ARPHA Conference Abstracts 8: e148864
doi: 10.3897/aca.8.e148864

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Conference Abstract

Microbial diversity of the Veryovkina cave after the 2018 flood

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Received: 05 Feb 2025 | Published: 06 Feb 2025

Citation: Hodzhev Y, Zhelyazkova V, Toshkova N, Tsafarova B, Panaiotov S, Stoev P (2025) Microbial diversity of the Veryovkina cave after the 2018 flood. ARPHA Conference Abstracts 8: e148864.
https://doi.org/10.3897/aca.8.e148864

Abstract

The Veryovkina Cave, located in the Abkhazia region, is the world's deepest known cave (approximately 2204 m) and hosts unique microbial ecosystems. Following a major flood in 2018, this study explored the impact on microbial diversity using 16S rRNA gene sequencing across ten sampling sites (A1–A10), for which a negative control was used. The ten samples were classified into "Upper," "Medium," and "Deeper" regions, with sediment types, moisture levels, and post-flood human access recorded to provide ecological context. 43,195 operational taxonomic units (OTUs) were identified, with an average yield of 284.18 per sample.

Sites such as A2 (Oiylia pass, - 350 m, wet clay, no human visits) and A10 (Captain Nemoisto's last stand - 2204 m, dry silt with human visits) were practically sterile, suggesting they were most severely impacted by the 2018 flood. The flood likely disrupted the ecosystem in these locations, flushing away most of the resident microbial diversity and leaving behind a biologically impoverished environment. In contrast, neighboring sites A4 (Pink meander, - 1100 m, wet clay, with human visits), place with a least human impact and A9 (Captain Nemoisto's last stand, - 2200 m, dry sand, no visits after the flood) exhibited the highest microbial abundance, suggesting these sites

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retained a microbiota state closer to pre-flood conditions. Proteobacteria and Acidobacteria were identified as key drivers of biogeochemical cycling within the cave ecosystem. Proteobacteria, known for their metabolic versatility, play a central role in organic matter decomposition, nitrogen fixation, and sulfur cycling. Acidobacteria often coexist with Proteobacteria, supporting interdependent microbial interactions influenced by nutrient availability and pH. Together, these phyla form the backbone of the microbial ecosystem, facilitating nutrient recycling and maintaining ecological balance.

The study underscores the ecological significance of microbial diversity in Veryovkina Cave, emphasizing the role of key phyla in maintaining ecosystem function and adapting to environmental disturbances such as flooding. This research serves as a foundation for further exploration of microbial life in deep subterranean ecosystems.

Keywords

Veryovkina cave, microbiome, amplicon sequencing, barcoding

Presenting author

Yordan Hodzhev

Presented at

First annual national meeting of the Bulgarian Barcode of Life consortium - BgBOL, 2024

Acknowledgements

This study was supported by the Bulgarian National Science Fund Grant number: KP 06-PN-51/9-2021

Grant title

Caves as a reservoir for novel and reoccurring zoonoses — ecological monitoring and metagenomic analysis in real time

KP 06-PN-51/9-2021

Conflicts of interest

The authors have declared that no competing interests exist.