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## Re-examination of *Hemidactylus tenkatei* van Lidth de Jeude, 1895: Populations from Timor provide insight into the taxonomy of the *H. brookii* Gray, 1845 complex (Squamata: Gekkonidae)

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### Abstract

Recent herpetofaunal investigations in Timor-Leste revealed populations similar to *Hemidactylus brookii* Gray, 1845 in four of 13 districts. In order to properly identify these populations, we examined their relationships to other *H. brookii*-complex populations, notably those from nearby Roti Island, Indonesia (to which the name *H. tenkatei* van Lidth de Jeude, 1895 has been applied) and topotypic Bornean samples. We evaluated both meristic and mensural data from a set of specimens that included the type material of *H. brookii* and *H. tenkatei*, and we generated nuclear (*RAG1*) and mitochondrial (*ND2*) DNA sequence data for Timor-Leste specimens and a topotypical Bornean specimen presumed to represent *H. brookii sensu stricto*. Morphologically, Timorese geckos are clearly distinct from *H. brookii* and identical to *H. tenkatei*. Our molecular data show that the Bornean specimen thought to be *H. brookii* is genetically congruent with Timor-Leste specimens, and this specimen is therefore identified as *H. tenkatei*. Our data also reveal that the Burmese species *H. subtriadroides* Annandale, 1905 is distinct from both *H. tenkatei* and *H. brookii*. While the current data do not allow us to determine with certainty whether *H. tenkatei* is the oldest available name for these widespread forms, it is the only name that can be reliably applied at this time.

**Key words:** *Hemidactylus tenkatei*, *H. brookii*, *H. subtriadroides*, Timor-Leste, Borneo, Roti, taxonomy

### Introduction

The genus *Hemidactylus* Oken, 1817 is one of the most species-rich clades of geckos with a trans-continental distribution (Kluge 1969). Currently represented by 127 species (Uetz 2014), these nocturnal geckos have adapted to a diverse array of habitat types including the tropics and subtropics of Africa, Asia, northern South America, the Caribbean, and Mediterranean Europe (Bauer *et al.* 2010b). Considering their adaptive plasticity, the majority of *Hemidactylus* species (approx. 94%) have relatively small distributions in Africa and Asia, while eight species, including *H. brookii*, *H. frenatus* Schlegel in Duméril and Bibron, 1836, *H. garnotii* Duméril and Bibron, 1836, *H. mabouia* Moreau de Jonnés, 1818, *H. persicus* Anderson, 1872, *H. platyurus* (Schneider, 1792), *H. parvimaclatus* Deraniyagala, 1953, and *H. turcicus* Linnaeus, 1758, are present in both the New and Old Worlds, having spread throughout these regions through the agency of humans (Carranza & Arnold 2006). Of these, *H. brookii* has one of the widest distributions and perhaps the most convoluted taxonomic history.

Herpetofaunal surveys in Timor-Leste, Asia's newest country, revealed several *brookii*-like populations (Fig. 1A) in four of the country's 13 districts (Kaiser *et al.* 2011; O'Shea *et al.* 2012; Sanchez *et al.* 2012). These were preliminarily identified as *H. cf. tenkatei* by O'Shea *et al.* (2012) and Sanchez *et al.* (2012), given their apparent similarity to *H. tenkatei* van Lidth de Jeude, 1895, a name coined to identify *brookii*-complex geckos from the nearby island of Roti. This name had fallen into disuse after being synonymized with *H. brookii* by de Rooij (1915), but two recent inquiries into the validity of *H. tenkatei* by Rösler and Glaw (2010) and Mahony (2011) led to the

attaches a taxon name to a tissue sample, a physical voucher specimen must be available, and this voucher must conform to the parameters represented by the type specimen of that taxon.

Unless as part of a trail of evidence in taxonomy the link between the past (i.e., a holotype, or a type series) and the present (the voucher specimen from which the tissue sample was extracted) is demonstrated, and information is provided to make these links reproducible (e.g., by providing accession numbers for both the voucher specimen and the corresponding tissue sample), the analysis must be considered inconclusive and ultimately of questionable value. This is not only a problem for taxonomists, it is also a problem for those who use or allocate public resources and expect reliable outcomes (Löbl 2014). We freely admit that verifying these links may be a tall order in some circumstances, due to high logistical cost in attempts to evaluate type specimens, unfamiliarity with the morphology of a group under investigation, or simply general time constraints. However, molecular studies are still invariably rooted in the morphology of real animals, and some of the challenges surrounding the identities of *H. brookii* and *H. tenkatei*, as identified in the works of Bauer *et al.* (2010a), Rösler and Glaw (2010), and Mahony (2011), might have been recognized and addressed had the type specimens been viewed together.

We appreciate the efforts to conduct broad molecular investigations with a biogeographic (as opposed to a taxonomic) focus, and we understand that evaluations of type material adds a layer of significant complexity to such studies: finding and evaluating specimens for each and every tissue sample used or for each DNA sequence obtained (such as from GenBank), makes for a significant workload. However, given that many GenBank accessions have not been verified (and we and others have identified a variety of taxonomic incongruities with these accessions; D. Mulcahy, pers. comm.), we urge extreme caution, and certainly communication with the depositor of a sequence, before the taxon name listed on GenBank is used to represent a species, sight unseen.

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