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### DNA methylation profiles in advanced breast cancer

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More than 25% of the patients with breast cancer (BC) develop metastatic disease. We investigated the relationship between DNA methylation levels in genes regulating cell growth, invasiveness, and metastasis and advanced BCs and evaluated the clinical utility of methylation profiles for detecting metastatic potential. Methylation levels in 11 cancer associated genes in primary tumors (PTs), lymph node metastases (LNMs), plasma (PL), and blood cells from 206 patients with invasive BC were quantified by pyrosequencing. PTs showed hypermethylation of *RASSF1A*, *APC*, *CXCL12*, and *ADAM23* genes with means 38.98%, 24.84%, 12.04%, and 10.01%, respectively. Positive correlations were identified between methylations in PTs and LNMs, but not between PL and PTs. The cumulative methylation of PTs and LNMs manifested similar spectrums of methylated genes that indicate the maintaining of aberrant methylation during breast tumorigenesis. Significantly increased methylation levels in *RASSF1A*, *APC*, *CXCL12*, and *ADAM23* were found in ER positive BCs in comparison with ER negative cases. Regarding these results, the evaluation of DNA methylation could be more informative in testing of patients with ER positive BC. The risk for LNMs development and higher proliferation of cancer cells measured through Ki-67 expression was increased by hypermethylation of *CXCL12* and *ADAM23*, respectively. Therefore, the quantification of *CXCL12* and *ADAM23* methylation could be useful for the prediction of advanced stage of BC.

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### Biography

Ivana Fridrichova has completed her university and PhD study from Comenius University in Bratislava and Cancer Research Institute, Slovak Academy of Sciences (CRI SAS) in Bratislava, Slovakia, in 1983 and 1991, respectively. Currently, she is senior scientist and head of Epigenetic Research Group at CRI SAS and she has supervised the research projects dealing with investigation of the aberrant epigenetic changes in cancer patients. Her research team is focused on aberrant methylation profiles of genes associated with metastatic breast cancer. She has published more than 25 papers in reputed journals.

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