



EvoLunch

Clines and inversions as evidence for local adaptation in *Drosophila melanogaster*

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Clines, which are gradual changes of genotypes or phenotypes along environmental transects, are often taken as *prima facie* evidence for the action of spatially varying selection. However, only due to recent advances in sequencing technology it now becomes possible to compare genome-wide clinal patterns and test for alternative models. We use the *Drosophila melanogaster* system to study genomic diversity along a latitudinal temperature gradient at the North American east coast. We found evidence for steep and temporally stable clinal variation associated with In(3R)Payne, a common cosmopolitan inversion, that cannot be explained by demography alone. To learn more about the potential adaptive effect of this inversion, we compare karyotype-specific genomic variation on multiple different continents. We find genomic regions in the center of the inversion that are in strong linkage disequilibrium with the inversion breakpoints possibly as a result of selection for inversion-specific genetic variation. Finally, with the help of a newly founded population genetics consortium, we now expand the genome-wide analysis of clinal genomic variation to the yet largely unexplored European continent and find further evidence for the clinal variation of In(3R)Payne despite complex demographic patterns.

Wednesday, September 20, 2017 12:30pm - 01:30pm

I22 Lakeside View (I22.01)



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