

Review

Kallikrein-related peptidases: proteolysis and signaling in cancer, the new frontier*

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Abstract

The exact mechanism(s) by which kallikrein-related peptidases (KLKs) function, their levels of activity and their potential endogenous targets *in vivo* have only recently begun to be revealed. Our group and others have shown that KLKs can have hormonal properties by signaling via proteinase-activated receptors (PARs), a family of G-protein-coupled receptors. Signals by PAR₁, PAR₂, and PAR₄ can regulate calcium release or mitogen-activated protein kinase activation and lead to platelet aggregation, vascular relaxation, cell proliferation, cytokine release, and inflammation. We have further documented the presence of active KLK6 and 10 (by activity-based ELISA or proteomics) and the presence of proteinase inhibitors, such as α_1 -antitrypsin, in cancer-derived fluids. We suggest that tumors and inflamed tissues can release active KLKs, which are under tight regulation by proteinase inhibitors. These enzymes can potentially control cell/tissue behavior by regulating PAR activation in specific settings and disease stages.

Keywords: hormone; inflammation; kallikrein-related peptidases; proteases; proteinase-activated receptors; proteinases; signaling; trypsin.

Introduction

The term hormone, by definition, refers to a messenger substance secreted by one tissue into the blood circulation to

reach another distant cell, tissue or organ and generate a chemical signal able to regulate tissue function. These characteristics of secretin led Bayliss and Starling (1902) to use the term hormone, possibly inspired by the Greek verb for excite or arouse, *ormao* (Henderson, 2005). Thereafter, several ligands such as amine-derived hormones (e.g., catecholamines), peptides/proteins (e.g., vasopressin and insulin), and lipid/phospholipid-derived mediators (e.g., steroids and prostaglandins) have been categorized as hormones.

According to this classical definition, even proteolytic enzymes can qualify as hormones. For example, thrombin, a well-recognized serine proteinase, is synthesized as a proenzyme in the liver and circulates through the bloodstream to signal to its target tissues (e.g., endothelium and platelets) (Barnhart, 1965). In addition, from a functional perspective, proteolytic enzymes can have other hormone-like characteristics. Apart from their roles in protein catabolism, which are well appreciated, several studies have shown that proteinases may mimic the action of traditional hormones. For example, work by Rieser and Rieser (1964) and Rieser (1967) showed that pepsin and chymotrypsin can mimic insulin action to promote glycogen formation in a rat diaphragm preparation. Soon thereafter it was shown that trypsin, like insulin, can stimulate glucose oxidation and inhibit lipolysis in isolated fat cells (Kono and Barham, 1971). This action of trypsin has been rationalized in terms of the tryptic cleavage of a regulatory domain of the insulin receptor (Shoelson et al., 1988). Furthermore, studies on thrombin and trypsin have revealed that these proteinases, like insulin and epidermal growth factor, can stimulate mitogenesis in cultured cell systems (Burger, 1970; Sefton and Rubin, 1970; Chen and Buchanan, 1975). Thus, the ability of proteinases to fulfill the criteria expected of a hormone and to trigger hormone-like signals in target tissues has been known for almost half a century, but it is only recently that several pieces of the puzzle relating to the mechanisms responsible for the hormonal actions of proteinases have been put together.

Kallikrein-related peptidases as hormones

Kallikrein-related peptidases (KLKs) are synthesized in several tissues and are secreted into the circulation and other major biological fluids, such as cerebrospinal fluid, vaginal fluid, nipple aspirate fluid, and tumor ascites fluid (Borgoño et al., 2004; Borgoño and Diamandis, 2004). Subsequently, KLKs can travel to surrounding and distant cells to exert their biological actions by means of proteolysis. For example, many KLKs, such as KLKs 4, 6, 8 and 10, are secreted by ovarian tumors and/or surrounding stromal cells and are

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thus overexpressed in ascites fluid and/or serum of ovarian cancer patients compared to non-malignant pathologies or normal controls (Borgoño et al., 2004; Borgoño and Diamandis, 2004; Obiezu and Diamandis, 2005). Likewise, KLK2, PSA/KLK3, and KLK11 are similarly highly expressed in prostate cancer patients, whereas KLK5 and 14 are overexpressed in breast carcinomas.

It has been shown *in vitro* that some of these KLKs can proteolytically activate hormones and growth factors, other proteinases or extracellular matrix components (Borgoño et al., 2004; Borgoño and Diamandis, 2004), possibly affecting tissue function (Figure 1). The KLKs can also induce cell proliferation, as demonstrated in the case of keratinocytes (Klucky et al., 2007), prostate-derived tumor cells (Klokk et al., 2007; Mize et al., 2008), and non-small-cell lung carcinoma cells (Heuzé-Vourc'h et al., 2009). Furthermore, it has long been known that kallikrein 1 (KLK1; formerly known as tissue kallikrein) has mitogenic effects by generating active kinin peptides from their kininogen precursor (Figure 1). The kinins can subsequently trigger the activation of the bradykinin B2 G-protein-coupled receptor (Roberts and Gullick, 1989; Bhoola et al., 1992) (Figure 1). These KLKs should not be confused with plasma kallikrein, which can also liberate active kinin peptides from kininogen, but does not belong to the kallikrein-related peptidase family (Schmaier and McCrae, 2007).

