.5	0.83	0.362
PHOMSP	67	PENIAURA	33	NEG	6	56	38	269	7.4	0.66	0.417
PHOMSP	67	PENIBREV	34	NEG	14	48	72	235	14.5	0.10	0.752
PHOMSP	67	PENICHRY	35	NEG	31	31	160	147	32.1	0.20	0.655
PHOMSP	67	PENICOMM	36	NEG	12	50	82	225	15.8	1.88	0.170
PHOMSP	67	PENICOPR	37	POS	2	60	8	299	1.7	0.02	0.888
PHOMSP	67	PENICORY	38	NEG	15	47	93	214	18.2	1.25	0.264
PHOMSP	67	PENICRUS	39	NEG	1	61	13	294	2.4	1.82	0.177
PHOMSP	67	PENICTNG	40	NEG	3	59	31	276	5.7	2.39	0.122
PHOMSP	67	PENICTRM	41	NEG	4	58	48	259	8.7	4.39	0.036
PHOMSP	67	PENIDECU	42	NEG	2	60	17	290	3.2	1.14	0.286
PHOMSP	67	PENIDIGI	43	POS	3	59	7	300	1.7	0.49	0.484
PHOMSP	67	PENIECHI	44	NEG	1	61	16	291	2.9	2.45	0.118
PHOMSP	67	PENIEXPA	45	NEG	9	53	60	247	11.6	1.22	0.269
PHOMSP	67	PENIGLAN	46	NEG	2	60	11	296	2.2	0.27	0.603
PHOMSP	67	PENIGRIS	47	NEG	1	61	22	285	3.9	3.75	0.053
PHOMSP	67	PENIIMPL	48	NEG	2	60	17	290	3.2	1.14	0.286
PHOMSP	67	PENIISLA	49	POS	2	60	9	298	1.9	0.08	0.777
PHOMSP	67	PENIITAL	50	NEG	1	61	10	297	1.9	1.22	0.269
PHOMSP	67	PENIMICZ	51	POS	3	59	11	296	2.4	0.01	0.920
PHOMSP	67	PENIOXAL	52	NEG	2	60	19	288	3.5	1.49	0.222
PHOMSP	67	PENIPURP	53	POS	2	60	7	300	1.5	0.00	1.000
PHOMSP	67	PENIRAIS	54	NEG	3	59	23	284	4.4	1.03	0.310
PHOMSP	67	PENIREST	55	NEG	1	61	8	299	1.5	0.83	0.362
PHOMSP	67	PENISIMP	56	POS	4	58	16	291	3.4	0.01	0.920
PHOMSP	67	PENISP	57	NEG	4	58	25	282	4.9	0.50	0.480
PHOMSP	67	PENISP01	58	NEG	0	62	9	298	1.5	3.30	0.069
PHOMSP	67	PENISP26	59	NEG	4	58	49	258	8.9	4.60	0.032
PHOMSP	67	PENISP64	60	NEG	0	62	10	297	1.7	3.50	0.061
PHOMSP	67	PENISPIN	61	POS	26	36	116	191	23.9	0.22	0.639
PHOMSP	67	PENIVARI	62	NEG	0	62	12	295	2.0	3.90	0.048
PHOMSP	67	PENIVERR	63	NEG	1	61	8	299	1.5	0.83	0.362
PHOMSP	67	PENIVIRI	64	NEG	7	55	61	246	11.4	3.13	0.077
PHOMSP	67	PENIVULP	65	NEG	2	60	20	287	3.7	1.67	0.196
PHOMSP	67	PHOMHERB	66	NEG	17	45	91	216	18.2	0.25	0.617
PITHCHAR	68	ACRESP	1	NEG	1	25	24	319	1.8	1.04	0.308
PITHCHAR	68	ALTEALTE	2	POS	24	2	303	40	23.0	0.09	0.764
PITHCHAR	68	ALTESP	3	POS	3	23	13	330	1.1	1.88	0.170
PITHCHAR	68	ASPECAND	4	POS	2	24	17	326	1.3	0.02	0.888
PITHCHAR	68	ASPEFUMI	5	POS	4	22	21	322	1.8	1.98	0.159
PITHCHAR	68	ASPEGLAU	6	POS	3	23	22	321	1.8	0.36	0.549
PITHCHAR	68	ASPENIGE	7	POS	13	13	113	230	8.9	2.41	0.121
PITHCHAR	68	ASPEOCHR	8	POS	6	20	66	277	5.1	0.05	0.823
PITHCHAR	68	ASPEORYZ	9	POS	1	25	8	335	0.6	0.03	0.862
PITHCHAR	68	ASPESP	10	NEG	3	23	64	279	4.7	1.37	0.242
PITHCHAR	68	ASPESYDO	11	POS	4	22	42	301	3.3	0.03	0.862
PITHCHAR	68	ASPEUSTU	12	POS	2	24	22	321	1.7	0.02	0.888
PITHCHAR	68	ASPEVERS	13	NEG	12	14	184	159	13.8	0.89	0.345
PITHCHAR	68	AUREPULL	14	NEG	17	9	276	67	20.6	4.35	0.037
PITHCHAR	68	CHAEGLOB	15	POS	3	23	21	322	1.7	0.45	0.502
PITHCHAR	68	CHRSPMSP	16	POS	4	22	10	333	1.0	7.16	0.007
PITHCHAR	68	CLADCLAD	17	NEG	11	15	174	169	13.0	1.06	0.303
PITHCHAR	68	CLADHERB	18	NEG	3	23	84	259	6.1	3.03	0.082
PITHCHAR	68	CLADSP	19	POS	9	17	55	288	4.5	4.60	0.032
PITHCHAR	68	CLADSPHA	20	POS	12	14	129	214	9.9	0.43	0.512
PITHCHAR	68	CONISP	21	POS	1	25	9	334	0.7	0.07	0.791

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
PITHCHAR	68	EMERNIDU	22	POS	1	25	9	334	0.7	0.07	0.791
PITHCHAR	68	EPICNIGR	23	POS	16	10	184	159	14.1	0.33	0.566
PITHCHAR	68	EUROHERB	24	NEG	12	14	233	110	17.3	6.16	0.013
PITHCHAR	68	FUSAOXYS	25	POS	4	22	16	327	1.4	3.53	0.060
PITHCHAR	68	FUSASP	26	NEG	2	24	57	286	4.2	2.17	0.141
PITHCHAR	68	GEOMPANN	27	NEG	0	26	12	331	0.9	2.38	0.123
PITHCHAR	68	MUCOPLUM	28	NEG	3	23	70	273	5.1	1.82	0.177
PITHCHAR	68	MUCORACE	29	NEG	6	20	85	258	6.4	0.19	0.663
PITHCHAR	68	PAECSP	30	POS	1	25	7	336	0.6	0.01	0.920
PITHCHAR	68	PAECVARI	31	NEG	3	23	47	296	3.5	0.37	0.543
PITHCHAR	68	PENIATRA	32	POS	2	24	7	336	0.6	1.30	0.254
PITHCHAR	68	PENIAURA	33	POS	4	22	40	303	3.1	0.06	0.806
PITHCHAR	68	PENIBREV	34	NEG	6	20	80	263	6.1	0.07	0.791
PITHCHAR	68	PENICHRY	35	NEG	12	14	179	164	13.5	0.64	0.424
PITHCHAR	68	PENICOMM	36	POS	9	17	85	258	6.6	0.77	0.380
PITHCHAR	68	PENICOPR	37	POS	1	25	9	334	0.7	0.07	0.791
PITHCHAR	68	PENICORY	38	POS	14	12	94	249	7.6	6.93	0.008
PITHCHAR	68	PENICRUS	39	POS	3	23	11	332	1.0	2.60	0.107
PITHCHAR	68	PENICTNG	40	POS	4	22	30	313	2.4	0.60	0.439
PITHCHAR	68	PENICTRM	41	NEG	2	24	50	293	3.7	1.60	0.206
PITHCHAR	68	PENIDECU	42	NEG	1	25	18	325	1.3	0.60	0.439
PITHCHAR	68	PENIDIGI	43	NEG	0	26	10	333	0.7	2.28	0.131
PITHCHAR	68	PENIECHI	44	POS	2	24	15	328	1.2	0.09	0.764
PITHCHAR	68	PENIEXPA	45	POS	5	21	64	279	4.9	0.04	0.841
PITHCHAR	68	PENIGLAN	46	POS	2	24	11	332	0.9	0.42	0.517
PITHCHAR	68	PENIGRIS	47	NEG	0	26	23	320	1.6	3.18	0.075
PITHCHAR	68	PENIIMPL	48	NEG	1	25	18	325	1.3	0.60	0.439
PITHCHAR	68	PENIISLA	49	POS	1	25	10	333	0.8	0.11	0.740
PITHCHAR	68	PENIITAL	50	NEG	0	26	11	332	0.8	2.33	0.127
PITHCHAR	68	PENIMICZ	51	POS	1	25	13	330	1.0	0.27	0.603
PITHCHAR	68	PENIOXAL	52	POS	2	24	19	324	1.5	0.00	1.000
PITHCHAR	68	PENIPURP	53	NEG	0	26	9	334	0.6	2.24	0.134
PITHCHAR	68	PENIRAIS	54	NEG	1	25	25	318	1.8	1.12	0.290
PITHCHAR	68	PENIREST	55	NEG	0	26	9	334	0.6	2.24	0.134
PITHCHAR	68	PENISIMP	56	POS	2	24	18	325	1.4	0.01	0.920
PITHCHAR	68	PENISP	57	NEG	1	25	28	315	2.0	1.36	0.244
PITHCHAR	68	PENISP01	58	POS	1	25	8	335	0.6	0.03	0.862
PITHCHAR	68	PENISP26	59	POS	5	21	48	295	3.7	0.20	0.655
PITHCHAR	68	PENISP64	60	POS	2	24	8	335	0.7	0.99	0.320
PITHCHAR	68	PENISPIN	61	NEG	10	16	132	211	10.0	0.04	0.841
PITHCHAR	68	PENIVARI	62	NEG	0	26	12	331	0.9	2.38	0.123
PITHCHAR	68	PENIVERR	63	NEG	0	26	9	334	0.6	2.24	0.134
PITHCHAR	68	PENIVIRI	64	POS	5	21	63	280	4.8	0.02	0.888
PITHCHAR	68	PENIVULP	65	NEG	1	25	21	322	1.6	0.81	0.368
PITHCHAR	68	PHOMHERB	66	NEG	7	19	101	242	7.6	0.25	0.617
PITHCHAR	68	PHOMSP	67	NEG	4	22	58	285	4.4	0.22	0.639
RHIZORYZ	69	ACRESP	1	NEG	3	50	22	294	3.6	0.42	0.517
RHIZORYZ	69	ALTEALTE	2	POS	48	5	279	37	47.0	0.06	0.806
RHIZORYZ	69	ALTESP	3	POS	3	50	13	303	2.3	0.02	0.888
RHIZORYZ	69	ASPECAND	4	POS	5	48	14	302	2.7	1.41	0.235
RHIZORYZ	69	ASPEFUMI	5	POS	4	49	21	295	3.6	0.00	1.000
RHIZORYZ	69	ASPEGLAU	6	POS	5	48	20	296	3.6	0.29	0.590
RHIZORYZ	69	ASPENIGE	7	POS	22	31	104	212	18.1	1.13	0.288
RHIZORYZ	69	ASPEOCHR	8	NEG	10	43	62	254	10.3	0.10	0.752
RHIZORYZ	69	ASPEORYZ	9	NEG	0	53	9	307	1.3	2.98	0.084
RHIZORYZ	69	ASPESP	10	POS	13	40	54	262	9.6	1.23	0.267
RHIZORYZ	69	ASPESYDO	11	POS	7	46	39	277	6.6	0.00	1.000
RHIZORYZ	69	ASPEUSTU	12	POS	5	48	19	297	3.5	0.40	0.527
RHIZORYZ	69	ASPEVERS	13	POS	32	21	164	152	28.2	0.99	0.320
RHIZORYZ	69	AUREPULL	14	NEG	39	14	254	62	42.1	1.73	0.188
RHIZORYZ	69	CHAEGLOB	15	NEG	2	51	22	294	3.5	1.37	0.242
RHIZORYZ	69	CHRSPMSP	16	POS	3	50	11	305	2.0	0.14	0.708

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
RHIZORYZ	69	CLADCLAD	17	NEG	26	27	159	157	26.6	0.10	0.752
RHIZORYZ	69	CLADHERB	18	NEG	12	41	75	241	12.5	0.12	0.729
RHIZORYZ	69	CLADSP	19	NEG	9	44	55	261	9.2	0.07	0.791
RHIZORYZ	69	CLADSPHA	20	NEG	19	34	122	194	20.3	0.29	0.590
RHIZORYZ	69	CONISP	21	POS	3	50	7	309	1.4	0.95	0.330
RHIZORYZ	69	EMERNIDU	22	POS	2	51	8	308	1.4	0.00	1.000
RHIZORYZ	69	EPICNIGR	23	POS	29	24	171	145	28.7	0.00	1.000
RHIZORYZ	69	EUROHERB	24	NEG	35	18	210	106	35.2	0.05	0.823
RHIZORYZ	69	FUSAOXYS	25	POS	3	50	17	299	2.9	0.06	0.806
RHIZORYZ	69	FUSASP	26	NEG	8	45	51	265	8.5	0.16	0.689
RHIZORYZ	69	GEOMPANN	27	POS	2	51	10	306	1.7	0.04	0.841
RHIZORYZ	69	MUCOPLUM	28	POS	19	34	54	262	10.5	8.92	0.003
RHIZORYZ	69	MUCORACE	29	POS	17	36	74	242	13.1	1.39	0.238
RHIZORYZ	69	PAECSP	30	NEG	1	52	7	309	1.2	0.44	0.507
RHIZORYZ	69	PAECVARI	31	POS	10	43	40	276	7.2	1.01	0.315
RHIZORYZ	69	PENIATRA	32	NEG	1	52	8	308	1.3	0.58	0.446
RHIZORYZ	69	PENIAURA	33	NEG	6	47	38	278	6.3	0.14	0.708
RHIZORYZ	69	PENIBREV	34	POS	13	40	73	243	12.4	0.00	1.000
RHIZORYZ	69	PENICHRY	35	POS	28	25	163	153	27.4	0.00	1.000
RHIZORYZ	69	PENICOMM	36	POS	15	38	79	237	13.5	0.12	0.729
RHIZORYZ	69	PENICOPR	37	NEG	0	53	10	306	1.4	3.13	0.077
RHIZORYZ	69	PENICORY	38	POS	22	31	86	230	15.5	3.82	0.051
RHIZORYZ	69	PENICRUS	39	POS	3	50	11	305	2.0	0.14	0.708
RHIZORYZ	69	PENICTNG	40	NEG	3	50	31	285	4.9	1.50	0.221
RHIZORYZ	69	PENICTRM	41	NEG	7	46	45	271	7.5	0.17	0.680
RHIZORYZ	69	PENIDECU	42	POS	3	50	16	300	2.7	0.02	0.888
RHIZORYZ	69	PENIDIGI	43	POS	2	51	8	308	1.4	0.00	1.000
RHIZORYZ	69	PENIECHI	44	POS	4	49	13	303	2.4	0.56	0.454
RHIZORYZ	69	PENIEXPA	45	POS	15	38	54	262	9.9	3.05	0.081
RHIZORYZ	69	PENIGLAN	46	POS	2	51	11	305	1.9	0.09	0.764
RHIZORYZ	69	PENIGRIS	47	POS	6	47	17	299	3.3	1.82	0.177
RHIZORYZ	69	PENIIMPL	48	POS	5	48	14	302	2.7	1.41	0.235
RHIZORYZ	69	PENIISLA	49	NEG	0	53	11	305	1.6	3.30	0.069
RHIZORYZ	69	PENIITAL	50	NEG	1	52	10	306	1.6	0.89	0.345
RHIZORYZ	69	PENIMICZ	51	NEG	2	51	12	304	2.0	0.16	0.689
RHIZORYZ	69	PENIOXAL	52	NEG	1	52	20	296	3.0	2.60	0.107
RHIZORYZ	69	PENIPURP	53	NEG	0	53	9	307	1.3	2.98	0.084
RHIZORYZ	69	PENIRAIS	54	POS	6	47	20	296	3.7	1.05	0.306
RHIZORYZ	69	PENIREST	55	POS	2	51	7	309	1.3	0.04	0.841
RHIZORYZ	69	PENISIMP	56	POS	3	50	17	299	2.9	0.06	0.806
RHIZORYZ	69	PENISP	57	POS	10	43	19	297	4.2	8.66	0.003
RHIZORYZ	69	PENISP01	58	POS	2	51	7	309	1.3	0.04	0.841
RHIZORYZ	69	PENISP26	59	POS	8	45	45	271	7.6	0.00	1.000
RHIZORYZ	69	PENISP64	60	NEG	0	53	10	306	1.4	3.13	0.077
RHIZORYZ	69	PENISPIN	61	NEG	17	36	125	191	20.4	1.41	0.235
RHIZORYZ	69	PENIVARI	62	NEG	1	52	11	305	1.7	1.05	0.306
RHIZORYZ	69	PENIVERR	63	NEG	1	52	8	308	1.3	0.58	0.446
RHIZORYZ	69	PENIVIRI	64	POS	12	41	56	260	9.8	0.44	0.507
RHIZORYZ	69	PENIVULP	65	NEG	3	50	19	297	3.2	0.17	0.680
RHIZORYZ	69	PHOMHERB	66	NEG	12	41	96	220	15.5	1.71	0.191
RHIZORYZ	69	PHOMSP	67	POS	9	44	53	263	8.9	0.03	0.862
RHIZORYZ	69	PITHCHAR	68	POS	4	49	22	294	3.7	0.02	0.888
SCOPBREV	70	ACRESP	1	NEG	1	32	24	312	2.2	1.59	0.207
SCOPBREV	70	ALTEALTE	2	NEG	27	6	300	36	29.2	2.48	0.115
SCOPBREV	70	ALTESP	3	POS	2	31	14	322	1.4	0.00	1.000
SCOPBREV	70	ASPECAND	4	NEG	1	32	18	318	1.7	0.98	0.322
SCOPBREV	70	ASPEFUMI	5	POS	3	30	22	314	2.2	0.04	0.841
SCOPBREV	70	ASPEGLAU	6	NEG	2	31	23	313	2.2	0.29	0.590
SCOPBREV	70	ASPENIGE	7	NEG	11	22	115	221	11.3	0.09	0.764
SCOPBREV	70	ASPEOCHR	8	POS	12	21	60	276	6.4	5.43	0.020
SCOPBREV	70	ASPEORYZ	9	POS	3	30	6	330	0.8	4.02	0.045
SCOPBREV	70	ASPESP	10	NEG	5	28	62	274	6.0	0.50	0.480

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
SCOPBREV	70	ASPESYDO	11	POS	5	28	41	295	4.1	0.05	0.823
SCOPBREV	70	ASPEUSTU	12	NEG	1	32	23	313	2.2	1.48	0.224
SCOPBREV	70	ASPEVERS	13	NEG	15	18	181	155	17.5	1.23	0.267
SCOPBREV	70	AUREPULL	14	NEG	23	10	270	66	26.2	2.79	0.095
SCOPBREV	70	CHAEGLOB	15	POS	5	28	19	317	2.2	3.03	0.082
SCOPBREV	70	CHRSPMSP	16	POS	2	31	12	324	1.3	0.06	0.806
SCOPBREV	70	CLADCLAD	17	NEG	15	18	170	166	16.5	0.56	0.454
SCOPBREV	70	CLADHERB	18	NEG	7	26	80	256	7.8	0.30	0.584
SCOPBREV	70	CLADSP	19	POS	7	26	57	279	5.7	0.14	0.708
SCOPBREV	70	CLADSPHA	20	NEG	11	22	130	206	12.6	0.63	0.427
SCOPBREV	70	CONISP	21	POS	1	32	9	327	0.9	0.20	0.655
SCOPBREV	70	EMERNIDU	22	POS	1	32	9	327	0.9	0.20	0.655
SCOPBREV	70	EPICNIGR	23	POS	18	15	182	154	17.9	0.02	0.888
SCOPBREV	70	EUROHERB	24	POS	28	5	217	119	21.9	4.66	0.031
SCOPBREV	70	FUSAOXYS	25	POS	4	29	16	320	1.8	1.90	0.168
SCOPBREV	70	FUSASP	26	NEG	4	29	55	281	5.3	0.78	0.377
SCOPBREV	70	GEOMPANN	27	NEG	1	32	11	325	1.1	0.35	0.554
SCOPBREV	70	MUCOPLUM	28	NEG	6	27	67	269	6.5	0.22	0.639
SCOPBREV	70	MUCORACE	29	NEG	7	26	84	252	8.1	0.48	0.488
SCOPBREV	70	PAECSP	30	POS	1	32	7	329	0.7	0.07	0.791
SCOPBREV	70	PAECVARI	31	POS	5	28	45	291	4.5	0.00	1.000
SCOPBREV	70	PENIATRA	32	POS	3	30	6	330	0.8	4.02	0.045
SCOPBREV	70	PENIAURA	33	POS	4	29	40	296	3.9	0.06	0.806
SCOPBREV	70	PENIBREV	34	POS	8	25	78	258	7.7	0.01	0.920
SCOPBREV	70	PENICHRY	35	NEG	9	24	182	154	17.1	9.81	0.002
SCOPBREV	70	PENICOMM	36	POS	14	19	80	256	8.4	4.55	0.033
SCOPBREV	70	PENICOPR	37	POS	1	32	9	327	0.9	0.20	0.655
SCOPBREV	70	PENICORY	38	POS	10	23	98	238	9.7	0.00	1.000
SCOPBREV	70	PENICRUS	39	POS	3	30	11	325	1.3	1.42	0.233
SCOPBREV	70	PENICTNG	40	NEG	2	31	32	304	3.0	0.94	0.332
SCOPBREV	70	PENICTRM	41	POS	6	27	46	290	4.7	0.20	0.655
SCOPBREV	70	PENIDECU	42	NEG	1	32	18	318	1.7	0.98	0.322
SCOPBREV	70	PENIDIGI	43	POS	2	31	8	328	0.9	0.46	0.498
SCOPBREV	70	PENIECHI	44	NEG	0	33	17	319	1.5	3.09	0.079
SCOPBREV	70	PENIEXPA	45	POS	12	21	57	279	6.2	6.22	0.013
SCOPBREV	70	PENIGLAN	46	NEG	0	33	13	323	1.2	2.71	0.100
SCOPBREV	70	PENIGRIS	47	NEG	1	32	22	314	2.1	1.38	0.240
SCOPBREV	70	PENIIMPL	48	NEG	1	32	18	318	1.7	0.98	0.322
SCOPBREV	70	PENIISLA	49	POS	1	32	10	326	1.0	0.27	0.603
SCOPBREV	70	PENIITAL	50	NEG	0	33	11	325	1.0	2.53	0.112
SCOPBREV	70	PENIMICZ	51	NEG	1	32	13	323	1.3	0.52	0.471
SCOPBREV	70	PENIOXAL	52	NEG	1	32	20	316	1.9	1.18	0.277
SCOPBREV	70	PENIPURP	53	POS	1	32	8	328	0.8	0.13	0.718
SCOPBREV	70	PENIRAIS	54	POS	5	28	21	315	2.3	2.40	0.121
SCOPBREV	70	PENIREST	55	POS	1	32	8	328	0.8	0.13	0.718
SCOPBREV	70	PENISIMP	56	POS	3	30	17	319	1.8	0.33	0.566
SCOPBREV	70	PENISP	57	POS	3	30	26	310	2.6	0.00	1.000
SCOPBREV	70	PENISP01	58	POS	1	32	8	328	0.8	0.13	0.718
SCOPBREV	70	PENISP26	59	POS	6	27	47	289	4.7	0.16	0.689
SCOPBREV	70	PENISP64	60	NEG	0	33	10	326	0.9	2.45	0.118
SCOPBREV	70	PENISPIN	61	POS	15	18	127	209	12.7	0.46	0.498
SCOPBREV	70	PENIVARI	62	POS	4	29	8	328	1.1	6.23	0.013
SCOPBREV	70	PENIVERR	63	POS	3	30	6	330	0.8	4.02	0.045
SCOPBREV	70	PENIVIRI	64	NEG	5	28	63	273	6.1	0.55	0.458
SCOPBREV	70	PENIVULP	65	POS	3	30	19	317	2.0	0.17	0.680
SCOPBREV	70	PHOMHERB	66	NEG	8	25	100	236	9.7	0.75	0.386
SCOPBREV	70	PHOMSP	67	NEG	3	30	59	277	5.6	2.21	0.137
SCOPBREV	70	PITHCHAR	68	NEG	2	31	24	312	2.3	0.35	0.554
SCOPBREV	70	RHIZORYZ	69	NEG	4	29	49	287	4.7	0.42	0.517
SCOPCAND	71	ACRESP	1	POS	4	23	21	321	1.8	1.77	0.183
SCOPCAND	71	ALTEALTE	2	POS	24	3	303	39	23.9	0.07	0.791
SCOPCAND	71	ALTESP	3	POS	2	25	14	328	1.2	0.10	0.752

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
SCOPCAND	71	ASPECAND	4	NEG	1	26	18	324	1.4	0.65	0.420
SCOPCAND	71	ASPEFUMI	5	POS	3	24	22	320	1.8	0.28	0.597
SCOPCAND	71	ASPEGLAU	6	NEG	1	26	24	318	1.8	1.12	0.290
SCOPCAND	71	ASPENIGE	7	POS	10	17	116	226	9.2	0.01	0.920
SCOPCAND	71	ASPEOCHR	8	POS	7	20	65	277	5.3	0.39	0.532
SCOPCAND	71	ASPEORYZ	9	POS	1	26	8	334	0.7	0.04	0.841
SCOPCAND	71	ASPESP	10	POS	8	19	59	283	4.9	1.81	0.179
SCOPCAND	71	ASPESYDO	11	POS	4	23	42	300	3.4	0.01	0.920
SCOPCAND	71	ASPEUSTU	12	POS	2	25	22	320	1.8	0.04	0.841
SCOPCAND	71	ASPEVERS	13	POS	17	10	179	163	14.3	0.75	0.386
SCOPCAND	71	AUREPULL	14	NEG	20	7	273	69	21.4	0.92	0.337
SCOPCAND	71	CHAEGLOB	15	POS	4	23	20	322	1.8	2.00	0.157
SCOPCAND	71	CHRSPMSP	16	NEG	0	27	14	328	1.0	2.54	0.111
SCOPCAND	71	CLADCLAD	17	NEG	13	14	172	170	13.5	0.17	0.680
SCOPCAND	71	CLADHERB	18	NEG	4	23	83	259	6.4	1.82	0.177
SCOPCAND	71	CLADSP	19	NEG	4	23	60	282	4.7	0.39	0.532
SCOPCAND	71	CLADSPHA	20	POS	13	14	128	214	10.3	0.81	0.368
SCOPCAND	71	CONISP	21	NEG	0	27	10	332	0.7	2.30	0.129
SCOPCAND	71	EMERNIDU	22	NEG	0	27	10	332	0.7	2.30	0.129
SCOPCAND	71	EPICNIGR	23	POS	16	11	184	158	14.6	0.12	0.729
SCOPCAND	71	EUROHERB	24	POS	19	8	226	116	17.9	0.06	0.806
SCOPCAND	71	FUSAOXYS	25	POS	2	25	18	324	1.5	0.00	1.000
SCOPCAND	71	FUSASP	26	NEG	3	24	56	286	4.3	0.98	0.322
SCOPCAND	71	GEOMPANN	27	POS	3	24	9	333	0.9	3.34	0.068
SCOPCAND	71	MUCOPLUM	28	POS	7	20	66	276	5.3	0.34	0.560
SCOPCAND	71	MUCORACE	29	POS	8	19	83	259	6.7	0.15	0.699
SCOPCAND	71	PAECSP	30	POS	1	26	7	335	0.6	0.01	0.920
SCOPCAND	71	PAECVARI	31	POS	9	18	41	301	3.7	8.00	0.005
SCOPCAND	71	PENIATRA	32	POS	1	26	8	334	0.7	0.04	0.841
SCOPCAND	71	PENIAURA	33	POS	5	22	39	303	3.2	0.62	0.431
SCOPCAND	71	PENIBREV	34	POS	9	18	77	265	6.3	1.09	0.296
SCOPCAND	71	PENICHRY	35	POS	15	12	176	166	14.0	0.04	0.841
SCOPCAND	71	PENICOMM	36	NEG	4	23	90	252	6.9	2.40	0.121
SCOPCAND	71	PENICOPR	37	POS	1	26	9	333	0.7	0.08	0.777
SCOPCAND	71	PENICORY	38	POS	14	13	94	248	7.9	6.05	0.014
SCOPCAND	71	PENICRUS	39	POS	2	25	12	330	1.0	0.25	0.617
SCOPCAND	71	PENICTNG	40	POS	3	24	31	311	2.5	0.00	1.000
SCOPCAND	71	PENICTRM	41	POS	5	22	47	295	3.8	0.16	0.689
SCOPCAND	71	PENIDECU	42	NEG	0	27	19	323	1.4	2.92	0.087
SCOPCAND	71	PENIDIGI	43	POS	1	26	9	333	0.7	0.08	0.777
SCOPCAND	71	PENIECHI	44	POS	2	25	15	327	1.2	0.06	0.806
SCOPCAND	71	PENIEXPA	45	NEG	5	22	64	278	5.1	0.08	0.777
SCOPCAND	71	PENIGLAN	46	POS	1	26	12	330	1.0	0.24	0.624
SCOPCAND	71	PENIGRIS	47	NEG	0	27	23	319	1.7	3.26	0.071
SCOPCAND	71	PENIIMPL	48	NEG	0	27	19	323	1.4	2.92	0.087
SCOPCAND	71	PENIISLA	49	POS	1	26	10	332	0.8	0.13	0.718
SCOPCAND	71	PENIITAL	50	POS	1	26	10	332	0.8	0.13	0.718
SCOPCAND	71	PENIMICZ	51	NEG	0	27	14	328	1.0	2.54	0.111
SCOPCAND	71	PENIOXAL	52	POS	2	25	19	323	1.5	0.00	1.000
SCOPCAND	71	PENIPURP	53	POS	1	26	8	334	0.7	0.04	0.841
SCOPCAND	71	PENIRAIS	54	NEG	1	26	25	317	1.9	1.20	0.273
SCOPCAND	71	PENIREST	55	POS	1	26	8	334	0.7	0.04	0.841
SCOPCAND	71	PENISIMP	56	POS	2	25	18	324	1.5	0.00	1.000
SCOPCAND	71	PENISP	57	NEG	2	25	27	315	2.1	0.21	0.647
SCOPCAND	71	PENISP01	58	POS	1	26	8	334	0.7	0.04	0.841
SCOPCAND	71	PENISP26	59	NEG	2	25	51	291	3.9	1.84	0.175
SCOPCAND	71	PENISP64	60	NEG	0	27	10	332	0.7	2.30	0.129
SCOPCAND	71	PENISPIN	61	POS	12	15	130	212	10.4	0.21	0.647
SCOPCAND	71	PENIVARI	62	POS	1	26	11	331	0.9	0.18	0.671
SCOPCAND	71	PENIVERR	63	POS	1	26	8	334	0.7	0.04	0.841
SCOPCAND	71	PENIVIRI	64	NEG	4	23	64	278	5.0	0.58	0.446
SCOPCAND	71	PENIVULP	65	POS	2	25	20	322	1.6	0.01	0.920

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
SCOPCAND	71	PHOMHERB	66	NEG	7	20	101	241	7.9	0.38	0.538
SCOPCAND	71	PHOMSP	67	NEG	3	24	59	283	4.5	1.19	0.275
SCOPCAND	71	PITHCHAR	68	POS	3	24	23	319	1.9	0.22	0.639
SCOPCAND	71	RHIZORYZ	69	NEG	2	25	51	291	3.9	1.84	0.175
SCOPCAND	71	SCOPBREV	70	NEG	2	25	31	311	2.4	0.41	0.522
SPHASP	72	ACRESP	1	POS	2	11	23	333	0.9	0.48	0.488
SPHASP	72	ALTEALTE	2	POS	13	0	314	42	11.5	0.76	0.383
SPHASP	72	ALTESP	3	NEG	0	13	16	340	0.6	2.17	0.141
SPHASP	72	ASPECAND	4	POS	1	12	18	338	0.7	0.05	0.823
SPHASP	72	ASPEFUMI	5	POS	1	12	24	332	0.9	0.18	0.671
SPHASP	72	ASPEGLAU	6	POS	1	12	24	332	0.9	0.18	0.671
SPHASP	72	ASPENIGE	7	NEG	3	10	123	233	4.4	1.33	0.249
SPHASP	72	ASPEOCHR	8	NEG	2	11	70	286	2.5	0.55	0.458
SPHASP	72	ASPEORYZ	9	NEG	0	13	9	347	0.3	2.24	0.134
SPHASP	72	ASPESP	10	POS	3	10	64	292	2.4	0.01	0.920
SPHASP	72	ASPESYDO	11	NEG	1	12	45	311	1.6	0.92	0.337
SPHASP	72	ASPEUSTU	12	NEG	0	13	24	332	0.9	2.37	0.124
SPHASP	72	ASPEVERS	13	NEG	5	8	191	165	6.9	1.85	0.174
SPHASP	72	AUREPULL	14	POS	13	0	280	76	10.3	2.31	0.129
SPHASP	72	CHAEGLOB	15	NEG	0	13	24	332	0.9	2.37	0.124
SPHASP	72	CHRSPMSP	16	POS	1	12	13	343	0.5	0.00	1.000
SPHASP	72	CLADCLAD	17	POS	9	4	176	180	6.5	1.25	0.264
SPHASP	72	CLADHERB	18	POS	6	7	81	275	3.1	2.62	0.106
SPHASP	72	CLADSP	19	NEG	1	12	63	293	2.3	1.71	0.191
SPHASP	72	CLADSPHA	20	NEG	4	9	137	219	5.0	0.73	0.393
SPHASP	72	CONISP	21	POS	2	11	8	348	0.4	3.98	0.046
SPHASP	72	EMERNIDU	22	NEG	0	13	10	346	0.4	2.20	0.138
SPHASP	72	EPICNIGR	23	POS	12	1	188	168	7.1	6.37	0.012
SPHASP	72	EUROHERB	24	NEG	8	5	237	119	8.6	0.46	0.498
SPHASP	72	FUSAOXYS	25	POS	1	12	19	337	0.7	0.07	0.791
SPHASP	72	FUSASP	26	NEG	1	12	58	298	2.1	1.48	0.224
SPHASP	72	GEOMPANN	27	NEG	0	13	12	344	0.4	2.16	0.142
SPHASP	72	MUCOPLUM	28	NEG	2	11	71	285	2.6	0.58	0.446
SPHASP	72	MUCORACE	29	POS	4	9	87	269	3.2	0.04	0.841
SPHASP	72	PAECSP	30	NEG	0	13	8	348	0.3	2.30	0.129
SPHASP	72	PAECVARI	31	NEG	1	12	49	307	1.8	1.08	0.299
SPHASP	72	PENIATRA	32	NEG	0	13	9	347	0.3	2.24	0.134
SPHASP	72	PENIAURA	33	POS	2	11	42	314	1.6	0.00	1.000
SPHASP	72	PENIBREV	34	NEG	3	10	83	273	3.0	0.13	0.718
SPHASP	72	PENICHRY	35	NEG	5	8	186	170	6.7	1.59	0.207
SPHASP	72	PENICOMM	36	NEG	1	12	93	263	3.3	3.32	0.068
SPHASP	72	PENICOPR	37	NEG	0	13	10	346	0.4	2.20	0.138
SPHASP	72	PENICORY	38	POS	4	9	104	252	3.8	0.04	0.841
SPHASP	72	PENICRUS	39	POS	1	12	13	343	0.5	0.00	1.000
SPHASP	72	PENICTNG	40	NEG	0	13	34	322	1.2	2.75	0.097
SPHASP	72	PENICTRM	41	NEG	0	13	52	304	1.8	3.58	0.058
SPHASP	72	PENIDECU	42	NEG	0	13	19	337	0.7	2.23	0.135
SPHASP	72	PENIDIGI	43	NEG	0	13	10	346	0.4	2.20	0.138
SPHASP	72	PENIECHI	44	NEG	0	13	17	339	0.6	2.19	0.139
SPHASP	72	PENIEXPA	45	NEG	2	11	67	289	2.4	0.45	0.502
SPHASP	72	PENIGLAN	46	POS	1	12	12	344	0.5	0.00	1.000
SPHASP	72	PENIGRIS	47	POS	3	10	20	336	0.8	3.89	0.049
SPHASP	72	PENIIMPL	48	POS	1	12	18	338	0.7	0.05	0.823
SPHASP	72	PENIISLA	49	POS	1	12	10	346	0.4	0.03	0.862
SPHASP	72	PENIITAL	50	POS	1	12	10	346	0.4	0.03	0.862
SPHASP	72	PENIMICZ	51	POS	2	11	12	344	0.5	2.21	0.137
SPHASP	72	PENIOXAL	52	POS	3	10	18	338	0.7	4.60	0.032
SPHASP	72	PENIPURP	53	POS	1	12	8	348	0.3	0.11	0.740
SPHASP	72	PENIRAIS	54	POS	1	12	25	331	0.9	0.21	0.647
SPHASP	72	PENIREST	55	NEG	0	13	9	347	0.3	2.24	0.134
SPHASP	72	PENISIMP	56	NEG	0	13	20	336	0.7	2.26	0.133
SPHASP	72	PENISP	57	POS	2	11	27	329	1.0	0.25	0.617

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
SPHASP	72	PENISP01	58	NEG	0	13	9	347	0.3	2.24	0.134
SPHASP	72	PENISP26	59	POS	4	9	49	307	1.9	1.73	0.188
SPHASP	72	PENISP64	60	NEG	0	13	10	346	0.4	2.20	0.138
SPHASP	72	PENISPIN	61	NEG	3	10	139	217	5.0	2.11	0.146
SPHASP	72	PENIVARI	62	NEG	0	13	12	344	0.4	2.16	0.142
SPHASP	72	PENIVERR	63	NEG	0	13	9	347	0.3	2.24	0.134
SPHASP	72	PENIVIRI	64	POS	5	8	63	293	2.4	2.35	0.125
SPHASP	72	PENIVULP	65	POS	2	11	20	336	0.8	0.75	0.386
SPHASP	72	PHOMHERB	66	POS	7	6	101	255	3.8	2.80	0.094
SPHASP	72	PHOMSP	67	NEG	2	11	60	296	2.2	0.27	0.603
SPHASP	72	PITHCHAR	68	POS	3	10	23	333	0.9	3.05	0.081
SPHASP	72	RHIZORYZ	69	POS	2	11	51	305	1.9	0.09	0.764
SPHASP	72	SCOPBREV	70	NEG	1	12	32	324	1.2	0.43	0.512
SPHASP	72	SCOPCAND	71	POS	1	12	26	330	1.0	0.24	0.624
STACCHAR	73	ACRESP	1	POS	1	12	24	332	0.9	0.18	0.671
STACCHAR	73	ALTEALTE	2	POS	12	1	315	41	11.5	0.00	1.000
STACCHAR	73	ALTESP	3	NEG	0	13	16	340	0.6	2.17	0.141
STACCHAR	73	ASPECAND	4	POS	1	12	18	338	0.7	0.05	0.823
STACCHAR	73	ASPEFUMI	5	NEG	0	13	25	331	0.9	2.41	0.121
STACCHAR	73	ASPEGLAU	6	POS	1	12	24	332	0.9	0.18	0.671
STACCHAR	73	ASPENIGE	7	NEG	4	9	122	234	4.4	0.31	0.578
STACCHAR	73	ASPEOCHR	8	POS	3	10	69	287	2.5	0.00	1.000
STACCHAR	73	ASPEORYZ	9	NEG	0	13	9	347	0.3	2.24	0.134
STACCHAR	73	ASPESP	10	POS	4	9	63	293	2.4	0.70	0.403
STACCHAR	73	ASPESYDO	11	POS	3	10	43	313	1.6	0.57	0.450
STACCHAR	73	ASPEUSTU	12	POS	1	12	23	333	0.9	0.16	0.689
STACCHAR	73	ASPEVERS	13	POS	8	5	188	168	6.9	0.11	0.740
STACCHAR	73	AUREPULL	14	NEG	10	3	283	73	10.3	0.33	0.566
STACCHAR	73	CHAEGLOB	15	POS	1	12	23	333	0.9	0.16	0.689
STACCHAR	73	CHRSPMSP	16	NEG	0	13	14	342	0.5	2.15	0.143
STACCHAR	73	CLADCLAD	17	POS	9	4	176	180	6.5	1.25	0.264
STACCHAR	73	CLADHERB	18	POS	7	6	80	276	3.1	5.22	0.022
STACCHAR	73	CLADSP	19	NEG	1	12	63	293	2.3	1.71	0.191
STACCHAR	73	CLADSPHA	20	POS	7	6	134	222	5.0	0.79	0.374
STACCHAR	73	CONISP	21	POS	1	12	9	347	0.4	0.07	0.791
STACCHAR	73	EMERNIDU	22	NEG	0	13	10	346	0.4	2.20	0.138
STACCHAR	73	EPICNIGR	23	POS	9	4	191	165	7.1	0.68	0.410
STACCHAR	73	EUROHERB	24	POS	9	4	236	120	8.6	0.01	0.920
STACCHAR	73	FUSAOXYS	25	POS	1	12	19	337	0.7	0.07	0.791
STACCHAR	73	FUSASP	26	NEG	0	13	59	297	2.1	3.95	0.047
STACCHAR	73	GEOMPANN	27	POS	1	12	11	345	0.4	0.02	0.888
STACCHAR	73	MUCOPLUM	28	NEG	1	12	72	284	2.6	2.16	0.142
STACCHAR	73	MUCORACE	29	NEG	3	10	88	268	3.2	0.21	0.647
STACCHAR	73	PAECSP	30	NEG	0	13	8	348	0.3	2.30	0.129
STACCHAR	73	PAECVARI	31	NEG	0	13	50	306	1.8	3.48	0.062
STACCHAR	73	PENIATRA	32	NEG	0	13	9	347	0.3	2.24	0.134
STACCHAR	73	PENIAURA	33	POS	2	11	42	314	1.6	0.00	1.000
STACCHAR	73	PENIBREV	34	NEG	1	12	85	271	3.0	2.85	0.091
STACCHAR	73	PENICHRY	35	NEG	6	7	185	171	6.7	0.48	0.488
STACCHAR	73	PENICOMM	36	NEG	3	10	91	265	3.3	0.28	0.597
STACCHAR	73	PENICOPR	37	NEG	0	13	10	346	0.4	2.20	0.138
STACCHAR	73	PENICORY	38	POS	7	6	101	255	3.8	2.80	0.094
STACCHAR	73	PENICRUS	39	NEG	0	13	14	342	0.5	2.15	0.143
STACCHAR	73	PENICTNG	40	NEG	0	13	34	322	1.2	2.75	0.097
STACCHAR	73	PENICTRM	41	POS	2	11	50	306	1.8	0.07	0.791
STACCHAR	73	PENIDECU	42	POS	1	12	18	338	0.7	0.05	0.823
STACCHAR	73	PENIDIGI	43	NEG	0	13	10	346	0.4	2.20	0.138
STACCHAR	73	PENIECHI	44	NEG	0	13	17	339	0.6	2.19	0.139
STACCHAR	73	PENIEXPA	45	POS	3	10	66	290	2.4	0.00	1.000
STACCHAR	73	PENIGLAN	46	NEG	0	13	13	343	0.5	2.15	0.143
STACCHAR	73	PENIGRIS	47	POS	1	12	22	334	0.8	0.13	0.718
STACCHAR	73	PENIIMPL	48	NEG	0	13	19	337	0.7	2.23	0.135

