

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

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### 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 non-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 included 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