MOLECULAR EVOLUTION

Did Birds Sail Through the K-T Extinction With Flying Colors?

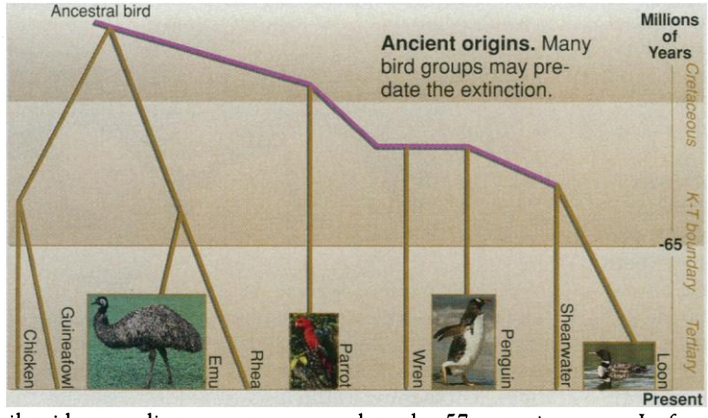
Even children's books can tell you that a giant asteroid or some such catastrophe killed off the dinosaurs 65 million years ago and cleared the way for birds and mammals to inherit the Earth. But paleontologists have long debated which other species—and how many—died out at the Cretaceous-Tertiary (K-T) boundary. The prevailing view has been that most archaic birds and mammals went the way of the dinosaurs, and that the few survivors rapidly hatched today's diverse array of birds and mammals (*Science*, 3 February 1995, p. 637). Now, a report on page 1109 combines molecular and fossil data to come to a different conclusion: that a diverse flock of birds flew through the cataclysm unscathed.

At least 21 different avian lineages survived the devastation, according to molecular evolutionist Alan Cooper of Oxford University and theoretical biologist David Penny of Massey University in New Zealand, who used differences in the DNA of modern birds as a "molecular clock" to determine the age of each lineage. Although other molecular researchers raise questions about the analysis, they generally agree with the conclusions, which match other molecular studies. "This makes the big disaster at the K-T boundary a much less dramatic event," says molecular evolutionist Svante Pääbo of the University of Munich in Germany. "It could change the textbook view that almost all the groups of birds died out."

Many paleontologists already think the fossil record shows that several groups of modern birds got an early start and made it through the extinction. But others point to fossil evidence suggesting that many other groups did suffer catastrophic extinction (*Science*, 22 November 1996, p. 1303). They also say the Cretaceous fossil record for modern birds is spotty, yielding little evidence for their presence before the K-T boundary. Ornithologist Alan Feduccia of the University of North Carolina, Chapel Hill, argues that the only truly modern birds who lived in the Cretaceous were a small group of transitional shorebirds. In his view, these were also the sole avian survivors of the extinction, and after the dust settled, they rapidly gave rise to other modern birds.

Given the uncertainties of the fossil record, Cooper and Penny turned to the genes of living birds for clues about their ancestry. Theirs is the latest in a series of studies that depend on the simple premise that as two species evolve, their genes gradually accumulate different mutations. The more differences between two species, the more time has passed since they diverged from a common ancestor. By measuring the genetic differences between lineages, researchers can construct a family tree that shows the order in which species branched from a common ancestor.

In the new work, Cooper and Penny looked at 16 orders of birds, using two small fragments of genes—600 base pairs of a protooncogene in the nucleus, and a 390–base pair region from the mitochondrion, a cellular organelle that has its own DNA. First, they measured the differences in the same snippet of gene between a pair of closely related birds, such as rheas and ostriches. They dated the split between these two using the earliest known fossil of each pair. For example, the oldest rhea dates to more than 60 million years ago, so the researchers reason that it took at least 60 million years to accumulate the 57 mutations that distinguish the rhea and ostrich genes. They analyzed another pair of closely related birds, such as loons and shearwaters, the same way, then averaged the mutation rates of the two pairs. Then they counted the additional mutations between the two pairs—38 in this case—and, using their average mutation rate of about one per million years, concluded that the last common ancestor of all four birds must have lived more than 98 million years ago, in the mid-Cretaceous.



Using this so-called quartet method developed by Penny and a new family tree, the team found that many lineages diverged long before the K-T extinction. These results point to an Early Cretaceous origin for modern birds as a whole and suggests that at least 21 lineages, including parrots, wrens, and penguins, survived the extinction (see diagram). These findings support other molecular genetic studies, notably one of both birds and mammals by evolutionary biologist S. Blair Hedges and colleagues at Pennsylvania State University, which appeared in the 16 May 1996 issue of *Nature*.

But because the molecular clock has to be calibrated with fossil dates, there is plenty of room for disagreement. Feduccia, for one, flatly dismisses the study as "a gross misrepresentation of the fossil record. The results are flawed because the molecular calibrations are based on erroneous identifications of the Cretaceous and early Paleocene fossils." For example, he says that a Cretaceous fossil identified as a 70-million-year-old loon, used to date the loon-shearwater split, may not be a loon at all. And the dates used for the loon and other bird fossils, such as the duck, are too old, he says. But others have more faith in the data used: "The fossil record is accurate," says vertebrate paleontologist Luis Chiappe of the American Museum of Natural History. "The dates are good."

Still, even some molecular systematists, including Hedges, Joel Cracraft of the American Museum of Natural History, and David Mindell of the University of Michigan, raise concerns about the study's methods and the calculated divergence dates for various birds, as well as the details of the family tree. Hedges says that the snippets of genes used are just too small to serve as reliable molecular clocks. And he'd like to see a statistical test to show that the divergence dates aren't being skewed by lineages with unusually fast or slow rates of evolution. Cooper and Penny say that they have done such statistical tests, and their work stands up. They add that they are already analyzing sequences of the entire mitochondrial genome to boost their data set.

In fact, they are so sure of their method that they extended it. Using other researchers' sequence data and fossil records, they conclude in their paper that at least 100 terrestrial vertebrate lineages survived the boundary, including primates, rodents, and other mammals. What this means—to Cooper, at least—is that doomsday scenarios of the K-T extinction are wrong: It was a selective culling and may not have been catastrophic for all terrestrial creatures, he says. But given the weight of fossil evidence to the contrary, it may take more data—and more debate—before most scientists are persuaded that the K-T mass extinction scenario is for the birds.

–Ann Gibbons

BENTOO PENGUIN AND LOON: VIREO; EMU: ADRIENNE T. GIBSON/ANNIMALS, ANIMALS; KING PARROT: PATTI MURRAY/ANIMALS, ANIMALS