CARBON FIXATION GENES IN BIOMINING MICROORGANISMS

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Background and aims: Studying metabolic pathways will help provide a better understanding of the role of different microorganisms within biomining environments. The majority of microorganisms involved in biomining are autotrophs which rely on atmospheric carbon fixation for growth. The aim of this study is to investigate genes involved with carbon fixation in a range of biomining microorganisms.

Methods: Genes that encode for key enzymes in the Calvin Cycle (the ribulose-1,5-bisphosphate carboxylase/oxygenase large-subunit genes cbbL and cbbM) and the Modified 3-Hydroxypropinase Cycle (the carboxyltransferase subunit gene pccB) were selected. Universal primers designed from multiple sequence alignments were used to amplify genes from Sulfolobus thermosulfidooxidans, Acidimicrobium ferrooxidans, Acidithiobacillus ferrooxidans, Acidithiobacillus thiooxidans, Acidithiobacillus caldus, Sulfolobus metallicus, Acidianus brierleyi and Metallosphaera sedula. Partial gene sequences were generated and specific primers were designed for each of the microorganisms.

Results: Universal primers designed were shown to amplify the following genes in the subsequent microorganism/s; cbbL red: S. thermosulfidooxidans, cbbL green: Am. ferrooxidans, At. thiooxidans and At. caldus, and pccB: S. metallicus, A. brierleyi and M. sedula. Partial sequences for the cbbL red gene of S. thermosulfidooxidans, the cbbL green of Am. ferrooxidans, At. thiooxidans and At. caldus and the pccB gene of M. sedula are described.

Conclusions: Sequences generated will assist in further research into the carbon fixation cycles of biomining microorganisms. The specifically designed primers will be used in quantitative reverse transcriptase polymerase chain reaction (qRT-PCR) to further investigate these microorganisms role within biomining environments.