

Community structure of Archaea in the western North Pacific and the Arctic Ocean

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Archaea are ubiquitously found in various environments. Many issues on their biological functions and ecological roles still remain to be investigated because they are often hard to be cultivated. Four phylogenetic groups, Marine Group I (MG-I) belonging to the phylum *Thaumarchaeota* and MG-II, MG-III, MG-IV belonging to the phylum *Euryarchaeota*, have been found so far in seawater environment. Although their abundance in mesopelagic and bathypelagic layers is comparable to bacteria, their ecological roles are not fully understood. Analyses of limited number of cultured strains, single-cell genomics and metagenomics of marine archaea have revealed that their contribution to energy flows and biogeochemical cycles in pelagic ecosystems can not be negligible. However, even basic information about their distribution, diversity and community structure is still very limited comparing with bacteria. Here we report archaeal community structure in the western North Pacific and the Arctic Ocean based on the deep sequencing of 16S rRNA genes directly amplified from seawater filtrates. Totally 44 samples including multiple depths of 8 different locations (4 in the North Pacific and 4 in the Arctic) were analyzed. Two size fractions, particle-associated ($>3.0\ \mu\text{m}$) and free-living ($0.22\text{--}3.0\ \mu\text{m}$), were obtained by seawater filtration. After extracting DNA, V4 hyper variable region of 16S rRNA gene was amplified and sequenced using an archaea specific primer set. Obtained sequences were clustered with 3 % cutoff value and assigned using Greengenes database. As a result, about 98 % of total reads were assigned to MG-I, MG-II, MG-III and the rest of 2 % reads were assigned to *Parvarchaeota*, Marine Benthic Group, MG-IV. Sequence reads assigned to MG-I were reanalyzed using our own database to have their subgroup assignment. The MG-I sequences were assigned to 9 of 10 subgroups. MG-I-alpha, MG-I-beta, MG-I-gamma were major subgroups and dominated about 93 % of total MG-I reads. Community structure showed depth-dependent patterns of each phylogenetic group. MG-II dominated in a surface layer (0-200 m) and MG-I dominated in subsurface and deep layers ($>200\ \text{m}$) in the Pacific Ocean. Also, MG-I-alpha was more abundant than other subgroups in the surface layer, whereas MG-I-gamma was abundant in the subsurface and deep layers. These depth-dependent patterns agreed well with previous knowledges. However, MG-I dominated in the surface layer at some Arctic locations and MG-I-beta was abundant in chlorophyll maximum depths at locations in the subtropical Pacific Ocean, which were previously unknown patterns and thus should be further investigated. In summary, we revealed seawater archaeal community structure in a wide climatic range of the ocean, from subtropical to the Arctic oceans. Our own database of MG-I archaea contains more detailed information of phylogenetic clustering than conventional 16S rRNA gene databases and thus enables subgroup assignments. Such subgroup assignment is important to understand archaeal contribution to biogeochemical cycles, because some of the MG-I subgroups such as MG-I-alpha, MG-I-beta, MG-I-gamma are known to be ammonia oxydizers and also ecotypes preferentially living in different habitats. Our MG-I database is useful for further analyses of archaeal community structure at the level of ecotypes and contributes to have more comprehensive view of their distribution in the ocean than before.

Keywords: Archaea, The western North Pacific Ocean, The Arctic Ocean

