



## Seasonal and spatial aspects of the eco-distribution of methanotrophic bacteria in floodplain soils

P.L.E. Bodelier (1), M. Meima-Franke (1), M. Kamst (1), L. Bodrossy (2), N. Stralis-Pavese (2), M.M. Hefting (3), and R. Laanbroek (1)

(1) Department of Microbial Wetland Ecology, Centre Limnology, Netherlands Institute of Ecology (NIOO-KNAW), Rijksstraatweg 6, 3631 AC Nieuwersluis, the Netherlands. Phone: 31 294239307; Email: p.bodelier@nioo.knaw.nl, (2) Department of Bioresources, ARC Seibersdorf Research GmbH, Seibersdorf, Austria, (3) Department of Landscape Ecology, Utrecht University, Utrecht, the Netherlands

METHECO is the acronym of a consortium of research groups funded by the European Science foundation (ESF) within the EuroDIVERSITY program. The consortium investigates the role of microbial diversity in the dynamics and stability of global methane consumption. The consortium covers various habitats (i.e. Landfills, rice paddies, alpine meadows, littoral wetlands, forests, arctic wetlands, peat soils and river floodplains) and assesses the effects of natural environmental perturbation on the function structure relationship of methane-consuming microbial communities. Consortium members follow the same experimental and methodological scheme using DNA and RNA based techniques (i.e. *pmoA*-based cloning, DGGE, micro arrays, Real Time PCR, stable isotope probing). This paper presents the results obtained in a river floodplain along the river Rhine in the Netherlands, a habitat anticipated to be subjected to major changes in flooding regime due to climate change. Experiments were carried out to assess methanotrophic diversity, methane oxidation kinetics and spatial variability of function and structure of methane-oxidizing communities. Flooding events affected methane consumption negatively on short term. However, the long –term consequences of the flooding regime where the establishment of a distinct maximum methane consumption activity exactly in the part of the floodplain intermediate between permanently and irregularly flooded, where moisture and organic matter content were optimal for methane cycling. The methanotrophic community composition as analysed by *pmoA* micro array mirrored the result of the activity measurements, demonstrating that the communities differed clearly according to the flooding gradient. Diversity as assessed by micro array and activity components (initial consumption,  $V_{max}$ ,  $V_{max}/K_m$ ) were positively correlated. QPCR analyses showed that main types of methanotrophic bacteria were differentially distributed throughout the flooding gradient. Type I mirrored the activity pattern with a distinct optimum in the gradient whereas type II increased with decreasing flooding intensity. In general it can be concluded that the environment and environmental disturbances shaped the methane-consuming microbial community and led to differential eco-distribution of methanotrophic bacterial groups. The relative abundance of specific subgroups controlled methane consuming activity which makes it evident that knowledge on the microbial community composition is necessary to predict effects of environmental disturbance on methane cycling.