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A new record and range extension for the endangered gecko *Paroedura masobe* Nussbaum & Raxworthy, 1994 from the highly disturbed forest of Betaikankana, eastern Madagascar

Rodlis Raphali Andriantsimanarilafy[1,*], Joseph Christian Randrianantoandro[2], Miguel Vences[3], and Alison Cameron[4]

The genus *Paroedura* comprises a diverse radiation of species endemic to Madagascar and the Comoro Islands (Rosa et al., 2011). This group of nocturnal, large-eyed geckoes is widely distributed in a great variety of habitats, from the north to the south of Madagascar (Nussbaum and Raxworthy, 2000; Glaw and Vences, 2007). After the latest species descriptions (Glaw et al., 2018; Köhler et al., 2019), the genus currently includes 22 species, with additional candidate species waiting to be formally described, especially in the *P. bastardi* complex (Köhler et al., 2019).

Paroedura masobe is the largest and one of the most distinct species in the genus. It has been recorded from low elevations (300–600 m) in the eastern rainforests of Madagascar (Glaw and Vences, 2007; Bora et al., 2020). This species is unable to survive in agricultural land and may disappear from even slightly degraded forests (Bora et al., 2020). It was classified as Endangered in 2011 because of its narrow distribution and small population size. Up to this point, *P. masobe* was known from only two sites, approximately 27 km apart: Betampona Strict Nature Reserve and Zahamena National Park (Glaw and Vences, 2007; Rosa et al., 2011). It was thought that it was unlikely to occur more widely than these localities (Bora et al., 2020). This gecko is also known from the international pet trade, where it is potentially in high demand (Jenkins et al., 2011), and the impact of trade on *P. masobe* populations has not yet been assessed (Bora et al., 2020). In 2016, the species was included on CITES Appendix II to control its exportation.

We conducted herpetofauna surveys in the eastern rainforest region of Madagascar, around the Corridor Ankeniheny-Zahamena protected area (Fig. 1) to assess the impact of land use change on amphibian and reptile distributions and abundances. A total of 44 sites were surveyed across five habitat types, including closed canopy forest, three stages of regeneration or degradation after forest loss (tree fallow, shrub fallow, and degraded land; Styger et al., 2007), and reforestation plots planted by the Tetik'Asa Mampody Savoka (TAMS) project around Andasibe.

The following standardised sampling was conducted at each site: (1) One 100-m transect with 11 bucket traps in a line and drift fences was set for seven nights. (2) We conducted standard nocturnal and diurnal active searches, over four nights and days, along four 50-m linear transects. (3) We attempted general collecting from target microhabitats. Geographic coordinates of each transect were recorded with a Garmin eTrex 30 GPS, microhabitat data were collected for each capture, and each animal was identified in the field using published reference material (e.g., Glaw and Vences, 2007). Photographs and morphometric measures were taken. Tissue was taken for DNA barcode verification of species identities, and a voucher specimen was collected.

Across all 44 sites only one individual (an adult female) of *Paroedura masobe* (Fig. 2) was encountered, in closed canopy forest in Betaikankana Forest (27 November 2014, 18.5079°S, 48.9897°E, elevation 411 m). Body length measured 109.3 mm and tail length was 64.5 mm. It was found perching 1 m above ground level on the third night of four active search transect surveys. The specimen was collected (RJC-0102, PAGES-TS-0163) and deposited in the herpetological collection of the University of Antananarivo (accession number UADBA-R 71834).

[1] Madagasikara Voakajy, BP 5181, Antananarivo (101), Madagascar.
[2] Faculty of Sciences, University of Antananarivo, BP 906, Antananarivo (101), Antananarivo, Madagascar.
[3] Technische Universität Braunschweig, Zoological Institute, Mendelssohnstraße 4, 38106 Braunschweig, Germany.
[4] School of Natural Sciences, Bangor University, Deiniol Road, Bangor, Gwynedd LL57 2UW, Wales, United Kingdom.
[*] Corresponding author. E-mail: arraphali@gmail.com

