Seminar/Talk

All roads lead to adaptation: Genomic signatures of parallel evolution in Drosophila

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Highly replicated experiments with microbes indicated that rewinding the tape of life results in more parallel evolution than previously anticipated. This high reproducibility is attributed to genetic constraints, resulting in different mutations in the same genes or pathways. Little is known about the reproducibility of adaptation from standing variation in sexual eukaryotes, where starting frequency, effective population size, and reservoir of mutations come into play. Furthermore, the adaptive traits are likely to be more complex than for microorganisms. We used the most highly replicated E&R study in Drosophila to study parallel evolution. The analysis of 10 replicate Drosophila simulans populations adapting to a hot environment uncovered a large number of candidate SNPs. To account for linkage, these SNPs were clustered into haplotype groups, each defining a selected genomic region. Interestingly, few clusters were selected in all replicates and most of them increased in frequency only in 1-5 replicates. Consistent with genetic drift being a major factor determining the heterogeneity among replicates, we found a strong positive correlation between the starting frequency of the selected clusters and the number of replicates showing a selection signature. Nevertheless, the clusters were significantly enriched for genes involved in oxidative phosphorylation pathway and TCA cycle, as well as genes with monosaccharide transmembrane transporter, triglyceride lipase, and endopeptidase activities. Moreover, all evolved replicates had a higher fecundity and metabolic rate than their ancestral populations. We conclude that natural D. simulans populations harbor sufficient standing variation to fuel parallel evolution of fitness and metabolism despite low parallelism on the gene level.

Wednesday, March 22, 2017 12:30pm - 01:30pm

I22 Lakeside View (I22.01)

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