Braf, Kras and Helicobacter pylori epigenetic changes-associated chronic gastritis in Egyptian patients with and without gastric cancer

Abstract

We aimed to study MLH1 and MGMT methylation status in Helicobacter pylori-associated chronic gastritis in Egyptian patients with and without gastric cancer. 39 patients were included in our study. They were divided into 2 groups; patients without (group I) and with gastric adenocarcinoma (group II). Patients were subjected to clinical examination, abdominal ultrasound and upper endoscopy for gastric biopsy. Biopsies were subjected to urease test, histological examination, and DNA purification. H. pylori, Braf, Kras, MLH1 and MGMT methylation were assessed by quantitative PCR. DNA sequencing was performed to assess Braf and Kras genes mutation. qPCR of H. pylori was significantly higher in patients with adenocarcinoma (group II) than those without adenocarcinoma (group I); with a $p<0.001$ as well as in patients with age above 50 years with a p value = 0.008. By applying logistic regression analysis it was reported that the H. pylori qPCR is a significant predictor to the adenocarcinoma with OR = 1.025 (95 % CI: 1. 002–1.048), with sensitivity of 90 % and specificity of 100 %. Adenocarcinoma patients had a significantly higher mean age and levels of H. Pylori, Braf, K-ras, methylated MGMT and methylated MLH1 than those of gastritis patients. DNA sequence analysis of Braf (codon 12) and Kras (codon 600) had genes mutation in gastric adenocarcinoma versus chronic gastritis. Conclusion: H. pylori may cause epigenetic changes predisposing the patients to cancer stomach. Estimation of H. pylori by qPCR can be a good predictor to adenocarcinoma. Braf and Kras genes mutation were reveled in gastritis and adenocarcinoma patients.