

Workshop: Computational Genomics

Adaptive evolution in *Drosophila* and humans

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An important goal of population genetics is to determine the forces that have shaped the pattern of genetic variation in natural populations. We developed a maximum likelihood method that allows us to infer demographic changes and detect recent positive selection (selective sweeps) in populations of varying size from DNA polymorphism data. Applying this approach to SNP data at more than 250 non-coding loci on the X chromosome of *Drosophila melanogaster* from an (ancestral) African population and a (derived) European, we found that the African population expanded about 60,000 years ago and that the European population split off from the African lineage about 15,800 years ago, thereby suffering a severe population size bottleneck. We estimated that about 160 beneficial mutations (with selection coefficients s between 0.05% and 0.5%) were fixed in the euchromatic portion of the X in the African population since population size expansion, and about 60 mutations (with s around 0.5%) in the diverging European lineage. Moreover, we developed a test which uses microsatellite markers and which examines the frequency spectrum of microsatellite alleles has a very low false positive rate while maintaining reasonable power. We show that under limited recombination selective sweeps produce an allele spectrum at a microsatellite which is characteristically different from that produced by any other examined evolutionary force. We apply our test to a dataset from malaria parasites (*Plasmodium falciparum*) in Asia and confirm the previously identified site of a selective sweep due to drug resistance. We also applied the test to a dataset from a Han-Chinese population and detected a signature of recent positive selection on eight markers. In six cases, at least one of the neighboring genes is involved in brain development or function.