MITOCHONDRIAL DNA PART B: RESOURCES, 2016
VOL. 1, NO. 1, 722–723
http://dx.doi.org/10.1080/23802359.2016.1229588

Taylor & Francis
Taylor & Francis Group

MITOGENOME ANNOUNCEMENT

OPEN ACCESS

The complete mitochondrial genome sequence of an Endangered powerful owl (*Ninox strenua*)

Subir Sarker[a,b], Shubhagata Das[b], Jade Forwood[c], Karla Helbig[a] and Shane R. Raidal[b]

[a]Department of Physiology, Anatomy and Microbiology, School of Life Sciences, La Trobe University, Melbourne, VIC, Australia; [b]Faculty of Science, School of Animal and Veterinary Sciences, Charles Sturt University, Wagga Wagga, New South Wales, Australia; [c]Faculty of Science, School of Biomedical Sciences, Charles Sturt University, Wagga Wagga, New South Wales, Australia

ABSTRACT

In this paper, the complete mitochondrial genome of an Endangered *Ninox strenua* is sequenced and reported for the first time. The mitogenome of *N. strenua* is a circular molecule of 16,206 bp in length, consisting of 13 protein-coding genes (PCGs), 22 tRNA, 2 rRNA, and a control region (D-loop). All the genes in *N. strenua* are distributed on the H-strand, except for the *ND6* subunit gene and eight *tRNA* genes, which are encoded on the L-strand. Phylogenetic analysis using an available mitogenome of *Strigidae* family revealed a close evolutionary relationship of *N. strenua* with *N. novaeseelandiae,* a Tasmanian spotted owl found throughout the Australasia.

ARTICLE HISTORY
Received 31 July 2016
Accepted 24 August 2016

KEYWORDS
Avian mtDNA; mitogenome phylogeny; family *Strigidae*; *Ninox strenua*

The avian order *Strigiformes* represents an intriguing model, which occupies the ecological niche of nocturnal raptor (Wink et al. 2009). Owls are birds from the order *Strigiformes* which includes about 200 species. Powerful owl (*Ninox strenua*), a member of the family *Strigidae* (order *Strigiformes*), is one of the largest and endemic Australian owl species (Ian & Dariel 2005). The Powerful owl is currently listed as Vulnerable or threatened in Queensland, New South Wales, and Victoria, whereas the species has been listed as Endangered in South Australia under the National Parks and Wildlife Act 1972 (NPW Act). The systematic position of the family *Strigidae* has been studied using morphological, and molecular characters' dependent on the *Cytochrome b* and the *Nuclear RAG-1* genes (Wink et al. 2009). A well-resolved avian phylogenetic tree is required for understanding biogeographic evolutionary structure, whilst there are still major uncertainties in the position of many avian species due to a lack of abundant mitochondrial (mt) data sets. Complete mitogenomes could play a vital role to understand the origin, evolution, and divergence time of speciation (Bagatharia et al. 2013), as well as influencing conservation and management decisions (Eo et al. 2010). In the present study, we report a complete mitogenome of *Ninox strenua* in order to provide further insights into the biology, host phylogeny, and conservation of the species.

The blood sample was obtained from a powerful owl in the wild (year of sampling: 2015; GPS location: 34°00′22.9″S, 151°02′18.6″E). The sample was immediately transferred to the Veterinary Diagnostic Laboratory (VDL), Charles Sturt University, and stored under the accession number CS15-3907. Animal sampling was obtained in accordance with approved guidelines set by the Australian Code of Practice for the Care and Use of Animals for Scientific Purposes (1997) and approved by the Charles Sturt University Animal Ethics Committee (Research Authority permit 09/046). The total genomic DNA was extracted using an established protocol (Sarker et al. 2016). The genomic libraries were prepared with an insert size of 150 paired-end. The next-generation sequencing (NGS) was performed on a HiSeq2500 sequencing platform (Illumina) at the Novogene, China, and generated approximately 11.9 million sequence reads from the genomic DNA of the Powerful owl. The sequences were assembled, and the construction of contigs with a minimum average PHRED score of 25 was considered in CLC Genomics workbench 9.0.1 under La Trobe University Genomics Platform.

