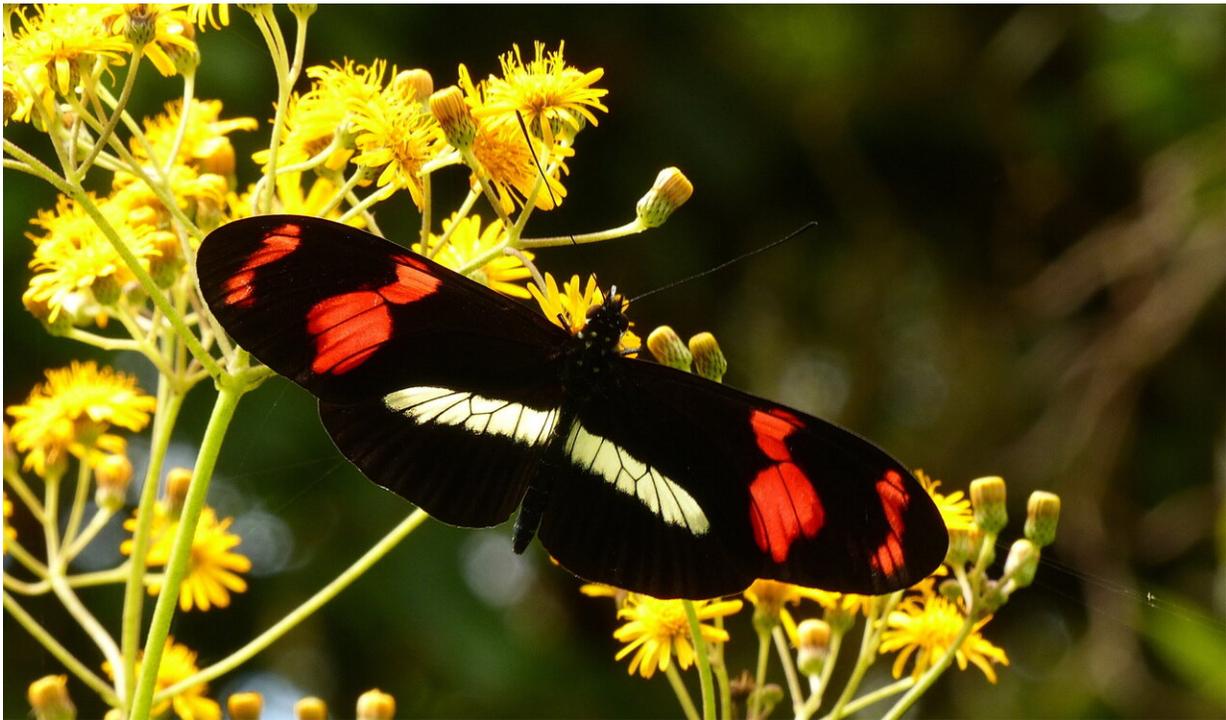


# Study reveals surprising amount of gene flow among butterfly species

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Photograph of a *Heliconius telesiphe* by Andrew Neild  
(<https://andrewneild.wixsite.com/home>) Credit: Andrew Neild, Photographer

An international team of researchers analyzed the genomes of 20 butterfly species and discovered a surprisingly high amount of gene flow among them - even between species that are distantly related. The findings, published in the journal *Science*, challenge conventional views

about species and point to hybridization as a key process in the emergence of biological diversity.

Different [species](#) of passion vine butterflies (Heliconius) have similar color patterns that serve as warnings to predators. Scientists have previously found that one reason for their similarity is that they actually share parts of their DNA, thanks to hybridization that occurred at some point in their ancestry. The new findings suggest that this process of DNA sharing is far more common than previously thought.

To understand how butterflies pass genes to other species by hybridizing, a process known as introgression, the researchers analyzed new [genome](#) assemblies of 20 Heliconius [butterfly species](#).

"DNA sharing had been shown in closely related species, but we wanted to probe deeper into the [phylogenetic tree](#)," said senior author James Mallet, Professor of Organismic and Evolutionary Biology in Residence and Associate of Population Genetics in the Museum of Comparative Zoology. "What we found is really astonishing: introgression even among species that are distantly related. "Species" are simply not what we thought they were, and now we have the data to show it. The evolutionary tree of butterflies is a complete morass of interconnectedness - every bit of the butterfly genome seems to have a different tree."

