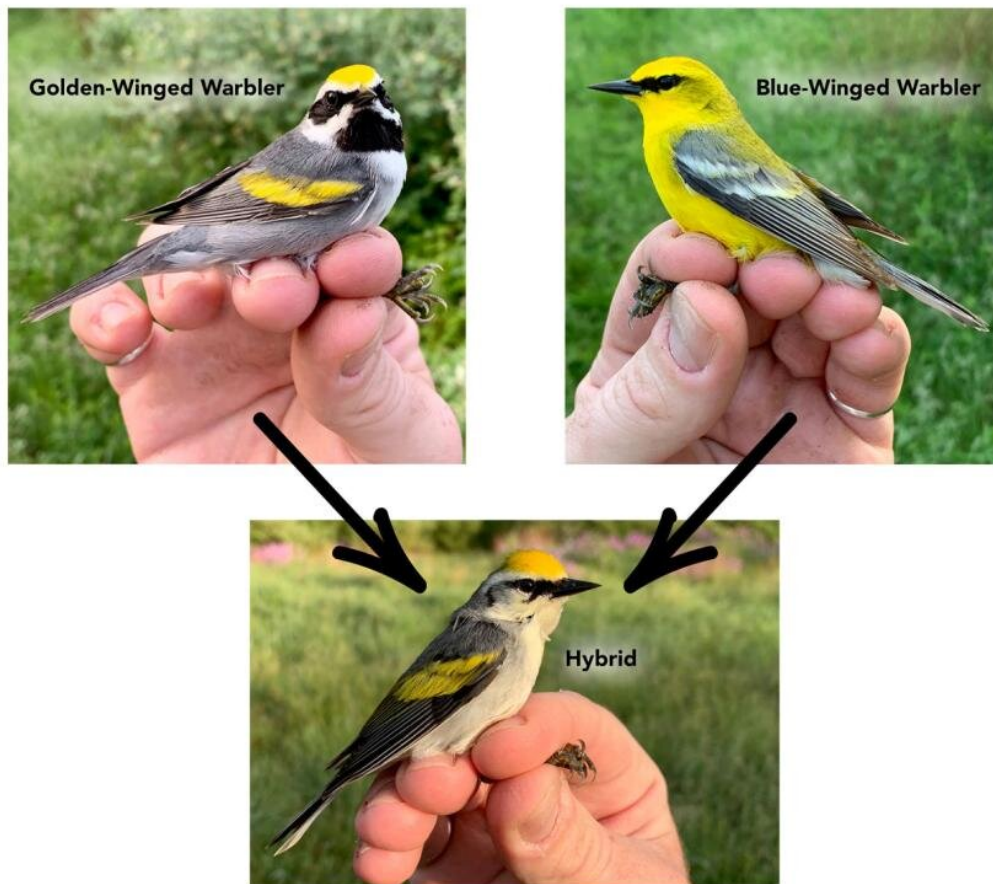


Biologists explore the secrets of the warbler genome

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While blue-winged warblers have predominantly yellow underparts, golden-winged warblers have white bellies and a black throat patch and face mask. Hybrid offspring of blue-winged and golden-winged warblers have a mix of coloration from the two parent species, and can thus be used to help identify which parts of the genome are associated with which color patterns. Credit: David Toews, Penn State

Looking through binoculars at the trees in their backyards during the pandemic, many brand-new birders may have been surprised by the diversity of visitors stopping by—finches, jays and warblers in an astounding array of yellows, blues and reds.

"Warblers in particular have an impressive diversity of colors and patterns across more than one hundred [species](#)," said David Toews, assistant professor of biology at Penn State. "My lab uses genomic tools to understand this diversity as well as how so many distinct species of these songbirds evolved so rapidly in evolutionary time."

Toews and his lab began with the most obvious differences between warblers: their colors. To pinpoint the [genes](#) associated with specific color patterns, they turned to the individual birds that result when two similar species of warblers interbreed. These hybrid offspring mix and match the color patterns of their parents, so by comparing the genomes of both parent species and the hybrids, the lab was able to identify which regions of the [genome](#) correspond to which color patterns.

"We identified a region of the genome that drives the black throat and face mask in these species," said Toews. "This region is located near a gene called Agouti-signaling protein (ASIP), which is known to regulate production of the pigment melanin."

In a separate study, his lab identified another gene, called beta-carotene oxygenase 2 (BCO2), which is thought to be involved in producing carotenoid pigments that result in bright yellow, red, and orange plumage.

"Once we had identified the [genetic regions](#) involved in color production in these species that hybridize, we could then compare these regions

across a larger group of warblers to understand how they might have evolved," said Toews.

Toews and his lab sequenced and compared the genomes of 34 [warbler](#) species within the genus Setophaga. Differences near the ASIP gene suggest that their black coloration likely arose through a common path of evolution, with mutations arising independently in different species. However, genetic differences near BCO2 paint a more interesting picture for yellow plumage.

The lab found evidence that genetic material had been shuffled between different pairs of warbler species through a process called introgression. This can occur when two separate species mate to produce a hybrid, and the hybrid goes on to mate with one of the original species. After several generations, genetic material from one species can be incorporated into the other.

"Genomes tell the story of all the ancestors that were involved in an individual's production, so we can look for ancient examples of hybridization and gene flow within the genomes of contemporary birds," said Toews. "Similarly, we weren't around to observe the hybridization of Homo sapiens and Neanderthals, but we can deduce that it occurred from genomic data. Ancestry tests can even reveal how many genetic variants from Neanderthals you have, which were introduced thanks to ancient instances of introgression."

The researchers also suspect that introgression may have occurred with species outside of the Setophaga genus. To explore this possibility, they are broadening their comparisons to include even more birds.

"Now we're expanding to the entire family of wood warblers, and instead of focusing on just genes related to color, we are looking at the whole genome," said Toews. "We're looking more broadly at how these birds

differ."

For example, Toews and colleagues have explored the genes responsible for warblers migrating south to winter in different locations. To determine where in Central and South America the birds spend their winters, the researchers track them using tiny bird backpacks, whose geolocators record light levels and reveal the bird's location.

"We are also using modern methods to ask some basic questions about the biology of these [birds](#)," said Toews. "For instance, it's really difficult to understand what insects they are eating unless you are high up in the canopy with them, so we're now using genomic tools to analyze fecal samples to reconstruct their diet and explore the microbes in their gut."

As the lab sequences the genomes of more and more species, they may be able to understand the genetics underlying different diets and behaviors.

"None of the species that we have worked on had previously had their genomes sequenced, so this is really unexplored territory," said Toews. "For a long time, people looked at the hundred or so species of warblers and thought they were ecologically pretty similar, like they were kind of redundant but just looked different. What we're finding is that obviously isn't the case, and that we can now pinpoint the individual genes that are involved with making them so diverse. It's a pretty exciting time to be a bird nerd studying genomics!"

Provided by Pennsylvania State University

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