Application of Genomics to Mineral Exploration

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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. Much bedrock geology is favourable to a wealth of mineral resources, but much of this geology is buried under transported overburden including glacial sediments and gravels, thus obscuring strong surface expression of these deposits and rendering them largely invisible to classical exploration approaches. In a pilot study, we have pioneered the use of soil microbial community fingerprinting with modern DNA sequencing technologies to find buried mineral deposits. To determine the potential use of microbial community fingerprinting to reveal buried mineral deposits a suite of 150 soil samples were collected over a known Cu-Au porphyry deposit (Deerhorn, British Columbia) with extensive geological, pedological, geochemical and geophysical metadata. From a subset of these samples we have extracted microbial genomic DNA to: tag sequence the small sub-unit of the ribosomal RNA gene (16S rRNA); shotgun sequence genomic DNA; and perform multi-locus sequencing of functional genes. Initial analysis of 16S RNA gene data, shows alpha diversity (Choa1 index) estimates of up to 4123 operational taxonomic units (97% sequence similarity), such deep coverage will enhance the statistical power of the data set. Community anlaysis reveals strong similarities across samples at high level taxonomic resolution, indicating consistency in the sampling of the upper-B horizon and suggesting that discrimination between background and anomalies will occur at the genius and species levels. Analysis of metagenomic data is leading to the development of a suite of multi-locus primers (e.g sulfide oxidation genes –*sox,* copper centered particulate methane monoxygenase –*pmmo*) that contribute most to the metabolic capacity that underpins anomalous soil microbial communities. In summary, the proposition to develop microbial community fingerprinting as an exploration tool will be of tremendous global value.