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## INTRODUCTION

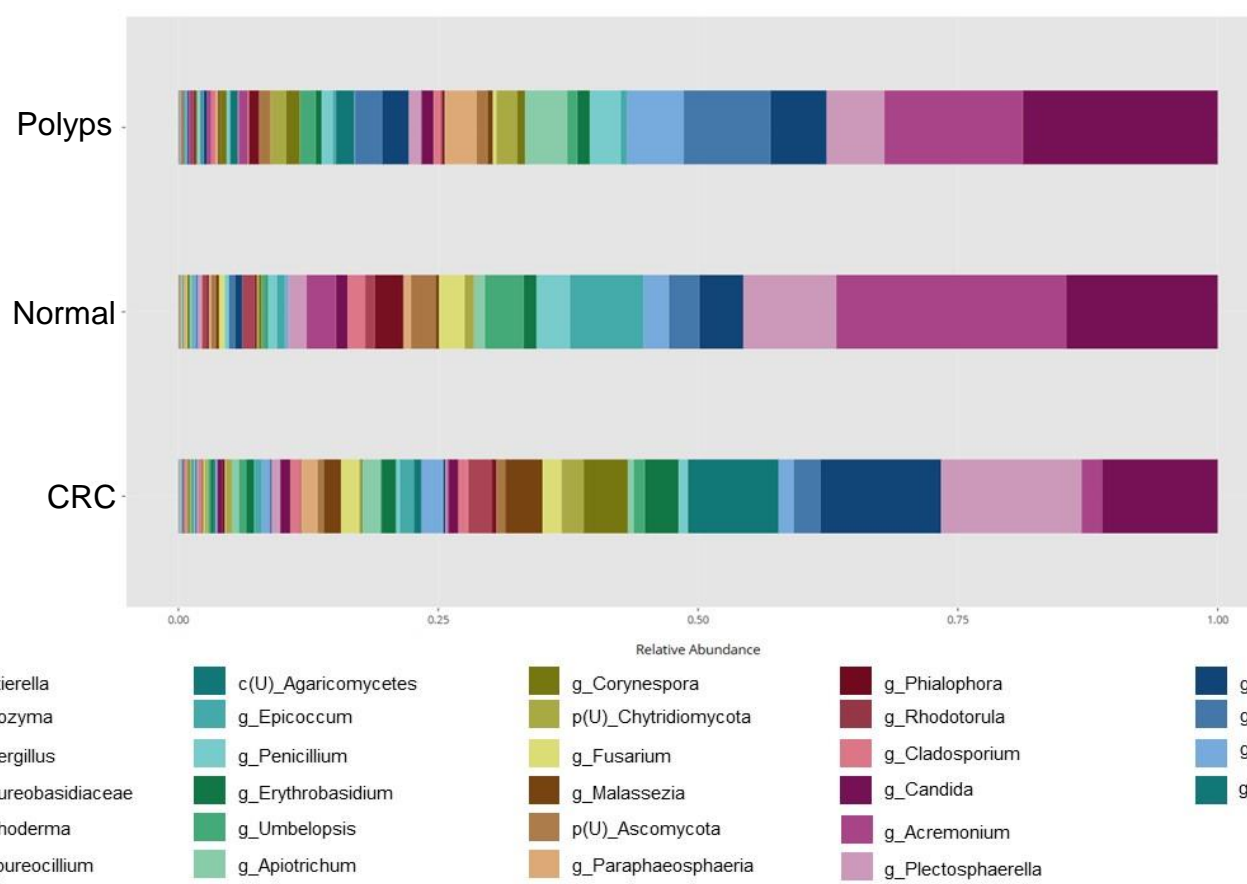
In Malaysia, colorectal cancer (CRC) is highly prevalent. The complex etiopathogenesis of CRC involves gut mycobiome. To date, little has been known about the composition and characteristics of the gut mycobiome in Malaysian CRC patients. We aimed to explore the presence of gut fungal pathogens in CRC patients.

