

## Vertical stratification and functional guilds in the bacterial community of Lake Kivu (East Africa)

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Lake Kivu, one of the East African great lakes is a deep (maximum 489 m), oligotrophic, high altitude (1,463 m) lake of tectonic origin. The lake has a permanent density stratification that separates an oxic mixolimnion (with an oxycline located around 20 to 60-m depth depending on the season) from an anoxic monimolimnion rich in dissolved salts, carbon dioxide (CO<sub>2</sub>) and methane (CH<sub>4</sub>). The various water layers present contrasting physical and chemical properties with well-developed vertical redox gradients. Although Lake Kivu is one of the largest surface reservoirs of biogenic CH<sub>4</sub> in the world, the CH<sub>4</sub> concentrations in the oxic mixolimnion are surprisingly low compared to other lakes globally. Little is known, however, about the diversity and ecology of the microbial communities that underpin the carbon and nutrient cycles in Lake Kivu. Our objectives were to study the spatial and temporal dynamics of the bacterial community composition (BCC) in Lake Kivu, to identify the main factors driving such dynamics and to link the BCC to microbial processes. The results presented here were obtained during 3 sampling campaigns at different periods of the year (October 2010, June 2011, January 2012). 16S rDNA pyrosequencing was used to investigate BCC in 72 samples from vertical profiles in three different stations. In parallel, a large set of biological and environmental parameters were measured.

Concerning the richness, the number of observed operational taxonomic units (OTU, 0.03) varied between 200 and 700, but in most samples the bacterial community was dominated by a limited number of abundant OTUs. Nevertheless, due to the high number of rare OTUs, the Chao richness indicator predicted up to 1800 different OTUs in some samples. The greatest diversity generally occurred within the redoxcline or the deepest waters sampled.

The BCC exhibited sharp stratification with the distribution of functional guilds co-varying vertically with numerous biogeochemical features. As expected, cyanobacteria were mainly observed in the photic layer accompanied by various groups of heterotrophic bacteria. A maximal bacterial activity (<sup>3</sup>H-thymidine uptake) was observed at the oxic-anoxic interface for each station and during each sampling campaign. In two of the sampling stations, this activity peak was strongly correlated with the relative abundance of *Methylobacter*. Rapid CH<sub>4</sub> oxidation rates at these depths linked to a pronounced negative excursion in the δ<sup>13</sup>C signatures of particulate organic

carbon suggests that much of the bacterial activity was related to aerobic CH<sub>4</sub> oxidation by *Methylomonas*. In other samples, the peak of bacterial activity corresponded to the maximal abundance of anoxygenic phototrophic bacteria (*Chlorobium*). Just below the oxycline, high H<sub>2</sub>S concentrations and a peak of sulphur-oxidizing epsilon-proteobacteria sequences (up to 50% of the sequences) were observed; some of these bacteria have been reported to respire NO<sub>3</sub><sup>-</sup> providing evidence for anaerobic sulfur-cycling. In conclusion, the various water layers harbor very different microbial communities supported by the vertical redox gradients. These results provide insight into the ecology of the bacteria coupling the major biogeochemical cycles in this stratified freshwater environment and provide a basis for further studies on the molecular mechanisms and interactions regulating these processes.