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Functional diversity of microbial eukaryotes in a meromictic lake: coupling between metatranscriptomic and a trait-based approach

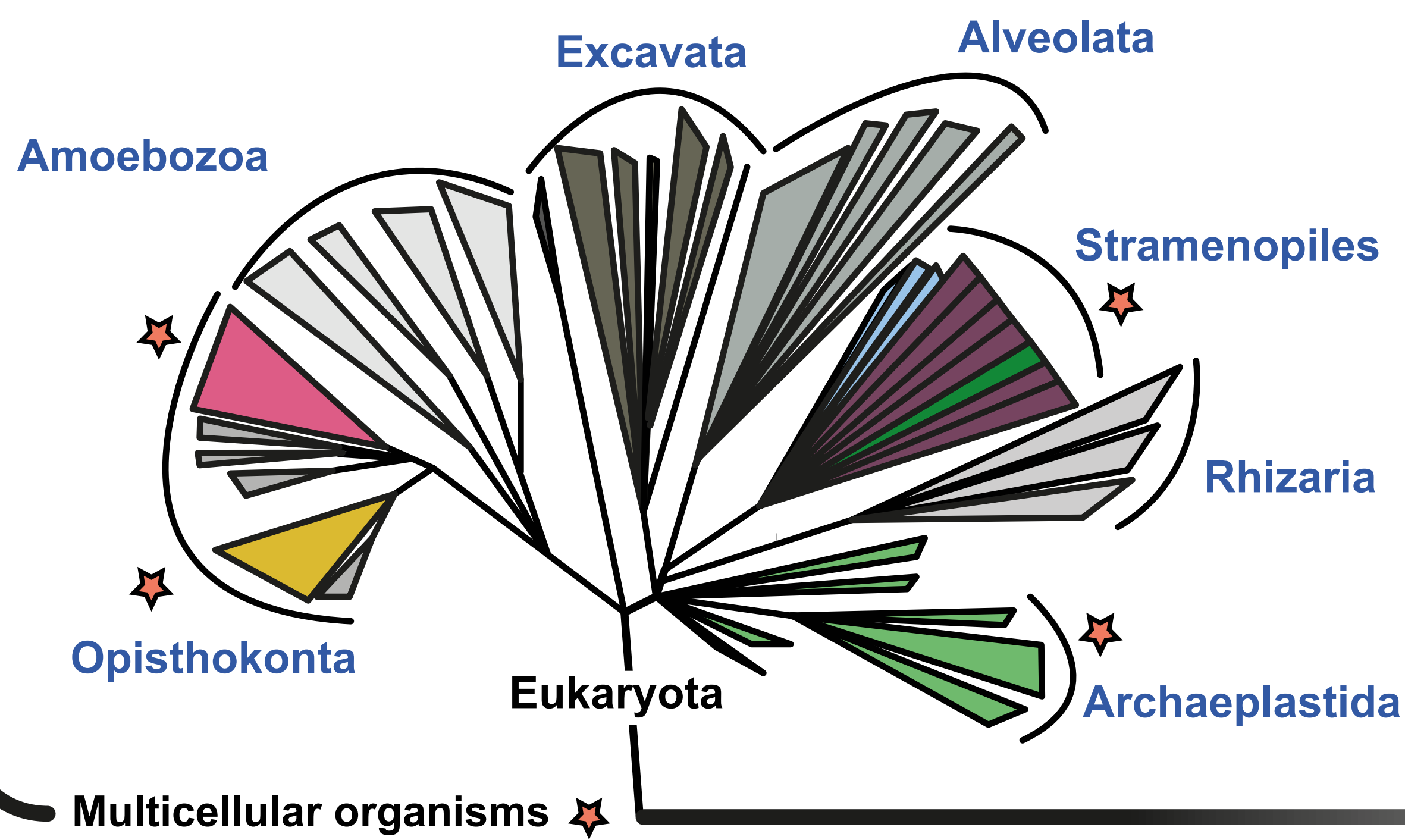
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Introduction



Background: While invisible to the naked eye, microorganisms are crucial components of the Earth's ecosystem, underpinning all biogeochemical cycles and supporting the existence of higher trophic life forms. Among microorganisms, our knowledge about microbial eukaryotes is poor compared to Bacteria. Moreover, in comparison to marine environments, freshwater ecosystems have received less attention although they contain a great microbial diversity.