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
STACCHAR	73	PENIISLA	49	NEG	0	13	11	345	0.4	2.17	0.141
STACCHAR	73	PENIITAL	50	NEG	0	13	11	345	0.4	2.17	0.141
STACCHAR	73	PENIMICZ	51	NEG	0	13	14	342	0.5	2.15	0.143
STACCHAR	73	PENIOXAL	52	POS	1	12	20	336	0.7	0.09	0.764
STACCHAR	73	PENIPURP	53	NEG	0	13	9	347	0.3	2.24	0.134
STACCHAR	73	PENIRAIS	54	POS	1	12	25	331	0.9	0.21	0.647
STACCHAR	73	PENIREST	55	NEG	0	13	9	347	0.3	2.24	0.134
STACCHAR	73	PENISIMP	56	NEG	0	13	20	336	0.7	2.26	0.133
STACCHAR	73	PENISP	57	NEG	0	13	29	327	1.0	2.55	0.110
STACCHAR	73	PENISP01	58	NEG	0	13	9	347	0.3	2.24	0.134
STACCHAR	73	PENISP26	59	NEG	0	13	53	303	1.9	3.63	0.057
STACCHAR	73	PENISP64	60	NEG	0	13	10	346	0.4	2.20	0.138
STACCHAR	73	PENISPIN	61	NEG	3	10	139	217	5.0	2.11	0.146
STACCHAR	73	PENIVARI	62	POS	1	12	11	345	0.4	0.02	0.888
STACCHAR	73	PENIVERR	63	POS	1	12	8	348	0.3	0.11	0.740
STACCHAR	73	PENIVIRI	64	NEG	2	11	66	290	2.4	0.43	0.512
STACCHAR	73	PENIVULP	65	NEG	0	13	22	334	0.8	2.31	0.129
STACCHAR	73	PHOMHERB	66	POS	5	8	103	253	3.8	0.19	0.663
STACCHAR	73	PHOMSP	67	POS	4	9	58	298	2.2	0.99	0.320
STACCHAR	73	PITHCHAR	68	POS	1	12	25	331	0.9	0.21	0.647
STACCHAR	73	RHIZORYZ	69	NEG	1	12	52	304	1.9	1.21	0.271
STACCHAR	73	SCOPBREV	70	POS	3	10	30	326	1.2	1.75	0.186
STACCHAR	73	SCOPCAND	71	POS	2	11	25	331	1.0	0.35	0.554
STACCHAR	73	SPHASP	72	POS	2	11	11	345	0.5	2.55	0.110
TRICSP	74	ACRESP	1	POS	2	5	23	339	0.5	2.43	0.119
TRICSP	74	ALTEALTE	2	POS	7	0	320	42	6.2	0.13	0.718
TRICSP	74	ALTESP	3	POS	1	6	15	347	0.3	0.14	0.708
TRICSP	74	ASPECAND	4	POS	1	6	18	344	0.4	0.06	0.806
TRICSP	74	ASPEFUMI	5	NEG	0	7	25	337	0.5	2.19	0.139
TRICSP	74	ASPEGLAU	6	POS	1	6	24	338	0.5	0.00	1.000
TRICSP	74	ASPENIGE	7	POS	3	4	123	239	2.4	0.01	0.920
TRICSP	74	ASPEOCHR	8	NEG	0	7	72	290	1.4	3.23	0.072
TRICSP	74	ASPEORYZ	9	POS	1	6	8	354	0.2	0.66	0.417
TRICSP	74	ASPESP	10	NEG	0	7	67	295	1.3	3.07	0.080
TRICSP	74	ASPESYDO	11	POS	1	6	45	317	0.9	0.19	0.663
TRICSP	74	ASPEUSTU	12	POS	1	6	23	339	0.5	0.00	1.000
TRICSP	74	ASPEVERS	13	NEG	2	5	194	168	3.7	2.88	0.090
TRICSP	74	AUREPULL	14	POS	6	1	287	75	5.6	0.00	1.000
TRICSP	74	CHAEGLOB	15	POS	1	6	23	339	0.5	0.00	1.000
TRICSP	74	CHRSPMSP	16	NEG	0	7	14	348	0.3	2.34	0.126
TRICSP	74	CLADCLAD	17	POS	6	1	179	183	3.5	2.31	0.129
TRICSP	74	CLADHERB	18	NEG	1	6	86	276	1.7	1.07	0.301
TRICSP	74	CLADSP	19	NEG	1	6	63	299	1.2	0.52	0.471
TRICSP	74	CLADSPHA	20	POS	4	3	137	225	2.7	0.42	0.517
TRICSP	74	CONISP	21	NEG	0	7	10	352	0.2	2.63	0.105
TRICSP	74	EMERNIDU	22	NEG	0	7	10	352	0.2	2.63	0.105
TRICSP	74	EPICNIGR	23	POS	5	2	195	167	3.8	0.29	0.590
TRICSP	74	EUROHERB	24	POS	5	2	240	122	4.7	0.01	0.920
TRICSP	74	FUSAOXYS	25	POS	1	6	19	343	0.4	0.04	0.841
TRICSP	74	FUSASP	26	POS	2	5	57	305	1.1	0.16	0.689
TRICSP	74	GEOMPANN	27	NEG	0	7	12	350	0.2	2.45	0.118
TRICSP	74	MUCOPLUM	28	NEG	1	6	72	290	1.4	0.72	0.396
TRICSP	74	MUCORACE	29	POS	3	4	88	274	1.7	0.47	0.493
TRICSP	74	PAECSP	30	NEG	0	7	8	354	0.2	2.92	0.087
TRICSP	74	PAECVARI	31	POS	2	5	48	314	1.0	0.38	0.538
TRICSP	74	PENIATRA	32	POS	1	6	8	354	0.2	0.66	0.417
TRICSP	74	PENIAURA	33	POS	1	6	43	319	0.8	0.16	0.689
TRICSP	74	PENIBREV	34	POS	2	5	84	278	1.6	0.01	0.920
TRICSP	74	PENICHRY	35	NEG	3	4	188	174	3.6	0.74	0.390
TRICSP	74	PENICOMM	36	NEG	0	7	94	268	1.8	4.00	0.046
TRICSP	74	PENICOPR	37	NEG	0	7	10	352	0.2	2.63	0.105
TRICSP	74	PENICORY	38	POS	6	1	102	260	2.1	8.38	0.004

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
TRICSP	74	PENICRUS	39	NEG	0	7	14	348	0.3	2.34	0.126
TRICSP	74	PENICTNG	40	POS	1	6	33	329	0.6	0.04	0.841
TRICSP	74	PENICTRM	41	POS	1	6	51	311	1.0	0.28	0.597
TRICSP	74	PENIDECU	42	NEG	0	7	19	343	0.4	2.21	0.137
TRICSP	74	PENIDIGI	43	NEG	0	7	10	352	0.2	2.63	0.105
TRICSP	74	PENIECHI	44	NEG	0	7	17	345	0.3	2.24	0.134
TRICSP	74	PENIEXPA	45	NEG	1	6	68	294	1.3	0.63	0.427
TRICSP	74	PENIGLAN	46	POS	1	6	12	350	0.3	0.28	0.597
TRICSP	74	PENIGRIS	47	POS	1	6	22	340	0.4	0.01	0.920
TRICSP	74	PENIIMPL	48	POS	1	6	18	344	0.4	0.06	0.806
TRICSP	74	PENIISLA	49	NEG	0	7	11	351	0.2	2.53	0.112
TRICSP	74	PENIITAL	50	NEG	0	7	11	351	0.2	2.53	0.112
TRICSP	74	PENIMICZ	51	NEG	0	7	14	348	0.3	2.34	0.126
TRICSP	74	PENIOXAL	52	POS	1	6	20	342	0.4	0.03	0.862
TRICSP	74	PENIPURP	53	NEG	0	7	9	353	0.2	2.75	0.097
TRICSP	74	PENIRAIS	54	NEG	0	7	26	336	0.5	2.19	0.139
TRICSP	74	PENIREST	55	POS	1	6	8	354	0.2	0.66	0.417
TRICSP	74	PENISIMP	56	NEG	0	7	20	342	0.4	2.20	0.138
TRICSP	74	PENISP	57	NEG	0	7	29	333	0.6	2.22	0.136
TRICSP	74	PENISP01	58	POS	1	6	8	354	0.2	0.66	0.417
TRICSP	74	PENISP26	59	POS	2	5	51	311	1.0	0.29	0.590
TRICSP	74	PENISP64	60	NEG	0	7	10	352	0.2	2.63	0.105
TRICSP	74	PENISPIN	61	NEG	2	5	140	222	2.7	0.88	0.348
TRICSP	74	PENIVARI	62	NEG	0	7	12	350	0.2	2.45	0.118
TRICSP	74	PENIVERR	63	POS	1	6	8	354	0.2	0.66	0.417
TRICSP	74	PENIVIRI	64	NEG	1	6	67	295	1.3	0.60	0.439
TRICSP	74	PENIVULP	65	POS	1	6	21	341	0.4	0.02	0.888
TRICSP	74	PHOMHERB	66	POS	5	2	103	259	2.1	4.23	0.040
TRICSP	74	PHOMSP	67	NEG	0	7	62	300	1.2	2.93	0.087
TRICSP	74	PITHCHAR	68	POS	1	6	25	337	0.5	0.00	1.000
TRICSP	74	RHIZORYZ	69	NEG	0	7	53	309	1.0	2.68	0.102
TRICSP	74	SCOPBREV	70	NEG	0	7	33	329	0.6	2.27	0.132
TRICSP	74	SCOPCAND	71	POS	1	6	26	336	0.5	0.00	1.000
TRICSP	74	SPHASP	72	POS	1	6	12	350	0.3	0.28	0.597
TRICSP	74	STACCHAR	73	POS	1	6	12	350	0.3	0.28	0.597
TRICVIRI	75	ACRESP	1	POS	9	102	16	242	7.5	0.20	0.655
TRICVIRI	75	ALTEALTE	2	NEG	96	15	231	27	98.4	1.05	0.306
TRICVIRI	75	ALTESP	3	NEG	2	109	14	244	4.8	3.41	0.065
TRICVIRI	75	ASPECAND	4	POS	8	103	11	247	5.7	0.84	0.359
TRICVIRI	75	ASPEFUMI	5	POS	12	99	13	245	7.5	3.23	0.072
TRICVIRI	75	ASPEGLAU	6	POS	8	103	17	241	7.5	0.00	1.000
TRICVIRI	75	ASPENIGE	7	NEG	37	74	89	169	37.9	0.11	0.740
TRICVIRI	75	ASPEOCHR	8	POS	27	84	45	213	21.7	1.92	0.166
TRICVIRI	75	ASPEORYZ	9	POS	3	108	6	252	2.7	0.02	0.888
TRICVIRI	75	ASPESP	10	NEG	20	91	47	211	20.2	0.04	0.841
TRICVIRI	75	ASPESYDO	11	NEG	11	100	35	223	13.8	1.32	0.251
TRICVIRI	75	ASPEUSTU	12	NEG	7	104	17	241	7.2	0.11	0.740
TRICVIRI	75	ASPEVERS	13	NEG	54	57	142	116	59.0	1.54	0.215
TRICVIRI	75	AUREPULL	14	POS	91	20	202	56	88.1	0.44	0.507
TRICVIRI	75	CHAEGLOB	15	NEG	6	105	18	240	7.2	0.63	0.427
TRICVIRI	75	CHRSPMSP	16	POS	10	101	4	254	4.2	9.87	0.002
TRICVIRI	75	CLADCLAD	17	POS	56	55	129	129	55.7	0.00	1.000
TRICVIRI	75	CLADHERB	18	NEG	26	85	61	197	26.2	0.03	0.862
TRICVIRI	75	CLADSP	19	POS	26	85	38	220	19.3	3.51	0.061
TRICVIRI	75	CLADSPHA	20	POS	46	65	95	163	42.4	0.52	0.471
TRICVIRI	75	CONISP	21	POS	5	106	5	253	3.0	1.09	0.296
TRICVIRI	75	EMERNIDU	22	POS	4	107	6	252	3.0	0.12	0.729
TRICVIRI	75	EPICNIGR	23	NEG	52	59	148	110	60.2	3.90	0.048
TRICVIRI	75	EUROHERB	24	NEG	72	39	173	85	73.7	0.28	0.597
TRICVIRI	75	FUSAOXYS	25	POS	8	103	12	246	6.0	0.55	0.458
TRICVIRI	75	FUSASP	26	NEG	17	94	42	216	17.8	0.15	0.699
TRICVIRI	75	GEOMPANN	27	POS	4	107	8	250	3.6	0.00	1.000

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
TRICVIRI	75	MUCOPLUM	28	POS	26	85	47	211	22.0	1.02	0.313
TRICVIRI	75	MUCORACE	29	POS	28	83	63	195	27.4	0.00	1.000
TRICVIRI	75	PAECSP	30	NEG	2	109	6	252	2.4	0.50	0.480
TRICVIRI	75	PAECVARI	31	NEG	10	101	40	218	15.0	3.38	0.066
TRICVIRI	75	PENIATRA	32	POS	5	106	4	254	2.7	1.74	0.187
TRICVIRI	75	PENIAURA	33	POS	15	96	29	229	13.2	0.20	0.655
TRICVIRI	75	PENIBREV	34	POS	33	78	53	205	25.9	3.17	0.075
TRICVIRI	75	PENICHRY	35	NEG	50	61	141	117	57.5	3.27	0.071
TRICVIRI	75	PENICOMM	36	POS	33	78	61	197	28.3	1.21	0.271
TRICVIRI	75	PENICOPR	37	POS	4	107	6	252	3.0	0.12	0.729
TRICVIRI	75	PENICORY	38	POS	38	73	70	188	32.5	1.56	0.212
TRICVIRI	75	PENICRUS	39	NEG	3	108	11	247	4.2	1.03	0.310
TRICVIRI	75	PENICTNG	40	POS	17	94	17	241	10.2	6.06	0.014
TRICVIRI	75	PENICTRM	41	POS	21	90	31	227	15.6	2.51	0.113
TRICVIRI	75	PENIDECU	42	POS	8	103	11	247	5.7	0.84	0.359
TRICVIRI	75	PENIDIGI	43	NEG	3	108	7	251	3.0	0.13	0.718
TRICVIRI	75	PENIECHI	44	POS	8	103	9	249	5.1	1.67	0.196
TRICVIRI	75	PENIEXPA	45	NEG	20	91	49	209	20.8	0.13	0.718
TRICVIRI	75	PENIGLAN	46	POS	4	107	9	249	3.9	0.06	0.806
TRICVIRI	75	PENIGRIS	47	POS	7	104	16	242	6.9	0.04	0.841
TRICVIRI	75	PENIIMPL	48	POS	9	102	10	248	5.7	2.05	0.152
TRICVIRI	75	PENIISLA	49	POS	4	107	7	251	3.3	0.02	0.888
TRICVIRI	75	PENIITAL	50	NEG	3	108	8	250	3.3	0.29	0.590
TRICVIRI	75	PENIMICZ	51	POS	6	105	8	250	4.2	0.59	0.442
TRICVIRI	75	PENIOXAL	52	NEG	6	105	15	243	6.3	0.16	0.689
TRICVIRI	75	PENIPURP	53	POS	3	108	6	252	2.7	0.02	0.888
TRICVIRI	75	PENIRAIS	54	NEG	4	107	22	236	7.8	3.67	0.055
TRICVIRI	75	PENIREST	55	POS	6	105	3	255	2.7	4.22	0.040
TRICVIRI	75	PENISIMP	56	NEG	5	106	15	243	6.0	0.58	0.446
TRICVIRI	75	PENISP	57	POS	13	98	16	242	8.7	2.54	0.111
TRICVIRI	75	PENISP01	58	NEG	1	110	8	250	2.7	2.64	0.104
TRICVIRI	75	PENISP26	59	POS	16	95	37	221	15.9	0.02	0.888
TRICVIRI	75	PENISP64	60	NEG	3	108	7	251	3.0	0.13	0.718
TRICVIRI	75	PENISPIN	61	POS	46	65	96	162	42.7	0.42	0.517
TRICVIRI	75	PENIVARI	62	POS	7	104	5	253	3.6	3.42	0.064
TRICVIRI	75	PENIVERR	63	POS	5	106	4	254	2.7	1.74	0.187
TRICVIRI	75	PENIVIRI	64	NEG	18	93	50	208	20.5	0.75	0.386
TRICVIRI	75	PENIVULP	65	POS	9	102	13	245	6.6	0.81	0.368
TRICVIRI	75	PHOMHERB	66	POS	33	78	75	183	32.5	0.00	1.000
TRICVIRI	75	PHOMSP	67	NEG	13	98	49	209	18.7	3.49	0.062
TRICVIRI	75	PITHCHAR	68	POS	9	102	17	241	7.8	0.09	0.764
TRICVIRI	75	RHIZORYZ	69	POS	21	90	32	226	15.9	2.18	0.140
TRICVIRI	75	SCOPBREV	70	POS	13	98	20	238	9.9	1.05	0.306
TRICVIRI	75	SCOPCAND	71	NEG	6	105	21	237	8.1	1.31	0.252
TRICVIRI	75	SPHASP	72	POS	6	105	7	251	3.9	0.96	0.327
TRICVIRI	75	STACCHAR	73	POS	4	107	9	249	3.9	0.06	0.806
TRICVIRI	75	TRICSP	74	POS	4	107	3	255	2.1	1.35	0.245
ULOCCHAR	76	ACRESP	1	POS	4	51	21	293	3.7	0.02	0.888
ULOCCHAR	76	ALTEALTE	2	POS	52	3	275	39	48.7	1.61	0.204
ULOCCHAR	76	ALTESP	3	POS	5	50	11	303	2.4	2.30	0.129
ULOCCHAR	76	ASPECAND	4	NEG	2	53	17	297	2.8	0.78	0.377
ULOCCHAR	76	ASPEFUMI	5	POS	5	50	20	294	3.7	0.20	0.655
ULOCCHAR	76	ASPEGLAU	6	NEG	3	52	22	292	3.7	0.51	0.475
ULOCCHAR	76	ASPENIGE	7	NEG	15	40	111	203	18.8	1.74	0.187
ULOCCHAR	76	ASPEOCHR	8	POS	15	40	57	257	10.7	1.93	0.165
ULOCCHAR	76	ASPEORYZ	9	NEG	1	54	8	306	1.3	0.64	0.424
ULOCCHAR	76	ASPESP	10	NEG	9	46	58	256	10.0	0.32	0.572
ULOCCHAR	76	ASPESYDO	11	NEG	6	49	40	274	6.9	0.36	0.549
ULOCCHAR	76	ASPEUSTU	12	NEG	0	55	24	290	3.6	5.84	0.016
ULOCCHAR	76	ASPEVERS	13	NEG	28	27	168	146	29.2	0.25	0.617
ULOCCHAR	76	AUREPULL	14	POS	50	5	243	71	43.7	4.44	0.035
ULOCCHAR	76	CHAEGLOB	15	POS	4	51	20	294	3.6	0.00	1.000

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
ULOCCHAR	76	CHRSPMSP	16	POS	3	52	11	303	2.1	0.10	0.752
ULOCCHAR	76	CLADCLAD	17	POS	36	19	149	165	27.6	5.37	0.020
ULOCCHAR	76	CLADHERB	18	NEG	9	46	78	236	13.0	2.37	0.124
ULOCCHAR	76	CLADSP	19	POS	11	44	53	261	9.5	0.14	0.708
ULOCCHAR	76	CLADSPHA	20	POS	27	28	114	200	21.0	2.72	0.099
ULOCCHAR	76	CONISP	21	NEG	0	55	10	304	1.5	3.21	0.073
ULOCCHAR	76	EMERNIDU	22	POS	3	52	7	307	1.5	0.83	0.362
ULOCCHAR	76	EPICNIGR	23	POS	37	18	163	151	29.8	3.85	0.050
ULOCCHAR	76	EUROHERB	24	POS	39	16	206	108	36.5	0.38	0.538
ULOCCHAR	76	FUSAOXYS	25	POS	4	51	16	298	3.0	0.11	0.740
ULOCCHAR	76	FUSASP	26	POS	11	44	48	266	8.8	0.46	0.498
ULOCCHAR	76	GEOMPANN	27	NEG	0	55	12	302	1.8	3.56	0.059
ULOCCHAR	76	MUCOPLUM	28	NEG	9	46	64	250	10.9	0.76	0.383
ULOCCHAR	76	MUCORACE	29	POS	16	39	75	239	13.6	0.43	0.512
ULOCCHAR	76	PAECSP	30	NEG	0	55	8	306	1.2	2.89	0.089
ULOCCHAR	76	PAECVARI	31	POS	9	46	41	273	7.5	0.20	0.655
ULOCCHAR	76	PENIATRA	32	POS	3	52	6	308	1.3	1.21	0.271
ULOCCHAR	76	PENIAURA	33	NEG	3	52	41	273	6.6	3.35	0.067
ULOCCHAR	76	PENIBREV	34	NEG	11	44	75	239	12.8	0.64	0.424
ULOCCHAR	76	PENICHRY	35	NEG	28	27	163	151	28.5	0.08	0.777
ULOCCHAR	76	PENICOMM	36	POS	18	37	76	238	14.0	1.37	0.242
ULOCCHAR	76	PENICOPR	37	NEG	0	55	10	304	1.5	3.21	0.073
ULOCCHAR	76	PENICORY	38	POS	20	35	88	226	16.1	1.19	0.275
ULOCCHAR	76	PENICRUS	39	POS	4	51	10	304	2.1	1.17	0.279
ULOCCHAR	76	PENICTNG	40	POS	7	48	27	287	5.1	0.52	0.471
ULOCCHAR	76	PENICTRM	41	POS	10	45	42	272	7.8	0.54	0.462
ULOCCHAR	76	PENIDECU	42	POS	4	51	15	299	2.8	0.20	0.655
ULOCCHAR	76	PENIDIGI	43	POS	2	53	8	306	1.5	0.00	1.000
ULOCCHAR	76	PENIECHI	44	POS	3	52	14	300	2.5	0.00	1.000
ULOCCHAR	76	PENIEXPA	45	POS	16	39	53	261	10.3	3.82	0.051
ULOCCHAR	76	PENIGLAN	46	POS	2	53	11	303	1.9	0.12	0.729
ULOCCHAR	76	PENIGRIS	47	POS	5	50	18	296	3.4	0.42	0.517
ULOCCHAR	76	PENIIMPL	48	NEG	1	54	18	296	2.8	2.38	0.123
ULOCCHAR	76	PENIISLA	49	POS	3	52	8	306	1.6	0.55	0.458
ULOCCHAR	76	PENIITAL	50	NEG	1	54	10	304	1.6	0.96	0.327
ULOCCHAR	76	PENIMICZ	51	NEG	2	53	12	302	2.1	0.20	0.655
ULOCCHAR	76	PENIOXAL	52	POS	4	51	17	297	3.1	0.05	0.823
ULOCCHAR	76	PENIPURP	53	NEG	0	55	9	305	1.3	3.04	0.081
ULOCCHAR	76	PENIRAIS	54	POS	5	50	21	293	3.9	0.13	0.718
ULOCCHAR	76	PENIREST	55	NEG	1	54	8	306	1.3	0.64	0.424
ULOCCHAR	76	PENISIMP	56	NEG	1	54	19	295	3.0	2.57	0.109
ULOCCHAR	76	PENISP	57	NEG	3	52	26	288	4.3	0.98	0.322
ULOCCHAR	76	PENISP01	58	POS	3	52	6	308	1.3	1.21	0.271
ULOCCHAR	76	PENISP26	59	POS	10	45	43	271	7.9	0.44	0.507
ULOCCHAR	76	PENISP64	60	NEG	0	55	10	304	1.5	3.21	0.073
ULOCCHAR	76	PENISPIN	61	NEG	21	34	121	193	21.2	0.04	0.841
ULOCCHAR	76	PENIVARI	62	POS	2	53	10	304	1.8	0.06	0.806
ULOCCHAR	76	PENIVERR	63	POS	4	51	5	309	1.3	4.18	0.041
ULOCCHAR	76	PENIVIRI	64	POS	12	43	56	258	10.1	0.26	0.610
ULOCCHAR	76	PENIVULP	65	POS	4	51	18	296	3.3	0.02	0.888
ULOCCHAR	76	PHOMHERB	66	POS	24	31	84	230	16.1	5.66	0.017
ULOCCHAR	76	PHOMSP	67	POS	14	41	48	266	9.2	2.77	0.096
ULOCCHAR	76	PITHCHAR	68	POS	4	51	22	292	3.9	0.05	0.823
ULOCCHAR	76	RHIZORYZ	69	NEG	6	49	47	267	7.9	1.00	0.317
ULOCCHAR	76	SCOPBREV	70	POS	8	47	25	289	4.9	1.75	0.186
ULOCCHAR	76	SCOPCAND	71	POS	7	48	20	294	4.0	1.93	0.165
ULOCCHAR	76	SPHASP	72	POS	5	50	8	306	1.9	4.13	0.042
ULOCCHAR	76	STACCHAR	73	POS	3	52	10	304	1.9	0.20	0.655
ULOCCHAR	76	TRICSP	74	POS	3	52	4	310	1.0	2.44	0.118
ULOCCHAR	76	TRICVIRI	75	NEG	14	41	97	217	16.5	0.94	0.332
WALLSEBI	77	ACRESP	1	POS	7	83	18	261	6.1	0.04	0.841
WALLSEBI	77	ALTEALTE	2	NEG	78	12	249	30	79.8	0.74	0.390

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
WALLSEBI	77	ALTESP	3	NEG	3	87	13	266	3.9	0.70	0.403
WALLSEBI	77	ASPECAND	4	NEG	4	86	15	264	4.6	0.39	0.532
WALLSEBI	77	ASPEFUMI	5	NEG	5	85	20	259	6.1	0.59	0.442
WALLSEBI	77	ASPEGLAU	6	POS	7	83	18	261	6.1	0.04	0.841
WALLSEBI	77	ASPENIGE	7	NEG	30	60	96	183	30.7	0.10	0.752
WALLSEBI	77	ASPEOCHR	8	POS	20	70	52	227	17.6	0.35	0.554
WALLSEBI	77	ASPEORYZ	9	POS	3	87	6	273	2.2	0.06	0.806
WALLSEBI	77	ASPESP	10	POS	23	67	44	235	16.3	3.75	0.053
WALLSEBI	77	ASPESYDO	11	NEG	10	80	36	243	11.2	0.40	0.527
WALLSEBI	77	ASPEUSTU	12	NEG	5	85	19	260	5.9	0.44	0.507
WALLSEBI	77	ASPEVERS	13	POS	59	31	137	142	47.8	6.75	0.009
WALLSEBI	77	AUREPULL	14	POS	72	18	221	58	71.5	0.00	1.000
WALLSEBI	77	CHAEGLOB	15	POS	9	81	15	264	5.9	1.69	0.194
WALLSEBI	77	CHRSPMSP	16	NEG	2	88	12	267	3.4	1.48	0.224
WALLSEBI	77	CLADCLAD	17	POS	48	42	137	142	45.1	0.33	0.566
WALLSEBI	77	CLADHERB	18	NEG	16	74	71	208	21.2	2.67	0.102
WALLSEBI	77	CLADSP	19	NEG	13	77	51	228	15.6	0.99	0.320
WALLSEBI	77	CLADSPHA	20	POS	43	47	98	181	34.4	4.09	0.043
WALLSEBI	77	CONISP	21	POS	3	87	7	272	2.4	0.00	1.000
WALLSEBI	77	EMERNIDU	22	POS	5	85	5	274	2.4	2.37	0.124
WALLSEBI	77	EPICNIGR	23	NEG	48	42	152	127	48.8	0.10	0.752
WALLSEBI	77	EUROHERB	24	POS	70	20	175	104	59.8	6.25	0.012
WALLSEBI	77	FUSAOXYS	25	POS	6	84	14	265	4.9	0.11	0.740
WALLSEBI	77	FUSASP	26	POS	17	73	42	237	14.4	0.49	0.484
WALLSEBI	77	GEOMPANN	27	POS	3	87	9	270	2.9	0.09	0.764
WALLSEBI	77	MUCOPLUM	28	NEG	16	74	57	222	17.8	0.49	0.484
WALLSEBI	77	MUCORACE	29	POS	23	67	68	211	22.2	0.01	0.920
WALLSEBI	77	PAECSP	30	POS	2	88	6	273	2.0	0.14	0.708
WALLSEBI	77	PAECVARI	31	NEG	9	81	41	238	12.2	1.71	0.191
WALLSEBI	77	PENIATRA	32	NEG	2	88	7	272	2.2	0.30	0.584
WALLSEBI	77	PENIAURA	33	NEG	10	80	34	245	10.7	0.21	0.647
WALLSEBI	77	PENIBREV	34	POS	23	67	63	216	21.0	0.19	0.663
WALLSEBI	77	PENICHRY	35	NEG	43	47	148	131	46.6	0.98	0.322
WALLSEBI	77	PENICOMM	36	POS	28	62	66	213	22.9	1.62	0.203
WALLSEBI	77	PENICOPR	37	NEG	2	88	8	271	2.4	0.49	0.484
WALLSEBI	77	PENICORY	38	POS	32	58	76	203	26.3	1.89	0.169
WALLSEBI	77	PENICRUS	39	POS	4	86	10	269	3.4	0.00	1.000
WALLSEBI	77	PENICTNG	40	NEG	7	83	27	252	8.3	0.56	0.454
WALLSEBI	77	PENICTRM	41	POS	15	75	37	242	12.7	0.40	0.527
WALLSEBI	77	PENIDECU	42	NEG	4	86	15	264	4.6	0.39	0.532
WALLSEBI	77	PENIDIGI	43	NEG	1	89	9	270	2.4	2.10	0.147
WALLSEBI	77	PENIECHI	44	POS	9	81	8	271	4.2	6.34	0.012
WALLSEBI	77	PENIEXPA	45	POS	23	67	46	233	16.8	3.11	0.078
WALLSEBI	77	PENIGLAN	46	NEG	3	87	10	269	3.2	0.19	0.663
WALLSEBI	77	PENIGRIS	47	POS	10	80	13	266	5.6	3.81	0.051
WALLSEBI	77	PENIIMPL	48	NEG	3	87	16	263	4.6	1.37	0.242
WALLSEBI	77	PENIISLA	49	NEG	2	88	9	270	2.7	0.71	0.399
WALLSEBI	77	PENIITAL	50	POS	3	87	8	271	2.7	0.02	0.888
WALLSEBI	77	PENIMICZ	51	NEG	3	87	11	268	3.4	0.34	0.560
WALLSEBI	77	PENIOXAL	52	POS	6	84	15	264	5.1	0.04	0.841
WALLSEBI	77	PENIPURP	53	NEG	1	89	8	271	2.2	1.77	0.183
WALLSEBI	77	PENIRAIS	54	POS	8	82	18	261	6.3	0.30	0.584
WALLSEBI	77	PENIREST	55	NEG	2	88	7	272	2.2	0.30	0.584
WALLSEBI	77	PENISIMP	56	POS	7	83	13	266	4.9	0.75	0.386
WALLSEBI	77	PENISP	57	NEG	6	84	23	256	7.1	0.50	0.480
WALLSEBI	77	PENISP01	58	POS	3	87	6	273	2.2	0.06	0.806
WALLSEBI	77	PENISP26	59	POS	15	75	38	241	12.9	0.30	0.584
WALLSEBI	77	PENISP64	60	NEG	1	89	9	270	2.4	2.10	0.147
WALLSEBI	77	PENISPIN	61	NEG	32	58	110	169	34.6	0.61	0.435
WALLSEBI	77	PENIVARI	62	POS	5	85	7	272	2.9	1.16	0.281
WALLSEBI	77	PENIVERR	63	NEG	1	89	8	271	2.2	1.77	0.183
WALLSEBI	77	PENIVIRI	64	NEG	11	79	57	222	16.6	3.62	0.057

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
WALLSEBI	77	PENIVULP	65	NEG	5	85	17	262	5.4	0.20	0.655
WALLSEBI	77	PHOMHERB	66	NEG	23	67	85	194	26.3	1.05	0.306
WALLSEBI	77	PHOMSP	67	NEG	13	77	49	230	15.1	0.72	0.396
WALLSEBI	77	PITHCHAR	68	NEG	2	88	24	255	6.3	5.26	0.022
WALLSEBI	77	RHIZORYZ	69	NEG	12	78	41	238	12.9	0.24	0.624
WALLSEBI	77	SCOPBREV	70	POS	11	79	22	257	8.1	1.08	0.299
WALLSEBI	77	SCOPCAND	71	POS	8	82	19	260	6.6	0.18	0.671
WALLSEBI	77	SPHASP	72	POS	4	86	9	270	3.2	0.05	0.823
WALLSEBI	77	STACCHAR	73	POS	6	84	7	272	3.2	2.35	0.125
WALLSEBI	77	TRICSP	74	POS	2	88	5	274	1.7	0.03	0.862
WALLSEBI	77	TRICVIRI	75	POS	35	55	76	203	27.1	3.85	0.050
WALLSEBI	77	ULOCCHAR	76	POS	16	74	39	240	13.4	0.50	0.480
YEAST	78	ACRESP	1	POS	22	290	3	54	21.1	0.04	0.841
YEAST	78	ALTEALTE	2	POS	279	33	48	9	276.5	0.83	0.362
YEAST	78	ALTESP	3	POS	15	297	1	56	13.5	0.47	0.493
YEAST	78	ASPECAND	4	NEG	16	296	3	54	16.1	0.14	0.708
YEAST	78	ASPEFUMI	5	POS	25	287	0	57	21.1	3.71	0.054
YEAST	78	ASPEGLAU	6	NEG	20	292	5	52	21.1	0.88	0.348
YEAST	78	ASPENIGE	7	POS	108	204	18	39	106.5	0.09	0.764
YEAST	78	ASPEOCHR	8	POS	61	251	11	46	60.9	0.02	0.888
YEAST	78	ASPEORYZ	9	NEG	7	305	2	55	7.6	1.07	0.301
YEAST	78	ASPESP	10	POS	58	254	9	48	56.7	0.10	0.752
YEAST	78	ASPESYDO	11	POS	42	270	4	53	38.9	1.29	0.256
YEAST	78	ASPEUSTU	12	NEG	18	294	6	51	20.3	2.66	0.103
YEAST	78	ASPEVERS	13	NEG	164	148	32	25	165.7	0.41	0.522
YEAST	78	AUREPULL	14	NEG	243	69	50	7	247.7	3.48	0.062
YEAST	78	CHAEGLOB	15	POS	24	288	0	57	20.3	3.51	0.061
YEAST	78	CHRSPMSP	16	POS	14	298	0	57	11.8	1.57	0.210
YEAST	78	CLADCLAD	17	NEG	148	164	37	20	156.4	6.61	0.010
YEAST	78	CLADHERB	18	NEG	64	248	23	34	73.6	11.66	0.001
YEAST	78	CLADSP	19	POS	58	254	6	51	54.1	1.66	0.198
YEAST	78	CLADSPHA	20	NEG	110	202	31	26	119.2	8.30	0.004
YEAST	78	CONISP	21	NEG	7	305	3	54	8.5	3.01	0.083
YEAST	78	EMERNIDU	22	POS	9	303	1	56	8.5	0.00	1.000
YEAST	78	EPICNIGR	23	NEG	168	144	32	25	169.1	0.22	0.639
YEAST	78	EUROHERB	24	POS	210	102	35	22	207.2	0.51	0.475
YEAST	78	FUSAOXYS	25	POS	19	293	1	56	16.9	1.02	0.313
YEAST	78	FUSASP	26	POS	50	262	9	48	49.9	0.02	0.888
YEAST	78	GEOMPANN	27	NEG	10	302	2	55	10.2	0.28	0.597
YEAST	78	MUCOPLUM	28	POS	64	248	9	48	61.7	0.41	0.522
YEAST	78	MUCORACE	29	NEG	75	237	16	41	76.9	0.67	0.413
YEAST	78	PAECSP	30	POS	7	305	1	56	6.8	0.07	0.791
YEAST	78	PAECVARI	31	NEG	40	272	10	47	42.3	1.37	0.242
YEAST	78	PENIATRA	32	POS	9	303	0	57	7.6	0.69	0.406
YEAST	78	PENIAURA	33	POS	39	273	5	52	37.2	0.33	0.566
YEAST	78	PENIBREV	34	NEG	72	240	14	43	72.7	0.17	0.680
YEAST	78	PENICHRY	35	NEG	159	153	32	25	161.5	0.75	0.386
YEAST	78	PENICOMM	36	POS	80	232	14	43	79.5	0.00	1.000
YEAST	78	PENICOPR	37	NEG	7	305	3	54	8.5	3.01	0.083
YEAST	78	PENICORY	38	POS	98	214	10	47	91.3	3.83	0.050
YEAST	78	PENICRUS	39	POS	12	300	2	55	11.8	0.06	0.806
YEAST	78	PENICTNG	40	NEG	28	284	6	51	28.8	0.39	0.532
YEAST	78	PENICTRM	41	POS	46	266	6	51	44.0	0.40	0.527
YEAST	78	PENIDECU	42	NEG	14	298	5	52	16.1	2.80	0.094
YEAST	78	PENIDIGI	43	NEG	7	305	3	54	8.5	3.01	0.083
YEAST	78	PENIECHI	44	NEG	14	298	3	54	14.4	0.36	0.549
YEAST	78	PENIEXPA	45	POS	61	251	8	49	58.3	0.64	0.424
YEAST	78	PENIGLAN	46	NEG	10	302	3	54	11.0	1.36	0.244
YEAST	78	PENIGRIS	47	NEG	17	295	6	51	19.5	3.08	0.079
YEAST	78	PENIIMPL	48	POS	18	294	1	56	16.1	0.87	0.351
YEAST	78	PENIISLA	49	POS	10	302	1	56	9.3	0.03	0.862
YEAST	78	PENIITAL	50	NEG	9	303	2	55	9.3	0.46	0.498

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	Σ(A+B+)	X^2	p
YEAST	78	PENIMICZ	51	POS	13	299	1	56	11.8	0.25	0.617
YEAST	78	PENIOXAL	52	NEG	17	295	4	53	17.8	0.61	0.435
YEAST	78	PENIPURP	53	POS	8	304	1	56	7.6	0.01	0.920
YEAST	78	PENIRAIS	54	POS	22	290	4	53	22.0	0.07	0.791
YEAST	78	PENIREST	55	POS	8	304	1	56	7.6	0.01	0.920
YEAST	78	PENISIMP	56	POS	19	293	1	56	16.9	1.02	0.313
YEAST	78	PENISP	57	POS	27	285	2	55	24.5	1.12	0.290
YEAST	78	PENISP01	58	POS	8	304	1	56	7.6	0.01	0.920
YEAST	78	PENISP26	59	POS	45	267	8	49	44.8	0.02	0.888
YEAST	78	PENISP64	60	POS	9	303	1	56	8.5	0.00	1.000
YEAST	78	PENISPIN	61	POS	123	189	19	38	120.1	0.52	0.471
YEAST	78	PENIVARI	62	POS	12	300	0	57	10.2	1.21	0.271
YEAST	78	PENIVERR	63	POS	9	303	0	57	7.6	0.69	0.406
YEAST	78	PENIVIRI	64	POS	61	251	7	50	57.5	1.25	0.264
YEAST	78	PENIVULP	65	POS	19	293	3	54	18.6	0.00	1.000
YEAST	78	PHOMHERB	66	NEG	88	224	20	37	91.3	1.46	0.227
YEAST	78	PHOMSP	67	NEG	47	265	15	42	52.4	5.21	0.022
YEAST	78	PITHCHAR	68	POS	26	286	0	57	22.0	3.92	0.048
YEAST	78	RHIZORYZ	69	POS	45	267	8	49	44.8	0.02	0.888
YEAST	78	SCOPBREV	70	POS	30	282	3	54	27.9	0.65	0.420
YEAST	78	SCOPCAND	71	NEG	22	290	5	52	22.8	0.54	0.462
YEAST	78	SPHASP	72	POS	11	301	2	55	11.0	0.15	0.699
YEAST	78	STACCHAR	73	POS	11	301	2	55	11.0	0.15	0.699
YEAST	78	TRICSP	74	POS	6	306	1	56	5.9	0.20	0.655
YEAST	78	TRICVIRI	75	POS	97	215	14	43	93.9	0.69	0.406
YEAST	78	ULOCCHAR	76	POS	47	265	8	49	46.5	0.00	1.000
YEAST	78	WALLSEBI	77	POS	79	233	11	46	76.1	0.65	0.420

