

Exploring for concealed kimberlites: increasing discovery success with soil microbial community fingerprints

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Introduction

Mineral exploration in northern latitudes is becoming increasingly more challenging as undiscovered deposits are likely buried beneath appreciable glacial overburden and/or bedrock. The effectiveness of many existing mineral exploration tools is diminished as these approaches frequently fail to detect mineralization through thick surface materials. Therefore, the development of innovative exploration strategies and robust techniques to see through cover is imperative to future mineral deposit discovery success.

Microorganisms kinetically enhance geochemical reactions, including the dissolution and formation of diverse minerals, and harness energy and materials from these reactions to support their metabolism and growth in nearly every Earth surface environment (Newman and Banfield 2002; Falkowski et al. 2008). They are acutely sensitive, responding to variability in the chemical and physical properties in their surrounding environments. Subtle changes in mineral bioavailability, for example, can be reflected in dramatic differences in the composition and activity of microbial communities (Wakelin et al. 2012; Reith et al. 2012; Leslie et al. 2014; Fierer 2017). Analyses of microbial community composition and structure thus have a strong potential to resolve chemical and physical differences between environments that are not readily discernible through conventional geochemical and geophysical surveys.

The advent of high-throughput sequencing platforms over the last decade has transformed our capacity to interrogate complex microbial communities across a wide-range of environmental matrices (Binladen et al. 2007; Zhou et al. 2015). The application of these technologies enables high-throughput profiling of the taxonomic compositions and metabolic potential of soil microbial communities across defined survey areas. Given that every individual soil sample comprises thousands of microbial taxa, each containing hundreds to thousands of genes sensing and interacting with the surrounding soil environment (Fierer 2017), the statistical power of this approach to identify anomalies is unprecedented.

Results

Soil microbial communities are sensitive to subtle environmental gradients, and they will reflect these gradients through spatial variability. Variations in microbial community profiles, induced by chemical and physical differences related to geology, are detectable and can be used to vector toward discrete geological features. Results to date demonstrate viability of DNA amplicon sequencing (16S rRNA gene) and microbial fingerprinting to directly identify the sub-crop of mineralization at the DO-18 kimberlite and the Kelvin kimberlite in the Slave Craton, Northwest Territories. Specifically, microbial community profiling of soils above these deposits reveals a well-resolved and statistically robust spatial correlation between microbial community compositions and structures and the surface expression of buried

kimberlites (Figures 1a and 1c). Importantly, suites of microbial taxonomic indicators yield anomalies that better resolve the surface expression of kimberlite mineralization than conventional geochemical pathfinder elements (Figures 1b and 1d).

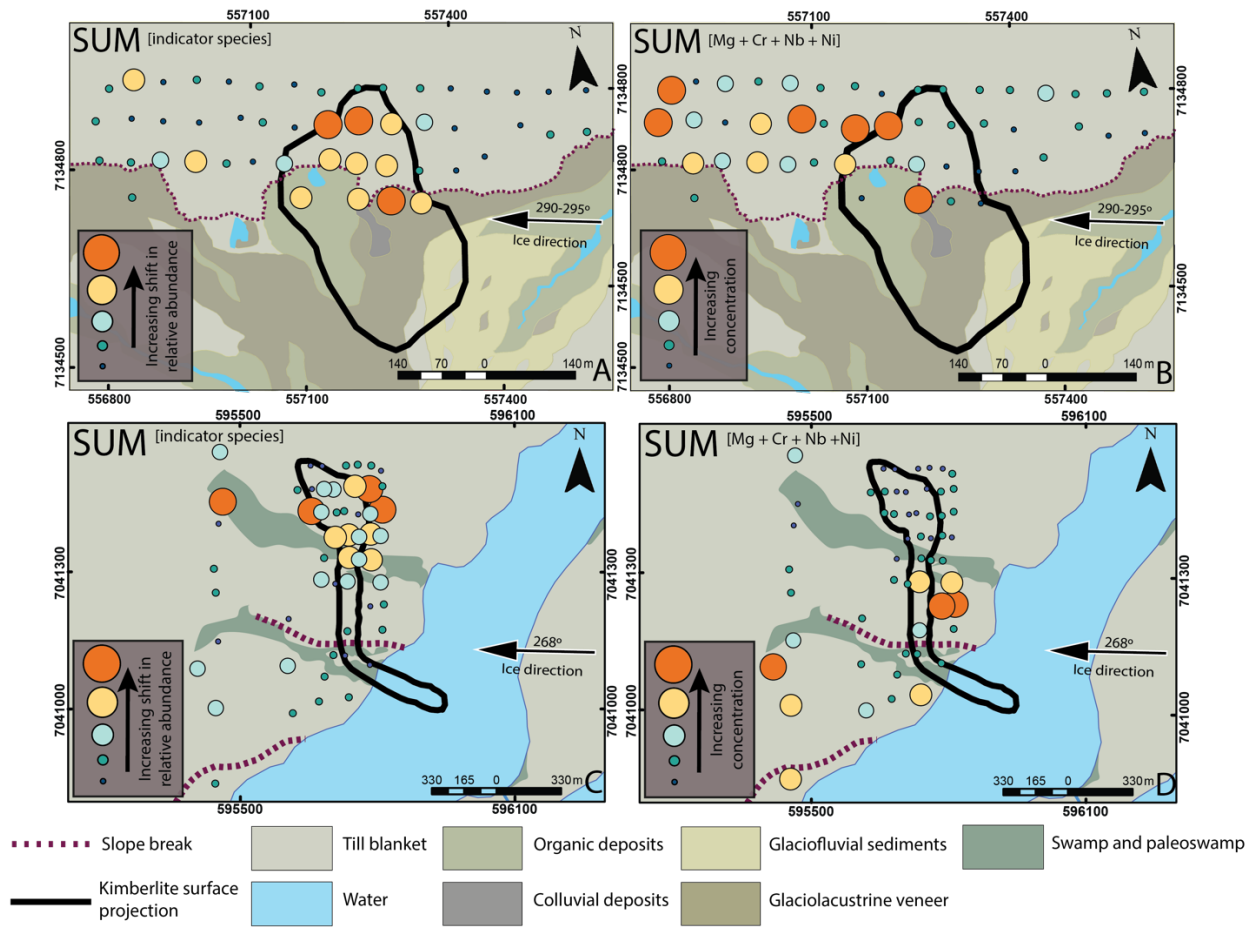


Figure 1: A normalized sum of microbial community indicator species anomalies at the DO-18 kimberlite (A) and Kelvin kimberlite (C) and a normalized sum of geochemical pathfinder elements at DO-18 (B) and Kelvin (D). All data are plotted onto surficial geology maps derived from field observations.

Future Work

Outcomes from these deposit-scale studies have highlighted the potential for geomicrobiological tools and techniques for successful application to through-cover mineral exploration. Microbial community anomalies that indicate buried kimberlites also appear to shape climate sensitive carbon pools, such as peatland bogs. Therefore, current research focuses specifically on reducing fundamental unknowns about the behaviour and variation of microbial communities in response to chemical and physical changes in the environment. This includes assessing how microorganisms sense and utilize economic minerals; exploring microbial community composition and metabolic potential in northern soils in response to changes in temperature and water content; and assessing the impact of ultramafic rock on the carbon feedbacks of soil microbial communities. These investigations serve to support the use of microbiological-based mineral exploration for concealed kimberlites in various terrains and climates, and to provide valuable information about northern Canadian carbon budgets.

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