

GENOMIC VARIATION AND EVOLUTION OF NATURAL MICROBIAL POPULATIONS INHABITING DEEP-SEA HYDROTHERMAL VENT HABITATS. R.E. Anderson^{1,2}, E.R. Reddington^{2,3}, J. Reveillaud^{2,4}, A.M. Eren^{2,5}, J. Seewald⁶, J. McDermott⁷, R. Stepanauskas⁸, and J. A. Huber²

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Since life first originated on Earth more than 4 billion years ago, it has adapted to dynamic conditions in diverse habitats across the planet. One of the most ancient, continuously inhabited environments on Earth is deep-sea hydrothermal vents, which are thought to have been an important site for the origin and early evolution of life [1–4]. Microbial communities in deep-sea hydrothermal vent habitats must adapt to dynamic conditions created by extreme environmental gradients, and have done so since the earliest stages of life's evolution. However, we lack a fundamental understanding of the microevolutionary processes that drive the evolution of seafloor microbial populations. Fundamental questions include: how do selection pressures vary across different environments in the subsurface? What is the relative role of the environment and other biotic interactions in driving selection? The Mid-Cayman Rise, hosting geologically diverse vent fields, is an ideal natural laboratory in which to examine these questions. We examined genomic variation among seafloor microbial lineages using both metagenomic binning and single cell genomics methods. Using metagenomics binning methods to examine variation across taxa, we observed that the environment had an important impact on microevolutionary dynamics. Von Damm, an ultramafic-hosted hydrothermal system with diverse energy sources and high microbial diversity, harbored microbial populations that appear to have undergone recent selective sweeps or immigration events. In contrast, at the mafic-hosted Piccard hydrothermal system, the deepest vent field discovered to date, evidence suggests that selective sweeps occurred less frequently or less recently relative to Von Damm. These results provide a case study illustrating the impact the environment can have on microevolutionary dynamics in hydrothermal systems. However, a closer examination of population variation within the genus *Methanothermococcus* using single-cell genomics revealed a potentially important role for viral infection in driving differentiation among strains, suggesting that interactions within the biological community contribute to diversification. Further work will provide further insight into the relative impact these factors play within different habitats of the ma-

rine subsurface. Analysis of the relative impact of these factors in driving microbial evolutionary trajectories is crucial for understanding the processes that have allowed life to adapt, persist and diversify in these ancient and dynamic environments, both now and in the deep past.

References: [1] Baross J.A. and Hoffman S.E. (1985) *Orig. Life Evol. Biosph.*, 15, 327–345. [2] Martin W., Baross J.A., Kelly D., and Russell M.J. (2005) *Nat. Rev. Microbiol.*, 6, 805–14. [3] Stüeken E.E., Anderson R.E., Bowman J.S., Brazelton W.J., Colangelo-Lillis J., et al. (2013) *Geobiology*, 11, 101–26. [4] Reysenbach A.L. and Shock E. (2002) *Science*, 296, 1077–1082.