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Mitogenome Announcement

The complete mitochondrial genome of North Island brown kiwi (*Apteryx mantelli*)

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Kiwi, belonging to very old bird group, is not only the national bird of New Zealand, but also the smallest bird among the flightless ratites (Prinzinger & Dietz [2004](#)). The genus *Apteryx* consists of three kiwi species and five subspecies, of which the North Island brown kiwi (*Apteryx mantelli*) is the most common one. The populations of *A. mantelli* is decreasing 3% every year (Holzapfel et al. [2008](#)), and thus, International Union for Conservation of Nature (IUCN) has included it in the Red List of Endangered species (Version 3.1, 2012). Although two complete mitochondrial (mt) genomes belonging to *Apteryx* have been determined (Haddrath & Baker [2001](#)), the *A. mantelli* mt genome sequence hasn't been reported.

Here, we sequenced and characterized the complete mt genome of *A. mantelli*. The mt genome reads were filtered from high through-output genome sequencing project of *A. mantelli* (Duc et al. [2015](#)) from European Nucleotide Archive (Accession: PRJEB6383) by Blast (Altschul et al. [1997](#)) using the *A. haastii* (NC_002782) mt genome sequence (Haddrath & Baker [2001](#)) as a reference. The data were from three sequenced *A. mantelli* female individuals, which originate from the far North (kiwi code 73) and central part - Lake Waikaremoana (kiwi code AT5 and kiwi code 16-12) of North Island, New Zealand.

Assembled by using the DOGMA pipeline, predicted genes were sequence accession number phylogenetic Pratt analysis replicate Whole mt genome of 16,694 bp, containing 22tRNA genes. The 30%, respectively. The proportion of 7%, which



encodes 3776 amino acids. All protein-coding genes started with Met. Remarkably, ND2, COX2, and COX3 ended by TAA as stop codon. The lengths of 12S ribosomal RNA and 16S ribosomal RNA are 973 bp and 1596 bp, respectively. The length of D-loop is 1112 bp, ranging from 15,583 to 16,694 bp.

Phylogenetic analysis included mt genome of *A. mantelli* and the other 10 species that are from the order Struthioniformes, Dinornithiformes, Rheiformes, Casuariiformes, and Apterygiformes, which belong to Ratitae, Using *Trogon viridi* (Trogoniformes) of Trogonidae family as an outgroup. Maximum-likelihood (ML) analysis exhibited that *A. mantelli* clustered with the other two *Apteryx* species, *A. haastii* and *A. owenii*, highly supported by a bootstrap value of 100 (Figure 1). The evolutionary relationships of these analyzed species are consistent with previously reported results (Mitchell et al. 2014). The newly determined mt genome will help to understand the evolution of ratite.

Figure 1. Maximum-likelihood (ML) phylogenetic tree of *A. mantelli* and the other 11 species using *T. viridis* as an outgroup. Number above each node indicates the ML bootstrap support values. All 12 species's accession numbers are listed as below: *A. mantelli* KU695537, *A. haastii* NC_002782, *A. owenii* NC_013806, *Casuarus casuarus* NC_002778, *Dromaius novaehollan* NC_002784, *Struthio camelus* NC_002785, *Dinornis giganteus* NC_002672, *Anomalopteryx didiformis* NC_002779, *Emeus crassus* NC_002673, *Pterocnemia pennata* NC_002783, *Rhea Americana* NC_000846, *T. viridis* NC



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The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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