

Expanding the known diversity of methanogenic microorganisms: Mcr- based methane production in *Archaeoglobaceae*

STEFFEN BUESSECKER¹, GRAYSON L. CHADWICK²,
MELANIE E. QUAN¹, BRIAN P. HEDLUND³, JEREMY A.
DODSWORTH⁴ AND ANNE E. DEKAS¹

¹Stanford University

²University of California, Berkeley

³University of Nevada Las Vegas

⁴California State University, San Bernardino

Presenting Author: dekas@stanford.edu

Methane is a potent greenhouse and also a substrate and product of microbial metabolism. Understanding its cycling is therefore of great interest to climatologists and geomicrobiologists alike, yet recent studies have indicated that the diversity of microbes capable of processing methane may be sorely underestimated. Biological methane is currently known to be produced nearly exclusively by anaerobic archaea via a pathway dependent on methyl-coenzyme M reductase (Mcr) and constrained to the well-studied and well-distributed Euryarchaeota. However, metagenomic data have revealed an abundance of divergent *mcr* sequences in the environment, undetected by previous PCR-based surveys, and found within metagenome assembled genomes (MAGs) from diverse archaea including the *Archaeoglobales*, *Korarchaeota*, *Nezhaarchaeota*, and *Verstraetearchaeota*. Whether these sequences are functional in methane production has remained unknown. Here, we detect one such divergent *mcr* sequence within a methane-producing enrichment culture from Great Boiling Springs, Nevada. A combination of metagenomics and manipulation experiments indicates that a novel lineage of the family *Archaeoglobaceae* within the enrichment, here designated *Methanoproducendum nevadense*, is capable of methane production using this diverged Mcr. This finding expands the known diversity of methanogenic microorganisms and suggests that other lineages containing closely related non-canonical *mcr* sequences may also be functional in methane production.