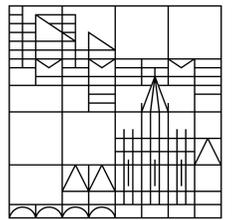


Characterizing the historical-cumulative interactions of the eukaryotic communities in sediments from Lake Constance, Germany

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May 5 2020

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Abstract

Lake Constance is a large peri-Alpine lake of glacial origin (SA 535 km²) divided into two major basins, western Lower Lake (depth, 40 m) and Upper Lake Constance (depth, 251m). Like other Alpine lakes, it underwent a major eutrophication event between the 1950s-1990s (Jenny et al, 2016). Using annual seasonal measurements, a major shift in the community composition was detected in the 1950s in response to rising phosphorus loads (Wessels et al., 1999). However, using sediments from lake Constance, we detected an earlier shift in the community composition using sediment historical DNA records (Ibrahim et al., *in review*). We here study the unique cumulative response of various eukaryotic groups detected by metabarcoding of the general 18S rRNA gene, their interactions with one another and within the trophic web (mainly copresence of parasites and macrophytes as substrates in relation to algae).

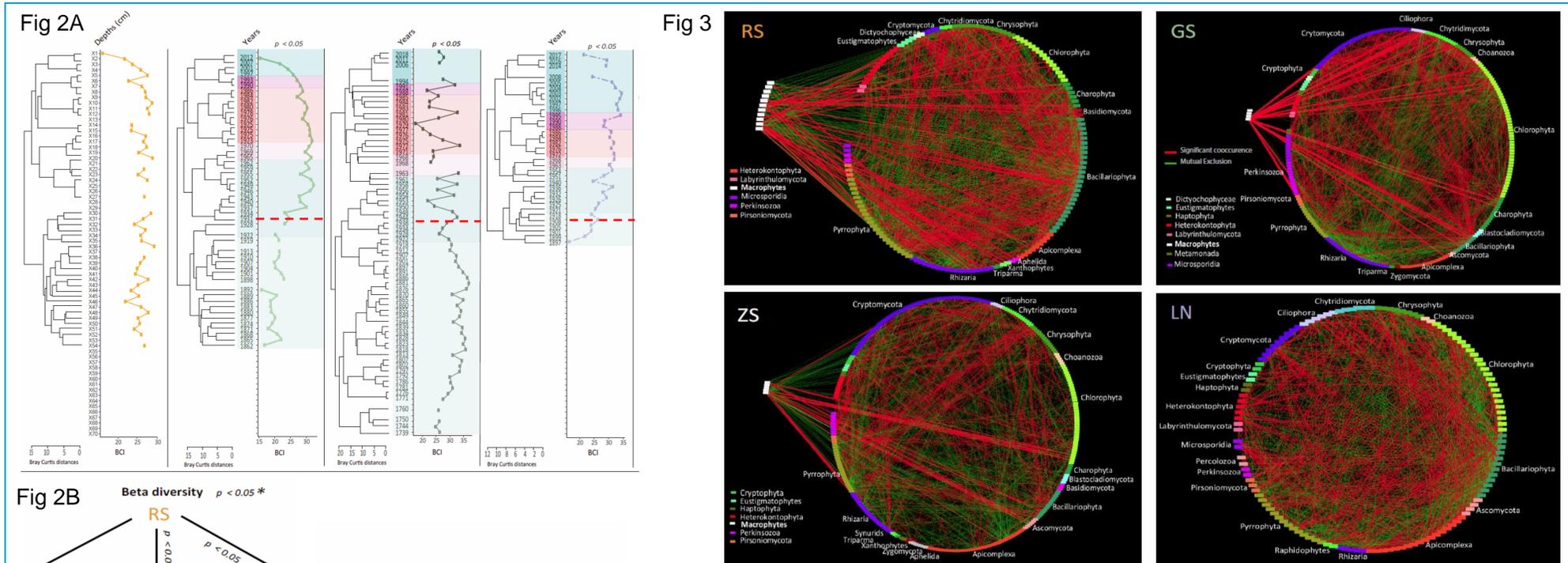


Figure 2: Spatial and temporal (A) Curve plots representing the Bray-Curtis similarity index of the cumulative eukaryotic community across sediment cores taken from Rheinsee, Gnadensee, Zellersee and Langenargen. (B) A graphical representation of the similarities between the shifts in the community compositions across the cores and along the different trophic states during the past 200 years as calculated by (i) Kruskal-Wallis chi-squared and (ii) Dunn (1964) Kruskal-Wallis multiple comparison using p-values adjusted with the Benjamini-Hochberg method. The (*) denotes the significant variations. Figure 3: Co-occurrence networks depicting the relation between the different classified algal groups and macrophytes (i.e. substrates) and parasites.

