

Profile of Scott Edwards

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Looking through Scott Edwards' curriculum vitae is like wandering the halls of the natural history collections he curates: an invitation to dive deeply into one area combined with permission to think broadly and zip enthusiastically from one exhibit to another. Zoologist and curator of ornithology of Harvard's Museum of Comparative Zoology, Edwards was elected to the National Academy of Sciences in 2015. Although Edwards primarily uses birds as models to study molecular evolution and biodiversity, he took a foray into amphibians in his Inaugural Article (1), analyzing the diminutive genome of the ornate burrowing frog. In the past, he has documented rapid genomic shifts in green anole lizards in response to winter storms in the southern United States and examined the genome sizes of organisms, ranging from bacteriophages to dinosaurs (2-4).

Birds are Biology

As a youth, Edwards became interested in birds when a neighbor in Riverdale, New York, invited him to go birdwatching in their Bronx neighborhood. Something about matching the species in the field with pictures in a book appealed to him. When he entered Harvard University in 1981, Edwards was not thinking about studying ornithology but was instead headed toward medical school. "My dad was a doctor," he says. "It just seemed like, 'Well, that's what biologists do.'" While still an undergraduate, he took a year off to learn the kinds of work that field biologists do. Edwards volunteered in collections at the Smithsonian Institution in Washington, DC, and participated in field work in Hawaii, where he was born and had lived briefly.

When he returned to Harvard, Edwards worked in the laboratory of Rodney Honeycutt on his undergraduate thesis, analyzing the mitochondrial DNA of African mole-rats (5). Seeing molecular tools and techniques applied outside of medicine was a gamechanger. "It was hard for me to believe that such hightech equipment could be used to study such a fun thing that wasn't related to human health. This was evolution," Edwards says. "In a weird way, I'm very thankful I took organic chemistry because I just hated that course. That's what inspired me to take a year off." These experiences in museum, field, and laboratory settings shaped Edwards' desire to pursue doctoral work.



Scott Edwards on his 76-day, 3,848-mile trek across the United States during the summer of 2020. Image credit: Scott Edwards.

Around this time, University of California, Berkeley biochemist Allan Wilson was using cutting-edge genetic techniques to study evolution. The work, as well as Berkeley's mild climate, appealed to Edwards. Edwards spent much of the first year of his doctoral studies in the field, ending up in Australia, where he found the eventual subject of his dissertation research, a group of birds called babblers. "It turned out it was a great group to study. They were relatively common. They were fairly easy to catch. They occurred in groups, so I could look at genetic variation within the groups and between groups," Edwards explains. "This was very early days in this field that today we call 'phylogeography'" (6).

Roots and Branches

"[Phylogeography] refers to looking at the pattern of genetic trees across [the] geography of a species,"

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Orioles (Icterus) in the ornithology collections of the Museum of Comparative Zoology at Harvard University. Image credit: Museum of Comparative Zoology at Harvard University/Jeremiah Trimble.

explains Edwards. "Back when I was in grad school, in the mid to late 1980s, it was really this new awareness that the phylogeny of a group of organisms was the appropriate framework in which to study their evolution. Until then, people thought of a group of species in some sort of linear order. It turns out that this branching pattern, or phylogeny, is central to how we can best understand how organisms have evolved and how their traits evolve," he says.

Edwards has continued to work on phylogeography, taking advantage of advances in genomics and data analytics. "It's been incredible to be doing science during this era because during my dissertation, we said, 'Wow, collecting 400 base pairs of DNA from 100 individuals, is just amazing.' And honestly, I don't think any of us imagined we would be sequencing whole genomes from these same individuals," he says. "That has been the most astounding change in our field."

More information has meant more choices to make in creating phylogenetic trees. "We have lots of data. How do we actually translate that into a statement of relationships between species? Some of our work in the last 10 years has tried to develop new ways to just build these trees from genetic data," explains Edwards. "We've developed ways to infer the species tree from the gene trees" (7). To do this, they build multiple trees using individual genes as starting points. These trees often differ from each other, especially when species have radiated quickly. "This is how evolution works," says Edwards. "It's a very noisy process. And so it behooves us to collect all the gene sequences, make trees of them, look at how variable the trees are-how much they differ from each other-and then take that information and produce an ensemble tree. It's not as simple as taking the most common tree."

Edwards recently received his first NIH grant to uncover the genetic basis of convergent evolution, a phenomenon that occurs when unrelated species develop similar phenotypes. The effort builds on his previous work in large flightless birds, like the emu, showing that loss of flight occurred multiple times over the course of evolution (8). "I'm really excited because this NIH grant is bringing together, of course, my interest in birds, but also my interest in statistical models using phylogenetics. Basically, we're going to be developing new models for linking genotype to phenotype using phylogenetic trees."

Multifaceted Major Histocompatibility

After earning his doctorate in 1992, Edwards found himself in a surprising place. "I actually did my postdoc at the University of Florida Medical School. To this day I sort of scratch my head: How did I end up in a medical school?" He had come to work with immunologists Wayne Potts and Edward Wakeland, both of whom were studying the major histocompatibility (MHC) complex in mice. Also found in humans, MHC genes act as unique molecular identifiers for an individual's cells. Edwards compared MHC gene sequences from three species of songbirds with mammalian MHC to analyze evolutionary relationships, finding that genes within each species of avian MHC were more closely related to each other than similar genes in related species (9). Work on MHC genes in blackbirds formed the basis of Edward's first successful National Science Foundation research grant after he took a position at the University of Washington's Burke Museum. "We did a lot of population genetics to try to understand the selective forces acting on MHC genes" (10).

