

The determination of population dynamics in a bioleaching column using T-RFLP.

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Background: Attempts to study the microbial ecology of harsh environments has been severely hampered as traditional techniques rely on the growth of organisms *ex situ* and reveal only a small fraction of the diversity of these microbial communities. Recent developments in microbial identification enable the analysis of microbial populations without cultivation. This culture-independent approach has greatly enhanced the ability to assess bacterial genetic diversity in natural ecosystems. One such method is terminal restriction fragment length polymorphism (T-RFLP). This method produces a “DNA fingerprint” of a microbial community by analysing the polymorphism of a certain gene, usually 16S rDNA. Bioleaching is a simple and effective technology for metal extraction from low-grade ores and metal concentrates by the oxidation of insoluble metal sulphides by microbes to soluble metal sulphates. This process relies on novel microbes that survive in harsh environments (acid and high temperature) and as such samples will be grossly contaminated with compounds that may interfere with DNA extraction and subsequent molecular manipulation. Bioleaching columns are inoculated with a known mixture of microorganisms, however, little is known of what happens to this population of microorganisms within the column over time or the extent that each microorganism contributes to the total bioleaching of the column.

Aims: This project aims to develop molecular based methods to be used in the determination of population diversity in a bioleaching column. This project, aims to utilise this assay to determine the abundance of each of the inoculant species in bioleaching columns. This will enable conclusions to be drawn on the effectiveness of each isolate in the bioleaching process and their longevity in these particularly harsh environments.

Methods: Skills developed will include the culturing of novel microbes, the extraction, recovery and purification of DNA from ore samples, PCR and T-RFLP optimisation and gene sequencing