APPENDIX C

Calculations of sampling efficiency

Sample No.	No.of isolates	Total No. Species	No. of spp. seen once	Percent Coverage	Sample No.	No.of isolates	Total No. Species	No. of spp. seen once	Percent Coverage
1	67	15	5	92.5	76	32	15	10	68.8
2	85	12	2	97.6	77	35	10	4	88.6
3	90	21	7	92.2	78	94	19	8	91.5
4	95	22	12	87.4	79	146	24	4	97.3
5	115	24	9	92.2	80	272	17	4	98.5
6	31	14	7	77.4	81	928	15	4	99.6
7	61	13	5	91.8	82	175	11	1	99.4
8	75	14	8	89.3	83	93	19	5	94.6
9	115	29	10	91.3	84	502	14	3	99.4
10	144	18	4	97.2	85	228	13	2	99.1
11	73	16	5	93.2	86	34	12	3	91.2
12	37	13	5	86.5	87	79	19	9	88.6
13	134	25	6	95.5	88	104	15	3	97.1
14	287	18	8	97.2	89	178	14	1	99.4
15	59	15	6	89.8	90	133	12	7	94.7
16	98	13	5	94.9	91	263	12	4	98.5
17	72	9	2	97.2	92	25	11	4	84.0
18	131	14	6	95.4	93	131	12	5	96.2
19	293	18	3	99.0	94	109	14	3	97.2
20	102	20	8	92.2	95	88	13	6	93.2
21	264	18	9	96.6	96	118	12	3	97.5
22	179	17	6	96.6	97	245	14	9	96.3
23	57	18	12	78.9	98	40	12	8	80.0
24	84	14	7	91.7	99	39	15	7	82.1
25	51	12	5	90.2	100	43	12	5	88.4
26	81	23	10	87.7	101	185	12	2	98.9
27	44	15	9	79.5	102	70	28	13	81.4
28	58	9	4	93.1	103	218	12	3	98.6
29	123	20	9	92.7	104	62	18	8	87.1
30	268	16	5	98.1	105	40	22	13	67.5
31	367	21	9	97.5	106	28	15	9	67.9
32	72	19	9	87.5	107	94	23	8	91.5
33	214	17	6	97.2	108	27	7	4	85.2
34	115	11	4	96.5	109	151	14	7	95.4
35	67	21	10	85.1	110	48	23	15	68.8
36	46	19	9	80.4	111	51	12	5	90.2
37	97	22	8	91.8	112	137	16	4	97.1
38	82	16	7	91.5	113	152	12	3	98.0
39	50	18	12	76.0	114	924	10	4	99.6
40	33	11	4	87.9	115	49	8	2	95.9
41	167	21	10	94.0	116	40	14	10	75.0
42	241	16	3	98.8	117	36	8	5	86.1
43	57	15	7	87.7	118	98	16	5	94.9
44	81	19	7	91.4	119	106	12	4	96.2
45	65	13	5	92.3	120	58	9	4	93.1
46	1647	17	3	99.8	121	231	10	2	99.1
47	70	22	8	88.6	122	81	6	2	97.5
48	80	16	7	91.3	123	54	17	5	90.7
49	23	7	6	73.9	124	144	12	3	97.9
50	51	9	4	92.2	125	68	18	10	85.3
51	16	8	5	68.8	126	37	10	3	91.9
52	860	11	2	99.8	127	132	20	8	93.9
53	101	19	7	93.1	128	44	12	4	90.9
54	77	18	7	90.9	129	22	12	10	54.5
55	87	13	2	97.7	130	99	13	5	94.9
56	93	16	6	93.5	131	31	15	7	77.4
57	186	16	6	96.8	132	73	11	3	95.9
58	71	17	7	90.1	133	24	9	3	87.5
59	52	13	4	92.3	134	74	10	4	94.6
60	108	12	4	96.3	135	65	10	4	93.8
61	230	20	4	98.3	136	13	7	4	69.2
62	113	18	8	92.9	137	8	6	4	50.0
63	52	17	8	84.6	138	27	12	6	77.8
64	65	15	8	87.7	139	109	10	2	98.2
65	156	12	1	99.4	140	65	23	12	81.5
66	147	12	4	97.3	141	97	12	3	96.9
67	59	11	3	94.9	142	32	7	2	93.8
68	124	14	5	96.0	143	60	14	7	88.3
69	105	13	3	97.1	144	155	12	4	97.4
70	76	15	6	92.1	145	263	14	4	98.5
71	72	20	8	88.9	146	60	9	2	96.7
72	196	23	7	96.4	147	187	15	5	97.3
73	51	15	7	86.3	148	732	14	3	99.6
74	80	20	7	91.3	149	53	12	7	86.8
75	161	8	3	98.1	150	35	11	5	85.7

Sample No.	No.of isolates	Total No. Species	No. of spp. seen once	Percent Coverage	Sample No.	No.of isolates	Total No. Species	No. of spp. seen once	Percent Coverage
151	88	12	5	94.3	226	542	14	2	99.6
152	40	8	1	97.5	227	149	16	4	97.3
153	145	18	9	93.8	228	207	17	6	97.1
154	141	7	3	97.9	229	26	10	4	84.6
155	189	9	3	98.4	230	221	11	4	98.2
156	18	8	3	83.3	231	120	11	2	98.3
157	199	11	3	98.5	232	137	6	0	100.0
158	22	11	6	72.7	233	80	15	4	95.0
159	106	15	4	96.2	234	295	15	6	98.0
160	112	11	2	98.2	235	112	15	3	97.3
161	109	14	5	95.4	236	154	24	6	96.1
162	44	8	0	100.0	237	55	11	3	94.5
163	106	15	7	93.4	238	58	7	2	96.6
164	93	12	5	94.6	239	140	12	5	96.4
165	160	14	6	96.3	240	152	10	4	97.4
166	652	14	2	99.7	241	247	18	6	97.6
167	134	14	2	98.5	242	35	13	5	85.7
168	125	8	2	98.4	243	22	6	2	90.9
169	194	20	4	97.9	244	136	13	2	98.5
170	276	16	2	99.3	245	272	15	4	98.5
171	88	8	1	98.9	246	43	6	3	93.0
172	137	13	4	97.1	247	70	9	5	92.9
173	159	23	6	96.2	248	52	6	2	96.2
174	201	19	7	96.5	249	17	8	5	70.6
175	202	15	1	99.5	250	25	11	5	80.0
176	83	7	4	95.2	251	48	14	3	93.8
177	282	16	5	98.2	252	24	10	5	79.2
178	98	10	2	98.0	253	210	15	5	97.6
179	190	10	1	99.5	254	129	18	6	95.3
180	71	14	5	93.0	255	23	7	3	87.0
181	177	22	8	95.5	256	368	21	5	98.6
182	147	19	4	97.3	257	45	9	3	93.3
183	53	8	2	96.2	258	25	13	4	84.0
184	44	12	6	86.4	259	234	10	4	98.3
185	129	25	11	91.5	260	366	19	4	98.9
186	108	15	5	95.4	261	59	8	2	96.6
187	45	12	5	88.9	262	98	14	6	93.9
188	166	17	3	98.2	263	27	8	2	92.6
189	300	11	1	99.7	264	66	15	5	92.4
190	82	21	6	92.7	265	33	7	1	97.0
191	33	8	4	87.9	266	30	11	5	83.3
192	24	7	4	83.3	267	125	15	5	96.0
193	1103	18	5	99.5	268	61	13	3	95.1
194	186	12	3	98.4	269	56	16	4	92.9
195	87	18	6	93.1	270	43	9	3	93.0
196	733	7	2	99.7	271	144	15	5	96.5
197	65	11	3	95.4	272	849	8	2	99.8
198	93	13	5	94.6	273	331	12	4	98.8
199	257	12	3	98.8	274	79	17	8	89.9
200	134	12	3	97.8	275	309	18	4	98.7
201	173	15	5	97.1	276	166	6	2	98.8
202	137	11	3	97.8	277	233	11	3	98.7
203	103	20	4	96.1	278	45	8	2	95.6
204	473	15	2	99.6	279	237	12	1	99.6
205	91	13	3	96.7	280	71	7	2	97.2
206	147	14	4	97.3	281	76	13	4	94.7
207	161	13	6	96.3	282	67	14	5	92.5
208	46	14	6	87.0	283	100	20	5	95.0
209	56	10	5	91.1	284	331	18	7	97.9
210	168	10	4	97.6	285	30	12	8	73.3
211	157	10	2	98.7	286	231	13	2	99.1
212	302	7	2	99.3	287	88	8	2	97.7
213	48	11	5	89.6	288	6	5	4	33.3
214	46	9	5	89.1	289	200	8	2	99.0
215	63	20	8	87.3	290	55	12	3	94.5
216	258	14	5	98.1	291	10	7	5	50.0
217	62	12	6	90.3	292	54	12	2	96.3
218	44	9	2	95.5	293	112	13	4	96.4
219	90	16	7	92.2	294	84	13	6	92.9
220	223	10	6	97.3	295	761	16	5	99.3
221	52	6	2	96.2	296	150	14	2	98.7
222	66	11	5	92.4	297	190	13	4	97.9
223	96	12	4	95.8	298	48	10	2	95.8
224	276	14	4	98.6	299	99	14	3	97.0
225	140	13	5	96.4	300	181	13	3	98.3

Sample No.	No.of isolates	Total No. Species	No. of spp. seen once	Percent Coverage	Sample No.	No.of isolates	Total No. Species	No. of spp. seen once	Percent Coverage
301	93	5	2	97.8	336	133	13	3	97.7
302	34	11	4	88.2	337	138	6	3	97.8
303	313	16	8	97.4	338	78	12	6	92.3
304	520	12	5	99.0	339	50	10	6	88.0
305	178	16	5	97.2	340	34	11	5	85.3
306	131	10	1	99.2	341	37	10	4	89.2
307	207	10	2	99.0	342	63	9	5	92.1
308	55	6	1	98.2	343	38	12	5	86.8
309	197	14	3	98.5	344	27	12	5	81.5
310	22	8	4	81.8	345	13	7	3	76.9
311	38	12	7	81.6	346	3	2	1	66.7
312	261	16	4	98.5	347	25	12	4	84.0
313	70	19	9	87.1	348	7	4	2	71.4
314	150	10	5	96.7	349	47	6	2	95.7
315	137	10	3	97.8	350	8	5	3	62.5
316	15	7	3	80.0	351	21	7	3	85.7
317	173	17	5	97.1	352	20	9	3	85.0
318	95	15	4	95.8	353	62	14	6	90.3
319	142	15	6	95.8	354	46	13	7	84.8
320	94	11	4	95.7	355	42	8	1	97.6
321	652	13	3	99.5	356	27	10	3	88.9
322	147	2	1	99.3	357	23	9	4	82.6
323	61	8	2	96.7	358	69	10	3	95.7
324	121	9	3	97.5	359	86	14	3	96.5
325	249	18	5	98.0	360	27	10	3	88.9
326	27	13	7	74.1	361	19	8	4	78.9
327	52	11	2	96.2	362	31	10	3	90.3
328	153	10	1	99.3	363	9	6	4	55.6
329	82	14	5	93.9	364	48	11	3	93.8
330	120	10	3	97.5	365	18	5	3	83.3
331	586	12	2	99.7	366	24	9	3	87.5
332	93	13	5	94.6	367	51	8	0	100.0
333	106	17	4	96.2	368	25	10	4	84.0
334	43	11	4	90.7	369	21	10	4	81.0
335	76	6	1	98.7					

APPENDIX D

Alignment of sequences of nuclear ribosomal DNA, ITS1-5.SS-ITS2
and partial 28S region from *Penicillium* subgen. *Penicillium*

