ARCHAEA BIODIVERSITY FROM CHOL BURI MANGROVE FOREST, THAILAND

Montri Yasawong [1]*, Pornpimon Kanjanavas[2], Sutatra Areekit[3], Kosum Chansiri [4]

[1]Department of Biochemistry, Faculty of Pharmacy, Mahidol University, 447 Sri-Ayuthaya Rd., Rajathevi, Bangkok 10400, Thailand
[2]Department of Industrial Microbiology, Faculty of Science and Technology, Huachiew Chalermprakiet University, Samutprakan 10540, Thailand
[3]Innovative Learning Center, Srinakharinwirot University, Bangkok 10110, Thailand
[4]Department of Biochemistry, Faculty of Medicine, Srinakharinwirot University, Sukhumvit 23, Bangkok 10110, Thailand
*Author to whom correspondence should be addressed; E-Mail: montri.yas@mahidol.ac.th

Abstract: Mangrove forests are one of the most typical coastline ecosystems in Thailand having importance for ecology of the country and exhibiting high biodiversity. The aim of the study was to characterize microbial community as well as to estimate methanogenesis in these mangrove sediments. The phylogenetic trees constructed from 16S rDNA of archaeal library revealed the strong dominance of two phylogenetic groups: ammonium oxidizers and methanogens. It was shown that the dominance of the classes *Delta*- and *Gammaproteobacteria* were dominant microbial groups in bacterial community. The former included sulphate-reducers from the genera *Desulfobulbus*, *Desulfobacterium* and *Desulfopila*. Archaeal community was dominated by ammonium oxidizers belonging to Candidatus *Nitrosopumilus* and methanogens from the orders *Methanomicrobiales* and *Methanosarcinales*. Methanogenesis in the samples incubated at 25°C has been strongly stimulated by trimethylamine and methanol, indicating the importance of methylotrophic pathway of CH_4 production. The 16S rRNA gene copy number of *Archaea* was approximatly two times higher than that of *Bacteria* according to qPCR. Statistical analysis revealed much higher diversity of bacteria compared to archaea. The microbial community of Chol Buri mangrove sediments comprises different trophic groups with predominance of sulphate-reducing bacteria as well as ammonia-oxidizing and methanogenic archaea. Thus, the 16S rRNA gene analysis exhibited the high microbial diversity in the sediments of Chol Buri mangrove of Thailand. The coexistence of two functional archaeal groups, namely anaerobic methanogens and aerobic ammonia-oxidizers which are highly abundant in the same sample site can be explained by the specific hydrology of mangrove ecosystems with highly varying red-ox potential resulted from the daily tidal period. The abundance of the above described three main functional groups of microorganisms in the sediment of Chol Buri mangrove in Thailand could be an indication of the primary importance of appropriative metabolic processes: sulphate reduction, ammonia-oxidation and methanogenesis. Methanogens and sulphate-reducers are likely to be the main terminal microbial groups in the anaerobic community of mangrove. This work is a contribution to the study of microbial diversity and microbial processes in mangrove ecosystems.

Keywords: Mangrove, Archaea, ammonium oxidizers, methanogens