

## Development of Methanogen Communities During a Primary Succession of Mire Ecosystems

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Mires are important sources of natural methane emissions and the emission rates have been connected to the successional stage of mires. However, knowledge of the development of methane producing microbial communities during the formation of mires is lacking. We postulated that, as in mire vegetation, there is a successional gradient in methanogenic microbial communities from young fens to bogs. Accordingly, we investigated the development of potential methane production and methanogen *Archaea* communities along a chronosequence of mires (ca. 100 - 2500 yrs) consisting of five mire sites (sites 1 to 5) located on the land-uplift coast of the Gulf of Bothnia. CH<sub>4</sub> production was measured in a laboratory incubation experiment. The methanogen communities were determined by amplification of a methyl coenzyme M-reductase (*mcr*) gene marker and further analysed by terminal restriction fragment chain length polymorphism (T-RFLP). The T-RFLP fingerprinting resulted in 15 terminal restriction fragments (T-RFs). The ordination configuration of T-RF data, using non-metric multidimensional scaling, showed a clear gradient in the methanogen community structures along the fen-bog succession. The fingerprint patterns of the samples from the water table level and 40 cm below were distinctively different from each other showing a depth-related distribution. Three T-RFs could be identified to belong to novel Fen-cluster methanogens earlier found in Finnish mires. The potential methane production showed the highest rates in the oligotrophic fen site (site 4) and clearly decreased towards the oldest site representing bog-fen transition stage (site 5). In the three youngest fen sites (sites 1 to 3) CH<sub>4</sub> production was negligible. However, the successful PCR amplification using *mcr* gene primers revealed the occurrence of methanogen community even in the young fen sites.