Fractionation of H and S isotopes in sulphate reducing bacteria with perturbed central energy metabolism

WILLIAM D. LEAVITT* AND ALEXANDER S. BRADLEY

Department of Earth and Planetary Sciences, Washington University in St. Louis, Saint Louis, MO 63130 USA (*wleavitt@eps.wustl.edu)

Bacterial sulphate reducers (BSRs) produce lipids that are strongly depleted in deuterium relative to growth water ($^{2}\varepsilon_{lipid\text{-}H2O}$ ~ -250‰) [1], along with sulphide that is depleted in ^{34}S relative to provided sulphate. The magnitude of hydrogen isotope fractionation may relate to central energy metabolism [2], while sulphur isotope fractionation ($^{34}\varepsilon_{SO4\text{-}H2S}$) scales inversely with sulphate reduction rate over a range of 70‰ [3-5]. Given that both isotope systems may relate to cellular energy conservation, we investigate metabolic conditions that may be recorded by both systems.

An important aspect of energy metabolism in some sulphate reducing bacteria is the activity of electron-bifurcating transhydrognase [6]. Recent work in aerobic methylotrophs [7] implicates transhydrogenase (TH) activity as a critical control on $^{2}\varepsilon_{lipid\text{-}H2O}$. We grew mutant strains of *Desulfovibrio alaskensis* strain G20 deficient in the locus *nfn*AB-2 encoding one of two copies of electron-bifurcating transhydrogenase [8]. These strains produce lipids with perturbed hydrogen isotopic fractionations between media water and lipid. Due to perturbed central energy metabolism, we predict altered $^{34}\varepsilon_{SO4\text{-}H2S}$ as well.

We discuss implications for understanding H-isotope fractionation during microbial fatty acid biosynthesis in BSRs and anaerobes in general, and joint sulfur and hydrogen isotopes as tracers of microbial metabolism in anoxic environments.

[1] Osburn (2013) *Dissertation (PhD)*. CalTech.
[2] Zhang et al. (2009) *PNAS* 106, 12580–86.
[3] Chambers & Trudinger (1975) *Can. J. Microbio*. 1602-07.
[4] Sim et al. (2011) *Science* 333, 74-77
[5] Leavitt et al. (2013) *PNAS* 110, 11244–49
[6] Price et al. (2014) *Frontiers in Microbiology*, 5, 1-20.
[7] Bradley et al. (2014). *AGU Fall Meeting*.
[8] Kuehl *et al*. (2014). *mBio* 5, 1-13.