GENOME-WIDE RECOMBINATION RATE VARIATION IN THE ARCHAEON SULFOLOBUS ISLANDICUS David J. Krause[1] and Rachel J. Whitaker[1], [1]Department of Microbiology, University of Illinois, 601 S. Goodwin Ave. CLSL C209, Urbana, IL. 61801.

Introduction: Recombination, or the exchange and stable incorporation of genetic material among organisms, is a feature of members of all three domains of life as well as viruses. The process is mediated by a diversity of mechanisms, both at the level of genetic exchange and at the level of DNA incorporation. In sexual eukaryotes, recombination does not occur at a constant rate throughout the genome, but rather there are regions with reduced recombination rates as well as counterpart recombination 'hotspots'. The divergence of Eukaryotes and Archaea represents one of the earliest defined branching events in the tree of life, therefore understanding factors that influence genomic recombination rates in the Archaea may yield insights into this same process in Eukaryotes, as well as meisosis and the origins of sex.

Results: In order to study recombination in the Archaea, a sympatric population of isolates of *Sulfolobus islandicus* from a single hot spring in the Mutnovsky Volcano region of Kamchatka, Russia, was cultured from a single sampling expedition in the year 2000. Ten individuals representing the diversity of the population were selected for genome sequencing [1]. Alignment of the core genomes using Mauve demonstrated variation in levels of polymorphism throughout the genome. These variations could not be accounted for by neither estimated mutation rate variation nor variation in selection. Instead, the levels of polymorphism are likely due to variation in recombination rates in the face of genome-wide purifying selection [2].

In order to identify whether recombination rates inferred from the population study are the result of genome-wide recombination rate variation, or instead are the result of higher-level epistatic selection on recombinant genotypes, recombination rates are being estimated directly in the laboratory. A triple-mutant genotype has been constructed that, when crossed with a wild-type strain, will form recombinant colonies on a selective plate that restricts the growth of either parent genotype. By crossing individuals that contain several thousand natural polymorphisms throughout their genomes, individual recombinants can be sequenced, and donor DNA incorporations can be identified in the resulting sequence data. This approach has shown that recombination does indeed occur throughout the genome; however, the number of colonies that need to be sequenced in order to reveal genome-wide recombination rate variation is too great to be accomplished using individual colony sequencing.

In contrast to single-colony sequencing, thousands of individual recombinant colonies can be pooled and sequenced in a single run. Individual recombination events have been identified from the sequence data of these pools, and genome-wide mapping of these events has yielded insight into genome-wide recombination rates. Future directions aim to identify the factors that define this genome-wide variation in recombination rates by developing an efficient method for identifying recombination rate variation in a variety of genetic mutants.

References: [1] Cadillo-Quiroz H. et al. (2012) *PLoS Biol.,* 10(2):e1001265. [2] Krause D. J. et al. (2014) *Genome Biol Evol* 6(1):170-8.