**Title: YEASTS IDENTIFICATION OF HUMAN ADULT GUT MICROBIOTA BY MALDI-TOF MS**

**Authors:** Borges, F.M., De Paula, T.O., Sarmiento, M.A., Ferreira-Machado, A. B., Resende, J. A.,Tavella, P. G., Oliveira, M.G., Nascimento, T.C., Silva, V. L., Diniz, C. G.

**Institution:** Universidade Federal de Juiz de Fora (Rua José Lourenço Kelmer, Martelos, Juiz de Fora – MG)

**Abstract:**

Fungi are components of human microbiota and their distribution vary considering different anatomical sites such as skin, scalp, oral cavity, lungs, genitourinary and gastrointestinal tracts. Differences in microbiota composition may be related to the host, to distinct colonization early in life, and also related to different environmental exposures such as chemotherapy, diet, and xenobiotics. As the bacteria species, the fungi associated to host's microbiota are amphibiontic microorganisms with important role in the health status, but also implicated in endogenous and opportunistic diseases, especially in the gut. To better address the role of resident fungi in health and disease, their diversity has to be evaluated and little information is available on the fungi gut microbiota. The objective of our study was to evaluate the aerobic yeasts diversity in human fecal microbiota, by culture-dependent methodology. Healthy adult individuals (n=21) with no use of antimicrobials in the prior 30 days, both genders and age between 18 and 60 years old were selected. Fresh fecal samples (100 mg) were serial tenfold diluted, spread into Sabouraud Dextrose Agar, and incubated aerobically at 28 ± 2°C, 48h. After UFC counting and colony isolation representative of all morphotypes in each plate, yeasts cultures were obtained and kept for further experiments. Isolated yeasts were identified by MALDI-TOF mass spectrometry. *Candida parapsilosis* was the most frequently identified yeast (66.6%), followed by *C. albicans* (28.5%) and *Rodothorula mucilaginosa* (19.0%)*. Other species were also identified in different samples: *Candida intermedia* (4.7%), *Candida glabrata* (4.7%)*, Candida metapsilosis* (4.7%)*, Candida robusta* (4.7%)*, Candida pararugosa* (4.7%)*, Geotrichum silvicola* (4.7%) and *Lodderomyces elongisporus* (4.7%). It was observed the predominance of *C. parapsilosis* in the human gastrointestinal tract, although *C. albicans* is thought to be the major yeast species in this ecossystem. Despite the number of evaluated samples, the results call to the relevance of regional studies on the investigation of microbial diversity in the human gut. These results are important not only considering ecological issues, but it is accepted that microbial shifts in gut microbiota may be associated with several non-infectious diseases.

**Keywords:** Gut microbiota, Yeasts, MALDI-TOF MS