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A revision of African helmeted terrapins (Testudines: Pelomedusidae: *Pelomedusa*), with descriptions of six new species

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Abstract

Using nearly range-wide sampling, we analyze up to 1848 bp of mitochondrial DNA of 183 helmeted terrapins and identify a minimum of 12 deeply divergent species-level clades. Uncorrected *p* distances of these clades equal or clearly exceed those between the currently recognized species of *Pelusios*, the genus most closely related to *Pelomedusa*. We correlate genetic discontinuities of *Pelomedusa* with data on morphology and endoparasites and describe six new *Pelomedusa* species. Moreover, we restrict the name *Pelomedusa subrufa* (Bonnaterre, 1789) to one genetic lineage and resurrect three further species from its synonymy, namely *P. galeata* (Schoepff, 1792), *P. gehafie* (Rüppell, 1835), and *P. olivacea* (Schweigger, 1812). In addition to these ten *Pelomedusa* species, we identify two further clades from Cameroon and Sudan with similar levels of genetic divergence that remain unnamed candidate species. We also note that some problematical terrapins from South Africa and Somalia may represent two additional candidate species. Some of the *Pelomedusa* species are morphologically distinctive, whilst others can only be identified by molecular markers and are therefore morphologically cryptic taxa.

Key words: Africa, Arabian Peninsula, integrative taxonomy, Madagascar, nomenclature, Reptilia, revision, species description

Introduction

Species delimitation has been flagged as a Renaissance issue in zoology (Sites & Marshall 2003), and to this end new DNA-based approaches have been developed (see the reviews in Carstens *et al.* 2013; Miralles & Vences 2013). Basically, two major approaches have gained much attention. One, DNA barcoding (e.g. Hebert *et al.* 2003), relies on genetic distances of typically a single marker gene, whilst the later proposed multilocus coalescent-based methods (e.g. Yang & Rannala 2010) seem at first glance much more sophisticated. It is well known that DNA barcoding suffers from several shortcomings, such as relying on a single (mitochondrial) marker and a rigid threshold for inferring species status. Moreover, hybridization, introgression, paralogues (in particular numts), incomplete sorting and recently split species pose serious challenges (e.g. Meyer & Paulay 2005; Galtier *et al.* 2009). For these reasons, DNA barcoding has been severely criticized as massive oversimplification (e.g. Will &

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Supporting Information

REFERENCE ALIGNMENT. 12S rRNA sequences (FASTA format) for *Pelomedusa* species.

TABLE S1. Used samples, GenBank sequences and their accession numbers.

TABLE S2. Evolutionary models selected by the Bayesian Information Criterion in PARTITIONFINDER (Lanfear *et al.* 2012).

The Supporting Information is available from the Dryad Repository using the link http://dx.doi.org/10.5061/dryad.288ft

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