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Conference Abstract

Different components of interconnected karst environment select for highly distinct microbial communities

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Abstract

Karst environments, formed by dissolution of rocks, present a unique opportunity to study groundwater and surface water as a single dynamic system. We aimed to explore the hydrological connections and identify shared microbiome between different components of this complex landscape (terrestrial, surface-subsurface freshwater networks and two different lake strata) on example of karst landscape at north shore of Lake Thun (CH).

52 samples from soil and 87 from the freshwater network were collected during low hydrological conditions. Additionally, 43 samples from 13 different lakes across Europe were included in the analysis. A 16S rRNA gene amplicon analysis revealed highly homogenous lake communities dominated by typical lake microbes represented by members of Alphaproteobacteria, Gammaproteobacteria and Actinobacteria. On the contrary, communities in soils and surface and subsurface water were observed to be highly heterogenous within the karst landscapes. Soil samples built two robust groups that corresponded to alkaline and acidic pH values associated with two types of bedrocks. Alkaline soils had higher abundance of Gammaproteobacteria and Alphaproteobacteria, while acidic soils were dominated by Acidobacteria. Alkaline cluster was better connected with aquatic environments and shared genotypes from the families Nitrosomonadaceae and Nitrospiraceae with cave sediments and lake hypolimnia, that implied ammonia and

nitrite oxidation as important chemotrophic processes in light depleted environments. *Rhodoferax, Limnohabitans* and *Sediminibacterium* were shared within subsurface network and lakes. Single *Rhodoferax* genotype was detected in all aquatic environments. Additionally, we observed that lineages from the families Pirellulaceae and Gemmataceae (phylum Planctomycetota) were alternatively distributed in both soil clusters and lakes. A similar pattern was observed in subsurface aquatic components and deeper lake strata within family Methylophilaceae, where *Methylotenera* was extensively replaced by *Methylopumilus*. This indicates that despite high hydrological connectedness between different karst landscape components, deterministic selective factors seem to prevail in the community assemblies.

Keywords

Karst, Freshwater networks, Microbial Communities, 16S rRNA amplicon

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Conflicts of interest

None.