We studied whether similar developmental genetic mechanisms are involved in both convergent and divergent evolution. Mimetic insects are known for their diversity of patterns as well as their remarkable evolutionary convergence, and they have played an important role in controversies over the respective roles of selection and constraints in adaptive evolution. Here we contrast three butterfly species, all classic examples of Müllerian mimicry. We used a genetic linkage map to show that a locus, Yb, which controls the presence of a yellow band in geographic races of Heliconius melpomene, maps precisely to the same location as the locus Cr, which has very similar phenotypic effects in its co-mimic H. erato. Furthermore, the same genomic location acts as a “supergene”, determining multiple sympatric morphs in a third species, H. numata. H. numata is a species with a very different phenotypic appearance, whose many forms mimic different unrelated ithomiine butterflies in the genus Melinaea. Other unlinked colour pattern loci map to a homologous linkage group in the co-mimics H. melpomene and H. erato, but they are not involved in mimetic polymorphism in H. numata. Hence, a single region from the multilocus colour pattern architecture of H. melpomene and H. erato appears to have gained control of the entire wing-pattern variability in H. numata, presumably as a result of selection for mimetic “supergene” polymorphism without intermediates. Although we cannot at this stage confirm the homology of the loci segregating in the three species, our results imply that a conserved yet relatively unconstrained mechanism underlying pattern switching can affect mimicry in radically different ways. We also show that adaptive evolution, both convergent and diversifying, can occur by the repeated involvement of the same genomic regions.

Introduction

Recent interest has focused on the genetic basis of convergent evolution [1,2]. Adaptive convergence between unrelated species, exemplified by colour pattern mimicry in insects [3], has led to a long-standing controversy about the relative contribution of gradual evolution driven by natural selection [4] versus occasional phenotypic leaps facilitated by conserved developmental pathways [5]. Recently, molecular genetic studies have shed new light on this controversy and have shown that regulation of the same genes [6,7], or even repeated recruitment of the same alleles [8], may explain convergent phenotypes in nature.

However, analysis of convergent phenotypes is only part of the story, because convergence and parallelism commonly occur in groups of organisms that have undergone recent adaptive radiations [9–11]. We are therefore interested in the evolution of phenotypic diversity and whether similar developmental genetic mechanisms are involved in convergent and divergent evolution. The repeated involvement of homologous loci in the evolution of convergent phenotypes would appear to support a hypothesis of strong developmental constraints on adaptive evolution [11–13]. If the same loci are also recruited in divergent evolution, then they may be generally important in phenotypic evolution rather than solely playing a role in convergence [14].

With strong divergence between geographic races of the same species and near-perfect local mimic convergence between species, the diverse wing patterns of Heliconius butterflies (Nymphalidae: Heliconiinae) provide an opportunity to link molecular genetics to adaptive evolution. A few genes of major effect are known to control patterns in the Müllerian co-mimics H. erato and H. melpomene [15]. This has led to proposals that homologous genetic pathways [16] or a limited number of loci capable of controlling colour pattern shifts [17] could play an important role in convergent mimicry. However, homology of genetic architecture in mimetic butterflies has never been directly tested, despite the key role that mimicry has played in the history of the controversy [4,5].

We investigated the genetic architecture of colour pattern

Academic Editor: Mohamed A. F. Noor, Duke University, United States of America
Received April 12, 2006; Accepted July 14, 2006; Published September 26, 2006
DOI: 10.1371/journal.pbio.0040303
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Abbreviations: BAC, bacterial artificial chromosome; cM, centimorgan
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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

A Conserved Supergene Locus Controls Colour Pattern Diversity in Heliconius Butterflies

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We investigated the genetic architecture of colour pattern diversity in Heliconius butterflies. PLoS Biol 4(10): e303. DOI: 10.1371/journal.pbio.0040303

Introduction

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Figure 1. Colour Pattern Diversity of H. numata, H. melpomene, and their Respective Co-Mimics

The upper half of the figure shows five sympatric forms of H. numata from northern Peru (second row, left to right: H. n. f. tarapotensis, H. n. f. silvana, H. n. f. aurora, H. n. f. bicoloratus, and H. n. f. arcuella) with their distantly related comimetic Melinaea species (Nymphalidae: Ithomiinae) from the same area (first row: M. menophilus ssp. nov., M. ludovica ludovica, M. m. rileyi, M. m. m. mothone, and M. m. m. phasiana) [20]. The lower half of the figure shows five colour pattern races of H. melpomene, each from a different area of South America (third row: H. m. rosina, H. m. cythera, H. m. agloape, H. m. m. m. plesseni, and H. m. m. notabilis) with their distantly related comimetic H. erato races from the same areas (fourth row: H. e. emma, H. e. cythera, H. e. plesseni, and H. e. notabilis). H. m. agloape and H. e. emma are known as rayed forms, whereas H. m. rosina, H. m. melpomene, and co-mimics are known as postman forms. H. m. plesseni and H. e. notabilis are from divergent clades of Heliconius and are identified in the field using minor morphological characters, such as the different form of the red rays on the hindwing between H. m. agloape and H. e. emma (third from left) or the arrangement of red versus white patches in H. m. plesseni and H. e. notabilis (first from right). Co-mimics H. numata and Melinaea spp. belong to different subfamilies of the Nymphalidae and have very different body morphology and wing venation. The phylogram on the left is a maximum-likelihood tree based on 1,541 bases of mitochondrial DNA (scale bar in substitutions per site, all bootstrap values over 99). DOI: 10.1371/journal.pbio.0040303.g001

in three Heliconius species that represent examples of both mimetic convergence and colour pattern diversification. H. melpomene and H. erato are distantly related, yet are phenotypically identical and have undergone a parallel radiation into over 30 named “rayed” or “postman” colour pattern races across the neotropics (Figure 1). H. erato is the probable model for this radiation [18], and local populations of the two co-mimics are monomorphic. The third species, H. numata, is closely related to H. melpomene but has extremely divergent wing patterns. Unlike the patterns in H. melpomene or H. erato, these patterns are highly polymorphic within populations, with up to seven “tiger”-patterned morphs in a single locality [20,21] (Figure 1). Each of these morphs is a precise mimic of a different species of Melinaea (Nymphalidae: Ithomiinae); polymorphism in H. numata is thought to be maintained by strong selection for mimicry in a fine-scale spatial mosaic of ithomiine communities [19,20].