## METHODOLOGY



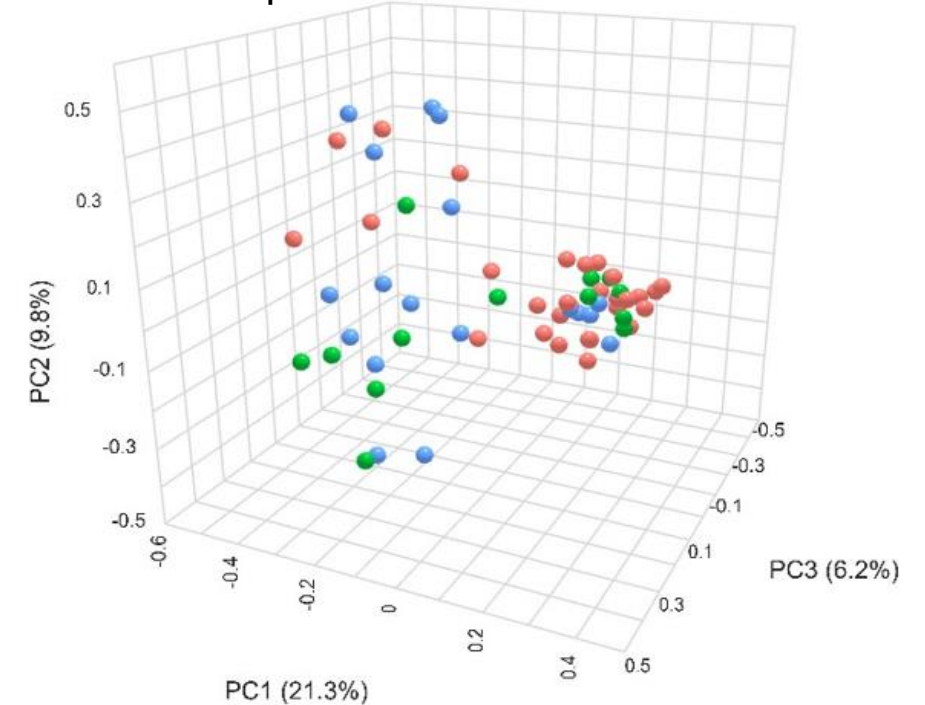
## RESULTS

**Figure 1:** Taxonomic composition abundant in 3 groups at the genus level



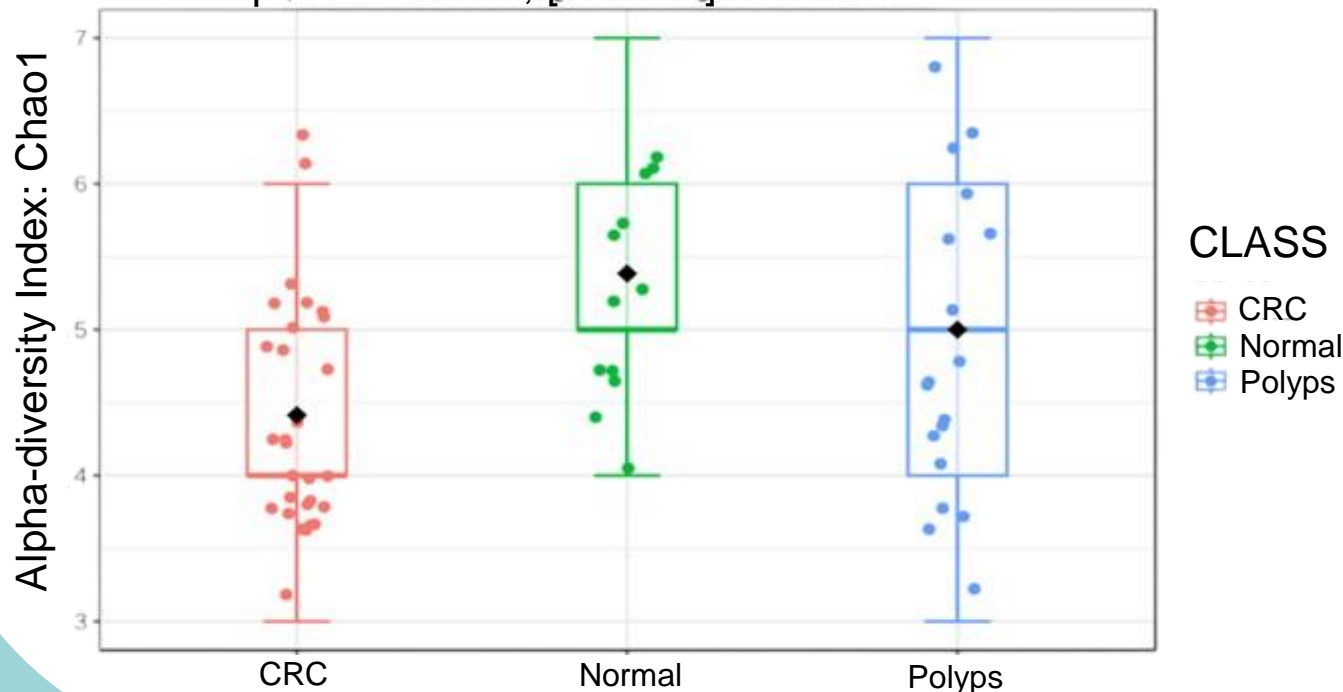
**Figure 3:** Beta-diversity analysis demonstrating mycobiota diversity within between groups ( $p < 0.05$ )