Objectives: In our study functional diversity of understudied freshwater microbial eukaryotes was investigated with an original approach which couples a trait-based methodology and a metatranscriptomic analysis. Expressed functions and ecological strategies of microbial eukaryotes were studied for the first time in relation to oxygen presence/absence and size fractions in a model meromictic lake (Pavin, France).

Materials & Methods

1° Taxonomic diversity

18S-V4 rDNA metabarcoding

DA|DA²

Community matrix

600 distinct taxonomic affiliations

3 358 ASVs

2° Functional diversity

Existing table (Ramond et al., 2018) + Literature

Morpho-physio-phenological traits table

Trait-based approach

- Gower distance
- PCoA
- Trait trade-off
- K-means clustering
- Cluster characterization
- Functional groups acquisition

3° Metabolic potential

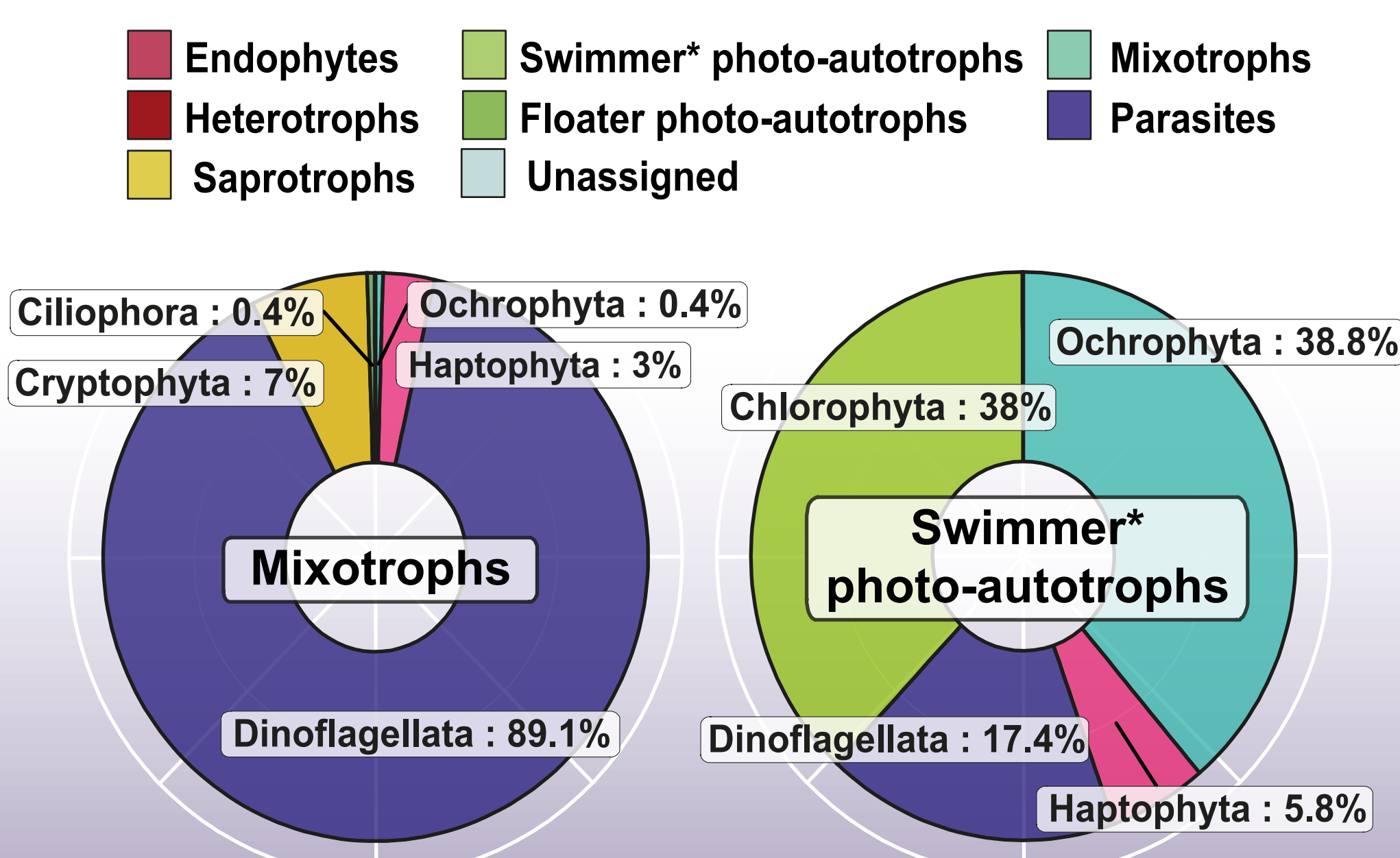
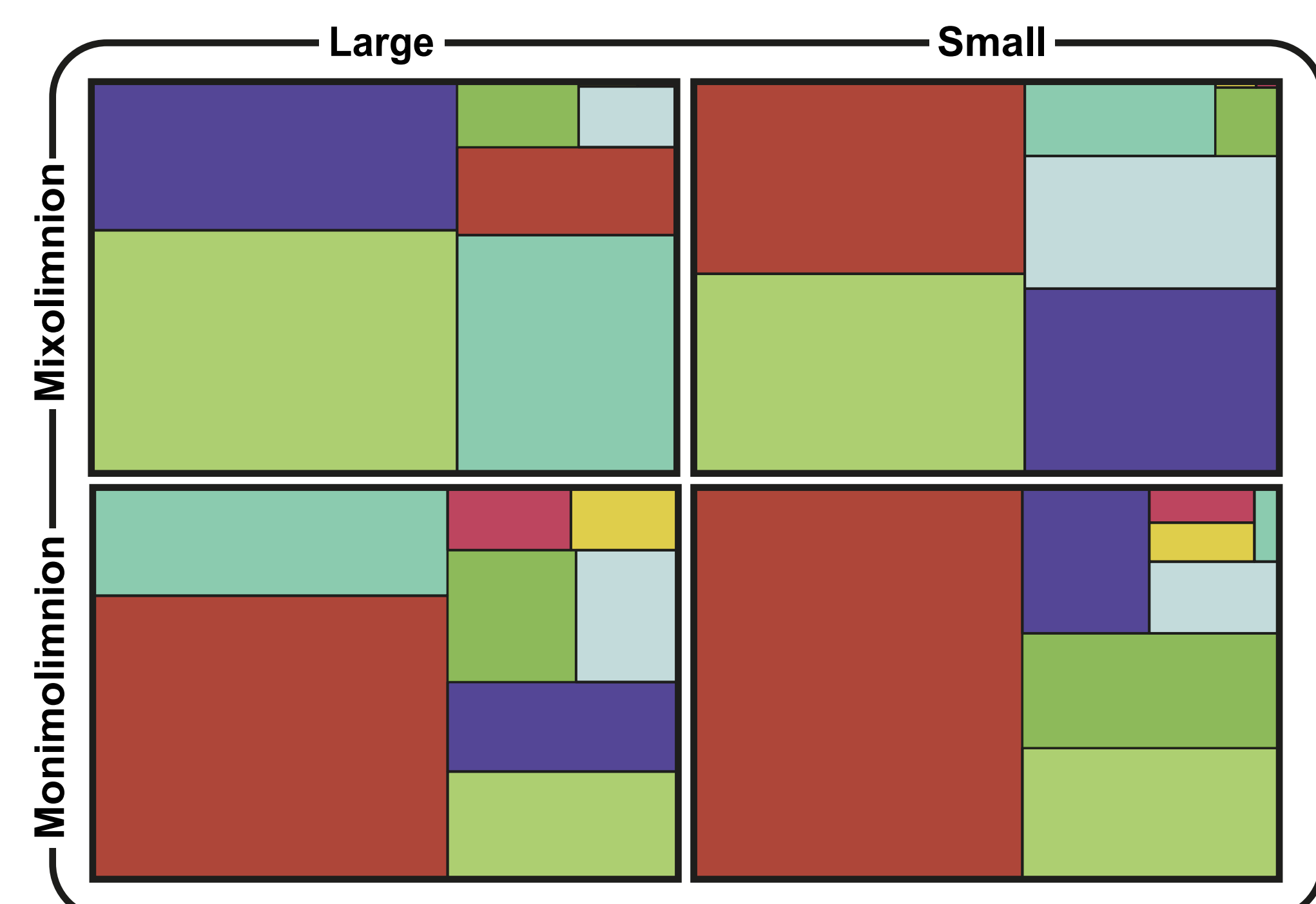
Metatranscriptomics gene catalog + protein prediction and annotation

