



Bird genomes are helping to reveal the relationships between species.

EVOLUTION

Bird family tree is in fine feather

Behind the most comprehensive tree of life lies a vast collaboration of like-minded researchers.

BY EWEN CALLAWAY

Evolutionary geneticist Tom Gilbert was sipping a coffee in Madrid five years ago when an idea hit him — literally. “A pigeon crapped on me,” he says, “and I thought to myself, ‘Huh, pigeons.’”

On 11 December, Gilbert, of the Natural History Museum of Denmark in Copenhagen, and dozens of his colleagues reported an evolutionary analysis of the genomes of 48 bird species (including pigeons), amounting to the most comprehensive genome study of any major branch of the tree of life¹. The results confirm a ‘big bang’ in bird diversity after dinosaurs went extinct, and settle long-standing questions on how different birds are related to each other.

On the same day, a consortium of researchers co-led by Gilbert published a further 18 bird-genome papers in various journals, on topics as diverse as the basis of birdsong, birds’ loss of teeth and the cold-weather adaptations of penguins (see avian.genomics.cn/en).

No one has ever used so much genome data from so many species to determine evolutionary relationships. Achieving this daunting task meant building a vast international collaboration that began, appropriately, with pigeons.

In 2010, Gilbert struck up a partnership with BGI, a sequencing powerhouse in Shenzhen, China, to map the first pigeon genome. The goals were to work out how different breeds relate to each other and the origins of their various traits. Gilbert met BGI genome scientist Guojie Zhang later that year and discovered that the BGI had sequenced several other bird genomes for a project led by neuroscientist Erich Jarvis of Duke University in Durham, North Carolina. The three researchers realized that, with a few more samples, they could get genomes from all branches of a group called Neoaves, which includes most modern birds except flightless species (such as ostriches and emus) and chickens, ducks and other fowl. “It struck me that there’s this pretty major unsolved question in avian evolutionary history, which is how do the different bird orders relate to each other?” Gilbert says.

No one had been able to determine which species split off first from the common ancestor of all Neoaves. Furthermore, study after study had thrown up different ways of mapping the evolutionary relationships between the subset of Neoaves

that exhibit vocal learning, a relatively rare trait that scientists see as analogous to human speech. Only entire genomes would reveal birds’ true evolutionary history, Gilbert and his colleagues surmised.

Gathering DNA samples was fairly straightforward. So, too, was sequencing the genomes, which BGI finished by summer 2011. But analysing the data and using them to build an evolutionary tree required another three years, new computational methods and 300 years of computing time. Hundreds of researchers asked if they could use the data, and the project swelled to 80 institutions in 20 countries; marathon Skype calls became a weekly fixture.

The results illuminate various aspects of bird biology, from neurophysiology to population genetics. In one effort, Jarvis and his co-workers discovered parallels between gene activity patterns in brain areas involved in birdsong and in human speech². Another effort dated the loss of teeth in birds to around 116 million years ago³. Yet another showed how inbreeding had shaped the genome of the crested ibis (*Nipponia nippon*) after a recovery programme brought its population up from seven individuals in the 1980s to hundreds now⁴.

The genomes also reveal the broad brushstrokes of the bird family tree. The results show that the first Neoaves species to peel off were ancestors of today’s doves, grebes and flamingos. The authors also conclude that vocal learning may have evolved independently in the ancestors of parrots, hummingbirds and songbirds, and that the ancestor of all land birds — which include eagles, woodpeckers, crows and parrots — was probably similar to a modern bird of prey or, as Gilbert puts it, “a mean-ass carnivore”.

The genomes also point to an explosion in diversity between 67 million and 50 million years ago, a period when non-bird dinosaurs are thought to have been wiped out by an asteroid impact. Mammals seem to have flourished then too, and both groups may have taken advantage of the niches that dinosaurs left behind.

Stephen Richards, a genomicist at Baylor College of Medicine in Houston, Texas, who is leading an effort to sequence 28 insect genomes, praises the team’s decision to systematically select bird species so that one from each taxonomic order was represented, rather than picking scientists’ favourite species. “It’s a foundational work for the next century of biological work into birds,” he says. “We need this revolution across all of biology.”

Gilbert, meanwhile, is a convert to super-sized projects that bring together multiple labs. No single group can do all the work to answer other questions he wants to tackle, such as the evolution of domestic crops. “I don’t spend all my time looking at hummingbirds,” he says. Or pigeons, for that matter. ■

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1. Jarvis, E. D. *et al. Science* **346**, 1320–1331 (2014).
2. Pfenning, A. R. *et al. Science* <http://doi.org/xqh> (2014).
3. Meredith, R. W. *et al. Science* <http://doi.org/xqn> (2014).
4. Li, S. *et al. Genome Biol.* **15**, 557 (2014).