The differences in colour pattern between races of H. melpomene and H. erato are controlled by several Mendelian factors of large phenotypic effect [15,17]. In H. melpomene, a complex of at least three tightly linked loci (N, Yb, and Sb) control most of the variation in yellow and white pattern elements (Figures 1 and 2A), and recombination between these loci suggests that they lie just a few centimorgans (cM) apart [15,17,21]. Another pair of loci (B and D), situated on a different linkage group, controls most of the variation in the red pattern elements and interacts with N to control the colour of the forewing band [15,17] (Figure 1). Locus Ac controls the presence of a yellow patch in the discal cell of the forewing in some crosses [22]. Finally, locus K, unlinked to N–Yb–Sb or B–D, turns white patches to yellow in crosses between H. melpomene and H. cydno [21,23] (Table S1).

The radiation in H. erato has a similar genetic architecture, with a locus Cr that has similar phenotypic effects to the combined action of N, Yb, and Sb in H. melpomene. In crosses between H. e. cythera and a sister species, H. himera, Cr controls a hindwing yellow bar (cf. Yb), a white hindwing margin (cf. Sb) and the yellow forewing band of H. himera (cf. N) [24] (Figure 2B). Nonetheless, there are differences between the species: in inter-racial H. erato crosses the forewing yellow band is controlled by an unlinked locus, D, rather than by Cr [17]. D also controls most of the variation in the red pattern elements in a way that is analogous to the B–D complex in H. melpomene.
In contrast, mimicry polymorphism affecting yellow, brown/orange, and black colour patterns in *H. numata* is inherited entirely at a single Mendelian locus, \( P \) (Figure 2C). Populations are locally polymorphic, and nine distinctive alleles have been identified for the \( P \) locus in a narrow geographic area of Peru (Figures 1 and 2C) [19,20]. Alleles at the \( P \) locus are nearly all completely dominant, with a linear hierarchy of dominance relationships [19,20], as might be expected in order to prevent the segregation of intermediate and nonmimetic phenotypes in wild populations. Occasional recombinant phenotypes occur, suggesting that the \( P \) locus may be a tight cluster of genes, or "supergene" [19,25].

Despite suggestions in the literature that there might be genetic homology between some of these mimicry genes in different *Heliconius* species [16,26,27], such homology has not been directly tested. Here we describe the development of molecular markers that are tightly linked to a colour pattern locus in *H. melpomene*; we used these markers to investigate synteny and homology of colour pattern genes between the three *Heliconius* species.

**Results**

We demonstrated homology of the genomic location of the \( P \) locus in *H. numata*, the \( N-Yb-Sb \) complex in *H. melpomene*, and the \( Cr \) locus in *H. erato* (Figure 3). A noncoding region (\( a41 \)), cloned from an amplified fragment length polymorphism marker in a linkage mapping study of *H. melpomene*, lies within 1.1 cM of the *H. melpomene* pattern locus \( Yb \) on linkage group 15 (out of a total map length of 1,616 cM) [22] (Figure S1). Among 413 individuals with both genotype and phenotype information from four mapping families, there were just five individuals recombinant between \( a41 \) and \( Yb \) (Table S1). This same marker is located within 0.7 cM of the \( P \) locus, which controls polymorphism in *H. numata*, with only two recombinant individuals identified among 306 individuals derived from six mapping families (Table S2). The probability of finding \( Yb \) and \( P \) so tightly linked to a homologous marker in the two species by chance is \( p < 0.002 \) (see Materials and Methods).

The primers for the noncoding \( a41 \) marker did not amplify a product in *H. erato*. However, we used a PCR amplicon of
Conserved Mimicry Genes in Heliconius

In both species, these end sequences showed complete linkage to a41 in at least 100 individuals. This clone was then sequenced and annotated by BLAST comparison with nucleotide and protein sequence databases (see Materials and Methods; Figure 4). In addition to identifying the a41 locus, we identified nine genes and three retrotransposon-associated coding regions (Figure 4).

None of the genes identified in the 118-kb BAC clone is a candidate for the Yb locus itself, because recombinants were identified between markers derived from the BAC end sequences and Yb in H. melpomene (unpublished data). However, coding sequences were used to design conserved PCR primers for gene-based markers that cross-amplify broadly across Heliconius. One of these markers, GerTra, amplifies using primers anchored in two putative exons of the Rab geranylgeranyl transferase beta subunit (ggt-II) gene and spans an intron showing substantial allelic size variation in H. erato (Figure S3). This region was 14 kb from the a41 marker in H. melpomene (Figure 4), and variation at this locus segregated nearly perfectly with the colour locus Cr in H. erato. Only one recombinant between Cr and GerTra alleles was identified among 197 individuals from two mapping families of H. erato (Table S2), thus locating GerTra within 0.3 cM of the Cr locus (Figure 3; total map length in H. erato was estimated at 1,430 cM [27,28]). The probability of the H. melpomene gene Yb and H. erato gene Cr being tightly linked to homologous markers by chance is p < 0.003.

At a broader scale, two microsatellite markers (Hm01 and Hm08) and three conserved gene regions (eIF3-S9, RpL22, and RpP40) map to the same linkage group as Yb in H. melpomene (Figure 2). In H. numata, Hm01, Hm08, and RpP40 show a conserved pattern of linkage with H. melpomene both in terms of gene order and estimated distances between loci (Figure 2; eIF3-S9 and RpL22 were not variable in mapped broods of H. numata). The two microsatellite loci unfortunately do not cross-amplify in H. erato, but RpL22 and eIF3-S9 both map to the linkage group containing the Cr locus (Figure 2). These data reinforce our observation that linkage order is preserved between distantly related Heliconius species [27] and suggest that the chromosomes bearing colour genes P, Yb, and Cr have not undergone large-scale rearrangement between the three species.

