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Vertical stratification of bacteria and archaea in sediments of a boreal stratified humic lake

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Boreal stratified humic lakes, with steep redox gradients in the water column and in the sediment, are important sources of methane (CH_4) to the atmosphere. CH_4 flux from these lakes is largely controlled by the balance between CH_4-production (methanogenesis), which takes place in the organic rich sediment and in the deepest water layers, and CH_4-consumption (methanotrophy), which takes place mainly in the water column. While there is already some published information on the activity, diversity and community structure of bacteria in the water columns of these lakes, such information on sediment microbial communities is very scarce. This study aims to characterize the vertical variation patterns in the diversity and the structure of microbial communities in sediment of a boreal stratified lake. Particular focus is on microbes with the potential to contribute to methanogenesis (fermentative bacteria and methanogenic archaea) and to methanotrophy (methanotrophic bacteria and archaea).

Two sediment cores (26 cm deep), collected from the deepest point ($\sim$6 m) of a small boreal stratified lake during winter-stratification, were divided into depth sections of 1 to 2 cm for analyses. Communities were studied from DNA extracted from sediment samples by next-generation sequencing (Ion Torrent) of polymerase chain reaction (PCR) - amplified bacterial and archaeal 16S rRNA gene amplicons. The abundance of methanogenic archaea was also specifically studied by quantitative-PCR of methyl coenzyme-M reductase gene (*mcrA*) amplicons. Furthermore, the community structure and the abundance of bacteria were studied by phospholipid fatty acid (PLFA) analysis.

Dominant potential fermentative bacteria belonged to families *Syntrophaceae*, *Clostridiaceae* and *Peptostreptococcaceae*. There were considerable differences in the vertical distribution among these groups. The relative abundance of *Syntrophaceae* started to increase from the sediment surface, peaked at depth layer from 5 to 10 cm (up to 21 % of bacterial 16S rRNA gene amplicons) and decreased gradually towards deeper layers while the relative abundances of *Clostridiaceae* and *Peptostreptococcaceae* started to increase at deeper depths, at 5 cm and 10 cm, respectively, both peaking at depth layer from 20 to 26 cm (*Clostridiaceae* up to 13 % and *Peptostreptococcaceae* up to 11 % of bacterial 16S rRNA amplicons). Methanogenic community was dominated by acetoclastic methanogens (genus *Methanosaeta*), which were most abundant at depth layer from sediment surface to 10 cm (up to 87 % of archaeal 16S rRNA gene amplicons) and decreased drastically until the depth of 18 cm having quite stable relative abundance from 18 to 26 cm (5 to 11 % of archaeal 16S rRNA gene amplicons). Hydrogenotrophic methanogens (*Methanoregula*, *Methanolinea*, *Methanospirillum*, *Methanocella*) (3 to 11 % of archaeal 16S rRNA gene amplicons) did not show any specific depth patterns. The proportion of methanotrophic microbes was very low and they consisted almost completely of type II methanotrophic bacteria (family *Methylocystaceae*), which had highest relative abundance at depth layer from 5 to 10 cm (up to 3 % of bacterial 16S rRNA gene amplicons) and were almost absent below 15 cm. Anaerobic methanotrophic archaea were not detected. These findings will be discussed with results from PLFA and q-PCR analyses.