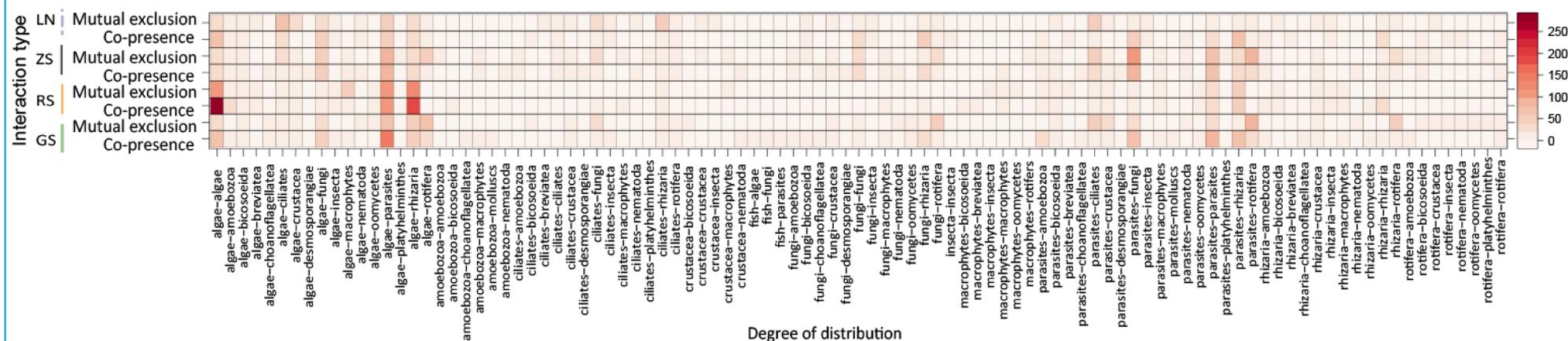
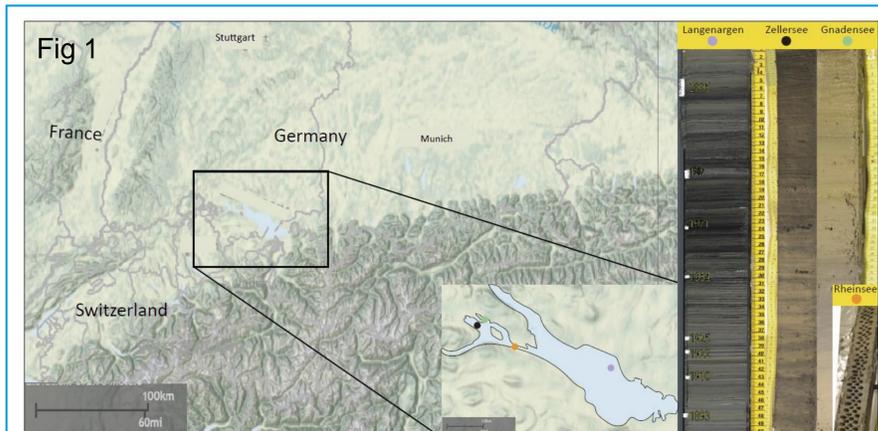


Figure 4: A heat map illustrating the degree of distributions as calculated by co-occurrence networks based on the merged p values (<0.05) obtained from an ensemble of similarity and dissimilarity indices (Spearman, Pearson, Bray-Curtis dissimilarity and Kulblak-Leibler). The co-occurrence networks display the only two significant interaction types, co-presence and mutual exclusion between the different eukaryotic groups successfully classified and detected by the sediment historical DNA. (also applies to Fig 3)



Conclusion

A congruent response in the cumulative eukaryotic community was detected across the four sites of lake Constance with an apparent earlier shift, ~1920-1930s in the community composition. Using sediment historical DNA, we were able to detect all possible eukaryotic interactions within the successfully classified communities along the cores. Amongst others, there was a noticeable co-presence between the algal and parasitic groups. Hence, we focused on displaying the degree of interaction between the various groups of alga, parasites and macrophytes, which majorly incorporated the *Potamogeton* group.

Acknowledgements

This study was funded by the Deutsche Forschungsgemeinschaft (DFG, German Research Foundation) – 298726046/GRK2272 as part of the RTG-R3 Resilience of Lake Ecosystems.

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