Although it is very likely that KLK1 is the only KLK that can signal via the generation of active kinin peptides *in vivo*, our recent studies have shown that KLKs can also regulate cell signaling by cleaving and triggering the activation of proteinase-activated receptors (PARs; Oikonomopoulou et al., 2006a,b, 2007; Figure 1). PAR 1–4 are members of the G-protein-coupled receptor superfamily (Macfarlane et al., 2001; Hollenberg and Compton, 2002). They have been implicated in a number of physiological and pathological signaling pathways in a variety of tissues (Coughlin, 2005; Steinhoff et al., 2005; Ramachandran and Hollenberg, 2008). Thus, we can now consider these receptors as additional targets by which KLKs, like hormones, can transmit their

chemical messages in an endocrine, paracrine or autocrine manner.

Pharmacology of PAR signaling by KLKs

We used a pharmacological approach to show that KLKs, represented by KLKs 5, 6, and 14, can mediate activation of PARs 1, 2, and 4 (Oikonomopoulou et al., 2006a,b). The main finding of our study was that signaling via human, rat, and mouse PARs can be regulated by human KLKs (Table 1). More specifically, KLKs 5, 6 and 14 caused PAR-dependent calcium signaling responses in cells expressing PAR₂, as well as endothelium-derived vascular relaxation via PAR₂. Interestingly, we found that among these three KLKs, it was only KLK14 that could also target the disarming/inhibition of PAR₁ and activation of PAR₄, and it could also cause platelet aggregation by means of PAR₄ activation.

Our studies principally focused on PAR₂, a major player in the settings of inflammation and nociception (Vergnolle et al., 2001a,b; Vergnolle, 2004), and on KLK14, a prognostic and diagnostic marker of ovarian and breast carcinoma (Borgoño et al., 2003, 2007b). KLK6 exhibited a comparable but unique potency for activation of PAR₂ compared with KLK14, whereas KLK5 was less efficient as an activator of this receptor (Oikonomopoulou et al., 2006a,b). Furthermore, the actions of these three KLKs were distinct from the effect of plasma kallikrein (which is a related proteinase but not a member of the KLK family), as well as tissue kallikrein (KLK1). It has been reported that these KLKs do not activate PAR₂ (Molino et al., 1997a,b), even though they can both act as agonists to trigger PAR₄ signaling (Houle et al., 2005). It has been suggested that this effect may involve activation of the bradykinin B2 receptor as a result of the KLK1-mediated release of active kinin peptides.

Later work by Stefansson et al. (2008) demonstrated that KLK14 is a strong and KLK5 a moderate activator of PAR₂ (Table 1). However, these authors could not conclude that KLK7 or KLK8 can induce a similar signal via this receptor.

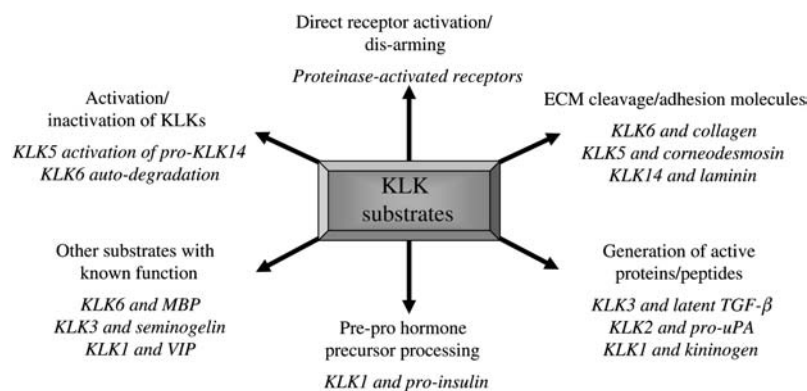


Figure 1 Potential substrates via which KLKs can regulate tissue function.

Selected examples are given for each suggested substrate group. MBP stands for myelin basic protein, VIP for vasoactive intestinal peptide, TGF- β for tissue growth factor type β , and pro-uPA for the zymogen of urokinase plasminogen activator. For details about the potential KLK substrates, see Borgoño et al. (2004), Borgoño and Diamandis (2004) and Sotiropoulou et al. (2009).

Table 1 Kallikrein-related peptidases as regulators of proteinase-activated receptor signalling.

