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Abstract Book

successfully identified prokaryotic lineages that predominated exclusively in the hypolimnion at multiple lakes. Majority of them were affiliated with phyla that had been considered as uncommon in epilimnion. Overall, the CL500-11 clade (*Chloroflexi*) was the most represented lineage in the hypolimnion of the studied lakes, followed by the diverse lineages of *Planctomycetes* (e.g. CL500-37, CL500-15, CL500-3), *Verrucomicrobia*, *Nitrospira*, and *Thaumarchaeota*. Fluorescent *in situ* hybridization demonstrated that some of the representative lineages often numerically accounted for more than 5% of the total prokaryotes in the hypolimnion, indicating that the biogeochemical cycling in the hypolimnion is driven by the bacterioplankton communities that are basically different from those in epilimnion. Moreover, each of them showed a different preference between the lakes, presumably reflecting their distinct ecological niche and physiological capabilities.

Does species diversity drive decomposition in boreal lake sediments?

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Organic matter (OM) derived from terrestrial ecosystems influences both the food webs and biogeochemical cycles of lakes. The boreal ecozone holds an estimated 60% of the world's fresh water, but lakes in this region tend to be nutrient-poor and less productive, making them especially reliant on carbon subsidies from riparian litterfall. The availability of these carbon subsidies for aquatic food webs depends on microbial communities, but little is known about how the taxonomic and functional diversity of heterotrophic bacteria might influence the rate at which this OM is decomposed in natural systems. Drawing upon biodiversity-ecosystem functioning theory, we predicted that decomposition rates, indicative of both food web production and whole-lake carbon cycling, increase with the taxonomic and functional diversity of bacterial communities. We characterized both bacterial community composition and microbial functional traits in nearshore sediments from 8 catchments along a gradient of terrestrial OM inputs using next-generation sequencing (16S rRNA amplicon sequencing and shotgun metagenomics). We found that both species richness and composition explained variation in rates of OM decomposition among sites. Differences in species composition were largely driven by 17 bacterial families, with abundances of *Acidobacteria*, *Firmicutes* and *Actinobacteria* changing along OM gradients. Ongoing shotgun sequencing will provide more detailed information on the functional traits present in lake sediments. This study highlights the role of microbial communities in the transfer of resources from terrestrial ecosystems, and improves our understanding of how catchment disturbances affect boreal aquatic ecosystems.

Vertical and seasonal distribution of ammonia-oxidizing communities in a warm-monomictic tropical crater lake

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Ammonia oxidation is the first and rate-limiting step in nitrification. Understanding this process is of high importance because it controls the availability of two major nitrogen compounds (ammonium and nitrate). Despite their crucial role in the nitrogen cycle, freshwater ecosystems are rarely studied

for ammonia oxidizers. In the oligotrophic monomictic Lake Alchichila (Mexico), ten depths were sampled in the stratification (November 2015) and mixing (February 2016) periods, covering the epilimnion (8, 17 and 27 m), oxycline (25, 29, 30 and 31 m), hypolimnion (32 and 45 m) and the bottom (60 m). The *amoA* gene abundance of ammonia-oxidizing archaea (AOA) and bacteria (AOB) was quantified by qPCR and compared with physicochemical parameters (temperature, oxygen and chlorophyll *a*) and nutrients (ammonium, nitrite, nitrate, dissolved inorganic nitrogen and phosphate). The quantitative distribution varied with depth and the highest copy numbers were observed in the transition zone (from 27 to 32 m). In theoxic zone, predation and competition for nutrients and CO₂ may have negatively influenced the population size of the ammonia oxidizers. In general, the AOA outnumbered the AOB abundance. However, in the epilimnion of the stratification period, AOB were more numerous than AOA. The AOA and AOB also showed a different temporal distribution pattern: AOA abundance significantly increased in the mixing period, probably due to the low availability of ammonium, and AOB abundance increased in theoxic zone of the stratification period. The results indicated that oxygen and ammonium concentration influence the abundance distribution of ammonia oxidizers in this lake.

Antibiotic resistant bacteria inhabiting Lake Sevan (Armenia)

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The increasing resistance of antibiotics is the result of uncontrolled application of antibiotics. Recently huge attention has been paid to the problem of bacterial resistance to antibiotics occurring in freshwater basins polluted by human sewage and agricultural wastewater. The aim of the present study was to determine distribution of antibiotic resistant (AR) isolates among allochthonous and autochthonous bacteria in Sevan Lake, the largest freshwater high-altitude (1,900 m) lake of Armenia. Target microbes were aeromonads and bacilli as models of the autochthonous microbiota, and *E. coli*, enterococci and staphylococci as common contaminants of water. The seasonal abundance of AR target microbes was estimated by plating of water samples on selective media supplemented with different antibiotics. Isolated AR bacteria were phenotypically characterized. The antibiotic susceptibility was determined using disk diffusion method. The highest numbers of AR bacteria were registered in summer season. Dominant group of gram-negatives AR bacteria was recorded for aeromonads, showing resistance to ciprofloxacin, doxycycline, imipenem and kanamycin, while among gram-positives, staphylococci appeared to be resistant to ciprofloxacin and erythromycin. Multi-resistance to kanamycin, imipenem, ampicillin, erythromycin and sulphonamides is widely distributed among both, allochthonous and autochthonous bacterial communities. The high resistance of isolates to ampicillin and erythromycin could be explained by their wide usage in agriculture and human health care during last decades. Competent bacteriophages for aeromonads and *E. coli* were also isolated to evaluate the role of transduction in AR gene transfer among allochthonous and autochthonous bacteria.

Drivers of microbial community structure and genome diversification in oligotrophic inland seas

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