Microbial community and its functions on methane metabolism in the wetland ecosystems

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Wetland ecosystems have been certified as the main natural source of atmospheric methane, the potent greenhouse gas that influences global climate and carbon fluxes. The metabolism of methane in a wetland environment is carried out by a diverse group of methane-metabolizing archaea through the biological decomposition of organic matter under anaerobic conditions. Recently, cultivation-independent genomic approaches are allowing us to explore genomic diversity and expand our understanding of the unidentified microbial lineages on their ecological lifestyles. However, clear evidence for methane metabolism and the functional methanogenic community is yet to be much documented. In this work, we characterized the microbial community structures in peats collected from the Bogatsuru Wetland, Oita Prefecture, Japan. The phylogenetic analysis based on 16S rRNA gene sequences and functional genes were used for investigating the key microbial groups and activity potentially involved with the metabolic pathways for methane production. The members of Methanomicrobia (mainly Methanomicrobiales and Methanosarcinales) were detected in anoxic sub-surface peat corresponded to the existence of the *mcrA* gene, a key functional gene for methanogenic archaea, indicating the methane production potentials. Additionally, the phylogenetic analyses of functional genes revealed that the Methanomassiliicoccales lineages, classified H_2-dependent methylotrophic archaea, were also detected from deeper peat. Interestingly, uncultured methanogenic Bathyarchaeota, the proposed methylotrophic methanogens, and unrecognized terrestrial archaeon were highly observed in this study. These findings emphasize the importance of discovering members of the methanogenic archaea in order to understand the ecological diversity and metabolic functions that play a vital role in the global carbon cycle.

Keywords: Wetland, Microbial community, Methane metabolism, Methanogen, Carbon cycle

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