In addition to genotyping a41 and the markers derived from the BAC sequence, we have genotyped and assigned to linkage groups a total of 48 codominant molecular markers from across the genome, including 12 markers for genes known to be involved in the development of wings and patterns in other butterflies or in Drosophila (so-called candidate genes) [29–31], and 37 other conserved single-copy nuclear genes and microsatellites used as anchor loci in comparative mapping [22,27,28] (see Materials and Methods). We found no conflicting linkage relationship between the three species on the 16 linkage groups anchored with shared markers (Table 1) out of a total of 21 in each species [22,27], suggesting a widely conserved pattern of synteny at the genome scale. In H. melpomene, we have also mapped the following: (a) patterning loci B and D, which lie 66.7 cM from the gene Cubitus-interruptus on linkage group 18, (b) locus Ar, which is assigned to LG10, and (c) a locus we here term Khw, which lies 10 cM from the gene wingless on linkage group 1 (Table 1). Khw controls the white/yellow switch of the

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**Figure 3.** Chromosomal Maps for Linkage Group Homologues in H. melpomene (LG15), H. numata (LG15), and H. erato (LG02)

Distances are in Haldane centimorgans. The alternative orders for P and a41 relative to Hm01 in H. numata are not significantly different (ΔLnL = −1.40). Similarly, most orders of N, Sb, Yb, and a41 in H. melpomene are not significantly different (from ΔLnL = −0.15 for the order a41–Yb–N–Sb– to ΔLnL = −0.77 for a41–N–Yb–Sb–). Finally, the two orders for Cr and GerTra in H. erato are also equally significant. Therefore, here we show the most likely gene orders but cannot exclude that the colour loci are on the other side of the anchor loci a41, Fox, or GerTra. In contrast, anchor loci order GerTra–RpP40–Hm01–Hm08 is robust, with alternative orders significantly worse (ΔLnL < −2), although the relative placement of RpL22 and eIF3-S9 is uncertain in H. melpomene and H. erato (ΔLnL > −2).

DOI: 10.1371/journal.pbio.0040303.g003

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this marker to probe a whole-genome bacterial artificial chromosomal (BAC) library of H. melpomene. A 118-kb BAC clone was identified and its genomic location confirmed by the following: (a) alignment with sequences of the a41 locus generated from H. melpomene genomic DNA and (b) recombination mapping of at least one marker derived from the end sequences of this clone in both H. melpomene and H. numata. In
hindwing margins in H. melpomene, and it is putatively distinct from K, which controls the yellow/white switch of the forewing patch in H. cydno [23]. In both cases, the allele for white is dominant to that for yellow.

Discussion

The data provide strong support for the hypothesis that a homologous gene or complex of genes regulates pattern diversity in H. numata, H. melpomene, and H. erato. The hypothesis of genetic homology of mimetic patterns in the geographic radiation of the Müllerian co-mimics H. erato and H. melpomene is a long-standing question, and our data provide the first explicit test, to our knowledge, of this hypothesis. It was initially suggested that shared developmental pathways might facilitate the convergence seen between mimetic species [5]. Subsequently, a more extreme hypothesis was proposed, which states that the actual genes (rather than merely pathways) might be homologous between species [16]. Here we have confirmed the hypothesis of homology, to under 10^{-3} of the Heliconius genome [22,27], of at least one of the major loci controlling convergent patterns between H. erato and H. melpomene (Figure 1).

Tight linkage of these elements could be involved in the switch supergene of the H. numata polymorphic mimicry. The three tightly linked colour pattern loci Yb, Sb, and N clearly segregate on LG15 in H. melpomene, whereas P (H. numata) and Cr (H. erato) show only extremely rare recombinant phenotypes, which could reflect higher crossing-over rates in this genomic region in H. melpomene and/or the involvement of more genetic elements (Figure 3).

Colour patterns develop by the maturation and spatial arrangement of different types of scales on the surface of the developing wing, each characterised by specific pigments and cuticular ultrastructure [16,38]. Our data show that genes on many different chromosomes are involved in the development of the colour pattern. The yellow, red, and orange pigments in Heliconius are ommochromes, and the ommochrome pathway genes — vermillion, white, and scarlet— are all

Figure 4. Annotation of Clone AEHM-41C10 from the Heliconius melpomene BAC Library

The region is situated on LG15 in the H. melpomene genome [22]. The sequence contains open reading frames of strong homology to 12 reported genes, three of which appear to be retrotranspon-associated coding regions (dotted boxes). Also highlighted in double frames are the a41 marker, which was used in H. numata and H. melpomene crosses and to isolate the clone from the library, and the Rab geranylgeranyl transferase gene, used as a marker in H. erato crosses.

DOI: 10.1371/journal.pbio.0040303.g004
Table 1. Linkage Group Associations in *H. melpomene*, *H. numata*, and *H. erato*