Lead author Nate Edelman, a graduate student in the Mallet group, explained that the new genome assemblies function as detailed genomic maps. They are constructed by sequencing short fragments of DNA, then assembling them in the proper order. Genome assemblies are an important resource for researchers, as they make it possible to map genes back to the genome.

"The cool thing about making genome assemblies instead of simple

genome "resequencing" is that it's not just the DNA bases that change - the entire structures of genomes can change through evolutionary time," Edelman said. "And using the assemblies, we can detect those changes."

When they began analyzing the assemblies, the team found evidence that some genes were capable of moving between species, and others were far more resistant to the process. One of the key factors that determining whether a gene could or could not move is a basic biological process called "recombination".

"In humans and most animals, every individual inherits two copies of their genome, one from her mother, and one from her father," explained Mallet. "The reason you differ genetically from your sibling is due to recombination. Your father contributed to you a newly scrambled, recombined copy of his own parents' genomes, as did your mother with her parents' genomes. So the combination of components from each parent is different in every individual."

Recombination is thought to be advantageous if the goal is to generate diverse genotypes for future generations. The system of recombination described in this study suggests that it also occurs during gene flow between species. According to the authors, this could provide a possible route for adaptive genes to be passed occasionally between species, as well within species.

"It might seem that useful genes are more likely to be transferred between species," said co-author Michael Miyagi of Harvard University. "That's true, but there are also more mundane structural issues with the genome that mean some regions are more likely to have genes go back and forth."

According to Edelman, whether those genes flow back and forth often depends on how much those different regions recombine.

"In low recombination regions, we tend to see more resistance to gene flow than in high recombination regions," he said. "What we think happens is that in very high recombination regions, the genes that are resistant or incompatible become dissociated from the [genes](#) that can flow across the species boundary."

The team was able to identify a key gene that acts to switch color patterns as one that moved between species.

"Heliconius butterflies are famous for their color patterns. We found that in one particular region of the genome, there are about 500,000 base pairs that have been inverted relative to the ancestral sequence," said Miyagi. "And smack in the middle of that inversion is that gene that we know controls color pattern. When you have an inversion like that, it means you're keeping all the things within it together, so they can't recombine."

The new genome assemblies also led to the discovery of a new, larger inversion on a different chromosome.

Using the new analysis method developed by Miyagi, the researchers showed that one of those inverted sequences was transferred among species.

"If we look at any specific chunk of DNA, each one has a specific history," Miyagi explained. "So the method we developed looks at these bits of DNA and can tell us which ones are more or less likely to be introgressed."

The study concludes that hybridization is one way for species to derive their genomes, and may be a key process in the creation of the diversity of life we see today.

"In nature, it's very unlikely that any individual will mate with a member of another species," Mallet said. "But over evolutionary time, it does happen. It probably only happens in the 'youngest' groups of species - species that are rapidly evolving. Most of the diversity of life is probably created in these rapid radiations. They are involved in events such as the origin of mammals. During these radiations, the hybridization and introgression we document here could be an important means of shuffling variation and recombining adaptations from different lineages."

The study has its roots in the Heliconius Genome Consortium, which set out in 2009 to address questions about evolution and adaptation by sequencing the genome of one Heliconius butterfly species. The new study has made 20 new genome assemblies available. Data from the study have been made freely available in public archives.

"Open data and sharing between laboratories is so important for understanding evolution, and how bursts of diversity happen," said Mallet. "In this international consortium we've each brought very different strengths and helped each other do much better science overall, and the result has been a resource that our collaborators, as well as anyone else, can use well into the future."

**More information:** N.B. Edelman et al., "Genomic architecture and introgression shape a butterfly radiation," *Science* (2019).  
[science.sciencemag.org/cgi/doi ... 1126/science.aaw2090](https://science.sciencemag.org/cgi/doi/10.1126/science.aaw2090)

Mapping footprints of past genetic exchange," *Science* (2019).  
[science.sciencemag.org/cgi/doi ... 1126/science.aaz1576](https://science.sciencemag.org/cgi/doi/10.1126/science.aaz1576)

Provided by Harvard University

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