Aberrant DNA methylation of $\textit{MGMT}$ and $\textit{hMLH1}$ 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 ($\textit{MGMT}$) and human mutL homolog 1 ($\textit{hMLH1}$) 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 $\textit{MGMT}$ and $\textit{hMLH1}$ were detected. The proportions of DNA hypermethylation in $\textit{MGMT}$ and $\textit{hMLH1}$ in cancer tissues were significantly higher than those in remote normal-appearing tissues. The DNA hypermethylation of $\textit{MGMT}$ 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 $\textit{MGMT}$ 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 $\textit{MGMT}$ could be a predictive biomarker for detecting gastric cancer.

Key words: Aberrant DNA methylation; $\textit{MGMT}$; $\textit{hMLH1}$; Gastric cancer