Usefulness of Epigenetic Biomarkers in Plasma for Detection of Colorectal Cancer

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Background and Aims: Colorectal cancer (CRC) developed from accumulation of genetic and epigenetic alterations in colonic epithelial cells. The aim of the study was evaluated promoter methylation in 5 genes, which are known to be involved in the pathogenesis of colorectal cancer and are frequently silenced by hypermethylation in colorectal cancer. Methods: Five markers were selected for analysis in plasma samples from 30 CRC and 50 non-CRC patients. The methylation states of promoter regions of the SMAD4, FHIT, DAPK1, APC and E-cadherin gene were examined. The methylation status of the 5 genes was determined using polymerase chain reaction - single strand conformation polymorphism (PCR-SSCP). Results: This study showed the most sensitive marker was E-cadherin, which amplified 90% of CRC patients, followed by APC (85%) and SMAD4 (71%). E-cadherin and APC had similar specificities and amplified 84% and 86% of CRC patients compared to non-CRC patients, respectively. Then we observed sensitivity and specificity to compare the methylation states of stages I CRC patients and normal control. The result indicated the most sensitive marker was APC, 50% of CRC patients, followed by E-cadherin (38%) and SMAD4 (31%). The most specific marker was APC, 89% of CRC patients, followed by E-cadherin (87%) and SMAD4 (87%). Conclusions: Among the five genes tested, E-cadherin methylation seems to have the highest probability of detection of CRC patients compared to non-CRC patients in blood. For detection stage I CRC compared to normal control, the most sensitive and specific marker was APC. Our exploratory study indicates that APC may be able to identify potentially early CRC. In this study, E-cadherin and APC were useful epigenetic biomarkers in blood for detection of CRC.