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

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The gDNA was extracted using the Ultra Deep Microbiome Prep Kit

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The amplicons of microbial genome libraries were targeted by sequencing the ITS1 regions

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The microbial genomic data was analyzed using state-of-the-art bioinformatic tools

Results:

- 6,477,706 read counts were generated from the samples.
- 1,364 amplicon sequence variants of fungi were found.
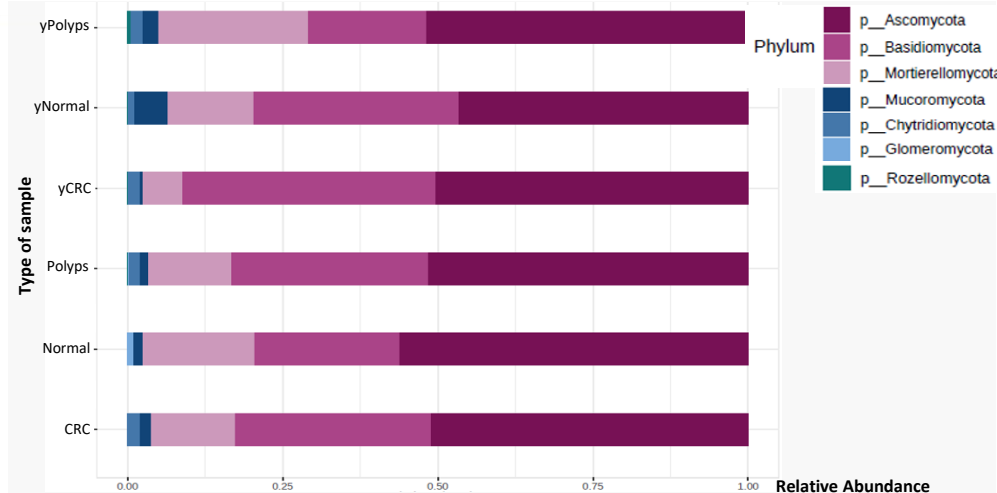
- *Ascomycota*, *Basidiomycota*, *Mortierellomycota*, and *Chytridiomycota* are the main fungal phyla found in both early and late-onset CRC patients.

p-value: 0.0017509; [ANOVA] F-value: 4.4272
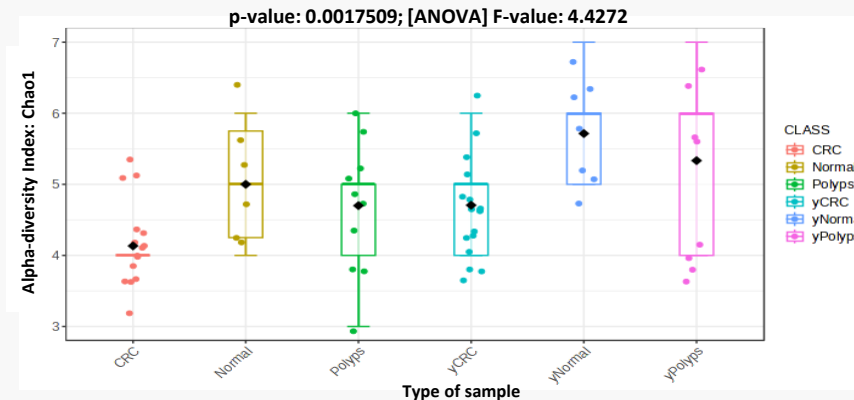
- Significant differences are observed in alpha diversity between early and late on-set CRC patients, polyps, and normal individuals, as measured by Chao1 diversity (p-value = 0.0017509).
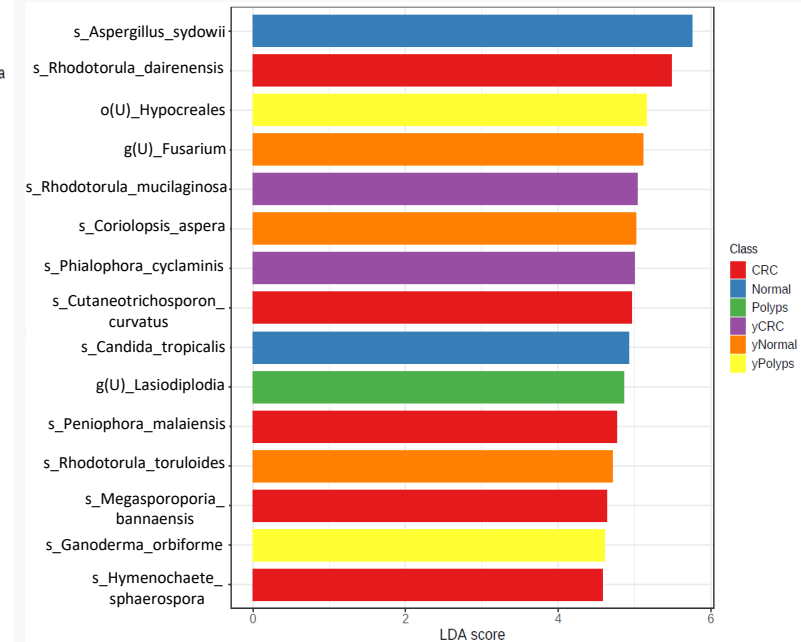
- *Aspergillus sydowii* and *Candida tropicalis* are associated with **healthy** individuals.
- *Rhodotorula dairenensis*, *Cutaneotrichosporon curvatus*, *Peniphora malaiensis*, *Megasporoporia bannaensis*, and *Hymenochaete sphaerospora* were found to have a positive correlation with **late-onset CRC** patients.
- *Rhodotorula mucilaginosa* and *Coriolopsis aspera* are associated with **early-onset CRC** patients.
- Previous studies have reported that CRC patients are at higher risk of *Rhodotorula* infection.

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.