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Semiquantitative detection of aberrant methylation as a tumor biomarker in the serum and plasma of gastric carcinoma patients

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Background & Aim: Epigenetic silencing of tumor-related genes, due to CpG island methylation, is considered to be an important mechanism for the development of many tumors, including gastric carcinoma (GC). We attempted to determine the feasibility and the clinical correlations of detecting tumor-associated aberrant methylation in the serum/plasma of patients with GC.

Materials & Methods: We examined promoter methylation of 6 genes using methylation-specific PCR (MSP) and methylation-sensitive high-resolution melting (MS-HRM) in paired serum, plasma and tumor samples of 50 GC patients. The tumor and the paired serum/plasma were investigated for aberrant methylation in *BLU, DAPK1, GADD45G, MGMT, p15* and *p16*.

Results: Promoter methylation in *BLU, DAPK1, GADD45G, MGMT, p15* and *p16* were detected in 47%, 37%, 59%, 32%, 14% and 43% of tumor tissues by MSP. In the serum/plasma of GC patients, *BLU, DAPK1, GADD45G, MGMT, p15* and *p16* were methylated at frequencies of 26%, 21%, 23%, 11%, 9% and 17%, respectively. Aberrant methylation in one or more genes was found in 74% (37/50) serum samples and 70% (35/50) plasma samples.

Conclusion: These results suggest that aberrant promoter methylation in serum/plasma can be detected in a substantial proportion of GC patients. Detection of DNA methylation in serum/plasma may be a biomarker for early detection of GC. MS-HRM is powerful technique for the analysis of promoter methylation. Application of HRM analysis to large number of clinical samples proves to be a fast and high-throughput way to investigate the epigenetic status of genes.

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