

SULFOLOBUS TURRETED ICOSAHEDRAL VIRUS IN SULFOLOBUS ACIDOCALDARIUS MAY PROVIDE INSIGHT FOR EVOLUTIONARY DIVERGENCE. A. Blancaflor^{1,2}, R. J. Whitaker^{1,2}, R. Anderson^{1,2}, and X. Ortiz-Mangual^{1,2}, ¹University of Illinois at Urbana-Champaign, ²Carl R. Woese Institute for Genomic Biology

Viruses infect all three domains of life and are thought to have played a key role the origin and early evolution of life [1]. The simultaneous diversity and homology of viruses across domains suggests that they originated early on, and co-evolved in parallel to life's divergence.

The study of archaeal viruses in particular can provide insights into evolutionary mechanisms within the archaea. *Sulfolobus* turreted icosahedral virus (STIV) is significant because it is genetically distinct from other *Sulfolobus* viruses yet shares structural similarity with viruses found in other domains [2]. The similarities in structure and assembly to viruses in other domains hint at deep evolutionary relationships among viruses. Furthermore STIV's thermophilic host can offer insight into survival on the harsh environments thought to dominate early planetary bodies. Continued research on viruses across domains may provide a better understanding of early life's evolutionary mechanisms and history.

We have examined a novel strain of STIV integrated into the genome of the thermophile *Sulfolobus acidocaldarius*. Previously STIV had only been found to infect (but not integrate into) *Sulfolobus solfataricus*. This virus was conserved across 16 different isolates of *S. acidocaldarius* taken from Yellowstone National Park in 2012, and are closely related to previously identified strains of STIV. The integration of the virus shows a greater host range than previously discovered for this virus. We compare this strain of STIV to others that have been previously isolated and to CRISPR/Cas spacer sequences in the host genome to identify how the evolutionary forces of virus-host interactions may have shaped the viral co-evolution. Further analysis will probe the virus integration into its host genome in order to identify co-evolutionary consequences of its integration.

[2] Rice, G., Tang, L., Stedman, K., Roberto, F., Spuhler, J., Gillitzer, E., Johnson, J., Douglas, T., Young, M. (2004) PNAS 101 7716-7720

References:

[1] Forterre, P., Prangishvili, D. (2009) Ann N Y Acad Sci 1178 65-77