

**International Symposium 1-2****Interplay of microbiota and the host for the maintenance of intestinal homeostasis**

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Bacterial community (microbiota) in human intestine has now been well characterized. In healthy state, microbiota contributes to generation of a variety of nutrients and regulation of the host mucosal immune system. In addition to bacteria, various types of fungi (mycobiota) reside in the human gut. However, interactions between microbiota and mycobiota remain poorly understood. In this study, we investigated the composition of bacteria and fungi in feces from the cohorts of Japanese and Indians using next-generation DNA sequencing. Japanese showed *Bacteroides*-dominated microbiota, while Indians possessed *Prevotella*-dominated microbiota. Regarding mycobiota, the relative abundance of *Saccharomyces* was the highest in Japanese, whereas *Candida* was most abundant in Indians. We then investigated the mechanism by which *Prevotella* and *Candida* are abundant in the intestine of Indians, who mainly take cereals abundant in dietary fibers as proteins sources. *Candida* showed a strong *in vitro* growth response to a component of dietary fibers, arabinoxylan. In contrast, the growth response of *Prevotella* to arabinoxylan was not potent. Furthermore, the growth of *Prevotella in vitro* was promoted by supernatants of *Candida* cultures in the presence of arabinoxylan. These findings indicate that the intestinal fungus *Candida* facilitates colonization of *Prevotella*. We will also discuss how *Candida* promotes the growth of *Prevotella*. This study demonstrates the transkingdom interaction of bacterium and fungus for the efficient colonization in the intestine.