

## MICROBIAL ARSENIC RESISTANCE IN CHAMPAGNE POOL, NEW ZEALAND

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### Rationale for study

Studies of microbial metal resistance strategies are key in developing an understanding in how early life on Earth was able to survive. Hot springs are considered modern analogues of early Earth conditions, and provide an ideal study site for the investigation into how microbial life dealt with metal toxicity. The presence of elevated arsenic (As) concentrations, a toxic metalloid, inflicts a high selective pressure on microbial communities in hot springs. In order to tolerate arsenic, microorganisms have had to evolve certain resistance mechanisms.

### Aims

The aim of this study was to identify abiotic and biotic arsenic transformation in hot springs, which gives insight into the earliest metal-resistance strategies.

### Methods

High temperature geothermal pools rich in arsenic species, near Waiotapu, NZ, were chosen as the study site. In these pools, meteoric water is heated by near surface magma, which travels via geological faults resulting in arsenic leaching from As-bearing rocks. Champagne Pool, the largest surface feature at Waiotapu, is highly enriched in arsenic. The inner pool, rim and outflow channel of the pool were chromatographically analysed for arsenic speciation. The arsenic resistant microbial communities responsible for arsenic transformation were captured via pyrosequencing.

### Result and Discussion

At all pool sites the reduced form arsenite, was established as the predominant As species, which is consistent with the alkali-chloride character of the spring suggesting a direct discharge of the deep hydrothermal fluid featuring arsenite. In this pool, relatively high sulphide concentrations are responsible

for significant formations of thio-arsenates (AsV-S), which were detected throughout all sites. In addition, the detection of methylated arsenic at the pool's outflow indicates a biotransformation of arsenic has occurred. Gene sequencing analysis, for microbial diversity, revealed a microbial population that appeared to be closely related to sulphur-cycling microorganisms. The closest relatives of gene sequences found in the inner pool and rim were shown to have sulphur-compounds-reducing capabilities to sulfide. The presence of orpiment, an orange precipitate, at the pool's rim suggests further oxidation of sulphide to elemental sulphur. The decrease in selective pressure on microbial communities by arsenic precipitation was illustrated in the increase of microbial diversity from the inner pool to the rim. At the outflow channel we found a gene sequence shift in microbial dominance to organisms more closely related to sulphur respiring archaea, suggesting a discharge of elemental sulphur. This marked shift of microbial dominance to archaea in the outflow channel correlated with the presence of methylated arsenic species, which indicates the activity of a rare arsenic resistance mechanism in thermophilic archaea.

### Conclusion

This study indicates the importance of sulphur compounds on the abiotic and biotic arsenic transformation and the implications for microorganisms living under these conditions not only in sulphur-rich hot springs found today but also on Early Earth.

### Importance and scientific interest

Arsenic speciation combined with microbial diversity studies in Champagne Pool leads to a better understanding of the overall arsenic cycle in hot springs and the implication for earliest life forms on Earth.