

Archaeal Metabolic Profiles at Deep-Sea Hydrothermal Vents in the Mid-Cayman Rise

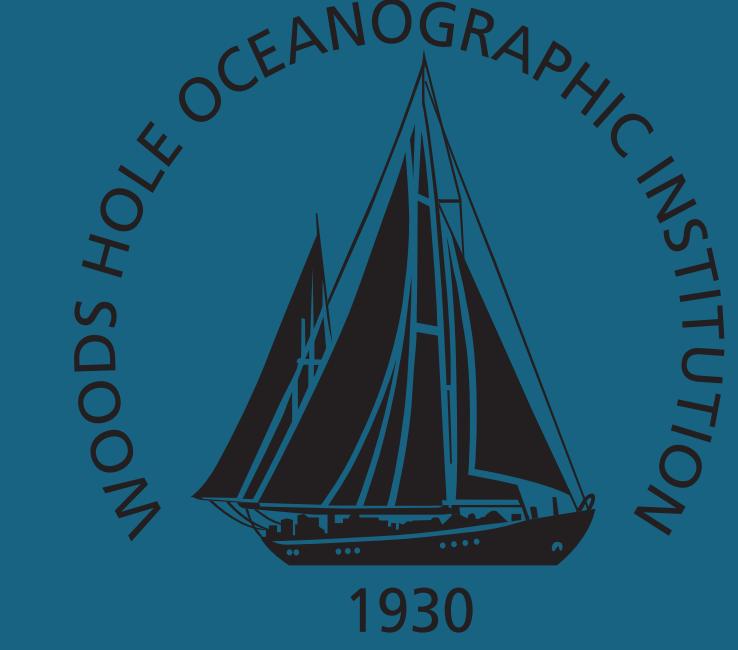


David Galambos¹, Julie Reveillaud², Rika E. Anderson¹, and Julie A. Huber³

¹Department of Biology, Carleton College, Northfield, MN

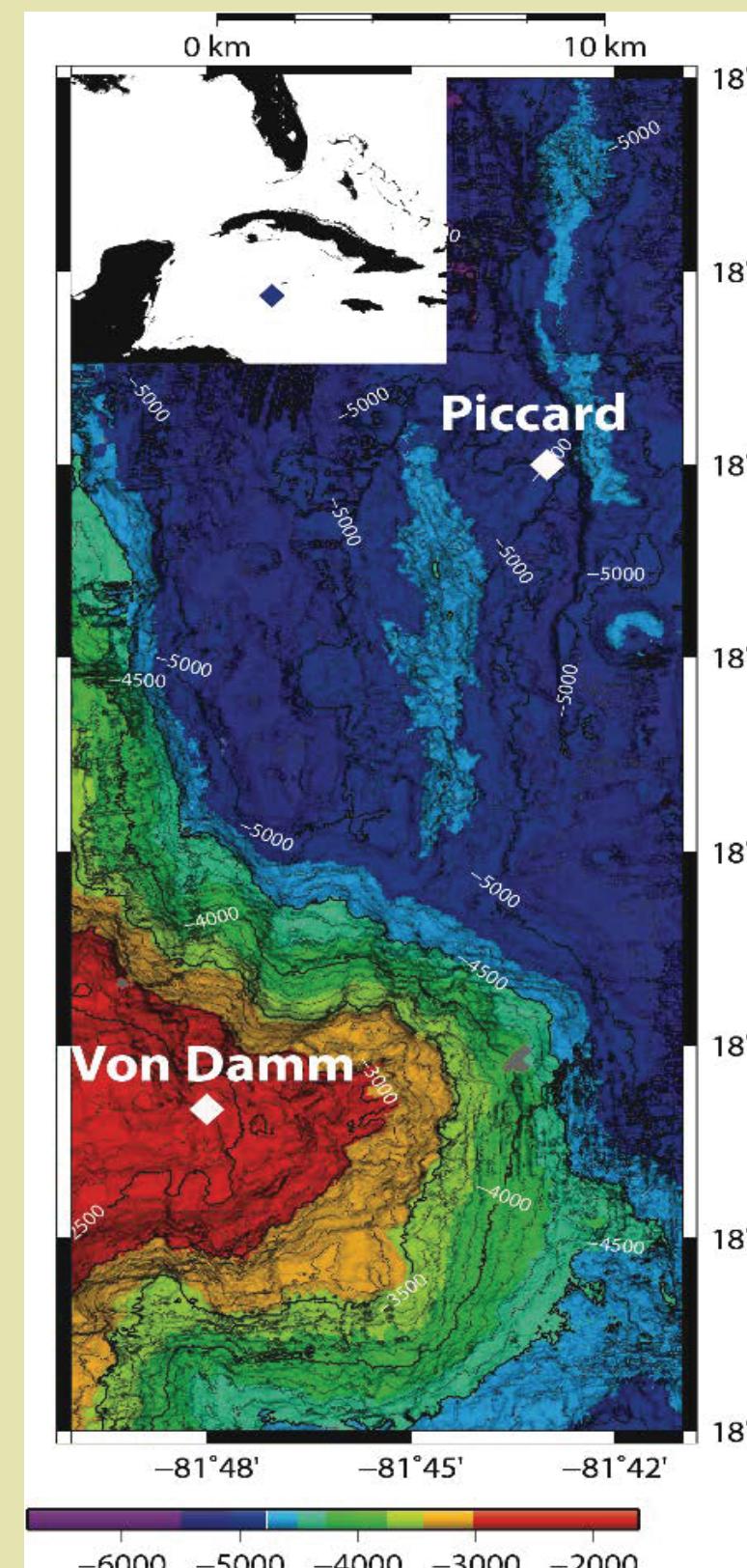
²Institut National de la Recherche Agronomique, Montpellier, France

