

Ciclo de conferências

CoBiG² - CBA

24 Maio, FCUL, Edifício C1, Piso 3, Anf. FFCUL

Programa

9.15-10.30h: Candidate genes and host race formation in aphids

ROGER BUTLIN, University of Sheffield

New sequencing approaches provide unprecedented opportunities to reveal the genetic basis of local adaptation and speciation. Both genome-wide scans and candidate gene approaches have provided useful insights but have shortcomings. I will describe an approach that combines benefits of the two alternatives, applied to chemosensory gene families in the pea aphid.

10.30-11.30h: Analysis of temporally sampled genetic data

MARK BEAUMONT, University of Bristol

Although potentially informative, the analysis of temporally sampled genetic data poses a number of interesting problems for analysis. This talk reviews an earlier approach based on the coalescent without migration, and a more recent application to the conservation biology of the Floreana Mockingbird. A model of serially sampled data with admixture events is then described and applied to data from freshwater bryozoans.

12.00-13.00h: Genomics of adaptation: Evolution of pigmentation alleles in beach mice

VERA DOMINGUES, Harvard University

With our ability to identify alleles contributing to adaptive variation, we are now in a position to understand their evolutionary histories. Specifically, we want to know the primary source of beneficial mutations (i.e., pre-existing mutations segregating as standing genetic variation or *de novo* mutations that occur after an environmental change), if those mutations have evolved repeatedly, and the timing and strength of selection acting on them. To address these questions, I study natural populations of oldfield mice, *Peromyscus polionotus*, which occupy oldfield habitat throughout the southeastern US, where they have dark coats. More recently, they have colonized the coastal dunes of Florida's Gulf Coast, where they have evolved pale coats for camouflage. A QTL mapping approach, identified three pigmentation genes, which together explain most of the variation in adaptive color differences between the beach and mainland subspecies. In the case of one gene, the *melanocortin-1 receptor (Mcl1r)*, we identified and functionally characterized a single derived amino acid change that reduces receptor signalling, consistent with its role in producing pale coat color. To determine the origin and selection strength acting on this mutation, I used next-generation sequencing technology to resequence non-coding regions scattered throughout the genome, as well as a 150-kb genomic region surrounding *Mcl1r*. Using this data I first showed that beach mice populations are young and have experienced a strong bottleneck. In this demographic context I determined a single origin of derived *Mcl1r* alleles that contribute to the differences in pigmentation between locally adapted populations of mice and I showed evidence of adaptation from ancestral variation.

In addition, I am using several complementary approaches to identify the precise regulatory mutation(s) in *Agouti signaling protein (Agouti)*, a second pigmentation gene that contributes to camouflaging pigmentation in beach mice. Together, these data allow us to reconstruct the evolutionary history of populations and adaptive alleles providing a model in which to study both the molecular basis and evolutionary history of adaptation in wild populations.