| Linkage Group Number | Markers (per Linkage Group) | Abbreviation | LG Assignment |
|----------------------|-----------------------------|--------------|---------------|
|                      |                             |              | *H. m.* | *H. n.* | *H. e.* |
| LG01, HEC04          | *H. melpomene* yellow/white switch | Khw          | ×       |
|                      | Dopa-decarboxylase          | DDC          | ×       | ×       | ×       |
|                      | Wingless                    | Wg           | ×       | ×       | ×       |
|                      | Ribosomal protein L3        | Rpl3         | ×       | ×       | ×       |
|                      | Microsatellite Hm21         | Hm21         | ×       | ×       | ×       |
|                      | Microsatellite Hm07         | Hm07         | ×       | ×       | ×       |
|                      | Microsatellite HeC005       | He05         | ×       | ×       | ×       |
|                      | Mannose phosphate isomerase | Mpi          | ×       | ×       | ×       |
|                      | Microsatellite Hm02         | Hm02         | ×       | ×       | ×       |
|                      | Microsatellite Hm12         | Hm12         | ×       | ×       | ×       |
|                      | Microsatellite Hm15         | Hm15         | ×       | ×       | ×       |
|                      | Microsatellite HeC005       | He17         | ×       | ×       | ×       |
|                      | Microsatellite Hm06         | Hm06         | ×       | ×       | ×       |
|                      | Ribosomal protein L11       | Rpl11        | ×       | ×       | ×       |
|                      | Microsatellite Hm03         | Hm03         | ×       | ×       | ×       |
|                      | Microsatellite Hm17         | Hm17         | ×       | ×       | ×       |
|                      | Microsatellite Hm05         | Hm05         | ×       | ×       | ×       |
|                      | *H. melpomene* yellow patch in forewing discal cell | Ac           | ×       |
|                      | *H. erato* length/shape of yellow forewing patch | Sd           | ×       |
|                      | *H. erato* yellow forewing "R-spot" | R-spot | ×       |
|                      | Patched                     | Ptc          | ×       | ×       | ×       |
|                      | Elongation factor 1-alpha   | EF-1a        | ×       | ×       | ×       |
|                      | Ribosomal protein L19       | Rpl19        | ×       | ×       | ×       |
|                      | Microsatellite Hm03         | Hm03         | ×       | ×       | ×       |
|                      | Microsatellite Hm17         | Hm17         | ×       | ×       | ×       |
|                      | Long-wavelength opsin       | Ops          | ×       | ×       |
|                      | Ribosomal protein L10a      | Rpl10a       | ×       | ×       | ×       |
|                      | Ribosomal protein P0        | Rpp0         | ×       | ×       | ×       |
|                      | Ribosomal protein S5        | Rps5         | ×       | ×       | ×       |
|                      | Ribosomal protein L5        | Rpl5         | ×       | ×       | ×       |
|                      | Ribosomal protein S8        | Rps8         | ×       | ×       | ×       |
|                      | Microsatellite Hm20         | Hm20         | ×       | ×       | ×       |
|                      | Ribosomal protein S9        | Rps9         | ×       | ×       | ×       |
|                      | *H. melpomene* yellow forewing band | N         | ×       |
|                      | *H. melpomene* yellow hindwing bar | Yb         | ×       |
|                      | *H. melpomene* white hindwing margin | Sb         | ×       |
|                      | *H. numata* colour form     | P            | ×       |
|                      | *H. erato* yellow patterns  | Cr           | ×       |
|                      | AFLP band a41              | a41          | ×       | ×       | ×       |
|                      | Forkhead Box J1            | Fox          | ×       | ×       | ×       |
|                      | Rab geranygeranyl transferase b| GerTra     | ×       | ×       | ×       |
|                      | Eukaryotic translation initiation factor subunit 9-eta | eIF3-S9 | ×       |
|                      | Ribosomal protein L22       | Rpl22        | ×       | ×       | ×       |
|                      | Ribosomal protein P40       | Rpp40        | ×       | ×       | ×       |
|                      | Microsatellite Hm01         | Hm01         | ×       | ×       | ×       |
|                      | Microsatellite Hm08         | Hm08         | ×       | ×       | ×       |
|                      | Scalloped                   | Sd           | ×       |
|                      | Ribosomal protein L31       | Rpl31        | ×       | ×       | ×       |
|                      | Ribosomal protein S2        | Rps2         | ×       |
|                      | *H. melpomene* red forewing patch | B         | ×       |
|                      | *H. melpomene* red forewing “dennis” and hindwing rays | D           | ×       |
|                      | *H. erato* red forewing “dennis” and hindwing rays, red/yellow forewing patch | D | ×       |
|                      | Cubitus-interruptus         | Ci           | ×       | ×       | ×       |
|                      | Microsatellite Hm14         | Hm14         | ×       | ×       | ×       |
|                      | Decapentaplegic             | Dpp          | ×       | ×       | ×       |
|                      | Ribosomal protein L44       | Rpl44        | ×       | ×       | ×       |
|                      | Microsatellite Hm13         | Hm13         | ×       | ×       | ×       |
|                      | Microsatellite Hm16         | Hm16         | ×       | ×       | ×       |
|                      | Scarlet                     | St           | ×       |
|                      | White                       | W            | ×       |
|                      | Microsatellite Hm19         | Hm19         | ×       | ×       | ×       |
| Z (sex chromosome)   | Sex                         | sex          | ×       | ×       | ×       |
|                      | Apterous                    | Ap           | ×       |
|                      | Triosephosphate isomerase   | TPI          | ×       | ×       | ×       |
unlinked to patterning genes segregating in our crosses in at least one of the species (Table 1). Furthermore, signalling-pathway genes known to be involved in establishing spatial information in developing butterfly wings—such as engrailed, Distal-less, and decapentaplegic [29,30,39,40]—are also unlinked to switch genes. Two candidate genes were found to be linked to patterning loci (Cubitus-interruptus with B and D, and wingless with Khw), but in both cases, recombination mapping ruled out a direct role for these loci (see below). We have shown that genes involved in wing development and pigment formation are distributed across the genome and not tightly linked to the patterning loci that we have mapped.

A number of observations from these and previous crosses, combined with the results obtained here, offer some clues as to the nature of the N-Yb–Sh/Cr/P complex. (a) The same pigment types are found in different genotypes at this locus in H. erato and H. melpomene (Figure 2B), demonstrating that these loci control placement of pigments but do not switch particular pigment pathways on or off constitutively. (b) In H. melpomene, several tightly linked loci control distinct pattern elements that can be separated by rare recombination. These loci have a similar function in that they all control placement of white or yellow pattern elements (Figure 2A), suggesting that they are either linked paralogous copies of the same gene, or clusters of cis regulatory elements of a single gene. (c) The locus controls patterns across both fore- and hindwings in all three species, but most strikingly in H. numata (Figure 2C). (d) The same allele can both increase and decrease the extent of the same pigment in different areas of the wing surface. In general, alleles adding yellow elements are recessive to those for black, but in the recessive silvana form of H. numata (allele P(B), Figure 2C), dominance of melanin elements is reversed relative to other forms such as tarapotensis (P(B)). Items (c) and (d) imply that the gene product(s) are not directly involved in determining spatial positioning across the wing but are more likely transcribed in response to spatial information. Therefore, this complex locus most likely acts by communicating between spatial coordinate pathways and pigment pathways to create colour pattern elements. We hypothesise that the switch gene is most likely a transcription factor with a number of cis regulatory elements that respond to the spatial information present in different parts of the wing. This transcription factor then triggers a response in sequentially acting downstream pathways to affect pigment deposition and scale morphology that are characteristic of each pattern element. Such regulatory elements would segregate in our crosses between wild forms and might vary in numbers and/or distance across species.

