129. Investigating the gut microbiome profiles associated with colorectal cancer in patients of African Descent

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Abstract

Colorectal cancer (CRC) is one of the leading causes of cancer in the world. In Kenya, CRC is the fifth most common cancer in the country and the third most frequent among Kenyan men. The human gut microbiome is a highly diverse microbial community that modulates human health through the production of short-chain fatty acids, vitamins, neurotransmitters and antimicrobial peptides. The human gut microbiome composition has been found to be a risk factor for the development of CRC. Bacteroides fragilis, Clostridium septicum, Enterococcus faecalis, Escherichia coli and Streptococcus gallolyticus are directly associated with colorectal carcinogenesis. The main object of this study is to explore the association between gut microbiome composition and diversity and CRC in patients of African descent. There is a paucity of data of the link between CRC and the gut microbiome among African patients. This will be a cross-sectional study that will involve a secondary analysis of publicly available 16S rRNA data obtained from analysing the gut microbiomes of patients with CRC. FastQ files will be retrieved from sequence databases by searching for specific keywords. DADA2 will be used to perform quality control and taxonomic classification on the obtained 16S rRNA sequence data in R 4.4.0. Phyloseq will be used to perform diversity analysis and generate data visualisations. PICRUSt2 will be used to predict microbial functions associated with CRC and MICOM for metabolic profiling of the gut microbiomes of patients with CRC. The findings from this study will generate a comprehensive analysis of the gut microbiome profiles of patients of African descent with colorectal cancer. Moreover, functional analysis will be key in identifying gene and protein families that are associated with CRC which may serve as diagnostic and prognostic biomarkers.

Keywords: *gut microbiome, colorectal cancer, diversity, functional, metabolic and dysbiosis.*