

Isotopic variations in mafic volcanic rocks from the western branch of the East African Rift

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Isotopic variations in lavas from regions of low tectonic extension, such as the western branch of the East African Rift (EAR), can be used to probe regional variability in the underlying continental lithospheric mantle. Volcanic rocks from the western branch of the EAR are isotopically among the most extreme young samples on Earth. Pb, Hf, Nd and Sr isotope compositions for mafic, undersaturated alkalic lavas from Rungwe, Kivu, Virunga and Toro-Ankole all show large variations over short lateral distances, indicating extensive isotopic heterogeneity in the continental lithospheric mantle source for these lavas, mostly due to ancient metasomatism associated with African orogenic events. Trends in the isotopic data show a convergence near values of $^{206}\text{Pb}/^{204}\text{Pb}=18.9\text{-}19.2$, $^{207}\text{Pb}/^{204}\text{Pb}=15.63\text{-}15.67$, $^{208}\text{Pb}/^{204}\text{Pb}=39.3\text{-}39.7$, $\epsilon_{\text{Nd}}=0$, $\epsilon_{\text{Hf}}=3$ and $^{87}\text{Sr}/^{86}\text{Sr}=0.705$. The isotopic variation within each volcanic province extends away from these values to distinct compositions. In contrast, $^3\text{He}/^4\text{He}$ within each province shows a restricted range; 7.5-9.0, 5.0-6.5, 6.7-7.5 and 5.6-6.8 R_A for Rungwe, Kivu, Virunga and Toro-Ankole, respectively. There is no evidence for the presence of high $^3\text{He}/^4\text{He}$ plume material such as that beneath the Ethiopian Rift and Afar. The convergence of the Pb-Hf-Nd-Sr isotopes suggests that primary magma is derived from a common mantle source beneath the western branch of the EAR, such as the lithosphere/asthenosphere boundary. In contrast, the distinct isotopic variations within each volcanic region represent the shallower, provincial characteristics of the underlying lithosphere and crust.

Electron shuttle production by *Shewanella oneidensis*

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Extracellular Respiration

Many dissimilatory metal reducing bacteria have evolved mechanisms to transfer electrons from the cytoplasmic membrane quinone pool to insoluble substrates (e.g. oxide minerals and electrodes) located beyond their outer membranes [1, 2]. *Shewanella oneidensis* strain MR-1 is the best understood model system for extracellular respiration. While biochemical evidence supports a direct mechanism for electron transfer to insoluble substrates, there is also strong physiological evidence for electron shuttling [3, 4]. Flavins (riboflavin and flavin mononucleotide (FMN)) were identified as the primary electron shuttle compounds produced by *Shewanella*. Our work seeks to define the contribution of electron shuttles to the reduction of insoluble substrates by *S. oneidensis* and understand the molecular mechanism underlying the production and processing of flavin shuttles produced by these bacteria.

Discussion of Results

We designed a mutagenesis screen in *S. oneidensis* to isolate strains that no longer accumulated flavins in culture supernatants. This work led to the identification of UshA, a 5'-nucleotidase involved in the processing of periplasmic flavin adenine dinucleotide (FAD) to FMN and adenosine monophosphate [5]. Strains defective in *ushA* accumulated FAD in culture supernatants instead of FMN or riboflavin. We repeated our mutagenesis screen in an *ushA* deletion mutant background to identify additional components involved in electron shuttle processing and secretion. This secondary screen identified mutants defective in flavin export and in regulation of flavin secretion. Here, we present the characterization of the two new components related to electron shuttle export by *S. oneidensis*. We have generated the first strain of *S. oneidensis* that is fully defective in electron shuttle secretion, allowing us to conclude that electron shuttling accounts for ~75% of the electron transfer activity to insoluble substrates. Moreover, electron shuttling mutants have no defect in respiration of soluble organic electron acceptors or chelated iron.

- [1] Lovley *et al.* (2004) *Adv Microb Physiol* **49**, 219-86.
[2] Shi *et al.* (2007) *Mol Microbiol* **65**, 12-20. [3] Marsili *et al.* (2008) *PNAS* **105**, 3968-73. [4] von Canstein *et al.* (2008) *Appl Environ Microbiol* **74**, 615-23. [5] Covington *et al.* (2010) *Mol Microbiol* **78**, 519-32.