We have shown that another major mimicry locus lies on a homologous chromosome in the two co-mimics (Table 1). Cubitus-interruptus is 75 cM from D in H. erato [27] and 66.7 cM from B and D in H. melpomene (unpublished data). Given the loose linkage, a more precise positional comparison of these loci awaits fine-scale mapping of this linkage group, but the similarity of phenotypic effects of those loci and their location on homologous chromosomes hint at possible genetic homology of B–D and D, and, together with colour pattern loci on other linkage groups (Table 1), hint at a largely shared multilocus colour pattern architecture between the distantly related co-mimics H. erato and H. melpomene. Taken together, these findings in turn reveal a probable route for the evolution of the unusual “supergene” pattern control of H. numata. Local mimicry polymorphism in H. numata is stable and is associated with selection favouring single-locus control of the entire pattern (P) with hierarchical dominance and avoiding nonmimetic intermediates [19,20,41]. However, the evolution of such supergene architecture, where the cosegregation of wing characters can be broken up by recombination [19], and which is most widely known from polymorphic Batesian mimics such as Papilio dardanus or P. memnon [42–44], is a puzzle. Theory predicts that selection against nonmimetic recombinants will rarely lead to the evolution of closer linkage between unlinked elements [41]. Genes must be rather tightly linked in the first place [41,45–47]—for instance via local gene duplications or regulatory element expansion [35,36]—to provide a useful starting point for the evolution of tighter linkage. In contrast to that of H. numata, geographic radiation in H. melpomene is controlled by several unlinked regulatory loci of large effect (N–Yb–Sh, B–D, Ac, and K), and nonadaptive recombinants are probably not a focus of selection because they occur only in narrow hybrid zones [15,17,21]. More distantly related Heliconius, such as H. erato, also have a similar and probably largely homologous multichromosomal mimicry architecture [17,27,38] (Table 1), so that the single-locus inheritance in H. numata is a derived state (Figure 1). Our results thus suggest that part or all of the existing N–Yb–Sh complex of H. melpomene has evolved into P in H. numata, by taking control of regulation of the entire wing pattern [43,47], whereas the remaining unlinked colour pattern loci (B, D, Ac, and K in H. melpomene; D and Sd in H. erato) do not cosegregate with major colour pattern variation in H. numata (Table 1). This result provides the first empirical evidence against the hypothesis of a “supergene” evolving via a gradual tightening of linkage between previously loosely linked or unlinked genes; this hypothesis has previously been challenged only on theoretical grounds [41,45–47]. The elucidation of the mechanism by which P may have gained control of the entire regulation of wing pattern in H. numata will require the precise identification of the regulatory regions involved at this locus and the developmental pathways in which they take part [35].

To this end, the markers we developed provide a decisive step towards positional cloning of loci underlying colour pattern shifts. Our markers on LG15 are situated within a fraction of a centimorgan of the actual loci under selection, which may represent as little as 130 kb, given the estimated physical-to-map distance of ~165–180 kb/cm [22,28]. The genomic resources now available for positional cloning and large-scale sequencing in the three Heliconius species mean that we are now close to identifying the genes involved in this adaptive radiation [48]. Fine-scale mapping using densely distributed markers will locate the recombination breakpoints in our crosses and narrow the segregating locus to a region of a few kilobases. Furthermore, the phenotypes...
studied occur in the wild and segregate across natural hybrid zones or in polymorphic populations [17,18,20], which will facilitate the use of association studies to test candidate loci [8]. On a broader phylogenetic scale, the identification of the colour pattern alleles segregating in different forms, races, and species in the wild will allow insights into the history of variation at these major loci and lead to testable hypotheses regarding the historical, developmental, or genetic constraints underlying the repeated recruitment of alleles at specific genes in mimetic lineages. Unravelling the molecular structure and developmental role of this locus in *Heliconius* will therefore provide important insights into the evolutionary basis of adaptive novelty.

**Materials and Methods**

**CROSSES.** *H. melpomene cythera* (Mindo, Ecuador) and *H. m. malletti* (Rio Quijos, Baecia, Ecuador) were each crossed to a stock of *H. m. melpomene* (French Guiana) to generate F2 mapping families in Gamboa, Panama, following methods described previously [17]. The *Yb* and *Sb* loci were scored in 419 individuals from four replicate *H. m. cythera × H. m. melpomene* F2 crosses. *Yb* was scored as codominant based on the altered reflectance of heterozygote phenotypes [15], whereas *Sb* was scored as a 1:1:1:1 ratio (Figure 2A). *N* was scored in 281 individuals from two *H. m. malletti × H. m. melpomene* F2 crosses (Table S1). Using a similar protocol, F2 and backcross families were derived from local forms of *H. numata* in Tarapoto, in eastern Peru [20]. Genotypes at the *P* locus in *H. numata* were scored in 306 individuals representing three F2 families of heterozygous *H. n. t. elegans* (p<sup>1</sup>(p<sup>2</sup>)<sup>1</sup>) fathers to *H. n. t. aurota* (p<sup>1</sup>(p<sup>1</sup>)<sup>1</sup>) or *H. n. t. arcuella* (p<sup>1</sup>(p<sup>1</sup>)<sup>1</sup>) mothers, and three individuals backcross to homozygous *H. n. t. silvana* (p<sup>1</sup>(p<sup>1</sup>)<sup>1</sup>) (Table S2; Figure 2C). In *H. erato*, the *Cr* locus was genotyped in a backcross (76 individuals) and an F2 intercross (117 individuals) between *H. e. cyria* (Guayquichuma Glen, Ecuador) and *H. himera* (Vilcabamba, Ecuador) generated in insectaries in Puerto Rico. Alternative alleles at the *Cr* locus are codominant in these crosses, although distinguishing *Cr<sup>a41</sup>Cr<sup>Cr</sup>* genotypes was more difficult in some genetic backgrounds [24,28] (Table S3; Figure 2B). In addition, a reference F2 intercross (97 individuals) between *H. e. notabilis* (Puyo, Ecuador) and *H. himera* (Vilcabamba, Ecuador) was genotyped for PCR markers GerTra and RflP2; this reference cross does not segregate for *Cr* (Table S3). Parents and progeny were either frozen at −80 °C or preserved in 20% dimethylsulfoxide, 0.25 M EDTA, and saturated NaCl solution (DMSO). DNA was extracted from thorax using the Qiagen DNeasy kit (Hilden, Germany) following manufacturer’s instructions.

