

## Assessing microbial metabolisms *in-situ*: Insights from carbon isotopic analyses at the molecular level

A. PEARSON

Dept. of Earth and Planetary Sciences, Harvard University,  
Cambridge, MA 02138 USA (pearson@eps.harvard.edu)

The sediment-water interface underlying productive water columns represents a rich environment for microorganisms. The flux of organic carbon and nutrients from overlying waters results in dense populations of bacteria and archaea, frequently observed as mats dominated visually by filamentous sulfur bacteria. Compositional data for lipids indicate that the organic material at these interfaces is composed of living and detrital remains of bacteria, archaea, phytoplankton, and other eukaryotes; and using molecular biological methods, including sequencing of nucleic acids and fluorescent imaging, many investigators have documented the presence of diverse communities. The phylogenetic data indicate that despite similarities in environmental setting, the populations at different locations are not the same; conversely, superficially similar populations can be seen at locations that actually are quite dissimilar in carbon source and flux. These observations suggest that geochemical environments exert strong pressure on microbial populations, and that differences in geochemistry between sites may be reflected in the response of the local microbial metabolisms.

One example is the contrast between the bacterial mat communities of the Guaymas Basin hydrothermal field and the Santa Barbara Basin. In both locations, samples harvested from the organic carbon-rich surface sediments have visible communities of filamentous sulfur bacteria. Compound-specific radiocarbon data indicate that in the Santa Barbara Basin, the primary source of carbon is heterotrophic consumption of fresh detrital carbon from the overlying water column. In contrast, in the Guaymas Basin, radiocarbon data show that most of the carbon must be coming from the sediments below, probably as a result of hydrothermal processes. An unanswered question, therefore, is the extent to which individual species are flexible with regard to preference for carbon substrates; or whether different species are optimized to dominate the total community production in these environments. Such questions are difficult to answer using methods based on the carbon isotopic analysis of lipids, as many bacterial groups do not contain specific molecular markers. New approaches such as stable isotope probing (SIP) or nucleic acid capture (NAC) may soon provide more insight.

## Population dynamics in acid mine drainage biofilms from the Richmond Mine at Iron Mountain, California

RACHEL WHITAKER, ERIC ALLEN, GENE TYSON AND  
JILLIAN BANFIELD

(rwhitaker@nature.berkeley.edu, eallen@nature.berkeley.edu,  
gtyson@nature.berkeley.edu, jill@seismo.berkeley.edu)

The dissolution of predominantly pyrite ( $\text{FeS}_2$ ) results in the formation of highly acidic ( $\text{pH} < 0.9$ ), metal-rich, toxic solutions referred to as acid mine drainage (AMD). In this drainage, communities of chemolithotrophic microorganisms grow as biofilms sustained solely by the oxidation of iron and sulfur. We are interested in how changes in geochemical conditions shape diversity in microbial communities with the ultimate goal of developing models that link geologic and evolutionary events on absolute times scales. To characterize population dynamics over time and space we use comparative genomics among DNA samples extracted from biofilms from different regions of the Richmond Mine at Iron Mountain, CA, over seasons and years, and across naturally occurring temperature gradients. The first community genome sequence of an AMD biofilm, revealed significant within-species strain variation in three closely related, recombining species of Archaea. For example, at least two distinct allele variants were uncovered for the majority of variable loci within the *Ferroplasma* type I strain populations. Using this variation as markers we test for fine scale changes in diversity within the *Ferroplasma* type I population to determine the population structure and relative genetic diversity within this species among biofilm samples. In addition we use molecular signals to test for evidence of natural selection among strain variants of *Ferroplasma* type I and between *Ferroplasma* and the other Archaeal species found within the AMD biofilm. Determining the effects of natural selection, recombination on population structure over time and space is essential to understanding the intimate link between microbial communities and their geochemical environments.