

Improving precision medicine through the identification of epigenetic biomarkers for colorectal cancer cases in a local setting- a study protocol

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ABSTRACT

Introduction: Colorectal cancer (CRC) is the second most common cancer in Malaysia, often diagnosed at late stages, leading to a substantial economic burden and reduced survival rates. Blood-based epigenetic markers, particularly circulating tumour DNA (ctDNA), hold promise for early CRC detection. However, data from local patients are limited, and marker effectiveness in diverse populations is uncertain. To address these gaps, we propose a study to identify and validate robust methylation markers that could effectively distinguish between CRC patients and those with colorectal polyps or adenomas. **Methods:** The study will include 120 histologically confirmed CRC, polyps or adenoma patients, with a total of 80 blood samples and 160 FFPE tissue samples collected. Patients receiving chemotherapy or radiotherapy treatment at recruitment will be excluded. Samples will be obtained through the MOH Biobank. Methylome profiling will be performed using Infinium Human MethylationEPIC v2.0 BeadChip arrays. Data analysis will include differential methylation analysis, gene set enrichment analysis, and logistic regression for CRC classification. **Results:** The study aims to identify and validate novel and known methylation markers for CRC detection, potentially contributing to the development of liquid biopsy and companion diagnostic tests for precision medicine in the local setting. **Conclusion:** This study addresses the scarcity of local methylation analysis data and the need for effective CRC screening methods. Validating blood-based methylation markers will enhance early detection efforts, reducing the burden of CRC in Malaysia, with advancing precision medicine and liquid biopsy tests for early CRC detection and treatment in the local population.