









Aflock of Genomes

by Guojie Zhang, Erich D. Jarvis, and M. Thomas P. Gilbert









INSIDE

OPINION

Valuing collections p. 1310

RESEARCH ARTICLES

Comparative genomics reveals insights into avian genome evolution and adaptation p. 1311

Whole-genome analyses resolve early branches in the tree of life of modern birds p. 1320

RESEARCH ARTICLE SUMMARIES

Complex evolutionary trajectories of sex chromosomes across bird taxa

Convergent transcriptional specializations in the brains of humans and song-learning birds p. 1333

Core and region-enriched networks of behaviorally regulated genes and the singing genome p. 1334

Three crocodilian genomes reveal ancestral patterns of evolution among archosaurs p. 1335

Evidence for a single loss of mineralized teeth in the common avian ancestor p. 1336

Statistical binning enables an accurate coalescent-based estimation of the avian tree p. 1337

SEE ALSO

- ▶ NEWS STORY P. 1275
- ▶ REVIEW p. 1341
- ▶ PODCAST

haracterization of genomic biodiversity through comprehensive species sampling has the potential to change our understanding of evolution. To study evolution across a major vertebrate class, dissect the genomics of complex traits, and resolve a centuries-old debate on the avian species tree, we formed a consortium focused on the sequencing and analyses of at least one genome per avian order. The resulting data set of 48 consistently annotated bird genomes spans 32 of the 35 recently proposed avian orders,* including all 30 neognath orders, and thus represents a wide range of avian evolutionary diversity. Our consortium's analyses have resulted in eight papers published today in *Science*, as well as 20 papers in other journals [avian.genomics.cn/en]. These include two flagship papers: one exploiting genomic-scale data to generate a highly supported avian order phylogeny that resolves many debates on the timing and topology of their radiation; the other a comparative genomic analysis exploring avian genome evolution and the genetic basis of complex traits. Other studies in Science describe convergent brain regions and gene expression for avian song learning and human speech, the singing activated genome in songbirds, complex evolutionary trajectories of avian sex chromosomes, a single loss of teeth in the ancestor of modern birds, the genomes of their closest extant outgroup (crocodilians) and inferred dinosaur ancestor, and computational methods developed for large-scale genomic analyses. Studies in companion papers explore the genomic adaptations of penguins, genomics of nearly extinct species, lineage-specific selection in birds, paleoviral infiltration in bird genomes, and many other questions. Thus, this study of a major vertebrate class highlights the future promise of large-scale comparative genomics, and we hope sets the stage for an approach for sequencing and analyses of many more genomes of birds and other vertebrate lineages.

^{*}J. Cracraft, in The Howard and Moore Complete Checklist of the Birds of the World, E. C. Dickinson, J. C. J. Remsen, Eds. (Aves Press, Eastbourne, UK, 2013), pp. xxi-xliii.