**Genome-Wide DNA Methylation Profiles of Low- and High-Grade Adenoma Reveals A Potential Biomarker for Early Detection of Colorectal Carcinoma**

**Abstract**

**Background:** Abnormal DNA methylation is a hallmark of human cancers, but it requires efforts to examine the changes in differential methylation regions (DMRs) identified in tumor genome could occur in precancerous lesions before cancer development.

**Methods:** In this study, we identified DMRs by genome-wide DNA methylation assay (Meth450K) to normal (N=20) and pre-colorectal cancer samples including 18 low-grade adenoma (LGA) and 22 high-grade adenoma (HGA), integrating with GEO and ArrayExpress datasets (N=833).

**Results:** We identified 209 hyper DMRs in LGA, which were further hyper-methylated in HGA and cancer samples. They showed better discrimination between normal, pre-cancerous, and cancerous tissues in comparison with hypo DMRs. DMRs specific to LGA were over-represented in nervous system-related pathways possibly related to early adenoma development. Together with GEO and ArrayExpress datasets, integration analysis revealed that DNA methylation in the promoter region of *ADHFE1* has the most potential for being an early detection biomarker for colorectal adenoma and cancer (sensitivity=0.96, specificity=0.95, area under the curve=0.97).

**Conclusions:** Overall, we demonstrated LGA and HGA provided an important proxy for early methylation event identification and the gene could be a promising methylation biomarker for colorectal cancer.