[PERMANOVA] F-value: 1.5224; R-squared: 0.050; p-value: 0.050

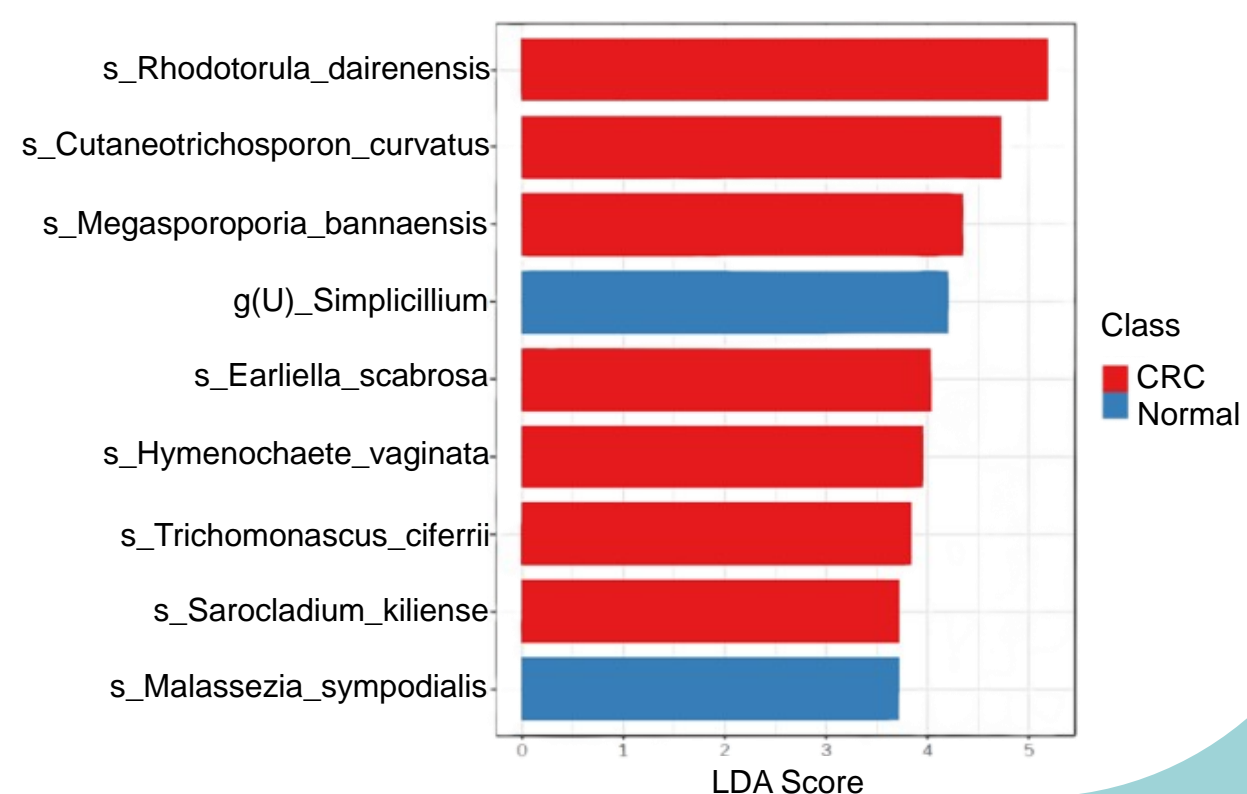


**Figure 2:** Alpha-diversity analysis demonstrating mycobiota diversity within each group ( $p < 0.05$ )

p-value: 0.004; [ANOVA] F-value: 5.9922



**Figure 4:** LDA score analysis showing 9 significant gut mycobiomes at the species level



## DISCUSSION

Fungi are understudied, but they play important roles as commensals or opportunistic pathogens that affect the host immunity of cancer patients. Previous research has linked *Rhodotorula dairenensis* and *Cutaneotrichosporon curvatus* to fungemia and cutaneous metastases, respectively, in CRC patients. Intriguingly, we detected an abundance of *Agaricomycetes* in CRC patients, which is related to their mushroom consumption.

## CONCLUSION

CRC, pre-CRC, and healthy controls exhibit a distinct mycobiome profile in Malaysia. Gut mycobiome signatures, such as *Rhodotorula dairenensis* and *Mortierella echinula*, may be involved in the pathogenesis of CRC and its precursor polyp, and may serve as future non-invasive mycobiome markers for the diagnosis of CRC.