Invariant bases are indicated by an asterisk

Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                  1       10        20        30        40        50
                                  +--------+---------+---------+---------+---------+
P.camemberti NRRL874              AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.camemberti NRRL875              AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.echinulatum NRRL1151            AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.crustosum NRRL968               AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.viridicatum NRRL961             AAGGATCATTACCGAGTGAGGGCCC-TTT-GGGTCCAACCTCCCACCCGT 48
P.aurantiogriseum NRRL971         AAGGATCATTACCGAGTGAGGGCCC-TTT-GGGTCCAACCTCCCACCCGT 48
P.polonicum NRRL995               AAGGATCATTACCGAGTGAGGGCCC-TTT-GGGTCCAACCTCCCACCCGT 48
P.viridicatum NRRL958             AAGGATCATTACCGAGTGAGGGCCC-TTT-GGGTCCAACCTCCCACCCGT 48
P.chrysogenum NRRL821             AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.chrysogenum NRRL807             AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.griseoroseum NRRL820            AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.chrysogenum NRRL824             AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.griseoroseum NRRL832            AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.griseofulvum NRRL734            AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.griseofulvum NRRL2300           AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.coprophilum NRRL13627           AAGGATCATTACCGAGTGAGGGCCC-TTT-GGGTCCAACCTCCCACCCAT 48
P.digitatum NRRL786               AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.sclerotigenum NRRL3461          AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
Eu.egyptiacum NRRL2090            AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
Eu.crustaceum NRRL3332            AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.expansum NRRL974                AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.turbatum NRRL757                AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
H.paradoxus NRRL2162              AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.atramentosum NRRL795            AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.swiecickii NRRL918              AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.kojigenum NRRL3442              AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.raistrickii NRRL2039            AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.soppii NRRL2023                 AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.canescens NRRL910               AAGGATCATTACCGAGCGAGAATTC-TCT-GAATTCAACCTCCCACCCGT 48
P.atrovenetum NRRL2571            AAGGATCATTACCGAGCGAGGATTC-TCTCGAATCCAACCTCCCACCCGT 49
P.canescens NRRL2147              AAGGATCATTACTGAGTGAGGGCCCCTCG-GGGTCCAACCTCCCACCCGT 49
P.waksmanii NRRL777               AAGGATCATTACTGAGTGAGGGCCCCTCG-GGGTCCAACCTCCCACCCGT 49
P.miczynskii NRRL1077             AAGGATCATTACTGAGTGAGGGCCCCTCG-GGGTCCAACCTCCCACCCGT 49
Eu.shearii NRRL715                AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.roseopurpureum NRRL733          AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.roseopurpureum NRRL2064         AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.sumatrense NRRL779              AAGGATCATTACTGAGTGAGGGCCCCTCG-GGGTCCAACCTCCCACCCGT 49
P.paxilli NRRL2008                AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.citrinum NRRL1841               AAGGATCATTACCGAGTGCGGGCCCCTCG-GGGCCCAACCTCCCACCCGT 49
P.sartoryi NRRL783                AAGGATCATTACCGAGTGCGGGCCCCTCG-GGGCCCAACCTCCCACCCGT 49
P.westlingii NRRL800              AAGGATCATTACCGAGTGCGGGCCCCTCG-GGGCCCAACCTCCCACCCGT 49
P.charlesii NRRL778               AAGGATCATTACTGAGTGCGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.fellutanum NRRL746              AAGGATCATTACTGAGTGCGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.spinulosum NRRL728              AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.spinulosum NRRL1750             AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.thomii NRRL2077                 AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
Eu.lapidosum NRRL718              AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.thomii NRRL760                  AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.purpurescens NRRL720            AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.glabrum NRRL766                 AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.asperosporum NRRL3411           AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.lividum NRRL754                 AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.adametzii NRRL736               AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.adametzii NRRL737               AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.bilaii  NRRL3391                AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.adametzioides NRRL3405          AAGGATCATTACTGAGTGAGGGCCT-TC--GGGTCCAACCTCCCACCCGT 47
P.herquei NRRL1040                AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.sclerotiorum NRRL2074           AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.decumbens NRRL742               AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.decumbens NRRL741               AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                  1       10        20        30        40        50
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759                AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.corylophilum NRRL803            AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCAT 48
P.corylophilum NRRL802            AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCAT 48
P.corylophilum NRRL793            AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCAT 48
P.melinii NRRL2041                AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.velutinum NRRL2069              AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.raciborskii NRRL2150            AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.restrictum NRRL25744            AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.restrictum NRRL1748             AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.citreonigrum NRRL761            AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.cinerascens NRRL748             AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.vinaceum NRRL739                AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.oxalicum NRRL790                AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.oxalicum NRRL787                AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.donkii NRRL5562                 AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.fuscum NRRL721                  AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.janthinellum NRRL2016           AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.raperi NRRL2674                 AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.daleae NRRL922                  AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.ochrochloron NRRL926            AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.simplicissimum NRRL1075         AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.rolfsii NRRL1078                AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
Eu.cinnamopurpureum NRRL3326      AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.chermesinum NRRL735             AAGGATCATTACCGAGTGCGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.clavariiformis NRRL2482         AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAAACCTCCACCCGT 48
                                  ************ *** * *      *   *    *** *  ****** *
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                  51        60        70        80        90       100
                                   +--------+---------+---------+---------+---------+
P.camemberti NRRL874              GTTTA-TTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC-TGGCCGCCG 96
P.camemberti NRRL875              GTTTA-TTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC-TGGCCGCCG 96
P.echinulatum NRRL1151            GTTTA-TTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC-TGGCCGCCG 96
P.crustosum NRRL968               GTTTA-TTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC-TGGCCGCCG 96
P.viridicatum NRRL961             GTTTA-TTTTACCTTGTTGCTTCGGCGGGCCCGCCTTTAC-TGGCCGCCG 96
P.aurantiogriseum NRRL971         GTTTA-TTTTACCTTGTTGCTTCGGCGGGCCCGCCTTTAC-TGGCCGCCG 96
P.polonicum NRRL995               GTTTA-TTTTACCTTGTTGCTTCGGCGGGCCCGCCTTTAC-TGGCCGCCG 96
P.viridicatum NRRL958             GTTTA-TTTTACCTTGTTGCTTCGGCGGGCCCGCCTTTAC-TGGCCGCCG 96
P.chrysogenum NRRL821             GTTTA-TTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC-TGGCCGCCG 96
P.chrysogenum NRRL807             GTTTA-TTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC-TGGCCGCCG 96
P.griseoroseum NRRL820            GTTTA-TTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC-TGGCCGCCG 96
P.chrysogenum NRRL824             GTTTA-TTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC-TGGCCGCCG 96
P.griseoroseum NRRL832            GTTTA-TTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC-TGGCCGCCG 96
P.griseofulvum NRRL734            GTTTA-TTT-ACCTTGTTGCTTCGGCGGGCCCGCCTTAAC-TGGCCGCCG 95
P.griseofulvum NRRL2300           GTTTA-TTT-ACCTTGTTGCTTCGGCGGGCCCGCCTTAAC-TGGCCGCCG 95
P.coprophilum NRRL13627           GTTTA-TTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC-TGGCCGCCG 96
P.digitatum NRRL786               GTTTA-TTTTACCTTGTTGCTTCGGCGGGCCCGCCTTTAC-TGGCCGCCG 96
P.sclerotigenum NRRL3461          GTTTA-TTT-ACCTTGTTGCTTCGGCGGGCCCGCCTTAAC-TGGCCGCCG 95
Eu.egyptiacum NRRL2090            GTTTA-TTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC-TGGCCGCCG 96
Eu.crustaceum NRRL3332            GTTTA-TTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC-TGGCCGCCG 96
P.expansum NRRL974                GTTTA-TTTTACCTTGTTGCTTCGGCGGGCCCGCCTTTAC-TGGCCGCCG 96
P.turbatum NRRL757                GTTTA-TTGTACCTTGTTGCTTCGGCGGGCCCGCCTTTA--TGGCCGCCG 95
H.paradoxus NRRL2162              GTTTA-TTGTACCTTGTTGCTTCGGCGGGCCCGCCCTTG--TGGCCGCCG 95
P.atramentosum NRRL795            GTTTA-TTGTACCTTGTTGCTTCGGCGGGCCCGCCTTTA--TGGCCGCCG 95
P.swiecickii NRRL918              GTTTA-TTATACCTTGTTGCTTCGGCGGGCCCGCCGTAT---GGCCGCCG 94
P.kojigenum NRRL3442              GTTTA-TTATACCTTGTTGCTTCGGCGGGCCCGCCGTAT---GGCCGCCG 94
P.raistrickii NRRL2039            GTTTA-TTATACCTTGTTGCTTCGGCGGGCCCGCCGTCA---GGCCGCCG 94
P.soppii NRRL2023                 GTTTA-TTATACCTTGTTGCTTTGGCGGGCCCGCCTCAC---GGCCGCCG 94
P.canescens NRRL910               GTTTA-TTGTACCTTGTTGCTTCGGCGGGCCCGCCTCAC---GGCCGCCG 94
P.atrovenetum NRRL2571            GTTTA-TTGTACCTTGTTGCTTCGGCGGGCCCGCCTCAC---GGCCGCCG 95
P.canescens NRRL2147              GTTTAACGAACC-TTGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 95
P.waksmanii NRRL777               GTTTAACGAACC-TTGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 95
P.miczynskii NRRL1077             GTTTAACGAACC-TTGTTGCTTTGGCGGGCCCGCC-TCAC--GGCCGCCG 95
Eu.shearii NRRL715                GTTTAACGAACC-TTGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.roseopurpureum NRRL733          GTTTAACGAACC-TTGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.roseopurpureum NRRL2064         GTTTAACGAACC-TTGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.sumatrense NRRL779              GTTTAACGAACCCTTGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 96
P.paxilli NRRL2008                GTTTAACTGTACCTTGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 95
P.citrinum NRRL1841               GTTGCCCGAACCTATGTTGCCTCGGCGGGCCC------------------ 81
P.sartoryi NRRL783                GTTGCCCGAACCTATGTTGCCTCGGCGGGCCC------------------ 81
P.westlingii NRRL800              GTTGCCCGAACCTATGTTGCCTCGGCGGGCCC------------------ 81
P.charlesii NRRL778               GTATACTTACCG--TGTTGCTTCGGCGGGCCCGCC-TGTCA-GGCCGCCG 94
P.fellutanum NRRL746              GTATACTTACCG--TGTTGCTTCGGCGGGCCCGCC-TGCCA-GGCCGCCG 94
P.spinulosum NRRL728              GTTTA-TTGTACCTTGTTGCTTCGGTGCGCCCGCC-TCAC--GGCCGCCG 94
P.spinulosum NRRL1750             GTTTA-TTGTACCTTGTTGCTTCGGTGCGCCCGCC-TCAC--GGCCGCCG 94
P.thomii NRRL2077                 GTTTA-TTGTACCTTGTTGCTTCGGTGCGCCCGCC-TCAC--GGCCGCCG 94
Eu.lapidosum NRRL718              GTTTA-TTGTACCTTGTTGCTTCGGTGCGCCCGCC-TCAC--GGCCGCCG 94
P.thomii NRRL760                  GTTTA-TTGTACCTTGTTGCTTCGGTGCGCCCGCC-TCAC--GGCCGCCG 94
P.purpurescens NRRL720            GTTTA-TTGTACCTTGTTGCTTCGGTGCGCCCGCC-TCAC--GGCCGCCG 94
P.glabrum NRRL766                 GTTTA-TTGTACCTTGTTGCTTCGGTGCGCCCGCC-TCAC--GGCCGCCG 94
P.asperosporum NRRL3411           GTTTA-TTGTACCTTGTTGCTTCGGTGAGCCCGCC-TCAC--GGCCGCCG 94
P.lividum NRRL754                 GTTTA-TTGTACCTTGTTGCTTCGGTGCGCCCGCC-TCAC--GGCCGCCG 94
P.adametzii NRRL736               GTTTTATTGTACCTTGTTGCTTCGGCAGGCCCGCC-TCAC--GGCCGCCG 95
P.adametzii NRRL737               GTTTTATTGTACCTTGTTGCTTCGGCAGGCCCGCC-TCAC--GGCCGCCG 95
P.bilaii  NRRL3391                GTCTC-TTGTACCATGTTGCTTCGGCGAGCCCGCC-TCAC--GGCCGCCG 94
P.adametzioides NRRL3405          GTCTA-TTGTACCATGTTGCTTCGGCAGGCCCGCC-TTAT--GGCCGCCG 93
P.herquei NRRL1040                GTTTA-TTGTACCTTGTTGCTTCGGCAGGCCCGCC-TCAC--GGCCGCCG 94
P.sclerotiorum NRRL2074           GTTTA-TTGTACCTTGTTGCTTCGGCAGGCCCGCC-TCAC--GGCCGCCG 94
P.decumbens NRRL742               GTCTA-TTGTACCTTGTTGCTTCGGCGGGCCCGCC-GCAA--GGCCGCCG 94
P.decumbens NRRL741               GTCTA-TTGTACCTTGTTGCTTCGGCGGGCCCGCC-GCAA--GGCCGCCG 94
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                 51        60        70        80        90       100
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759                GTCTA-TTGTACCTTGTTGCTTCGGCGGGCCCGCC-GCAA--GGCCGCCG 94
P.corylophilum NRRL803            GTTTA-TTGTACCTTGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.corylophilum NRRL802            GTTTA-TTGTACCTTGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.corylophilum NRRL793            GTTTA-TTGTACCTTGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.melinii NRRL2041                GTTTA-TCGTACCTTGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.velutinum NRRL2069              GTTTA-TCGTACCTTGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.raciborskii NRRL2150            GTTTA-TCGTACCTTGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.restrictum NRRL25744            GTTTA-TCGTACCTTGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.restrictum NRRL1748             GTTTA-TCGTACCTTGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.citreonigrum NRRL761            GTTTA-TCGTACCTTGTTGCTTCGGCGGGCCCGCC-GCAA--GGCCGCCG 94
P.cinerascens NRRL748             GTTTA-TCGTACCTTGTTGCTTCGGCGGGCCCGCC-GCAA--GGCCGCCG 94
P.vinaceum NRRL739                GTTTA-TCGTACCTTGTTGCTTCGGCGGGCCCGCC-GCAA--GGCCGCCG 94
P.oxalicum NRRL790                GTTTA-TCGTACCTTGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.oxalicum NRRL787                GTTTA-TCGTACCTTGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.donkii NRRL5562                 GTCTA-TTGTACCTTGTTGCTTCGGCGGGCCCGCCATCATGTGGCCGCCG 97
P.fuscum NRRL721                  GTCTA-TTGTACCTTGTTGCTTCGGTGGGCCCGCCTTTAT--GGCCGCCG 95
P.janthinellum NRRL2016           GTTTA-TCATACCTAGTTGCTTCGGCGGGCCCGCCGTCA---GGCCGCCG 94
P.raperi NRRL2674                 GTTTA-TCATACCTAGTTGCTTCGGCGGGCCCGCCGTCAT--GGCCGCCG 95
P.daleae NRRL922                  GTTTA-TCGTACCTTGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.ochrochloron NRRL926            GTTTA-TT-TACCTTGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 93
P.simplicissimum NRRL1075         GTTTA-TT-TACCTTGTTGCTTCGGCGAGCCCGCC-TCAC--GGCCGCCG 93
P.rolfsii NRRL1078                GTTTA-TCGTACCTTGTTGCTTCGGCGAGCCCGCC-TCAC--GGCCGCCG 94
Eu.cinnamopurpureum NRRL3326      GTTTA-TCGTACCTTGTTGCTTCGGCGGGCCCGCCGTCA---GGCCGCCG 94
P.chermesinum NRRL735             GTTTA-TCGTACCTTGTTGCTTCGGCGGGCCCGCCGCCA---GGCCGCCG 94
P.clavariiformis NRRL2482         GTTTA-TTGTACCATGTTGCTTCGGCGGGCCCGCCATTGC--GGCCGCCG 95
                                  **             ***** * **   ****
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                101      110       120       130       140       150
                                  +--------+---------+---------+---------+---------+
P.camemberti NRRL874              GGGGGCT--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 142
P.camemberti NRRL875              GGGGGCT--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 142
P.echinulatum NRRL1151            GGGGGCT--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 142
P.crustosum NRRL968               GGGGGCT--TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 142
P.viridicatum NRRL961             GGGGGCT--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 142
P.aurantiogriseum NRRL971         GGGGGCTT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 143
P.polonicum NRRL995               GGGGGCT--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--CCGAA 142
P.viridicatum NRRL958             GGGGGCT--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 142
P.chrysogenum NRRL821             GGGGGCT--TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 142
P.chrysogenum NRRL807             GGGGGCT--TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 142
P.griseoroseum NRRL820            GGGGGCT--TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 142
P.chrysogenum NRRL824             GGGGGCT--TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 142
P.griseoroseum NRRL832            GGGGGCT--TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 142
P.griseofulvum NRRL734            GGGGGCT--TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 141
P.griseofulvum NRRL2300           GGGGGCT--TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 141
P.coprophilum NRRL13627           GGGGGCT--TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 142
P.digitatum NRRL786               GGGGGCT--CACGCTCCCGGGCCCGCGCCCGCCGAAGACACCC--CCGAA 142
P.sclerotigenum NRRL3461          GGGGGCT--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 141
Eu.egyptiacum NRRL2090            GGGGGCT--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 142
Eu.crustaceum NRRL3332            GGGGGCT--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 142
P.expansum NRRL974                GGGGGCT--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 142
P.turbatum NRRL757                GGGGGCT--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACC---TCGAA 140
H.paradoxus NRRL2162              GGGGGCT--TACGCTCCCGGGCCCGCGCCCGCCGAAGACACCC--ACGAA 141
P.atramentosum NRRL795            GGGGGCT--TACGCTCCCGGGCCCGCGCCCGCCGAAGACACCC--TCGAA 141
P.swiecickii NRRL918              GGGGGCT--TCTGCCCCCGGGCCCGCGCCCGCCGAAGACATCT--C-GAA 139
P.kojigenum NRRL3442              GGGGGCT--TCTGCCCCCGGGCCCGCGCCCGCCGAAGACATCT--C-GAA 139
P.raistrickii NRRL2039            GGGGGCT--TCTGCCCCCGGGCCCGCGCCCGCCGAAGACATCT--C-GAA 139
P.soppii NRRL2023                 GGGGGCT--TCTGCCCCCGGGCCCGTGCCCGCCGAAGACACCT--TAGAA 140
P.canescens NRRL910               GGGGGCA--TCTGCCCCCGGGCCCGCGCCCGCCGAAGACACCT--T-GAA 139
P.atrovenetum NRRL2571            GGGGGCA--TCTGCTCCCGGGCCCGCGCCCGCCGAAGACACCT--T-GAA 140
P.canescens NRRL2147              GGGGGCAT--CTGCCCCCGGGCCCGCGCCCGCCGAAGCCACC--TGTGAA 141
P.waksmanii NRRL777               GGGGGCAT--CCGCCCCCGGGCCCGCGCCCGCCGAAGCCACC--TGTGAA 141
P.miczynskii NRRL1077             GGGGGCAT--CTGCCCCCGGGCCCGCGCCCGCCGAAGCCACC--TGTGAA 141
Eu.shearii NRRL715                GGGGGCAT--CCGCCCCCGGGCCCGCGCCCGCCGAAGACACC--TGTGAA 140
P.roseopurpureum NRRL733          GGGGGCAT--CCGCCCCCGGGCCCGCGCCCGCCGAAGACACC--TGTGAA 140
P.roseopurpureum NRRL2064         GGGGGCAT--CCGCCCCCGGGCCCGCGCCCGCCGAAGACACC--TGTGAA 140
P.sumatrense NRRL779              GGGGGCTC--CTGCCCCCGGGCCCGCGCCCGCCGAAGCCCCC--CCTGAA 142
P.paxilli NRRL2008                GGGGGCTCTCCTGCCCCCGGGCCCGCGCCCGCCGAAGACACC--TGTGAA 143
P.citrinum NRRL1841               ----------------------C-GCGCCCGCCGACGGCCCC--CCTGAA 106
P.sartoryi NRRL783                ----------------------C-GCGCCCGCCGACGGCCCC--CCTAAA 106
P.westlingii NRRL800              ----------------------C-GCGCCCGCCGACGGCCCC--CCTGAA 106
P.charlesii NRRL778               GGGGGCAA--CCGCCCCCGGGCCCGCGCCCGCCGAAGACCCC--AACGAA 140
P.fellutanum NRRL746              GGGGGCAA--CCGCCCCCGGGCCCGCGCCCGCCGAAGACCCC--CACGAA 140
P.spinulosum NRRL728              GGGGGCTTCT--GCCCCCGGGTCCGCGCGCACCGGAGACACC--ATTGAA 140
P.spinulosum NRRL1750             GGGGGCTTCT--GCCCCCGGGTCCGCGCGCACCGGAGACACC--ATTGAA 140
P.thomii NRRL2077                 GGGGGCTTCT--GCCCCCGGGTCCGCGCGCACCGGAGACACC--ATTGAA 140
Eu.lapidosum NRRL718              GGGGGCTTCT--GCCCCCGGGTCCGCGCGCACCGGAGACACC--ATTGAA 140
P.thomii NRRL760                  GGGGGCTTCT--GCCCCCGGGTCCGCGCGCACCGGAGACACC--ATTGAA 140
P.purpurescens NRRL720            GGGGGCTTCT--GCCCCCGGGTCCGCGCGCACCGGAGACACC--ATTGAA 140
P.glabrum NRRL766                 GGGGGCTTCT--GCCCCCGGGTCCGCGCGCACCGGAGACACT--ATTGAA 140
P.asperosporum NRRL3411           GGGGGCTTCT--GCCCCCGGGCCCGCGCCCACCGAAGACACC--ATTGAA 140
P.lividum NRRL754                 GGGGGCTTCT--GCCCCCGGGTCCGCGCGCACCGAAGACACC--ATTGAA 140
P.adametzii NRRL736               GGGGGCCTCT--GCCCCCGGGCCCGCGCCTGCCGAAGACACC--CTTGAA 141
P.adametzii NRRL737               GGGGGCCTCT--GCCCCCGGGCCCGCGCCTGCCGAAGACACC--CTTGAA 141
P.bilaii  NRRL3391                GGGGGCATCT--GCCCCCGGGCCCGCGCCCGCCGAAGCCCCC--TCTGAA 140
P.adametzioides NRRL3405          GGGGCTAACC--GCCC-CGGGCCCGCGCCTGCCGAAGACCCC--TCTGAA 138
P.herquei NRRL1040                GGGGGCTTCTC-GCCCCCGGGCCCGCGCCTGCCGGAGACACC--TTTGAA 141
P.sclerotiorum NRRL2074           GGGGGCTTCT--GCCCCCGGGCCCGCGCCTGCCGGAGACAAT--CTTGAA 140
P.decumbens NRRL742               GGGGGCTTCT--GCCCCCGGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.decumbens NRRL741               GGGGGCTTCT--GCCCCCGGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                101      110       120       130       140       150
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759                GGGGGCTTCT--GCCCCCGGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.corylophilum NRRL803            GGGGGCTTCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.corylophilum NRRL802            GGGGGCTTCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.corylophilum NRRL793            GGGGGCTTCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.melinii NRRL2041                GGGGGCTTCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.velutinum NRRL2069              GGGGGCTTCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.raciborskii NRRL2150            GGGGGCTTCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.restrictum NRRL25744            GGGGGCTTCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.restrictum NRRL1748             GGGGGCTTCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.citreonigrum NRRL761            GGGGGCATCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.cinerascens NRRL748             GGGGGCATCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.vinaceum NRRL739                GGGGGCTTCC--GTCCCCGGGCCCGCGCCCGCCGAAGACACC--TGTGAA 140
P.oxalicum NRRL790                GGGGGCATCC--GCCCCCGGGCCCGCGCCCGCCGAAGACACACAAACGAA 142
P.oxalicum NRRL787                GGGGGCATCC--GCCCCCGGGCCCGCGCCCGCCGAAGACACACAAACGAA 142
P.donkii NRRL5562                 GGGGGCATCT--GCCCCCGGGCCCGCGCCCGCCGAAGACACC--CCTGAA 143
P.fuscum NRRL721                  GGGGGCATCC--GCCCCCGGGCCCGCGCCCGCCGAAGACACC--CCTGAA 141
P.janthinellum NRRL2016           GGGGGCATCC--GCCCCCGGGCCCGCGCCCGCCGAAGCCCCC--CCTGAA 140
P.raperi NRRL2674                 GGGGGCACCC--GCCCCCGGGCCCGCGCCCGCCGAAGACCCC--CCTGAA 141
P.daleae NRRL922                  GGGGGCACCC--GCCCCCGGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.ochrochloron NRRL926            GGGGGCATCT--GCCCCCGGGCCCGCGCCCGCCGAAGACACC--ATTGAA 139
P.simplicissimum NRRL1075         GGGGGCACCC--GCCCCCGGGCCCGCGCCCGCCGAAGACACC--ATTGAA 139
P.rolfsii NRRL1078                GGGGGCATCC--GCCCCCGGGCCCGCGCTCGCCGAAGACACC--ATTGAA 140
Eu.cinnamopurpureum NRRL3326      GGGG-CTTCG-TGCCC-CGGGCCCGTGCCCGCCGAAGACACC--ATTGAA 139
P.chermesinum NRRL735             GGGG-CATCC--GCCC-CGGGCCCGCGCCCGCCGAAGACACC--CCTGAA 138
P.clavariiformis NRRL2482         GGGGGCCTTT-TGTCCCCGGGCCTGTGCCCGCCGAAGACACT----TGAA 140
                                                        * * **   ***  * *         **
```

Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                151      160       170       180       190       200
                                  +--------+---------+---------+---------+---------+
P.camemberti NRRL874              CTCT-GTCTGAAGATTGAAGTCTGAGTGA---AAATATAAATTATTTAAA 188
P.camemberti NRRL875              CTCT-GTCTGAAGATTGAAGTCTGAGTGA---AAATATAAATTATTTAAA 188
P.echinulatum NRRL1151            CTCT-GTCTGAAGATTGAAGTCTGAGTGA---AAATATAAATTATTTAAA 188
P.crustosum NRRL968               CTCT-GTCTGAAGATTGAAGTCTGAGTGA---AAATATAAATTATTTAAA 188
P.viridicatum NRRL961             CTCT-GTCTGAAGATTGAAGTCTGAGTGA---AAATATAAATTATTTAAA 188
P.aurantiogriseum NRRL971         CTCT-GTCTGAAGATTGAAGTCTGAGTGA---AAATATAAATTATTTAAA 189
P.polonicum NRRL995               CTCT-GTCTGAAGATTGAAGTCTGAGTGA---AAATATAAATTATTTAAA 188
P.viridicatum NRRL958             CTCT-GTCTGAAGATTGAAGTCTGAGTGA---AAATATAAATTATTTAAA 188
P.chrysogenum NRRL821             CTCT-GTCTGAAGATTGTAGTCTGAGTGA---AAATATAAATTATTTAAA 188
P.chrysogenum NRRL807             CTCT-GTCTGAAGATTGTAGTCTGAGTGA---AAATATAAATTATTTAAA 188
P.griseoroseum NRRL820            CTCT-GTCTGAAGATTGTAGTCTGAGTGA---AAATATAAATTATTTAAA 188
P.chrysogenum NRRL824             CTCT-GTCTGAAGATTGTAGTCTGAGTGA---AAATATAAATTATTTAAA 188
P.griseoroseum NRRL832            CTCT-GTCTGAAGATTGTAGTCTGAGTGA---AAATATAAATTATTTAAA 188
P.griseofulvum NRRL734            CTCT-GTCTGAAGATTGTAGTCTGAGTGA---AAATATAAATTATTTAAA 187
P.griseofulvum NRRL2300           CTCT-GTCTGAAGATTGTAGTCTGAGTGA---AAATATAAATTATTTAAA 187
P.coprophilum NRRL13627           CTCT-GTCTGAAGATTGTAGTCTGAGTGA---AAATATAAATTATTTAAA 188
P.digitatum NRRL786               CTCT-GTCTGAAGATTGCAGTCTGAGTGA---AAAC-GAAATTATTTAAA 187
P.sclerotigenum NRRL3461          CTCT-GTCTGAAGATTGCAGTCTGAGTGA---AAATAGAAATTATTTAAA 187
Eu.egyptiacum NRRL2090            CTCT-GTCTGAAGATTGTAGTCTGAGTGA---AAATATAAATTATTTAAA 188
Eu.crustaceum NRRL3332            CTCT-GTCTGAAGATTGTAGTCTGAGTGA---AAATATAAATTATTTAAA 188
P.expansum NRRL974                CTCT-GTCTGAAGATTGTAGTCTGAGTGA---AAATATAAATTATTTAAA 188
P.turbatum NRRL757                CTCT-GTCTGAAGATTGTAGTCTGAGTGA---AAATATAAATTATTTAAA 186
H.paradoxus NRRL2162              CTCT-GTATGAAGATTGCAGTCTGAGTGA---AAATATAAATTATTTAAA 187
P.atramentosum NRRL795            CTCT-GTCTGAAGATTGTAGTCTGAGTGA---AAATATAAATTATTTAAA 187
P.swiecickii NRRL918              CTCT-GTCTGAAGATTGTAGTCTGAGTAA---AAATATAAATTATTTAAA 185
P.kojigenum NRRL3442              CTCT-GTCTGAAGATTGTAGTCTGAGTAA---AAATATAAATTATTTAAA 185
P.raistrickii NRRL2039            CTCT-GTCTGAAGATTGTAGTCTGAGTAT---AAATATAAATTATTTAAA 185
P.soppii NRRL2023                 CTCT-GTCTGAAGATTGTAGTCTGAGTAA---AAATATAAATTATTTAAA 186
P.canescens NRRL910               CTCT-GTATGAAAATTGCAGTCTGAGTCT---AAATATAAATTATTTAAA 185
P.atrovenetum NRRL2571            CTCT-GTATGAAAATTGCAGTCTGAGTCT---AAATATAAATTATTTAAA 186
P.canescens NRRL2147              CGCT-GTCTGAAGTATGCAGTCTGAGACA---ATTATTAAATTAATTAAA 187
P.waksmanii NRRL777               CGCT-GTCTGAAGTATGCAGTCTGAGACA---ATTATTAAATTAATTAAA 187
P.miczynskii NRRL1077             CTCT-GTCTGAAGTATGCAGTCTGAGACA---ATTATTAAATTAATTAAA 187
Eu.shearii NRRL715                CTCT-GTCTGAAGT-TGCAGTCTGAGAAA---CTATTTAAATTAGTTAAA 185
P.roseopurpureum NRRL733          CACT-GTCTGAAGT-TGCAGTCTGAGAAA---CTAGCTAAATTAGTTAAA 185
P.roseopurpureum NRRL2064         CACT-GTCTGAAGT-TGCAGTCTGAGAAA---CTAGCTAAATTAGTTAAA 185
P.sumatrense NRRL779              CGCT-GTCTGAAGT-TGCAGTCTGAGAAA---CTAGCTAAATTAGTTAAA 187
P.paxilli NRRL2008                CGCT-GTCTGAAGTATGCAGTCTGAGAAAA--CTAGCTAAATTAGTTAAA 190
P.citrinum NRRL1841               CGCT-GTCTGAAGT-TGCAGTCTGAGACCT--ATAACGAAATTAGTTAAA 152
P.sartoryi NRRL783                CGCT-GTCTGAAGT-TGCAGTCTGAGACCT--ATAACGAAATTGGTTAAA 152
P.westlingii NRRL800              CGCT-GTCTGAAGT-TGCAGTCTGAGACCT--ATAACGAAATTAGTTAAA 152
P.charlesii NRRL778               CTCT-TG-T--ACCTTGCAGTCTGAGCGAT--AAGCATAAATTA-TTAAA 183
P.fellutanum NRRL746              CTCT-TTCT--ACCTTGCAGTCTGAGCGAT--AAGCATAAATTA-TTAAA 184
P.spinulosum NRRL728              CTCT-GTCTGAAGATTGCAGTCTGAGCATA--AA--CTAAATAAGTTAAA 185
P.spinulosum NRRL1750             CTCT-GTCTGAAGATTGCAGTCTGAGCATA--AA--CTAAATAAGTTAAA 185
P.thomii NRRL2077                 CTCT-GTCTGAAGATTGCAGTCTGAGCATA--AA--CTAAATAAGTTAAA 185
Eu.lapidosum NRRL718              CTCT-GTCTGAAGATTGCAGTCTGAGCATA--AA--CTAAATAAGTTAAA 185
P.thomii NRRL760                  CTCT-GTCTGAAGATTGCAGTCTGAGCATA--AA--CTAAATAAGTTAAA 185
P.purpurescens NRRL720            CTCT-GTCTGAAGATTGCAGTCTGAGCATA--AA--CTAAATAAGTTAAA 185
P.glabrum NRRL766                 CTCT-GTCTGAAGATTGCAGTCTGAGCATA--AA--CTAAATAAGTTAAA 185
P.asperosporum NRRL3411           CTCT-GTCTGAAGATTGCAGTCTGAGCATA--AA--CTAAATAAGTTAAA 185
P.lividum NRRL754                 CTCT-GTATGAAGATTGCAGTCTGAGCGAA--AA--CTAAATGAGTTAAA 185
P.adametzii NRRL736               CGCT-GTCTGAAGTTTGCAGTCTGAGCGAA--AAGCAAAATTTA-TTAAA 187
P.adametzii NRRL737               CGCT-GTCTGAAGTTTGCAGTCTGAGCGAA--AAGCAAAATTTA-TTAAA 187
P.bilaii  NRRL3391                CGCT-GTCTGAAGATTGCAGTCTGAGCGAT--AAGCAAAAATTATTTAAA 187
P.adametzioides NRRL3405          CGCT-GTCTGAAGATTGCCGTCTGAGCGAA--ACATATAAATTATTTAAA 185
P.herquei NRRL1040                CGCT-GTCTGAAGTTTGCAGTCTGAGCGA---TTAGCTAAATTAGTTAAA 187
P.sclerotiorum NRRL2074           CGCT-GTCTGAAGAATGCAGTCTGAGCGAT--TAAGCAAAATTAGTTAAA 187
P.decumbens NRRL742               CGCT-GTCTGAAGATTGCAGTCTGAGCAA---TTAGCTAAATAAGTTAAA 186
P.decumbens NRRL741               CGCT-GTCTGAAGATTGCAGTCTGAGCAA---TTAGCTAAATAAGTTAAA 186
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                151      160       170       180       190       200
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759               CGCT-GTCTGAAGATTGCAGTCTGAGCAA---TTAGCTAAATAAGTTAAA 186
P.corylophilum NRRL803          CACT-GTCTGAAGATTGCAGTCTGAGCAA---TTAGCTAAATAAGTTAAA 186
P.corylophilum NRRL802          CACT-GTCTGAAGATTGCAGTCTGAGCAA---TTAGCTAAATAAGTTAAA 186
P.corylophilum NRRL793          CACT-GTCTGAAGATTGCAGTCTGAGCAA---TTAGCTAAATAAGTTAAA 186
P.melinii NRRL2041              CGCT-GTCTGAAGATTGCAGTCTGAGCAA---TTAGCTAAATAAGTTAAA 186
P.velutinum NRRL2069            CGCT-GTCTGAAGATTGCAGTCTGAGCAA---TTAGCTAAATAAGTTAAA 186
P.raciborskii NRRL2150          CGCT-GTCTGAAGATTGCAGTCTGAGCAA---TTAGCTAAATAAGTTAAA 186
P.restrictum NRRL25744          CGCT-GTCTGAAGATTGCAGTCTGAGCAA---TTAGCTAAATAAGTTAAA 186
P.restrictum NRRL1748           CGCT-GTCTGAAGATTGCAGTCTGAGCAA---TTAGCTAAATAAGTTAAA 186
P.citreonigrum NRRL761          CGCT-GTCTGAAGATTGCAGTCTGAGCAA---TTAGTTAAATAACTTAAA 186
P.cinerascens NRRL748           CGCT-GTCTGAAGATTGCAGTCTGAGCAA---TTAGTTAAATAACTTAAA 186
P.vinaceum NRRL739              CGCT-GTATGAAGATTGCAGTCTGAGCGA---AAAGCTAAATTTGTTAAA 186
P.oxalicum NRRL790              CTCTTGTCTGAAGATTGCAGTCTGAG-TAC--TTGACTAAATCAGTTAAA 189
P.oxalicum NRRL787              CTCTTGTCTGAAGATTGCAGTCTGAG-TAC--TTGACTAAATCAGTTAAA 189
P.donkii NRRL5562               CGCT-GTCTGAAGATTGCAGTCTGAGCAGA--TTAGCTAAATCAGTTAAA 190
P.fuscum NRRL721                CGCT-GTCTGAAGATTGCAGTCTGAGCAGA--TTAGCTAAATCAGTTAAA 188
P.janthinellum NRRL2016         CGCT-GTCTGAAGATTGCAGTCTGAGCGA---TTAGCTAAATCAGTTAAA 186
P.raperi NRRL2674               CGCT-GTCTGAAGATTGCAGTCTGAGCGA---TTAGCTAAATCAGTTAAA 187
P.daleae NRRL922                CGCT-GTCTGAAGATTGCAGTCTGAGCATC--TTAGCTAAATCAGTTAAA 187
P.ochrochloron NRRL926          CTCT-GTCTGAAGATTGCAGTCTGAGCGA---TTAACTAAATCAGTTAAA 185
P.simplicissimum NRRL1075       CTCT-GTCTGAAGATTGCAGTCTGAGCGA---TTAGCTAAATCAGTTAAA 185
P.rolfsii NRRL1078              CTCT-GTCTGAAGATTGCAGTCTGAGTGA---TTAACTAAATCAGTTAAA 186
Eu.cinnamopurpureum NRRL3326    CGCT-GTCTGAAGATTGCAGTCTGAGCGA---TTAGCTAAATTAGTTAAA 185
P.chermesinum NRRL735           CGCT-GTCTGAAGATTGCAGTCTGAGCGA---TTA-TTAAATTATTTAAA 183
P.clavariiformis NRRL2482       CTCTTGTCTGATGGTTGCAGTCTGAGTTGTGATTATTATAATCAATTAAA 190
                                * **    *       **  *******             * *   *****
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                201      210       220       230       240       250
                                  +--------+---------+---------+---------+---------+
P.camemberti NRRL874              ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 238
P.camemberti NRRL875              ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 238
P.echinulatum NRRL1151            ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 238
P.crustosum NRRL968               ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 238
P.viridicatum NRRL961             ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 238
P.aurantiogriseum NRRL971         ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 239
P.polonicum NRRL995               ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 238
P.viridicatum NRRL958             ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 238
P.chrysogenum NRRL821             ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 238
P.chrysogenum NRRL807             ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 238
P.griseoroseum NRRL820            ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 238
P.chrysogenum NRRL824             ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 238
P.griseoroseum NRRL832            ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 238
P.griseofulvum NRRL734            ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 237
P.griseofulvum NRRL2300           ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 237
P.coprophilum NRRL13627           ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 238
P.digitatum NRRL786               ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 237
P.sclerotigenum NRRL3461          ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 237
Eu.egyptiacum NRRL2090            ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 238
Eu.crustaceum NRRL3332            ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 238
P.expansum NRRL974                ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 238
P.turbatum NRRL757                ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 236
H.paradoxus NRRL2162              ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 237
P.atramentosum NRRL795            ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 237
P.swiecickii NRRL918              ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
P.kojigenum NRRL3442              ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
P.raistrickii NRRL2039            ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
P.soppii NRRL2023                 ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 236
P.canescens NRRL910               ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
P.atrovenetum NRRL2571            ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 236
P.canescens NRRL2147              ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 237
P.waksmanii NRRL777               ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 237
P.miczynskii NRRL1077             ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 237
Eu.shearii NRRL715                ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
P.roseopurpureum NRRL733          ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
P.roseopurpureum NRRL2064         ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
P.sumatrense NRRL779              ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 237
P.paxilli NRRL2008                ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 240
P.citrinum NRRL1841               ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 202
P.sartoryi NRRL783                ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 202
P.westlingii NRRL800              ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 202
P.charlesii NRRL778               ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 233
P.fellutanum NRRL746              ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 234
P.spinulosum NRRL728              ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
P.spinulosum NRRL1750             ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
P.thomii NRRL2077                 ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
Eu.lapidosum NRRL718              ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
P.thomii NRRL760                  ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
P.purpurescens NRRL720            ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
P.glabrum NRRL766                 ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
P.asperosporum NRRL3411           ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
P.lividum NRRL754                 ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
P.adametzii NRRL736               ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 237
P.adametzii NRRL737               ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 237
P.bilaii  NRRL3391                ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 237
P.adametzioides NRRL3405          ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
P.herquei NRRL1040                ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 237
P.sclerotiorum NRRL2074           ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 237
P.decumbens NRRL742               ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 236
P.decumbens NRRL741               ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 236
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                201      210       220       230       240       250
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759               ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 236
P.corylophilum NRRL803           ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 236
P.corylophilum NRRL802           ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 236
P.corylophilum NRRL793           ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 236
P.melinii NRRL2041               ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 236
P.velutinum NRRL2069             ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 236
P.raciborskii NRRL2150           ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 236
P.restrictum NRRL25744           ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 236
P.restrictum NRRL1748            ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 236
P.citreonigrum NRRL761           ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 236
P.cinerascens NRRL748            ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 236
P.vinaceum NRRL739               ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 236
P.oxalicum NRRL790               ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 239
P.oxalicum NRRL787               ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 239
P.donkii NRRL5562                ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 240
P.fuscum NRRL721                 ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 238
P.janthinellum NRRL2016          ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 236
P.raperi NRRL2674                ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 237
P.daleae NRRL922                 ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 237
P.ochrochloron NRRL926           ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
P.simplicissimum NRRL1075        ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
P.rolfsii NRRL1078               ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 236
Eu.cinnamopurpureum NRRL3326     ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 235
P.chermesinum NRRL735            ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 233
P.clavariiformis NRRL2482        ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA 240
                                  **************************************************
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                251      260       270       280       290       300
                                  +--------+---------+---------+---------+---------+
P.camemberti NRRL874              AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 287
P.camemberti NRRL875              AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 287
P.echinulatum NRRL1151            AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 287
P.crustosum NRRL968               AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 287
P.viridicatum NRRL961             AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 287
P.aurantiogriseum NRRL971         AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 288
P.polonicum NRRL995               AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 287
P.viridicatum NRRL958             AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 287
P.chrysogenum NRRL821             AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 287
P.chrysogenum NRRL807             AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 287
P.griseoroseum NRRL820            AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 287
P.chrysogenum NRRL824             AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 287
P.griseoroseum NRRL832            AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 287
P.griseofulvum NRRL734            AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 286
P.griseofulvum NRRL2300           AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 286
P.coprophilum NRRL13627           AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 287
P.digitatum NRRL786               AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 286
P.sclerotigenum NRRL3461          AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 286
Eu.egyptiacum NRRL2090            AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 287
Eu.crustaceum NRRL3332            AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 287
P.expansum NRRL974                AATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTT 287
P.turbatum NRRL757                AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
H.paradoxus NRRL2162              AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 287
P.atramentosum NRRL795            AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 287
P.swiecickii NRRL918              AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.kojigenum NRRL3442              AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.raistrickii NRRL2039            AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.soppii NRRL2023                 AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.canescens NRRL910               AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.atrovenetum NRRL2571            AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.canescens NRRL2147              AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 287
P.waksmanii NRRL777               AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 287
P.miczynskii NRRL1077             AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 287
Eu.shearii NRRL715                AATGCGATAAATAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.roseopurpureum NRRL733          AATGCGATAAATAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.roseopurpureum NRRL2064         AATGCGATAAATAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.sumatrense NRRL779              AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 287
P.paxilli NRRL2008                AATGCGATAATTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 290
P.citrinum NRRL1841               AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 252
P.sartoryi NRRL783                AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 252
P.westlingii NRRL800              AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 252
P.charlesii NRRL778               AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 283
P.fellutanum NRRL746              AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 284
P.spinulosum NRRL728              AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.spinulosum NRRL1750             AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.thomii NRRL2077                 AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
Eu.lapidosum NRRL718              AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.thomii NRRL760                  AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.purpurescens NRRL720            AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.glabrum NRRL766                 AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.asperosporum NRRL3411           AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.lividum NRRL754                 AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.adametzii NRRL736               AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 287
P.adametzii NRRL737               AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 287
P.bilaii  NRRL3391                AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 287
P.adametzioides NRRL3405          AATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.herquei NRRL1040                AATGCGATAATTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 287
P.sclerotiorum NRRL2074           AATGCGATAATTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 287
P.decumbens NRRL742               AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.decumbens NRRL741               AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                251      260       270       280       290       300
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759               AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.corylophilum NRRL803           AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.corylophilum NRRL802           AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.corylophilum NRRL793           AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.melinii NRRL2041               AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.velutinum NRRL2069             AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.raciborskii NRRL2150           AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.restrictum NRRL25744           AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.restrictum NRRL1748            AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.citreonigrum NRRL761           AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.cinerascens NRRL748            AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.vinaceum NRRL739               AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.oxalicum NRRL790               AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 289
P.oxalicum NRRL787               AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 289
P.donkii NRRL5562                AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 290
P.fuscum NRRL721                 AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 288
P.janthinellum NRRL2016          AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.raperi NRRL2674                AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 287
P.daleae NRRL922                 AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 287
P.ochrochloron NRRL926           AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.simplicissimum NRRL1075        AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.rolfsii NRRL1078               AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
Eu.cinnamopurpureum NRRL3326     AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.chermesinum NRRL735            AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 283
P.clavariiformis NRRL2482        AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 290
                                 *********  ************** ************************
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                301      310       320       330       340       350
                                  +--------+---------+---------+---------+---------+
P.camemberti NRRL874              GAACGCACATTGCGCCCCCTGGTATTCCGGAGGGCATGCCTGTCCGAGCG 337
P.camemberti NRRL875              GAACGCACATTGCGCCCCCTGGTATTCCGGAGGGCATGCCTGTCCGAGCG 337
P.echinulatum NRRL1151            GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.crustosum NRRL968               GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.viridicatum NRRL961             GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.aurantiogriseum NRRL971         GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 338
P.polonicum NRRL995               GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.viridicatum NRRL958             GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.chrysogenum NRRL821             GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.chrysogenum NRRL807             GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.griseoroseum NRRL820            GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.chrysogenum NRRL824             GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.griseoroseum NRRL832            GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.griseofulvum NRRL734            GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
P.griseofulvum NRRL2300           GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
P.coprophilum NRRL13627           GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.digitatum NRRL786               GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
P.sclerotigenum NRRL3461          GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
Eu.egyptiacum NRRL2090            GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
Eu.crustaceum NRRL3332            GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.expansum NRRL974                GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.turbatum NRRL757                GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
H.paradoxus NRRL2162              GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.atramentosum NRRL795            GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.swiecickii NRRL918              GAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCG 335
P.kojigenum NRRL3442              GAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCG 335
P.raistrickii NRRL2039            GAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCG 335
P.soppii NRRL2023                 GAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCG 336
P.canescens NRRL910               GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 335
P.atrovenetum NRRL2571            GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
P.canescens NRRL2147              GAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCG 337
P.waksmanii NRRL777               GAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCG 337
P.miczynskii NRRL1077             GAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCG 337
Eu.shearii NRRL715                GAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCG 335
P.roseopurpureum NRRL733          GAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCG 335
P.roseopurpureum NRRL2064         GAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCG 335
P.sumatrense NRRL779              GAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCG 337
P.paxilli NRRL2008                GAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCG 340
P.citrinum NRRL1841               GAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCG 302
P.sartoryi NRRL783                GAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCG 302
P.westlingii NRRL800              GAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCG 302
P.charlesii NRRL778               GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 333
P.fellutanum NRRL746              GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 334
P.spinulosum NRRL728              GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 335
P.spinulosum NRRL1750             GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 335
P.thomii NRRL2077                 GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 335
Eu.lapidosum NRRL718              GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 335
P.thomii NRRL760                  GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 335
P.purpurescens NRRL720            GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 335
P.glabrum NRRL766                 GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 335
P.asperosporum NRRL3411           GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 335
P.lividum NRRL754                 GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 335
P.adametzii NRRL736               GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.adametzii NRRL737               GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.bilaii  NRRL3391                GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.adametzioides NRRL3405          GAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCG 335
P.herquei NRRL1040                GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.sclerotiorum NRRL2074           GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.decumbens NRRL742               GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
P.decumbens NRRL741               GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                301      310       320       330       340       350
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759               GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
P.corylophilum NRRL803           GAACGCACATTGCGCCCCTTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
P.corylophilum NRRL802           GAACGCACATTGCGCCCCTTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
P.corylophilum NRRL793           GAACGCACATTGCGCCCCTTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
P.melinii NRRL2041               GAACGCACATTGCGCCCCTTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
P.velutinum NRRL2069             GAACGCACATTGCGCCCCTTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
P.raciborskii NRRL2150           GAACGCACATTGCGCCCCTTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
P.restrictum NRRL25744           GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
P.restrictum NRRL1748            GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
P.citreonigrum NRRL761           GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
P.cinerascens NRRL748            GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
P.vinaceum NRRL739               GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
P.oxalicum NRRL790               GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 339
P.oxalicum NRRL787               GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 339
P.donkii NRRL5562                GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 340
P.fuscum NRRL721                 GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 338
P.janthinellum NRRL2016          GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
P.raperi NRRL2674                GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.daleae NRRL922                 GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 337
P.ochrochloron NRRL926           GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 335
P.simplicissimum NRRL1075        GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 335
P.rolfsii NRRL1078               GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 336
Eu.cinnamopurpureum NRRL3326     GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 335
P.chermesinum NRRL735            GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 333
P.clavariiformis NRRL2482        GAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCG 340
                                 *****************  *********** *******************
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                351      360       370       380       390       400
                                  +--------+---------+---------+---------+---------+
P.camemberti NRRL874              TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 385
P.camemberti NRRL875              TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 385
P.echinulatum NRRL1151            TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 385
P.crustosum NRRL968               TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC-GT-CCCCCGA 385
P.viridicatum NRRL961             TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 385
P.aurantiogriseum NRRL971         TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 386
P.polonicum NRRL995               TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 385
P.viridicatum NRRL958             TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 385
P.chrysogenum NRRL821             TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 385
P.chrysogenum NRRL807             TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 385
P.griseoroseum NRRL820            TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 385
P.chrysogenum NRRL824             TCATTTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 385
P.griseoroseum NRRL832            TCATTTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 385
P.griseofulvum NRRL734            TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 384
P.griseofulvum NRRL2300           TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 384
P.coprophilum NRRL13627           TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 385
P.digitatum NRRL786               TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC-GT-CCCCCGA 384
P.sclerotigenum NRRL3461          TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC-GT-CCTCCGT 384
Eu.egyptiacum NRRL2090            TCATTACTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 385
Eu.crustaceum NRRL3332            TCATTACTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 385
P.expansum NRRL974                TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 385
P.turbatum NRRL757                TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 384
H.paradoxus NRRL2162              TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC-GT-CCCCCGA 385
P.atramentosum NRRL795            TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 385
P.swiecickii NRRL918              TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGT-CCCCCGA 383
P.kojigenum NRRL3442              TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 383
P.raistrickii NRRL2039            TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 383
P.soppii NRRL2023                 TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC-GT-CCTCCGA 384
P.canescens NRRL910               TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGTCTC-GT-CCCCCTT 383
P.atrovenetum NRRL2571            TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGTCTC-GT-CCCCCTC 384
P.canescens NRRL2147              TCATTGCTGCCCTCCAGCCCGGCTGGTGTGTTGGGCCCC-G-CCCCCCTT 385
P.waksmanii NRRL777               TCATTGCTGCCCTCCAGCCCGGCTGGTGTGTTGGGCCCC-G-CCCCCCTT 385
P.miczynskii NRRL1077             TCATTGCTGCCCTCCAGCCCGGCTGGTGTGTTGGGCCCC-G-CCCCCCTT 385
Eu.shearii NRRL715                TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC-GTCCCCCCCC 384
P.roseopurpureum NRRL733          TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCCGT-CCCCCCC 384
P.roseopurpureum NRRL2064         TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCCGT-CCCCCCC 384
P.sumatrense NRRL779              TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCCGTCCCCCCCT 387
P.paxilli NRRL2008                TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCTCGTCCCCCC-- 388
P.citrinum NRRL1841               TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC-GTCCCCCCC- 350
P.sartoryi NRRL783                TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC-GTCCCCCCC- 350
P.westlingii NRRL800              TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC-GTCCCCCCC- 350
P.charlesii NRRL778               TCATTACTGCCCTCAAGCCCGGCTTGTGTGTTGGGCG-CCG-CCCCCC-- 379
P.fellutanum NRRL746              TCATTACTGCCCTCAAGCCCGGCTTGTGTGTTGGGCG-CCG-CCCCCC-- 380
P.spinulosum NRRL728              TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCCCCC-- 382
P.spinulosum NRRL1750             TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCCCCC-- 382
P.thomii NRRL2077                 TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCCCCC-- 382
Eu.lapidosum NRRL718              TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCCCCC-- 382
P.thomii NRRL760                  TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCCCCC-- 382
P.purpurescens NRRL720            TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCCCCC-- 382
P.glabrum NRRL766                 TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCCCCC-- 382
P.asperosporum NRRL3411           TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCCCCC-- 382
P.lividum NRRL754                 TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCT-GTCCCCCTC- 383
P.adametzii NRRL736               TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCTCCGT-CCCCCA- 385
P.adametzii NRRL737               TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCTCCGT-CCCCCA- 385
P.bilaii  NRRL3391                TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCTCCGT-CCTCCC- 385
P.adametzioides NRRL3405          TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGTCTC-GT-CCCC--- 380
P.herquei NRRL1040                TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCTC-GTCCCCCCT- 385
P.sclerotiorum NRRL2074           TCATTGCTGCCCTCAAGCACGGCTTGTTTGTTGGGTCTT-GTTCCCCC-- 384
P.decumbens NRRL742               TCATTGCTGCCCTTAAGCACGGCTTATGTGTTGGGCCTCCGT-CCTCCT- 384
P.decumbens NRRL741               TCATTGCTGCCCTTAAGCACGGCTTATGTGTTGGGCCTCCGT-CCTCCT- 384
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                351      360       370       380       390       400
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759               TCATTGCTGCCCTTAAGCACGGCTTATGTGTTGGGCCTCCGT-CCTCCT- 384
P.corylophilum NRRL803           TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGT-CCTCCT- 383
P.corylophilum NRRL802           TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGT-CCTCCT- 383
P.corylophilum NRRL793           TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGT-CCTCCT- 383
P.melinii NRRL2041               TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGT-CCTCCT- 383
P.velutinum NRRL2069             TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGT-CCTCCT- 383
P.raciborskii NRRL2150           TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGT-CCTCCT- 383
P.restrictum NRRL25744           TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCTCCGT-CCTCCT- 384
P.restrictum NRRL1748            TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCTCCGT-CCTCCT- 384
P.citreonigrum NRRL761           TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGT-CCTCCT- 383
P.cinerascens NRRL748            TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGT-CCTCCT- 383
P.vinaceum NRRL739               TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCTCGT-CCCCC-- 383
P.oxalicum NRRL790               TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCTCG-CCCCCCGC 388
P.oxalicum NRRL787               TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCTCG-CCCCCCGC 388
P.donkii NRRL5562                TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCCG-CCCCCCGG 389
P.fuscum NRRL721                 TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCCG-CCCCCCGG 387
P.janthinellum NRRL2016          TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCCG-CCCCCCGG 385
P.raperi NRRL2674                TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-CCCG-CCCCCCGG 385
P.daleae NRRL922                 TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCCG-CCCCCCGG 386
P.ochrochloron NRRL926           TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-CCCG-CCCCCCGG 383
P.simplicissimum NRRL1075        TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-CCCG-CCCCCCGG 383
P.rolfsii NRRL1078               TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC-CCCG-CCCCCCGG 384
Eu.cinnamopurpureum NRRL3326     TCATTGCTGCCCTCAAGCACGGCTTGT-TGTTGGGTCTACGTCCCCCC-- 382
P.chermesinum NRRL735            TCATTTCTGCCCTCAAGCCCGGCTTGTGTGTTGGG-CCGCGTCCCCCC-- 380
P.clavariiformis NRRL2482        TCATTGCTACCCTCAAGCCCGGCTTGTGTGTTGGGTCGTCGTCCCCCCTC 390
                                  ***** ** ****  *** *****  * *******      *  ** *
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                401      410       420       430       440       450
                                  +--------+---------+---------+---------+---------+
P.camemberti NRRL874             TC-TCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 434
P.camemberti NRRL875             TC-TCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 434
P.echinulatum NRRL1151           TT-TCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 434
P.crustosum NRRL968              TC-TCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 434
P.viridicatum NRRL961            T--TCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 433
P.aurantiogriseum NRRL971        T--TCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 434
P.polonicum NRRL995              T--TCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 433
P.viridicatum NRRL958            T--CCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 433
P.chrysogenum NRRL821            T--CCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 433
P.chrysogenum NRRL807            T--CCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 433
P.griseoroseum NRRL820           T--CCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 433
P.chrysogenum NRRL824            T--CCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 433
P.griseoroseum NRRL832           T--CCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 433
P.griseofulvum NRRL734           T--TCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 432
P.griseofulvum NRRL2300          T--TCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 432
P.coprophilum NRRL13627          T--TCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 433
P.digitatum NRRL786              T--CCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 432
P.sclerotigenum NRRL3461         T--CCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 432
Eu.egyptiacum NRRL2090           T--CCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 433
Eu.crustaceum NRRL3332           T--CCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 433
P.expansum NRRL974               T--TCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 433
P.turbatum NRRL757               T--TCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 432
H.paradoxus NRRL2162             T--CCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 433
P.atramentosum NRRL795           T--CCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 433
P.swiecickii NRRL918             T--CCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 431
P.kojigenum NRRL3442             T--CCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 431
P.raistrickii NRRL2039           T--CCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 431
P.soppii NRRL2023                T--CCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT 432
P.canescens NRRL910              C--CCGGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 431
P.atrovenetum NRRL2571           C--CCGGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 432
P.canescens NRRL2147             C--CCGGGGGGGCGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 433
P.waksmanii NRRL777              C--CCGGGGGGGCGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 433
P.miczynskii NRRL1077            C--CCGGGGGGGCGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 433
Eu.shearii NRRL715               T-CCCGGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 433
P.roseopurpureum NRRL733         A--CCGGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 432
P.roseopurpureum NRRL2064        A--CCGGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 432
P.sumatrense NRRL779             CTGCCGGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 437
P.paxilli NRRL2008               -------GGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 431
P.citrinum NRRL1841              --GCCGGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 398
P.sartoryi NRRL783               --GCCGGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 398
P.westlingii NRRL800             --GCCGGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 398
P.charlesii NRRL778              ---C---GGGGGCGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 423
P.fellutanum NRRL746             ---C---GGGGGCGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 424
P.spinulosum NRRL728             -------GGGGACGGGCCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT 425
P.spinulosum NRRL1750            -------GGGGACGGGCCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT 425
P.thomii NRRL2077                -------GGGGACGGGTCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT 425
Eu.lapidosum NRRL718             -------GGGGACGGGTCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT 425
P.thomii NRRL760                 -------GGGGACGGGTCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT 425
P.purpurescens NRRL720           -------GGGGACGGGTCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT 425
P.glabrum NRRL766                -------GGGGACGGGTCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT 425
P.asperosporum NRRL3411          -------GGGGACGGGCCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT 425
P.lividum NRRL754                --TCC-GGGGGACAGGCCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT 430
P.adametzii NRRL736              --CCC-GGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGTGTCCGGTCCT 432
P.adametzii NRRL737              --CCC-GGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGTGTCCGGTCCT 432
P.bilaii  NRRL3391               --CCCGGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGTGTCCGGTCCT 433
P.adametzioides NRRL3405         --CCC-GGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGTGTCCGGTCCT 427
P.herquei NRRL1040               --CCGCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGTGTCCGGTCCT 433
P.sclerotiorum NRRL2074          -------GGGAACAGGCCCGAAAGGCAGTGGCGGCACCG--TCCGATCCT 425
P.decumbens NRRL742              T-TGG--GGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 431
P.decumbens NRRL741              T-TGG--GGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 431
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                401      410       420       430       440       450
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759                T-TGG--GGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 431
P.corylophilum NRRL803            T-CCC-GGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 431
P.corylophilum NRRL802            T-CCC-GGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 431
P.corylophilum NRRL793            T-CCC-GGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 431
P.melinii NRRL2041                T-CCC-GGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 431
P.velutinum NRRL2069              T-CCC-GGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 431
P.raciborskii NRRL2150            T-CCC-GGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 431
P.restrictum NRRL25744            C-CCG--GGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 431
P.restrictum NRRL1748             T-CCG-GGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 432
P.citreonigrum NRRL761            C-CCG--GGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 430
P.cinerascens NRRL748             C-CCG--GAGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 430
P.vinaceum NRRL739                --------GGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 425
P.oxalicum NRRL790                T-TCC-GGGGGGCGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 436
P.oxalicum NRRL787                T-TCC-GGGGGGCGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 436
P.donkii NRRL5562                 T-CTC-GGGGGGCGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 437
P.fuscum NRRL721                  T-CTC-GGGGGGCGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 435
P.janthinellum NRRL2016           C-TCCCGGGGGGCGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 434
P.raperi NRRL2674                 C-TCC-GGGGGGCGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 433
P.daleae NRRL922                  C-TCCCGGGGGGCGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 435
P.ochrochloron NRRL926            T-CCC-GGGGGGCGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 431
P.simplicissimum NRRL1075         T-CCC-GGGGGGCGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 431
P.rolfsii NRRL1078                T-TTC-GGGGGGCGGACCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 432
Eu.cinnamopurpureum NRRL3326      -------GGGGACGGGCCCGAAAGGCAGCGGCGGCATCGCGTCCGGTCCT 425
P.chermesinum NRRL735             -------GGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT 423
P.clavariiformis NRRL2482         CTGTGGGGGGGACGGGCCCGAAAGGCAGCGGCGGCACTGTGCCTGGTCCT 440
                                           *  * *  *********** *******  *    * * ****
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                451       460       470       480       490       500
                                  +---------+---------+---------+---------+---------+
P.camemberti NRRL874              CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 482
P.camemberti NRRL875              CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 482
P.echinulatum NRRL1151            CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 482
P.crustosum NRRL968               CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 482
P.viridicatum NRRL961             CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 481
P.aurantiogriseum NRRL971         CGAGCGTATGGG-GCTTTGTCACCCGCTCC-GTAGGCCCGGCCGGCGCTT 482
P.polonicum NRRL995               CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 481
P.viridicatum NRRL958             CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 481
P.chrysogenum NRRL821             CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 481
P.chrysogenum NRRL807             CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 481
P.griseoroseum NRRL820            CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 481
P.chrysogenum NRRL824             CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 481
P.griseoroseum NRRL832            CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 481
P.griseofulvum NRRL734            CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 480
P.griseofulvum NRRL2300           CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 480
P.coprophilum NRRL13627           CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 481
P.digitatum NRRL786               CGAGCGTATGGG-GCTTTGTCACCCGCTCC-GTAGGCCCGGCCGGCGCCT 480
P.sclerotigenum NRRL3461          CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCT 480
Eu.egyptiacum NRRL2090            CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 481
Eu.crustaceum NRRL3332            CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 481
P.expansum NRRL974                CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 481
P.turbatum NRRL757                CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 480
H.paradoxus NRRL2162              CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 481
P.atramentosum NRRL795            CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 481
P.swiecickii NRRL918              CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 479
P.kojigenum NRRL3442              CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 479
P.raistrickii NRRL2039            CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 479
P.soppii NRRL2023                 CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 480
P.canescens NRRL910               CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 479
P.atrovenetum NRRL2571            CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGGCCGGCCGGCGCCT 480
P.canescens NRRL2147              CGAGCGTATGGG-GCTTTGTCACCCGCTCTTGTAGGCCCGGCCGGCGTCA 482
P.waksmanii NRRL777               CGAGCGTATGGG-GCTTTGTCACCCGCTCTTGTAGGCCCGGCCGGCGTCA 482
P.miczynskii NRRL1077             CGAGCGTATGGG-GCTTTGTCACCCGCTCTTGTAGGCCCGGCCGGCGCCA 482
Eu.shearii NRRL715                CGAGCGTATGGG-GCTTTGTCACCCGCTCTTGTAGGCCCGGCCGGCGCTT 482
P.roseopurpureum NRRL733          CGAGCGTATGGG-GCTCTGTCACCCGCTCTTGTAGGCCCGGCCGGCGCCA 481
P.roseopurpureum NRRL2064         CGAGCGTATGGG-GCTCTGTCACCCGCTCTTGTAGGCCCGGCCGGCGCCA 481
P.sumatrense NRRL779              CGAGCGTATGGG-GCTTCGTCACCCGCTCTTGTAGGCCCGGCCGGCGCCA 486
P.paxilli NRRL2008                CGAGCGTATGGG-GCTTCGTCACCCGCTCGT-TAGGCCCGGCCGGCGCCA 479
P.citrinum NRRL1841               CGAGCGTATGGG-GCTTCGTCACCCGCTCTAGTAGGCCCGGCCGGCGCCA 447
P.sartoryi NRRL783                CGAGCGTATGGG-GCTTCGTCACCCGCTCTAGTAGGCCCGGCCGGCGCCA 447
P.westlingii NRRL800              CGAGCGTATGGG-GCTTCGTCACCCGCTCTAGTAGGCCCGGCCGGCGCCA 447
P.charlesii NRRL778               CGAGCGTATGGG-GCTTTGTCACCCGCCC--GTAGGCCCGGCCGGCGCCC 470
P.fellutanum NRRL746              CGAGCGTATGGG-GCTTTGTCACCCGCCC--GTAGGCCCGGCCGGCGCCC 471
P.spinulosum NRRL728              CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCA 473
P.spinulosum NRRL1750             CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCA 473
P.thomii NRRL2077                 CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCA 473
Eu.lapidosum NRRL718              CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCA 473
P.thomii NRRL760                  CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCA 473
P.purpurescens NRRL720            CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCA 473
P.glabrum NRRL766                 CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCA 473
P.asperosporum NRRL3411           CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCA 473
P.lividum NRRL754                 CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCA 478
P.adametzii NRRL736               CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCT 480
P.adametzii NRRL737               CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCT 480
P.bilaii  NRRL3391                CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTG 481
P.adametzioides NRRL3405          CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCT 475
P.herquei NRRL1040                CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCT 481
P.sclerotiorum NRRL2074           CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 473
P.decumbens NRRL742               CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGTCCGGCCGGCGCCT 479
P.decumbens NRRL741               CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGTCCGGCCGGCGCCT 479
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                451      460       470       480       490       500
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759               CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGTCCGGCCGGCGCCT 479
P.corylophilum NRRL803           CGAGCGTATGGG-GCTTTGTCACCCGCTCTTGTAGGCCCGGCCGGCGCTT 480
P.corylophilum NRRL802           CGAGCGTATGGG-GCTTTGTCACCCGCTCTTGTAGGCCCGGCCGGCGCTT 480
P.corylophilum NRRL793           CGAGCGTATGGG-GCTTTGTCACCCGCTCTTGTAGGCCCGGCCGGCGCTT 480
P.melinii NRRL2041               CGAGCGTATGGG-GCTTCGTCTTCCGCTCTTGTAGGCCCGGCCGGCGCTT 480
P.velutinum NRRL2069             CGAGCGTATGGG-GCTTCGTCTTCCGCTCTTGTAGGCCCGGCCGGCGCTT 480
P.raciborskii NRRL2150           CGAGCGTATGGG-GCTTCGTCTTCCGCTCTTGTAGGCCCGGCCGGCGCTT 480
P.restrictum NRRL25744           CGAGCGTATGGG-GCTTCGTCACCCGCTCTTGTAGGCCCGGCCGGCGCTT 480
P.restrictum NRRL1748            CGAGCGTATGGG-GCTTCGTCACCCGCTCTTGTAGGCCCGGCCGGCGCTT 481
P.citreonigrum NRRL761           CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGCCCGGCCGGCGCTT 478
P.cinerascens NRRL748            CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGTCCGGCCGGCGCTT 478
P.vinaceum NRRL739               CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGCCCGGCCGGCGTCT 473
P.oxalicum NRRL790               CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCC 484
P.oxalicum NRRL787               CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCC 484
P.donkii NRRL5562                CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCC 485
P.fuscum NRRL721                 CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAAGCCCGGCCGGCGCCC 483
P.janthinellum NRRL2016          CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCC 482
P.raperi NRRL2674                CGAGCGTATGGG-GCTTCGTCACCCGCTCC-GTAGGCCCGGCCGGCGCCC 481
P.daleae NRRL922                 CGAGCGTATGGG-GCTTTGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCC 483
P.ochrochloron NRRL926           CGAGCGTATGGG-GCTTTGTCACCCGCTCC-GTAGGCCCGGCCGGCGCCC 479
P.simplicissimum NRRL1075        CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCC 479
P.rolfsii NRRL1078               CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGCCCGGCCGGCGCCC 480
Eu.cinnamopurpureum NRRL3326     CGAGCGTATGGG-GCTTCGTCACCCGCTCTTGTAGGCCCGGCCGGCGCCA 474
P.chermesinum NRRL735            CGAGCGTATGGG-GCTTTGTCACCCGCTCTTGCAGGCCCGGCCGGCGCCA 472
P.clavariiformis NRRL2482        CGAGCGTATGGGAGCTTTGTCACCCGCTCT-GTAGGCCAGGCCGGCGCCT 489
                                 ************ ***  ***  **** *    * * * ********
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                501      510       520       530       540       550
                                  +--------+---------+---------+---------+---------+
P.camemberti NRRL874              --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 524
P.camemberti NRRL875              --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 524
P.echinulatum NRRL1151            --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 524
P.crustosum NRRL968               --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 524
P.viridicatum NRRL961             --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.aurantiogriseum NRRL971         --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 524
P.polonicum NRRL995               --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.viridicatum NRRL958             --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.chrysogenum NRRL821             --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.chrysogenum NRRL807             --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.griseoroseum NRRL820            --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.chrysogenum NRRL824             --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.griseoroseum NRRL832            --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.griseofulvum NRRL734            --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 522
P.griseofulvum NRRL2300           --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 522
P.coprophilum NRRL13627           --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.digitatum NRRL786               --GCCGATCAAC---CCCAAATT-TTTAATCCAGGTTGACCTCGGATCAG 524
P.sclerotigenum NRRL3461          --GCCGATCAAC---CCCAA-TT-TTTTATCCAGGTTGACCTCGGATCAG 523
Eu.egyptiacum NRRL2090            --GCCGATCAAC---CCAAA--C-TTCTAT--AGGTTGACCTCGGATCAG 521
Eu.crustaceum NRRL3332            --GCCGATCAAC---CCCAA--T-TTTTAT--AGGTTGACCTCGGATCAG 521
P.expansum NRRL974                --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.turbatum NRRL757                --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 522
H.paradoxus NRRL2162              --GCCGATCAAC---CAAAT----TTTTATCCAGGTTGACCTCGGATCAG 522
P.atramentosum NRRL795            --GCCGATCAAC---CAAAA----TTTTTTCCAGGTTGACCTCGGATCAG 522
P.swiecickii NRRL918              --GCCGATCAAC---CAAAT----TTTTATCCAGGTTGACCTCGGATCAG 520
P.kojigenum NRRL3442              --GCCGATCAAC---CAAAT----TTTTATCCAGGTTGACCTCGGATCAG 520
P.raistrickii NRRL2039            --GCCGATCAAC---CAAAT----TTTTATCCAGGTTGACCTCGGATCAG 520
P.soppii NRRL2023                 --GCCGATCAAC---CAAAT----TTTT-TCCAGGTTGACCTCGGATCAG 520
P.canescens NRRL910               --GCCGATCAAC---CAAAA--C-TTTTTTCCAGGTTGACCTCGGATCAG 521
P.atrovenetum NRRL2571            --GCCGATCAAC---CACAA--A-TTTTTTCCAGGTTGACCTCGGATCAG 522
P.canescens NRRL2147              --GCCGACCCCC----TCAATCTATTTTTT-CAGGTTGACCTCGGATCAG 525
P.waksmanii NRRL777               --GCCGACCCCC----TCAATCTATTTTTT-CAGGTTGACCTCGGATCAG 525
P.miczynskii NRRL1077             --GCCGACCCCC----TCAATCTATTTTTT-CAGGTTGACCTCGGATCAG 525
Eu.shearii NRRL715                --GCCGACCCCC----TCAATCTATTTTT--CAGGTTGACCTCGGATCAG 524
P.roseopurpureum NRRL733          --GCCGACCCCCC---TCAATCTATTTTTT-CAGGTTGACCTCGGATCAG 525
P.roseopurpureum NRRL2064         --GCCGACCCCCC---TCAATCTATTTTTT-CAGGTTGACCTCGGATCAG 525
P.sumatrense NRRL779              --GCCGACCCCAA---CCCTAAATTTTTTT-CAGGTTGACCTCGGATCAG 530
P.paxilli NRRL2008                --GCCGACCCCC----CCTCAATCTTTAAC-CAGGTTGACCTCGGATCAG 522
P.citrinum NRRL1841               --GCCGACCCCCA---ACCTTTAATTATCT-CAGGTTGACCTCGGATCAG 491
P.sartoryi NRRL783                --GCCGACCCCCA---ACCTTTAATTATCT-CAGGTTGACCTCGGATCAG 491
P.westlingii NRRL800              --GCCGACCCCCA---ACCTTTAATTATCT-CAGGTTGACCTCGGATCAG 491
P.charlesii NRRL778               --GCCGACCCCC--CAACCTTTTTTTTT---CAGGTTGACCTCGGATCAG 513
P.fellutanum NRRL746              --GCCGACCCCCTCCAACCTTTTTTTTTTTTCAGGTTGACCTCGGATCAG 519
P.spinulosum NRRL728              --GCCGACA--AC---CCATCATCCTTT--TCAGGTTGACCTCGGATCAG 514
P.spinulosum NRRL1750             --GCCGACA--AC---CCATCATCCTTT--TCAGGTTGACCTCGGATCAG 514
P.thomii NRRL2077                 --GCCGACA--AC---CAATCATCCTTTTTTCAGGTTGACCTCGGATCAG 516
Eu.lapidosum NRRL718              --GCCGACA--AC---CAATCATCCTTTTTTCAGGTTGACCTCGGATCAG 516
P.thomii NRRL760                  --GCCGACA--AC---CAATCATCCTTTTTTCAGGTTGACCTCGGATCAG 516
P.purpurescens NRRL720            --GCCGACA--AC---CAATCATCCTTTTTTCAGGTTGACCTCGGATCAG 516
P.glabrum NRRL766                 --GCCGACA--AC---CAATCATCCTTTTTTCAGGTTGACCTCGGATCAG 516
P.asperosporum NRRL3411           --GCCGACA--AC---CCATCATCCTTT--TCAGGTTGACCTCGGATCAG 514
P.lividum NRRL754                 --GCCGACA--AC---CCATCATCCTTT--TCAGGTTGACCTCGGATCAG 519
P.adametzii NRRL736               --GCCGACC--CT---C-ATCATCCTTTTTTCAGGTTGACCTCGGATCAG 522
P.adametzii NRRL737               --GCCGACC--CT---C-ATCATCCTTTTTTCAGGTTGACCTCGGATCAG 522
P.bilaii  NRRL3391               --GCCGACC--CT---CCAACCCCATTTTTTCAGGTTGACCTCGGATCAG 524
P.adametzioides NRRL3405          --GTCGACC--CC---C-AATCTATTTTTTTCAGGTTGACCTCGGATCAG 517
P.herquei NRRL1040                TAGCCGACG--AC---ACAATCT-TTTTTTTCAGGTTGACCTCGGATCAG 525
P.sclerotiorum NRRL2074           --GCCGAC----C---CCAATCAATCTTTTTCAGGTTGACCTCGGATCAG 514
P.decumbens NRRL742               --GCCGAACA-CA---TCAATCTTTTTT-C-CAGGTTGACCTCGGATCAG 521
P.decumbens NRRL741               --GCCGAACA-CA---TCAATCTTTTTT-C-CAGGTTGACCTCGGATCAG 521
```

Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                501      510       520       530       540       550
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759                --GCCGAACA-CA---TCAATCTTTTTT-C-CAGGTTGACCTCGGATCAG 521
P.corylophilum NRRL803            --GCCGACAACCA---TCAATCTTTTTT---CAGGTTGACCTCGGATCAG 522
P.corylophilum NRRL802            --GCCGACAACCA---TCAATCTTTTTT---CAGGTTGACCTCGGATCAG 522
P.corylophilum NRRL793            --GCCGACAACCA---TCAATCTTTTTT---CAGGTTGACCTCGGATCAG 522
P.melinii NRRL2041                --GCCGACAACAA---TCAATCTTTTTT---CAGGTTGACCTCGGATCAG 522
P.velutinum NRRL2069              --GCCGACAACAA---TCAATCTTTTTT---CAGGTTGACCTCGGATCAG 522
P.raciborskii NRRL2150            --GCCGACAACAA---TCAATCTTTTTT-T-CAGGTTGACCTCGGATCAG 523
P.restrictum NRRL25744            --GCCGACA--CA---TCAATCTTTTTTTC-CAGGTTGACCTCGGATCAG 522
P.restrictum NRRL1748             --GCCGACA--CA---TCAATCTTTTTT-C-CAGGTTGACCTCGGATCAG 522
P.citreonigrum NRRL761            --GCCGACA--CA---TCAATCTTTTTT-C-CAGGTTGACCTCGGATCAG 519
P.cinerascens NRRL748             --GCCGACA--CA---TCAATCTTTTTT-T-CAGGTTGACCTCGGATCAG 519
P.vinaceum NRRL739                --GCCGACA-CCA---TCAATCTTTTTT-C-CAGGTTGACCTCGGATCAG 515
P.oxalicum NRRL790                --GCCGGCGAACA---C-CATCAATCTTAACCAGGTTGACCTCGGATCAG 528
P.oxalicum NRRL787                --GCCGGCGAACA---C-CATCAATCTTAACCAGGTTGACCTCGGATCAG 528
P.donkii NRRL5562                 --GCCGGCGACCC---C-AATCAATCTATC-CAGGTTGACCTCGGATCAG 528
P.fuscum NRRL721                  --GCCGGCAACCC---C-AATCAATCTATC-CAGGTTGACCTCGGATCAG 526
P.janthinellum NRRL2016           --GCCGGCGACCC---C-CCTCAATCTTTCTCAGGTTGACCTCGGATCAG 526
P.raperi NRRL2674                 --GCCGGCGACCC---C-CCTCAATCTTTCTCAGGTTGACCTCGGATCAG 525
P.daleae NRRL922                  --GCCGGCGACCC---C-CCTCAATCTTTC-CAGGTTGACCTCGGATCAG 526
P.ochrochloron NRRL926            --GCCGGCGACCC---CCAATCAATCTATC-CAGGTTGACCTCGGATCAG 523
P.simplicissimum NRRL1075         --GCCGGCGACCC---C-AATCAATCTATC-CAGGTTGACCTCGGATCAG 522
P.rolfsii NRRL1078                --GCCGGCGACCC---C-AATCAATCTATC-CAGGTTGACCTCGGATCAG 523
Eu.cinnamopurpureum NRRL3326      --GCCGAC----C---CCAACCATT-TTTCTCAGGTTGACCTCGGATCAG 514
P.chermesinum NRRL735             --GCCGAC----C---CCAACCATTCTTTCTCAGGTTGACCTCGGATCAG 513
P.clavariiformis NRRL2482         --GCCACAA-------CCA-T--TTTTTATCCAGGTTGACCTCGGATCAG 527
                                    * *                          ******************
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                551       560       570       580       590       600
                                  +--------+---------+---------+---------+---------+
P.camemberti NRRL874              GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 574
P.camemberti NRRL875              GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 574
P.echinulatum NRRL1151            GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 574
P.crustosum NRRL968               GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 574
P.viridicatum NRRL961             GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 573
P.aurantiogriseum NRRL971         GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 574
P.polonicum NRRL995               GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 573
P.viridicatum NRRL958             GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 573
P.chrysogenum NRRL821             GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 573
P.chrysogenum NRRL807             GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 573
P.griseoroseum NRRL820            GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 573
P.chrysogenum NRRL824             GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 573
P.griseoroseum NRRL832            GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 573
P.griseofulvum NRRL734            GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.griseofulvum NRRL2300           GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.coprophilum NRRL13627           GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 573
P.digitatum NRRL786               GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 574
P.sclerotigenum NRRL3461          GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 573
Eu.egyptiacum NRRL2090            GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 571
Eu.crustaceum NRRL3332            GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 571
P.expansum NRRL974                GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 573
P.turbatum NRRL757                GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
H.paradoxus NRRL2162              GTAGGGATACCCGCTCAACTTAAGCATATCAATGAGCGGAGGAAAAGAAA 572
P.atramentosum NRRL795            GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.swiecickii NRRL918              GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 570
P.kojigenum NRRL3442              GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 570
P.raistrickii NRRL2039            GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 570
P.soppii NRRL2023                 GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 570
P.canescens NRRL910               GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 571
P.atrovenetum NRRL2571            GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.canescens NRRL2147              GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 575
P.waksmanii NRRL777               GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 575
P.miczynskii NRRL1077             GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 575
Eu.shearii NRRL715                GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 574
P.roseopurpureum NRRL733          GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 575
P.roseopurpureum NRRL2064         GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 575
P.sumatrense NRRL779              GTAGGGATACCCGCTGAACTTAAGCATATCAATGAGCGGAGGAAAAGAAA 580
P.paxilli NRRL2008                GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.citrinum NRRL1841               GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 541
P.sartoryi NRRL783                GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 541
P.westlingii NRRL800              GTAGGGATACCCGCTGAACTTAAGCATATCAATGAGCGGAGGAAAAGAAA 541
P.charlesii NRRL778               GTAGGGATACCCGCTGAACTTAAGCATATCAATCAGCGGAGGAAAAGAAA 563
P.fellutanum NRRL746              GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 569
P.spinulosum NRRL728              GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 564
P.spinulosum NRRL1750             GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 564
P.thomii NRRL2077                 GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 566
Eu.lapidosum NRRL718              GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 566
P.thomii NRRL760                  GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 566
P.purpurescens NRRL720            GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 566
P.glabrum NRRL766                 GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 566
P.asperosporum NRRL3411           GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 564
P.lividum NRRL754                 GTAGGGATACCCGCTGAACTTAAGCATATCAATGAGCGGAGGAAAAGAAA 569
P.adametzii NRRL736               GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.adametzii NRRL737               GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.bilaii  NRRL3391                GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 574
P.adametzioides NRRL3405          GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 567
P.herquei NRRL1040                GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 575
P.sclerotiorum NRRL2074           GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 564
P.decumbens NRRL742               GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 571
P.decumbens NRRL741               GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 571
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                551      560       570       580       590       600
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759               GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 571
P.corylophilum NRRL803           GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.corylophilum NRRL802           GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.corylophilum NRRL793           GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.melinii NRRL2041               GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.velutinum NRRL2069             GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.raciborskii NRRL2150           GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 573
P.restrictum NRRL25744           GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.restrictum NRRL1748            GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.citreonigrum NRRL761           GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 569
P.cinerascens NRRL748            GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 569
P.vinaceum NRRL739               GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 565
P.oxalicum NRRL790               GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 578
P.oxalicum NRRL787               GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 578
P.donkii NRRL5562                GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 578
P.fuscum NRRL721                 GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 576
P.janthinellum NRRL2016          GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 576
P.raperi NRRL2674                GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 575
P.daleae NRRL922                 GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 576
P.ochrochloron NRRL926           GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 573
P.simplicissimum NRRL1075        GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.rolfsii NRRL1078               GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 573
Eu.cinnamopurpureum NRRL3326     GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 564
P.chermesinum NRRL735            GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 563
P.clavariiformis NRRL2482        GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 577
                                 *************** ***************** ****************
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                 601      610       620       630       640       650
                                   +--------+---------+---------+---------+---------+
P.camemberti NRRL874               CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 624
P.camemberti NRRL875               CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 624
P.echinulatum NRRL1151             CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 624
P.crustosum NRRL968                CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 624
P.viridicatum NRRL961              CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 623
P.aurantiogriseum NRRL971          CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 624
P.polonicum NRRL995                CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 623
P.viridicatum NRRL958              CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 623
P.chrysogenum NRRL821              CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 623
P.chrysogenum NRRL807              CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 623
P.griseoroseum NRRL820             CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 623
P.chrysogenum NRRL824              CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 623
P.griseoroseum NRRL832             CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 623
P.griseofulvum NRRL734             CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.griseofulvum NRRL2300            CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.coprophilum NRRL13627            CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 623
P.digitatum NRRL786                CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 624
P.sclerotigenum NRRL3461           CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 623
Eu.egyptiacum NRRL2090             CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 621
Eu.crustaceum NRRL3332             CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 621
P.expansum NRRL974                 CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 623
P.turbatum NRRL757                 CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
H.paradoxus NRRL2162               CCAACAGGGATTGCCCCACTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.atramentosum NRRL795             CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.swiecickii NRRL918               CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 620
P.kojigenum NRRL3442               CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 620
P.raistrickii NRRL2039             CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 620
P.soppii NRRL2023                  CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 620
P.canescens NRRL910                CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 621
P.atrovenetum NRRL2571             CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.canescens NRRL2147               CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 625
P.waksmanii NRRL777                CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 625
P.miczynskii NRRL1077              CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 625
Eu.shearii NRRL715                 CCAACCGGGATTACCCTAGTAACGGCGAGTGAAGCGGTAAGAGCTCAAAT 624
P.roseopurpureum NRRL733           CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 625
P.roseopurpureum NRRL2064          CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 625
P.sumatrense NRRL779               CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 630
P.paxilli NRRL2008                 CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.citrinum NRRL1841                CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 591
P.sartoryi NRRL783                 CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 591
P.westlingii NRRL800               CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 591
P.charlesii NRRL778                CCAACAGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 613
P.fellutanum NRRL746               CCAACAGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 619
P.spinulosum NRRL728               CCAACAGGGATTACCTCAGTAACGGCGAGTGAAGCGGTAAGAGCTCAAAT 614
P.spinulosum NRRL1750              CCAACAGGGATTACCTCAGTAACGGCGAGTGAAGCGGTAAGAGCTCAAAT 614
P.thomii NRRL2077                  CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 616
Eu.lapidosum NRRL718               CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 616
P.thomii NRRL760                   CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 616
P.purpurescens NRRL720             CCAACAGGGATTACCTCAGTAACGGCGAGTGAAGCGGTAAGAGCTCAAAT 616
P.glabrum NRRL766                  CCAACAGGGATTACCTCAGTAACGGCGAGTGAAGCGGTAAGAGCTCAAAT 616
P.asperosporum NRRL3411            CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 614
P.lividum NRRL754                  CCAACAGGGATTACCTCAGTAACGGCGAGTGAAGCGGTAAGAGCTCAAAT 619
P.adametzii NRRL736                CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.adametzii NRRL737                CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.bilaii  NRRL3391                 CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 624
P.adametzioides NRRL3405           CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 617
P.herquei NRRL1040                 CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 625
P.sclerotiorum NRRL2074            CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 614
P.decumbens NRRL742                CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 621
P.decumbens NRRL741                CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 621
```

Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                601      610       620       630       640       650
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759               CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 621
P.corylophilum NRRL803           CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.corylophilum NRRL802           CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.corylophilum NRRL793           CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.melinii NRRL2041               CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.velutinum NRRL2069             CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.raciborskii NRRL2150           CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 623
P.restrictum NRRL25744           CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.restrictum NRRL1748            CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.citreonigrum NRRL761           CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 619
P.cinerascens NRRL748            CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 619
P.vinaceum NRRL739               CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 615
P.oxalicum NRRL790               CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 628
P.oxalicum NRRL787               CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 628
P.donkii NRRL5562                CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 628
P.fuscum NRRL721                 CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 626
P.janthinellum NRRL2016          CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 626
P.raperi NRRL2674                CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 625
P.daleae NRRL922                 CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 626
P.ochrochloron NRRL926           CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 623
P.simplicissimum NRRL1075        CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.rolfsii NRRL1078               CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 623
Eu.cinnamopurpureum NRRL3326     CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 614
P.chermesinum NRRL735            CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 613
P.clavariiformis NRRL2482        CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 627
                                  ***** ****** **  * ***************** ************
```

Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                651       660       670       680       690       700
                                  +--------+---------+---------+---------+---------+
P.camemberti NRRL874              TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 674
P.camemberti NRRL875              TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 674
P.echinulatum NRRL1151            TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 674
P.crustosum NRRL968               TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 674
P.viridicatum NRRL961             TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 673
P.aurantiogriseum NRRL971         TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 674
P.polonicum NRRL995               TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 673
P.viridicatum NRRL958             TTGAAAGCTGGCTCCTTCGGGGCCCGCATTGTAATTTGCAGAGGATGCTT 673
P.chrysogenum NRRL821             TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGTAGAGGATGCTT 673
P.chrysogenum NRRL807             TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGTAGAGGATGCTT 673
P.griseoroseum NRRL820            TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGTAGAGGATGCTT 673
P.chrysogenum NRRL824             TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGTAGAGGATGCTT 673
P.griseoroseum NRRL832            TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGTAGAGGATGCTT 673
P.griseofulvum NRRL734            TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGTAGAGGATGCTT 672
P.griseofulvum NRRL2300           TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGTAGAGGATGCTT 672
P.coprophilum NRRL13627           TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGTAGAGGATGCTT 673
P.digitatum NRRL786               TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 674
P.sclerotigenum NRRL3461          TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 673
Eu.egyptiacum NRRL2090            TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 671
Eu.crustaceum NRRL3332            TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 671
P.expansum NRRL974                TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 673
P.turbatum NRRL757                TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
H.paradoxus NRRL2162              TTGAAAGCTGACTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.atramentosum NRRL795            TTGAAAGCTGACTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.swiecickii NRRL918              TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 670
P.kojigenum NRRL3442              TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 670
P.raistrickii NRRL2039            TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 670
P.soppii NRRL2023                 TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 670
P.canescens NRRL910               TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 671
P.atrovenetum NRRL2571            TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATACTT 672
P.canescens NRRL2147              TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 675
P.waksmanii NRRL777               TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 675
P.miczynskii NRRL1077             TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGTAGAGGATGCTT 675
Eu.shearii NRRL715                TTGAAAGCTGGCCCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 674
P.roseopurpureum NRRL733          TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 675
P.roseopurpureum NRRL2064         TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 675
P.sumatrense NRRL779              TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 680
P.paxilli NRRL2008                TTGAAAGCTGGCCCCTGCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.citrinum NRRL1841               TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 641
P.sartoryi NRRL783                TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 641
P.westlingii NRRL800              TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 641
P.charlesii NRRL778               TTGAAAGCTGGCCCCCTCGGGGCCCGCATTGTAATTTGCAGAGGATGCTT 663
P.fellutanum NRRL746              TTGAAAGCTGGCCCCCTCGGGGCCCGCATTGTAATTTGCAGAGGATGCTT 669
P.spinulosum NRRL728              TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT 664
P.spinulosum NRRL1750             TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT 664
P.thomii NRRL2077                 TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT 666
Eu.lapidosum NRRL718              TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT 666
P.thomii NRRL760                  TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT 666
P.purpurescens NRRL720            TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT 666
P.glabrum NRRL766                 TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT 666
P.asperosporum NRRL3411           TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 664
P.lividum NRRL754                 TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT 669
P.adametzii NRRL736               TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.adametzii NRRL737               TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.bilaii  NRRL3391                TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 674
P.adametzioides NRRL3405          TTGAAAGCTGGCTCCTTCGGGGCCCGCATTGTAATTTGCAGAGGATGCTT 667
P.herquei NRRL1040                TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 675
P.sclerotiorum NRRL2074           TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT 664
P.decumbens NRRL742               TTGAAAGCTGGCCCCCTTGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 671
P.decumbens NRRL741               TTGAAAGCTGGCCCCCTTGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 671
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                651      660       670       680       690       700
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759                TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 671
P.corylophilum NRRL803            TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.corylophilum NRRL802            TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.corylophilum NRRL793            TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.melinii NRRL2041                TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.velutinum NRRL2069              TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.raciborskii NRRL2150            TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 673
P.restrictum NRRL25744            TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.restrictum NRRL1748             TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.citreonigrum NRRL761            TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 669
P.cinerascens NRRL748             TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 669
P.vinaceum NRRL739                TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 665
P.oxalicum NRRL790                TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 678
P.oxalicum NRRL787                TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 678
P.donkii NRRL5562                 TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 678
P.fuscum NRRL721                  TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 676
P.janthinellum NRRL2016           TTGAAAGCTGGCCCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 676
P.raperi NRRL2674                 TTGAAAGCTGGCCCCTTCGGGGTCCGCGTTGTAATTTGCAGAGGATGCTT 675
P.daleae NRRL922                  TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 676
P.ochrochloron NRRL926            TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 673
P.simplicissimum NRRL1075         TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.rolfsii NRRL1078                TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 673
Eu.cinnamopurpureum NRRL3326      TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 664
P.chermesinum NRRL735             TTGAAAGCTGGCCCCCTCGGGGTCCGCATTGTAATTTGCAGAGGATGCTT 663
P.clavariiformis NRRL2482         TTGAAATCTGGCGTCTTTGGCGTCCGAGTTGTAATTTGCAGAGGATGCTT 677
                                  ****** *** *  *   ** * ***  ********** *******  **
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                701      710       720       730       740       750
                                  +--------+---------+---------+---------+---------+
P.camemberti NRRL874              CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 724
P.camemberti NRRL875              CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 724
P.echinulatum NRRL1151            CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 724
P.crustosum NRRL968               CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 724
P.viridicatum NRRL961             CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 723
P.aurantiogriseum NRRL971         CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 724
P.polonicum NRRL995               CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 723
P.viridicatum NRRL958             CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 723
P.chrysogenum NRRL821             CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 723
P.chrysogenum NRRL807             CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 723
P.griseoroseum NRRL820            CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 723
P.chrysogenum NRRL824             CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 723
P.griseoroseum NRRL832            CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 723
P.griseofulvum NRRL734            CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 722
P.griseofulvum NRRL2300           CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 722
P.coprophilum NRRL13627           CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 723
P.digitatum NRRL786               CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 724
P.sclerotigenum NRRL3461          CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 723
Eu.egyptiacum NRRL2090            CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 721
Eu.crustaceum NRRL3332            CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 721
P.expansum NRRL974                CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 723
P.turbatum NRRL757                CGGGAGCGGTCCCCATCTAAGTTCCCTGGAACGGGACGTCATAGAGGGTG 722
H.paradoxus NRRL2162              CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 722
P.atramentosum NRRL795            CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 722
P.swiecickii NRRL918              CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 720
P.kojigenum NRRL3442              CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 720
P.raistrickii NRRL2039            CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 720
P.soppii NRRL2023                 CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGACGTCATAGAGGGTG 720
P.canescens NRRL910               CGGGAGCGGTCCCCATCTAAGTTCCCTGGAACGGGACGTCATAGAGGGTG 721
P.atrovenetum NRRL2571            CGGGAGCGGTCCCCATCTAAGTTCCCTGGAACGGGACGTCATAGAGGGTG 722
P.canescens NRRL2147              CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 725
P.waksmanii NRRL777               CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 725
P.miczynskii NRRL1077             CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 725
Eu.shearii NRRL715                CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 724
P.roseopurpureum NRRL733          CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 725
P.roseopurpureum NRRL2064         CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 725
P.sumatrense NRRL779              CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 730
P.paxilli NRRL2008                CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 722
P.citrinum NRRL1841               CGGGAACGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 691
P.sartoryi NRRL783                CGGGAACGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 691
P.westlingii NRRL800              CGGGAACGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 691
P.charlesii NRRL778               CGGGCGTGGCCCCTGTCTAAGTGCCCTGGAACGGGCCGTCAGAGAGGGTG 713
P.fellutanum NRRL746              CGGGCGTGGCCCCTGTCTAAGTGCCCTGGAACGGGCCGTCAGAGAGGGTG 719
P.spinulosum NRRL728              CGGGAGCAGCCCCCATCTAAGTGTCCTGGAACGGACCGTCATAGAGGGTG 714
P.spinulosum NRRL1750             CGGGAGCAGCCCCCATCTAAGTGTCCTGGAACGGACCGTCATAGAGGGTG 714
P.thomii NRRL2077                 CGGGAGCAGCCCCCATCTAAGTGTCCTGGAACGGACCGTCATAGAGGGTG 716
Eu.lapidosum NRRL718              CGGGAGCAGCCCCCATCTAAGTGTCCTGGAACGGACCGTCATAGAGGGTG 716
P.thomii NRRL760                  CGGAAGCAGCCCCCATCTAAGTGTCCTGGAACGGACCGTCATAGAGGGTG 716
P.purpurescens NRRL720            CGGGAGCAGCCCCCATCTAAGTGTCCTGGAACGGACCGTCATAGAGGGTG 716
P.glabrum NRRL766                 CGGGAGCAGCCCCCATCTAAGTGTCCTGGAACGGACCGTCATAGAGGGTG 716
P.asperosporum NRRL3411           CGGGAGCAGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 714
P.lividum NRRL754                 CGGAAGCAGCCCCCATCTAAGTACCCTGGAACGGGTCGTCATAGAGGGTG 719
P.adametzii NRRL736               CGGGAGCGGCCCCCATCTAAGTGCCCTGGAACGGGCTGTCATAGAGGGTG 722
P.adametzii NRRL737               CGGGAGCGGCCCCCATCTAAGTGCCCTGGAACGGGCTGTCATAGAGGGTG 722
P.bilaii  NRRL3391                CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGCTGTCATAGAGGGTG 724
P.adametzioides NRRL3405          CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGCTGTCATAGAGGGTG 717
P.herquei NRRL1040                CGGGAGCGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 725
P.sclerotiorum NRRL2074           CGGGAGTGGCCCCCATCTAAGTGTCCTGGAACGGACCGTCATAGAGGGTG 714
P.decumbens NRRL742               CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 721
P.decumbens NRRL741               CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 721
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                701      710       720       730       740       750
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759                CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 721
P.corylophilum NRRL803            CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 722
P.corylophilum NRRL802            CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 722
P.corylophilum NRRL793            CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 722
P.melinii NRRL2041                CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 722
P.velutinum NRRL2069              CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 722
P.raciborskii NRRL2150            CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 723
P.restrictum NRRL25744            CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 722
P.restrictum NRRL1748             CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 722
P.citreonigrum NRRL761            CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 719
P.cinerascens NRRL748             CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 719
P.vinaceum NRRL739                CGGGAGCGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 715
P.oxalicum NRRL790                CGGGAGCGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 728
P.oxalicum NRRL787                CGGGAGCGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 728
P.donkii NRRL5562                 CGGGAGCGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 728
P.fuscum NRRL721                  CGGGAGCGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 726
P.janthinellum NRRL2016           CGGGAGCGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 726
P.raperi NRRL2674                 CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 725
P.daleae NRRL922                  CGGGAGCGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 726
P.ochrochloron NRRL926            CGGGAGTGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 723
P.simplicissimum NRRL1075         CGGGAGTGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 722
P.rolfsii NRRL1078                CGGGAGTGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 723
Eu.cinnamopurpureum NRRL3326      CGGGAGCGGTCCCCATCTAAGTACCCTGGAACGGGTCGTCATAGAGGGTG 714
P.chermesinum NRRL735             CGGAGGCAGCCCCCGTCTAAGTACCCTGGAACGGGTCGTCATAGAGGGTG 713
P.clavariiformis NRRL2482         CGGATACAGCCCCTGTCTAAGTGCCCTGGAACGGGCCGTCGGAGAGGGTG 727
                                  ***     * ***  ********  *********   ***  ********
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                751      760       770       780       790       800
                                  +--------+---------+---------+---------+---------+
P.camemberti NRRL874              AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 774
P.camemberti NRRL875              AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 774
P.echinulatum NRRL1151            AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 774
P.crustosum NRRL968               AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 774
P.viridicatum NRRL961             AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 773
P.aurantiogriseum NRRL971         AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 774
P.polonicum NRRL995               AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 773
P.viridicatum NRRL958             AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 773
P.chrysogenum NRRL821             AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 773
P.chrysogenum NRRL807             AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 773
P.griseoroseum NRRL820            AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 773
P.chrysogenum NRRL824             AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 773
P.griseoroseum NRRL832            AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 773
P.griseofulvum NRRL734            AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 772
P.griseofulvum NRRL2300           AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 772
P.coprophilum NRRL13627           AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 773
P.digitatum NRRL786               AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 774
P.sclerotigenum NRRL3461          AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 773
Eu.egyptiacum NRRL2090            AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 771
Eu.crustaceum NRRL3332            AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 771
P.expansum NRRL974                AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 773
P.turbatum NRRL757                AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 772
H.paradoxus NRRL2162              AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 772
P.atramentosum NRRL795            AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 772
P.swiecickii NRRL918              AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 770
P.kojigenum NRRL3442              AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 770
P.raistrickii NRRL2039            AGAATCCCGTATGGGATGGGGTGTCCGCGCCCATGTGAAGCTCCTTCGAC 770
P.soppii NRRL2023                 AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 770
P.canescens NRRL910               AAAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 771
P.atrovenetum NRRL2571            AAAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGTTCCTTCGAC 772
P.canescens NRRL2147              AGAATCCCGTATGGGATGGGGTGCCCGCGCCCGTGTGAAGCTCCTTCGAC 775
P.waksmanii NRRL777               AGAATCCCGTATGGGATGGGGTGCCCGCGCCCGTGTGAAGCTCCTTCGAC 775
P.miczynskii NRRL1077             AGAATCCCGTATGGGATGGGGTGCCCGCGCCCGTGTGAAGCTCCTTCGAC 775
Eu.shearii NRRL715                AGAATCCCGTATGGGATGGGGTGCCCGCGCCCGTGTGAAGCTCCTTCGAC 774
P.roseopurpureum NRRL733          AGAATCCCGTATGGGATGGGGTGCCCGCGCCCGTGTGAAGCTCCTTCGAC 775
P.roseopurpureum NRRL2064         AGAATCCCGTATGGGATGGGGTGCCCGCGCCCGTGTGAAGCTCCTTCGAC 775
P.sumatrense NRRL779              AGAATCCCGTCTGGGATGGGGTGCCCGCGCCCGTGTGAAGCTCCTTCGAC 780
P.paxilli NRRL2008                AGAATCCCGTATGGGATGGGGTGCCCGCGCCCGTGTGAAGCTCCTTCGAC 772
P.citrinum NRRL1841               AGAATCCCGTCTGGGATGGGGTGGCCGCGCCCGTGTGAAGCTCCTTCGAC 741
P.sartoryi NRRL783                AGAATCCCGTCTGGGATGGGGTGGCCGCGCCCGTGTGAAGCTCCTTCGAC 741
P.westlingii NRRL800              AGAATCCCGTCTGGGATGGGGTGGCCGCGCCCGTGTGAAGCTCCTTCGAC 741
P.charlesii NRRL778               AGAATCCCGTATGGGATGGGGTGCCCACGCCCGTGTGAAGCTCCTTCGAC 763
P.fellutanum NRRL746              AGAATCCCGTATGGGATGGGGTGCCCACGCCCGTGTGAAGCTCCTTCGAC 769
P.spinulosum NRRL728              AGAATCCCGTATGGGATGGGGTGTCTGCGCCCATGTGAAACTCCTTCGAC 764
P.spinulosum NRRL1750             AGAATCCCGTATGGGATGGGGTGTCTGCGCCCATGTGAAACTCCTTCGAC 764
P.thomii NRRL2077                 AGAATCCCGTATGGGATGGGGTGTCTGCGCCCATGTGAAACTCCTTCGAC 766
Eu.lapidosum NRRL718              AGAATCCCGTATGGGATGGGGTGTCTGCGCCCATGTGAAACTCCTTCGAC 766
P.thomii NRRL760                  AGAATCCCGTATGGGATGGGGTGTCTGCGTCCATGTGAAACTCCTTCGAC 766
P.purpurescens NRRL720            AGAATCCCGTATGGGATGGGGTGTCTGCGCCCATGTGAAACTCCTTCGAC 766
P.glabrum NRRL766                 AGAATCCCGTATGGGATGGGGTGTCTGCGCCCATGTGAAACTCCTTCGAC 766
P.asperosporum NRRL3411           AAAATCCCGTATGGGATGGGGTGTCTGCGCCCATGTGAAGCTCCTTCGAC 764
P.lividum NRRL754                 AGAATCCCGTATGGGATGGGGTGTCTGCGCCCATGTGAAACTCCTTCGAC 769
P.adametzii NRRL736               AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 772
P.adametzii NRRL737               AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 772
P.bilaii  NRRL3391                AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 774
P.adametzioides NRRL3405          AGAATCCCGTATGGGATGGGGTGCCCGCGCCCGTGTGAAGCTCCTTCGAC 767
P.herquei NRRL1040                AGAATCCCGTATGGGATGGGGTGCCCGCGCCCGTGTGAAGCTCCTTCGAC 775
P.sclerotiorum NRRL2074           AGAATCCCGTATGGGATGGGGTGCCCACGCCCGTGTGAAACTCCTTCGAC 764
P.decumbens NRRL742               AGAATCCCGTATGGGATGGGGTGTCCGCGACCATGTGAAGCTCCTTCGAC 771
P.decumbens NRRL741               AGAATCCCGTATGGGATGGGGTGTCCGCGACCATGTGAAGCTCCTTCGAC 771
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                751      760       770       780       790       800
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759               AGAATCCCGTATGGGATGGGGTGTCCGCGACCATGTGAAGCTCCTTCGAC 771
P.corylophilum NRRL803           AGAATCCCGTATGGGATGGGGTGTCCGCGACCATGTGAAGCTCCTTCGAC 772
P.corylophilum NRRL802           AGAATCCCGTATGGGATGGGGTGTCCGCGACCATGTGAAGCTCCTTCGAC 772
P.corylophilum NRRL793           AGAATCCCGTATGGGATGGGGTGTCCGCGACCATGTGAAGCTCCTTCGAC 772
P.melinii NRRL2041               AGAATCCCGTATGGGATGGGGTGTCCGCGACCATGTGAAGCTCCTTCAAC 772
P.velutinum NRRL2069             AGAATCCCGTATGGGATGGGGTGTCCGCGACCATGTGAAGCTCCTTCAAC 772
P.raciborskii NRRL2150           AGAATCCCGTATGGGATGGGGTGTCCGCGACCATGTGAAGCTCCTTCAAC 773
P.restrictum NRRL25744           AGAATCCCGTATGGGATGGGGTGTCCGCGACCATGTGAAGCTCCTTCAAC 772
P.restrictum NRRL1748            AGAATCCCGTATGGGATGGGGTGTCCGCGACCATGTGAAGCTCCTTCAAC 772
P.citreonigrum NRRL761           AGAATCCCGTATGGGATGGGGTGTCCGCGACCATGTGAAGCTCCTTCGAC 769
P.cinerascens NRRL748            AGAATCCCGTATGGGATGGGGTGTCCGCGACCATGTGAAGCTCCTTCGAC 769
P.vinaceum NRRL739               AGAATCCCGTCTGGGATGGGGTGCCCGCGACCATGTGAAGCTCCTTCGAC 765
P.oxalicum NRRL790               AAAATCCCGTCTGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 778
P.oxalicum NRRL787               AAAATCCCGTCTGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 778
P.donkii NRRL5562                AGAATCCCGTCTGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 778
P.fuscum NRRL721                 AGAATCCCGTCTGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 776
P.janthinellum NRRL2016          AGAATCCCGTCTGGGATGGGGTGCCCGCGCCCGTGTGAAGCTCCTTCGAC 776
P.raperi NRRL2674                AGAATCCCGTCTGGGATGGGGTGCCCGCGCCCGTGTGAAGCTCCTTCGAC 775
P.daleae NRRL922                 AGAATCCCGTCTGGGATGGGGTGCCCGCGCCCGTGTGAAGCTCCTTCGAC 776
P.ochrochloron NRRL926           AGAATCCCGTCTGGGATGGGGTGCCCACGCCCGTGTGAAGCTCCTTCGAC 773
P.simplicissimum NRRL1075        AGAATCCCGTCTGGGATGGGGTGCCCACGCCCGTGTGAAGCTCCTTCGAC 772
P.rolfsii NRRL1078               AGAATCCCGTCTGGGATGGGGTGCCCACAACCGTGTGAAGCTCCTTCGAC 773
Eu.cinnamopurpureum NRRL3326     AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC 764
P.chermesinum NRRL735            AGAATCCCGTACGGGACGGGGTGTCTGCCACCGTGTGAAGCTCCTTCGAC 763
P.clavariiformis NRRL2482        AGAATCCCGTCTGGGACAGGGTGTCTGTGTCTGTGTGAAGCTCCTTCGAC 777
                                 * ********  ****  ***** *     *  ******  ****** **
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                801      810       820       830       840       850
                                  +--------+---------+---------+---------+---------+
P.camemberti NRRL874             GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 824
P.camemberti NRRL875             GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 824
P.echinulatum NRRL1151          GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 824
P.crustosum NRRL968             GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 824
P.viridicatum NRRL961           GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 823
P.aurantiogriseum NRRL971       GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 824
P.polonicum NRRL995             GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 823
P.viridicatum NRRL958           GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 823
P.chrysogenum NRRL821           GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 823
P.chrysogenum NRRL807           GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 823
P.griseoroseum NRRL820          GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 823
P.chrysogenum NRRL824           GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 823
P.griseoroseum NRRL832          GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 823
P.griseofulvum NRRL734          GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 822
P.griseofulvum NRRL2300         GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 822
P.coprophilum NRRL13627         GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 823
P.digitatum NRRL786             GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 824
P.sclerotigenum NRRL3461        GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 823
Eu.egyptiacum NRRL2090          GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 821
Eu.crustaceum NRRL3332          GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 821
P.expansum NRRL974              GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 823
P.turbatum NRRL757              GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 822
H.paradoxus NRRL2162            GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 822
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P.swiecickii NRRL918           GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 820
P.kojigenum NRRL3442            GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 820
P.raistrickii NRRL2039         GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 820
P.soppii NRRL2023               GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 820
P.canescens NRRL910             GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 821
P.atrovenetum NRRL2571          GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 822
P.canescens NRRL2147            GAGTCGAGTTGTTTGGGAATGCAGCTCTAATTGGGTGGTAAATTTCATCT 825
P.waksmanii NRRL777             GAGTCGAGTTGTTTGGGAATGCAGCTCTAATTGGGTGGTAAATTTCATCT 825
P.miczynskii NRRL1077          GAGTCGAGTTGTTTGGGAATGCAGCTCTAATTGGGTGGTAAATTTCATCT 825
Eu.shearii NRRL715              GAGTCGAGTTGTTTGGGAATGCAGCTCTAATTGGGTGGTAAATTTCATCT 824
P.roseopurpureum NRRL733        GAGTCGAGTTGTTTGGGAATGCAGCTCTAATTGGGTGGTAAATTTCATCT 825
P.roseopurpureum NRRL2064       GAGTCGAGTTGTTTGGGAATGCAGCTCTAATTGGGTGGTAAATTTCATCT 825
P.sumatrense NRRL779            GAGTCGAGTTGTTTGGGAATGCAGCTCTAATTGGGTGGTAAATTTCATCT 830
P.paxilli NRRL2008              GAGTCGAGTTGTTTGGGAATGCAGCTCTAATTGGGTGGTAAATTTCATCT 822
P.citrinum NRRL1841             GAGTCGAGTTGTTTGGGAATGCAGCTCTAATTGGGTGGTAAATTTCATCT 791
P.sartoryi NRRL783              GAGTCGAGTTGTTTGGGAATGCAGCTCTAATTGGGTGGTAAATTTCATCT 791
P.westlingii NRRL800            GAGTCGAGTTGTTTGGGAATGCAGCTCTAATTGGGTGGTAAATTTCATCT 791
P.charlesii NRRL778             GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 813
P.fellutanum NRRL746            GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 819
P.spinulosum NRRL728            GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 814
P.spinulosum NRRL1750           GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 814
P.thomii NRRL2077               GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 816
Eu.lapidosum NRRL718            GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 816
P.thomii NRRL760                GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 816
P.purpurescens NRRL720          GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 816
P.glabrum NRRL766               GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 816
P.asperosporum NRRL3411         GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 814
P.lividum NRRL754               GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 819
P.adametzii NRRL736             GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 822
P.adametzii NRRL737             GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 822
P.bilaii  NRRL3391              GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 824
P.adametzioides NRRL3405        GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 817
P.herquei NRRL1040              GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 825
P.sclerotiorum NRRL2074         GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 814
P.decumbens NRRL742             GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 821
P.decumbens NRRL741             GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 821
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                801      810       820       830       840       850
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759                GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 821
P.corylophilum NRRL803            GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 822
P.corylophilum NRRL802            GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 822
P.corylophilum NRRL793            GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 822
P.melinii NRRL2041                GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 822
P.velutinum NRRL2069              GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 822
P.raciborskii NRRL2150            GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 823
P.restrictum NRRL25744            GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 822
P.restrictum NRRL1748             GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 822
P.citreonigrum NRRL761            GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 819
P.cinerascens NRRL748             GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 819
P.vinaceum NRRL739                GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 815
P.oxalicum NRRL790                GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 828
P.oxalicum NRRL787                GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 828
P.donkii NRRL5562                 GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 828
P.fuscum NRRL721                  GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 826
P.janthinellum NRRL2016           GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 826
P.raperi NRRL2674                 GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 825
P.daleae NRRL922                  GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 826
P.ochrochloron NRRL926            GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 823
P.simplicissimum NRRL1075         GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 822
P.rolfsii NRRL1078                GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 823
Eu.cinnamopurpureum NRRL3326      GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 814
P.chermesinum NRRL735             GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 813
P.clavariiformis NRRL2482         GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTCATCT 827
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                851       860       870       880       890       900
                                  +---------+---------+---------+---------+---------+
P.camemberti NRRL874             AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 874
P.camemberti NRRL875             AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 874
P.echinulatum NRRL1151           AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 874
P.crustosum NRRL968              AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 874
P.viridicatum NRRL961            AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 873
P.aurantiogriseum NRRL971        AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 874
P.polonicum NRRL995              AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 873
P.viridicatum NRRL958            AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 873
P.chrysogenum NRRL821            AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 873
P.chrysogenum NRRL807            AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 873
P.griseoroseum NRRL820           AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 873
P.chrysogenum NRRL824            AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 873
P.griseoroseum NRRL832           AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 873
P.griseofulvum NRRL734           AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.griseofulvum NRRL2300          AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.coprophilum NRRL13627          AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 873
P.digitatum NRRL786              AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 874
P.sclerotigenum NRRL3461         AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 873
Eu.egyptiacum NRRL2090           AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 871
Eu.crustaceum NRRL3332           AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 871
P.expansum NRRL974               AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 873
P.turbatum NRRL757               AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
H.paradoxus NRRL2162             AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.atramentosum NRRL795           AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.swiecickii NRRL918             AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 870
P.kojigenum NRRL3442             AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 870
P.raistrickii NRRL2039           AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 870
P.soppii NRRL2023                AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 870
P.canescens NRRL910              AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 871
P.atrovenetum NRRL2571           AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.canescens NRRL2147             AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 875
P.waksmanii NRRL777              AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 875
P.miczynskii NRRL1077           AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 875
Eu.shearii NRRL715               AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 874
P.roseopurpureum NRRL733         AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 875
P.roseopurpureum NRRL2064        AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 875
P.sumatrense NRRL779             AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 880
P.paxilli NRRL2008               AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.citrinum NRRL1841              AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 841
P.sartoryi NRRL783               AAAGCTAAATATTGGCCGGAGACCGATCGCGCACAAGTAGAGTGATCGAA 841
P.westlingii NRRL800             AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 841
P.charlesii NRRL778              AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 863
P.fellutanum NRRL746             AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 869
P.spinulosum NRRL728             AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 864
P.spinulosum NRRL1750            AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 864
P.thomii NRRL2077                AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 866
Eu.lapidosum NRRL718             AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 866
P.thomii NRRL760                 AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 866
P.purpurescens NRRL720           AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 866
P.glabrum NRRL766                AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 866
P.asperosporum NRRL3411          AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 864
P.lividum NRRL754                AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 869
P.adametzii NRRL736              AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.adametzii NRRL737              AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.bilaii  NRRL3391               AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 874
P.adametzioides NRRL3405         AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 867
P.herquei NRRL1040               AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 875
P.sclerotiorum NRRL2074          AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 864
P.decumbens NRRL742              AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 871
P.decumbens NRRL741              AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 871
```

Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                851      860       870       880       890       900
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759                AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 871
P.corylophilum NRRL803            AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.corylophilum NRRL802            AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.corylophilum NRRL793            AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.melinii NRRL2041                AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.velutinum NRRL2069              AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.raciborskii NRRL2150            AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 873
P.restrictum NRRL25744            AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.restrictum NRRL1748             AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.citreonigrum NRRL761            AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 869
P.cinerascens NRRL748             AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 869
P.vinaceum NRRL739                AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 865
P.oxalicum NRRL790                AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 878
P.oxalicum NRRL787                AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 878
P.donkii NRRL5562                 AAAGCTAAATACTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 878
P.fuscum NRRL721                  AAAGCTAAATACTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 876
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P.raperi NRRL2674                 AAAGCTAAATACTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 875
P.daleae NRRL922                  AAAGCTAAATACTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 876
P.ochrochloron NRRL926            AAAGCTAAATACTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 873
P.simplicissimum NRRL1075         AAAGCTAAATACTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.rolfsii NRRL1078                AAAGCTAAATACTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 873
Eu.cinnamopurpureum NRRL3326      AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 864
P.chermesinum NRRL735             AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 863
P.clavariiformis NRRL2482         AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 877
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                901      910       920       930       940       950
                                  +--------+---------+---------+---------+---------+
P.camemberti NRRL874              AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 924
P.camemberti NRRL875              AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 924
P.echinulatum NRRL1151            AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 924
P.crustosum NRRL968               AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 924
P.viridicatum NRRL961             AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 923
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P.viridicatum NRRL958             AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 923
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P.griseofulvum NRRL2300           AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 922
P.coprophilum NRRL13627           AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 923
P.digitatum NRRL786               AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 924
P.sclerotigenum NRRL3461          AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 923
Eu.egyptiacum NRRL2090            AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 921
Eu.crustaceum NRRL3332            AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 921
P.expansum NRRL974                AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 923
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P.herquei NRRL1040                AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 925
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P.decumbens NRRL742               AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 921
P.decumbens NRRL741               AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 921
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                901      910       920       930       940       950
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P.turbatum NRRL759               AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 921
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P.corylophilum NRRL793           AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 922
P.melinii NRRL2041               AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 922
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P.raciborskii NRRL2150           AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 923
P.restrictum NRRL25744           AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 922
P.restrictum NRRL1748            AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 922
P.citreonigrum NRRL761           AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 919
P.cinerascens NRRL748            AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 919
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P.oxalicum NRRL787               AGATGAAAAGCACTTTGAAAAGAGAGTTAAACAGCACGTGAAATTGTTGA 928
P.donkii NRRL5562                AGATGAAAAGCACTTTGAAAAGAGAGTTAAACAGCACGTGAAATTGTTGA 928
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P.raperi NRRL2674                AGATGAAAAGCACTTTGAAAAGAGAGTTAAACAGCACGTGAAATTGTTGA 925
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P.clavariiformis NRRL2482        AGATGAAAAGCACTTTGGAAAGAGAGTTAAACAGCACGTGAAATTGTTGA 927
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                951      960       970       980       990      1000
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P.camemberti NRRL874              AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 973
P.camemberti NRRL875              AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 973
P.echinulatum NRRL1151            AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 973
P.crustosum NRRL968               AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 973
P.viridicatum NRRL961             AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 972
P.aurantiogriseum NRRL971         AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 973
P.polonicum NRRL995               AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 972
P.viridicatum NRRL958             AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 972
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P.chrysogenum NRRL807             AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 972
P.griseoroseum NRRL820            AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 972
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P.griseoroseum NRRL832            AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 972
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P.coprophilum NRRL13627           AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 972
P.digitatum NRRL786               AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCACTC 973
P.sclerotigenum NRRL3461          AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 972
Eu.egyptiacum NRRL2090            AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 970
Eu.crustaceum NRRL3332            AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 970
P.expansum NRRL974                AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 972
P.turbatum NRRL757                AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 971
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P.swiecickii NRRL918              AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 969
P.kojigenum NRRL3442              AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 969
P.raistrickii NRRL2039            AAGGGAAGCGCTTGCGATCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 969
P.soppii NRRL2023                 AAGGGAAGCGCTTGCGACCAGACTCGCTCGTGGGGTT-CAGCCGGCATTC 969
P.canescens NRRL910               AAGGGAAGCGCTTGCGACCAGACTCGCTCGCGGGGTT-CAGCCGGCATTC 970
P.atrovenetum NRRL2571            AAGGGAAGCGCTTGCGACCAGACTCGGTCGCGGGGTT-CAGCCGGCATTC 971
P.canescens NRRL2147              AAGGGAAGCGCTTGCGATCAGACTCGCTCGCGGGGTT-CAGCCGGCCTTC 974
P.waksmanii NRRL777               AAGGGAAGCGCTTGCGATCAGACTCGCTCGCGGGGTT-CAGCCGGCCTTC 974
P.miczynskii NRRL1077             AAGGGAAGCGCTTGCGATCAGACTCGCTCGCGGGGTT-CAGCCGGCCTTC 974
Eu.shearii NRRL715                AAGGGAAGCGCTTGCGATCAGACTCGCTCGCGGGGTT-CAGCCGGCCTTC 973
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P.roseopurpureum NRRL2064         AAGGGAAGCGCTTGCGATCAGACTCGCCCACGGGGTT-CAGCCGGCATTC 974
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P.thomii NRRL2077                 AAGGGAAGCGCTTGCGATCAGACTCGCCTTGGGGGTT-CAGCCGGCATTC 965
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P.glabrum NRRL766                 AAGGGAAGCGCTTGCGATCAGACTCGCCTTGGGGGTT-CAGCCGGCATTC 965
P.asperosporum NRRL3411           AAGGGAAGCGCTTGCGATCAGACTCGCCTTGGGGGTT-CAGCCGGCATTC 963
P.lividum NRRL754                 AAGGGAAGCGCTTGCGACCAGACTCGCCTCGGGGGTT-CAACCGGCATTC 968
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P.adametzioides NRRL3405          AAGGGAAGCGTTTGCGACCAGACTCGCCTACGGGGTT-CAGCCTGCCTTC 966
P.herquei NRRL1040                AAGGGAAGCGTTTGCGACCAGACTCGCCTACGGGGTT-CAGCCGGCTTTC 974
P.sclerotiorum NRRL2074           AAGGGAAGCGTTTGCGATCAGACTCGCCGACGGGGTT-CAGCCTGCCTTC 963
P.decumbens NRRL742               AAGGGAAGCGCTTGCGACCAGACTCGCCTGCGGGGTT-CAGCCGGTATTC 970
P.decumbens NRRL741               AAGGGAAGCGCTTGCGACCAGACTCGCCTGCGGGGTT-CAGCCGGTATTC 970
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                951      960       970       980       990      1000
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759               AAGGGAAGCGCTTGCGACCAGACTCGCCTGCGGGGTT-CAGCCGGTATTC 970
P.corylophilum NRRL803           AAGGGAAGCGCTTGCGACCAGACTCGCCTACGGGGTT-CAGCCGGTATTC 971
P.corylophilum NRRL802           AAGGGAAGCGCTTGCGACCAGACTCGCCTACGGGGTT-CAGCCGGTATTC 971
P.corylophilum NRRL793           AAGGGAAGCGCTTGCGACCAGACTCGCCTACGGGGTT-CAGCCGGTATTC 971
P.melinii NRRL2041               AAGGGAAGCGCTTGCGACCAGACTCGCCTACGGGGTT-CAGCCGGTATTC 971
P.velutinum NRRL2069             AAGGGAAGCGCTTGCGACCAGACTCGCCTACGGGGTT-CAGCCGGTATTC 971
P.raciborskii NRRL2150           AAGGGAAGCGCTTGCGACCAGACTCGCCTACGGGGTT-CAGCCGGTATTC 972
P.restrictum NRRL25744           AAGGGAAGCGCTTGCGACCAGACTCGCCTGCGGGGTT-CAGCCGGTATTC 971
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P.citreonigrum NRRL761           AAGGGAAGCGCTTGCGACCAGACTCGCCTACGGGGTT-CAGCCGGTATTC 968
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P.vinaceum NRRL739               AAGGGAAGCGCTTGCGACTAGACTCGCCCACGGGGTAACAGCCGCTATTC 965
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P.ochrochloron NRRL926           AAGGGAAGCGCTTGCGACCAGACTCGCCCACGGGGTT-CAGCCGGCATTC 972
P.simplicissimum NRRL1075        AAGGGAAGCGCTTGCGACCAGACTCGCCCACGGGGTT-CAGCCGGCATTC 971
P.rolfsii NRRL1078               AAGGGAAGCGCTTGCGACCAGACTCGCCCACGGGGTT-CAGCCGGCATTC 972
Eu.cinnamopurpureum NRRL3326     AAGGGAAGCGCTTGCGACCAGACTCGCCCACGGGGTT-CAGCCGGCATTC 963
P.chermesinum NRRL735            AAGGGAAGCGCTTGCGACCAGACTCGCCCACGGGGTT-CAGCCGGCATTC 962
P.clavariiformis NRRL2482        AAGGGAAGCGCTTGCGACCAGACTCGCTTGCAGGGTT-CAGCCGGGATTC 976
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                               1001     1010      1020      1030      1040      1050
                                  +--------+---------+---------+---------+---------+
P.camemberti NRRL874              GTGCCGGTGTATTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1023
P.camemberti NRRL875              GTGCCGGTGTATTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1023
P.echinulatum NRRL1151            GTGCCGGTGTATTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1023
P.crustosum NRRL968               GTGCCGGTGTATTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1023
P.viridicatum NRRL961             GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1022
P.aurantiogriseum NRRL971         GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1023
P.polonicum NRRL995               GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1022
P.viridicatum NRRL958             GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1022
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P.chrysogenum NRRL807             GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1022
P.griseoroseum NRRL820            GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1022
P.chrysogenum NRRL824             GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1022
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P.griseofulvum NRRL2300           GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1021
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P.sclerotigenum NRRL3461          GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1022
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P.expansum NRRL974                GTGCCGGTGTATTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1022
P.turbatum NRRL757                GTGCCGGTGTACTTCCCCGCGAGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1021
H.paradoxus NRRL2162              GTGCCGGTGTATTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1021
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P.kojigenum NRRL3442              GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGTGGTCGG 1019
P.raistrickii NRRL2039            GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1019
P.soppii NRRL2023                 GTGCCGGTGTACTTCCCCGCGAGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1019
P.canescens NRRL910               GTGCCGGTGTACTTCCCCGCGGGCGGGCCAACGTCGGTTTGGGCGGTCGG 1020
P.atrovenetum NRRL2571            GTGCCGGTGTACTTCCCCGCGGCCGGGCCAACGTCAGTTTGGATGGTCGG 1021
P.canescens NRRL2147              GGGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1024
P.waksmanii NRRL777               GGGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1024
P.miczynskii NRRL1077             GGGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1024
Eu.shearii NRRL715                GGGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1023
P.roseopurpureum NRRL733          GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1024
P.roseopurpureum NRRL2064         GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1024
P.sumatrense NRRL779              GTGCCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1029
P.paxilli NRRL2008                GTGCCGGTGTACTTCCCCGGGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1021
P.citrinum NRRL1841               GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 990
P.sartoryi NRRL783                GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 990
P.westlingii NRRL800              GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 990
P.charlesii NRRL778               GGGCCGGTGTACTTCCCCCGGGGCGGGCCAGCGTCGGTTTTGGCGGCCGG 1012
P.fellutanum NRRL746              GGGCCGGTGTACTTCCCCCGGGGCGGGCCAGCGTCGGTTTTGGCGGCCGG 1018
P.spinulosum NRRL728              GTGCCGGTGTACTTCCCCCAGGGCGGGCCAGCGTCGGTTTGGGTGGCTGG 1013
P.spinulosum NRRL1750             GTGCCGGTGTACTTCCCCCAGGGCGGGCCAGCGTCGGTTTGGGTGGCTGG 1013
P.thomii NRRL2077                 GTGCCGGTGTACTTCCCCCAGGGCGGGCCAGCGTCGGTTTGGGTGGCTGG 1015
Eu.lapidosum NRRL718              GTGCCGGTGTACTTCCCCCAGGGCGGGCCAGCGTCGGTTTGGGTGGCTGG 1015
P.thomii NRRL760                  GTGCCGGTGTACTTCCCCCAGGGCGGGCCAGCGTCGGTTTGGGTGGCTGG 1015
P.purpurescens NRRL720            GTGCCGGTGTACTTCCCCCAGGGCGGGCCAGCGTCGGTTTGGGTGGCCGG 1015
P.glabrum NRRL766                 GTGCCGGTGTACTTCCCCCAGGGCGGGCCAGCGTCGGTTTGGGTGGCCGG 1015
P.asperosporum NRRL3411           GTGCCGGTGTACTTCCCCCAGGGCGGGCCAGCGTCGGTTTGGGTGGCCGG 1013
P.lividum NRRL754                 GTGCCGGTGTACTTCCCCCGGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG 1018
P.adametzii NRRL736               GGGTAGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1021
P.adametzii NRRL737               GGGTAGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1021
P.bilaii  NRRL3391                GGGCTGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1023
P.adametzioides NRRL3405          GGGCAGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1016
P.herquei NRRL1040                GGGCCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1024
P.sclerotiorum NRRL2074           GGGCAGGTGTACTTCCCCGCCGGCGGGCCAGCGTCGGTTTGGGTGGCCGG 1013
P.decumbens NRRL742               GTACCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1020
P.decumbens NRRL741               GTACCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1020
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                               1001     1010      1020      1030      1040      1050
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759                GTACCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1020
P.corylophilum NRRL803            GTACCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1021
P.corylophilum NRRL802            GTACCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1021
P.corylophilum NRRL793            GTACCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1021
P.melinii NRRL2041                GTACCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1021
P.velutinum NRRL2069              GTACCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1021
P.raciborskii NRRL2150            GTACCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1022
P.restrictum NRRL25744            GTACCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1021
P.restrictum NRRL1748             GTACCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1021
P.citreonigrum NRRL761            GTACCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1018
P.cinerascens NRRL748             GTACCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1018
P.vinaceum NRRL739                GTAGCGGTGCACTTCCCCGTGGTCGGGCCAGCGTCGGTTTGGGCGGCCGG 1015
P.oxalicum NRRL790                GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1027
P.oxalicum NRRL787                GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1027
P.donkii NRRL5562                 GTGCCGGTGTACTTCCCCGCGAGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1027
P.fuscum NRRL721                  GTGCCGGTGTACTTCCCCGCGAGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1025
P.janthinellum NRRL2016           GGGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1025
P.raperi NRRL2674                 GGGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1024
P.daleae NRRL922                  GTGCCGGTGTACTTCCCCACGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1025
P.ochrochloron NRRL926            GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1022
P.simplicissimum NRRL1075         GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1021
P.rolfsii NRRL1078                GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1022
Eu.cinnamopurpureum NRRL3326      GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1013
P.chermesinum NRRL735             GTGCCGGTGTACTTCCCCGCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1012
P.clavariiformis NRRL2482         GTCCCGGTGTACTTCCCTGCTGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1026
                                  *    **** * *****      ******* **** **** *  **  **
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                               1051     1060      1070      1080      1090      1100
                                  +--------+---------+---------+---------+---------+
P.camemberti NRRL874              TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1071
P.camemberti NRRL875              TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1071
P.echinulatum NRRL1151            TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1071
P.crustosum NRRL968               TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1071
P.viridicatum NRRL961             TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1070
P.aurantiogriseum NRRL971         TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1071
P.polonicum NRRL995               TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1070
P.viridicatum NRRL958             TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1070
P.chrysogenum NRRL821             TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1070
P.chrysogenum NRRL807             TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1070
P.griseoroseum NRRL820            TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1070
P.chrysogenum NRRL824             TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1070
P.griseoroseum NRRL832            TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1070
P.griseofulvum NRRL734            TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1069
P.griseofulvum NRRL2300           TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1069
P.coprophilum NRRL13627           TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1070
P.digitatum NRRL786               TCAAAGGCCCTCGGAAGGTAACGCCCCT--CGGGGCGTCTTATAGCCGAG 1071
P.sclerotigenum NRRL3461          TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1070
Eu.egyptiacum NRRL2090            TCAAAGGCCCTCGGAAGGTAACGCCCCT--CGGGGCGTCTTATAGCCGAG 1068
Eu.crustaceum NRRL3332            TCAAAGGCCCTCGGAAGGTAACGCCCCT--CGGGGCGTCTTATAGCCGAG 1068
P.expansum NRRL974                TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1070
P.turbatum NRRL757                TCAAAGGCCCTCGGAAGGTAACGCCCCC--AGGGGCGTCTTATAGCCGAG 1069
H.paradoxus NRRL2162              TCAAAGGCCCTCGGAAGGTAACGCCCCC--AGGGGCGTCTTATAGCCGAG 1069
P.atramentosum NRRL795            TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1069
P.swiecickii NRRL918              TCAAAGGCCCTCGGAAGGTAACGCCCCCTCGGGGGCGTCTTATAGCCGAG 1069
P.kojigenum NRRL3442              TCAAAGGCCCTCGGAAGGTAACGCCCCCTCGGGGGCGTCTTATAGCCGAG 1069
P.raistrickii NRRL2039            TCAAAGGCCCTCGGAAGGTAACGCCCCCTCGGGGGCGTCTTATAGCCGAG 1069
P.soppii NRRL2023                 TCAAAGGCCCTCGGAAGGTAACGCCCCCTCGGGGGCGTCTTATAGCCGAG 1069
P.canescens NRRL910               TCAAAGGCCCTCGGAAGGTAACGCCCCC--AGGGGCGTCTTATAGCCGAG 1068
P.atrovenetum NRRL2571            TTAAAGGCTCTCGGAAGGTAACGCCTCT--AGGGGCGTCTTATAGCCGAG 1069
P.canescens NRRL2147              TCAAAGGCCCCTGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCAGG 1072
P.waksmanii NRRL777               TCAAAGGCCCCTGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCAGG 1072
P.miczynskii NRRL1077            TCAAAGGCCCCTGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCAGG 1072
Eu.shearii NRRL715                TCAAAGGCCCCTGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCAGG 1071
P.roseopurpureum NRRL733          TCAAAGGCCCCTGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCAGG 1072
P.roseopurpureum NRRL2064         TCAAAGGCCCCTGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCAGG 1072
P.sumatrense NRRL779              TCAAAGGCCCCTGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCAGG 1077
P.paxilli NRRL2008                TCAAAGGCCCCTGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCAGG 1069
P.citrinum NRRL1841               TCAAAGGCCTCTGGAAGGTAACGCCTCT--CGGGGCGTCTTATAGCCAGG 1038
P.sartoryi NRRL783                TCAAAGGCCTCTGGAAGGTAACGCCTCT--CGGGGCGTCTTATAGCCAGG 1038
P.westlingii NRRL800              TCAAAGGCCCTCGGAAGGTAACGCCCCT--AGGGGCGTCTTATAGCCGAG 1038
P.charlesii NRRL778               TCAAAGGCCCCTGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCAGG 1060
P.fellutanum NRRL746              TCAAAGGCCCCTGGAATGTAACGCCCCC--CGGGGCGTCTTATAGCCAGG 1066
P.spinulosum NRRL728              TCAAAGGCCCTTGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCAAG 1061
P.spinulosum NRRL1750             TCAAAGGCCCTTGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCAAG 1061
P.thomii NRRL2077                 TCAAAGGCCCTTGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCAAG 1063
Eu.lapidosum NRRL718              TCAAAGGCCCTTGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCAAG 1063
P.thomii NRRL760                  TCAAAGGCCCTTGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCAAG 1063
P.purpurescens NRRL720            TCAAAGGCCCTTGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCAAG 1063
P.glabrum NRRL766                 TCAAAGGCCCTTGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCAAG 1063
P.asperosporum NRRL3411           TCAAAGGCCCTTGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCAAG 1061
P.lividum NRRL754                 TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1066
P.adametzii NRRL736               TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1069
P.adametzii NRRL737               TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1069
P.bilaii  NRRL3391               TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1071
P.adametzioides NRRL3405          TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1064
P.herquei NRRL1040                TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1072
P.sclerotiorum NRRL2074           TCAAAGGCCCTAGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCTAG 1061
P.decumbens NRRL742               TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1068
P.decumbens NRRL741               TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1068
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                               1051     1060      1070      1080      1090      1100
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759                TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1068
P.corylophilum NRRL803            TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1069
P.corylophilum NRRL802            TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1069
P.corylophilum NRRL793            TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1069
P.melinii NRRL2041                TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGCCTTATAGCCGAG 1069
P.velutinum NRRL2069              TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1069
P.raciborskii NRRL2150            TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGGG 1070
P.restrictum NRRL25744            TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1069
P.restrictum NRRL1748             TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1069
P.citreonigrum NRRL761            TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1066
P.cinerascens NRRL748             TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1066
P.vinaceum NRRL739                TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGGG 1063
P.oxalicum NRRL790                TCAAAGGCCCTCGGAATGTAACGCCCCC--CGGGGCGTCTTATAGCCGAG 1075
P.oxalicum NRRL787                TCAAAGGCCCTCGGAATGTAACGCCCCC--CGGGGCGTCTTATAGCCGAG 1075
P.donkii NRRL5562                 TCAAAGGCCCTCGGAATGTAACGCCCCC--CGGGGCGTCTTATAGCCGAG 1075
P.fuscum NRRL721                  TCAAAGGCCCTCGGAATGTAACGCCCCC--CGGGGCGTCTTATAGCCGAG 1073
P.janthinellum NRRL2016           TCAAAGGCCCTCGGAATGTAACGCCCCC--CGGGGCGTCTTATAGCCGAG 1073
P.raperi NRRL2674                 TCAAAGGCCCTCGGAATGTAACGCCCCC--CGGGGCGTCTTATAGCCGAG 1072
P.daleae NRRL922                  TCAAAGGCCCTCGGAATGTAACGCCCCC--CGGGGCGTCTTATAGCCGAG 1073
P.ochrochloron NRRL926            TCAAAGGCCCTTGGAATGTACCGCCCCC--CGGGGCGGCTTATAGCCAAG 1070
P.simplicissimum NRRL1075         TCAAAGGCCCTTGGAATGTACCGCCCCC--CGGGGCGGCTTATAGCCAAG 1069
P.rolfsii NRRL1078                TCAAAGGCCCTTGGAATGTAACGCCCCC--CGGGGCGTCTTATAGCCAAG 1070
Eu.cinnamopurpureum NRRL3326      TCAAAGGCCCTCGGAATGTAACGCCCCT--CGGGGCGTCTTATAGCCGAG 1061
P.chermesinum NRRL735             TCAAAGGCCCTCGGAATGTAACGCCCCC--CGGGGCGTCTTATAGCCGAG 1060
P.clavariiformis NRRL2482         TCAAAGGCCCCTGGAATGTAGCACCCTC----GGGTGTCTTATAGCCAGG 1072
                                  * ******    **** *** * **       *** * *********  *
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                               1101     1110      1120      1130      1140      1150
                                  +--------+---------+---------+---------+---------+
P.camemberti NRRL874              GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1121
P.camemberti NRRL875              GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1121
P.echinulatum NRRL1151            GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1121
P.crustosum NRRL968               GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1121
P.viridicatum NRRL961             GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1120
P.aurantiogriseum NRRL971         GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1121
P.polonicum NRRL995               GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1120
P.viridicatum NRRL958             GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1120
P.chrysogenum NRRL821             GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1120
P.chrysogenum NRRL807             GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1120
P.griseoroseum NRRL820            GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1120
P.chrysogenum NRRL824             GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1120
P.griseoroseum NRRL832            GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1120
P.griseofulvum NRRL734            GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1119
P.griseofulvum NRRL2300           GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1119
P.coprophilum NRRL13627           GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1120
P.digitatum NRRL786               GGTGCAATGCGACCTGCCCAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1121
P.sclerotigenum NRRL3461          GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1120
Eu.egyptiacum NRRL2090            GGTGCAATGCGACCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1118
Eu.crustaceum NRRL3332            GGTGCAATGCGACCTGCCCAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1118
P.expansum NRRL974                GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1120
P.turbatum NRRL757                GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1119
H.paradoxus NRRL2162              GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1119
P.atramentosum NRRL795            GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1119
P.swiecickii NRRL918              GGTGCAATGCGACCTGCCTGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1119
P.kojigenum NRRL3442              GGTGCAATGCGACCTACCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1119
P.raistrickii NRRL2039            GGTGCAATGCGACCTGCCTGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1119
P.soppii NRRL2023                 GGTGCAATGCGACCTGCCTGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1119
P.canescens NRRL910               GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGTT 1118
P.atrovenetum NRRL2571            GGTGTAATGCGACCTATCCGGACTGAGGAACGCGCTTCGGCTCGGACGTT 1119
P.canescens NRRL2147              GGTGCCATGCGGCCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1122
P.waksmanii NRRL777               GGTGCCATGCGGCCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1122
P.miczynskii NRRL1077             GGTGCCATGCGGCCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1122
Eu.shearii NRRL715                GGTGCCATGCGGCCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1121
P.roseopurpureum NRRL733          GGTGCCATGCGACCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1122
P.roseopurpureum NRRL2064         GGTGCCATGCGACCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1122
P.sumatrense NRRL779              GGTGCCATGCGGCCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1127
P.paxilli NRRL2008                GGTGCCATGCGGCCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1119
P.citrinum NRRL1841               GGTGCCATGCGGCCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1088
P.sartoryi NRRL783                GGTGCCATGCGGCCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1088
P.westlingii NRRL800              GGTGCAATGCGACCTGCCTAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1088
P.charlesii NRRL778               GGTGCCATGCGGCCCGCCGGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1110
P.fellutanum NRRL746              GGTGCCATGCGGCCCGCCGGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1116
P.spinulosum NRRL728              GGTGCCATGCAGCCTACCTGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1111
P.spinulosum NRRL1750             GGTGCCATGCAGCCTACCTGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1111
P.thomii NRRL2077                 GGTGCCATGCAGCCTACCTGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1113
Eu.lapidosum NRRL718              GGTGCCATGCAGCCTACCTGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1113
P.thomii NRRL760                  GGTGCCATGCAGCCTACCTGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1113
P.purpurescens NRRL720            GGTGCCATGCGGCCTACCTGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1113
P.glabrum NRRL766                 GGTGCCATGCGGCCTACCTGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1113
P.asperosporum NRRL3411           GGTGCCATGCGGCCTACCTGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1111
P.lividum NRRL754                 GGTGCCATGCGACCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1116
P.adametzii NRRL736               GGTGCCATGCGGCCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1119
P.adametzii NRRL737               GGTGCCATGCGGCCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1119
P.bilaii  NRRL3391                GGTGCCATGCGGCCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1121
P.adametzioides NRRL3405          GGTGCCATGCGGCCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1114
P.herquei NRRL1040                GGTGCCATGCGGCCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1122
P.sclerotiorum NRRL2074           GGTGTCATGCGGCCTACCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1111
P.decumbens NRRL742               GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCACGGACGCT 1118
P.decumbens NRRL741               GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCACGGACGCT 1118
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

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                               1101     1110      1120      1130      1140      1150
                                  +--------+---------+---------+---------+---------+
P.turbatum NRRL759                GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCACGGACGCT 1118
P.corylophilum NRRL803            GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCACGGACGCT 1119
P.corylophilum NRRL802            GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCACGGACGCT 1119
P.corylophilum NRRL793            GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCACGGACGCT 1119
P.melinii NRRL2041                GGTGCCATGCGGCCAGCCCAGACCGAGGAACGCGCTTCGGCACGGACGCT 1119
P.velutinum NRRL2069              GGTGCCATGCGGCCAGCCCAGACCGAGGAACGCGCTTCGGCACGGACGCT 1119
P.raciborskii NRRL2150            GGTGCCATGCGGCCAGCCCAGACCGAGGAACGCGCTTCGGCACGGACGCT 1120
P.restrictum NRRL25744            GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCACGGACGCT 1119
P.restrictum NRRL1748             GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCACGGACGCT 1119
P.citreonigrum NRRL761            GGTGCCATGCGGCCAGCCCAGACCGAGGAACGCGCTTCGGCACGGACGCT 1116
P.cinerascens NRRL748             GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCACGGACGCT 1116
P.vinaceum NRRL739                GGTGCCATGCGGCCAGCCCAGACCGAGGATCGCGCTTCGGCACGGACGCT 1113
P.oxalicum NRRL790                GGTGCCATGCGGCCAGCCCAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1125
P.oxalicum NRRL787                GGTGCCATGCGGCCAGCCCAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1125
P.donkii NRRL5562                 GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1125
P.fuscum NRRL721                  GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1123
P.janthinellum NRRL2016           GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1123
P.raperi NRRL2674                 GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1122
P.daleae NRRL922                  GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1123
P.ochrochloron NRRL926            GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1120
P.simplicissimum NRRL1075         GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1119
P.rolfsii NRRL1078                GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1120
Eu.cinnamopurpureum NRRL3326      GGTGCCATGCGGCCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1111
P.chermesinum NRRL735             GGTGCCATGCGGCCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1110
P.clavariiformis NRRL2482         GGTGCAATGCGGCCTGCCTGGACCGAGGAACGCGCTTCGGCACGGACGCT 1122
                                  ****  ****  **   *  *** ***** *********** ****** *
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Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                              1151     1160      1170
                                 +--------+---------+--
P.camemberti NRRL874             GGCATAATGGTCGTAAGCGACC 1143
P.camemberti NRRL875             GGCATAATGGTCGTAAGCGACC 1143
P.echinulatum NRRL1151           GGCATAATGATCGTAAGCGACC 1143
P.crustosum NRRL968              GGCATAATGATCGTAAGCGACC 1143
P.viridicatum NRRL961            GGCATAATGGTCGTAAGCGACC 1142
P.aurantiogriseum NRRL971        GGCATAATGGTCGTAAGCGACC 1143
P.polonicum NRRL995              GGCATAATGGTCGTAAGCGACC 1142
P.viridicatum NRRL958            GGCATAATGGTCGTAAGCGACC 1142
P.chrysogenum NRRL821            GGCATAATGGTCGTAAACGACC 1142
P.chrysogenum NRRL807            GGCATAATGGTCGTAAACGACC 1142
P.griseoroseum NRRL820           GGCATAATGGTCGTAAACGACC 1142
P.chrysogenum NRRL824            GGCATAATGGTCGTAAACGACC 1142
P.griseoroseum NRRL832           GGCATAATGGTCGTAAACGACC 1142
P.griseofulvum NRRL734           GGCATAATGGTCGTAAGCGACC 1141
P.griseofulvum NRRL2300          GGCATAATGGTCGTAAGCGACC 1141
P.coprophilum NRRL13627          GACATAATGATCGTAAGCGACC 1142
P.digitatum NRRL786              GACATAATGATCGTAAGCGACC 1143
P.sclerotigenum NRRL3461         GGCATAATGGTCGTAAGCGACC 1142
Eu.egyptiacum NRRL2090           GGCATAATGGTCGTAAACGACC 1140
Eu.crustaceum NRRL3332           GGCATAATGGTCGTAAACGACC 1140
P.expansum NRRL974               GGCATAATGGTCGTAAGCGACC 1142
P.turbatum NRRL757               GGCATAATGGTCGTAAGCGACC 1141
H.paradoxus NRRL2162             GGCATAATGGTCGTAAGCGACC 1141
P.atramentosum NRRL795           GGCATAATGGTCGTAAGCGACC 1141
P.swiecickii NRRL918             GGCATAATGGTCGTAAGCGACC 1141
P.kojigenum NRRL3442             GGCATAATGGTCGTAAGCGACC 1141
P.raistrickii NRRL2039           GGCATAATGGTCGTAAGCGACC 1141
P.soppii NRRL2023                GGCATAATGGTCGTAAGCGACC 1141
P.canescens NRRL910              GGCATAATGGTCGTAAGCGACC 1140
P.atrovenetum NRRL2571           GGCATAATGGTCGTAAGCGACC 1141
P.canescens NRRL2147             GGCATAATGGTCGTAAGCGACC 1144
P.waksmanii NRRL777              GGCATAATGGTCGTAAGCGACC 1144
P.miczynskii NRRL1077            GGCATAATGGTCGTAAGCGACC 1144
Eu.shearii NRRL715               GGCATAATGGTCGTAAGCGACC 1143
P.roseopurpureum NRRL733         GGCATAATGGTCGTAAGCGACC 1144
P.roseopurpureum NRRL2064        GGCATAATGGTCGTAAGCGACC 1144
P.sumatrense NRRL779             GGCATAATGGTCGTAAGCGACC 1149
P.paxilli NRRL2008               GGCATAATGGTCGTAAGCGACC 1141
P.citrinum NRRL1841              GGCATAATGGTCGTAAGCGACC 1110
P.sartoryi NRRL783               GGCATAATGGTCGTAAGCGACC 1110
P.westlingii NRRL800             GGCATAATGGTCGTAAACGACC 1110
P.charlesii NRRL778              GGCATAATGGTCGTAAGCGACC 1132
P.fellutanum NRRL746             GGCATAATGGTCGTAAGCGACC 1138
P.spinulosum NRRL728             GGCATAATGGTCGTAAGCGACC 1133
P.spinulosum NRRL1750            GGCATAATGGTCGTAAGCGACC 1133
P.thomii NRRL2077                GGCATAATGGTCGTAAGCGACC 1135
Eu.lapidosum NRRL718             GGCATAATGGTCGTAAGCGACC 1135
P.thomii NRRL760                 GGCATAATGGTCGTAAGCGACC 1135
P.purpurescens NRRL720           GGCATAATGGTCGTAAGCGAC- 1134
P.glabrum NRRL766                GGCATAATGGTCGTAAGCGACC 1135
P.asperosporum NRRL3411          GGCATAATGGTCGTAAGCGACC 1133
P.lividum NRRL754                GGCATAATGGTCGTAAGCGACC 1138
P.adametzii NRRL736              GGCATAATGGTCGTAAACGACC 1141
P.adametzii NRRL737              GGCATAATGGTCGTAAACGACC 1141
P.bilaii  NRRL3391               GGCTTAATGGTCGTCAACGACC 1143
P.adametzioides NRRL3405         GGCTTAATGGTCGTAAACGACC 1136
P.herquei NRRL1040               GGCATAATGGTCGTAAACGACC 1144
P.sclerotiorum NRRL2074          GGCATAATGGTCGTAAACGACC 1133
P.decumbens NRRL742              GGCATAATGGTCGTAAGCGACC 1140
P.decumbens NRRL741              GGCATAATGGTCGTAAGCGACC 1140
```

Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                               1151     1160      1170
                                  +--------+---------+--
P.turbatum NRRL759                GGCATAATGGTCGTAAGCGACC 1140
P.corylophilum NRRL803            GGCATAATGGTCGTAAGCGACC 1141
P.corylophilum NRRL802            GGCATAATGGTCGTAAGCGACC 1141
P.corylophilum NRRL793            GGCATAATGGTCGTAAGCGACC 1141
P.melinii NRRL2041                GGCATAATGGTCGTAAGCGACC 1141
P.velutinum NRRL2069              GGCATAATGGTCGTAAGCGACC 1141
P.raciborskii NRRL2150            GGCATAATGGTCGTAAGCGACC 1142
P.restrictum NRRL25744            GGCATAATGGTCGTAAGCGACC 1141
P.restrictum NRRL1748             GGCATAATGGTCGTAAGCGACC 1141
P.citreonigrum NRRL761            GGCATAATGGTCGTAAGCGACC 1138
P.cinerascens NRRL748             GGCATAATGGTCGTAAGCGAC- 1137
P.vinaceum NRRL739                GGCTTAATGGTCGTAAGCGACC 1135
P.oxalicum NRRL790                GGCATAATGGTCGTAAGCGACC 1147
P.oxalicum NRRL787                GGCATAATGGTCGTAAGCGACC 1147
P.donkii NRRL5562                 GGCATAATGGTCGTAAGCGACC 1147
P.fuscum NRRL721                  GGCATAATGGTCGTAAGCGACC 1145
P.janthinellum NRRL2016           GGCATAATGGTCGTAAGCGACC 1145
P.raperi NRRL2674                 GGCATAATGGTCGTAAGCGACC 1144
P.daleae NRRL922                  GGCATAATGGTCGTAAGCGACC 1145
P.ochrochloron NRRL926            GGCATAATGGTCGTAAGCGACC 1142
P.simplicissimum NRRL1075         GGCATAATGGTCGTAAGCGACC 1141
P.rolfsii NRRL1078                GGCATAATGGTCGTAAGCGACC 1142
Eu.cinnamopurpureum NRRL3326      GGCATAATGGTCGTAAGCGACC 1133
P.chermesinum NRRL735             GGCATAATGGTCGTAAGCGACC 1132
P.clavariiformis NRRL2482         GGCATAATGGTCGTAAGCGACC 1144
                                  * * ***** **** * ****
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APPENDIX E

Alignment of sequences of nuclear ribosomal DNA, ITS1-5.8S-ITS2 region from 46 taxa from *Penicillium* subgen. *Pencillium*

Invariant bases indicated by an asterisk

Penicillium subgenus *Penicillium*, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                    1       10        20        30        40        50
                                    +--------+---------+---------+---------+---------+
P.canescens NRRL910[T]              AAGGATCATTACCGAGCGAGAATTCTCT-GAATTCAACCTCCCACCCGTG
P.atrovenetum NRRL2571[T]           AAGGATCATTACCGAGCGAGGATTCTCTCGAATCCAACCTCCCACCCGTG
P.chrysogenum NRRL807[T]            AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.chrysogenum C8.24                 AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.notatum NRRL821[T]                AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.griseoroseum NRRL820[T]           AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.chrysogenum C8.12                 AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.nalgiovense NRRL911[T]            AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.chrysogenum NRRL824 Fleming strn  AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.notatum NRRL832 Biourge strn      AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
Eu.egyptiacum NRRL2090[T]           AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
Eu.crustaceum NRRL3332[T]           AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.viridicatum NRRL5880              AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.aethiopicum CBS484.84[T]          AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.gris.v.dipodomyicola NRRL13487[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.camemberti NRRL874[T]             AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.caseicolum NRRL875[T]             AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.crustosum NRRL968                 AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.viridicatum NRRL961               AAGGATCATTACCGAGTGAGGGCCCTTT-GGGTCCAACCTCCCACCCGTG
P.aurantiogriseum NRRL971[T]        AAGGATCATTACCGAGTGAGGGCCCTTT-GGGTCCAACCTCCCACCCGTG
P.polonicum NRRL995[T]              AAGGATCATTACCGAGTGAGGGCCCTTT-GGGTCCAACCTCCCACCCGTG
P.polonicum C74.1                   AAGGATCATTACCGAGTGAGGGCCCTTT-GGGTCCAACCTCCCACCCGTG
P.viridicatum NRRL958[T]            AAGGATCATTACCGAGTGAGGGCCCTTT-GGGTCCAACCTCCCACCCGTG
P.echinulatum NRRL1151[T]           AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.sclerotigenum NRRL786[T]          AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.sclerotigenum NRRL3461[T]         AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.olsonii CBS232.32[T]              AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.coprophilum NRRL13627[T]          AAGGATCATTACCGAGTGAGGGCCCTTT-GGGTCCAACCTCCCACCCATG
P.griseofulvum NRRL734[T]           AAGGATCATTACTGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.griseofulvum NRRL2300[T]          AAGGATCATTACTGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.chrys.v.dipodomyis NRRL13485[T]   AAGGATCATTACTGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.expansum NRRL974 Biourge strn     AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.turbatum NRRL757[T]               AAGGATCATTACTGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
?H.paradoxus NRRL2162[T]            AAGGATCATTACTGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.atramentosum NRRL795[T]           AAGGATCATTACTGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.swiecickii NRRL918[T]             AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.kojigenum NRRL3442[T]             AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.raistrickii NRRL2039[T]           AAGGATCATTACTGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.soppii NRRL2023[T]                AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.brevicompactum B65.4              AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.brevicompactum DAOM193712[T]      AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.stoloniferum ATCC10111[T]         AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCTTG
P.brevicompactum B251               AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.brevicompactum B132.1             AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
Eu.lapidosum NRRL718[T]             AAGGATCATTACTGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.bilaii  NRRL3391[T]               AAGGATCATTACTGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
                                    ************ *** ***    ** * *  * ************* **
```

Penicillium subgenus *Penicillium*, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                   51        60        70        80        90       100
                                    +--------+---------+---------+---------+---------+
P.canescens NRRL910[T]              TTTATTGTACCTTGTTGCTTCGGCGGGCCCGCCTCAC--GGCCGCCGGGG
P.atrovenetum NRRL2571[T]           TTTATTGTACCTTGTTGCTTCGGCGGGCCCGCCTCAC--GGCCGCCGGGG
P.chrysogenum NRRL807[T]            TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.chrysogenum C8.24                 TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.notatum NRRL821[T]                TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.griseoroseum NRRL820[T]           TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.chrysogenum C8.12                 TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.nalgiovense NRRL911[T]            TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.chrysogenum NRRL824 Fleming strn  TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.notatum NRRL832 Biourge strn      TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
Eu.egyptiacum NRRL2090[T]           TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
Eu.crustaceum NRRL3332[T]           TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.viridicatum NRRL5880              TTTATTTTTCCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.aethiopicum CBS484.84[T]          TTTATTTTTCCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.gris.v.dipodomyicola NRRL13487[T] TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.camemberti NRRL874[T]             TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.caseicolum NRRL875[T]             TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.crustosum NRRL968                 TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.viridicatum NRRL961               TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTTACTGGCCGCCGGGG
P.aurantiogriseum NRRL971[T]        TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTTACTGGCCGCCGGGG
P.polonicum NRRL995[T]              TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTTACTGGCCGCCGGGG
P.polonicum C74.1                   TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTTACTGGCCGCCGGGG
P.viridicatum NRRL958[T]            TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTTACTGGCCGCCGGGG
P.echinulatum NRRL1151[T]           TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.sclerotigenum NRRL786[T]          TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTTACTGGCCGCCGGGG
P.sclerotigenum NRRL3461[T]         TTTATTT-ACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.olsonii CBS232.32[T]              TTTATTT-ACCTTATTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.coprophilum NRRL13627[T]          TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.griseofulvum NRRL734[T]           TTTATTT-ACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.griseofulvum NRRL2300[T]          TTTATTT-ACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.chrys.v.dipodomyis NRRL13485[T]   TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGG
P.expansum NRRL974 Biourge strn     TTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTTACTGGCCGCCGGGG
P.turbatum NRRL757[T]               TTTATTGTACCTTGTTGCTTCGGCGGGCCCGCCTTTA-TGGCCGCCGGGG
?H.paradoxus NRRL2162[T]            TTTATTGTACCTTGTTGCTTCGGCGGGCCCGCCCTTG-TGGCCGCCGGGG
P.atramentosum NRRL795[T]           TTTATTGTACCTTGTTGCTTCGGCGGGCCCGCCTTTA-TGGCCGCCGGGG
P.swiecickii NRRL918[T]             TTTATTATACCTTGTTGCTTCGGCGGGCCCGCCGTAT--GGCCGCCGGGG
P.kojigenum NRRL3442[T]             TTTATTATACCTTGTTGCTTCGGCGGGCCCGCCGTAT--GGCCGCCGGGG
P.raistrickii NRRL2039[T]           TTTATTATACCTTGTTGCTTCGGCGGGCCCGCCGTCA--GGCCGCCGGGG
P.soppii NRRL2023[T]                TTTATTATACCTTGTTGCTTTGGCGGGCCCGCCTCAC--GGCCGCCGGGG
P.brevicompactum B65.4              TTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTTTT--GGCTGCCGGGG
P.brevicompactum DAOM193712[T]      TTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTTTT--GGCTGCCGGGG
P.stoloniferum ATCC10111[T]         TTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTTTT--GGCTGCCGGGG
P.brevicompactum B251               TTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTTTT--GGCTGCCGGGG
P.brevicompactum B132.1             TTTATTT-ACCTTGTTGCTTCGGCGAGCCTGCCTTTT--GGCTGCCGGGG
Eu.lapidosum NRRL718[T]             TTTATTGTACCTTGTTGCTTCGGTGCGCCCGCCTCAC--GGCCGCCGGGG
P.bilaii  NRRL3391[T]               TCTCTTGTACCATGTTGCTTCGGCGAGCCCGCCTCAC--GGCCGCCGGGG
                                    * * **   ** * ****** ** * *** ***      *** *******
```

