Detection of Colorectal Neoplasia by Multigene Methylation Analysis of Circulating Tumor DNA

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Abstract

Background: Colorectal cancer (CRC) is considered most widely recognized malignant growth around the world. CRC is caused by precancerous polyps within the colon as well as rectum and can be prevented by early detection and excision of precursor lesions. In this work, we evaluated the methylation of *SEPT9* and *SPG20* genes as bio markers for CRC patients in cell free DNA extracted from plasma.

Methods: This case-control study was carried out on 25 cases with verified CRC and 25 apparently healthy individual controls as dictated by colonoscopy. The workflow consisted of plasma cell-free DNA isolation, bisulfite treatment of DNA, purified of bisulfite treated DNA, and detection of treated DNA by "methylation specific PCR".

Results: The bisulfite conversion assay yielded 45%–50% of the circulating plasma genomic DNA. The *SEPT9* and *SPG20* combined assay successfully identified CRC samples 100% as sensitivity and 100 % as specificity with 100% of positive predictive value and AUC 1.000{95% confidence interval, (1.000-1.000)}. A significant increase of m*SEPT9*-m*SPG20* in CRC correlated with histological grade, tumor size, and overall histological type were correlated with CRC (P < 0 05).

Conclusion: Circulating methylated SEPT9 and *SPG20* DNA sounds like a promising detection tool for colorectal cancer in Gaza strip.

Keywords: Biomarker, colorectal cancer, cf-DNA, DNA methylation, *SEPT9, SPG20*.