

UNRAVELING THE IMPACT OF ECOLOGICAL SELECTION PRESSURES ON THE PANGENOME OF *SULFOLOBUS ACIDOCALDARIUS*. R. A. Anderson¹, A. Kouris², C. Seward¹ and R. J. Whitaker¹,¹Carl R. Woese Institute for Genomic Biology, University of Illinois at Urbana-Champaign, ²Roy J. Carver Biotechnology Center, University of Illinois at Urbana-Champaign.

While the evolution and spread of microbial communities has profoundly shaped our planet's biogeochemical cycles and biosphere, we lack a solid understanding of the microevolutionary processes that facilitate the spread of microbes into new ecological niches. Generally, microorganisms adapt to their environment through genomic variation, which can consist of individual point mutations or the gain or loss of large genomic regions. However, the extent to which this genomic variation is driven by genetic drift or by natural selection through adaptation to the physical environment or to biological interactions is unknown. Here, we explore these questions through a comparative analysis of 47 genomes of the thermophilic crenarchaeon *Sulfolobus acidocaldarius*. First, we show that relative to *S. islandicus*, the genome of *S. acidocaldarius* is highly conserved, with only a few single nucleotide polymorphisms differentiating the core genomes, even across large scales of space and time. However, the SNPs we observe do indicate some differentiation among geographically separated populations, suggesting that geographic barriers to gene flow do exist for this species. Single nucleotide polymorphisms differentiating the geographically separated populations encoded nonsynonymous changes to membrane proteins. Patterns of gene gain and loss indicated that much of the variation occurs between closely related strains, and thus occurred in the relatively recent past. While gene gain was a more common mechanism of variation than gene loss, membrane proteins were disproportionately lost rather than gained, and a large genomic island encoding glycosyltransferases was among the genomic regions differentiating geographically isolated populations. Thus, variation in both the core and variable genomes favors differentiation in terms of membrane protein presence or structure. We hypothesize that this variation is evidence of selection pressures resulting from the virus-host arms race. These results raise the question of why some species' genomes appear to be more dynamic than others, and demonstrate that biological interactions such as viral infection can play a powerful role in determining the evolutionary trajectory of a given species.