Methylmercury production by Desulfovibrio desulfuricans ND132: Influences of natural organic matter and growth stage

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Mercury (Hg) is a widely distributed pollutant that can be methylated by sulfate-reducing bacteria (SRB) in sedimentary environments to form the neurotoxin methylmercury (MeHg) that can bioaccumulate up aquatic foodwebs. Studies of MeHg production have indicated that total Hg is not directly correlated to total MeHg in many aquatic systems [1], which has stimulated interest in variables controlling Hg uptake by bacterial cells (eg. Hg speciation [2, 3]) and controls on bacterial metabolic processes that could affect rates of Hg methylation. Natural organic matter (NOM) is a ubiquitous environmental variable that can strongly complex with Hg in natural systems and whose effect on Hg methylation has been understudied.

Cultures of the known methylating SRB Desulfovibrio desulfuricans ND-132 were grown under respirative conditions (sulfate-free media with pyruvate and fumarate added) and spiked with inorganic Hg or Hg pre-equilibrated with Suwanee River (SR-)NOM. Sacrificial samples collected at mid-log, late-log, and late stationary phases were sampled for MeHg, filter-passing $(0.2 \mu m)$ and filter-retained total Hg, organic acids, and cell enumeration. Methylmercury produced by ND132, expressed as picograms MeHg per 10⁶ cells (pg/Mcell), was not influenced by the presence of SRNOM at any sampling time, though ND132 did grow faster in the presence of SRNOM. MeHg increased from 0.058 pg/Mcell at mid-log phase to 0.09 pg/Mcell at late stationary phase. The addition of Hg or Hg-SRNOM to a late stationary phase culture (~98% of the pyruvate and fumarate had been consumed) produced a 4X increase in MeHg production (0.35 pg/Mcell, equivalent to 70% methylation; samples collected 48 hours after Hg addition) and suggests that ND132 in this stressed condition may be a more active methylator. Results offer a first step toward a better understanding of controls on MeHg production under natural environmental conditions.

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Subsolidus cooling effects on the trace element systematics of mantle peridotite pyroxenes

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The trace element systematics of peridotitic clinopyroxenes place important constrains on the mechanisms of melt extraction in the upper mantle. Peridotites sampled at the surface, however, go through subsolidus cooling that redistributes elements within the peridotite mineralogy. Opx/cpx concentration ratios (Dopx/cpx) for many lithophile elements (e.g. REE, HFSE) in fresh Hawaiian spinel peridotites and other samples from the literature are lower than experimentally determined (solidus) Dopx/cpx ratios and vary systematically with equilibration T, or the Ca-Mg exchange between cpx-opx.

Here we present a melting model that incorporates temperature dependent subsolidus cooling. Melting rate, melt reactions and mineral phase major element compositions of a depleted mantle source are calculated with the pMELTS algorithm. Trace elements are modelled by an incremental melting model with Ds varying as a function of pressure. We model subsolidus cooling by redistributing Ca and Mg between opx - cpx from their model solidus compositions to the measured compositions in the natural samples while changing the opx-cpx modal abundance accordingly (i.e. exsolution). Trace elements are then redistributed in the new residual mineralogy based on apparent (subsolidus) Dopx/cpx determined from Hawaiian peridotites and from the literature. This model results in higher concentrations (x10-1000) in residual peridotite cpx for the highly incompatible elements (e.g. Zr, Nd, Ce) at high degrees (>10%) of melting than conventional models.

The incorporation of subsolidus cooling in the modelling of clinopyroxene trace element compositions in mantle peridotites relaxes the requirements for metasomatism or meltinfiltration in the mantle and can explain some abyssal and Hawaiian peridotite clinopyroxene compositions previously thought of metasomatic origin.