Penicillium subgenus *Penicillium*, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                  101       110       120       130       140       150
                                    +--------+---------+---------+---------+---------+
P.canescens NRRL910[T]              GGCA-TCTGCCCCCGGGCCCGCGCCCGCCGAAGACACCT-TGAACTCTGT
P.atrovenetum NRRL2571[T]           GGCA-TCTGCTCCCGGGCCCGCGCCCGCCGAAGACACCT-TGAACTCTGT
P.chrysogenum NRRL807[T]            GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.chrysogenum C8.24                 GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.notatum NRRL821[T]                GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.griseoroseum NRRL820[T]           GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.chrysogenum C8.12                 GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.nalgiovense NRRL911[T]            GGCT-TACGCCCCCGGGCCCGCGCCCGCGGAAGACACCCTCGAACTCTGT
P.chrysogenum NRRL824 Fleming strn  GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.notatum NRRL832 Biourge strn      GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
Eu.egyptiacum NRRL2090[T]           GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
Eu.crustaceum NRRL3332[T]           GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.viridicatum NRRL5880              GGCT-CACGCTCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.aethiopicum CBS484.84[T]          GGCT-CACGCTCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.gris.v.dipodomyicola NRRL13487[T] GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.camemberti NRRL874[T]             GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.caseicolum NRRL875[T]             GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.crustosum NRRL968                 GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.viridicatum NRRL961               GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.aurantiogriseum NRRL971[T]        GGCTTCACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.polonicum NRRL995[T]              GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCCGAACTCTGT
P.polonicum C74.1                   GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCCGAACTCTGT
P.viridicatum NRRL958[T]            GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.echinulatum NRRL1151[T]           GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.sclerotigenum NRRL786[T]          GGCT-CACGCTCCCGGGCCCGCGCCCGCCGAAGACACCCCCGAACTCTGT
P.sclerotigenum NRRL3461[T]         GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.olsonii CBS232.32[T]              GGTT-CACACCCCCGGGCCCGCGCCCGCCGAAGACACTC-CGAACTCTGT
P.coprophilum NRRL13627[T]          GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.griseofulvum NRRL734[T]           GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.griseofulvum NRRL2300[T]          GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.chrys.v.dipodomyis NRRL13485[T]   GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.expansum NRRL974 Biourge strn     GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.turbatum NRRL757[T]               GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCT-CGAACTCTGT
?H.paradoxus NRRL2162[T]            GGCT-TACGCTCCCGGGCCCGCGCCCGCCGAAGACACCCACGAACTCTGT
P.atramentosum NRRL795[T]           GGCT-TACGCTCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGT
P.swiecickii NRRL918[T]             GGCT-TCTGCCCCCGGGCCCGCGCCCGCCGAAGACATCT-CGAACTCTGT
P.kojigenum NRRL3442[T]             GGCT-TCTGCCCCCGGGCCCGCGCCCGCCGAAGACATCT-CGAACTCTGT
P.raistrickii NRRL2039[T]           GGCT-TCTGCCCCCGGGCCCGCGCCCGCCGAAGACATCT-CGAACTCTGT
P.soppii NRRL2023[T]                GGCT-TCTGCCCCCGGGCCCGTGCCCGCCGAAGACACCTTAGAACTCTGT
P.brevicompactum B65.4              GACG-TCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGT
P.brevicompactum DAOM193712[T]      GACG-TCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGT
P.stoloniferum ATCC10111[T]         GACG-TCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGT
P.brevicompactum B251               GACA-TCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGT
P.brevicompactum B132.1             GACG-TCAGTCCCCGGGTCCGTGCTCGCCGGAGACACCTTAGAACTCTGT
Eu.lapidosum NRRL718[T]             GGCT-TCTGCCCCCGGGTCCGCGCACCGGAGACACCATTGAACTCTGT
P.bilaii  NRRL3391[T]               GGCA-TCTGCCCCCGGGCCCGCGCCCGCCGAAGCCCCCTCTGAACGCTGT
                                    *          ****** *** ** * * * ** *      **** ****
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Penicillium subgenus *Penicillium*, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                  151      160       170       180       190       200
                                    +--------+---------+---------+---------+---------+
P.canescens NRRL910[T]             ATGAAAATTGCAGTCTGAGT-CTAAATATAAATTATTTAAAACTTTCAAC
P.atrovenetum NRRL2571[T]          ATGAAAATTGCAGTCTGAGT-CTAAATATAAATTATTTAAAACTTTCAAC
P.chrysogenum NRRL807[T]           CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.chrysogenum C8.24                CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.notatum NRRL821[T]               CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.griseoroseum NRRL820[T]          CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.chrysogenum C8.12                CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.nalgiovense NRRL911[T]           CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.chrysogenum NRRL824 Fleming strn CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.notatum NRRL832 Biourge strn     CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
Eu.egyptiacum NRRL2090[T]          CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
Eu.crustaceum NRRL3332[T]          CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.viridicatum NRRL5880             CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.aethiopicum CBS484.84[T]         CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.gris.v.dipodomyicola NRRL13487[T] CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.camemberti NRRL874[T]            CTGAAGATTGAAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.caseicolum NRRL875[T]            CTGAAGATTGAAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.crustosum NRRL968                CTGAAGATTGAAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.viridicatum NRRL961              CTGAAGATTGAAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.aurantiogriseum NRRL971[T]       CTGAAGATTGAAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.polonicum NRRL995[T]             CTGAAGATTGAAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.polonicum C74.1                  CTGAAGATTGAAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.viridicatum NRRL958[T]           CTGAAGATTGAAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.echinulatum NRRL1151[T]          CTGAAGATTGAAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.sclerotigenum NRRL786[T]         CTGAAGATTGCAGTCTGAGT-GAAAAC-GAAATTATTTAAAACTTTCAAC
P.sclerotigenum NRRL3461[T]        CTGAAGATTGCAGTCTGAGT-GAAAATAGAAATTATTTAAAACTTTCAAC
P.olsonii CBS232.32[T]             CTGAAGAATGCAGTCTGAGA-ACAAATATAAATTATTTAAAACTTTCAAC
P.coprophilum NRRL13627[T]         CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.griseofulvum NRRL734[T]          CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.griseofulvum NRRL2300[T]         CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.chrys.v.dipodomyis NRRL13485[T]  CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.expansum NRRL974 Biourge strn    CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.turbatum NRRL757[T]              CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
?H.paradoxus NRRL2162[T]           ATGAAGATTGCAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.atramentosum NRRL795[T]          CTGAAGATTGTAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.swiecickii NRRL918[T]            CTGAAGATTGTAGTCTGAGT-AAAAATATAAATTATTTAAAACTTTCAAC
P.kojigenum NRRL3442[T]            CTGAAGATTGTAGTCTGAGT-AAAAATATAAATTATTTAAAACTTTCAAC
P.raistrickii NRRL2039[T]          CTGAAGATTGTAGTCTGAGT-ATAAATATAAATTATTTAAAACTTTCAAC
P.soppii NRRL2023[T]               CTGAAGATTGTAGTCTGAGT-AAAAATATAAATTATTTAAAACTTTCAAC
P.brevicompactum B65.4             CTGAAGATTGTAGTCTGAGA-TTAAATATAAATTATTTAAAACTTTCAAC
P.brevicompactum DAOM193712[T]     CTGAAGATTGTAGTCTGAGA-TTAAATATAAATTATTTAAAACTTTCAAC
P.stoloniferum ATCC10111[T]        CTGAAGATTGTAGTCTGAGA-TTAAATATAAATTATTTAAAACTTTCAAC
P.brevicompactum B251              CTGAAGATTGTAGTCTGAGA-TTAAATATAAATTATTTAAAACTTTCAAC
P.brevicompactum B132.1            CTGAAGATTGTAGTCTGAGA-TTAAATATAAATTATTTAAAACTTTCAAC
Eu.lapidosum NRRL718[T]            CTGAAGATTGCAGTCTGAGC-ATAAACTAAA-TAAGTTAAAACTTTCAAC
P.bilaii  NRRL3391[T]              CTGAAGATTGCAGTCTGAGCGATAAGCAAAAATTATTTAAAACTTTCAAC
                                    **** * ** ********    **    ** * * **************
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Penicillium subgenus *Penicillium*, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                  201      210       220       230       240       250
                                    +--------+---------+---------+---------+---------+
P.canescens NRRL910[T]              AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.atrovenetum NRRL2571[T]           AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.chrysogenum NRRL807[T]            AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.chrysogenum C8.24                 AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.notatum NRRL821[T]                AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.griseoroseum NRRL820[T]           AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.chrysogenum C8.12                 AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.nalgiovense NRRL911[T]            AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.chrysogenum NRRL824 Fleming strn  AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.notatum NRRL832 Biourge strn      AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
Eu.egyptiacum NRRL2090[T]           AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
Eu.crustaceum NRRL3332[T]           AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.viridicatum NRRL5880              AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.aethiopicum CBS484.84[T]          AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.gris.v.dipodomyicola NRRL13487[T] AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.camemberti NRRL874[T]             AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.caseicolum NRRL875[T]             AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.crustosum NRRL968                 AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.viridicatum NRRL961               AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.aurantiogriseum NRRL971[T]        AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.polonicum NRRL995[T]              AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.polonicum C74.1                   AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.viridicatum NRRL958[T]            AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.echinulatum NRRL1151[T]           AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.sclerotigenum NRRL786[T]          AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.sclerotigenum NRRL3461[T]         AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.olsonii CBS232.32[T]              AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.coprophilum NRRL13627[T]          AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.griseofulvum NRRL734[T]           AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.griseofulvum NRRL2300[T]          AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.chrys.v.dipodomyis NRRL13485[T]   AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.expansum NRRL974 Biourge strn     AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.turbatum NRRL757[T]               AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
?H.paradoxus NRRL2162[T]            AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.atramentosum NRRL795[T]           AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.swiecickii NRRL918[T]             AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.kojigenum NRRL3442[T]             AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.raistrickii NRRL2039[T]           AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.soppii NRRL2023[T]                AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.brevicompactum B65.4              AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.brevicompactum DAOM193712[T]      AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.stoloniferum ATCC10111[T]         AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.brevicompactum B251               AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.brevicompactum B132.1             AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
Eu.lapidosum NRRL718[T]             AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.bilaii  NRRL3391[T]               AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATA
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Penicillium subgenus *Penicillium*, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                  251      260       270       280       290       300
                                    +--------+---------+---------+---------+---------+
P.canescens NRRL910[T]              CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.atrovenetum NRRL2571[T]           CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.chrysogenum NRRL807[T]            CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.chrysogenum C8.24                 CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.notatum NRRL821[T]                CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.griseoroseum NRRL820[T]           CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.chrysogenum C8.12                 CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.nalgiovense NRRL911[T]            CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.chrysogenum NRRL824 Fleming strn  CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.notatum NRRL832 Biourge strn      CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
Eu.egyptiacum NRRL2090[T]           CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
Eu.crustaceum NRRL3332[T]           CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.viridicatum NRRL5880              CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.aethiopicum CBS484.84[T]          CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.gris.v.dipodomyicola NRRL13487[T] CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.camemberti NRRL874[T]             CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.caseicolum NRRL875[T]             CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.crustosum NRRL968                 CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.viridicatum NRRL961               CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.aurantiogriseum NRRL971[T]        CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.polonicum NRRL995[T]              CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.polonicum C74.1                   CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.viridicatum NRRL958[T]            CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.echinulatum NRRL1151[T]           CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.sclerotigenum NRRL786[T]          CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.sclerotigenum NRRL3461[T]         CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.olsonii CBS232.32[T]              CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.coprophilum NRRL13627[T]          CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.griseofulvum NRRL734[T]           CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.griseofulvum NRRL2300[T]          CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.chrys.v.dipodomyis NRRL13485[T]   CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.expansum NRRL974 Biourge strn     CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.turbatum NRRL757[T]               CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
?H.paradoxus NRRL2162[T]            CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.atramentosum NRRL795[T]           CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.swiecickii NRRL918[T]             CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.kojigenum NRRL3442[T]             CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.raistrickii NRRL2039[T]           CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.soppii NRRL2023[T]                CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.brevicompactum B65.4              CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.brevicompactum DAOM193712[T]      CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.stoloniferum ATCC10111[T]         CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.brevicompactum B251               CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.brevicompactum B132.1             CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
Eu.lapidosum NRRL718[T]             ACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.bilaii  NRRL3391[T]               ACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
                                      ************** *********************************
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Penicillium subgenus *Penicillium*, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                  301      310       320       330       340       350
                                    +--------+---------+---------+---------+---------+
P.canescens NRRL910[T]              TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.atrovenetum NRRL2571[T]           TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.chrysogenum NRRL807[T]            TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.chrysogenum C8.24                 TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.notatum NRRL821[T]                TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.griseoroseum NRRL820[T]           TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.chrysogenum C8.12                 TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTTCTG
P.nalgiovense NRRL911[T]            TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTTCTG
P.chrysogenum NRRL824 Fleming strn  TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTTCTG
P.notatum NRRL832 Biourge strn      TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTTCTG
Eu.egyptiacum NRRL2090[T]           TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTACTG
Eu.crustaceum NRRL3332[T]           TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTACTG
P.viridicatum NRRL5880             TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.aethiopicum CBS484.84[T]          TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.gris.v.dipodomyicola NRRL13487[T] TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.camemberti NRRL874[T]             TTGCGCCCCCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTCATTGCTG
P.caseicolum NRRL875[T]             TTGCGCCCCCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTCATTGCTG
P.crustosum NRRL968                 TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.viridicatum NRRL961               TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.aurantiogriseum NRRL971[T]        TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.polonicum NRRL995[T]              TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.polonicum C74.1                   TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.viridicatum NRRL958[T]            TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.echinulatum NRRL1151[T]           TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.sclerotigenum NRRL786[T]          TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.sclerotigenum NRRL3461[T]         TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.olsonii CBS232.32[T]              TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.coprophilum NRRL13627[T]          TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.griseofulvum NRRL734[T]           TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.griseofulvum NRRL2300[T]          TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.chrys.v.dipodomyis NRRL13485[T]   TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.expansum NRRL974 Biourge strn     TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.turbatum NRRL757[T]               TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
?H.paradoxus NRRL2162[T]            TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.atramentosum NRRL795[T]           TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.swiecickii NRRL918[T]             TTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTCATTGCTG
P.kojigenum NRRL3442[T]             TTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTCATTGCTG
P.raistrickii NRRL2039[T]           TTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTCATTGCTG
P.soppii NRRL2023[T]                TTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTCATTGCTG
P.brevicompactum B65.4              TTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTCATTGCTG
P.brevicompactum DAOM193712[T]      TTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTCATTGCTG
P.stoloniferum ATCC10111[T]         TTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTCATTGCTG
P.brevicompactum B251               TTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTCATTGCTG
P.brevicompactum B132.1             TTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTCATTGCTG
Eu.lapidosum NRRL718[T]             TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.bilaii  NRRL3391[T]               TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
                                    ******** ************ ************************ ***
```

Penicillium subgenus *Penicillium*, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                  351      360       370       380       390       400
                                    +--------+---------+---------+---------+---------+
P.canescens NRRL910[T]              CCCTCAAGCCCGGCTTGTGTGTTGGGT-CTCGTCCCCC-TTCCCGGGGGG
P.atrovenetum NRRL2571[T]           CCCTCAAGCCCGGCTTGTGTGTTGGGT-CTCGTCCCCC-TCCCCGGGGGG
P.chrysogenum NRRL807[T]            CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATC-CCGGGGG
P.chrysogenum C8.24                 CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATC-CCGGGGG
P.notatum NRRL821[T]                CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATC-CCGGGGG
P.griseoroseum NRRL820[T]           CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATC-CCGGGGG
P.chrysogenum C8.12                 CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATC-CCGGGGG
P.nalgiovense NRRL911[T]            CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATC-CCGGGGG
P.chrysogenum NRRL824 Fleming strn  CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATC-CCGGGGG
P.notatum NRRL832 Biourge strn      CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATC-CCGGGGG
Eu.egyptiacum NRRL2090[T]           CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATC-CCGGGGG
Eu.crustaceum NRRL3332[T]           CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCGTCCTCCGATC-CCGGGGG
P.viridicatum NRRL5880              CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATC-CCGGGGG
P.aethiopicum CBS484.84[T]          CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATC-CCGGGGG
P.gris.v.dipodomyicola NRRL13487[T] CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATC-CCGGGGG
P.camemberti NRRL874[T]             CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCGTCCTCCGATCTCCGGGGG
P.caseicolum NRRL875[T]             CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCGTCCTCCGATCTCCGGGGG
P.crustosum NRRL968                 CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCGTCCCCCGATCTCCGGGGG
P.viridicatum NRRL961               CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCGTCCTCCGATT-CCGGGGG
P.aurantiogriseum NRRL971[T]        CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCGTCCTCCGATT-CCGGGGG
P.polonicum NRRL995[T]              CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCGTCCTCCGATT-CCGGGGG
P.polonicum C74.1                   CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCGTCCTCCGATT-CCGGGGG
P.viridicatum NRRL958[T]            CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCGTCCTCCGATC-CCGGGGG
P.echinulatum NRRL1151[T]           CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCGTCCTCCGATTTCCGGGGG
P.sclerotigenum NRRL786[T]          CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCGTCCCCCGATC-CCGGGGG
P.sclerotigenum NRRL3461[T]         CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGTTC-CCGGGGG
P.olsonii CBS232.32[T]              CCCTCAAGCCCGGCTTGTGTGTTGGGT-CTCGTCCTCCGATT-CTGGAGG
P.coprophilum NRRL13627[T]          CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCGTCCTCCGATT-CCGGGGG
P.griseofulvum NRRL734[T]           CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATT-CCGGGGG
P.griseofulvum NRRL2300[T]          CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATT-CCGGGGG
P.chrys.v.dipodomyis NRRL13485[T]   CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATT-CCGGGGG
P.expansum NRRL974 Biourge strn     CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATT-CCGGGGG
P.turbatum NRRL757[T]               CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATT-CCGGGGG
?H.paradoxus NRRL2162[T]            CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCCCCGATC-CCGGGGG
P.atramentosum NRRL795[T]           CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATC-CCGGGGG
P.swiecickii NRRL918[T]             CCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCCCCGATC-CCGGGGG
P.kojigenum NRRL3442[T]             CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATC-CCGGGGG
P.raistrickii NRRL2039[T]           CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATC-CCGGGGG
P.soppii NRRL2023[T]                CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCCGATC-CCGGGGG
P.brevicompactum B65.4              CCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCTCC--TT-CCGGGGG
P.brevicompactum DAOM193712[T]      CCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCTCC--TT-CCGGGGG
P.stoloniferum ATCC10111[T]         CCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCTCC--TT-CCGGGGG
P.brevicompactum B251               CCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCTCC--TT-CCGGGGG
P.brevicompactum B132.1             CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCGTCCTCC--TT-CCGGGGG
Eu.lapidosum NRRL718[T]             CCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCCCC--C-----GGGG
P.bilaii  NRRL3391[T]               CCCTCAAGCACGGCTTGTGTGTTGGGCCTCCGTCCTCC--CCCCGGGGGG
                                    ********* ****************    ***** **        * **
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Penicillium subgenus *Penicillium*, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                  401      410       420       430       440       450
                                    +--------+---------+---------+---------+---------+
P.canescens NRRL910[T]              ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.atrovenetum NRRL2571[T]           ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.chrysogenum NRRL807[T]            ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.chrysogenum C8.24                 ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.notatum NRRL821[T]                ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.griseoroseum NRRL820[T]           ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.chrysogenum C8.12                 ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.nalgiovense NRRL911[T]            ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.chrysogenum NRRL824 Fleming strn  ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.notatum NRRL832 Biourge strn      ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
Eu.egyptiacum NRRL2090[T]           ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
Eu.crustaceum NRRL3332[T]           ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.viridicatum NRRL5880              ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.aethiopicum CBS484.84[T]          ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.gris.v.dipodomyicola NRRL13487[T] ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.camemberti NRRL874[T]             ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.caseicolum NRRL875[T]             ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.crustosum NRRL968                 ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.viridicatum NRRL961               ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.aurantiogriseum NRRL971[T]        ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.polonicum NRRL995[T]              ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.polonicum C74.1                   ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.viridicatum NRRL958[T]            ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.echinulatum NRRL1151[T]           ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.sclerotigenum NRRL786[T]          ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.sclerotigenum NRRL3461[T]         ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.olsonii CBS232.32[T]              ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTTCCTCGAGCGTATG
P.coprophilum NRRL13627[T]          ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.griseofulvum NRRL734[T]           ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.griseofulvum NRRL2300[T]          ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.chrys.v.dipodomyis NRRL13485[T]   ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.expansum NRRL974 Biourge strn     ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.turbatum NRRL757[T]               ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
?H.paradoxus NRRL2162[T]            ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.atramentosum NRRL795[T]           ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.swiecickii NRRL918[T]             ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.kojigenum NRRL3442[T]             ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.raistrickii NRRL2039[T]           ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.soppii NRRL2023[T]                ACGGGCCCGAAAGGCAGCGGCGGCACCGAGTCCGGT-CCTCGAGCGTATG
P.brevicompactum B65.4              ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCAAGCGTATG
P.brevicompactum DAOM193712[T]      ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCAAGCGTATG
P.stoloniferum ATCC10111[T]         ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCAAGCGTATG
P.brevicompactum B251               ACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCAAGCGTATG
P.brevicompactum B132.1             ACGGGTCCGAAAGGCAGCGGCGGCACCGCGTCCGGT-CCTCAAGCGTATG
Eu.lapidosum NRRL718[T]             ACGGGTCCGAAAGGCAGCGGCGGCACCGAGTCCGGT-CCTCGAGCGTATG
P.bilaii  NRRL3391[T]               ACGGGCCCGAAAGGCAGCGGCGGCACCGTGTCCGGT-CCTCGAGCGTATG
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Penicillium subgenus *Penicillium*, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

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                                  451      460       470       480       490       500
                                    +--------+---------+---------+---------+---------+
P.canescens NRRL910[T]              GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCA
P.atrovenetum NRRL2571[T]           GGGCTTTGTCACCCGCTCTGTAGGGCCGGCCGGCGCCTGCCGATCAACCA
P.chrysogenum NRRL807[T]            GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.chrysogenum C8.24                 GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.notatum NRRL821[T]                GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.griseoroseum NRRL820[T]           GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.chrysogenum C8.12                 GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.nalgiovense NRRL911[T]            GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.chrysogenum NRRL824 Fleming strn  GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.notatum NRRL832 Biourge strn      GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
Eu.egyptiacum NRRL2090[T]           GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
Eu.crustaceum NRRL3332[T]           GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.viridicatum NRRL5880             GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.aethiopicum CBS484.84[T]          GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.gris.v.dipodomyicola NRRL13487[T] GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.camemberti NRRL874[T]             GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.caseicolum NRRL875[T]             GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.crustosum NRRL968                 GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.viridicatum NRRL961               GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.aurantiogriseum NRRL971[T]        GGGCTTTGTCACCCGCTCCGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.polonicum NRRL995[T]              GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.polonicum C74.1                   GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.viridicatum NRRL958[T]            GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.echinulatum NRRL1151[T]           GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.sclerotigenum NRRL786[T]          GGGCTTTGTCACCCGCTCCGTAGGCCCGGCCGGCGCCTGCCGATCAACCC
P.sclerotigenum NRRL3461[T]         GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCCTGCCGATCAACCC
P.olsonii CBS232.32[T]              GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.coprophilum NRRL13627[T]          GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.griseofulvum NRRL734[T]           GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.griseofulvum NRRL2300[T]          GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.chrys.v.dipodomyis NRRL13485[T]   GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.expansum NRRL974 Biourge strn     GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
P.turbatum NRRL757[T]               GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
?H.paradoxus NRRL2162[T]            GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACC-
P.atramentosum NRRL795[T]           GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACC-
P.swiecickii NRRL918[T]             GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACC-
P.kojigenum NRRL3442[T]             GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACC-
P.raistrickii NRRL2039[T]           GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACC-
P.soppii NRRL2023[T]                GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACC-
P.brevicompactum B65.4              GGGCTTTGTCACCCGCTTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-
P.brevicompactum DAOM193712[T]      GGGCTTTGTCACCCGCTTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-
P.stoloniferum ATCC10111[T]         GGGCTTTGTCACCCGCTTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-
P.brevicompactum B251               GGGCTTTGTCACCCGCTTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-
P.brevicompactum B132.1             GGGCTTTGTCACTCGCTTTGTAGGCCTGGCCGGCGCTTGCCGATCAACC-
Eu.lapidosum NRRL718[T]             GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCCAGCCGA-CAACCA
P.bilaii  NRRL3391[T]               GGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTGGCCGA-CCCTCC
                                    ************ ****  ***** * *********  ***** *   *
```

Penicillium subgenus *Penicillium*, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

```
                                  501      510       520       530
                                    +--------+---------+---------+------
P.canescens NRRL910[T]              AAA--CTTTTTTCCAGGTTGACCTCGGATCAGGTAG
P.atrovenetum NRRL2571[T]           CAA--ATTTTTTCCAGGTTGACCTCGGATCAGGTAG
P.chrysogenum NRRL807[T]            AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.chrysogenum C8.24                 AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.notatum NRRL821[T]                AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.griseoroseum NRRL820[T]           AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.chrysogenum C8.12                 AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.nalgiovense NRRL911[T]            AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.chrysogenum NRRL824 Fleming strn  AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.notatum NRRL832 Biourge strn      AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
Eu.egyptiacum NRRL2090[T]           AAA--CTTCTAT--AGGTTGACCTCGGATCAGGTAG
Eu.crustaceum NRRL3332[T]           CAA--TTTTTAT--AGGTTGACCTCGGATCAGGTAG
P.viridicatum NRRL5880              AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.aethiopicum CBS484.84[T]          AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.gris.v.dipodomyicola NRRL13487[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.camemberti NRRL874[T]             AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.caseicolum NRRL875[T]             AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.crustosum NRRL968                 AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.viridicatum NRRL961               AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.aurantiogriseum NRRL971[T]        AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.polonicum NRRL995[T]              AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.polonicum C74.1                   AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.viridicatum NRRL958[T]            AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.echinulatum NRRL1151[T]           AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.sclerotigenum NRRL786[T]          CAAATTTTTAATCCAGGTTGACCTCGGATCAGGTAG
P.sclerotigenum NRRL3461[T]         CAA-TTTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.olsonii CBS232.32[T]              AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.coprophilum NRRL13627[T]          AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.griseofulvum NRRL734[T]           AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.griseofulvum NRRL2300[T]          AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.chrys.v.dipodomyis NRRL13485[T]   AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.expansum NRRL974 Biourge strn     AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.turbatum NRRL757[T]               AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
?H.paradoxus NRRL2162[T]            AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.atramentosum NRRL795[T]           AAA--ATTTTTTCCAGGTTGACCTCGGATCAGGTAG
P.swiecickii NRRL918[T]             AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.kojigenum NRRL3442[T]             AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.raistrickii NRRL2039[T]           AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.soppii NRRL2023[T]                AAA---TTTTTTCCAGGTTGACCTCGGATCAGGTAG
P.brevicompactum B65.4              AAA--CTTTTTTCCAGGTTGACCTCGGATCAGGTAG
P.brevicompactum DAOM193712[T]      AAA--CTTTTTTCCAGGTTGACCTCGGATCAGGTAG
P.stoloniferum ATCC10111[T]         AAA--CTTTTTTCCAGGTTGACCTCGGATCAGGTAG
P.brevicompactum B251               AAA--CTTTTTTCCAGGTTGACCTCGGATCAGTGAG
P.brevicompactum B132.1             AAA--CTTTTTATCAGGTTGACCTCGGATCAGGTAG
Eu.lapidosum NRRL718[T]             ATCATCCTTTTTTCAGGTTGACCTCGGATCAGGTAG
P.bilaii  NRRL3391[T]               AACCCCATTTTTTCAGGTTGACCTCGGATCAGGTAG
                                           *      *****************   **
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APPENDIX F

Alignments of gene sequences from *P. brevicompactum*

Invariant bases indicated by an asterisk

Penicillium brevicompactum, benA locus

CLUSTAL X (1.8) multiple sequence alignment

```
               1       10        20        30        40        50        60
               +--------+---------+---------+---------+---------+---------+
B132.1         TGGTATGTACCGCATCACGGTCTTTTTTTC-TCCCGCAATGGCTGGGCATCAATTGACAT 59
B65.4          TGGTATGTATCGCACCATG-TCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTGACAT 59
B251           TGGTATGTATCGCACCATG-TCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTGACAT 59
DAOM 193712    TGGTATGTATCGCACCATG-TCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTGACAA 59
ATCC 10111     TGGTATGTATCGCACCATG-TCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTGACAA 59
B306.2         TGGTATGTATCGCACCATG-TCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTGACAA 59
B117           TGGTATGTATCGCACCATG-TCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTGACAA 59
B99            TGGTATGTATCGCACCATG-TCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTAACAT 59
B244.1         TGGTATGTATCGCACCATGGTCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTGACAT 60
B65.6          TGGTATGTATCGCACCATG-TCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTGACAA 59
B75.3          TGGTATGTATCGCACCATG-TCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTGACAA 59
DAOM 193710    TGGTAAGTCTCGGA----G--CTTTTTTTT---TCGC----GTTGGGTATCAATTGACAA 47
               ***** **  ** *    *  ****** *     ***    * **** ******* ***

              61       70        80        90       100       110       120
               +--------+---------+---------+---------+---------+---------+
B132.1         CTTGCTAACTGACATCAAGGCAAACTATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
B65.4          TTTGCTAACTGGCTCTAAGGCAAACTATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
B251           TTTGCTAACTGGCTCTAAGGCAAACTATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
DAOM 193712    TTTGCTAACTGGCTCAAAGGCAAACTATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
ATCC 10111     TTTGCTAACTGGCTCAAAGGCAAACTATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
B306.2         TTTGCTAACTGGCTCAAAGGCAAACTATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
B117           TTTGCTAACTGGCTCAAAGGCAAACTATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
B99            TTTGCTAACTGATTCAAAGGCAAACTATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
B244.1         TTTGCTAACTGGCTCAAAGGCAAACTATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 120
B65.6          TTTGCTAACTGGCTTAAAGGCAAACTATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
B75.3          TTTGCTAACTGGCTTAAAGGCAAACTATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
DAOM 193710    GTTGCTAACTGGATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGAC 107
                **********      ******** ***** ****************************

             121      130       140       150       160       170       180
               +--------+---------+---------+---------+---------+---------+
B132.1         AGTAAGTGG---AGCGTACTGGGATCCCATGTGGATTGG--TTCTGATATATTGTTAGGT 174
B65.4          AGTAAGTGGACGACTGTGTTCGAATTACGCGTGGATTGG--GTCTGAGATCTTGTTAGGT 177
B251           AGTAAGTGGACGACTGTGTTCGAATTACGCGTGGATTGG--GTCTGAGATCTTGTTAGGT 177
DAOM 193712    AGTAAGTGGACGACTGTGTTCGAATTACGCGTGTATTGG--GTCTGAGATCTTGTTAGGT 177
ATCC 10111     AGTAAGTGGACGACTGTGTTCGAATTACGCGTGTATTGG--GTCTGAGATCTTGTTAGGT 177
B306.2         AGTAAGTGGACGACTGTGTTCGAATTACGCGTGGATTGG--GTCTGAGATCTTGTTAGGT 177
B117           AGTAAGTGGACGACTGTGTTCGAATTACGCGTGGATTGG--GTCTGAGATCTTGTTAGGT 177
B99            AGTAAGTGGACGACTGTGTTCGAATTACGCGTGGATTGG--GTCTGAGATCTTGTTAGGT 177
B244.1         AGTAAGTGGACGACTGTGTTCGAATTACGCGTGGATTGG--GTCTGAGATCTTGTTAGGT 178
B65.6          AGTAAGTGGACGACTGTGTTCGAATTATGCGTGGATGGG--GTCTGAGATCTTGTTAGGT 177
B75.3          AGTAAGTGGACGACTGTGTTCGAATTATGCGTGGATGGG--GTCTGAGATCTTGTTAGGT 177
DAOM 193710    AGTAAGTTTA--ACAGTGATGGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGT 165
               *******     *  **  * *        *** **      ***** ** *** *****
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             181      190       200       210       220       230       240
               +--------+---------+---------+---------+---------+---------+
B132.1         ACAACGGTACCTCCGACCTCCAGCTGGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 234
B65.4          ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 237
B251           ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 237
DAOM 193712    ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 237
ATCC 10111     ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 237
B306.2         ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 237
B117           ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 237
B99            ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 237
B244.1         ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 238
B65.6          ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 237
B75.3          ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 237
DAOM 193710    ACAATGGTACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 225
               **** ** ***************** **********************************

             241      250       260       270       280       290       300
               +--------+---------+---------+---------+---------+---------+
B132.1         CAATGCCTTGGATAAATTTTGTTGTGTGTTTGCTCACCCGG----ATTCTTTGACCTCCC 290
B65.4          CAATGATGTGAAGAACTCTGGTTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 293
B251           CAATGATGTGAAGAACTCTGGTTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 293
DAOM 193712    CAATGATGTGAAGAACTCTGGTTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 293
ATCC 10111     CAATGATGTGAAGAACTCTGGTTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 293
B306.2         CAATGATGTGAAGAACTCTGGTTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 293
B117           CAATGATGTGAAGAACTCTGGTTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 293
B99            CAATGATGTGAAGAACTCTTGTTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 293
B244.1         CAATGATGTGAAGAACTCTTGTTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 294
B65.6          CAATGATGTGAAGAACTCTTGTTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 293
B75.3          CAATGATGTGAAGAACTCTTGTTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 293
DAOM 193710    CAATGACTGGG--AATCTTAATTGTGCATCATCTGATCGGGCGTTTTTCTTTGACAATCT 283
               *****    *   **   *  *****  *   ** * *         *  *****   * 

             301      310       320       330       340       350       360
               +--------+---------+---------+---------+---------+---------+
B132.1         AGGCTAGCGGTGACAAGTATGTTCCCCGTGCCGTCCTCGTCGATTTGGAGCCCGGTACCA 350
B65.4          AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 353
B251           AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 353
DAOM 193712    AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 353
ATCC 10111     AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 353
B306.2         AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 353
B117           AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 353
B99            AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 353
B244.1         AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 354
B65.6          AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 353
B75.3          AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 353
DAOM 193710    AGGCCAGCGGTGACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCA 343
               **** ** *********** ************** ** ***** ****************

             361      370       380       390       400       410       420
               +--------+---------+---------+---------+---------+---------+
B132.1         TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCG 410
B65.4          TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCG 413
B251           TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCG 413
DAOM 193712    TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCG 413
ATCC 10111     TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCG 413
B306.2         TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCG 413
B117           TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCG 413
B99            TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCG 413
B244.1         TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCG 414
B65.6          TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCG 413
B75.3          TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCG 413
DAOM 193710    TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCG 403
               ************************************************************
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               421      430       440  445
                 +--------+---------+----+
B132.1           GTCAGTCCGGTGCTGGTAACAACTG 435
B65.4            GTCAATCCGGTGCTGGTAACAACTG 438
B251             GTCAATCCGGTGCTGGTAACAACTG 438
DAOM 193712      GTCAATCCGGTGCTGGTAACAACTG 438
ATCC 10111       GTCAATCCGGTGCTGGTAACAACTG 438
B306.2           GTCAATCCGGTGCTGGTAACAACTG 438
B117             GTCAATCCGGTGCTGGTAACAACTG 438
B99              GTCAGTCCGGTGCTGGTAACAACTG 438
B244.1           GTCAGTCCGGTGCTGGTAACAACTG 439
B65.6            GTCAGTCCGGTGCTGGTAACAACTG 438
B75.3            GTCAGTCCGGTGCTGGTAACAACTG 438
DAOM 193710      GTCAGTCCGGTGCTGGTAACAACTG 428
                 **** ********************
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Penicillium brevicompactum, rDNA ITS1-5.8S-ITS2 locus

CLUSTAL X (1.8) multiple sequence alignment

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               1       10        20        30        40        50        60
               +--------+---------+---------+---------+---------+---------+
B132.1         TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
B65.4          TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
B251           TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
DAOM 193712    TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
ATCC 10111     TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
B306.2         TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
B117           TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
B99            TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
B244.1         TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
B65.6          TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
B75.3          TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
DAOM 193710    TTCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 60
               ************** *********************************************

              61       70        80        90       100       110       120
               +--------+---------+---------+---------+---------+---------+
B132.1         CCACCCGTGTTTATTT-ACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 116
B65.4          CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
B251           CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
DAOM 193712    CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
ATCC 10111     CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
B306.2         CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
B117           CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
B99            CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
B244.1         CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
B65.6          CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
B75.3          CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
DAOM 193710    CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGG 120
               **************** ***************** *** *****   **** ********

             121       130       140       150       160       170       180
               +--------+---------+---------+---------+---------+---------+
B132.1         ACGTCAGTCCCCGGGTCCGTGCTCGCCGGAGACACCTTAGAACTCTGTCTGAAGATTGTA 176
B65.4          ACGTCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
B251           ACATCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
DAOM 193712    ACGTCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
ATCC 10111     ACGTCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
B306.2         ACATCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
B117           ACGTCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
B99            ACGTCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
B244.1         ACATCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
B65.6          ACATCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
B75.3          ACATCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
DAOM 193710    GCTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTA 180
                * *  * ******* *** ** ***** ******* * *********************
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              181       190       200       210       220       230       240
                +---------+---------+---------+---------+---------+---------+
B132.1          GTCTGAGATTAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCAT 236
B65.4           GTCTGAGATTAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCAT 237
B251            GTCTGAGATTAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCAT 237
DAOM 193712     GTCTGAGATTAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCAT 237
ATCC 10111      GTCTGAGATTAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCAT 237
B306.2          GTCTGAGATTAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCAT 237
B117            GTCTGAGATTAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCAT 237
B99             GTCTGAGATTAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCAT 237
B244.1          GTCTGAGATTAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCAT 237
B65.6           GTCTGAGATTAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCAT 237
B75.3           GTCTGAGATTAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCAT 237
DAOM 193710     GTCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCAT 240
                *******   **************************************************

              241       250       260       270       280       290       300
                +---------+---------+---------+---------+---------+---------+
B132.1          CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC 296
B65.4           CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC 297
B251            CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC 297
DAOM 193712     CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC 297
ATCC 10111      CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC 297
B306.2          CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC 297
B117            CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC 297
B99             CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC 297
B244.1          CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC 297
B65.6           CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC 297
B75.3           CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC 297
DAOM 193710     CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATC 299
                ******************************************* ****************