KLK	PAR ^a	Response	Tissue/cell line ^b	Comment	Reference
KLK1	PAR ₂	Ca ²⁺ ; phosphoinositide hydrolysis	HUVEC; COS-1-PAR ₂ cells	Negative assay	Molino et al., 1997b
KLK1	PAR ₁	Ca ²⁺	NSC34 neurons; Neu7 astrocytes	Negative assay	Vandell et al., 2008
KLK1	PAR ₄	Edema	Mouse paw		
KLK2	PAR ₂	ERK	DU145 prostate cancer cells; KOLF-PAR ₂ cells	Indirect activation via kinin-dependent triggering of B2 receptor	Houle et al., 2005
KLK4	PAR ₁	Ca ²⁺	LMF-PAR ₁ cells	Proliferation	Mize et al., 2008
KLK4	PAR ₂	Ca ²⁺ and ERK		Possible PAR ₁ disarming at high KLK4 concentrations	Ramsay et al., 2008a
KLK4	PAR ₂	Ca ²⁺	LMF-PAR ₂ cells	PAR ₂ ERK>PAR ₂ Ca ²⁺ >PAR ₁ Ca ²⁺	Ramsay et al., 2008a
KLK4	PAR ₂	Ca ²⁺	PC3 prostate cancer cells	PAR ₂ and KLK4 co-localization in primary and bone metastatic cancer	Ramsay et al., 2008a
KLK4	PARs 1 and 2	ERK	DU145 prostate cancer cells; KOLF-PAR ₁ and KOLF-PAR ₂ cells	Proliferation	Mize et al., 2008
KLK4	PAR ₁	ERK	WPMY-1 prostatic stromal cells; CHO-TO-PAR ₁ cells		Wang et al., 2010
KLK5	PAR ₂	Ca ²⁺	HEK/KNRK-PAR ₂ cells	Stromal-epithelial interaction: KLK4 (prostatic epithelium) triggers PAR ₁ (stroma) to produce IL-6 → secretion of PSA and KLK4 from prostate cancer cells	Oikonomopoulou et al., 2006a,b; Stefansson et al., 2008
KLK5	PAR ₂	Relaxation	Rat aorta	Different KLK potencies dependent on the expressing system and PAR species	
KLK5	PAR ₄	Aggregation	Platelets	Endothelium-dependent	Oikonomopoulou et al., 2006a,b
KLK5	PAR ₂	NF-κβ	Keratinocytes	Negative assay	Oikonomopoulou et al., 2006a,b
KLK6	PAR ₂	Ca ²⁺	HEK/KNRK-PAR ₂ cells	Upregulation of TLSP confirmed in Netherton syndrome patients	Briot et al., 2009
KLK6	PAR ₂	Relaxation		Possible disarming of PAR ₂ at high KLK6 concentrations	Oikonomopoulou et al., 2006a,b
KLK6	PAR ₄	Aggregation	Rat aorta	Endothelium-dependent	Oikonomopoulou et al., 2006a,b
KLK6	PAR ₁	Ca ²⁺ /ERK	Platelets	Negative assay	Oikonomopoulou et al., 2006a,b
KLK6	PAR ₁ and PAR ₂	Ca ²⁺	NSC34 neurons	Major part of signaling is mediated by B2 receptor; possible ERK/AKT activation favoring neuronal cell death	Vandell et al., 2008
KLK6	PAR ₁ and PAR ₂	Ca ²⁺	Neu7 astrocytes	Possible ERK/AKT activation favoring astrocyte survival	
KLK7	PAR ₂	Ca ²⁺	KNRK-PAR ₂ cells	Negative assay	Stefansson et al., 2008
KLK8	PAR ₂	Ca ²⁺	KNRK-PAR ₂ cells	Negative assay	Stefansson et al., 2008
KLK14	PAR ₁ and PAR ₂	Ca ²⁺	HEK/KNRK-PAR ₂ cells	Disarming of PAR ₁ at lower KLK14 concentrations	Oikonomopoulou et al., 2006a,b

Table 1 (Continued)

KLK	PAR ^a	Response	Tissue/cell line ^b	Comment	Reference
KLK 14	PAR ₂	Ca ²⁺	KNRK-PAR ₂ cells	KLK 14 more potent than KLK5; co-localization of KLK14 and PAR ₂ in inflammatory skin disorders (atopic dermatitis and rosacea)	Stefansson et al., 2008
KLK 14	PAR ₂	Relaxation	Rat/mouse aorta	Endothelium-dependent; absent in PAR ₂ ^{-/-}	Oikonomopoulou et al., 2006a,b
KLK 14	PAR ₄	Aggregation/Ca ²⁺	Platelets/HEK-PAR ₄ cells	KLK 14 is the only KLK thus far shown to activate PAR ₄ and trigger platelet aggregation	Oikonomopoulou et al., 2006a,b

^a For the majority of the studies summarized in this Table, investigation of whether the activation or inhibition of a PAR is the result of direct or indirect KLK-mediated proteolytic activity is not always a straightforward procedure. Therefore, the intermediate involvement of other receptors or other KLK-related substrates within the KLK-PAR signaling pathways cannot be excluded.

^b CHO-TO, Chinese hamster ovary Tet-On; HEK, human embryonic kidney epithelial cells; HUVECs, human umbilical vein endothelial cells; KNRK, Kirsten murine sarcoma virus-transformed rat kidney epithelial cells; KOLF, PAR₁ knockout mouse lung fibroblast cells (lacking PAR₁ and PAR₂); LMF, lung murine fibroblasts. HEK cells naturally express PARs 1 and 2, but no other PAR unless otherwise indicated. CHO-TO, COS-1, KOLF, and LMF cells were transfected to overexpress the PAR indicated. KNRK cells were either transfected to express rat PAR₂ (Oikonomopoulou et al., 2006a,b) or human PAR₂ (Stefansson et al., 2008).