**Marker loci.** Development of most of the molecular markers we used is described elsewhere [22,49–51]. Specific primers for single-copy nuclear loci, such as ribosomal proteins, were developed from EST sequences, amplification length variation and RFLPs were used to genotype segregating alleles in mapping families and PCR products were visualised on 1.5% agarose gels. Microsatellites were genotyped using fluorescent-labelled primers on an ABI 3730 capillary sequencing machine (Applied Biosystems, Foster City, California, United States). Specific primers were developed for the amplified fragment length polymorphism marker *a41*, previously identified as being linked to the *H. melpomene* *Yb* locus [21], to allow amplification of this locus in both *H. numata* and *H. melpomene* (Beltrán M, Mavárez J, González M, Bermingham E, Jiggins F, unpublished data). An alignment of *H. melpomene* and *H. numata* *a41* sequences is given in Figure S1. The *a41* region was amplified in *H. numata* and *H. melpomene* with a fluorescent-labelled primer, and the product was visualised as for microsatellite loci. In all broods except one, length variation segregated at the *a41* locus and could be scored as for microsatellites.

**Mapping.** Alleles derived from the mother (female-informative) were used to confirm synteny of linked markers [21], because chromatin intacts in the mother occur in the lack of crossing over in female Lepidoptera [52]. Alleles derived from the brood father (male-informative) were scored as for a backcross brood, and recombination distances were calculated using MapMaker [53]. Linkage group assignment was carried out using JoinMap 3.0 [54].

**BAC clone identification and sequencing.** An *H. melpomene* BAC library was constructed by Ampiclon Express (Pullman, Washington, United States) from high-molecular weight DNA derived from six larvae of *H. melpomene*. A total of 18,816 clones were picked, with an average insert size of 123 kb, giving an estimated 85% genome coverage. The entire library was gridded onto nylon membranes in a high-density 4 x 4 array of 6,144 (16 x 384) spots, each representing a single clone gridded once. These arrays were hybridised with a PCR-derived probe for the *a41* marker labelled with P32 using the Prime-It II Random Primer Labeling Kit (Stratagene, La Jolla, California, United States). Probe cleanup was carried out using a NucTrap Probe Purification Column (Stratagene). Hybridisation of the filters was carried out using protocols recommended by the Sanger Institute (http://www.sanger.ac.uk/HPG/methods/mapping/screening/hyb. shtml). A single positive clone was identified and confirmed by PCR. This clone was then sequenced, assembled, and finished by the Sanger Institute. Briefly, the clone was sheared to create 4- to 6-kb fragments that are cloned as a library into pUC19. Approximately 6x sequence coverage of each BAC was then generated in paired 600- to 800-bp reads. Data were assembled using Phrap software and edited in a GAP4 database. Contigs were extended by oligo walking. The BAC sequence was annotated using BLAST comparison with a UniRef100 database and with our Heliconius EST dataset.

**Development of the GerTra marker.** The following primers were then designed to span a 3-kb intron between two exons showing homology to the *Rab geranylgeranyl transferase beta subunit* (RGGII; *Homo sapiens*) (Figure 4 and Figure S3): GerTra-Int-F 5′-ctggtctgtgtttccttt-3′ and GerTra-Int-R 5′-gaggaactacctacggctt-3′. These primers amplified a single 1.2-kb product in *H. erato*, which was sequenced to confirm homology with the *H. melpomene* region (see Figure S2 for an alignment with the *H. melpomene* BAC clone sequence). New *H. erato*-specific primers (GerTra-Int-HeF 5′-ggtgtgtttgttgaag-3′ and GerTra-Int-HeR 5′-attgtgatctaaasaggc-3′) were designed that gave more consistent amplification from genomic DNA. Genotypes at the *Cr* locus were determined by following the segregation of allele size variants in 1%-2% agarose gels.

**Supporting Information**

Figure S1. Alignment of *a41* Sequences for *H. melpomene* and *H. numata*

The high homology of the sequences (scores > 84) confirms that the fragments represent orthologous markers in both species. The large insertions and deletions in the middle of the sequence allowed easy genotyping (Beltrán M, Mavárez J, González M, Bermingham E, Jiggins F, unpublished data).

Found at DOI: 10.1371/journal.pbio.0040303.sg001 (30 KB DOC).

Figure S2. Alignment of a *H. melpomene* *a41* Sequence with BAC Clone AEHM-41C10

The marker corresponds to positions 5,829-6,170 on the BAC sequence.

Found at DOI: 10.1371/journal.pbio.0040303.sg002 (27 KB DOC).

Figure S3. Alignment of *H. erato* GerTra Sequences with *H. melpomene* BAC Clone AEHM-41C10

Because the PCR amplics in *H. erato* are too large for complete sequencing, we provide here the alignment of both end sequences with the respective *H. melpomene* *Rab geranylgeranyl transferase* exons from which the primers were designed. exon 1 lies at position 19,970:20,290 and exon 2 at 21,535:21,846, with a 1,245-bp intron in between.

Found at DOI: 10.1371/journal.pbio.0040303.sg003 (38 KB DOC).

