



Conference Abstract

# Revisiting global biogeography of freshwater diatoms: new insights from molecular data

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## Abstract

The high-dispersal rates of microorganisms have driven to the expectation of their cosmopolitan geographic distribution. However, recent studies demonstrate that microorganisms instead show particular biogeography. Despite the existence of cosmopolitan species, geographically limited microbial groups have been found in aquatic and terrestrial environments worldwide.

Diatoms are long time used model to study the biogeography of microorganisms. They are unicellular eukaryotic microalgae that contribute significantly to the aquatic primary production and have huge taxonomic diversity and marked species-specific ecological preferences. Several authors considered that diatoms have no limits in dispersion and are ubiquitously present. On the other hand, recent studies have shown that endemism exists for several genera, and species may have low dispersal capacity. However, all these studies are based on data obtained by microscopy and therefore suffer from the many well-identified biases associated with the optical identification of microorganisms at large scale.

Metabarcoding technologies provide an access to taxonomic precision with a higher resolution compared to microscopy and open therefore the possibility of analyzing microbial diversity at genetic level. Recent bioinformatics tools allow reliable and standardized comparison of large datasets originating from distant geographic regions, overcoming issues related to biases in species identification.

In this study we used metabarcoding data to revisit central questions in freshwater diatom biogeography. We assembled a large dataset of samples of benthic diatoms collected from rivers in seven different geographic regions. These regions cover the subpolar (Fennoscandia), temperate (France Mainland) and tropical (West Africa, French Guyana, New Caledonia, Tahiti island and Mayotte island) climate zones. The selected geographic regions can also be classified into four continental areas (Fennoscandia, France Mainland, West Africa, and French Guyana) and three islands (New Caledonia, Tahiti and Mayotte).

We analyzed diatom alpha, beta and gamma diversity patterns in this dataset to address two main questions: 1) the presence of a latitudinal gradient in diatom diversity and 2) the cosmopolitanism of diatoms.

Similarly to results previously reported by Soininen et al. 2016, our data showed a decrease in diatom richness with a decrease in latitude. However, testing the effect of land type (island vs. mainland) showed that this factor explains the actual variability of richness along the climatic gradient and the effect of latitude is not significant. Differences in community structure between regions and climate zones were significant. In multivariate analysis, tropical samples did not overlap with any of the other climate zones, suggesting the specificity of these communities.

## **Keywords**

diatoms, DNA metabarcoding, microbial diversity, spatial ecology, rivers, latitudinal diversity gradient, endemism

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