The "cool tropic paradox": Reassessing aberrant $\delta^{18}O$ in foraminifera by SIMS

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Cool tropical sea surface temperatures (SSTs) are reported based on planktonic foraminiferal tests from warm Paleogene and Cretaceous greenhouse climates. This "cool tropic paradox" is difficult to reconcile with greenhouse-gas-forced climate models; hence it has been proposed to result from postdepositional alteration of foraminiferal calcite that secondarily increases the $\delta^{18}O$ signal. However, the degree of diagenetic alteration can be difficult to assess as recrystallization may occur on a sub-micrometer scale without obliterating internal test structures. Consequently, new analytical approaches are required to test the cool tropic paradox and extract a reliable temperature signal from potentially altered foraminiferal tests.

We applied Secondary Ion Mass Spectrometry (SIMS) to determine the $\delta^{18}O$ in tests of the tropical planktonic foraminiferal species *Morozovella velascoensis, M. allisonensis* and *M. aragonensis* from a deep-sea section (ODP Site 865, central Pacific) spanning the Paleocene-Eocene boundary. Scanning electron microscope (SEM) images of chamber wall crossections revealed that the muricae, calcareous outgrowths from the chamber walls, are nonporous and therefore less susceptible to postdepositional alteration. Consequently, SIMS analysis was performed on the muricae of numerous morozovellid tests using ~15 μm pits with an average precision of 0.41‰ (2 SD). The identical appearance of ion microprobe pits in muricae and calcite standard indicates that the muricae are crystalline.

We found that the $\delta^{18}O$ of muricae varies from -2.6 to -4.4‰ [PDB] (n = 73). Averaged $\delta^{18}O$ values of muricae are consistently 1.1 to 2.2‰ lower than published $\delta^{18}O$ values derived from conventional analyses of pooled, multi-specimen samples from the same core depth. The $\delta^{18}O$ values of muricae, as determined by SIMS, are similar to published $\delta^{18}O$ values for "glassy" unaltered planktonic foraminiferal tests from impermeable clay-rich sediments [Pearson *et al*. 2007 *Geology*], implying that Early Paleogene tropical SSTs in the central Pacific were higher than indicated by previously published $\delta^{18}O$ records.

Comparative genome analysis of *M. yellowstoni*: Diversity of O_2 reductases and evolution scenarios for acidophilic Fe oxidation

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A draft genome has been assembled for the novel iron oxidizing *M. yellowstoni* isolated from a geothermal spring in Yellowstone National Park. This study compares the putative genes involved in Fe^{2+} oxidation and O_2 reduction between *M. yellowstoni* and Fe^{2+} oxidizing prokaryotes with genomes available including *S. tokodaii*, *A. ferrooxidans*, *F. acidimarnus* and *L. ferrooxidans* Group II. This study also compares the diversity of all known iron oxidizing acidophilic prokaryotes along with possible scenarios for the evolution of Fe^{2+} oxidation based on 16S rRNA phylogenetic analysis (Fig 1) and the link between blue copper proteins and heme copper oxidases (HCOs).

M. yellowstoni contains homologous genes to *M. sedula* and *S. tokodaii* in regards to Fe oxidation including a novel *fox* HCO gene cluster, a multicopper oxidase (*mco*), and $cytb_{558/566}$ which differ from the proteins discussed in the putative Fe^{2+} oxidation pathways of *A. ferrooxidans*, *F. acidimarnus* and *L. ferrooxidans* [1, 2, 3]. Blue copper proteins appear to be important in most Fe^{2+} oxiding prokaryotes along with HCOs and surprisingly, the Sulfolobales contain the vast (Fig 2) majority of HCOs among aerobic organisms with seven copies found in the draft genome.

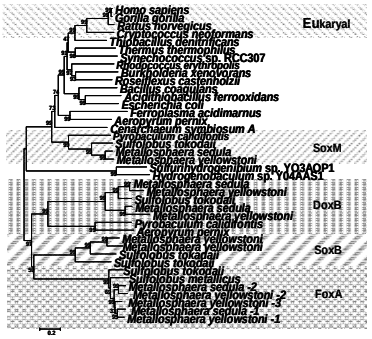

Figure 1. 16S rRNA phylogenetic tree of known acidophilic Fe^{2+} oxidizing prokaryotes (Highlighted; * genomes available)

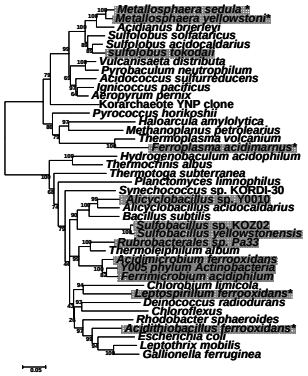

Figure 2. Protein tree of HCO subunit I.

[1] Dopson (2005) *Microbiology* **151,** 4127–4137. [2] Rawlings (2005) *Microbial Cell Factories*. **4**,13. [3] Singer *et al.* (2008) *Appl Environ Microbiol*. **74**, 4454-62.