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Presentation Title: **Expression analysis and prognostic significance of SR-A1 gene, encoding for a new member of the human ser/arg-rich family of pre-mRNA splicing factors, in breast and ovarian cancer**

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Author Block: *Theoni Leoutsakou, Maroulio Talieri, Konstantina Mathioudaki, Panagiota Stavropoulou, Niki Arnogianaki, Eleftherios P. Diamandis, Andreas Scorilas.* NCSR Demokritos, Athens, Greece, Saint Savas Hospital, Athens, Greece, Mount Sinai Hospital and University of Toronto, Toronto, ON, Canada, NCSR Demokritos and University of Athens, Athens, Greece

We cloned recently the SR-A1 gene which encodes for a new member of the human Ser/Arg-rich family of pre-mRNA splicing factors. The SR-A1 gene, located between the interferon regulator factor 3 (IRF3) gene and RRAS oncogene is a member of the SR family of proteins and has been shown to interact with the C-terminal domain (CTD) of the large subunit of RNA polymerase II, and participate in pre-mRNA splicing. There is evidence that SR protein splicing factors are involved in cancer pathobiology through their involvement in alternative processing events. In the present study we have examined the prognostic value of SR-A1 expression in 80 breast and 100 ovarian tissues from patients undergone surgery for primary breast and ovarian cancer at the Oncologic Hospital of Athens "Saint Savas". Total RNA was extracted from pulverized tumors, and cDNA was prepared by reverse transcription. SR-A1 was amplified by PCR using gene specific primers, and its identity was verified by sequencing. Breast and ovarian tissues were then classified as SR-A1 positive or negative, based on ethidium bromide visualization of the PCR products on agarose gels. Actin was used as a control gene. SR-A1 gene was expressed in 43/80 (53%) breast cancer tissue. SR-A1 overexpression was found to be more frequent in breast cancer patients with tumors of large size ($p=0.02$), as well as in node positive and progesterone receptor negative patients ($p<0.001$ and $p=0.04$ respectively). Also SR-A1, was found to be expressed in 40/100 ovarian tumors and its overexpression was found more frequently in grade III ($p=0.03$) as well as in stage III tumors ($p=0.02$). In univariate analysis, SR-A1 overexpression proved to be a predictor of statistical significance for decreased progression-free (PFS) and overall survival (OS) of breast and ovarian cancer. Cox multivariate analysis indicated that SR-A1 was an independent prediction factor for PFS ($p=0.02$) and OS ($p=0.01$) of ovarian cancer patients. Our results suggest that SR-A1 gene, is involved in cancer progression and may be characterised as a new marker of unfavourable prognosis for breast and ovarian cancer. **Acknowledgements:** This work was supported by a PENED grant (Code # 01ED622) from European Community, the General Secretariat for Research & Technology of Greece (EPAN.M.8.3) and BioSURE- R&T Cell Co. Athens, Greece.

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