

Investigation of role and metabolic potentials of the microorganisms in sites of gas and oil containing mineralized fluids in Lake Baikal using molecular methods

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In freshwater environments, gas hydrates have to date been reported only from Lake Baikal (De Batist *et al*, 2002), the largest freshwater basin in the world. Known that the oxidation of methane in aerobic and anaerobic conditions carry out microorganisms (Valentine, Reeburgh, 2000). In Lake Baikal was proved presence of process of aerobic methane oxidation by methanotrophic bacteria (Hamsaraev, Zemskaia, 2000). Profiles of distribution curves of methane concentrations in deep water sediments at sites of discharge gas and oil fluids indicate talk about presence of process anaerobic oxidation of methane (AOM) (Egorov 2003). However, what microorganisms and electron acceptor is used for AOM in Lake Baikal. In process of AOM might be involved alternative electron acceptors (sulfate, iron (III), manganese (IV), nitrite and ammonium) (Zehnder, Brock, 1980; 1989; Valentine, Reeburgh, 2000; Conrad, 2009).

High concentration these ions were detected in deep water sediments at sites of discharge gas and oil fluids on the Lake Baikal (Pogodaeva *et al*, 2012, 2013). Using fluorescent *in situ* hybridization with labeled oligonucleotide probes has confirmed the presence of groups ANME1 and ANME2. But, phylogenetic analysis of 16S rRNA gene fragments of *Archaea* has not confirmed presence these groups. Among of *Archaea* was detected representatives *Euryarchaeota* (*Methanomicrobiales* and *Methanosarcinales*), *Crenarchaeota* and *Thaumarchaeota*. Baikal archaea have formed separate clade with archaea with not known metabolism. Among *Bacteria* was investigated phylum *Planctomycetes*. Baikal *Planctomycetes* are similar to bacteria participating in anaerobic ammonium oxidation and belonged to the phylogenetic cluster of the candidate species (ANAMMOX group) anaerobically oxidizing ammonium. However, the degree of similarity with the closest homologues was as low as 90-97%, thus, indicating the relation of Baikal *Planctomycetes* to new, unknown taxa of this phylum.

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