In addition, it has been shown that KLK4 can induce signals via PAR₂ in PAR-transfected cells [Ca²⁺ and extracellular signal-regulated kinase (ERK) signaling] and prostate cancer cultured cells (Ca²⁺ signaling), and could also immobilize a lower Ca²⁺ response via PAR₁, but not PAR₄ (Ramsay et al., 2008a; Table 1). This study also showed that KLK4 can act as a more potent activator of PAR₂-mediated ERK1/2 signaling at a lower concentration of the enzyme compared with the Ca²⁺ response triggered by higher levels of the proteinase. Similar work on KLK1 and 6 has also shown that KLK6 can trigger Ca²⁺ release from both cultured neurons (PAR₁-mediated) and astrocytes (PAR₁ or PAR₂-mediated), whereas both KLKs exhibited a variable pattern of regulation of ERK, Jun N-terminal kinase (JNK) and AKT (Vandell et al., 2008; Table 1). Notably, the neuronal KLK1-triggered ERK response and a major part of KLK6 neuronal signaling were attributed to activation of the bradykinin B2 receptor.

The data derived from these pharmacological studies, and summarized in Table 1, suggest that the KLKs not only target different members of the G-protein coupled proteinase-activated receptor family or other G-protein coupled receptors, but also exhibit variable pharmacological potencies for cleaving at the same tethered ligand site of catalysis and can trigger distinct G-protein-coupled mechanisms (e.g., G_q-coupled increases in intracellular calcium versus G_i/G_{12,13}-coupled activation of mitogen-activated protein kinase). It is therefore important to note the variable signaling potential of the different members of the same enzyme family. We suggest that all human KLKs, as well as KLKs from other species, can have both common and distinct actions via the different PARs in cells and tissues expressing these receptors.

KLKs and PARs in cancer and inflammation

During the past few years, interest in the field of KLK signaling via PARs has increased and it has been confirmed that there is an association between KLK levels and processes associated with both inflammation and cancer. This finding is not surprising, since inflammation and carcinogenesis share important features and should therefore be considered as biochemically and biophysically related pathologies. This idea was first introduced in 1863 by Rudolf Virchow, who pointed out the increased presence of inflammatory cells (leukocytes) in neoplastic tissue (reviewed by Macarthur et al., 2004). The hypothesis linking inflammation to the development of cancer has been regularly revisited, and there are currently several experimental, clinical and epidemiological studies that support a relationship between chronic inflammation and cancer and a possible signaling pathway crosstalk between these two pathological conditions (Coussens and Werb, 2002; Macarthur et al., 2004; Rogers and Fox, 2004; Allavena et al., 2008a,b).

It has also been noted that the extracellular tumor micro-environment can be characterized by the presence of mediators found in inflamed tissues (Macarthur et al., 2004; Allavena et al., 2008a,b). These common mediators include growth factors, proteinases and cytokines, which can pro-

mote cell survival, regulate adaptive immunity, increase angiogenesis, and initiate tissue destruction either to facilitate tumor invasion and metastasis (Macarthur et al., 2004; Allavena et al., 2008b) or to promote the resolution of inflammation. A number of cell-derived proteinases are expressed by either the tumor tissue or stromal cells (including invading leukocytes and macrophages) that share the tumor microenvironment. Apart from the well-appreciated roles of matrix metalloproteinases (MMPs) in either promoting or inhibiting cancer spread (Seiki, 2003; López-Otín and Matrisian, 2007), serine proteinases can also be of considerable importance in the tumor microenvironment. Many of these serine proteinases and metalloproteinases have been implicated in the pathology of ovarian cancer (Stack et al., 1998; Camerer, 2007), including urokinase plasminogen activator (uPA) (Choong and Nadesapillai, 2003), a serine proteinase that converts plasminogen to plasmin.

The pharmacological work mentioned above indicates that KLK4–6 and 14, which are highly expressed tumor-associated proteinases, can be potential stimulators of PARs in the settings of cancer and inflammation (Table 1). Much of the data supporting a role for KLKs in regulating cell function have come from studying the effects of KLKs on PAR-expressing cell lines *in vitro* (either naturally occurring PARs, as in human HEK cells, or as recombinantly expressed receptors in background cells, such as rat KNRK cells). Thus, the next step in testing the hypothesis that PARs might play a role in cancer and inflammation was to design experiments performed with cultured cells and *in vivo* systems related to the settings of a specific disease.

Confirmation of KLK signaling *in vivo*

Data obtained from pharmacological studies using PAR-derived receptor-activating peptides and agonists, known to activate cells and tissues *in vitro*, are of considerable value in predicting what can *potentially* happen in a physiological setting. However, it would be misleading to predict the *in vivo* role of PAR-activating enzymes, such as KLKs, based solely on data obtained *in vitro*. This reservation arises for three main reasons: (a) all of the *in vitro* protocols include an unavoidable bias, since the experiments target only one or two receptors, which are often abundant in the cell expression systems; (b) many of the studies of PAR-mediated calcium signaling have used cells in suspension, so that the impact of the extracellular matrix network on PAR responses has not been taken into account; and (c) cell lines, platelets, and tissues are assayed after extensive washing, which in principle might underestimate a potential role for serine proteinase inhibitors in regulating proteinase-mediated PAR signaling. Therefore, the next important step was to investigate if KLKs can have a functional role *in vivo*.

