

Group builds most comprehensive family tree of birds to date

October 8 2015, by Bob Yirka



A first-year Penn State College of Information Sciences and Technology doctoral student spent four months observing birds in an effort to learn what it would mean to design technologies from a more-than-human perspective. Her autoethnographic study contributes to addressing the challenging research problem of how to operationalize posthuman concepts into practice for human-computer interaction. House finchnigel. Credit: Wikimedia Commons

(Phys.org)—A team of researchers from several institutions in the U.S. has created the most comprehensive family tree of birds to date. In their paper published in the journal *Nature* the team describes the genomic sequencing technique they used and the structure of the tree they created. Gavin Thomas with the University of Sheffield, in the U.K. offers a News & Views piece on the work done by the team in the same issue, highlighting differences in phylogeny between this newer work and that conducted by another team last year.

Building a family tree for modern [birds](#) has been difficult for scientists because of the dearth of fossil evidence going past 66 million years—the time before the mass extinction that wiped out the other dinosaurs. After the extinction, bird species evolved so rapidly that it has been difficult to use traditional genomic techniques to follow the paths of the evolution of new species, which in turn has made it almost impossible to create an accurate tree. To overcome such problems the [researchers](#) with this latest effort used a different type of genomic sequencing technique—it is called anchored hybrid enrichment and allows for sampling parts of the genome that evolved both slowly and more quickly in the flanking regions.

In all the team collected and tested samples from 198 bird species (which included 390,000 bases of genomic sequence data) that together represented approximately 90 percent of all known birds—a group known collectively as Neoaves. In looking at the data they retrieved, the team found that virtually all birds (excluding flightless and some chickens and ducks) could be grouped into five sub-groups, i.e. major clads. They also found evidence that suggested that all modern birds likely evolved from a single ancestor, one that lived approximately 75 million years ago, or ten million years before all the other dinosaurs went extinct—birds in general are believed to have evolved from the dinosaur family, developing feathers approximately 150 million years ago.

In addition, the researchers claim their results show (and agree with paleontology records) that there was a major radiation event following the mass extinction.

More information: A comprehensive phylogeny of birds (Aves) using targeted next-generation DNA sequencing, *Nature* (2015) [DOI: 10.1038/nature15697](https://doi.org/10.1038/nature15697)

Abstract

Although reconstruction of the phylogeny of living birds has progressed tremendously in the last decade, the evolutionary history of Neoaves—a clade that encompasses nearly all living bird species—remains the greatest unresolved challenge in dinosaur systematics. Here we investigate avian phylogeny with an unprecedented scale of data: >390,000 bases of genomic sequence data from each of 198 species of living birds, representing all major avian lineages, and two crocodilian outgroups. Sequence data were collected using anchored hybrid enrichment, yielding 259 nuclear loci with an average length of 1,523 bases for a total data set of over 7.8×10^7 bases. Bayesian and maximum likelihood analyses yielded highly supported and nearly identical phylogenetic trees for all major avian lineages. Five major clades form successive sister groups to the rest of Neoaves: (1) a clade including nightjars, other caprimulgiforms, swifts, and hummingbirds; (2) a clade uniting cuckoos, bustards, and turacos with pigeons, mesites, and sandgrouse; (3) cranes and their relatives; (4) a comprehensive waterbird clade, including all diving, wading, and shorebirds; and (5) a comprehensive landbird clade with the enigmatic hoatzin (*Opisthocomus hoazin*) as the sister group to the rest. Neither of the two main, recently proposed Neoavian clades—Columbea and Passerea¹—were supported as monophyletic. The results of our divergence time analyses are congruent with the palaeontological record, supporting a major radiation of crown birds in the wake of the Cretaceous–Palaeogene (K–Pg) mass extinction.

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