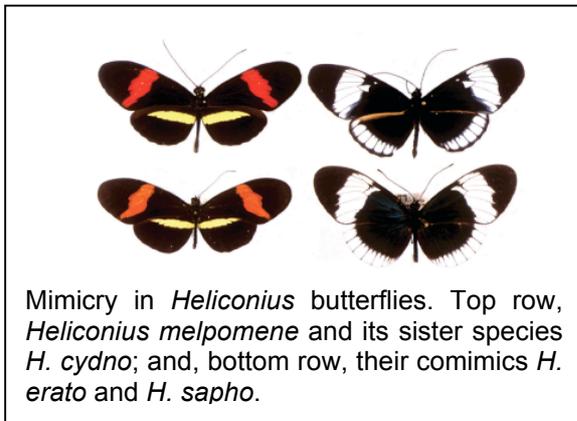


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Report on work achieved during Varley-Gradwell Traveling Fellowship in Insect Ecology

## Ecological speciation in tropical butterflies

Speciation is the process ultimately responsible for generating biodiversity, and understanding its mechanisms remains a fundamental goal. I was awarded the Varley-Gradwell Traveling Fellowship in Insect Ecology in May 2012 to support my work on mimetic *Heliconius* butterflies. My research focuses on the ecological, genetic and developmental basis of adaptive behaviours that contribute to the evolution of new species. In particular, I am interested in how behavioural isolation evolves, and how genetic architecture and other factors may influence this process.



It is now widely accepted that adaptation to different ecological niches can drive speciation. However, if populations remain in contact, speciation is constrained because recombination breaks down associations between key traits that characterize emerging species. A number of mechanisms may overcome this by ‘coupling’ traits involved in speciation, including for example, pleiotropy and genetic linkage. In *Heliconius* butterflies colour pattern is both used to warn predators and as a mate recognition cue. I have previously demonstrated that loci underlying differences in colour pattern and the corresponding mate preference, between the sister species *H. cydno* and *H. melpomene*, are physically associated in the genome. Thus individuals that have the same colour pattern genes, which are under disruptive selection for mimicry, are strongly predisposed to mate with one another.

Despite this, we are largely ignorant of the genetic structures underlying these associations. I now am addressing this through multiple approaches. In 2012 and ‘13, supported by the Varley-Gradwell Traveling Fellowship, I spent over 4 months in Panama collecting tissue from *H. melpomene* and *H. cydno* across a developmental time course. In total, I collected eye and brain tissue from 226 individuals, including various pupal and adult stages, raised in a common garden. I have now extracted RNA from these samples and a subset of these are awaiting sequencing at a genomics facility in Edinburgh. This will produce vast amounts of data allowing me to examine gene expression differences both across the colour/preference candidate region and the larger transcriptome. This will first allow me to ask whether there a correlated difference in expression between genes associated with mimetic wing pattern shifts and expression in eye and brain tissue. Second, I will be able to combine the resulting expression data with quantitative trait loci analyses. This will hopefully lead to the

identification of candidate genes underlying divergent mate preferences in *Heliconius*. The project is ongoing and I am still awaiting the sequencing data. However, I am confident that this work will produce interesting results and will be published. (Resulting publications will be available online: <http://www.zoo.cam.ac.uk/directory/richard-merrill>).

I would very much like to thank the board of the fund of the award, which has supported a key aspect of this project. My current position has no associated funds for research, and so funding from the Varley-Gradwell fellowship has been particularly valuable.