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20 September 2006 The Genetics of Wing Pattern Mimicry, Food-Web Models Predict Abundance, and More - Press Release from PLoS Biology under embargo until 26 Sep 2006 01:00 GMT

### How butterflies got their spots: a "supergene" controls wing pattern diversity

Butterflies are known to employ some interesting convergent evolutionary tactics to survive—some nonpoisonous species have similar wing patterns to those of noxious species that predators avoid. In a new study published online today in the open access journal PLoS Biology, Mathieu Joron, Chris Jiggins, and colleagues investigate the underlying genetic mechanisms of such molecular mimicry in three species of *Heliconius* butterflies.

In this study, the authors investigate two distantly related species (*H. melpomene* and *H. erato*) that have similar wing patterns and a third species, *H. numata*, that is closely related to *H. melpomene*, but displays very different wing patterns. Each of these three species is also known to mimic a different species within another butterfly genus, *Melinaea*. Several genomic loci are already known to be responsible in part for encoding the wing patterns and colorings. To explore the genetic backgrounds of each of these species, the authors crossed different races of each species and genotyped the offspring in order to identify genes responsible for the color patterns. Thus, they were able to map the color pattern controlling loci in each species: N, Yb, and Sb for *H. melpomene*; Cr for *H. erato*; and P for *H. numata*. Using molecular markers within the pattern encoding genic regions, the authors then found that the loci controlling color pattern variation for each species lie within the same genomic equivalent locations.

This "supergene" region therefore seems to be responsible for producing wing pattern diversity in *Heliconius* butterflies. Such a locus plays what researchers call a "jack-of-all-trades flexibility" rather than a constraining role. Under natural selection, this region presumably functions as a "developmental switching mechanism" by responding to a wide range of mimetic pressures to produce radially divergent, locally adapted wing patterns.

Citation: Joron M, Papa R, Beltrán M, Chamberlain N, Mavárez J, et al. (2006) A conserved supergene locus controls colour pattern diversity in *Heliconius* butterflies. PLoS Biol 4(10): e303. DOI: 10.1371/journal.pbio.0040303.

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- Caption: *Heliconius numata*, f. *silvana* feeding from a *Psiguria* flower.  
(Photo: Mathieu Joron)

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#### Predicting species abundance in the face of habitat loss

Habitat loss poses the greatest threat to the survival of a species, and often precipitates the demise of top predators and wide-ranging animals, like the Siberian tiger and the orangutan. Any hope of recovering such critically endangered species depends on understanding what drives changes in population size following habitat contraction. In a new study published in *PLoS Biology*, Nicholas Gotelli and Aaron Ellison test the relative contributions of habitat contraction, keystone species effects, and food-web interactions on species abundance, and provide experimental evidence that trophic interactions exert a dominant effect. Until now, direct evidence that trophic interactions play such an important role has been lacking, in part because manipulating an intact food web has proven experimentally intractable, and in part because these different modeling frameworks have not been explicitly compared.

Gotelli and Ellison overcame such technical limitations by using the carnivorous pitcher plant (*Sarracenia purpurea*) and its associated food web as a model for studying what regulates abundance in shrinking habitats. Every year, the pitcher plant, found in bogs and swamps throughout southern Canada and the eastern United States, grows six to 12 tubular leaves that collect enough water to support an entire aquatic food web. The pitcher plant food web starts with ants, flies, and other arthropods unlucky enough to fall into its trap. Midges and sarcophagid fly larvae "shred" and chew on the hapless insect. This shredded detritus is further broken down by bacteria, which in turn are consumed by protozoa, rotifers, and mites. Pitcher plant mosquito larvae feed on bacteria, protozoa, and rotifers. Older, larger sarcophagid fly larvae also feed on rotifers as well as on younger, smaller mosquito larvae.

Working with 50 pitcher plants in a bog in Vermont, Gotelli and Ellison subjected the plants to one of five experimental treatments, in which they manipulated habitat size (by changing the volume of water in the leaves), simplified the trophic structure (by removing the top trophic level—larvae of the dipterans fly, midge, and mosquito), did some combination of the two, or none of the above (the control condition). Dipteran larvae and water were measured as each treatment was maintained; both were replaced in the control condition and more water was added in the habitat expansion treatment. These treatments mimic the kinds of changes that occur in nature as habitat area shrinks and top predators disappear from communities.

The best predictors of abundance were models that incorporated trophic structure—including the "mosquito keystone model." This model accurately reflected the pitcher plant food web, with mosquito larvae preying on rotifers, and sarcophagid flies preying on mosquito larvae. "Bottom-up" food-web models (in which links flow from prey to predator) predicted that changes in bacteria population size influence protozoa abundances, which in turn affect mosquito numbers, and that changes in bacteria abundance also affect mite numbers, which impact rotifer abundance. This scenario lends support to the model of a *Sarracenia* food web in which each link in the chain performs a specialized service in breaking down the arthropod prey that is used by the next species in the processing chain.

With over 200 million acres of the world's forestlands destroyed in the 1990s alone, and an estimated 40% increase in the human population by 2050, a growing number of species will be forced to cope with shrinking

habitat. Instead of trying to determine how individual species might respond to habitat loss, Gotelli and Ellison argue that incorporating trophic structure into ecological models may yield more-accurate predictions of species abundance—a critical component of species restoration strategies.

Citation: Gotelli NJ, Ellison AM (2006) Food-web models predict species abundances in response to habitat change. *PLoS Biol* 4(10): e324. DOI: 10.1371/journal.pbio.0040324.

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- Caption: *Sarracenia purpurea*. (Photo: Nicholas J. Gotelli)

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#### Implicit Multisensory Associations Influence Voice Recognition

This study illustrates that recognition of natural objects under conditions where only one sensory modality is available can rely on implicit access to multisensory representations of the stimulus.

Citation: von Kriegstein K, Giraud AL (2006) Implicit multisensory associations influence voice recognition. *PLoS Biol* 4(10): e326. DOI: 10.1371/journal.pbio.0040326.

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#### Munc18-Bound Syntaxin Readily Forms SNARE Complexes with Synaptobrevin in Native Plasma Membranes

The authors take a fresh look at the role of Munc-18, an SM protein, in vesicle fusion and find that it facilitates the formation of fusion-competent SNARE complexes by binding to syntaxin.

Citation: Zilly FE, Sørensen JB, Jahn R, Lang T (2006) Munc18-bound syntaxin readily forms SNARE complexes with synaptobrevin in native plasma membranes. *PLoS Biol* 4(10): e330. DOI: 10.1371/journal.pbio.0040330.

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