We used a murine paw edema inflammation model to study the response of KLKs *in vivo* (Vergnolle et al., 1999). Based on our data showing that KLKs mimic the action of trypsin to activate PAR₂ in rodent and human cell systems expressing this receptor, we anticipated that KLKs would also mimic the inflammatory action of trypsin mediated via PAR₂ (Vergnolle et al., 1999, 2001b; Cenac et al., 2002,

Nguyen et al., 2003) in this murine paw edema model. KLK14 was able to trigger a murine inflammatory response in this model *in vivo*, an effect that is very likely due to PAR activation (Oikonomopoulou et al., 2006b, 2007). These preliminary data suggest that a more in-depth evaluation of the role played by KLKs and the participation of proteinase inhibitors in this interesting model of inflammatory response triggered either by PARs or via a non-specific inflammatory stimulus, such as carrageenan, will be fruitful in the future.

Prostate cancer

Among the different tumors, prostate cancer is one of the best-studied types of carcinoma in which KLKs are highly expressed (Borgoño et al., 2004; Borgoño and Diamandis, 2004). Of the 15 members of the KLK family, PSA/KLK3 (prostate-specific antigen) has served as the most valuable biomarker for monitoring prostate cancer patients and has been extensively used for the diagnosis and prognosis of the disease (Loeb and Catalona, 2007). Apart from PSA, the closely-related enzyme, KLK2, as well as other members of the family, are promising biomarkers for the detection of prostate cancer (Becker et al., 2001; Borgoño et al., 2004; Borgoño and Diamandis, 2004; Obiezu and Diamandis, 2005). Despite the suggested clinical applicability of monitoring levels of several members of the KLK family by immunoassay for the detection or prognosis of prostate cancer, their biological roles and their levels of enzyme activity are essentially unknown. The same caveat applies for the PARs, which are also highly expressed in primary prostate cancer and prostate tumor-derived cell lines (Ramsay et al., 2008b).

Recent data have pointed for the first time to one of the KLKs as a major potential regulator of prostate tumor signaling (Ramsay et al., 2008a). More specifically, it was shown that KLK4 can initiate Ca²⁺ responses in prostate tumor-derived PC3 cells expressing PARs 1 and 2. It is possible that these signals were generated by preferential PAR₂ activation. KLK4 has also been co-localized with PAR₂ in primary prostate cancer and metastatic prostate cancer bone lesions, pointing to a role for this enzyme in the progression of prostate cancer (Ramsay et al., 2008a). Similar observations have subsequently been reported by another group documenting the proliferative role of KLK2 and 4 in the aggressive and androgen-independent DU145 prostate cancer cells (Mize et al., 2008). This study concluded that KLK4 can trigger ERK-activating signals via both PAR 1 and 2. Interestingly, KLK2 was able to initiate phosphorylation of ERK1/2 only via PAR₂.

A more important observation followed: the KLK4 interaction with PAR₁ and the subsequent initiation of ERK1/2 signaling can play a major role in tumor-stroma interactions in androgen-independent prostate cancer (Wang et al., 2010). Thus far, most of the studies that have evaluated KLKs as potential regulators of PAR signaling have considered tumor cells as the primary targets of KLK action. However, it is possible that stromal cells, rather than the tumor, play the major regulatory role in the tumor microenvironment. In this regard, the study by Wang et al. (2010) provided molecular

and immunohistochemical evidence that KLK4 produced by prostate cancer epithelial cells can trigger, in a paracrine manner, a reaction from the surrounding stroma by means of PAR₁ activation. This action resulted in cytokine release. One of the cytokine molecules released, interleukin (IL)-6, was able to stimulate ERK-dependent signaling by the epithelial cancer cells. This signal in turn caused secretion of KLKs 4 and 3 and resulted in cell proliferation.

Multiple sclerosis

Among the KLKs expressed in the central nervous system (CNS), KLK6 has been implicated in multiple sclerosis (Scarlsbrick et al., 2002; Blaber et al., 2004), Alzheimer's disease (Little et al., 1997; Diamandis et al., 2000; Ogawa et al., 2000; Mitsui et al., 2002; Zarghooni et al., 2002), and Parkinson's disease (Ogawa et al., 2000; Iwata et al., 2003). Furthermore, KLK8 (also known as brain serine peptidase or neuropsin) may play a role in synaptic plasticity (Shimizu et al., 1998; Yousef et al., 2003), long-term potentiation (Tamura et al., 2006), and neurodegeneration (Terayama et al., 2007). Several KLKs are also highly expressed by immune cells, such as T-cells and macrophages, in inflammatory conditions like multiple sclerosis, and are under steroid hormone regulation (Scarlsbrick et al., 2002, 2006). Recent data suggest that KLKs 1 and 6 can serve as serological markers of progressive multiple sclerosis and contribute directly to the development of neurodegeneration (Scarlsbrick et al., 2008). Given that the KLKs can regulate PAR₂ activity and that PAR₂ has been implicated in a murine experimental autoimmune encephalitis model of multiple sclerosis (Noorbakhsh et al., 2006), we can predict that a PAR₂-KLK interaction may play an important role not only in multiple sclerosis, but also in other types of neurodegenerative diseases. It has also been shown that many of the PARs are highly expressed both in the central and peripheral nervous system by neurons and their associated cells, such as astrocytes (Steinhoff et al., 2005; Luo et al., 2007). PARs 1 and 2, specifically expressed in neuronal cells, are primarily responsible for triggering inflammation (Steinhoff et al., 2000; de Garavilla et al., 2001). Therefore, interactions of KLKs with many members of the PAR family in neurological disease are likely.

