Pathogenic fungi of genera *Rhodotorula* is linked with early and late-onset colorectal cancer patients in Malaysia

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**Background:**
- Colorectal cancer (CRC) is a deadly disease that caused 0.9 million deaths worldwide in 2020.
- The prevalence of CRC is expected to increase steadily each year.
- Studies have linked gut microbiota to CRC, but it’s unclear how fungal communities in the gut are involved.
- This study aims to explore the role of opportunistic fungal pathogens and the host’s phenotypes in CRC patients.

**Methodology:**
- Biopsy samples were taken from 64 individuals during colonoscopy sessions.
- The gDNA was extracted using the Ultra Deep Microbiome Prep Kit.
- The amplicons of microbial genome libraries were targeted by sequencing the ITS1 regions.
- The microbial genomic data was analyzed using state-of-the-art bioinformatic tools.

**Results:**
- 6,477,706 read counts were generated from the samples.
- 1,564 amiploc sequence variants of fungi were found.
- Significant differences are observed in alpha diversity between early and late on-set CRC patients, polyps, and normal individuals, as measured by Chao1 diversity (p-value = 0.0017509).

**Conclusion:**
- The study found a correlation between the presence of the fungal genera *Rhodotorula* and CRC patients in Malaysia.
- Further studies are needed to understand the role of this opportunistic pathogen in the progression of CRC.