

Invited Talk

Inferring genomic footprints of adaptation from SNP data

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Abstract

An important goal of population genetics is to determine the forces that have shaped the pattern of genetic variation in natural populations. For inferring the adaptive history of populations, we developed likelihood methods using the coalescent approach. We applied these techniques to *Drosophila melanogaster*, an originally African species that colonized temperate regions around the world after the last ice age. Our analyses suggest that the ancestral African population expanded its size about 60,000 years ago. The non-African populations split off from the African lineage about 16,000 years ago, thereby suffering severe population size bottlenecks. These demographic changes were accompanied by the fixation of numerous beneficial mutations, as revealed by signatures of positive directional selection in the genome (“selective sweeps”). The estimated rate of adaptive substitution is very high (in the order of one per genome per 100 generations). In several of the genomic regions exhibiting selective sweeps, we found genes with significant expression differences between African and non-African lines, suggesting that regulatory elements were the targets of selection and facilitated adaptation of fruit flies to temperate climates.