Inspired by these observations, a recent study has investigated the hypothesis that KLKs 1 and 6 are physiological regulators of PAR signaling in neurons and astrocytes (Vandell et al., 2008). The authors found that KLK6 could evoke PAR₁-dependent signaling responses in neurons and astrocytes, whereas activation of PAR₂ occurred only in the case of astrocytes, which express low levels of PAR₁. Furthermore, it was found that KLK1 acts primarily via the bradykinin B2 receptor. It is intriguing that the KLK6 responses were the result of the combined activation of both PAR₁ and B2 receptors. These findings point to a potential major regulatory role for the KLKs and the bradykinin receptor in the CNS, complementary to the role of the PARs, possibly involving a synergistic interaction between the two receptors. The authors postulated that signaling via these mechanisms

could promote astrocyte survival while triggering neuronal death (Vandell et al., 2008).

Skin pathology

Three KLKs, KLK5, 7 and 14, have been isolated in their active forms from the outermost layers of the stratum corneum (Hansson et al., 1994; Brattsand and Egelrud, 1999; Stefansson et al., 2006). Other KLKs are also expressed in the epidermis (Komatsu et al., 2005, 2006). Despite the fact that accumulating data indicate the involvement of many KLKs in skin (patho)physiology, knowledge of their specific contributions to trypsin- or chymotrypsin-like activity in the skin is still limited. A KLK cascade involving KLKs 5 and 7 has been identified and may effect skin desquamation via the degradation of intercellular (corneo)desmosomal adhesion molecules (Caubet et al., 2004; Brattsand et al., 2005). Moreover, it has been suggested that KLK5, 6, and 14 are also involved in this process owing to their immunolocalization and ability to degrade desmoglein-1, one of the adhesive proteins in the corneodesmosome (Borgoño et al., 2007a). Finally, of the skin-abundant KLKs, KLK5 regulates signaling responses via PAR₂ (Oikonomopoulou et al., 2006a,b; Stefansson et al., 2008). The activity of several of the aforementioned KLKs can be regulated by the proteinase inhibitor lymphoepithelial Kazal-type-related inhibitor (LEKTI; Borgoño et al., 2007a; Deraison et al., 2007). Genetic mutations of LEKTI diminish its inhibitory activity and therefore increase constitutive proteinase activity, resulting in stratum corneum overdesquamation, which can lead to pathological conditions of the skin, such as Netherton syndrome, in which several KLKs are also overexpressed (Chavanas et al., 2000; Komatsu et al., 2008).

Recent data have shed additional light on the potential role of one of these KLKs in the pathobiology of Netherton syndrome (Briot et al., 2009). The authors proposed a signaling pathway in which KLK5 has the leading role and activates skin PAR₂ to increase expression of proinflammatory cytokines and chemokines. More specifically, KLK5 caused a nuclear factor- κ B (NF- κ B)-mediated induction of thymic stromal lymphopoietin (TSLP), tumor necrosis factor α , and IL-8, as well as an increase in intercellular adhesion molecule 1 in human primary keratinocytes. TSLP secretion was further confirmed in keratinocytes from patients with Netherton syndrome. These data indicated that KLK5 hyperactivity in the epidermis of patients can trigger skin inflammation via PAR₂, independently of environmental stimuli and the adaptive immune system (Briot et al., 2009).

The data summarized in this manuscript have now added KLKs 1, 2, 4–6 and 14 to the list of potential regulators of PARs. The studies discussed indicate that active KLKs can single out these receptors as targets in the settings of cancer and inflammation *in vivo*. However, the exact roles assumed by KLKs within a specific (patho)physiological setting will depend on the absolute amount of enzyme activity. This issue raises a very important question: what are the levels of *enzymatically active* KLKs released by tumor or stromal cells into biological fluids related to inflammation and cancer? These secretions may be a significant reservoir of active pro-

teinasases capable of regulating signaling in tumor and inflammatory cells.

Activity of KLKs in cancer-derived fluids

Activity-based probe ELISA

To investigate the levels of KLK activity in cancer-derived fluids with high sensitivity and specificity, we used a biotinylated activity-based probe (ABP) with selectivity for trypsin-like serine proteinases (Bio-PK-DPP 4; Pan et al., 2006; Figure 2A). Since KLKs are all secreted proteins, we reasoned that this type of ABP would be an efficient reagent to target KLK activity in biological fluids. This approach, targeting secreted enzymes, circumvents problems encountered with the use of biotin-tagged reagents for cell-based analyses, because in cells or tissues the high levels of endogenous background biotin-containing proteins can be problematic (Sadaghiani et al., 2007; Fonović et al., 2007). The ABP we used was designed in accordance with the strategy for tagging serine proteinases with a biotinylated diphenylphosphonate probe (Hawthorne et al., 2004). The phosphonate reactive group (which alkylates the serine residue within the active site of any serine proteinase) is preceded by a proline-lysine sequence in the P2/P1 enzyme target site to restrict the probe specificity to trypsin-like serine proteinases (Figure 2A). This enzyme target is separated from the biotin tag with an N-terminal-attached spacer (Bio-PK-DPP 4; Pan et al., 2006; Paulick and Bogoy, 2008). The interaction between the probe and the enzyme is characterized as a suicide inhibitor mechanism, such that the inhibitor is covalently and irreversibly bound to the proteinase. This reaction mimics the interaction of serine proteinases with many of their naturally occurring inhibitors belonging to the family of serpins (Law et al., 2006).

