Duplicated Recombination Genes in the Cyanobacterium *Acaryochloris*: Consequences for Genome Evolution. S. R. Miller[1], E. B. Sano[1] and A. L. Gallagher[1]. [1] 32 Campus Dr. #4824, Division of Biological Sciences, The University of Montana, Missoula, MT 59812.

Homologous recombination (HR) by members of the ancient recombinase A (*recA*) gene family is a potent creative force in evolution through its assortment of standing variation into novel genetic combinations, and HR-mediated gene duplication was a central mechanism of the origin of organismal complexity through the evolution of new functions. HR is also essential for maintaining genome integrity by repairing DNA damage but must be tightly regulated, as it is also an important source of destabilizing genomic rearrangements.

We are investigating the contribution of the extraordinary genetic variation exhibited by duplicated *recA* gene copies in the genomes of the cyanobacterium *Acaryochloris* to both its high levels of genome instability (including a high gene duplication rate) and its ability to adapt to novel environments. Although the vast majority of bacteria only possess a single copy of recA, presumably to regulate HR activity, *Acaryochloris* genomes may have at least seven actively expressed copies of this gene. Here, we show that these duplicated *recA* copies are differentially expressed in response to different environmental stresses, which suggests that they have functionally diverged. Differences in recombinase activity of the duplicates also provide evidence of functional divergence. Although gene duplication at other loci is typically non-adaptive, it may also be a mechanism of adaptation to novel environments through positive dosage effects, as we observe for the case of iron limitation.