Gene catalog

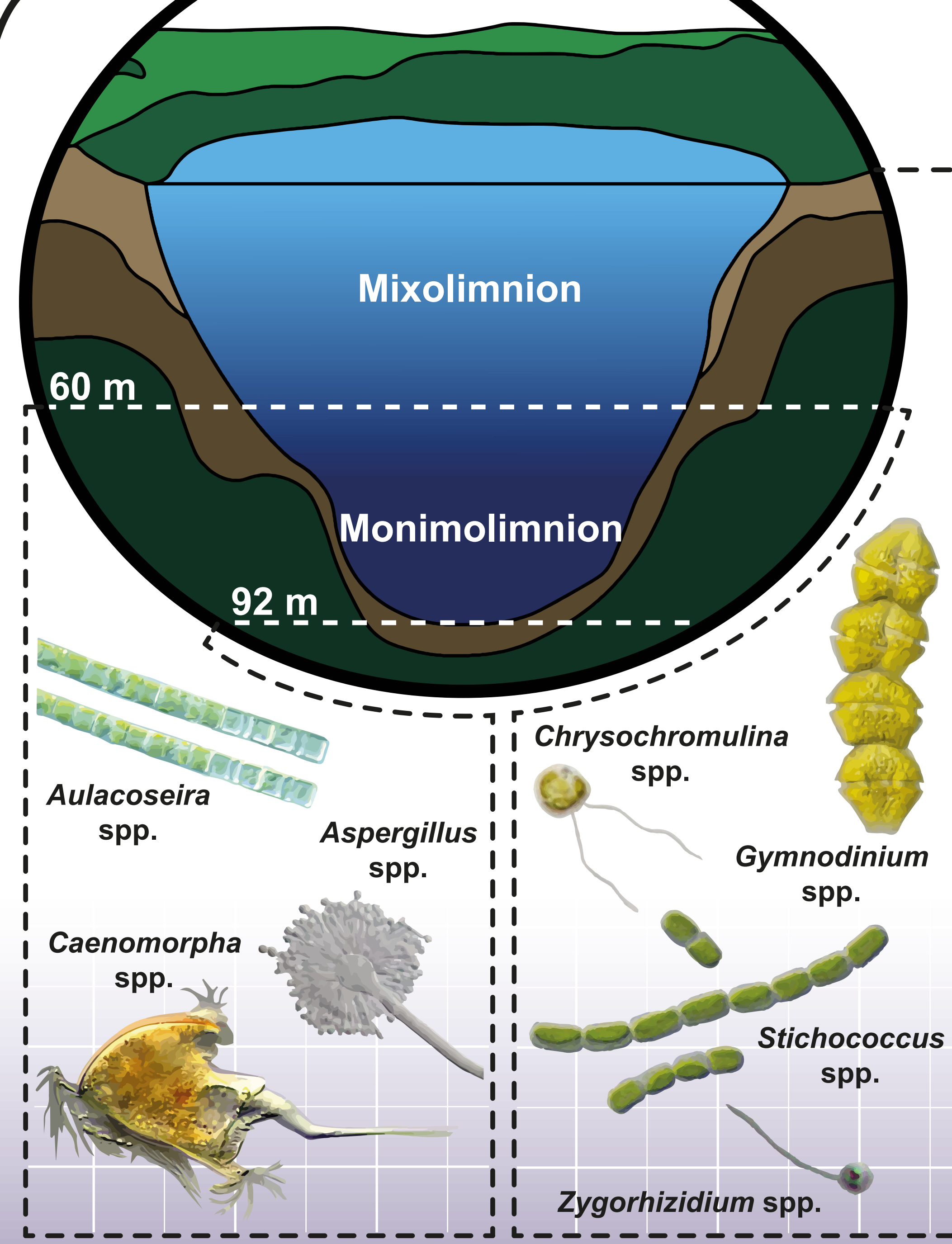
9 182 313 unigenes (30% with KO annotation, 11% with taxonomic affiliation to species rank and 3% associated to functional groups)



