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Avian phylogeny and divergence times
based on mitogenomic sequences

Kerryn Elizabeth Slack

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Institute of Molecular BioSciences
Massey University
Palmerston North,
New Zealand

Abstract

Despite decades of research using a variety of data sources (such as morphological, paleontological, immunological, DNA hybridization and short DNA sequences) both the relationships between modern bird orders and their times of origin remain uncertain. Complete mitochondrial (mt) genomes have been extensively used to study mammalian and fish evolution. However, at the very beginning of my study only the chicken mt sequence was available for birds, though seven more avian mt genomes were published soon after. In order to address these issues, I sequenced eight new bird mt genomes: four (penguin, albatross, petrel and loon) from previously unrepresented orders and four (goose, brush-turkey, gull and lyrebird) to provide improved taxon sampling. Adding these taxa to the avian mt genome dataset aids in resolving deep bird phylogeny and confirms the traditional placement of the root of the avian tree (between paleognaths and neognaths). In addition to the mt genomes, in a collaboration between paleontologists and molecular biologists, the oldest known penguin fossils (which date from 61- 62 million years ago) are described. These fossils are from the Waipara Greensand, North Canterbury, New Zealand, and establish an excellent calibration point for estimating avian divergence times. Bayesian analysis of the DNA sequence data, using the penguin calibration point plus two others, indicates a substantial radiation of modern bird orders in the Late Cretaceous (80 - 65 million years ago). Biotic interactions between modern birds and declining groups such as pterosaurs and early bird groups (e.g. *Hesperornis* and *Ichthyornis*) may thus have played an important role during this time.

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G. L. (Abby) Harrison (University of Oxford, Oxford, U.K.),

P. A. (Trish) McLenachan (Institute of Molecular BioSciences, Massey University, NZ),

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