Mechanisms underlying control of sulfur isotope fractionation during sulfate reduction

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We have previously examined [1] the concentration dependence of sulfur isotope fractionation in sulfate reducing bacteria. Using continuous culture devices we grew two strains under constant growth rates, varying sulfate concentration from 0.1 to 10 mM. Each relationship can be fit with a Monod curve, but the fitted constants differ markedly between strains. In related work [2] we held sulfate concentrations constant and examined the relationship between sulfur isotope fractionation and sulfate reduction over a wide range of rates – the resulting relationship is a hyperbolic fit between rate and fractionation.

Recent work [3] has provided a framework for understanding controls on these fractionations. We have combined our results in a model framework in which we represent the magnitude of sulfur isotope fractionation as a function of two parameters. These are the rates of electron donor supply and sulfate supply to the cellular machinery responsible for transformation of sulfate to sulphide. Fitting parameters account for strain specific factors, such as sulfate and electron donor affinity constant.

These results are best understood by casting them into an enzymatic reaction network in which fluxes and fractionations may be imposed at any given step. In combination with recent work aimed at uncovering enzyme-specific sulfur isotope fractionations, this work moves us towards an understanding of the biological underpinnings of sulfur isotope fractionation, and the genetic variations that may impose phenotypic differences between strains. We consider the effects of selective pressure on the evolution of sulfate and electron acquisition machinery over the course of evolutionary and Earth history. These results will aid efforts to reconstruct ambient sulfate concentrations from sedimentary sulfur isotopic compositions.

[1] Bradley, Leavitt, Schmidt, Knoll, Girguis & Johnston (2015) *Geobiology* in revision. [2] Leavitt, Halevy, Bradley & Johnston (2013) *PNAS* **110**, 11244-11249 [3] Wing & Halevy (2014) *PNAS* **111**, 18116-18125