Targeted drilling for Re-Os geochronology to decipher complex history of overmature source rocks and migrated hydrocarbons

G. YANG[1], H. STEIN[1,2], J. HANNAH[1,2] AND A. ZIMMERMAN[1]

[1]AIRIE Program, Colorado State University, Fort Collins, CO 80523 USA (*correspondence: gangyang@colostate.edu)
[2]Geological Survey of Norway, 7491 Trondheim, Norway

Successful Re-Os geochronology depends on acquisition of samples with identical age and initial $^{187}Os/^{188}Os$ (Os_i), *but* varied Re/Os concentration ratios. Black shales and migrated hydrocarbons present unique challenges. Sampling strategy must be grounded in knowledge of the local sedimentology and maturation history, as these factors contribute to small-scale heterogeneity.

Two sampling strategies were employed for Re-Os geochronology using core from ICDP FAR-DEEP drillhole 13A, intersecting the ca. 2 Ga Zaonezhskaya Formation black siltstones near Shunga village in the Onega Basin, Russian Fennoscandia [1, 2]. First, six 7-9 g samples were taken from discrete segments spanning 5 m of drill core; each sample was pulverized and homogenized to minimize any Os_i heterogeneity. These samples yield an errorchron of 1852 ± 300 Ma (Os_i = 1.5 ± 2.0, MSWD = 40). Scatter is likely caused by migration of hydrocarbons in the section. Vitreous 'shungite', up to 70% carbon, is visible under a binocular microscope. These *large* 7-9 g samples contain both primary organic matter and locally migrated hydrocarbons, and thus are heterogeneous mixtures with variable Os_i and age.

Second, using the binocular scope, eight much *smaller* 450-500 mg samples were taken from drillhole 13A by targeted drilling of homogeneous black C-rich siltstone within a 3-cm section. These samples yield a Model 3 isochron age of ~1730 Ma with an Os_i of 5. Four additional samples from a new 3-cm section (0.5 m up section) improve the isochron statistics without a change in the nominal age or Os_i. We interpret this as the age of isotopic homogenization (maturation?) for the fossil hydrocarbons. This age is consistent with younger phases of the Svecofennian orogeny [3], known to have impacted the siltstones.

This is but one of many localities yielding meaningful ages by targeted drilling of heterogeneous shale-hydrocarbon sequences. Small samples (500 mg) can yield big results.

Supported by ICDP FAR-DEEP Project (Melezhik *et al.*) and NSF award EAR-0820848 to J. Hannah and H. Stein.

[1] Melezhik *et al.* (2009) *Terra Nova* **21**, 119–126. [2] Hannah *et al.* (2008) *33rd IGC*, Oslo, **#1352701**. [3] Stein (2006) *Lithos* **87**, 300–327.

Using hydrogen isotopes to assess proton flux during biological hydrogen production: Part 1

H. YANG[1], H.W. KREUZER[2]*, L. SHI[2], N.E. OSTROM[3], H. GANDHI[3] AND E.L. HEGG[1]*

[1]Department of Biochemistry & Molecular Biology, Michigan State Univ., East Lansing, MI 48824 (*correspondence: EricHegg@msu.edu)
[2]Chemical and Biological Sciences, Pacific Northwest National Laboratory, Richland, WA 99352 (*correspondence: Helen.Kreuzer@pnl.gov)
[3]Department of Zoology, Michigan State University, East Lansing, MI 48824 (Ostromn@msu.edu)

Biological hydrogen production is mainly mediated by hydrogenase (H_2ase) enzymes, which combine protons from water with electrons to generate H_2. One major impediment to improving our understanding of H_2 metabolism is our inability to define adequately the regulation of and the flux through key pathways involved in H_2 production. To fill this need, we are developing the use of hydrogen isotopes as a tool to address fundamental questions related to hydrogenases and intracellular proton trafficking.

In the first phase of the project, we have overexpressed and purified a number of different H_2ases under anaerobic conditions, quantified the specific activity of the purified H_2ases, and constructed a custom-built GC-IRMS system to measure the isotope ratio of the collected H_2 with good precision (error ≤ 3‰) and sensitivity (0.2 μM in 1 mL headspace). As predicted, isotopic analysis of the H_2 generated by 7 different enzymes (including one nitrogenase) revealed that each H_2ase has a unique fractionation factor and produces H_2 with a distinct isotopic signature. In addition, our research will provide the first fractionation factors for these classes of enzymes.

In a second phase of the project, we are also performing *in vivo* experiments (see accompanying poster). Preliminary results indicate that the isotopic content of H_2 produced *in vitro* is remarkably similar to that measured *in vivo*. Together our results provide compelling evidence that hydrogen isotopes can be used to study biological H_2 production.