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NATURAL SELECTION AND THE FORMATION OF A MIMICRY SUPERGENE IN BUTTERFLIES

par

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Butterfly mimicry is characterised by powerful natural selection shaping extraordinary wing pattern convergence between species, as well as a rich diversity of distinct mimicry groups. With increasing genomic resources and huge natural diversity of phenotypes and ecologies, butterflies are an excellent system to explore the basis of adaptation and diversification.

I will present integrative research combining ecological, morphometric, genomic and population genetic data to understand the factors influencing adaptive diversity. My talk will focus on the maintenance of adaptive polymorphism in an Amazonian butterfly, *Heliconius numata*, in which multiple wing pattern forms coexist and mimic the diversity of local mimicry groups in every locality. Ecological experiments show strong frequency-dependent selection which varies spatially in its direction, participating to the maintenance of polymorphism.

Wing pattern variation is controlled by a supergene, a co-adapted cluster of loci locked together by polymorphic inversions. We studied the differentiation of allelic blocks using population genomics and whole-genome resequencing of populations of *H. numata* and closely related species. Shared polymorphisms with a non-sister species suggest this supergene was probably initiated through ancient introgression. Genotype-phenotype association helps pinpointing the few co-adapted genes within the cluster, and reveal that many other genes seem to follow by mere hitchhiking, suggesting that coadaptation here could have direct evolutionary consequences for neighbouring genes. Behavioural experiments reveal disassortative mating based on inversion genotypes, suggesting sexual selection on inversions, perhaps influencing the stability of adaptive polymorphisms. Finally, polymorphism seems to have favoured the evolution of dominance relationships between wing patterns alleles.

Our results suggest that an initial inversion kick-started the formation of a complex genomic architecture with multiple evolutionary and ecological outcomes, and far-reaching consequences in terms of demographics, population differentiation, cladogenesis and community ecology.