**Table S1.** Mapping Families and Colour Pattern Genotypes in *H. melpomene*

Details of the *H. m. cythera × H. m. melpomene* F2 crosses segregating for *Yb/Yb, S/Sb*, and *Khw/Khw*, and *H. m. malletti × H. m. melpomene* F2 crosses segregating for *N′/N′, B/b*, and *Dδ/Dδ* (full pedigree information available upon request; codes in brackets identify the brood from which each parent originates; *Khw* is only expressed in a *S′/S*′ background. See Figure 2A for details of wing patterns.

Found at DOI: 10.1371/journal.pbio.0040303.s001 (98 KB DOC).

**Table S2.** Mapping Families and Colour Pattern Genotypes in *H. erato*

Details of the F2 cross (CH-CH5) and the backcross (CH-Cy6) of *H. e.*
References
1. Carroll SB, Grenier JK, Weatherbee SD (2001) From DNA to diversity: Molecular genetics and the evolution of animal design. Malden (Massachusetts): Blackwell Science. 214 p.
2. Gompel N, Prud’homme B, Witzkopp PJ, Kassner VA, Carroll SB (2005) Chance caught on the wing: cis-regulatory evolution and the origin of pigment patterns in Drosophila. Nature 435: 481–487.
3. Müller F (1879). Müller F (1879) Imitation and Thrydias: A remarkable case of mimicry in butterflies. Trans Entomol Soc Lond 1879: xx–xxi.
4. Fisher RA (1958) The genetic theory of natural selection, 2nd revised edition. New York: Dover. 291 p.
5. Goldschmidt RB (1945) Mimetic polymorphism, a controversial chapter of genetics. New York: Reinhold. 471 p.
6. Cresko WA, Amores A, Wilson C, Murphy J, Currey M, et al. (2004) Parallel evolution in the NOTF2–9 reference F2 cross was used to map gene markers in the Heliconius erato BAC clone AEHM-41C10 is CR974474. Coloured superscript numbers identify chromosomes identical by descent in different broods (full pedigree information available upon request; codes in brackets give the brood from which each parent originates). See Figure 2C for details of wing patterns. Proc Natl Acad Sci U S A 101: 6050–6055.
7. Cresko WA, Amores A, Wilson C, Murphy J, Currey M, et al. (2004) Parallel genetic basis for repeated evolution of armor loss in Alaskan threespine stickleback populations. Proc Natl Acad Sci U S A 101: 6050–6055.
8. Sorensen N, Bennet J, Leroi A, Queiroz K, Rodriguez-Schettino L (2005) Widespread parallel evolution in shavenbaby/oovari underlies multiple cases of morphological parallelism. Nature 424: 935–938.
9. Cresko WA, Amores A, Wilson C, Murphy J, Currey M, et al. (2004) Parallel genetic basis for repeated evolution of armor loss in Alaskan threespine stickleback populations. Proc Natl Acad Sci U S A 101: 6050–6055.
10. Sturmbauer C, Hainz U, Baric S, Verheyen E, Salzburger W (2003) The genomic location of wingless. Proc Natl Acad Sci U S A 100: 9704–9709.
11. Schluter D (2000) The ecology of adaptive radiation. Oxford: Oxford University Press. 214 p.
12. Wake DB (1991) Homoplasy—The result of natural selection, or evidence of design limitations. Am Nat 138: 543–567.
13. Price T, Pavella M (1996) Evolution of a colour pattern: History, development, and selection. J Evol Biol 9: 451–470.
14. Mundy NI (2005) A window on the genetics of evolution: MC1R and plumage colouration in birds. Proc R Soc Lond B Biol Sci 272: 1633–1640.
15. Sheppard PM, Turner JRG, Brown KS, Benson WW, Singer MC (1985) Genetics and the evolution of Mullerian mimicry in Heliconius butterflies. Philos Trans R Soc Lond B Biol Sci 308: 433–610.
16. Nijhout HF (1991) The development and evolution of butterfly wing patterns. Washington (D. C.): Smithsonian Institution Press. 297 p.
17. Mallet J (1989) The genetics of warning colour in Peruvian hybrid zones of Mullerian mimicry. Proc R Soc Lond B Biol Sci 264: 236–242.
18. Mundy NI (2005) The evolution of the genomic location of wingless. Proc Natl Acad Sci U S A 100: 9704–9709.
19. Brown KS, Benson WW (1974) Adaptive polymorphism associated with multiple Mullerian mimicry in Heliconius numata. Biotropica 6: 205–228.
20. Mallet J, Wynne IR, Lamas G, Mallet J (1999) Variable selection and the coexistence of multiple mimetic forms of the butterfly Heliconius numata. Evol Ecol 13: 721–754.
21. Naisbit RE, Jiggins CD, Mallet J (2003) Mimicry: Developmental genes that contribute to speciation. Evol Dev 5: 269–280.
22. Jiggins CD, Mallet J, Beltrán M, McMillan WO, Johnston JS, et al. (2005) A genetic linkage map of the mimetic butterfly, Heliconius numata. Genetics 171: 557–570.
23. Kronforst MR, Young LG, Kapan DD, McNeely C, O’Neill RJ, et al. (2006) Linkage of butterfly mate preference and wing color preference cue at the genomic location of wingloss. Proc Natl Acad Sci U S A 103: 6575–6580.
24. Jiggins CD, McMillan WO (1997) The genetic basis of an adaptive radiation: Warning colour in two Heliconius species. Proc R Soc Lond B Biol Sci 264: 1167–1175.
25. Mather K (1950) The genetic architecture of heterozygosity in Primula elatior. Evolution 4: 340–352.
26. Turner JRG (1968) Natural selection for and against a polymorphism which interacts with sex. Evolution 22: 481–495.
27. Kapan DD, Flanagan NS, Tobler A, Papa R, Reed RD, et al. (2006) Localization of Mullerian mimicry genes on a dense linkage map of Heliconius erato. Genetics 173: 735–757.
