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Střevní mykobiom asociovaný s diagnózou zánětlivého střevního onemocnění založený na tkáňových biopsiích

Rigorózní práce

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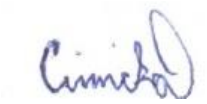
Cimická, J., 2022: Střevní mykobiom asociovaný s diagnózou zánětlivého střevního onemocnění založený na tkáňových biopsiích. [Intestinal mycobiome associated with diagnosis of inflammatory bowel disease based on tissue biopsies. RNDr. Thesis, in Czech.] - 1 p., Faculty of Science, University of South Bohemia, České Budějovice, Czech Republic.

Annotation:

This thesis reveals results of NGS mycobiome analysis from formalin-fixed, paraffin-embedded samples of Crohn's disease, ulcerative colitis patients and healthy controls, divides fungal genera into three experimental groups, determines their affiliation to health and disease, suggests fungal genera interactions, and shows specific fungal genera related to the diagnosis.

Prohlašuji, že jsem autorem této kvalifikační práce a že jsem ji vypracoval(a) pouze s použitím pramenů a literatury uvedených v seznamu použitých zdrojů.

V Plzni, dne 3.1.2021



Cimická, J., Riegert, J., Kavková, M., & Černá, K. (2021). Intestinal mycobiome associated with diagnosis of inflammatory bowel disease based on tissue biopsies. Medical Mycology. https://doi.org/10.1093/mmy/myab076

Abstract

Analysis of mycobiome from formalin-fixed, paraffin-embedded (FFPE) biopsies should preferentially detect only fungi which are actually present in the intestine wall, in contrast to stool samples, which are limited by the diet composition. Next generation sequencing provides the advantage of analysing many species from a single sample. Consequently, Canonical correspondence analysis divided fungal genera present in FFPE intestinal tissues into three well defined experimental groups (negative controls - NC, Crohn's disease - CD, ulcerative colitis - UC). Simultaneously, the analysis showed that particular fungal genera are associated with these experimental groups and several fungal genera occurred in all experimental groups equally. Our results also showed a noticeable increase of Ascomycota proportion from NC, through CD to UC. Fungal genera *Malassezia*, *Cladosporium* and *Toninia* occurred in all experimental groups assuming that they are common components of the intestinal mycobiome. Other fungal genera found only in the NC experimental group were non-pathogenic and might bring some benefits. In contrast, CD and UC samples were characterized by an accumulation of genera with inhibitive effects on growth of other fungal genera and the presence of opportunistic pathogens. Furthermore, a decrease in the fungal genus *Malassezia* in inflammatory tissues was observed; Specifically, the UC experimental group showed a connection between the presence of *Candida* and seven time's lower amounts of *Malassezia* (compared to amounts found in NC). The CD experimental group was characterized by the simultaneous presence of *Engyodontium album* with *Lecanicillium*, and indicate a possible pathogenic effect of *Ramularia* in disease development.