Genomic adaptations of *Acidithiobacillus* enabling survival in diverse hot springs

Chanenath Sriaporn
Kathleen A. Campbell
Martin J. Van Kranendonk
Kim M. Handley

Video Byte

Keywords: *Acidithiobacillus*, genome streamlining, adaptation, hot spring, temperature, pH, Taupo Volcanic Zone, 16S rRNA, RNA sequencing, RNA-seq, bioinformatics, genomic adaptation, thermostability, thermostable, microbes, extremophile, extremophilic, thermophile, thermophilic, Microbiome

Posted Date: October 13th, 2021

DOI: <https://doi.org/10.21203/rs.3.rs-967290/v1>

License: This work is licensed under a Creative Commons Attribution 4.0 International License.
[Read Full License](#)

Abstract

The microbial compositions of hot springs are strongly influenced by temperature and pH.

Acidithiobacillus bacteria are found in diverse hot springs, but the genomic features that enable their adaptability are unclear. A recent DNA sequencing study analyzed the genomes of *Acidithiobacillus* from hot springs in New Zealand and compared them to published non-hot-spring *Acidithiobacillus* sequences. *Acidithiobacillus* typically accounted for over 10% of the prokaryote abundance in the springs. Three species, including two novel species (TVZ_G2 and TVZ_G3), accounted for over 90% of *Acidithiobacillus* and were found in springs with wide-ranging characteristics. A fourth related novel species was also found, although in low abundance. All four species were found at temperatures and pHs above the known limits for *Acidithiobacillus*, likely because they had more GC bases and proline codons in their DNA than other species, increasing their thermostability. The four species' genomes also appeared to be streamlined, as they had lower paralog/coding sequence ratios and were smaller than other *Acidithiobacillus* genomes. For pH tolerance, the three novel species (TVZ_G2-G4) seemed to rely on more mechanisms than the TVZ_G1 clade (*A. caldus*). Although culture-based confirmation is needed, the results reveal distinct features of hot-spring-resident *Acidithiobacillus* and provide insights into extensive adaptations in these bacteria.