³Department of Marine Chemistry and Geochemistry, Woods Hole Oceanographic Institution, Woods Hole, MA



Motivating Questions

- What kinds of metabolic genes are found in the Mid-Cayman Rise vent fields?
- Which genes are most highly expressed at the community level?
- Which taxonomic groups have the highest rates of overall gene expression?
- What is the metabolic potential of each taxonomic group?



Introduction

Deep-sea hydrothermal vent systems host a wide diversity of bacteria, archaea and viruses. Although the geochemical conditions at these vents are well-documented, the relative metabolic activity of microbial lineages, especially among archaea, remains poorly characterized. The deep, slow-spreading Mid-Cayman Rise, which hosts the mafic-influenced Picard and ultramafic-influenced Von Damm vent fields, allows for the comparison of vent sites with different geochemical characteristics. Previous metagenomic work (Reveillaud et al., 2016) indicates that despite the distinct geochemistry at Von Damm and Picard, the overall functional profile of microbial communities between the two sites is similar.

Methods

Sequencing of metagenomes and metatranscriptomes was conducted on an Illumina Hi Seq 1000. Reads were assembled with IDBA (Peng et al., 2010). Mapping was done with Bowtie2 (Langmead and Salzberg, 2012). We used anvi'o v2.3.2 (Eren et al., 2015) for supervised binning of the metagenome-assembled genomes (MAGs) based on coverage and tetranucleotide frequency. We also used anvi'o v2.3.2 for the pangenomic analysis. Figures were generated using matplotlib (Hunter, 2007) and seaborn.

