Prokaryotic Diversity of the Hypersaline Environments of Qiaohou Salt Mine in Yunnan, China

Author(s) Zhi-Gang Wang, Yong-Xia Wang, Wei Xiao, Qin-Yuan Li, Meng-Liang Wen, Xiao-Long Cui

Institution(s) 1. YIM, Yunnan Institute of Microbiology, Yunnan University, Cuihu Beilu 2, Kunming, Yunnan 650091, P. R. China

Abstract:

Prokaryotic diversity of the hypersaline environments of Qiaohou salt mine in Yunnan, southwest of China has been analyzed by using cultivation or culture-independent molecular approaches. 102 no redundant bacterial isolates were obtained from 3 samples collected from the hypersaline environments of Qiaohou salt mine, and the phylogenetic analysis results based on the partial/full length 16S rRNA gene sequences of 43 selected strains showed that the bacteria distributed in the environments included the members assigning into more than 18 genera of 4 bacterial phyla Actinobacteria (53.5% of the total isolates), Firmicutes (23.2%), Proteobacteria (16.3%) and Bacteroidetes (7%), i.e. Bacillus, Brevibacterium, Exiguobacterium, Georgenia, Halobacillus, Halomonas, Idiomarina, Knoellia, Kocuria, Marinobacter, Micrococcus, Phycococcus, Paracoccus, Pseudomonas, Rhodococcus, Salegentibacter, Staphylococcus and Streptomyces, which indicates higher culturable bacterial diversity in the habitat. However, no archaeal strains were isolated. Samples of the salt mine were analyzed by culture-independent methods. A total of 120 archaeal and 125 bacterial 16S rRNA gene clones from the salt mine were analyzed by amplified ribosomal DNA restriction analysis (ARDRA), and formed 33 and 31 different ARDRA types, respectively. Phylogenetic analyses based on nonchimeric sequences revealed that the bacteria include members assigning into 5 groups (Bacteroidetes, Proteobacteria, Firmicutes, uncultured bacteria of environment samples and Chloroflexi), and the archaea included members affiliated with genera (Halobacterium, Halorubrum, Haloarcula and Halomicrobium) and uncultured archaea of the family Halobacteriaceae of the phylum Euryarchaeota. Additionally, the results by culture-independent approaches have proved that the uncultured bacteria and archaea were the major components of the natural microbial communities, and few microorganisms of them were isolated. This indicates that the salt mine harbor a unique and novel prokaryotic diversity that is different from what has been described in other hypersaline environments.

Key words: prokaryotic diversity, hypersaline environment, salt mine, Yunnan