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**Methylation-Specific PCR Assay for Quantification of DNA Methylation of SPG20 Gene in Colorectal Cancer**

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**ABSTRACT**

Colorectal cancer (CRC) is one of the most common cancers worldwide that arise from successive accumulation of genetic and epigenetics alterations. It is a major cause of morbidity and mortality globally. It is highly curable if detected early, as the polyps can be removed before they divide and overgrow. Unremoved polyps may invade other parts of the body. Hence, earlier detection would significantly reduce the number of death due to this cancer. The discovery of aberrant DNA methylation in CpG islands of a number of genes might be one of the important pathways involved in CRC initiation and development. Therefore, the aim of our study was to examine the relationship of DNA methylation levels of SPG20 gene, one of the gene that is commonly epigenetically methylated in CRC, using genomic DNA derived from the tissues of patients with this cancer. The case control studies consisted of 29 cancerous tissues and 29 normal tissues taken from CRC patients. The extracted DNA was bisulfite converted and the percentage of methylation of the DNA samples were calculated based on their Cq values assayed using quantitative methylation-specific PCR (qMSP) procedure. We found that the percentage of SPG20 methylation showed a statistically significant difference in CRC samples as compared to normal tissues. Our results showed high level of SPG20 methylation in CRC tissue samples, thus suggesting the involvement of methylation as one of the mechanism in CRC pathogenesis. Hence, the identification of methylation level of SPG20 may serve as potential indicator in early detection of CRC and provide useful insights in better understanding of CRC progression. However, the finding of the study is limited due to small sample size and evaluation at a larger scale involving other prevalent genes is necessary.