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## Using microbial indicators in mineral exploration: Lessons from Australia

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The discovery of new world-class gold (Au) and base metal deposits is becoming increasingly difficult, because worldwide many un(der)explored regions are covered by thick layers of *in situ* and/or transported weathered materials, e.g., soils, sediments and saprolite. An on-going revolution in molecular biology now offers the prospect of using the microbial signatures of these materials to explore for underlying deposits [1].

Weathered materials are highly active zones of the environment hosting large microbial communities of commonly  $>10^9$  cells  $g^{-1}$ . These communities are primary drivers of C-, N-, S- and P- cycling. They also drive metal cycles, because many metals are used as micro-nutrients and for energy generation. If contents of mobile heavy metals, e.g., Ag, Cu, Au, Ni, Pb, U and Zn, exceed certain thresholds, metals become cytotoxic. This changes the microbial community composition; while some species thrive others decline. Generally, thriving species display increased capability in dealing with metal toxicity by expressing more genetic metal-resistance determinants. This allows them to detoxify their immediate cell environment, and is commonly also linked to the immobilisation of metals via the formation of intra- and extra-cellular biominerals.

Modern molecular techniques (e.g., next generation sequencing and high throughput microarrays) have enabled the generation of highly detailed profiles of composition and functions of microorganisms inhabiting these metal-anomalous zones, as well as understanding of the genetic pathways that enable organisms to survive in metal enriched environments. Using advanced statistical modelling allows us to link the genetic profiles to geochemical/geological parameters of underlying deposits. In a number of recent Australian studies of soils overlying VMS-, Au-, Pt-, Cu-Au-U- and base deposits microbial community compositions and abundances of metal-resistance genes were closely linked to the underlying mineralisation, demonstrating that pinpointing underlying ore bodies is feasible using these techniques [2, 3, 4]. To provide a dataset against which these anomalies can be compared the Biomes of Australian Soil Environments (BASE) project is currently underway, with 1400 sites across the Australian continent currently in the database. As this database will keep growing and the price of sequencing will decrease even further, these new geobiological tools using easy to obtain surface soils/sediments samples, will provide critical advantages for exploration in covered terrains.

References:

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