

Microbial communities and bioactive metabolite potential of microbialites from extreme Australian environments

DAVID VARDEH^{1*}, JASON N. WOODHOUSE¹ AND
BRETT A. NEILAN¹

¹School of Biotechnology and Biomolecular Sciences,
University of New South Wales, Sydney, 2052 NSW
Australia

(correspondence:d.vardeh@unsw.edu.au,
j.woodhouse@unsw.edu.au, b.neilan@unsw.edu.au)

Extreme habitats support complex but poorly characterised microbial assemblages which can form accreted microbial mats or microbialites, widespread life forms of Early Earth.

Here we report the hitherto unexplored communities of extant microbialites from caves in New South Wales and hypersaline lakes in South Australia based on 16S rRNA Illumina sequencing and assess their bioactive metabolite potential by sequencing of domains of the nonribosomal peptide synthetase (NRPS) and polyketide synthase (PKS) pathways.

A wide array of microbial taxa harbouring a high percentage of unknown sequences has been unveiled, most notably Actinobacteria and Cyanobacteria.

In the caves, the extremophile *Chroococcidiopsis* is a dominant cyanobacterial taxon and has previously been shown to possess a variety of biosynthetic pathways [1]. Most predominant groups share low similarities even to uncultured organisms and may comprise unknown taxa.

From the salt lakes, a potentially new branch of halophilic Cyanobacteria outside of the *Euhalothece* cluster was found along an increasing salinity gradient and first culturing efforts are underway.

Pathways of NRPS and PKS have been detected in almost all sites and in-depth sequencing results will be presented.

Exploration and conservation of these environments is critical in times of climate change and anthropogenic alterations. The lack of awareness of these rich microbial assemblages jeopardises the chance to tap their full potential for bioactive compound production.

[1] Shih *et al.* (2013) *PNAS* **110**(3), 1053-1058