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Geomicrobiology of arsenic: how genes influence As geochemistry

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The toxic element arsenic is a major contaminant of many groundwaters and surface waters throughout the world. The reduction of arsenate to arsenite by bacteria is known to promote the release of arsenic from contaminated sediments and ultimately to drinking water supplies. Arsenate is reduced to arsenite by bacteria either as a mechanism of detoxification or as a terminal electron acceptor during anaerobic respiration. Arsenate respiratory reduction and arsenate detoxification are attributed to genes encoding for an As(V) respiratory reductase complex (*arrAB*) and an As detoxification operon *arsRDABC*, respectively. Much is known about the environmental factors that turn on the *ars* detoxification pathway in bacteria. However little is known about the environmental factors that control the expression of arsenate respiration genes. We have developed a model organism to study arsenate reduction in the facultative anaerobe *Shewanella* sp. strain ANA-3. This strain contains both the detoxification and respiratory arsenate reductases and is the only known genetically tractable As(V) respiring bacterium. We have quantitatively characterized the gene expression patterns and dynamics of both *arr* and *ars* genes in bacterial cultures grown under a variety of environmental conditions (e.g. aerobic/anaerobic, competing electron acceptors with or without arsenate or arsenite, and in various growth phases). Our results show that the arsenate respiratory reduction pathway is induced by arsenate and arsenite only under anaerobic conditions and that the gene expression is 1,000 times more sensitive to arsenite than the expression of the arsenate reductase gene of the detoxification pathway. Current work is focused on understanding how microbes sense arsenic in the environment and how gene expression changes when arsenic is associated with mineral surfaces.