

Songbirds' epic migrations connected to a small cluster of genes

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Swainson's thrush in the wild, British Columbia, Canada. Credit: Darren Irwin, University of British Columbia

Scientists from the University of British Columbia have shown that there is a genetic basis to the migratory routes flown by songbirds, and have narrowed in on a relatively small cluster of genes that may govern the behaviour.

"It's amazing that the routes and timing of such complex behaviour could be genetically determined and associated with a very small portion of the genome," said researcher Kira Delmore, lead author of the paper published today in *Current Biology*.

"What's even more amazing is that differences in this behaviour could be helping to maintain the huge diversity of songbirds we see in the natural world."

Seasonal migration is one of the most remarkable biological phenomena in the world, with routes spanning thousands of kilometres and involving billions of animals. Songbirds travel up to 15,000 kilometres, despite often weighing under ten grams. They undertake these journeys alone at night and return to the same locations year after year.

Delmore and her colleagues used coin-sized light-level geolocators to track songbirds' migrations, and next-generation sequencing techniques to get an in-depth view of their genomes. They applied these two recently-developed techniques to two closely related groups of Swainson's thrushes in B.C., and their hybrids.



Swainson's thrush wearing a geolocator. Credit: Kira Delmore, University of British Columbia

While the groups are evolutionarily and genetically related, they take different routes on migration each year. A coastal group migrates down the west coast, southward to Mexico and Central America, while an inland group near Kamloops migrates southeastward to the southeastern USA and then South America. The groups interbreed northeast of Vancouver, in the coastal mountains.

Previous work conducted by the team showed that birds from the hybrid population take intermediary migration routes, which cross deserts and mountainous regions. These inferior routes likely cause hybrids to have

lower reproductive success, resulting in less gene flow between the groups and more differentiation between them.

By linking the [migratory behavior](#) of hybrids to their genetic makeup, these researchers pinpointed a single cluster of roughly 60 genes on one chromosome that largely accounts for the difference in migration patterns.

The genes play an important role in the birds' circadian, nervous and cell signalling systems. They are also located in regions of the genome that have reduced movement of genes from one population of thrushes to the other.

"Smaller scale studies have associated some genes in this region with migratory behavior in organisms as diverse as butterflies, fish and other birds," said UBC zoologist Darren Irwin, senior author of the study. "These results provide even stronger evidence that evolution of this genetic cluster can cause different [migratory routes](#), facilitating the evolution of two species from one."

Delmore conducted the research while at UBC and is now with the Max Planck Institute for Evolutionary Biology, where she will continue to winnow down the set of [genes](#) responsible for migration, and use the same cutting edge techniques to investigate other populations of birds.

Provided by University of British Columbia

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