

Prospective study of species diversity and colonization ratio of the large intestine by unicellular fungi identified by mass spectrometry

Robert Kuthan^{1,2}, Magdalena Sikora^{2,3}, Dariusz Domański⁴,
Ewa Swoboda-Kopec'^{1,2}

¹ Chair and Department of Medical Microbiology, Medical University of Warsaw, Warsaw, Poland; ² Department of Medical Microbiology, Infant Jesus Teaching Hospital, Warsaw, Poland; ³ Department of Dental Microbiology, Medical University of Warsaw, Warsaw, Poland; ⁴ Salus Medycyna Medical Center, Siedlce, Poland

INTRODUCTION. Opportunistic fungal infections have dramatically increased in recent years, mainly among immunocompromised patients. Fungal complications constitute a vital clinical issue concerning various groups of patients. The most common etiological infection factors, concerning the mentioned patients are the yeast-like fungi. In clinical specimens, the predominant genus of yeast-like fungi is *Candida*. Apart from frequent infections caused by well-known pathogens, such as *Candida albicans*, the number of fungal infections caused by often drug-resistant pathogens or strains earlier rarely causing infections, including *C. glabrata*, *C. parapsilosis*, *C. tropicalis*, *C. krusei*, *C. inconspicua*, *C. kefyr*, *Trichosporon* spp., *Geotrichum candidum* and *Geotrichum capitatum*, has been recently increasing. *Candida* species are known as harmless commensals of the human body. However, in the wrong location and under decreased immune functions, it can cause a systemic mycosis. *Candida* fungi produce various pathogenicity factors enabling invasion process and proceeding of the subsequent infection stages. Due to the insignificant pathogenic potential of the *Candida* spp., associated with the fact of their natural existence on the skin and mucous membrane, the research is currently often directed at detection of the factors responsible for the colonization and development of the fungal infections. The aim of the study was to determine species diversity and colonization ratio of the large intestine by unicellular fungi.

MATERIALS AND METHODS. The research included yeast-like fungal strains cultured from anus swabs of 2063 patients admitted to the Infant Jesus Teaching Hospital in Warsaw. Samples were collected in the period from March to June 2019. Isolation of strains have been conducted in compliance with the standard procedures of mycological diagnostics. The clinical samples were cultured on Sabouraud agar and incubated at 30° C for 24–72h until representative single colonies were formed. Species were identified by Matrix-Assisted Laser Desorption/Ionization – Time-Of-Flight Mass Spectrometry (MALDI-TOF MS).

RESULTS. Results revealed that the prevalence of unicellular fungi was 28,16%. In total 24 species were isolated. The identified species belonged to the six genera: *Candida*, *Saccharomyces*, *Rhodotorula*, *Geotrichum*, *Trichosporon*, *Exophiala*. The most predominant species was *Candida albicans* (n = 295). *C. glabrata* (n = 132) was predominant among the non-albicans *Candida* followed by *C. tropicalis* (n = 42) and *C. dubliniensis* (n = 39).

CONCLUSIONS. Our results indicated that 45,87% of patients, with positive mycological culture, were colonized by non-albicans *Candida* species. The isolation of non-albicans *Candida* may have clinical implication because of their reduced susceptibility to antimicrotics, and the fact that most of the infections have the endogenous origin.

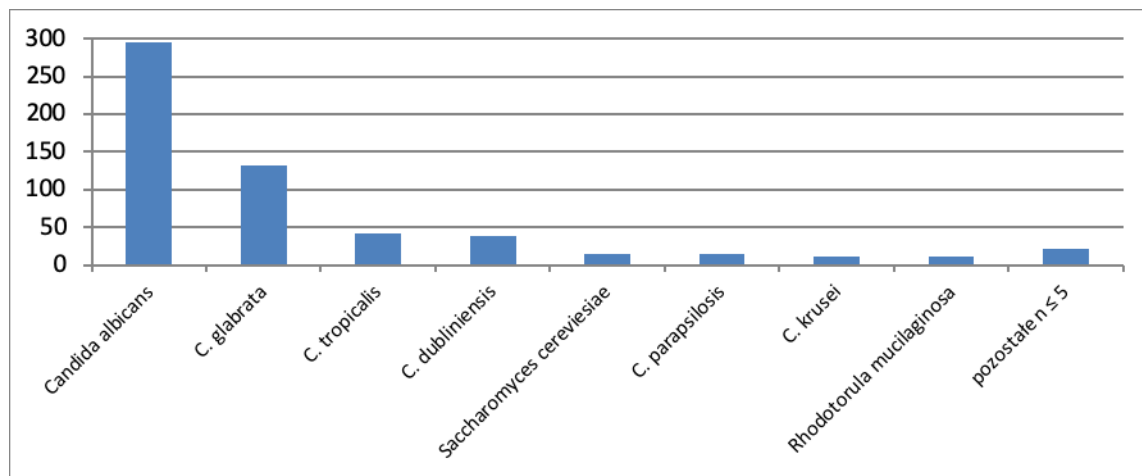


Figure 1. Occurrence of different unicellular fungi colonizing large intestine.