In a previous study, we used immunological isolation to capture KLK6 reactive to the ABP from cerebrospinal fluids, cultured cancer cell supernatants, and ovarian cancer-associated ascites fluids (Oikonomopoulou et al., 2008). By detecting the biotin moiety of the probe, we showed that only a low proportion (approx. 0.1–5% of the total enzyme) of the immunoreactive KLK6 in such samples represents active enzyme not complexed to inhibitors. However, even though the absolute concentrations of active enzyme in our clinical and cell-derived samples were low, the total amount of enzyme, if generated in a restricted environment, would in principle be sufficient to cause cell and tissue signals. Furthermore, the *total* levels of immunoreactive KLK6 (possibly in zymogen form) in all the samples we surveyed were relatively high. Thus, a change in the microenvironment (e.g., an increase in pH) or an increase in the levels of a KLK-activating proteinase could potentially trigger the generation of active KLK6 from the zymogen reservoir.

Therefore, the active enzyme produced by tissues at a localized site could be present in concentrations able to cleave and regulate PARs, as well as cleave extracellular matrix molecules, all of which have been established as tar-

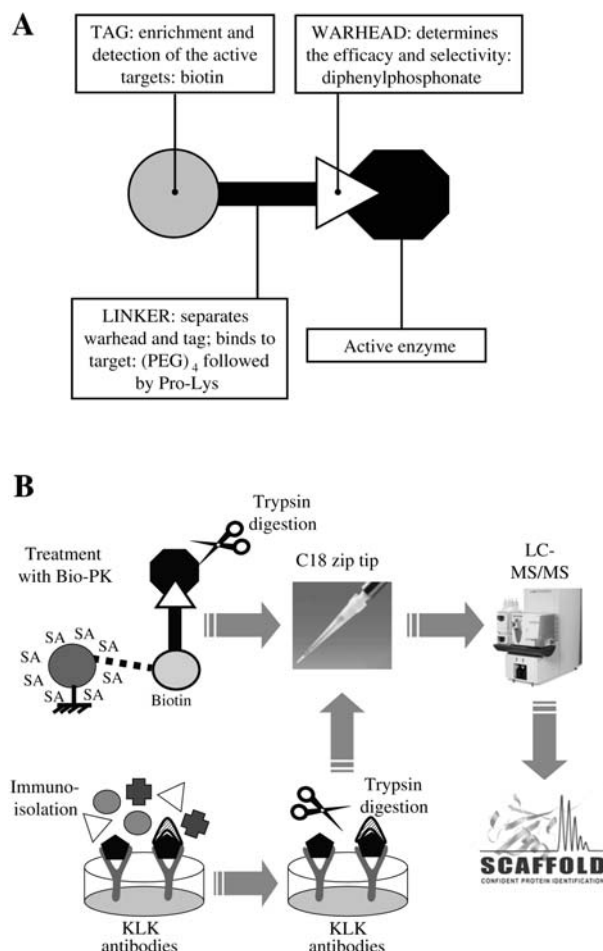


Figure 2 Activity-based probe for serine proteinases with trypsin-like activity.

(A) Structure of the Bio-PK-DPP 4 probe. The probe consists of three groups: a biotin molecule followed by a linker moiety poly(ethylene glycol)₄ or (PEG)₄ joined to a P2/P1 enzyme target site, Pro-Lys-peptide, followed by a warhead, diphenylphosphonate, which alkylates the active serine of the proteinase. The biotin tag facilitates enrichment and detection of active trypsin-like serine proteinases covalently bound to the probe. For details, see Pan et al. (2006). (B) Functional proteomics analysis of ovarian cancer ascites fluid. Samples were enriched either (1) for active proteinases using the activity-based probe followed by immobilization to Streptavidin beads (SA), or (2) for the total content of kallikrein-related peptidases, captured by KLK-specific monoclonal antibodies. Captured proteins (KLKs: black pentagons; KLK complexes: grey arrowheads) were fragmented with trypsin and subjected to mass spectrometric identification. For details, see Oikonomopoulou et al. (2010).

gets of KLK6 *in vitro*. This proteolytic activity could contribute to disease pathogenesis (Borgoño and Diamandis, 2004).

ABP proteomics

Having examined the activity of KLK6 in cancer-derived fluids, question to address was whether several members of the KLK family and other enzyme classes can be present and active in the same microenvironment. These proteinases can

form potential cascades that may lead to activation of the effector enzyme and progression of the carcinogenic or inflammatory effect. To test this hypothesis, we coupled the ABP used for the immunofluorometric detection assay with tandem mass spectrometry to investigate the presence of active proteinases in ovarian cancer ascites, one of the best-studied cancer-related fluids (Figure 2B).