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- Key metabolic gene expression similar between

Von Damm and Picard

- Von Damm: Higher evenness of gene expression
- Methanogenesis gene (*mcr*) highly active compared to other metabolic groups
- Key methane oxidation gene (*pmoA*) not expressed at any sites

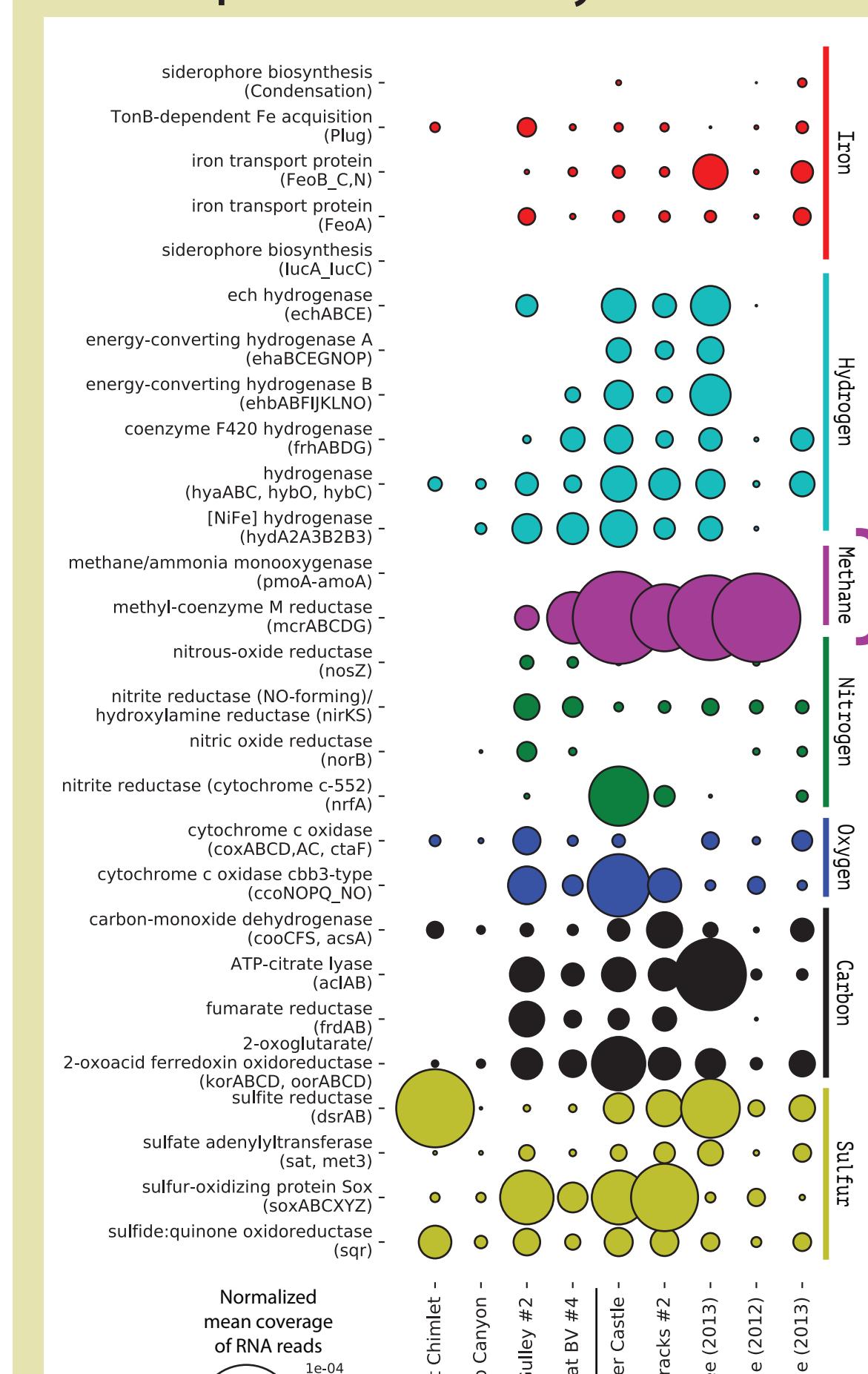


Fig. 1. RNA expression of key metabolic genes

Results

Tree indicates clustering of MAGs based on presence/absence pattern

- Methanomicrobia: FULL acetate => methane, partial CO₂ => methane
- Methanococci: partial CO₂ => methane, partial acetate => methane
- Archaeoglobi: partial CO₂ => methane, partial acetate => methane
- Clostridia (Bacteria): partial trimethylamine => methane

