The Link Between The Opportunistic Gut Fungal Pathogens With Colorectal Adenocarcinoma

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Objective(s): Colorectal cancer (CRC) is highly prevalent in Malaysia. Etiopathogenesis of CRC is complex involving gut mycobiome. To date, little is known about the composition and characteristics of the gut mycobiome among patients with CRC in Malaysia. We aimed to explore the presence of gut fungal pathogens in CRC patients.
Methodology: Biopsy samples were obtained from 61 individuals of 3 groups; 29 CRC (n=29), 19 polyps (pre-CRC) (n=19), and healthy controls (n=13). The gDNA was extracted for amplicon sequencing by targeting the ITS1 region and proceeded for diversities and biomarkers analyses using state-of-art bioinformatics approaches.
Results: The analysis of 6,265,412 read-counts revealed 1,364 fungal ASV, with variable fungal species abundance across the groups. *Ascomycota* and *Basidiomycota* formed the highest phyla in all samples, with *Mucoromycota* (3.99%) and *Mortierellomycota* (18.76%) being significant among the control and pre-CRC groups, respectively. At the genera level, *Aspergillus* (13.63%), *Mortierella* (18.76%), and *Saitozyma* (22.83%) were abundant among the CRC, pre-CRC, and control groups, respectively. Alpha and beta-diversities analyses showed significant differences between the groups; Chao1 index (*p*-value = 0.004) and Bray-Curtis index (*p*-value = 0.05), respectively. Remarkedly, machine learning analysis predicted that CRC patients were positively correlated with *Rhodotorula* and *Cutaneotrichosporon.*
Discussion: Fungi are understudied but play significant roles as commensals or opportunistic pathogens that influence cancer patients' host immunity. Previous studies showed *Rhodotorula dairenensis* and *Cutaneotrichosporon curvatus* were associated with fungemia and cutaneous metastases among the CRC, respectively. Interestingly, we discovered a profusion of *Agaricomycetes* in CRC patients, which are connected to the patients' mushroom diet.
Conclusion(s): In Malaysia, a distinctive mycobiome profile is observed among CRC, pre-CRC, and healthy controls. Gut mycobiome signatures including *Rhodotorula dairenensis*, and *Mortierella echinula* may be involved in the CRC pathogenesis and its precursor polyp, and potentially serve as future non-invasive mycobiome markers for the detection of CRC.