

Sulfur-dependent arsenic resistance in hot springs: Insights from the metagenome of Champagne Pool, New Zealand

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In Champagne Pool, New Zealand, a potential early Earth analog site, microbes mediate and respond to the coupled cycling of arsenic and sulfur in a way that yields insights into the evolution of the microbial arsenic resistome. Linking arsenic and sulfur chemical speciation to metagenomic analyses facilitates the detection of key microorganisms and their arsenic adaptation strategies.

Detection of the *ars* arsenic detoxification operon at all sites along major chemical gradients in Champagne Pool supported its prioritization over the energy conserving arsenite oxidase, which was not detected anywhere despite the ubiquitous presence of arsenite. The detection of the arsenate reductase, *arsC*, at all sites, together with the widespread distribution of thioarsenate in Champagne Pool, supports an early evolution for arsenate resistance irrespective of the presence of molecular oxygen. Arsenic methylation occurred uniquely associated with a fundamental shift in microbial community structure in the outflow channel of Champagne Pool, with thioarsenate as a likely reactant.

The unraveling of direct and indirect microbial impacts on arsenic cycling in hot springs yields insights into how Earth's earliest microorganisms survived in metal-enriched environments and in response to evolutionary selection by arsenic on the early Earth.