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Microbiome analysis and mycobacteria presence in microbiome of Hranice Abyss and Zbrasov Aragonite Caves (Hranice Karst, Czech Republic)

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The composition of microbiome and presence of mycobacteria was studied in 63 samples from Hranice Abyss, the deepest L abyss around the world and in the Zbrasov Aragonite Caves. Microbiome DNA was isolated and amplified by PCR. The amplicons were sequenced by Illumina MiSeq. A total 238 different bacterial families above 1% of a total number of OTU were identified. Following families were found as the most frequent: Lachnospiraceae (4.41%), Moraxellaceae (3.60%), Ignavibacteriaceae (3.04%), Ruminococcaceae (2.68%), Weeksellaceae (2.29%), Gallionellaceae (1.85%), Bacillaceae (1.58%), Methylomirabiliaceae (1.46%) and Thermodesulfovibrionaceae (1.35%). Different mycobacterial species were identified by culture examinations and by the presence of mycobacterial DNA. Nontuberculous mycobacteria were cultured from 10.9% and their DNA was directly detected in 21.8% samples. In the Hranice Abyss M. florentinum in soil was identified by culture. M. arupense (in bacterial slimes), M. mucogenicum and M. sediminis (in hot spring water) were determined by PCR methods. In Zbrasov Aragonite Caves, M. intracellulare was presented in residual sediments and M. avium complex in fluvial sediments. The all cultured mycobacterial species belong to slow-growing mycobacteria. The family Mycobacteriaceae was less than 1% in all analyzed matrices. Completely distinct species composition could be caused by the presence of two ecosystems. The geochemical characteristics of all different zones (photic, cave dry and cave flooded zones) did not have any impact on the presence of mycobacteria. The total organic carbon (TOC) was detected only in Hranice Abyss dry zone material (soil) with pH between 7.12 and 7.56 and in fluvial sediments from Zbrašov Aragonite caves with pH 7.91±0.04. It could be concluded that in the Czech Republic Hranice Karst environment does not represent favourable conditions for mycobacteria presence.

Biography

Milan Bartos is an Associate Professor at the Department of Microbiology, Faculty of Science, Masaryk University in Brno where he delivers two special lectures (Special methods of analysis microorganisms I, and II). His professional fields of research are molecular biology, molecular epidemiology, and biotechnology. He studies epidemiology and epizootology of human pathogens and zoonosis, he prepares recombinant genes and special gene constructs used in diagnostics of microorganisms, study of DNA polymorphisms in human genome and in detection of genetically modified organisms. Some recombinant proteins are prepared for kinetic studies of human enzymes and hormones (focused on diabetes mellitus, Cohn's disease, and cardiovascular diseases). He is also a Research Scientist in his own private company (Molecular Epidemiology).

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