Environmental drivers of plankton and sediment microbial communities along latitudinal and vertical gradients in the deepest freshwater lake (Baikal, Southern Siberia)

Purificacion Lopez-Garcia¹, Guillaume Reboul¹, Gwendoline David¹, Ludwig Jardillier¹, Nataliia Annenkova², Paola Bertolino¹, Ana I. Lopez-Archilla³, Konstantin Vershinin², and David Moreira¹

¹Ecologie Systématique Evolution, Centre National de la Recherche Scientifique - CNRS, Université Paris-Saclay, AgroParisTech, Orsay, France (puri.lopez@u-psud.fr)
²Limnological Institute, Siberian Branch of the Russian Academy of Sciences, Irkutsk, Russia
³Departamento de Ecologia. Universidad Autonoma de Madrid, Madrid, Spain

Understanding how abiotic and biotic factors influence microbial community assembly and function is crucial to understand ecological processes and predict how communities will respond to environmental change. Lake Baikal (Russian Federation) is the oldest, deepest and most voluminous freshwater lake on Earth, resembling in several respects sea environments. It thus offers a unique opportunity to test the effect of horizontal versus vertical gradients in community structure. Since climate change is rapidly affecting Siberia and Lake Baikal, this information can be useful both, as a reference for future monitoring of the lake and to help predictions about how local communities change as a function of environmental parameters. In order to address these questions, in 2017, we carried out a comprehensive sampling of Lake Baikal water columns and sediments along a North-South latitudinal gradient (ca. 600 km) across the three major basins of the lake, from coastal to pelagic areas and from surface to the deepest zones (0.5 to 1450 m deep). We then applied metabarcoding approaches based on 16S and 18S rRNA gene amplicon sequencing to characterize the composition of microbial communities, in particular, both prokaryotes and eukaryotes in sediments and microbial eukaryotes (0.2-30 µm cell size) in plankton (65 samples from 17 water columns). As expected, depth had a strong significant effect on protist community stratification in the water column. The effect of the latitudinal gradient was marginal and no significant difference was observed between coastal and surface open water communities. Co-occurrence network analyses showed that epipelagic protist communities were significantly more interconnected than in the dark water column. Surprisingly, Baikal benthic communities (13 sites) displayed remarkable stability across sites and seemed not determined by depth or latitude. Comparative analyses with other freshwater, brackish and marine sediments confirmed the distinctness of Baikal benthic communities, which show some similarity to marine and hydrothermally-influenced systems likely owing to its high oligotrophy, depth and fault-associated seepage. Metagenomic analyses of sediment samples show a wide metabolic potential of Baikal benthos and highlight the relative importance ammonia-oxidizing archaea in upper sediment layers.