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Distribution of Methane and Methanogen Populations in the Qilian Mountain Permafrost, Qinghai Province, China

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Qilian Mountain permafrost locates in northern Qinghai-Tibet plateau. Four scientific experimental wells were drilled there in 2008 and 2009, three of which contained gas hydrate. Soil samples were collected about 10cm beneath the ground of swamp zone and meadow zone near these wells in 2011. Eight samples were selected, four from swamp zone and four from meadow zone, for methane and methanogen populations analysis. The methane concentrations of the swamp samples were all higher than the meadow ones. The analyses of methanogen populations in swamp zone and meadow zone were used the methyl coenzyme-M reductase (mcrA) gene as the target. The mcrA gene were amplified by polymerase chain reaction (PCR) and sequenced. All the samples from swamp were amplified successfully and three of them sequenced, while the four samples from meadow all failed to be amplified. Eventually, swamp

samples mcrA gene clone library was constructed with a total of 62 sequences. Phylogenetic analysis indicated the dominant methanogen populations in the swamp zone were *Methanosarcinales* and *Methanomicrobiales*. As the methane concentrations of meadow samples were very low and the mcrA gene of them were all failed to be amplified after several times, while the methane concentrations of swamp samples were very high and the mcrA gene of them were successfully amplified easily, the conclusion can be drawn that the methane concentrations were positively related to the methanogen populations in the Qilian Mountain permafrost. It can be inferred that the methane probably mainly generated from methanogens in the surface soil in the Qilian Mountain permafrost.

Key words: Qilian Mountain permafrost, methane, methanogen populations, mcrA gene

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