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Distinct methanotrophs modulate soil methane oxidation in cold-temperate rice fields

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Methane is a potent greenhouse gas in the atmosphere causes global warming. Methanotrophic Bacteria (MOB) have the capacity to alleviate CH₄ emissions from rice based ecosystems to the atmosphere. In this study, we provide molecular evidence for distinctly different phylotypes of methanotrophs through DNA-based Stable Isotope Probing (SIP) and high throughput MiSeq amplicon sequencing of the 16S rRNA and *pmoA* genes in paddy soils from cold-temperate region in China. To know the active MOB in total microbimes and their *pmoA* genotypes, we incubated four paddy soils with ambient CH₄, high ¹²C-CH₄ and ¹³C-CH₄ amendment. The results showed strong activity of MOB and their ability of methane consumption in cold-temperate rice fields. The *pmoA* gene copies increased significantly with high ¹³C-CH₄ incubated microcosms and reached the peak in heavy DNA fractions suggesting strong labeling of active MOB community. The *pmoA* and 16S rRNA gene sequences showed a high diversity of active methanotrophs and it seems that type-I was leading than type-II in three soils while only ones soil exhibited high abundance of type II- like methanotrophs. With all ¹³C-labeled methanotrophic 16S rRNA and *pmoA* gene sequences demonstrated that active MOB were affiliated with type-Ia including genera *Methylobacter*, *Methylosarcina*, *Methylocaldum* and *Methylmicrobium* while *Methylocystis* and *Methylosinus*-related to type-II methanotrophs. So, our study suggests that a wide variety of methanotrophs can modulate soil methane oxidation in cold-temperate rice fields that might be able to reducing the methane emissions to the atmosphere.

Biography

Nasrin Sultana completed Ph.D. at Institute of Soil Science-Chinese Academy of Sciences, China. Her research interest is on Environmental microbiology.

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