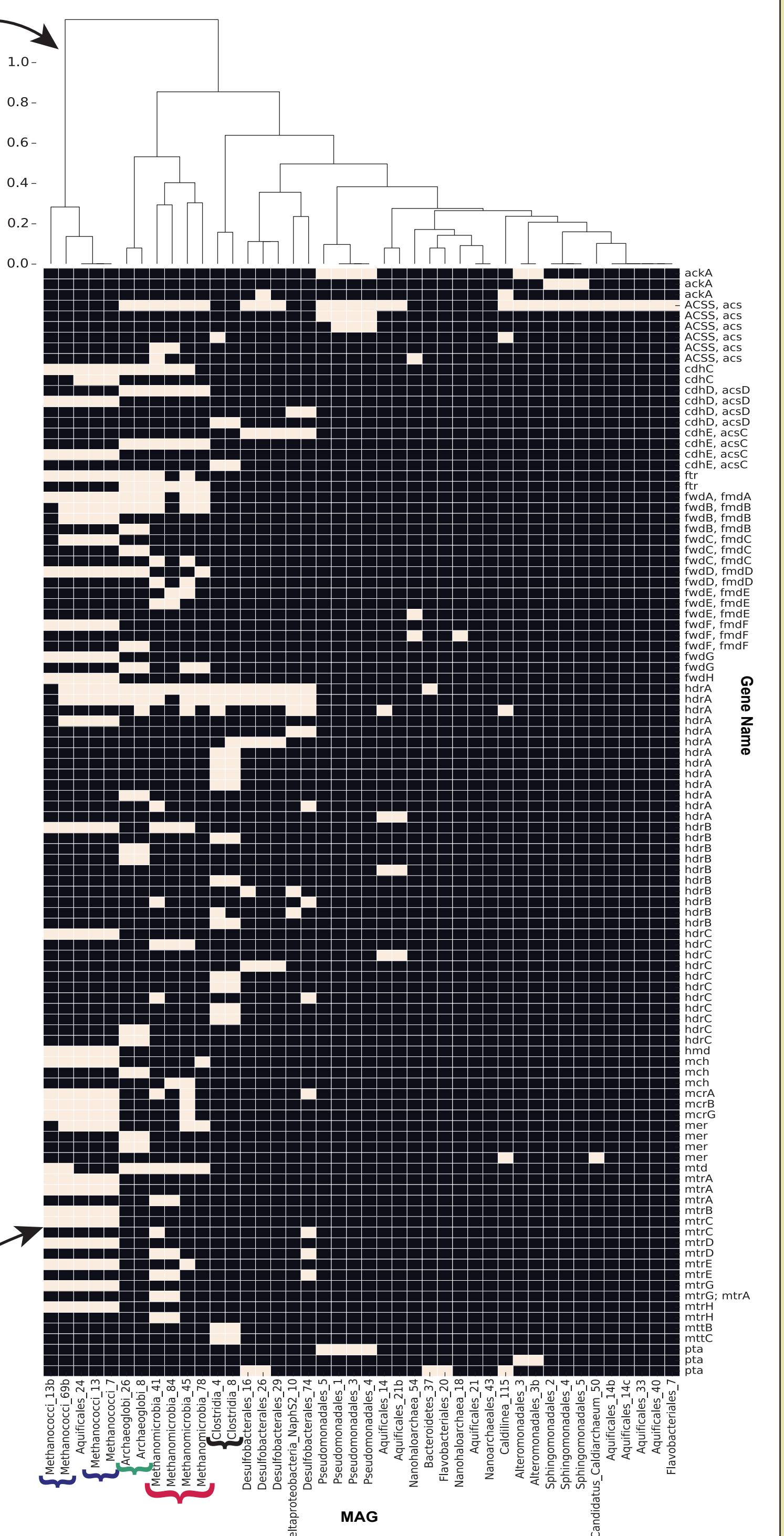


Fig. 2. RNA expression of archaeological MAGs

- Methanomicrobia: Only active at Shrimp Hole site
- Methanococci: active at all other sites

