EEB Seminar Series 2018 - 2019

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Adaptive evolution of meiotic recombination in response to whole genome duplication and habitat

Eukaryotes produce progeny through the union of haploid gametes. Importantly, gametes contain recombined versions of the parental chromosomes, making each individual unique. This process of recombination of genetic material is a critical factor in inheritance and evolution, yet is also essential (in most species) for the mechanics of chromosome segregation. Recombination rates are known to vary among species, populations, even individuals. Whether or how this variation is adaptive has seen extensive debate. Here, I will discuss two separate instances of recombination rate evolution in diploid and tetraploid Arabidopsis arenosa. In the tetraploid lineage, we have evidence that reduced recombination rates were achieved via modification of core structural meiosis proteins, and that reduced recombination directly stabilizes tetraploid meiosis by preventing chromosome tangling. We also discovered selection acting independently on some of the same genes in a diploid population, where we think the driving force is temperature adaptation. This raises important questions about what we are actually looking at when we observe recombination rate variation. Our results highlight how recombination rates can evolve mechanistically, and show that both climate and genome change may influence recombination rate evolution in surprisingly similar ways.

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