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P60-S6K1 mRNA TRANSCRIPT EXPRESSION PROFILE IN A PANEL OF CELL LINES AND BREAST CANCER TISSUE SAMPLES

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Introduction. The *RPS6KB1* (S6K1 (ribosomal protein S6 kinase 1) gene is frequently amplified in breast cancer that is associated with shorter survival of patients suggesting that S6K1 protein overexpression (p85- and p70-S6K1 isoforms) plays a significant part in breast cancer biology. Unlike the major p85- and p70-S6K1 isoforms, expression and a role of the p60-S6K1 isoform in breast cancer has been poorly studied to date. The aim of the study was to analyze the expression profile of p60-S6K1 mRNA transcript in different cell types and breast tumors of various clinical subtypes.

Methods. RNA isolation, RT-PCR, DNA gel electrophoresis, DNA sequencing.

Results. Initially, we focused on confirmation of the existence of the p60-S6K1 mRNA transcript by PCR. PCR analysis of cDNA from HEK-293 and subsequent DNA sequencing verified that the sequence of the PCR product corresponded to the p60-S6K1 transcript-specific nucleotide sequence. Expression levels of the p60-S6K1 transcript were estimated using PCR analysis of cDNA from 8 different cell lines (MCF-7, HEK-293, HeLa, HepG2, U-87, U-373, U-937, Jurkat), 20 breast cancer tissue samples grouped according to the clinical subtype (Luminal A (7), Luminal B (7), HER^+ (6) and 6 normal breast tissue samples adjacent to breast tumors. Data showed the presence of heterogeneity of p60-S6K1 mRNA expression between different cell lines and also heterogeneity between 3 clinical breast cancer subtypes. What is more, the expression levels of the given transcript were elevated in the samples of Luminal B and HER^+ subtypes, which are associated with poor prognosis, compared to that of Luminal A subtype associated with good prognosis. In addition, there was no correlation observed between expression of the p60-S6K1 transcript and total S6K1 RNA transcripts in all tested cell lines and tissue samples.

Conclusions. Additional evidence of the existence of the p60-S6K1 mRNA transcript, which supposedly encodes the p60-S6K1 isoform, was received. The given transcript exhibits a differential expression pattern in a number of cell lines, as well as in breast cancer tissue samples of different clinical subtypes. The increased expression levels of the p60-S6K1 transcript seem to correlate with poor prognosis in patients with breast cancer.