

Exploring microbial contribution to the biogeochemical cycling of gold from the genomic and proteomic perspective

SANTONU KUMAR SANYAL^{1,2}, JOËL BRUGGER²,
BARBARA ETSCHMANN² AND JEREMIAH SHUSTER³

¹Jagannath University

²Monash University

³University of Tuebingen

Presenting Author: santonu@mib.jnu.ac.bd

In natural environments, gold is dissolved (oxidized), dispersed, and reconcentrated. Collectively, these processes constitute the biogeochemical cycle of gold, which can be directly or indirectly catalysed by bacteria. Earlier studies investigated bacterial roles in gold biogeochemistry by performing *in-vitro* experiments using proxy pure culture or consortia; however, the role of indigenous bacteria inhabiting gold-bearing soil/sediments has remained unknown. To address this gap, a bacterial consortium was cultured from gold particles obtained from an abandoned gold mine in Donnybrook, Western Australia. Remnants of bacterial cells were observed within the polymorphic layers on gold particles, indicating that these crevices might provide a protective niche for bacteria and could be ‘hot-spots’ for bacteria-gold interactions. Bacteria, with their diverse metabolic activities (e.g., excretion of low molecular weight organic acids), and environmental conditions (e.g., pH, rainfall) may create microenvironments on particle surfaces (i.e., polymorphic layers) that facilitate the dissolution of soluble gold from particles. This is coupled to the reduction to micro- to nanometer-sized secondary gold particles with the polymorphic layers. Therefore, in terms of bacteria-gold interaction, a fundamental question arises: how do bacteria mediate the toxicity of soluble Au during the biogeochemical dissolution of gold?

The enrichment of bacteria directly from gold particles using a culture-dependent microbiological technique demonstrated that viable bacteria exist on particles. *In-vitro* experiments using these enriched bacteria consortia and soluble gold at concentrations similar to those expected to develop at the surface of dissolving gold particles resulted in the selective enrichment of a gold-resistant bacterial consortium. The genomic characterisation of the Au-tolerant bacterium *Serratia proteamaculans* isolated via this process demonstrated that these bacteria harbour various types of genes involved in heavy-metal resistance and oxidative stress tolerance. Proteomic experiments further revealed that this bacterium upregulated the synthesis of various proteins related to oxidative stress response (e.g., Monothiol Glutaredoxin, Thiol Peroxidase, etc.) and cellular damage repair as a result of the biotoxicity of ionic gold. In conclusion, the genomic and proteomic approach has provided a holistic biomolecular perspective on bacterial interactions with gold on Earth’s surficial environment (Fig) and biogeochemical