Beige square indicates gene PRESENT in MAG

Fig. 3. Presence/absence of key methane genes in selected MAGs

Conclusions

- No obvious correlations between vent geochemistry and community-level expression of metabolic genes in the Mid-Cayman Rise
- Genes for methane oxidation and sulfur redox most highly expressed
- Previously identified methanogens Methanococci and Methanomicrobia (Evans et al., 2015) control last step of methanogenesis (*mcr* gene)
- Despite having similar methane metabolism profiles, Methanococci & Methanomicrobia show different expression levels at Shrimp Hole
- In terms of metabolic potential, Archaeoglobi, Methanomicrobia and Methanococci are methane generalists rather than specialists

References

- Altschul, S.F., Gish, W., Miller, W., Myers, E.W., and Lipman, D.J. (1990). Basic Local Alignment Search Tool. *J Mol Biol* 215, 403-410.
 Anantharaman, K., Breier, J.A., Sheik, C.S., and Dick, G.J. (2013). Evidence for hydrogen oxidation and metabolic plasticity in widespread deep-sea sulfur-oxidizing bacteria. *P Natl Acad Sci USA* 110, 330-335.
 Anantharaman, K., Brown, C.T., Hug, L.A., Sharon, I., Castelle, C.J., Probst, A.J., Thomas, B.C., Singh, A., Wilkins, M.J., Karaoz, U., et al. (2016). Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. *Nat Commun*.
 Enright, A.J., Van Dongen, S., and Ouzounis, C.A. (2002). An efficient algorithm for large-scale detection of protein families. *Nucleic Acids Res* 30, 1575-1584.
 Eren, A.M., Esen, O.C., Quince, C., Vineis, J.H., Morrison, H.G., Sogin, M.L., and Delmont, T.O. (2015). Anvi'o: an advanced analysis and visualization platform for 'omics' data. *PeerJ* 3, e1319.
 Evans, P.N., Parks, D.H., Chadwick, G.L., Robbins, S.J., Orphan, V.J., Golding, S.D., and Tyson, G.W. (2015). Methane metabolism in the archaeal phylum Bathyrhizobacteria revealed by genome-centric metagenomics. *Science* 350, 434-438.
 Hunter, J.D. (2007). Matplotlib: A 2D graphics environment. *Comput Sci Eng* 9, 90-95.
 Langmead, B., and Salzberg, S.L. (2012). Fast gapped-read alignment with Bowtie 2. *Nat Methods* 9, 357-U354.
 Meier, D.V., Pjevac, P., Bach, W., Hourdez, S., Girguis, P.R., Vidoudez, C., Amann, R., and Meyer-Dierks, A. (2017). Niche partitioning of diverse sulfur-oxidizing bacteria at hydrothermal vents. *ISME J*.
 Orcutt, B.N., Sylvan, J.B., Knob, N.J., and Edwards, K.J. (2011). Microbial Ecology of the Dark Ocean above, at, and below the Seafloor. *Microbiol Mol Biol R* 75, 351-356.
 Peng, Y., Leung, H.C.M., Liu, S.M., and Chin, F.Y.L. (2010). IDBA - A Practical Iterative de Bruijn Graph De Novo Assembler. *Lect N Bioinform* 6044, 426-440.
 Reveillaud, J., Reddington, E., McDermott, J., Algar, C., Meyer, J.L., Sylva, S., Seewald, J., German, C.R., and Huber, J.A. (2016). Subseafloor microbial communities in hydrogen-rich vent fluids from hydrothermal systems along the Mid-Cayman Rise. *Environ Microbiol* 18, 1970-1987.
 Stewart, F.J., Ulloa, O., and DeLong, E.F. (2012). Microbial metatranscriptomics in a permanent marine oxygen minimum zone. *Environmental Microbiology* 14, 23-40.