

# Abundance and diversity of Sulfate-Reducing Bacteria in Tagejia and Quzhuomu geothermal zones of Tibet, western China

\*Weiyu She<sup>1</sup>, Geng Wu<sup>1</sup>, Hongchen Jiang<sup>1</sup>

1. China university of geosciences, Wuhan

Sulfate-reducing bacteria (SRB) play an important role in the sulfur cycles of hot springs. However, little is known about the distribution of SRB and their response to temperature in terrestrial hot springs of the Tibetan Plateau. In this study, sediments from eight hot springs and two geothermal channels in the Tagejia (TGJ) and Quzhuomu (QZM) geothermal zone. These sampled hot springs possessed temperature ranging from 32 °C to 82°C and circumneutral pH. The TGJ hot springs contained lower (< 100 mg/L vs. > 250mg/L) sulfate content than the QZM hot springs. The QZM hot springs were inhabited by thick green or red microbial mats, while the TGJ hot springs contained green/grey/pink microbial mat. The abundance and diversity of SRB in the collected hot springs sediment were investigated by using quantitative polymerase chain reaction (QPCR) and cloning-based phylogenetic analysis on the *dsrB* gene (beta subunit of dissimilatory sulfite reductase in SRB), respectively. The QPCR data showed *dsrB* gene abundance ranged from  $1.75 \times 10^6$  to  $0.96 \times 10^8$  copies per gram of sediments in the studied hot springs and *dsrB*-containing microorganisms comprised ~ 8% of the total bacteria in the studied hot springs. The relative abundance of *dsrB* gene to total bacterial 16S rRNA gen was positively correlated with temperature ( $R=0.4$  and  $R=0.82$  for the two geothermal channels, respectively). The phylogenetic analysis showed that SRB populations in the studied Tibetan hot springs were diverse and were mainly composed of *Desulfobacterales*, *Desulfovibrionales*, *Syntrophobacterales*, *Clostridia* and *Nitrospirales*, and unclassified *dsrB* gene. The molecular diversity analysis showed that *Syntrophobacterales*-related *dsrB* gene clones were dominant in the high-sulfate hot springs ( $\text{Fe}^{2+}$  up to 2.39 mg/L), in contrast with dominance of *Desulfobacterales*-related clones in the low-sulfate hot springs. The *dsrB* gene diversity at the OTU level (97% cutoff) was negatively correlated with increasing temperature ( $R=0.98$  and  $R=0.7$  for the two geothermal channels, respectively). These results suggested that temperature and sulfate concentration played an important role in affecting the *dsrB* gene distribution in the studied Tibetan hot springs.

Keywords: sulfate-reducing bacteria, *dsrB* gene, hot spring, temperature, Tibetan Plateau