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Denitrification in Great Basin hot springs

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Hydrogen has been proposed to fuel primary production in the *Aquificae*-dominated hot springs of Yellowstone National Park (Spear, et al. 2005), a finding the authors generalized to all hot springs. However, clone libraries derived from Great Basin springs contain few 16S ribosomal RNA (rRNA) gene sequences from *Aquificae* and many from unknown microorganisms. In the same springs, alternative electron donors rival the reducing power of hydrogen. This project will try to cultivate the uncharacterized microbes of two Great Basin springs and determine which electron donors they can use.

Nitrogen is key to life. In its reduced form, ammonia, it is a primary constituent of nucleic acids and proteins. In its oxidized form, nitrate, it frequently substitutes for oxygen in anoxic conditions as microbes' preferred electron acceptor for respiration. In this capacity, it drives energy capture—typically, though not always, in the process of denitrification [8]. Understanding the supply, demand, and interconversion of nitrogen through an ecosystem is essential to understanding the life within it. Although denitrification has been predicted to occur within hot springs on thermodynamic grounds, and some thermophilic isolates reduce nitrate, denitrification has never been examined in a hot spring. The hot springs of the Great Basin are under studied reservoirs of novel metabolisms and microbes, and are well worth in-depth exploration. Our project adapts techniques regularly used in marine and soil microbiology [6,7,9] to higher temperatures to test our hypothesis: that some thermophiles within the hot springs respire nitrate, in the process of denitrification, for a significant amount of energy capture.