This protocol took advantage of the chemical properties of the probe to facilitate sample enrichment and specific isolation of active proteinases, with preference for cleavage after Lys, from the complex proteome of a biological fluid such as ovarian cancer ascites (Oikonomopoulou et al., 2010). We also included parallel enrichment of the same fluids using KLK-specific antibodies to replace the probes (Figure 2B). We anticipated that the isolated proteins would be either active KLKs or partners of these peptidases in complex with the enzymes.

Despite the low overall serine proteinase activity of ovarian cancer ascites, our preliminary work using the ABP proteomics approach singled out KLK10 among the active serine proteinases of ovarian cancer ascites fluid (Oikonomopoulou et al., 2010). By contrast, other KLKs abundantly expressed in ovarian cancer ascites as indicated by immunoassay results (such as KLKs 5, 6, and 8) remained undetected by the ABP assay and were therefore presumed to be enzymatically inactive (zymogens, fragmented proteinases or proteinases complexed to inhibitors). In keeping with this conclusion, the four members of the family detected in ovarian cancer ascites fluid by immunoassay (KLKs 5, 6, 8, and 10) were also detected by mass spectral analysis, along with proteinase inhibitors. This finding suggests that enzymatically active KLKs can be generated in the setting of cancer, but the enzymes are rapidly sequestered by inhibitors in the environment of tumors.

Conclusions and future directions

Our work to date has focused on the KLK family of serine proteinases, which are highly expressed in various types of cancer and inflammation. As summarized in Figure 1, there are many potential target substrates for these enzymes that can lead to their biological effects *in vivo* in the settings of a tumor or an inflamed tissue. In this regard, an extensive body of literature suggests a role for the measurement of immunoreactive KLK levels in the diagnosis, prognosis or monitoring of several types of cancer, including ovarian, prostate, and breast cancers (Borgoño et al., 2004; Borgoño and Diamandis, 2004). For example, KLK3 is an established biomarker for monitoring of prostate cancer patients. Another member of the family, KLK6, is a putative biomarker of ovarian cancer prognosis and response to treatment. However, apart from KLK3, no other KLK, measured either alone or in combination with other members of the KLK family, has thus far served as an optimal tumor marker with clinical utility for cancer diagnosis and prognosis. Furthermore, despite recent reports documenting KLK expression in inflammatory diseases (Scarlsbrick et al., 2008), strong evidence of the role of KLKs in these settings is only starting to emerge.

We suggest that identification of the functional roles of KLKs will facilitate their use as potential disease markers in the settings of inflammation and cancer. It will therefore be important to investigate the signaling pathways that KLKs activate downstream of PARs, or other as yet unknown receptors, to trigger inflammatory and tumorigenic responses *in vivo*. PAR-null animals are a valuable tool that can be used to investigate the role of these receptors in KLK-mediated inflammation and carcinogenesis.

Furthermore, it is essential to determine the proportion of KLKs detected by immunoassay that are catalytically active *in vivo* in inflamed tissues, tumor cells and related fluids, or in samples derived from patients experiencing chronic inflammation and pain. As knowledge on the catalytic specificity of serine proteinases and their endogenous substrates is rapidly increasing, selection of an optimal probe for activity-based assays will significantly increase both the sensitivity and specificity of proteinase detection. Despite the restriction of such activity-based tools to specific groups of proteinases, they have the potential to be used in clinical practice. In this regard, we foresee a major clinical importance for our recently developed high-throughput ABP proteomics concept, which may facilitate rapid identification or quantification of all active proteinases (e.g., serine, cysteine, metalloproteinases) in clinical samples.

The levels of proteinase inhibitors in pathological settings may also be used as clinical markers of disease. Supporting this proposal is the finding that the percentage of free KLK3 (not complexed to inhibitors but mainly enzymatically inactive) is lower in serum samples from patients with prostate cancer, which, with the use of the appropriate set of probes, may be associated with a more aggressive form of prostate cancer for reasons that are yet unknown (Carter et al., 1997; Arcangeli et al., 1998; Catalona et al., 1998).

The activity-based proteomics approach can also serve to identify simultaneously active KLKs or other serine proteinases in several inflammatory or tumor settings. Targeting the analysis of multiple active proteinases (and their inhibitors) may provide insights into the network of proteinases critical for the inflammatory response or for tumor survival and progression. This information may point the way to appropriately customized therapeutic modalities.

Finally, it is of major importance to delineate the specific components that act both upstream and downstream of KLKs and PARs. Identification of naturally occurring specific activators or inhibitors of KLK activity *in vivo* may lead to the development of regimens for the treatment of diseases such as cancer, multiple sclerosis and Netherton syndrome. Furthermore, as discussed, the different KLKs may have differential effects on cells and tissues via the activation of multiple signaling pathways. These effects may also depend on the presence of several co-factors. Identification of these distinct signal pathways will also contribute to the selection of therapeutic targets for the treatment of patients suffering from inflammatory diseases or cancer in which KLKs may be involved.

In summary, the future of KLK research will involve delineation of the components of the signaling pathways

upstream or downstream of the active proteinases and their receptors, as well as their levels of function and activity. These findings may lead to the development of clinical assays for disease detection, prognosis or monitoring, as well as to the production of therapeutic compounds for pathological conditions, such as cancer and inflammation.

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