Butterfly wing patterns: Multiple approaches to understand supergene evolution

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Laboratory

Origins, Structure and Evolution of Biodiversity UMR 7205 CNRS/MNHN
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Subjects / Tools-Methodologies

1 : Evolutionary genetics/Linkage mapping, IlluminaRADtag sequencg
2 : Ecological bioinformatics/Fst genomic scans, High-throughput sequencing data
3 : Modelling/Coalescence/genealogy models, Bayesian inference

Website : www.mnhn.fr/oseb

Summary of lab's interests

The large OSEB laboratory (www.mnhn.fr/oseb) aims to provide answers to important questions about the origins of biodiversity, such as the modes of diversification of species, the shaping of multispecies communities and how those interact with the spatial and temporal evolution of taxa. Approaches to tackle those questions are based on phylogenetic inference and genealogical studies, molecular ecology, molecular population and evolutionary genetics, modelling, and morphometric analysis.

The host team (Genetics of adaptive traits, ERC/ATIP funded) studies the evolution of adaptive diversity and the associated genetic changes, using the colour patterns of butterflies as a model. Butterflies have extremely diverse colour patterns with clear adaptive functions (such as camouflage, sexual signalling, or advertisement to predators). We are now starting to uncover how gene networks underlie the formation of wing patterns and their natural variation. This knowledge will provide the tools for a better understanding of the evolution of adaptive traits, and their importance from individual physiology and life history, to population genetics, and to the shaping of entire communities. We work with tropical butterflies involved in mimicry, mainly passion-vine butterflies in the genus Heliconius, but also with Papilio swallowtails.

Summary of project

Butterflies in the genus Heliconius (Nymphalidae) have emerged as excellent models for the study of the evolutionary genetics of adaptive traits and the processes shaping tropical diversity. This clade has undergone a spectacular adaptive radiation of wing colour patterns, used as warning signals of their toxicity to predators, and involved in mimicry between coexisting species. In Heliconius, the diversity of patterns is controlled by a conserved set (toolkit) of loci on 5 chromosomes. However, the species H. numata shows tremendous local poplymorphism controlled by only one of the toolkit loci. This supergene locus (cluster of genes) shows a great flexibility of expression and a series of dominance between its alleles, each of which controls a different mimetic wing pattern. This genetic architecture allows multiple mimetic forms to coexist in a geographic area via balancing selection, while avoiding the occurrence of unfit intermediate (non-mimetic) morphologies.

The aim of the proposed subject is to understand the concentration of the ancestral genetic architecture on this genomic \"hotspot\" of adaptation, and to trace the evolutionary origins of the multiple alleles underlying the rapid mimetic radiation within the neotropical region. The project will use the combination of molecular ecology approaches, bioinformatics and modelling approaches:
1) a dense linkage mapping of colour pattern variation in the clade H. numata, using Illumina RAD-tag linkage mapping, to define the genetic homologies between closely related species and trace the origins of the supergene;
2) a population genetic and genealogical study of the colour pattern loci and at the genome-wide scale, to study the history of variation associated with the adaptive radiation.
3) a modelling approach using coalescence models will be implemented (a) to confront the above data to predictions on the evolution of the condensed genetic architecture with dominance from a multilocus architecture, (b) to test the importance of hybridisation and introgression in adaptation in the clade, and (c) to test biogeographic scenarios on the mode and tempo of tropical diversification during the quaternary geological period.