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1728 Expression analysis of the SR-A1 gene, encoding for a novel member of the human Ser/Arg-rich family of proteins, in breast cancer.

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SR proteins can complement splicing-inactive S100 fractions and alter splice-site selection in alternatively spliced pre-mRNAs. Moreover, there is evidence that SR protein splicing factors are involved in cancer pathobiology through their effect on alternative processing decisions. Recently the SR-A1 gene, encoding for a new member of the human Ser/Arg-rich family of pre-mRNA splicing factors, was cloned by members of our group (Scorilas A et al. Br J Cancer 2001;85:190-8). Also, overexpression of the gene was documented in aggressive ovarian cancer. In the present study, the expression of SR-A1 gene was examined in tumor samples of 80 patients who underwent surgery for primary breast cancer. Total RNA was reverse-transcribed to cDNA. The SR-A1 gene was amplified by PCR using gene specific primers(1) and product identity was verified by sequencing. Breast 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. The SR-A1 gene was expressed in 43/80 (53%) of breast cancer tissues. SR-A1 overexpression was found to be more frequent in 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). Our results suggest that the newly cloned gene SR-A1, may be involved in breast cancer progression and is a marker of unfavourable prognosis for breast cancer.

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