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**Whole Genome Sequencing of Malaysian Colorectal Cancers Identifies SNVs, Indels and Actionable Mutations**

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**ABSTRACT**

Whole genome sequencing (WGS) has enabled the in-depth characterisation of cancer tissues, by providing the base-by-base view of the entire cancer genome. In today’s era of precision medicine, this insight into the complete genome of an individual tumour is valuable for the determination of personalised treatment as well as for the advancement of cancer pharmacogenetics. By sequencing the DNA from a tumour and the corresponding normal cells, we can identify the somatic variants within the tumour that are of clinical importance. In this study, paired tumour-normal samples were collected from thirteen patients diagnosed with primary colorectal cancer and treated at Universiti Kebangsaan Malaysia Medical Centre (UKMMC). The extracted genomic DNA samples were subjected to WGS on the Illumina Hiseq X Ten platform. We looked at the somatic mutations (single nucleotide variants and indels) present in the tumours, and characterized the mutational profiles of the patients. All 26 samples achieved at least 30x sequencing coverage. At least 93% of the raw reads passed the quality check and pre-processing criteria. At least 97.9% of the clean reads mapped to hg19 with more than 97.5% uniquely mapped reads. There were 3,353 - 823,647 somatic single nucleotide variants and 454 - 156,760 indels identified in all samples. By focusing on the deleterious variants located in exonic region, we identified an average of 143 somatic variants. After prioritizing the variants according to actionability, at least one actionable variant was identified in KRAS, BRAF, PIK3CA, SMAD4 and FBXW7, all of which are potentially involved in determining responses towards chemotherapeutic drugs, such as 5-fluorouracil, cetuximab and panitumumab. These preliminary findings could assist in determining the optimal tailored treatment for each individual patient.