

#3106 The SR-A1 Gene, Encoding a New Member of the Human Ser/Arg-Rich Family of Pre-mRNA Splicing Factors, is Overexpressed in Aggressive Ovarian Tumors and is an Independent Unfavorable Prognostic Indicator in Ovarian Cancer. Andreas Scorilas, D. Katsaros, A. Kwamie, S. Fracchioli, and E. Diamandis. *Mount Sinai Hospital, Toronto, ON, Canada, Mount Sinai Hospital and University of Toronto, Toronto, ON, Canada, University of Toronto, Toronto, ON, Canada, and University of Turin, Turin, Italy.*

The SR-A1 gene, located between the interferon regulator factor 3 (IRF3) and RRAS genes, is one of the newly discovered members of the human Ser/Arg-rich family (SR) of pre-mRNA splicing factors which appears to be the human homolog of the rat A1 gene. Members of the SR family of proteins have 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, and we have undertaken the examination of the prognostic value of SR-A1 expression in 140 malignant ovarian tissues. 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. Ovarian tissues were then classified as SR-A1 positive or negative, based on ethidium bromide visualization of the PCR product on agarose gels. SR-A1 was found to be expressed in 58/140 (41%) of ovarian tumors. SR-A1 overexpression was found more frequently in grade III tumors ($P=0.034$) as well as in stage III ($P=0.028$) and suboptimal debulking patients ($P=0.001$). In univariate analysis, SR-A1 overexpression proved to be a significant predictor of decreased progression-free (PFS) ($P=0.006$) and overall survival (OS) ($P<0.001$). Cox multivariate analysis indicated that SR-A1 was an independent factor to predict the PFS ($P=0.025$) and OS ($P=0.01$). These regression models were adjusted for stage of disease, tumor grade, residual tumor, histologic type and age. In conclusion, SR-A1 is a new potential independent unfavorable prognostic factor in ovarian cancer patients.