

## Cultured bacterial communities from Australian and African gold grains

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Bacterial biofilms living on gold (Au) grain surfaces affect Au biogeochemistry by enabling its dissolution, transport and biomineralisation [1]. These processes contribute to the (trans)formation Au grains and nuggets. This study aims to isolate and characterise bacterial strains that contribute to Au cycling on Au grains. Gold grains were collected aseptically from a gold mining site near Donnybrook (Western Australia). In addition samples from a number of deposits in the Barberton region of South Africa were collected. High-resolution scanning electron microscopy of Donnybrook grains reveal that they are dendritic and show surface textures indicative of Au and silver (Ag) dissolution. These zones contain up to 99.1% Au, whereas the centre of the grains is far richer in Ag. Crevices on the surface gold grains were filled with cells, residual organics and clay minerals in which bacteriomorphic and nanophase particles and octahedral platelets were abundant. This was also observed on grains from South Africa. The formation of these secondary gold structures can be attributed to Au cycling catalyzed by bacteria such as those resident on the grains. Bacterial enrichment cultures from Donnybrook grains were able to grow up to concentrations of 20  $\mu\text{M}$  of highly toxic Au(III)-chloride amended Tris Minimal Medium. Phylogenetic analyses reveal that in Gammaproteobacteria dominated Au(III)-amended enrichment cultures with their abundance shifting significantly after Au stress from 67 to 95 % (compared to unamended controls). To date, several isolates were capable of growing at concentrations of up to 100  $\mu\text{M}$  of Au(III); among these were novel strains of *Micrococcus luteus*, *Serratia proteomaculans* and *Pseudomonas fluorescens*. Further research on enriched and isolated Au-resident bacteria will unveil how their physiological and biochemical reactions influence Au biogeochemical cycle.

[1] Rea MAD, Zammit CM Reith F 2016. FEMS Microbiol Ecol. 92, fw082.