Microbial community structure at Champagne Pool, Waiotapu, New Zealand

A. CHILDS[1], B.W. MOUNTAIN[1] AND R. O'TOOLE[2]

[1] GNS Science, Wairakei Research Centre, Private Bag 2000, Taupo, New Zealand; a.childs@gns.cri.nz
[2] School of Biological Sciences, Victoria University of Wellington, Wellington, New Zealand

The unique geology and geochemistry of Champagne Pool, Waiotapu, New Zealand, has been well documented but to date there has been very little information on the relationship between microbial community structure and the physico-chemical environments in and around the pool. Champagne Pool contains alkali-chloride water that maintains a constant 75ºC in which the pH is lowered to 5.5 due to the formation of bicarbonate from the ascending CO_2. The water itself contains a variety of elements such as arsenic, antimony, sulfur, gold, silver, thallium, and mercury. Silica is precipitated out and deposited around the edge of the pool forming siliceous microstromatolites. This study aims to identify organisms around the margins of Champagne Pool and assess their spatial distribution with reference to the pool's geochemistry.

The sample site was divided into four zones spanning the margin of the pool: the sub-aqueous precipitate at 75ºC and pH 5.5; the air/water interface containing elemental sulfur and amorphous silica; the silica microstromatolites consisting of layers of microbes and precipitated silica which are kept moist by wave action, steam, and wicking effect; and the organic mat which coats the underside of the silica sinter ledge. This has a pH of 2.5 due to the oxidation of airborne H_2S and is kept moist by steam emanating from the pool.

Molecular methods were used to identify the community structure and relate this to the geochemical environment. Community genomic DNA was extracted and 16S ribosomal DNA amplified using a variety of universal and specific primers for archaea and bacteria. Sequences were then compared with current databases using BLAST. DGGE has been used to assess variation in microbial diversity associated with each cross-sectional zone.

The sub-aqueous precipitate, sulfur and sinter samples showed a number of organisms that originate near the base of the 16S phylogeny tree including the archaeal families *Sulfolobales*, *Thermoproteales*, *Desulfurococcales* and *Thermofilaceae*. Bacteria identified to date include *Thermodesulfobacterium* and *Aquificales*. These results reveal a predominance of anaerobic sulphur-respiring microbes. The microbial mat revealed a different community containing β, δ and γ *Proteobacteria,* and *Cyanidiaceae.*