ORIGINAL ARTICLE

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Study of DNA Methylation Pattern at the Tumor Suppressor Gene RASSF1A Promoter in Two Breast Cancer Cell Lines

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Abstract

Introduction: Breast cancer represents a significant health problem in women worldwide and improvements in our ability to prevent, diagnose, and treat the disease requires a greater understanding of the molecular basis of breast carcinogenesis. Methylation analysis of cell cycle genes can be used as a way of identifying important genes in tumorigenesis and can have diagnostic/prognostic value. The aim of this study was to investigate the methylation status of RASSF1A promoter, as a cell cycle regulatory gene, in two breast cancer cell lines.

Method: In this basic research, MSP (methylation-specific PCR) was used as a qualitative method to assess the methylation pattern of RASSF1A promoter in two breast cancer cell lines (MCF-7 and MDA-MB-231). This method involves initial modification of DNA by sodium bisulfite, converting all unmethylated, but not methylated, cytosines to uracil, and subsequent amplification with primers specific for methylated and unmethylated DNA.

Results: MSP results show that in both MCF-7 and MDA-MB-231 cell lines, regardless of their molecular subtype, promoter of the tumor suppressor gene RASSF1A is completely methylated. The lack of unmethylated band in both mentioned cell lines also indicate this issue.

Conclusion: These findings confirm that RASSF1A promoter region hypermethylation may play an important role in breast cancer pathogenesis. Considering that epigenetic changes are reversible, screening for aberrant methylation patterns of CpG sites within the promoter of essential genes during the tumorigenic process, such as cell cycle genes, can contribute to the development and application of therapeutic agents targeting these alterations in human breast cancers.

Key words: Breast Cancer, Cell Cycle Genes, Aberrant Methylation Patterns, Promoter of the Tumor Suppressor Gene RASSF1A.