              301       310       320       330       340       350       360
                +---------+---------+---------+---------+---------+---------+
B132.1          GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC 356
B65.4           GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC 357
B251            GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC 357
DAOM 193712     GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC 357
ATCC 10111      GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC 357
B306.2          GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC 357
B117            GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC 357
B99             GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC 357
B244.1          GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC 357
B65.6           GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC 357
B75.3           GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC 357
DAOM 193710     GAGTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTC 359
                ************************* ************ *********************

              361       370       380       390       400       410       420
                +---------+---------+---------+---------+---------+---------+
B132.1          ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCC--TTCCGGGGGACGGG 414
B65.4           ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCCTCC--TTCCGGGGGACGGG 415
B251            ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCCTCC--TTCCGGGGGACGGG 415
DAOM 193712     ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCCTCC--TTCCGGGGGACGGG 415
ATCC 10111      ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCCTCC--TTCCGGGGGACGGG 415
B306.2          ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCCTCC--TTCCGGGGGACGGG 415
B117            ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCCTCC--TTCCGGGGGACGGG 415
B99             ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCCTCC--TTCCGGGGGACGGG 415
B244.1          ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCCTCC--TTCCGGGGGACGGG 415
B65.6           ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCCTCC--TTCCGGGGGACGGG 415
B75.3           ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCCTCC--TTCCGGGGGACGGG 415
DAOM 193710     ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGG 419
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             421      430       440       450       460       470       480
               +--------+---------+---------+---------+---------+---------+
B132.1         TCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCAAGCGTATGGGGCTTTGTCACTCGC 474
B65.4          CCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCAAGCGTATGGGGCTTTGTCACCCGC 475
B251           CCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCAAGCGTATGGGGCTTTGTCACCCGC 475
DAOM 193712    CCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCAAGCGTATGGGGCTTTGTCACCCGC 475
ATCC 10111     CCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCAAGCGTATGGGGCTTTGTCACCCGC 475
B306.2         CCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCAAGCGTATGGGGCTTTGTCACCCGC 475
B117           CCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCAAGCGTATGGGGCTTTGTCACCCGC 475
B99            CCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCAAGCGTATGGGGCTTTGTCACCCGC 475
B244.1         CCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCAAGCGTATGGGGCTTTGTCACCCGC 475
B65.6          CCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCAAGCGTATGGGGCTTTGTCACCCGC 475
B75.3          CCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCAAGCGTATGGGGCTTTGTCACCCGC 475
DAOM 193710    CCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGC 479
                ********************************** ******************** ***

             481      490       500       510       520       530       540
               +--------+---------+---------+---------+---------+---------+
B132.1         TTTGTAGGCCTGGCCGGCGCTTGCCGATCAACC-AAACTTTTTATCAGGTTGACCTCGGA 533
B65.4          TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
B251           TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
DAOM 193712    TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
ATCC 10111     TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
B306.2         TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
B117           TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
B99            TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
B244.1         TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
B65.6          TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
B75.3          TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
DAOM 193710    TCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGA 539
               * ****** * ********* ************ *** ****   ***************

             541    548
               +------+
B132.1         TCAGGTAG 541
B65.4          TCAGGTAG 542
B251           TCAGGTAG 542
DAOM 193712    TCAGGTAG 542
ATCC 10111     TCAGGTAG 542
B306.2         TCAGGTAG 542
B117           TCAGGTAG 542
B99            TCAGGTAG 542
B244.1         TCAGGTAG 542
B65.6          TCAGGTAG 542
B75.3          TCAGGTAG 542
DAOM 193710    TCAGGTAG 547
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APPENDIX G

Alignments of gene sequences from *Penicillium chrysogenum*

Invariant bases indicated by an asterisk

Penicillium chrysogenum, acuA locus

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CLUSTAL X (1.8) multiple sequence alignment

                 1       10        20        30        40        50        60
                 +--------+---------+---------+---------+---------+---------+
NRRL_13485       GACACTTACTTGAATGTGTACAAGGGTTACTACGTAAGACGCC-CGCAGC--CTGACTCA
NRRL_911         GACACTTACTTGAATGTGTACAAGGGTTACTACGTAAGACGCC-CGCAGC--CTGACTCA
CBS_484.84       GACACTTACTTGAATGTGTACAAGGGTTACTACGTAAGACTCCTCGCAGCGCCTGGCTTA
C8.24            GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTCGCAAC--CTGACTTG
DAOM_193710      GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTCGCAAC--CTGACTTG
DAOM_155631      GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTCGCAAC--CTGACTTG
DAOM_171025      GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTCGCAAC--CTGACTTG
DAOM_178623      GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTCGCAAC--CTGACTTG
DAOM_215337      GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTCGCAAC--CTGACTTG
DAOM_216701      GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTCGCAAC--CTGACTTG
ATCC_10108       GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTCGCAAC--CTGACTTG
DAOM_215336      GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCTTCGCAGC--CTGCCTTG
DAOM_216700      GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCTTCGCAGC--CTGCCTTG
DAOM_212031      GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCTTCGCAGC--CTGCCTTG
DAOM_190864      GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCTTCGCAGC--CTGCCTTG
DAOM_175758      GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCTTCGCAGC--CTGCCTTG
DAOM_175176      GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCTTCGCAGC--CTGCCTTG
DAOM_175157      GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCTTCGCAGC--CTGCCTTG
DAOM_167036      GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCTTCGCAGC--CTGCCTTG
DAOM_155628      GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCTTCGCAGC--CTGCCTTG
DAOM_155627      GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCTTCGCAGC--CTGCCTTG
DAOM_59494C      GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCTTCGCAGC--CTGCCTTG
C200             GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCTTCGCAGC--CTGCCTTG
C317.1           GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCTTCGCAGC--CTGCCTTG
NASA             GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCTTCGCAGC--CTGCCTTG
NRRL_824         GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCTTCGCAGC--CTGCCTTG
C8.12            GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCTTCGCAGC--CTGCCTTG
C238             GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTCGCAGC--CTGACTTG
NRRL_13487       GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGCCGCCCCGCAGT-CCGAATTTA
                 ************** *********************** * *  ****    *    *
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Penicillium chrysogenum, acuA locus

CLUSTAL X (1.8) multiple sequence alignment

```
                 61      70        80        90       100       110       120
                 +--------+---------+---------+---------+---------+---------+
NRRL_13485       CAAGATTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCGTGACCACGAC
NRRL_911         CAAGATTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCGTGACCACGAC
CBS_484.84       CATGATTGGTAACTTACTTATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
C8.24            CAGGATCGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
DAOM_193710      CAGGATCGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
DAOM_155631      CAGGATCGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
DAOM_171025      CAGGATCGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
DAOM_178623      CAGGATCGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
DAOM_215337      CAGGATCGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
DAOM_216701      CAGGATCGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
ATCC_10108       CAGGATCGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
DAOM_215336      CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
DAOM_216700      CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
DAOM_212031      CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
DAOM_190864      CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
DAOM_175758      CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
DAOM_175176      CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
DAOM_175157      CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
DAOM_167036      CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
DAOM_155628      CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
DAOM_155627      CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
DAOM_59494C      CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
C200             CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
C317.1           CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
NASA             CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
NRRL_824         CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
C8.12            CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
C238             CAGGATTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGCCGTGACCACGAC
NRRL_13487       TGGAATTGATA-CTAACCCGTCTATAGTTCACCGGAGATGGTGCTGGCCGTGATCACGAC
                      * * ** ** **   * ************************* ***** ******
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Penicillium chrysogenum, acuA locus

CLUSTAL X (1.8) multiple sequence alignment

```
                121      130       140       150       160       170       180
                  +--------+---------+---------+---------+---------+---------+
NRRL_13485        GGTTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
NRRL_911          GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
CBS_484.84        GGCTACTACTGGATCCGCGGTCGCGTCGACGATGTTGTCAATGTTTCTGGACACCGTCTG
C8.24             GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_193710       GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_155631       GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_171025       GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_178623       GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_215337       GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_216701       GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
ATCC_10108        GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_215336       GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_216700       GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_212031       GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_190864       GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_175758       GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_175176       GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_175157       GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_167036       GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_155628       GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_155627       GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_59494C       GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
C200              GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
C317.1            GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
NASA              GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
NRRL_824          GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
C8.12             GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
C238              GGCTACTACTGGATCCGTGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
NRRL_13487        GGCTACTACTGGATCCGTGGCCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
                  ** ** *********** ** ** ** ******** ***** ******************
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Penicillium chrysogenum, acuA locus

CLUSTAL X (1.8) multiple sequence alignment

```
               181      190       200       210       220       230       240
                 +--------+---------+---------+---------+---------+---------+
NRRL_13485       TCCACCGCTGAGATCGAGGCTGCTCTTCTCGAGCACCGTAAGTGCAACCACAGTACCTGT
NRRL_911         TCCACCGCTGAGATCGAGGCTGCTCTTCTCGAGCACCGTAAGTGCAACCACAGTACCTGT
CBS_484.84       TCCACCGCCGAGATCGAGGCTGCTCTTCTCGAGCACCGTAAGTGCAACCACAGTACCTGT
C8.24            TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTACCTGC
DAOM_193710      TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTACCTGC
DAOM_155631      TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTACCTGC
DAOM_171025      TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTACCTGC
DAOM_178623      TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTACCTGC
DAOM_215337      TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTACCTGC
DAOM_216701      TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTACCTGC
ATCC_10108       TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTACCTGC
DAOM_215336      TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
DAOM_216700      TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
DAOM_212031      TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
DAOM_190864      TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
DAOM_175758      TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
DAOM_175176      TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
DAOM_175157      TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
DAOM_167036      TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
DAOM_155628      TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
DAOM_155627      TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
DAOM_59494C      TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
C200             TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
C317.1           TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
NASA             TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
NRRL_824         TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
C8.12            TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
C238             TCCACCGCCGAGATTGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTACCTGC
NRRL_13487       TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTGCAACCACAGTACATTC
                 ******** ***** ***** ********************** ***********  *
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Penicillium chrysogenum, acuA locus

CLUSTAL X (1.8) multiple sequence alignment

```
               241      250       260       270       280       290
                 +--------+---------+---------+---------+---------+----
NRRL_13485       CAAAACTTGCAACTGAGCCCAAACTAACTATGAACAGCTTCTGTTGCCGAGGCT
NRRL_911         CAAAACTTGCAACTGAGCCCAAACTAACCATGAACAGCTTCTGTTGCCGAGGCT
CBS_484.84       CAAAAATCGCAAATGAGCCCAAACTAACTATGAACAGCTTCTGTTGCCGAGGCT
C8.24            CAAAAATTGGAACTGAGCCCAAACTAACTACGAACAGCTTCCGTTGCCGAGGCT
DAOM_193710      CAAAAATTGGAACTGAGCCCAAACTAACTACGAACAGCTTCCGTTGCCGAGGCT
DAOM_155631      CAAAAATTGGAACTGAGCCCAAACTAACTACGAACAGCTTCCGTTGCCGAGGCT
DAOM_171025      CAAAAATTGGAACTGAGCCCAAACTAACTACGAACAGCTTCCGTTGCCGAGGCT
DAOM_178623      CAAAAATTGGAACTGAGCCCAAACTAACTACGAACAGCTTCCGTTGCCGAGGCT
DAOM_215337      CAAAAATTGGAACTGAGCCCAAACTAACTACGAACAGCTTCCGTTGCCGAGGCT
DAOM_216701      CAAAAATTGGAACTGAGCCCAAACTAACTACGAACAGCTTCCGTTGCCGAGGCT
ATCC_10108       CAAAAATTGGAACTGAGCCCAAACTAACTACGAACAGCTTCCGTTGCCGAGGCT
DAOM_215336      CAAAAATTGCAACTGAGCCCAAACTAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_216700      CAAAAATTGCAACTGAGCCCAAACTAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_212031      CAAAAATTGCAACTGAGCCCAAACTAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_190864      CAAAAATTGCAACTGAGCCCAAACTAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_175758      CAAAAATTGCAACTGAGCCCAAACTAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_175176      CAAAAATTGCAACTGAGCCCAAACTAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_175157      CAAAAATTGCAACTGAGCCCAAACTAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_167036      CAAAAATTGCAACTGAGCCCAAACTAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_155628      CAAAAATTGCAACTGAGCCCAAACTAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_155627      CAAAAATTGCAACTGAGCCCAAACTAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_59494C      CAAAAATTGCAACTGAGCCCAAACTAACTATGAACAGCTTCCGTTGCCGAGGCT
C200             CAAAAATTGCAACTGAGCCCAAACTAACTATGAACAGCTTCCGTTGCCGAGGCT
C317.1           CAAAAATTGCAACTGAGCCCAAACTAACTATGAACAGCTTCCGTTGCCGAGGCT
NASA             CAAAAATTGCAACTGAGCCCAAACTAACTATGAACAGCTTCCGTTGCCGAGGCT
NRRL_824         CAAAAATTGCAACTGAGCCCAAACTAACTATGAACAGCTTCCGTTGCCGAGGCT
C8.12            CAAAAATTGCAACTGAGCCCAAACTAACTATGAACAGCTTCCGTTGCCGAGGCT
C238             CAAAAATTGCAACTGAGCCCAAACTAACTATGAACAGCCTCCGTTGCCGAGGCT
NRRL_13487       AAAGATTGCCAACTGAGCCCAAACTGACTATAAACAGCTTCTGTTGCCGAAGCT
                  ** * *   ** ************ ** *  ****** ** ******** ***
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Penicillium chrysogenum, Bt2 locus

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CLUSTAL X (1.8) multiple sequence alignment

                 1       10        20        30        40        50        60
                 +--------+---------+---------+---------+---------+---------+
NRRL_911         TGGTAAGTCTCGGATCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTACTAACTG
NRRL_13485       TGGTAAGTGCCGGAGCTTTTTTTTTTCCGCGTTGGGTATCAATTGACAAGTTACTAACTG
C8.24            TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
ATCC_10108       TGGTAAGTCTCGGAGCTTTTTTTT---CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
C238             TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_155631      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_171025      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_178623      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_193710      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_215337      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_216701      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
C200             TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
C317.1           TGGTAAGTCTCGGAGCTTTTTTTT---CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
NASA             TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
NRRL_824         TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_216700      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_215336      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_212031      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_189864      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_175758      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_175176      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_175157      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_167036      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_155628      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_155627      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_59494C      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
C8.12            TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
CBS_484.84       TGGTAAGTGTTTGAGCTTTTTT-----CGCGTTGGGTATCAATTGACAAGTTACTAACCG
NRRL_13487       TGGTATGTGCC-GAGCTTTTTTTCC--CGCGTTGGGTATCAATTGACAAGTTACTAACTG
                 ***** **    ** *******     ************************* ***** *
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Penicillium chrysogenum, Bt2 locus

```
CLUSTAL X (1.8) multiple sequence alignment

                61       70        80        90       100       110       120
                 +--------+---------+---------+---------+---------+---------+
NRRL_911         GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
NRRL_13485       GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
C8.24            GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
ATCC_10108       GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
C238             GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_155631      GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_171025      GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_178623      GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_193710      GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_215337      GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_216701      GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
C200             GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
C317.1           GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
NASA             GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
NRRL_824         GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_216700      GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_215336      GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_212031      GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_189864      GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_175758      GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_175176      GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_175157      GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_167036      GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_155628      GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_155627      GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_59494C      GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
C8.12            GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
CBS_484.84       AATTACAGGCAGACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
NRRL_13487       GATTACAGGCAAACCATTTCCGGCGAGCACGGTCTCGATGGTGATGGACAGTAAGTT-AA
                  ********** ***** ** ******************** *************** **
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Penicillium chrysogenum, Bt2 locus

CLUSTAL X (1.8) multiple sequence alignment

```
               121      130       140       150       160       170       180
                 +--------+---------+---------+---------+---------+---------+
NRRL_911         CAGTGATGGGGATTCTGGTGGACTACACGTCTGATATATTGCTAGGTACAATGGTACCTC
NRRL_13485       CAGTGATGGGGATTCTGGTGGACCACACGTCTGATATATTGCTAGGTACAATGGTACCTC
C8.24            CAGTGATGGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
ATCC_10108       CAGTGATGGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
C238             CAGTGATGGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_155631      CAGTGATGGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_171025      CAGTGATGGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_178623      CAGTGATGGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_193710      CAGTGATGGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_215337      CAGTGATGGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_216701      CAGTGATGGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
C200             CAGTGATGGGGATTTTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
C317.1           CAGTGATAGGGATTTTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
NASA             CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
NRRL_824         CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_216700      CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_215336      CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_212031      CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_189864      CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_175758      CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_175176      CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_175157      CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_167036      CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_155628      CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_155627      CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_59494C      CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
C8.12            CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
CBS_484.84       CAGTGATGGGG-TTTTGGTGGATAGCACGTCTGATATCTTGCTAGGTACAATGGTACCTC
NRRL_13487       TAGCGATGGCTTCTCCAGTAGATGACATGTCTGATATCTTGTTAGGTACAATGGTACCTC
                  ** *** *    *   ** **   ** ********* *** ******************
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Penicillium chrysogenum, Bt2 locus

CLUSTAL X (1.8) multiple sequence alignment

```
               181      190       200       210       220       230       240
                 +--------+---------+---------+---------+---------+---------+
NRRL_911         CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
NRRL_13485       CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
C8.24            CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
ATCC_10108       CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
C238             CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_155631      CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_171025      CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_178623      CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_193710      CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_215337      CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_216701      CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
C200             CGACCTCCAGCTCGAACGCATGAACGTCTACTTCAACCATGTGAGTACAAT-GGCTGGGA
C317.1           CGACCTCCAGCTCGAACGCATGAACGTCTACTTCAACCATGTGAGTACAAT-GGCTGGGA
NASA             CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
NRRL_824         CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_216700      CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_215336      CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_212031      CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_189864      CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_175758      CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_175176      CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_175157      CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_167036      CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_155628      CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_155627      CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_59494C      CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
C8.12            CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
CBS_484.84       CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGG
NRRL_13487       CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTATAGCCGATTGGGA
                 *************** ** **************************** *   *  ****
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Penicillium chrysogenum, Bt2 locus

CLUSTAL X (1.8) multiple sequence alignment

```
              241      250       260       270       280       290       300
                +--------+---------+---------+---------+---------+---------+
NRRL_911        ATCGATCAATCGTGCATCATCTGATCGGATGTTTTTCTTTGATAATCTAGGCCAGCGGTG
NRRL_13485      ATCGATCAATCGTGCATCATCTGATCGGATATTTTTCTTTGATAATCTAGGCCAGCGGTG
C8.24           ATC--TTAATTGTGCATCATCTGATCGGGCGTTTTTCTTTGACAATCTAGGCCAGCGGTG
ATCC_10108      ATC--TTAATTGTGCATCATCTGATCGGGCGTTTTTCTTTGACAATCTAGGCCAGCGGTG
C238            ATC--TTAATTGTGCATCATCTGATCGGGCGTTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_155631     ATC--TTAATTGTGCATCATCTGATCGGGCGTTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_171025     ATC--TTAATTGTGCATCATCTGATCGGGCGTTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_178623     ATC--TTAATTGTGCATCATCTGATCGGGCGTTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_193710     ATC--TTAATTGTGCATCATCTGATCGGGCGTTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_215337     ATC--TTAATTGTGCATCATCTGATCGGGCGTTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_216701     ATC--TTAATTGTGCATCATCTGATCGGGCGTTTTTCTTTGACAATCTAGGCCAGCGGTG
C200            ATCGATTAATTGTGCATCATCTGATCGGGCGTTTTTCTTTGACAATCTAGGCCAGCGGTG
C317.1          ATCGATTAATTGTGCATCATCTGATCGGGCGTTTTTCTTTGACAATCTAGGCCAGCGGTG
NASA            ATCGATTGATTGTGCATCATCTGATCGGACGTTTTTCTTTGACAATCTAGGCCAGCGGTG
NRRL_824        ATCGATTGATTGTGCATCATCTGATCGGACGTTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_216700     ATCGATTGATTGTGCATCATCTGATCGGACGTTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_215336     ATCGATTGATTGTGCATCATCTGATCGGACGTTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_212031     ATCGATTGATTGTGCATCATCTGATCGGACGTTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_189864     ATCGATTGATTGTGCATCATCTGATCGGACGTTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_175758     ATCGATTGATTGTGCATCATCTGATCGGACGTTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_175176     ATCGATTGATTGTGCATCATCTGATCGGACGTTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_175157     ATCGATTGATTGTGCATCATCTGATCGGACGTTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_167036     ATCGATTGATTGTGCATCATCTGATCGGACGTTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_155628     ATCGATTGATTGTGCATCATCTGATCGGACGTTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_155627     ATCGATTGATTGTGCATCATCTGATCGGACGTTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_59494C     ATCGATTGATTGTGCATCATCTGATCGGACGTTTTTCTTTGACAATCTAGGCCAGCGGTG
C8.12           ATCGATTGATTGTGCATCATCTGATCGGACGTTTTTCTTTGACAATCTAGGCCAGCGGTG
CBS_484.84      ACCAATCAATCGTGCATCATCTGATCGGACGTTTCTCTTTGATAATCTAGGCCAGCGGTG
NRRL_13487      ACCGAT-AATCGTGCATCATCTGATCGGATCTTTTTCTTTGATAATCTAGGCCAGCGGTG
                * *  *  ** *****************   *** ******* *****************
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Penicillium chrysogenum, Bt2 locus

CLUSTAL X (1.8) multiple sequence alignment

```
                301      310       320       330       340       350       360
                  +--------+---------+---------+---------+---------+---------+
NRRL_911        ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
NRRL_13485      ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
C8.24           ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
ATCC_10108      ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
C238            ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
DAOM_155631     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
DAOM_171025     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
DAOM_178623     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
DAOM_193710     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
DAOM_215337     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
DAOM_216701     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
C200            ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
C317.1          ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
NASA            ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
NRRL_824        ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_216700     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_215336     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_212031     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_189864     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_175758     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_175176     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_175157     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_167036     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_155628     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_155627     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_59494C     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
C8.12           ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
CBS_484.84      ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
NRRL_13487      ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
                **************************************************** *******
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Penicillium chrysogenum, Bt2 locus

CLUSTAL X (1.8) multiple sequence alignment

```
              361      370       380       390       400       410       420
                +--------+---------+---------+---------+---------+---------+
NRRL_911        GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCATTCGGGTG
NRRL_13485      GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
C8.24           GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
ATCC_10108      GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
C238            GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
DAOM_155631     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
DAOM_171025     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
DAOM_178623     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
DAOM_193710     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
DAOM_215337     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
DAOM_216701     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
C200            GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
C317.1          GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
NASA            GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
NRRL_824        GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
DAOM_216700     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
DAOM_215336     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
DAOM_212031     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
DAOM_189864     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
DAOM_175758     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
DAOM_175176     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
DAOM_175157     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
DAOM_167036     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
DAOM_155628     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
DAOM_155627     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
DAOM_59494C     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
C8.12           GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
CBS_484.84      GCTCCGGTCCTTTCGGCAAGCTTTTCCGCCCCGACAACTTCGTCTTCGGTCAGTCCGGTG
NRRL_13487      GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGATAACTTCGTCTTCGGTCAGTCCGGTG
                ********** *********************** ***************** ** ****
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Penicillium chrysogenum, Bt2 locus

CLUSTAL X (1.8) multiple sequence alignment

```
               421      430
                 +--------+----
NRRL_911         CTGGTAACAACTGG
NRRL_13485       CTGGTAACAACTGG
C8.24            CTGGTAACAACTGG
ATCC_10108       CTGGTAACAACTGG
C238             CTGGTAACAACTGG
DAOM_155631      CTGGTAACAACTGG
DAOM_171025      CTGGTAACAACTGG
DAOM_178623      CTGGTAACAACTGG
DAOM_193710      CTGGTAACAACTGG
DAOM_215337      CTGGTAACAACTGG
DAOM_216701      CTGGTAACAACTGG
C200             CTGGTAACAACTGG
C317.1           CTGGTAACAACTGG
NASA             CTGGTAACAACTGG
NRRL_824         CTGGTAACAACTGG
DAOM_216700      CTGGTAACAACTGG
DAOM_215336      CTGGTAACAACTGG
DAOM_212031      CTGGTAACAACTGG
DAOM_189864      CTGGTAACAACTGG
DAOM_175758      CTGGTAACAACTGG
DAOM_175176      CTGGTAACAACTGG
DAOM_175157      CTGGTAACAACTGG
DAOM_167036      CTGGTAACAACTGG
DAOM_155628      CTGGTAACAACTGG
DAOM_155627      CTGGTAACAACTGG
DAOM_59494C      CTGGTAACAACTGG
C8.12            CTGGTAACAACTGG
CBS_484.84       CTGGTAACAACTGG
NRRL_13487       CTGGTAACAACTGG
                 **************
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Penicillium chrysogenum, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

```
                1       10        20        30        40        50        60
                +--------+---------+---------+---------+---------+---------+
C8.24           TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
NRRL13485       TCCGTAGGTGAACCTGCGGAAGGATCATTACTGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM193710      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
C317.1          TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
C238            TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM155631      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM171025      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM178623      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM215337      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM216701      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
ATCC_10108      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
C200            TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
NRRL911         TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM175157      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM215336      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM216700      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM212031      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM190864      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM175758      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM175176      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM167036      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM155628      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM155627      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM59494C      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
NRRL824         TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
NASA            TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
C8.12           TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
NRRL13487       TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
CBS484.84       TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
                ******************************* ****************************
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Penicillium chrysogenum, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

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               61       70        80        90        100       110       120
                +--------+---------+---------+---------+---------+---------+
C8.24           CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
NRRL13485       CACCCGTGTTTATTT-ACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
DAOM193710      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
C317.1          CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
C238            CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
DAOM155631      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
DAOM171025      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
DAOM178623      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
DAOM215337      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
DAOM216701      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
ATCC_10108      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
C200            CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
NRRL911         CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
DAOM175157      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
DAOM215336      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
DAOM216700      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
DAOM212031      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
DAOM190864      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
DAOM175758      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
DAOM175176      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
DAOM167036      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
DAOM155628      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
DAOM155627      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
DAOM59494C      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
NRRL824         CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
NASA            CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
C8.12           CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
NRRL13487       CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
CBS484.84       CACCCGTGTTTATTTTTCCTTGTTGCTTCGGCGGGCCCGCCTTAACTGGCCGCCGGGGGG
                ***************  *******************************************
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Penicillium chrysogenum, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

```
              121      130       140       150       160       170       180
                +--------+---------+---------+---------+---------+---------+
C8.24           CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
NRRL13485       CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM193710      CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
C317.1          CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
C238            CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM155631      CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM171025      CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM178623      CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM215337      CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM216701      CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
ATCC_10108      CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
C200            CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
NRRL911         CTTACGCCCCCGGGCCCGCGCCCGCGGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM175157      CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM215336      CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM216700      CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM212031      CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM190864      CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM175758      CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM175176      CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM167036      CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM155628      CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM155627      CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM59494C      CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
NRRL824         CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
NASA            CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
C8.12           CTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
NRRL13487       CTCACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
CBS484.84       CTCACGCTCCCGGGCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
                ** **** ***************** **********************************
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Penicillium chrysogenum, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

```
               181      190       200       210       220       230       240
                 +--------+---------+---------+---------+---------+---------+
C8.24           TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
NRRL13485       TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
DAOM193710      TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
C317.1          TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
C238            TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
DAOM155631      TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
DAOM171025      TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
DAOM178623      TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
DAOM215337      TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
DAOM216701      TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
ATCC_10108      TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
C200            TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
NRRL911         TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
DAOM175157      TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
DAOM215336      TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
DAOM216700      TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
DAOM212031      TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
DAOM190864      TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
DAOM175758      TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
DAOM175176      TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
DAOM167036      TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
DAOM155628      TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
DAOM155627      TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
DAOM59494C      TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
NRRL824         TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
NASA            TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
C8.12           TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
NRRL13487       TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
CBS484.84       TCTGAGTGAAAATATAAATTATTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATC
                ************************************************************
```

Penicillium chrysogenum, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

```
               241      250       260       270       280       290       300
                 +--------+---------+---------+---------+---------+---------+
C8.24            GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
NRRL13485        GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM193710       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
C317.1           GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
C238             GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM155631       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM171025       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM178623       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM215337       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM216701       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
ATCC_10108       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
C200             GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
NRRL911          GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM175157       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM215336       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM216700       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM212031       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM190864       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM175758       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM175176       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM167036       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM155628       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM155627       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM59494C       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
NRRL824          GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
NASA             GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
C8.12            GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
NRRL13487        GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
CBS484.84        GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
                 ************************************************************
```

Penicillium chrysogenum, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

```
               301      310       320       330       340       350       360
                 +--------+---------+---------+---------+---------+---------+
C8.24            GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
NRRL13485        GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM193710       GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
C317.1           GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
C238             GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM155631       GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM171025       GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM178623       GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM215337       GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM216701       GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
ATCC_10108       GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
C200             GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
NRRL911          GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM175157       GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM215336       GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM216700       GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM212031       GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM190864       GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM175758       GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM175176       GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM167036       GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM155628       GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM155627       GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM59494C       GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
NRRL824          GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
NASA             GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
C8.12            GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
NRRL13487        GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
CBS484.84        GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCAT
                 ************************************************************
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Penicillium chrysogenum, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

```
              361      370       380       390       400       410       420
                +--------+---------+---------+---------+---------+---------+
C8.24           TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
NRRL13485       TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATTCCGGGGGACGGGCC
DAOM193710      TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
C317.1          TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
C238            TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM155631      TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM171025      TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM178623      TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM215337      TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM216701      TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
ATCC_10108      TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
C200            TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
NRRL911         TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM175157      TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM215336      TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM216700      TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM212031      TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM190864      TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM175758      TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM175176      TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM167036      TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM155628      TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM155627      TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM59494C      TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
NRRL824         TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
NASA            TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
C8.12           TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
NRRL13487       TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
CBS484.84       TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
                * ******************************************* **************
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Penicillium chrysogenum, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

```
               421      430       440       450       460       470       480
                  +--------+---------+---------+---------+---------+---------+
C8.24             CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
NRRL13485         CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM193710        CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
C317.1            CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
C238              CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM155631        CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM171025        CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM178623        CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM215337        CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM216701        CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
ATCC_10108        CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
C200              CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
NRRL911           CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM175157        CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM215336        CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM216700        CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM212031        CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM190864        CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM175758        CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM175176        CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM167036        CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM155628        CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM155627        CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM59494C        CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
NRRL824           CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
NASA              CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
C8.12             CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
NRRL13487         CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
CBS484.84         CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
                  ************************************************************
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Penicillium chrysogenum, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

```
              481      490       500       510       520       530       540
                +--------+---------+---------+---------+---------+---------+
C8.24           TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
NRRL13485       TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
DAOM193710      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
C317.1          TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
C238            TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
DAOM155631      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
DAOM171025      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
DAOM178623      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
DAOM215337      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
DAOM216701      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
ATCC_10108      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
C200            TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCGAATTTTTATCCAGGTTGACCTCGGATC
NRRL911         TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
DAOM175157      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
DAOM215336      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
DAOM216700      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
DAOM212031      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
DAOM190864      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
DAOM175758      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
DAOM175176      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
DAOM167036      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
DAOM155628      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
DAOM155627      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
DAOM59494C      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
NRRL824         TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
NASA            TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
C8.12           TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
NRRL13487       TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
CBS484.84       TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGATC
                ******************************** ***************************
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Penicillium chrysogenum, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

```
              541
                +-----
C8.24           AGGTAG
NRRL13485       AGGTAG
DAOM193710      AGGTAG
C317.1          AGGTAG
C238            AGGTAG
DAOM155631      AGGTAG
DAOM171025      AGGTAG
DAOM178623      AGGTAG
DAOM215337      AGGTAG
DAOM216701      AGGTAG
ATCC_10108      AGGTAG
C200            AGGTAG
NRRL911         AGGTAG
DAOM175157      AGGTAG
DAOM215336      AGGTAG
DAOM216700      AGGTAG
DAOM212031      AGGTAG
DAOM190864      AGGTAG
DAOM175758      AGGTAG
DAOM175176      AGGTAG
DAOM167036      AGGTAG
DAOM155628      AGGTAG
DAOM155627      AGGTAG
DAOM59494C      AGGTAG
NRRL824         AGGTAG
NASA            AGGTAG
C8.12           AGGTAG
NRRL13487       AGGTAG
CBS484.84       AGGTAG
                ******
```

Penicillium chrysogenum, trxB locus

CLUSTAL X (1.8) multiple sequence alignment

```
                1       10        20        30        40        50        60
                +--------+---------+---------+---------+---------+---------+
C317.1          CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
C200            CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
C8.24           CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
D193710         CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
C238            CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM155631      CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM171025      CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM178623      CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM215337      CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM216701      CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
ATCC10108       CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
NRRL824         CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
C8.12           CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
NASA            CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM59494C      CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM155627      CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM155628      CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM167036      CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM215336      CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM216700      CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM212031      CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM190864      CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM175758      CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM175176      CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM175157      CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
CBS_484.84      CTCTTCTACGCCGTTGGTCACGACCCCGCTAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
NRRL13485       CTCTTCTACGCTGTTGGTCACGACCCTGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTT
NRRL911         CTCTTCTACGCTGTTGGTCACGACCCTGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
NRRL13487       CTCTTCTACGCTGTTGGTCACGACCCCGCCAATGCTCTCGTTAAGGGCCAGGTTGAGCTC
                *********** ************** ** * ** ****** ***************** 
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Penicillium chrysogenum, trxB locus

CLUSTAL X (1.8) multiple sequence alignment

```
               61       70        80        90       100       110       120
                +--------+---------+---------+---------+---------+---------+
C317.1          GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTTGAGGGTGTT
C200            GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTTGAGGGTGTT
C8.24           GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
D193710         GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
C238            GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
DAOM155631      GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
DAOM171025      GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
DAOM178623      GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
DAOM215337      GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
DAOM216701      GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
ATCC10108       GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
NRRL824         GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
C8.12           GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
NASA            GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
DAOM59494C      GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
DAOM155627      GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
DAOM155628      GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
DAOM167036      GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
DAOM215336      GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
DAOM216700      GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
DAOM212031      GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
DAOM190864      GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
DAOM175758      GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
DAOM175176      GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
DAOM175157      GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGTT
CBS_484.84      GACAGCGAGGGATATATCATCACCAAGCCCGGTACCAGCTTCACTAACGTCGAGGGTGTC
NRRL13485       GATGACGAACAATACATCATCACCAAGCCCGGTACCAGCTTCACTAACGTCGAGGGTGTC
NRRL911         GATGACGAACAATACATCATCACCAAGCCCGGTACCAGCTTCACTAACGTCGAGGGTGTC
NRRL13487       AATGATGAAGGATACATCGTCACCAAGCCCGGTACCAGCTTCACTAACGTCGAGGGTGTC
                 *    **   *** *** **************** ************** ********
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Penicillium chrysogenum, trxB locus

CLUSTAL X (1.8) multiple sequence alignment

```
              121      130       140       150       160       170       180
                +--------+---------+---------+---------+---------+---------+
C317.1          TTCGCCTGCGGTGATGTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
C200            TTCGCCTGCGGTGATGTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
C8.24           TTCGCCTGCGGTGATGTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
D193710         TTCGCCTGCGGTGATGTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
C238            TTCGCCTGCGGTGATGTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
DAOM155631      TTCGCCTGCGGTGATGTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
DAOM171025      TTCGCCTGCGGTGATGTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
DAOM178623      TTCGCCTGCGGTGATGTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
DAOM215337      TTCGCCTGCGGTGATGTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
DAOM216701      TTCGCCTGCGGTGATGTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
ATCC10108       TTCGCCTGCGGTGATGTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
NRRL824         TTCGCCTGCGGTGATGTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
C8.12           TTCGCCTGCGGTGATGTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
NASA            TTCGCCTGCGGTGATGTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM59494C      TTCGCCTGCGGTGATGTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM155627      TTCGCCTGCGGTGATGTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM155628      TTCGCCTGCGGTGATGTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM167036      TTCGCCTGCGGTGATGTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM215336      TTCGCCTGCGGTGATGTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM216700      TTCGCCTGCGGTGATGTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM212031      TTCGCCTGCGGTGATGTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM190864      TTCGCCTGCGGTGATGTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM175758      TTCGCCTGCGGTGATGTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM175176      TTCGCCTGCGGTGATGTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM175157      TTCGCCTGCGGTGATGTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
CBS_484.84      TTCGCCTGCGGTGATGTCCAGGATAAGCGCTACCGCCAGGCTATCACCAGTGCCGGTATC
NRRL13485       TTCGCCTGCGGTGATGTCCAGGATAAGCGCTACCGCCAGGCTATCACCAGTGCCGGTATG
NRRL911         TTCGCCTGCGGTGATGTCCAGGATAAGCGCTACCGCCAGGCTATCACCAGTGCCGGTATG
NRRL13487       TTCGCCTGCGGTGATGTTCAGGATAAGCGTTACCGCCAGGCTATCACCAGTGCCGGTATG
                ***************** ***** ***** ***** *********************** 
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Penicillium chrysogenum, trxB locus

CLUSTAL X (1.8) multiple sequence alignment

```
              181      190       200       210       220       230       240
                +--------+---------+---------+---------+---------+---------+
C317.1          TTCATACTTCAGCATCTCGTTCATAGTAATTGTAAGTTGGCTAACTCAATATTCTACCAG
C200            TTCATACTTCAGCATCTCGTTCATAGTAATTGTAAGTTGGCTAACTCAATATTCTACCAG
C8.24           TTCATACTTCAGCATCTCGTTCATAGTAATTGCAAGTTGGCTAACTCAGTATTCTACCAG
D193710         TTCATACTTCAGCATCTCGTTCATAGTAATTGCAAGTTGGCTAACTCAGTATTCTACCAG
C238            TTCATACTTCAGCATCTCGTTCATAGTAATTGCAAGTTGGCTAACTCAGTATTCTACCAG
DAOM155631      TTCATACTTCAGCATCTCGTTCATAGTAATTGCAAGTTGGCTAACTCAGTATTCTACCAG
DAOM171025      TTCATACTTCAGCATCTCGTTCATAGTAATTGCAAGTTGGCTAACTCAGTATTCTACCAG
DAOM178623      TTCATACTTCAGCATCTCGTTCATAGTAATTGCAAGTTGGCTAACTCAGTATTCTACCAG
DAOM215337      TTCATACTTCAGCATCTCGTTCATAGTAATTGCAAGTTGGCTAACTCAGTATTCTACCAG
DAOM216701      TTCATACTTCAGCATCTCGTTCATAGTAATTGCAAGTTGGCTAACTCAGTATTCTACCAG
ATCC10108       TTCATACTTCAGCATCTCGTTCATAGTAATTGCAAGTTGGCTAACTCAGTATTCTACCAG
NRRL824         TTCATACTTCAGCATCTCATTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
C8.12           TTCATACTTCAGCATCTCATTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
NASA            TTCATACTTCAGCATCTCATTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM59494C      TTCATACTTCAGCATCTCATTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM155627      TTCATACTTCAGCATCTCATTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM155628      TTCATACTTCAGCATCTCATTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM167036      TTCATACTTCAGCATCTCATTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM215336      TTCATACTTCAGCATCTCATTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM216700      TTCATACTTCAGCATCTCATTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM212031      TTCATACTTCAGCATCTCATTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM190864      TTCATACTTCAGCATCTCATTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM175758      TTCATACTTCAGCATCTCATTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM175176      TTCATACTTCAGCATCTCATTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM175157      TTCATACTTCAGCATCTCATTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
CBS_484.84      TTCATACTCCAGCG------ACATTTTAATTATAGTT--GCTAACTCAAT-TTCTACTAG
NRRL13485       TTCATACCCCAGCATTTCCGTTGTCGTAATTGCGATTTAGCTAACTCAATATTCTACTAG
NRRL911         TTCATACCCCAGCATTTCCGTTGTCGTAATTGCGATTTAGCTAACTCAATATTCTACTAG
NRRL13487       TTCATACTCTATTGTTTCCTTTATATTAGCTGCATTTC-GCTAACTCAACGTTCTACCAG
                *******   *            *  **  *     *  *********   ****** **
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Penicillium chrysogenum, trxB locus

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CLUSTAL X (1.8) multiple sequence alignment

              241      250       260       270       280       290       300
                +--------+---------+---------+---------+---------+---------+
C317.1          GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
C200            GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
C8.24           GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
D193710         GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
C238            GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM155631      GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM171025      GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM178623      GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM215337      GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM216701      GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
ATCC10108       GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
NRRL824         GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
C8.12           GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
NASA            GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM59494C      GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM155627      GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM155628      GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM167036      GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM215336      GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM216700      GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM212031      GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM190864      GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM175758      GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM175176      GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM175157      GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
CBS_484.84      GATCTGGCTGTGTTGCCGCCCTTGAGGCCGAGAAGTTCCTCGCCGACCTTGAGACTCACC
NRRL13485       GATCTGGCTGTGTCGCCGCCCTCGAGGCCGAGAAGTTCCTCGCCGAGACTGAGACTCACC
NRRL911         GATCTGGCTGTGTCGCCGCCCTCGAGGCCGAGAAGTTCCTCGCCGAGACTGAGACTCACC
NRRL13487       GATCTGGCTGTGTCGCCGCCCTCGAAGCCGAGAAGTTCCTCTCTGAGACCGAGACTCACC
                ************* ** ** ** ** ** ********* ** * **     **********
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Penicillium chrysogenum, trxB locus

CLUSTAL X (1.8) multiple sequence alignment

```
              301
                +-----
C317.1          AGGAGG
C200            AGGAGG
C8.24           AGGAGG
D193710         AGGAGG
C238            AGGAGG
DAOM155631      AGGAGG
DAOM171025      AGGAGG
DAOM178623      AGGAGG
DAOM215337      AGGAGG
DAOM216701      AGGAGG
ATCC10108       AGGAGG
NRRL824         AGGAGG
C8.12           AGGAGG
NASA            AGGAGG
DAOM59494C      AGGAGG
DAOM155627      AGGAGG
DAOM155628      AGGAGG
DAOM167036      AGGAGG
DAOM215336      AGGAGG
DAOM216700      AGGAGG
DAOM212031      AGGAGG
DAOM190864      AGGAGG
DAOM175758      AGGAGG
DAOM175176      AGGAGG
DAOM175157      AGGAGG
CBS_484.84      AGGAGG
NRRL13485       AGGAGG
NRRL911         AGGAGG
NRRL13487       AGGAGG
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