

Structure and functions of a methane-driven microbial food chain in rice field soil

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Methane oxidation is a key process controlling methane emission from wetlands into the atmosphere. Methanotrophs, responsible for aerobic methane oxidation, do not only oxidize but also assimilate methane. Once assimilated, methane carbon may be utilized by other organisms. Here we present the evidence of a methane-driven microbial food chain in a rice field soil and its potential impact on methanotrophs. Stable-isotope probing of nucleic acids using ¹³C-labelled methane demonstrated that methane carbon is incorporated not only into methanotrophs but also into non-methanotrophic bacteria, phagotrophic protists, bacteriovorous nematodes in a rice field soil. Methane carbon could be also incorporated into the capsid gene of T4 type bacteriophages. These results suggest that methane carbon is linked to the soil microbial food chain that involves cross feeding, grazing, and viral lysis—once assimilated. The rice rhizosphere—the active site of methane oxidation—can have a distinct community of phagotrophic protists involved in a methanotrophic food chain that is influenced by elevated atmospheric CO₂; this implies a variation of prey-predator interaction in the methanotrophic food chain. Protistan grazing shapes the community structure of methanotrophs most likely by selective grazing. Protistan grazing also has a potential to affect methane oxidation in the surface of water-saturated rice field soil. Altogether, a series of our study suggests the potential importance of microbe-microbe interactions in methane dynamics in a rice field soil.

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