

# Determining the Taxonomic and Conservation Status of the Forest Owlet (*Heteroglaux blewitti*)

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Department of  
BioTechnology,  
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## **Funding agency**

Department of Biotechnology, Govt. of India

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August, 2016



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***Recommended Citation***

Mukherjee, S., V.V. Robin, P. Mehta and P. Koparde. (2016). Determining taxonomic and conservation status of the critically endangered Forest Owlet (*Heteroglaux blewitti*). Sálim Ali Centre for Ornithology and Natural History. Technical Report No. PR-4812. 1-82 pp.

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***Front and back cover design:*** Pankaj Koparde

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## **Acknowledgements**

*We would like to thank Department of Biotechnology, Government of India for funding and Dr Omkar Nath Tiwari (Scientist, DBT) for extending all the support during this project. We thank Maharashtra, Madhya Pradesh and Chhattisgarh State Forest Departments for granting us permission to work on the Critically Endangered species.*

*We thank Dr K. Sankar (Director, SACON) and Dr P.A. Azeez (Former Director, SACON) for helping us with obtaining Forest Department permits and helping in logistics. We are grateful to Dr Uma Ramakrishnan (Associate Professor, NCBS) for allowing us to use her laboratory for conducting most of the genetic work and assisting us to use sequencing facility at NCBS. We would like to thank Dr Sushma Reddy (Loyola University, Chicago, USA) and Field Museum of Natural History for making the sequence data on *A. superciliaris* available for our analysis. Thanks are also due to Dr Asad Rahmani for permitting us to sample owls from the museum of Bombay Natural History Society, Mumbai. We would like to thank Dr Rajah Jaypal (Principal Scientist, SACON) for helping us in interpreting the possible reflection of molecular phylogeny in traditional taxonomy of owls.*

*We express our thanks to Dr Prachi Mehta's team that collected samples from field. We thank NCBS Lab-3 members for supporting us throughout the research-work conducted in Dr Uma Ramakrishnan's laboratory. We thank Mr. C.K. Vishnudas and Mr. Kaushal Patel for their help on field. We also thank Mr. Kunal Patel and Mr. Jugal Tiwari (Jivdaya Charitable Trust) for providing samples of Spotted Owlets. We would also like to thank Mr Arpit Deomurari for allowing us to use his photograph of Forest Owlet as the front cover of this report and Handbook of the Birds of the World for open access bird illustrations.*

# Summary

The Forest Owlet *Heteroglaux blewitti*, belonging to a monotypic genus, is a Critically Endangered species endemic to Central India. Since the discovery of the species, the taxonomic placement of the species has always been debatable. In addition, the data on the population structure and species distribution is scanty. There exists a report on hybridization between *Athene brama* and *H. blewitti*, which needs further scrutiny. Since *H. blewitti* is a conservation priority species, studies on its phylogeny, population connectivity, and hybridization status are of utmost importance to realize its conservation needs. Given this background, in the present study we addressed three objectives –

1. To identify any genetically unique populations through a phylogeographic study.
2. To compare molecular based phylogeny to current taxonomy. Does molecular data support the existing taxonomic position?
3. To resolve the taxonomic ambiguity surrounding *Heteroglaux blewitti* with respect to possible hybrid individuals in the populations.

To study the population connectivity, we planned to sample across the species range, however, we did not receive permits to sample. Hence, to check if the species is continuously distributed or not, and what drives its distribution, we modeled the species contemporary and past niche. We field tested our model, and during ground-truthing detected two new records of *H. blewitti* from Gujarat. The past climatic niche models showed that the species has possibly been restricted to Central India since Last Glacial Maxima; however the area under suitable niche has reduced since significantly.

To clarify taxonomic status of the species, we sequenced two mitochondrial and four nuclear genes, generating around 4100 bp data, from moulted feathers of *H. blewitti*, *A. brama* and *Glaucidium radiatum*. We performed standard phylogenetic analysis on the datasets. Our phylogenetic analysis showed that *H. blewitti* is not sister to *A. brama*, but nested within the *Athene* clade. Our molecular dating analyses showed that *H. blewitti* is evolutionary distinct, having a possible African ancestry.

To clarify the hybridization status, we compared gene sequences of *A. brama* and *H. blewitti*. In our analysis, we did not find any cases of hybridization between *H. blewitti* and *A. brama*.

The present study shows that the Critically Endangered *H. blewitti* is nested within the *Athene* clade, which may warrant updating information on its taxonomic status. Further, the species may be widespread than previously thought as apparent from our field validated niche model, and the species niche might have been impacted by past climate change. In our dataset, we did not find signature of hybridization. Our findings underline that the basic research on ecology and evolutionary biology of endangered and endemic species such as *H. blewitti* are necessary to bring about essential information which may have conservation significance.

We recommend sampling areas of highly suitable habitat, given by our niche model, to detect the species across its range. To further resolve the phylogenetic position of *H. blewitti*, and to understand functional connectivity of *H. blewitti* populations, a population genetic approach to devise population level conservation strategies to conserve the species is highly recommended.

**Keywords:** Conservation, Endemic, Endangered, Forest Owlet, Niche model, Phylogeny



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