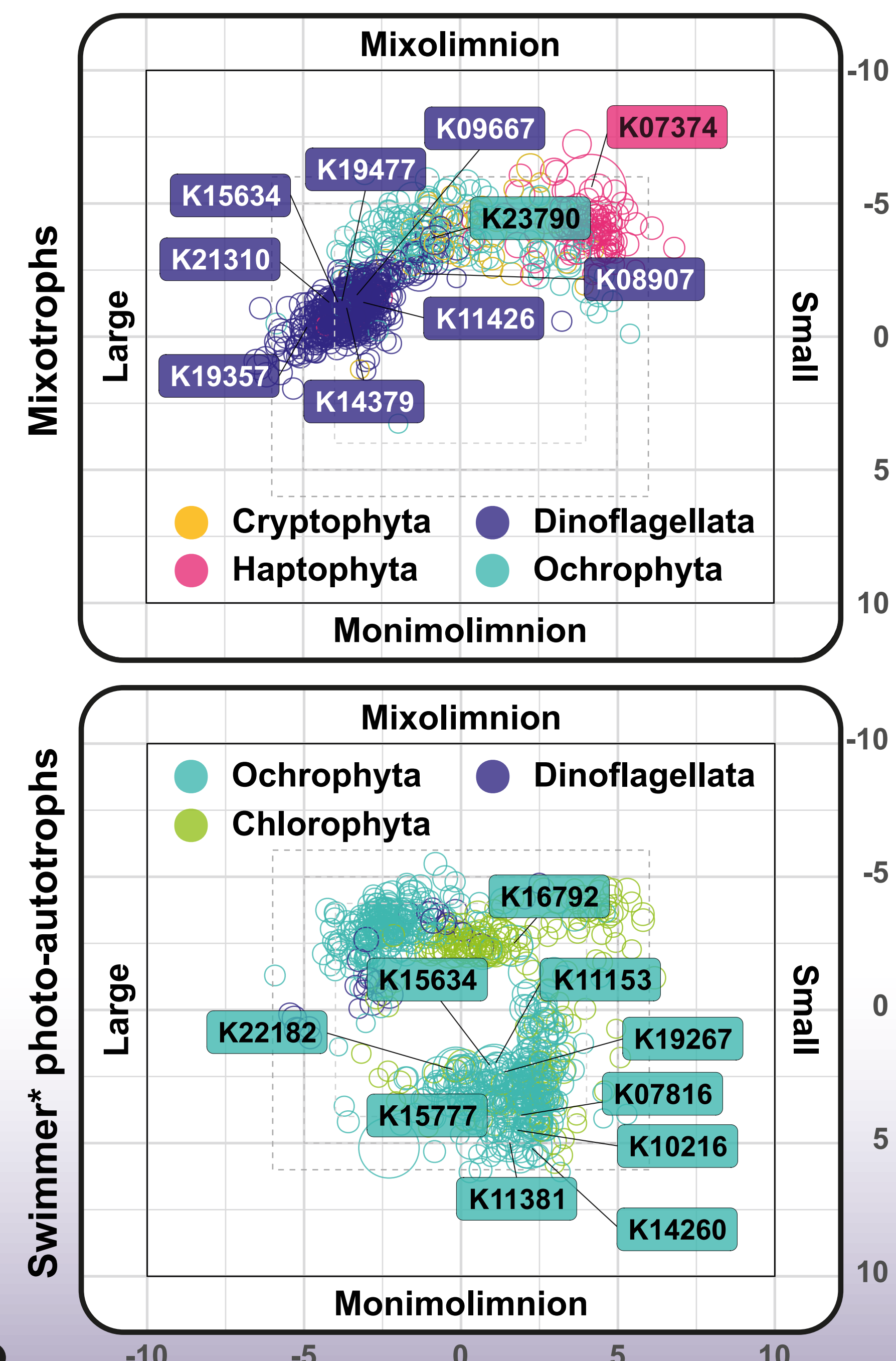
Functional diversity



Lake Pavin



Metabolic potential



Conclusion

This study targeting microbial eukaryotes is the first combining trait-based approach and metatranscriptomic in a freshwater meromictic lake. The analysis of differentially expressed genes with taxonomic affiliation and functional group allows the identification of differentially expressed orthologous genes (KOs) as well as metabolic and cellular processes that could complement trait-based definition of functional groups. This approach allows to highlight microbial eukaryote ecological strategies according to different forcing variables. Parasites (*i.e.* fungi) and mixotrophs strongly differed according to the living zone, parasites in relation to their phytoplankton hosts occurring in surface and mixotrophs in relation to genera trophic abilities (obligate/facultative mixotrophs). Numerous microbial eukaryotes are also able to thrive in absence of oxygen such as saprotrophs expressing transcripts related to sulfur and nitrate metabolism as well as organic matter degradation in the monimolimnion. Photosynthetic microbial eukaryotes are also present in this zone raising the hypothesis of unknown anaerobic metabolisms.

*Swimmer & heavy-covered photo-autotrophs

