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Effect of rice cultivars on root-associated methanotrophic communities

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Rice agriculture represents a major source of the greenhouse gas methane. However, a large amount of methane is oxidized by methanotrophic bacteria before being released to the atmosphere. Methanotrophs are characterized by their unique ability to use methane as sole source for carbon and energy. They are located at oxic-anoxic interfaces where methane and oxygen are present, such as the rhizosphere. Although they have been studied extensively in the past, only little is known about natural or anthropogenic factors influencing their large diversity.

In this study, we investigated the effect of 20 different rice cultivars on methanotrophic communities associated with the roots of rice plants. The pmoA gene encoding a subunit of the particulate methane monooxygenase (catalyzing the first step of methane oxidation) was used as a functional and phylogenetic marker and analyzed using two different fingerprinting methods. The well established terminal restriction fragment length polymorphism (T-RFLP) analysis was compared to results obtained using a diagnostic pmoA microarray.

Both methods indicated that type Ib (Methylococcus/Methylocaldum) and type II (Methylosinus/Methylocystis) were the predominat methanotrophs located on rice roots. Interestingly, analysis of pmoA transcripts suggested Methylobacter/Methylomonas (type Ia) to present the actively methane oxidizing population in this environment.