28. Tobler A, Kapan DD, Flanagan N, Gonzalez C, Peterson E, et al. (2005) First-generation linkage map of the warningly colored butterfly Heliconius erato. Heredity 94: 408–417.
29. Carroll SB, Gates J, Keys DN, Paddock SW, Panganihan GEF, et al. (1994) Patterns of formation and eyepatch determination in butterfly wings. Science 265: 109–114.
30. Brakefield PM, Gates J, Keys DN, Kesbeke F, Wijngaarden PJ, et al. (1996) Development, plasticity and evolution of butterfly eyepatch patterns. Nature 384: 236–242.
31. Beldade P, Brakefield PM, Long AD (2002) Contribution of Distal-less to quantitative variation in butterfly eyepatches. Nature 415: 315–318.
32. Schluter D, Clifford EA, Nemethy M, McKinnon J (2004) Parallel evolution and inheritance of quantitative traits. Am Nat 163: 809–829.
33. Shubin N, Wake DB, Crawford AJ (1995) Morphological variation in the limbs of Taricha granulosa (Caudata, Salamandridae)—Evolutionary and phylogenetic implications. Evolution 49: 874–884.
34. Richardson MK, Brakefield PM (2003) Hotspots for evolution. Nature 424: 894–895.
35. Carroll SB, Gompel N, Prud’homme B, Witzkopp TJ, Kassner VA (2005) Chance caught on the wing: cis-regulatory evolution and the origins of novelty. Dev Biol 283: 584–594.
36. Ranson H, Claudianos C, Ortelli F, Abgrall C, Hemingway J, et al. (2002) Linkage of butterfly mate preference and wing color preference cue at the genomic location of wingloss. Proc Natl Acad Sci U S A 103: 6575–6580.
37. Petkov PM, Graber JH, Churchill GA, DiPetrillo K, King BL, et al. (2005) Evidence of a large-scale functional organization of mammalian chromosomes. PLoS Genet 1: e33. DOI: 10.1371/journal.pgen.0010033
38. Gilbert LE (2003) Adaptive novelty through intragenre introgression in Heliconius wing patterns: Evidence for a shared genetic ‘tool box’ from synthetic hybrid zones and a theory of diversification. In: Boggs CL, Watt WB, Ehrlich PR, editors. Ecology and evolution taking flight: Butterflies as model systems. Chicago: University of Chicago Press. pp. 281–318.
39. Keys DN, Lewis BL, Selegue JE, Pearson BJ, Goodrich LV, et al. (1999) Recruitment of a hedgehog regulatory circuit in butterfly eyepatch evolution. Science 283: 532–534.
40. Beldade P, Brakefield PM (2002) The genetics and evo-devo of butterfly wing patterns. Nat Rev Genet 3: 442–452.
41. Charlesworth D, Charlesworth B (1975) Theoretical genetics of Batesian mimicry II. Evolution of supergenes. J Theor Biol 55: 305–324.
42. Clarke CA, Sheppard PM (1963) Interactions between major genes and polygenes in the determination of the mimetic patterns of Papilio dardanus. Evolution 17: 404–413.
43. Turner JRG (1984) Mimicry: The palatability spectrum and its consequences. In: Vane-Wright RI, Ackery PR, editors. The biology of butterflies. London: Academic Press. pp. 141–161.
44. Nijhout HF (2003) Polymorphic mimicry in Papilio dardanus: Mosaic dominance, big effects, and origins. Evol Dev 5: 579–592.
45. Sheppard PM (1959) The evolution of mimicry: A problem in ecology and genetics. Cold Spring Harb Symp Quant Biol 24: 131–140.
46. Turner JRG (1977) Butterfly mimicry: The genetical evolution of an adaptation. Evol Biol 10: 163–206.
47. Le Thierry d’Ennequin M, Toupane B, Robert T, Godelle B, Gouyon PH (1999) Plant domestication: A model for studying the evolution of linkage. J Evol Biol 12: 1138–1147.
48. Joron M, Jiggins CD, Papanicolaou A, McMillan WO (2006) Heliconius wing patterns: An evo-devo model for understanding phenotypic diversity. Heredity. E-pub ahead of print.
49. Kronforst MR (2005) Primers for the amplification of nuclear introns in Heliconius butterflies. Mol Ecol Notes 5: 158–162.
50. Mavarez J, Gonzalez M (2006) A set of microsatellite markers for Heliconius melpomene and closely related species. Mol Ecol Notes 6: 20–23.
51. Papanicolaou A, Joron M, McMillan WO, Blaxter ML, Jiggins CD (2005) Genomic tools and cDNA derived markers for butterflies. Mol Ecol 14: 2883–2897.
52. Suomalainen E, Cook LM, Turner JRG (1973) Achiasmatic oogenesis in the heliconine butterflies. Hereditas 74: 302–304.
53. Lander E, Abrahamsen J, Barlow A, Daly M, Lincoln S, et al. (1987) Mapmaker: A computer package for constructing genetic-linkage maps. Cytogenet Cell Genet 46: 642–642.
54. Stam P (1993) Construction of integrated genetic-linkage maps by means of a new computer package—JoinMap. Plant J 3: 739–744.
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Joron, M; Papa, R; Beltran, M; Chamberlain, N; Mavarez, J; Baxter, S; Abanto, M; Bermingham, E; Humphray, SJ; Rogers, J; Beasley, H; Barlow, K; ffrench-Constant, RH; Mallet, J; McMillan, WO; Jiggins, CD

Title:
A conserved supergene locus controls colour pattern diversity in Heliconius butterflies

Date:
2006-10-01

Citation:
Joron, M., Papa, R., Beltran, M., Chamberlain, N., Mavarez, J., Baxter, S., Abanto, M., Bermingham, E., Humphray, S. J., Rogers, J., Beasley, H., Barlow, K., ffrench-Constant, R. H., Mallet, J., McMillan, W. O. & Jiggins, C. D. (2006). A conserved supergene locus controls colour pattern diversity in Heliconius butterflies. PLOS BIOLOGY, 4 (10), pp.1831-1840. https://doi.org/10.1371/journal.pbio.0040303.

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