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Microbial ecology on the microcosm level: Activity and population dynamics of methanotrophic bacteria during early succession in a flooded rice field soil

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Methane oxidizing bacteria (methanotrophs) play an important role in natural wetlands and rice fields preventing large amounts of methane from escaping into the atmosphere. The occurrence of both type I and type II methanotrophs in the soil surface layer has been demonstrated in many studies. However, there is no profound understanding which of them are responsible for the oxidizing activity and how they differ ecologically. Hence, a gradient microcosm system was applied simulating oxic-anoxic interfaces of water saturated soils to unravel population dynamics in early succession of methanotrophs in a flooded rice paddy. Additionally, environmental parameters were analyzed to link environment, populations, and their specific activity. We measured pmoA-based (particulate methane monooxygenase) terminal restriction fragment length polymorphism (T-RFLP) profiles both on transcription and population level. DNA T-RFLP patterns showed no major differences in the methanotrophic community structure remaining relatively constant over time. In contrast the active methanotrophic community structure as detected by pmoA mRNA T-RFLP analysis clearly demonstrated a distinct pattern from DNA T-RFLP profiles. While type II represented the most prominent group on the population level it seems to play a minor role on the transcription level. Furthermore there were no clear implications towards a link between soil parameters (e.g. NH4+ concentration) and methanotrophic community structure.