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Aberrant DNA methylation of *MGMT* and *hMLH1* genes in prediction of gastric cancer

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ABSTRACT. We aimed to explore the association between aberrant DNA methylation of the O(6)-methylguanine-DNA methyltransferase (MGMT) and human mutL homolog 1 (hMLH1) genes with gastric cancer. A total of 283 gastric cancer patients who were confirmed by pathological diagnosis were included in our study. Aberrant DNA methylation of *MGMT* and *hMLH1* were detected. The proportions of DNA hypermethylation in *MGMT* and *hMLH1* in cancer tissues were significantly higher than those in remote normal-appearing tissues. The DNA hypermethylation of *MGMT* was correlated with the tumor-necrosis-metastasis stage in gastric cancer tissues. Results showed that individuals with gastric cancer in the N1 and M1 stages had a significantly higher risk of DNA hypermethylation of *MGMT* in cancer tissues [odds ratio (OR) = 1.97, 95% confidence interval (CI) = 1.15-3.37 for the N1 stage; OR (95%CI) = 5.39 (2.08-14.98) for the M1 stage]. In conclusion, we found that aberrant hypermethylation of *MGMT* could be a predictive biomarker for detecting gastric cancer.

Key words: Aberrant DNA methylation; MGMT; hMLH1; Gastric cancer

