

MICROARRAY ANALYSIS OF MICROBIAL WEATHERING.

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Microbial activity has been linked to volcanic rock weathering. It is thought that the process is generally driven by the nutrient requirement of the microbial community and occurs as a result of the sequestration of bio-essential elements (1). Although we know that metabolising bacteria influence rock weathering, the molecular processes involved are unknown.

For the first time, we have used DNA microarray technology to investigate the genes involved in weathering, in particular the sequestering of iron using the heavy metal resistant bacterium, *Cupriavidus metallidurans* CH34. Extensive studies have characterised the heavy metal resistant and iron uptake mechanisms of this bacterium. CH34 employs siderophores, which are iron-chelating compounds, to sequester iron in iron-limited conditions (2). Furthermore, plasmid-based heavy metal resistant genes are expressed in the presence of certain heavy metals (3).

For this study we grew CH34 in MM284 (iron) and MM284 (iron-limited) with and without volcanic basalt. Low levels of heavy metals were detected in the basalt, using ICP-MAS. Microarray analysis demonstrated that siderophore genes were not differentially expressed when grown in MM284 (iron-limited) with basalt. This was in concurrence with siderophore measurements using the CAS assay. Instead, a large number of porins and membrane transporters in concomitantly with genes associated with biofilm formation were up-regulated. Furthermore, genes linked to heavy metal resistance were up-regulated. This included the plasmid borne cation efflux metal resistant operons, *czc* (resistance to Cd^{II}, Zn^{II} and Co^{II}), and *cnr* (resistance to Co^{II} and Ni^{II}).

The findings in this paper are the first insight into the molecular processes involved in microbial weathering. Some of the earliest environments on the Earth were volcanic. Therefore, these results not only elucidate the mechanisms by which bacteria might have sequestered nutrients on the early Earth but also provide an explanation for the evolution of multiple heavy metal resistance genes long before the creation of contaminated industrial biotopes by human activity.

Reference: (1) Cockell CS, Olsson K, Herrera A, Meunier A (2009). *Geobiol.*, **7**, 50-65. (2) Bhatt G, Denny T (2004). *J. Bacteriol.*, **186**, 7896-7904. (3) Mergeay M, Monchy S, Vallaeys T, Auquier V, Benotmane A, Bertin P, Taghavi S, Dunn J, van der Lelie D, Wattiez R (2003). *FEMS Microbiol. Rev.*, **27**, 385-41.