



Bacterial diversity and distribution in the Holocene sediments of a northern temperate lake

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Sediments contain an abundance of microorganisms. However, the diversity and distribution of microorganisms associated with sediments are poorly understood, particularly in lacustrine environments. We used banding patterns from denaturing gradient gel electrophoresis (DGGE) and 16S rDNA sequences to assess the structure of bacterial communities in the Holocene sediments of a meromictic lake in Minnesota. Cluster analysis of the DGGE banding patterns indicates that the early- and middle-Holocene samples group separately from the late-Holocene samples. About 79% of the recovered bacterial sequences cluster with the alpha-, beta-, delta-, epsilon-, and gamma-Proteobacteria and *Firmicutes*. The remaining ~21% lack cultured representatives. The taxonomic lineages of bacteria differ statistically among the early-, middle-, and late-Holocene samples, although the difference is smallest between early- and middle-Holocene samples. Early- and middle-Holocene samples are dominated by epsilon- proteobacteria, and late-Holocene samples are dominated by sequences from uncultured sub-phyla. We only recovered delta-Proteobacteria in late-Holocene sediments and alpha- and gamma-Proteobacteria in late- and middle-Holocene sediments. Diversity estimates derived from early-, middle-, and late-Holocene clone libraries indicate that the youngest (late-Holocene) samples had significantly greater bacterial diversity than the oldest (early-Holocene) samples, and the middle-Holocene samples contained intermediate levels of diversity. The observed patterns of diversity may be caused by increased bacterial niche-partitioning in younger sediments that contain a greater abundance of labile organic-matter than older sediments.