A 1994 outbreak of Mycoplasma in house finches and its subsequent spread presented opportunities for Edwards and collaborator Geoff Hill of Auburn University to reconstruct the pathogen's spread and study the coevolution of the host and bacteria using MHC genetics (11). Edwards has also explored the behavioral aspects of MHC by focusing on chemical ecology and mate choice in Leach's storm-petrels with ecologist Gabrielle Nevitt at the University of California, Davis. "The storm-petrel is probably the best system that we have studied," Edwards says. "I'm more of a museum type, so my interaction with the organism, it's often a very temporary thing, whereas Gaby's system was amazing because she had been studying these storm-petrel for years. She knew who was mated to whom. She knew all the chicks. It's a great system to look at MHC variation, and we found some evidence for biased mating depending on the chooser and the recipient's genotype, which is pretty exciting" (12).

Diversity of Size

"I had been interested in genome size for a long time. Birds have pretty small genomes among the vertebrates," he says. "We did some work using osteocytes in dinosaur bones to estimate what genome sizes they had, which of course is kind of a crazy idea" (4). Frogs are known for their large genomes. This ornate burrowing frog's diminutive genome, however, is smaller even than many bird genomes. These frogs live in the seasonally arid regions of Australia, and the vernal pools that provide a nursery for the species' young evaporate rapidly. "In the case of this frog, it seems very likely that selection for rapid tadpole development has caused its genome size to shrink."

One way to shrink a genome is to reduce the proliferation of transposable elements, which are pieces of DNA that can copy and paste themselves throughout an organism's genome. Edwards and colleagues identified Piwi genes in the frog that are known to suppress

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transposable elements (1). "We know that transposable elements often proliferate in the germline, and so we were very excited when we found evidence for gene duplication of Piwi-interacting RNA genes, as well as really high expression in the germline as opposed to other tissues."

Important Job

In addition to a love of birds, Edwards is also a baker, a drummer with a passion for music, and recently biked 3,848 miles across the United States in 76 days during the summer of 2020. He began planning the trip against the backdrop of the COVID-19 pandemic that spring. Shortly before he set off in June, protests against systemic racism and police violence toward Black people filled the country. "It just started as, 'I want to get out of the house and I've always wanted to ride my bicycle across country, so let's do it.' Somehow it morphed into a little bit of a protest. I had my Black Lives Matter signs on my bicycle." A Go-Fund Me site organized by fellow NAS member Sally Otto during the ride raised more than \$61,000 to support diversity initiatives by the Society of Systematic Biologists, The American Society of Naturalists, and The Society for the Study of Evolution.

Supporting the participation of minorities in science has been a career-long pursuit for Edwards, who last year won the inaugural Inclusiveness, Diversity, Equity, and Access (IDEA) Award from the Society for Study of Evolution and participated in the University of Washington's Howard Hughes High School Program for Minority High School Science Student's for nearly a decade. "I think it's fair to say there are not many scientists of color in evolutionary biology. I've spent a fair bit of my career trying to foster diverse students and basically increase diversity in evolutionary biology, and that's been really, really fulfilling," says Edwards. "It's an important job that I think all of us are learning how to do better. I think it's not just for people of color to do this. I think everyone has something to contribute to that effort."

- 1 S. Lamichhaney et al., A bird-like genome from a frog: Mechanisms of genome size reduction in the ornate burrowing frog, Platyplectrum ornatum. Proc. Natl. Acad. Sci. U.S.A. 118, e2011649118 (2021).
- 2 S. C. Campbell-Staton et al., Winter storms drive rapid phenotypic, regulatory, and genomic shifts in the green anole lizard. *Science* 357, 495–498 (2017).
- 3 K. J. O'Keefe et al., Geographic differences in sexual reassortment in RNA phage. Evolution 64, 3010-3023 (2010).
- 4 C. L. Organ, A. M. Shedlock, A. Meade, M. Pagel, S. V. Edwards, Origin of avian genome size and structure in non-avian dinosaurs. *Nature* 446, 180–184 (2007).
- 5 R. L. Honeycutt, S. V. Edwards, K. Nelson, E. Nevo, Mitochondrial DNA variation and the phylogeny of African mole-rats (Rodentia: Bathyergidae). Syst. Zool. 36, 280–292 (1987).
- 6 S. V. Edwards, Long-distance gene flow in a cooperative breeder detected in genealogies of mitochondrial DNA sequences. Proc. Biol. Sci. 252, 177–185 (1993).
- 7 L. Liu, L. Yu, S. V. Edwards, A maximum pseudo-likelihood approach for estimating species trees under the coalescent model. BMC Evol. Biol. 10, 302 (2010).
- 8 T. B. Sackton et al., Convergent regulatory evolution and loss of flight in paleognathous birds. Science 364, 74–78 (2019).
- 9 S. V. Edwards, E. K. Wakeland, W. K. Potts, Contrasting histories of avian and mammalian MHC genes revealed by class II B sequences
- from songbirds. Proc. Natl. Acad. Sci. U.S.A. 92, 12200–12204 (1995).
 10 S. V. Edwards, J. Gasper, D. Garrigan, D. Martindale, B. F. Koop, A 39-kb sequence around a blackbird MHC class II gene: Ghost of selection past and songbird genome architecture. Mol. Biol. Evol. 17, 1384–1395 (2000).
- 11 N. F. Delaney et al., Ultrafast evolution and loss of CRISPRs following a host shift in a novel wildlife pathogen, Mycoplasma gallisepticum. PLoS Genet. 8, e1002511 (2012).
- 12 B. Hoover et al., Ecology can inform genetics: Disassortative mating contributes to MHC polymorphism in Leach's storm-petrels (Oceanodroma leucorhoa). Mol. Ecol. 27, 3371–3385 (2018).

