

**Elucidating the evolution of extremophile viruses by comparative genomics and genetics.** K. M. Stedman<sup>1</sup>, E. A. Iverson<sup>1</sup>, D. A. Goodman<sup>1</sup>, J. Hartunians<sup>1,2</sup>, and V. P. Huang<sup>1</sup>. <sup>1</sup>Center for Life in Extreme Environments, Department of Biology, Portland State University, P.O. Box 751, Portland, OR 97201. kstedman@pdx.edu, <sup>2</sup>Université de Bretagne Occidentale, Brest, France.

**Introduction:** The fuselloviruses of archaea are, arguably, the best studied of all archaeal viruses. Extensive comparative genomic work on environmental isolates of fuselloviruses from volcanic hot springs from throughout the world has been assembled [1-3]. The viral genomes are 15-20kbp double stranded circular DNA. Preliminary genetic analysis has been performed on the prototypical fusellovirus, SSV1 [5-7]. Surprisingly the viral integrase gene was found not to be essential for SSV1 function, but did provide a competitive advantage [6].

**Results:** We have now completed both random and site directed mutagenesis in every putative protein-coding gene in the SSV1 genome. Interestingly, about ½ of the genes tolerate either insertion or deletion or both. We have also recently developed synchronous infection protocols for SSV1 infection of the hyperthermophilic and acidophilic archaeon, *Sulfolobus*. Together with the recently published structure of SSV1 [8] these results lead to profound insights into the structure and function of these viruses. Comparative infection studies indicate which genes are important for the evolutionary success of this widespread but understudied group of viruses.

**References:**

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