Mitochondrial genome sequence of black paradise flycatcher (Aves: Monarchidae) and its phylogenetic position

Soo Hyung Eoa and Junghwa Anb

a Department of Forest Resources, Kongju National University, Chungnam, Republic of Korea; b Animal Resources Division, National Institute of Biological Resources, Incheon, Republic of Korea

ABSTRACT

We generated the complete mitochondrial genome of the black paradise flycatcher (Terpsiphone atrocaudata; Family: Monarchidae), an ecologically important insectivorous bird in Asian forest ecosystems. The mitogenome was 16,984 bp in length and consisted of 13 protein-coding genes, 22 tRNAs, two rRNAs and a control region. Gene composition and arrangement in the mitogenome were similar to those of related families Corvidae and Laniidae available in GenBank. However, tRNA\[^{Ala}\] was located between COXII and ATP8 genes in the mitogenome of T. atrocaudata while tRNA\[^{Lys}\], was in the same location in the mitogenomes of Corvidae and Laniidae. The phylogenetic tree based on the mitogenomes of T. atrocaudata and the related families supported that Monarchidae was the sister taxa to the clade of Laniidae and Corvidae. The mitogenome of T. atrocaudata will be a valuable genetic resource for phylogenetic analyses and implication of conservation and management of the species.

MITOCHONDRIAL DNA PART B: RESOURCES, 2016
VOL. 1, NO. 1, 454–455
http://dx.doi.org/10.1080/23802359.2016.1181996

CONTACT Junghwa An safety@korea.kr Animal Resources Division, National Institute of Biological Resources, Hwangyeong-ro 42, Seo-gu, Incheon 404-708, Republic of Korea

© 2016 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.
The result is similar to those of the phylogenetic trees based on multilocus nuclear genes (Barker et al. 2002, 2004). The complete mitogenome of T. atrocaudata will be a valuable genetic resource for phylogenetic relationships and implication of conservation and management of the species.

Acknowledgements

The authors thank Conservation Genome Resource Bank for Korean Wildlife (CGRB) for donating samples of Terpsiphone atrocaudata. This work was supported by a grant from the National Institute of Biological Resources (NIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea (NIBR 201503103).

Disclosure statement

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

References

Barker FK, Barrowclough GF, Groth JG. 2002. A phylogenetic hypothesis for passerine birds: Taxonomic and biogeographic implications of an analysis of nuclear DNA sequence data. Proc Biol Sci. 269:295–308.

Barker FK, Cibois A, Schikler P, Feinstein J, Cracraft J. 2004. Phylogeny and diversification of the largest avian radiation. Proc Natl Acad Sci USA. 101:11040–11045.

BirdLife International. 2015. Terpsiphone atrocaudata. The IUCN red list of threatened species version 2015; [cited 2015 Nov 26]. Available at: http://www.iucnredlist.org/.

Del Hoyo J, Elliot A, Christie D. 2006. Handbook of the birds of the world, old world flycatchers to old world warblers, vol. 11. Barcelona, Sapin: Lynx Edicions.

Eo SH, An J. 2015. The complete mitochondrial genome sequence of Japanese murrelet (aves: Alcidae) and its phylogenetic position in Charadriiformes. Mitochondrial DNA [Epub ahead of print]. doi:10.3109/19401736.2015.1101570.

Eo SH, DeWoody JA. 2010. Evolutionary rates of mitochondrial genomes correspond to diversification rates and to contemporary species richness in birds and reptiles. Proc Biol Sci. 277:3587–3592.

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.

Gill F, Donsker D. 2015. IOC World Bird List v 5.4; [cited 2016 Jan 15]. Available at: http://www.worldbirdnames.org/.

Kim Y, Kim W, Oh H. 2011. Studies on breeding ecology of black paradise flycatcher Terpsiphone atrocaudata on Jeju Island. Kor J Orni. 18:263–272.

Kim Y, Oh H, Jang Y, Choi S. 2010. Nest environment selection of black paradise flycatcher (Terpsiphone atrocaudata). Kor J Orni. 17:11–19.

Mizuta T. 1998. The breeding biology of the black paradise flycatcher Terpsiphone atrocaudata. Jpn J Ornitol. 47:25–28.

Sibley CG, Ahlquist JE. 1990. Phylogeny and classification of birds: a study in molecular evolution. New Haven, CT: Yale University Press.