The complete mitochondrial genome sequence of *N. strenua* was 16,206 bp in length (GenBank accession no. KX529654) with a 47.2% GC content. It encodes 37 genes containing 13 PCGs, 22 tRNA genes, 2 rRNA genes, and a control region. Among these, 9 genes are encoded on the L-strand, including *ND6* and 8 tRNA genes ($tRNA^{Gln}$, $tRNA^{Ala}$, $tRNA^{Asn}$, $tRNA^{Cys}$, $tRNA^{Tyr}$, $tRNA^{Ser}$, $tRNA^{Pro}$, and $tRNA^{Glu}$), the remaining 28 genes are encoded on the H-strand. The gene arrangement is similar to the complete mitochondrial genome of other *Strigidae* species.

The complete mitochondrial genome sequences relevant to the family *Strigidae* available in GenBank was aligned using the MAFFT L-INS-i algorithm (Katoh et al. 2002), and the neighbour-joining (NJ) tree with 1000 nonparametric bootstrap resamplings were generated using CLC Genomics

CONTACT Subir Sarker S.Sarker@latrobe.edu.au Department of Physiology, Anatomy and Microbiology, School of Life Sciences, La Trobe University, Melbourne, VIC 3086, Australia

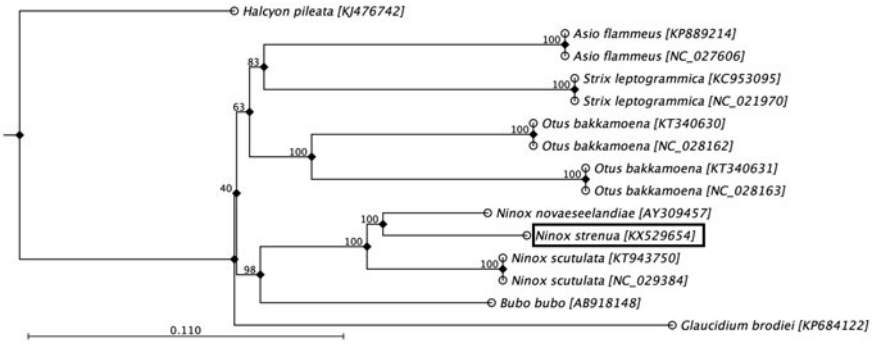

Figure 1. Host-phylogenetic inference of evolutionary relationship among *Strigidae* family. NJ-tree was constructed using complete mitochondrial genome sequences of species belonging to the *Strigidae* family, and a Black-capped kingfisher (*Halcyon pileata*; GenBank accession: KJ476742) as an outgroup.

workbench 9.0.1. The phylogenetic tree revealed that *N. strenua* was clustered most closely to *N. novaeseelandiae,* Tasmanian spotted owl which is found throughout Tasmania and New Zealand (Figure 1), and is consistent with previous research (Wink et al. 2009). We expect the complete mitogenome of *N. strenua* will be a useful database for further research and host-phylogenetic analysis of *Strigidae* species, and their implication for the conservation of the species.

Disclosure statement

The authors declare no competing financial interests. The authors alone are responsible for the content and writing of the article.

Funding

This research was supported by Australian Research Council's Discovery Projects funding scheme [DP1095408]. We are grateful for the financial support from the La Trobe University Start Up Grant to SS.

References

Bagatharia SB, Joshi MN, Pandya RV, Pandit AS, Patel RP, Desai SM, Sharma A, Panchal O, Jasmani FP, Saxena AK. 2013. Complete mitogenome of asiatic lion resolves phylogenetic status within Panthera. BMC Genomics. 14:1–9.

Eo SH, Wares JP, Carroll JP. 2010. Subspecies and units for conservation and management of the northern bobwhite in the eastern United States. Conserv Genet. 11:867–875.

Ian AWM, Dariel L. 2005. Historical records of the powerful owl *Ninox strenua* in Sydney and comments on the species' status. Aust Field Ornithol. 22:29–37.

Katoh K, Misawa K, Kuma K, Miyata T. 2002. MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic Acids Res. 30:3059–3066.

Sarker S, Lloyd C, Forwood J, Raidal SR. 2016. Forensic genetic evidence of beak and feather disease virus infection in a powerful owl, *Ninox strenua*. Emu. 116:71–74.

Wink M, El-Sayed AA, Sauer-Gürth H, Gonzalez J. 2009. Molecular phylogeny of owls (*Strigiformes*) inferred from DNA sequences of the mitochondrial cytochrome b and the nuclear RAG-1 gene. Ardea. 97:581–591.