

Genome analysis and distribution of cyanobacteria belonging to *Thermosynechococcus* in varying geochemical environments

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Cyanobacteria are photosynthetic microorganisms that have greatly changed Earth's geo- and biosphere through their release of oxygen to the environment. In ancient times, they likely inhabited a planet with quite different chemistry from the one we know today. This may have inhibited or delayed their growth and evolutionary radiation. Some hot springs on Earth today resemble potential ancient environments, and the organisms present there might give us insights into Earth's early biosphere.

Some cyanobacteria are known to be able to live in diverse chemical environments [1] but the genetic basis for this is unknown. Here we look at the genomes of cyanobacteria belonging to the genus *Thermosynechococcus* from hot springs with varying geochemical parameters. These environments all show high temperatures in addition to varying pH, sulfur and iron concentrations. Out of seven total genomes, two originate from iron rich hot springs with iron concentrations $> 100 \mu\text{M}$.

We compare the phylogeny and taxonomy of the strains with respect to the geochemical settings they were found in and specifically the differences of those strains found in iron rich environments. In comparison to strains from other genera, the species described here have a smaller total genome but a bigger core genome with genes shared by all strains. Additionally, no genes specific to iron tolerance were found in the genomes from high iron environments.

We are hoping that by understanding the relationships between genomes and their environment we can put these organisms, their physiologies, and their stress adaptations, into an evolutionary context.

[1] Papke, R. T., Ramsing, N. B., Bateson, M. M. & Ward, D. M. Geographical isolation in hot spring cyanobacteria. *Environ. Microbiol.* **5**, 650–659 (2003).