



Conference Abstract

# Environmental DNA variability in lake sediment cores

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## Abstract

Lake sediments are natural archives that accumulate information about biological communities and their surrounding catchments. Paleolimnology has traditionally focussed on identifying fossilized organisms to reconstruct past environments. In the last decade, the application of molecular methodologies has increased in paleolimnological studies, but further studies investigating factors such as sample heterogeneity and DNA degradation are required. Here we investigated bacterial community heterogeneity (16S rRNA metabarcoding) within depth slices. Sediment cores were collected from three lakes with differing sediment compositions. Samples were collected from a variety of depths (1-cm width) which represent a period of time of approximately 1,200 years. Triplicate samples were collected from each slice and bacterial 16S rRNA metabarcoding was undertaken on each sample. Rarefaction curves showed that except for the deepest (oldest) slices, the combination of three replicate samples were insufficient to characterise the entire bacterial diversity. However, shared Amplicon Sequence Variants (ASVs) accounted for the majority of the reads in each slice (max. shared proportional read abundance 96%, 86%, 65% in the three lakes). Within slice similarity was higher than between slice similarity. No general trend was observed in variability among replicates with depth amongst the lakes. In one core, there was a higher community dissimilarity in older sediment, which may be due to laminae not being horizontal. These results highlight the fact that microbial communities

can be differentiated with depth however it is critical to interpret these results in the context of the stratigraphic data of the core.

## **Keywords**

paleolimnology, lakes, metabarcoding, bacteria,

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