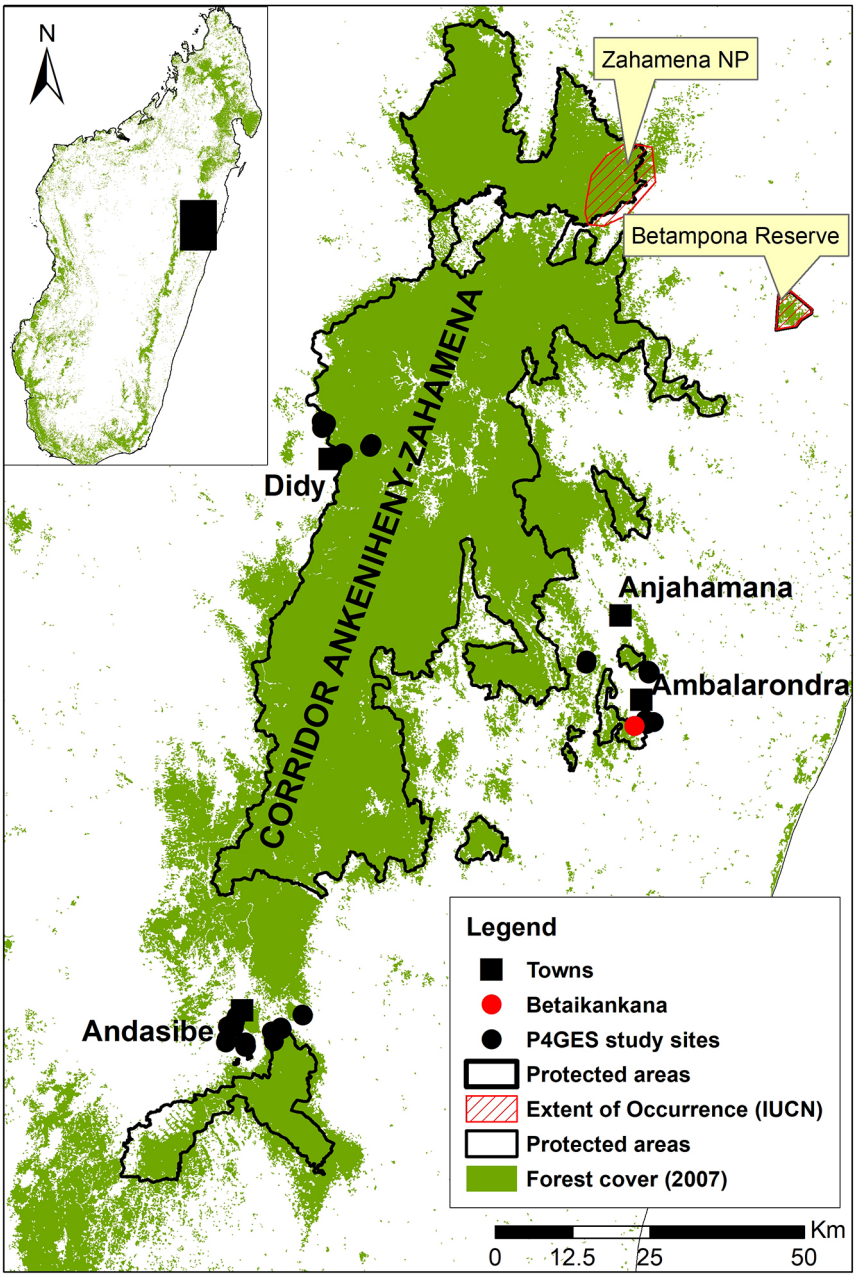

Figure 1. Map showing the current Extent of Occurrence of *Paroedura masobe* from the IUCN Red List assessment (Zahamena National Park and Betampona Strict Nature Reserve) and the new locality for the species.

DNA extracted from a tissue sample of this specimen was submitted to metabarcoding following the protocol established by Vences et al. (2016). In brief, a short segment of the mitochondrial 16S rRNA gene was PCR-amplified (indexed primers and protocols as in Vences et al., 2016) for several hundred samples, pooled and sequenced on an Illumina Miseq instrument using 2x250 v2 chemistry. Consensus sequences of the obtained reads were computed with the QIIME pipeline. Reads assigned to the sample PAGES-TS-0163 yielded a consensus sequence of 251 nucleotides (submitted to GenBank and available under accession number MN748972) that

Figure 2. Adult female of *Paroedura masobe* from Betaikankana Forest (specimen number RJC-0102, UADBA-R 71834).

matched 100% with the corresponding stretch of the only other *P. masobe* 16S sequence (accession number GU129003; Aprea et al., 2013). This reference sequence was obtained from the voucher specimen FAZC 11702, purportedly originating from "Fiherenana" but probably collected at some distance from the actual location of Fierenana Village, which is located at the western edge of the Ankeniheny-Zahamena Forest Corridor. So far, no molecular data are available for *P. masobe* samples with reliable collecting data, and therefore, no analysis of phylogeographic differentiation can be performed. However, given the strong divergences among populations of *P. gracilis* along Madagascar's northern east coast (Mohan et al., 2019), some genetic differentiation can also be expected among populations of *P. masobe*.

Our standardised survey in the Ankeniheny-Zahamena Corridor represents a substantial effort, with a good chance of detecting species if present. In the surroundings of Betaikankana Forest we surveyed nine sites (two closed canopy, two tree fallows, three shrub fallows, and two degraded agriculture) located on the eastern side of the Ankeniheny-Zahamena Corridor. Eight sites were located between Betaikankana Forest and Betampona and Zahamena, the previously known localities for species. These localities are approximately 26 km apart, and Betaikankana Forest is approximately 66 km south of the closest one of those sites (Betampona Strict Nature Reserve). Thus, our finding represents a significant range extension. The specimen was collected at an elevation of 411 m, well within the species' previously known elevational range of 300–600 m. Despite our substantial survey effort, and some extra effort invested trying to find more individuals at the same site, only one adult female of *P. masobe* was found, confirming that the species is either difficult to find or exists at low densities (Bora et al., 2020).

Betaikankana Forest comprises several non-connected fragments. As with other eastern lowland habitats, this forest is highly disturbed and under strong pressure from agriculture, timber extraction, and subsistence resource use. This locality is outside of the Ankeniheny-Zahamena Corridor protected area, it is a property of the state, and is currently without a management structure. However, it is approximately 2 km away from the boundary of the nearest parcel of the Anheniheny-Zahamena Corridor, which has Category VI protection (protected area with sustainable use of natural resources). The forest between Betaikankana Forest and the boundary of the protected area is contiguous, so it is possible that this parcel of the Corridor and others within the area may provide some protection to the species.

We recommended the extension of protection of the closest parcel of the Ankeniheny-Zahamena Corridor to include the forest contiguous with the new locality, or implementation of a local community management agreement (*transfert de gestion*) to ensure the conservation of this *P. masobe* population. As this species is now listed on CITES Appendix II, export controls should be enforced and the forest parcel should also be excluded for collection of similar-looking species, such as *P. gracilis*, to prevent accidental collection of *P. masobe*. Due to the rarity of this species, a population assessment is likely to be challenging, but further information on the

species' distribution, demography, dispersal ability, and natural history would assist with refining its IUCN and CITES statuses and enable the development of a Species Action Plan.

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