

CLINICOPATHOLOGICAL SIGNIFICANCE OF BRCA1 PROMOTER HYPERMETHYLATION IN THAI BREAST-CANCER PATIENTS

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ABSTRACT

Breast cancer susceptibility gene 1 (BRCA1) is mapped on chromosome 17q21. It is implicated in the repair mechanism of cellular DNA. Inactivation of this gene is involved in the development of many human cancers, including breast cancer. This study investigated the prognostic value of BRCA1 promoter hypermethylation and expression in breast cancer. Sixty-one breast tumors were examined for BRCA1 hypermethylation by methylation-specific PCR and 45 paired normal breast tissues were analyzed for BRCA1 mRNA level by quantitative real-time reverse transcription-polymerase chain reaction (RT-PCR). Aberrant methylation status in BRCA1 was detected in 15 of 61 cases (24.6%), while reduced expression was found in 7 of 45 cases (15.6%). BRCA1 hypermethylation was significantly associated with tumor grade III ($P=0.04$), a high frequency of stage IIB ($P=0.02$) and triple-negative tumor (OR= 3.64, 95%CI =1.1-12.3, $P=0.033$). No association was observed between BRCA1 mRNA under-expression and the clinicopathological features of breast cancer. Our findings indicate that BRCA1 promoter hypermethylation could serve as a prognostic marker for the development of breast cancer.

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