

Hidden biodiversity – challenge in abundance

Authors:

Martin Schlegel
Institute of Biology, Leipzig University

Abstract:

We applied metabarcoding with group-specific primers for a comprehensive assessment of the diverse protist phyla Cercozoa (Rhizaria) and Oomycota (Stramenopiles) across all ecological compartments from forest soils to the canopy region in a temperate and tropical biome.

In the Leipzig floodplain forest, we detected distinct communities of ~ 400 Oomycota OTUs and >700 Cercozoa OTUs. Most variation in beta diversity was explained by microhabitat differences within tree canopies. We observed obligate biotrophic species, showing tree canopies to be a hitherto overlooked reservoir for parasitic protists. In addition, we found a high diversity in air samples. In spring, heterogeneity within alpha diversity was high during initial colonization. Subsequently, communities underwent compositional changes in autumn, reflecting recurring phenological changes during colonization.

In a tropical rainforest in the northeast of Papua New Guinea we detected distinct communities of 652 and 283 OTUs for Cercozoa and Oomycota, in three autochthonous tree species. In Cercozoa most taxa corresponded to those known from temperate zones. However, in Oomycetes, approximately 50% of all OTUs showed a sequence identity of less than 70% to any reference sequence, pointing to a substantial unknown diversity of microbial eukaryotes.

In a metatranscriptomic approach we assessed the entire living canopy bark microbiome in the Leipzig floodplain forest. With almost 1500 genera, we found a high microbial diversity on three tree species with distinct bark textures (*Quercus robur*, *Tilia cordata*), both with rough bark, and maple (*Acer pseudoplatanus*) with smooth bark. Regarding Cercozoa and Oomycota we found a broad taxonomic overlap with our metabarcoding data. Core co-occurrence network analysis revealed a rich food web dominated by algal primary producers, and bacterial and fungal decomposers, sustaining a diverse community of consumers, including protists, microscopic Metazoa and predatory bacteria. Co-occurring algae and fungi highlight the importance of algal-fungal lichen symbioses even at the microscopic scale.