Health & Medical Sciences Abstracts

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Edited by Gregory T. Papanikos

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DNA Hypermethylation Detected in Invasive Breast Cancer

Objective: DNA methylation as an early event in breast carcinogenesis has been frequently studied in tumour samples. The aim of this study was to compare the relationship between DNA methylation levels of genes associated with invasivity and metastasising and aberrant protein expression (breast cancer progression).

Methods: A total 55 healthy controls and 185 patients with primary breast cancer, as well as plasma and peripheral blood cells has been analysed by using pyrosequencing method. The expression of 11 proteins in paraffinembedded biopsy was evaluated by immunohistochemistry. Genes containing CpG islands in promotor region were suggested for screening because they could be epigenetic upregulated with high probability. DNA methylation of APC, ADAM23, CXCL12, ESR1, PGR B, CDH1, RASSF1A, SYK, TIMP3, BRMS1 and SOCS1 genes has been detected.

Results: DNA hypermethylation of tumor suppressor genes is tumorspecific and could be used for recognition of tumor cells. We observed higher methylation status for 4 genes (RASSF1A, APC, CXCL12 and ADAM23) from 11 genes evaluated in tumors. The highest promoter methylation level was 88%, detected in RASSF1A and APC genes. Variable expression profiles were identified in analyzed genes ranging from negative expression to high expression. Our present results indicate the variability in expression of the proteins studied in tumor tissue of patients with breast cancer. Conclusion: We can conclude that the quantitative analyses of tumor DNA methylation in any of RASSF1A, ADAM23, CXCL12 and APC genes could have prognostic potential. Supported by the grant APVV-0076-10 - the Slovak Research and Development Agency and Research and Development Operational Programme (ERDF)-26240220058.