Microbial-Community Fingerprints as Indicators for Buried Mineralization

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In light of strong projected demand for metal resources into the foreseeable future, rates of new mineral deposit discovery are declining, while existing deposits are being progressively mined-out. Although little explored, biological anomalies may be robust indicators of buried mineralization, and such anomalies may be detectable through low-cost, high-throughput geobiological surveys. Application of DNA sequcening technologies allows profiling of the taxonomic diversity and metabolic potential of soil microbial communities across defined survey areas. British Columbia (BC), Canada is host to numerous mineral deposits of economic value, including a wealth of Cu-porphyry mineralization. The province is an ideal region to evaluate microbial-community sequencing as an exploration methodology for 'seeing' through overburden, as multiple field sites can be tested. Data have been collected from two different Cu-porphyry systems: 1) the Deerhorn Cu-Au porphyry of Consolidated Woodjam Copper Corp. in central BC, and 2) the Highland Valley Copper Highmont South Cu-Mo porphyry of Teck Resources Ltd. in south-central BC. Microbial-community DNA was extracted from soil transects at Deerhorn and Highland Valley Copper and the 16S rRNA gene was sequenced. Analysis of these sequences reveals that the number of observed OTUs is 2417 ±344 at Deerhorn and 2671 ±445 at Highland Valley Copper, indicating that the sequencing coverage was sufficient to capture 65% of the microbial-community diversity. There was no pronounced difference in species richness across the mineralized zones at either Deerhorn or Highland Valley Copper. Most microbial-community members belong to the Proteobacteria, Acidobacteria and Verrucomicrobia phyla at both sites, suggesting that discrimination between background and anomalies will occur at the genus and species levels, for example *Rhodanobacteria* sp., and *Acidimicrobiales* sp. increase in relative abundance in response to chalcopyrite ore presence. Standard hierarchical-clustering analysis and multivariate statistical analyses (UniFrac, ANOSIM) of the samples is being used to discriminate between background and anomalous values. Indicator analyses will be used to identify microbial taxa responsible for these community anomalies. In summary, the proposition to develop microbial community fingerprinting as an exploration tool will be of tremendous global value.

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