MteI-PCR assay – a new method of methylation status determination for GC-rich regulatory regions of human tumor suppressor genes

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A novel method of MteI-PCR analysis of GC-rich DNA regions has been proposed based on the unique methyl-dependent site-specific DNA endonuclease MteI, which recognizes a long highly methylated site. The method includes DNA hydrolysis with MteI followed by real-time PCR or PCR with electrophoretic determination of the obtained products. Methylation status of regulatory regions of a number of tumor supressor genes has been determined by this method in comparison with the similar data obtained by previously proposed method of BlsI- and GlaI-PCR analysis. An applicability of MteI-PCR analysis has been shown by analysis of methylation status of *CEBPD, HS3ST2, RASSF1A, SEPT9b* and *TWIST1* genes regulatory regions. In case of *RASSF1A* regulatory region, real-time MteI-PCR analysis in contrast to BlsI- and GlaI-PCR analysis, does not show methylation of this DNA region in a control healthy lung fibroblast cell line. Thus, MteI-PCR analysis allows to perform more distinct determination and discrimination of *RASSF1A* regulatory region methylation and, probably, some other GC-rich regions of human DNA as well.

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