Correspondence

Another candidate species of *Pelomedusa* (Testudines: Pelomedusidae) from the Democratic Republic of the Congo?

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Helmeted terrapins (Testudines: Pelomedusidae: Pelomedusa) have a wide distribution and occur in most of sub-Saharan Africa and on the southwestern Arabian Peninsula (IVERSON 1992, GASPERETTI et al. 1993). In addition, introduced *Pelomedusa subrufa* (BONNATERRE, 1789) sensu stricto (VARGAS-RAMÍREZ et al. 2010, WONG et al. 2010, PETZOLD et al. 2014) occur in most of western and southern Madagascar (IVERSON 1992). For a long time, Pelomedusa was thought to comprise a single species only, P. subrufa. However, in 2010 two independent studies challenged this view: VARGAS-RAMÍREZ et al. (2010) and WONG et al. (2010) identified nine deeply divergent genetic lineages of Pelomedusa. These lineages differed for the mitochondrial cytochrome b gene (cyt-b), a frequently used marker for species delimitation in turtles and tortoises (e.g., FRITZ et al. 2012a, b, KINDLER et al. 2012), to a degree equalling or exceeding the divergences between many other congeneric turtle species (VARGAS-RAMÍREZ et al. 2010). Recently, FRITZ et al. (2014) and PETZOLD et al. (2014) examined the situation in more detail and discovered additional genetic lineages of Pelomedusa. These authors concluded that Pelomedusa is a species complex, and PETZOLD et al. (2014) described six new species and resurrected three further taxa from the synonymy of P. subrufa, so that ten species of Pelomedusa were now recognized formally. In addition, PETZOLD et al. (2014) identified up to four genetically distinct candidate species of which too few specimens were available for naming them.

Although PETZOLD et al. (2014) used range-wide sampling, many parts of the vast distribution range of *Pelomedusa* remained insufficiently covered. Thus, it seems plausible that further undescribed species might exist. In the present paper, we report the discovery of another possible candidate species of *Pelomedusa* from southwest of the Albertine Rift. On 22 November 2011, we found an adult *Pelomedusa* (Fig. 1) in a shallow flooded roadside ditch, approximately 10 km north of Gombela on the road to Katwe in the Kundelungu National Park (Katanga, Democratic Republic of the Congo; 10.688680° S, 27.830932° E, 1,365 m above sea level; locality marked with a red star in Fig. 2. This specimen with the field tag UP497 had a carapace length of approximately 152 mm and is now in the collection of the Royal Belgian Institute of Natural Sciences (RBINS:ZTN:UP497).

A tissue sample from this terrapin was used to generate 12S, cyt-b and ND4 sequences (GenBank accession numbers 12S: LM993295; cyt-b: LM993296; ND4: LM993297) as described in FRITZ et al. (2014). The resulting mitochondrial sequences were concatenated and merged with the data set of PETZOLD et al. (2014). Maximum likelihood analyses were performed as described there. In the resulting best tree (not shown), UP497 is with bootstrap support of 95% sister to P. neumanni. PETZOLD et al. (2014) used uncorrected p-distances for the 12S and cyt-b genes as a tool for species delimitation in Pelomedusa. If such values are calculated using MEGA 6.06 (TAMURA et al. 2014) and the pairwise deletion option, UP497 and P. neumanni differ by mean divergences of 1.34% (12S) and 4.78% (cyt-b), respectively. According to PETZOLD et al. (2014), the ten recognized species of Pelomedusa and two unnamed candidate species differ in the 12S gene by average uncorrected p-distances ranging from 2.60 to 12.15% and in the cyt-b gene, by values between 5.64 and 18.60%. In addition, two genetic lineages provisionally identified with P. galeata differ by 1.79 (12S) and 7.50% (cyt-b); and two lineages within P. somalica, by 1.83 (12S) and 5.98% (cyt-b). Each of these

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four lineages could represent a distinct species (PETZOLD et al. 2014). The divergences of *P. neumanni* and UP497 fall just short of these values, and we conclude that UP497 could either represent a genetically divergent population of *P. neumanni* or a recently split species. Following PETZOLD et al. (2014), *P. neumanni* is known from Kenya and Tanzania, with the holotype originating from the Kakamega forest in Kenya. The hitherto known localities of this species are situated exclusively to the east of the Albertine Rift, at least 1,000 km northeast of the col-



Figure 1. A) *Pelomedusa* cf. *neumanni* (UP497), found in a shallow flooded roadside ditch, Kundelungu National Park, Democratic Republic of the Congo; B) ventral aspect of the same specimen. Note the dark plastral colouration and pectoral scutes meeting on the midline.



Figure 2. Distribution of Pelomedusa species in East and Central Africa using data of PETZOLD et al. (2014) and the present study.

Correspondence

lection site of our specimen. Furthermore, both P. kobe and P. gehafie, the two most closely related species of P. neumanni, occur in East Africa; in Tanzania as well as in Eritrea and perhaps in Sudan. At the same time, the genetically highly distinct P. subrufa sensu stricto is known from southern Katanga in the Democratic Republic of the Congo (Kalakundi Mine; 11°12.48' S, 27°22.92' E; PETZOLD et al. 2014), which is only approximately 100 km distant from the collection site of our terrapin. Pelomedusa subrufa, P. kobe, and P. neumanni occur in the Arusha region of Tanzania in sympatry or at least close proximity (PETZOLD et al. 2014), and we suppose that a similar situation exists in the Democratic Republic of the Congo with respect to P. subrufa and UP497. Further sampling is needed to clarify this situation, in particular to find out whether the two taxa occur in sympatry, and to allow a thorough morphological and genetic characterization of the putative new candidate species.

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