Os isotope systematics of Jorullo Lavas, Mexico: Petrogenetic implications

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Arc lavas are generally radiogenic in $^{187}Os/^{188}Os$ compared to depleted mantle, which has been variously attributed to crustal assimilation [1] or to addition of subduction components to the mantle wedge [2]. However, the low Os abundances in most arc lavas make the Os isotope signatures highly susceptible to crustal assimilation. The 1759-1774 eruption of the Jorullo volcano in the Michoacán Guanajuato Volcanic field (MGVF), Mexico produced relatively primitive lavas that can potentially help address the origin of radiogenic Os in arc magmas. Os concentrations in Jorullo lavas vary from 18 to 173 ppt, and $^{187}Os/^{188}Os$ ranges from 0.13031 to 0.14066. A previous regional Os isotope study of MGVF cinder cones invoked lower crustal assimilation to explain such elevated ratios [1, 3]. However, our preliminary work on Jorullo lavas shows a lack of correlation between $^{187}Os/^{188}Os$ and indices of fractionation (e.g. MgO, SiO_2), suggesting a limited role for crustal assimilation processes in their petrogenesis. In addition, a positive correlation between $^{187}Os/^{188}Os$ and $^{206}Pb/^{204}Pb$ argues against lower crust assimilation assuming typical lower crustal compositions. Instead, $^{187}Os/^{188}Os$ is positively correlated with elemental ratios characteristic of slab derived fluids (e.g. Ba/Zr, Sr/Ta), thus apparently consistent with addition of a slab-derived fluid containing radiogenic Os to the overlying mantle wedge. In addition, the negative correlation between the $^{187}Os/^{188}Os$ and some incompatible elements (e.g. Ta) appears to be inconsistent with upper crustal assimilation, and may reflect variable degrees of partial melting of a mantle source, in which greater fluid addition to the mantle wedge results in more radiogenic Os and higher degrees of melting.

[1] Chesley *et al*. (2002) *Earth Planet Sci. Lett*. **195,** 211–221. [2] Saha *et al*. (2005*) Earth Planet Sci. Lett*. **236,** 182-194. [3] Lassiter & Luhr (2001) G3 2, 1525-2027.

Insights into anaerobic respiration from the genome of the selenate respiring bacterium *"Desulfurispirillum indicum"* strain S5

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Background

The bioreduction of dissolved selenate and selenite oxyanions to sparingly soluble elemental selenium is one of the primary processes by which selenium can be detoxified in contaminanted environments. In order to employ Se-reducing bacteria for *in situ* bioremediation purposes, reliable models must be developed to predict microbial behavior, including when they are active, what mechanisms are involved, and under what conditions the mechanisms function. '*Desulfurispirillum indicum*' strain S5, a novel species belonging to the family of *Chrysiogenes,* is capable of respiring selenate, selenite, arsenate, and nitrate. The annotation of its whole genome sequence enabled us to identify and characterize the reductases and molybdoenzymes involved in selenate, arsenate, and nitrate respiration.

Methods

To process the genome sequence information of '*Desulfurispirillum indicum*' and make possible predictions about the function of genes, the JGI databases (IMG) and various other tools, such as BLAST and Artemis were used. The genome data analysis was set in the comparative context of multiple microbial genomes to identify homologous genes, open reading frames and proteins.

Results and Discussion

Genome analysis uncovered 17 sequences carrying the signatures of molybdoenzymes. Two of the molybdoenzyme sequences were found to cluster with the respiratory arsenate reductase Arr, the alpha subunit of the membrane-bound nitrate reductase NarG, and the periplasmic nitrate reductase subunit NapA, respectively. Further analysis of the genome context revealed the presence of additional sequences encoding operons of each enzyme, and a gene organization resembling typical *arr, nar*, and *nap* operons. Homologs of YnfE and YnfG, known to be involved in selenate reduction in *Escherichia coli* and *Salmonella*, were also identified in the S5 genome. The results of this genomic analysis provide a springboard for further investigations into metabolic pathways for energy production in contaminated environments, and how these pathways are regulated depending on the availability of oxyanions.