



Description of two *Werneria* tadpoles from Cameroon (Amphibia: Anura: Bufonidae)

MAREIKE HIRSCHFELD¹, MICHAEL F. BAREJ¹, SIMON P. LOADER² & MARK-OLIVER RÖDEL¹

¹Museum für Naturkunde, Leibniz Institute for Research on Evolution and Biodiversity at the Humboldt University Berlin, Invalidenstraße 43, 10115 Berlin, Germany

²Institute of Biogeography, University of Basel, Basel, Switzerland.

E-mails: mareike.hirschfeld@mfn-berlin.de, michael.barej@mfn-berlin.de, simon.loader@unibas.ch, mo.roedel@mfn-berlin.de

Detailed tadpole descriptions for toads of the genus *Werneria* Poche, 1903 have been only published for *W. preussi* (Matschie, 1893) (Mertens 1938) and *W. tandyi* (Amiet, 1972) (Rödel *et al.* 2004), the latter description assigned to this species with reservation. A few characters of *W. bambutensis* (Amiet, 1972) tadpoles were mentioned by Amiet (1972). So far the assignment of tadpoles to a particular *Werneria* species was based on geography (locality and altitude). Three *Werneria* species, *W. mertensiana*, *W. tandyi* and *W. bambutensis* (Fig. 1), co-occur on Mount Manengouba in south-western Cameroon. There they inhabit forests and river edges in different but slightly overlapping altitudes (Rödel *et al.* 2004). During recent field work (November / December 2010) on Mount Manengouba we collected *Werneria* tadpoles which are herein described.



FIGURE 1. Three *Werneria* species live at different altitudes on Mount Manengouba (d), Cameroon. *W. mertensiana* (a, ZMB 76693) occurs at lowest altitudes (950–1350 m asl), followed by *W. tandyi* (b, ZMB 76697; 1200–1750 m asl) and *W. bambutensis* (c, ZMB 76699; 1750–2200 m asl).

Tadpoles were collected with nets and preserved in 8% formalin. Pieces of the tail were stored in 96% ethanol. Adults of all three species have been collected on Mount Manengouba and liver samples of these were taken for genetic comparisons. All voucher specimens were deposited at the Museum für Naturkunde Berlin (ZMB; Appendix 1). Tadpoles were identified using DNA-barcoding, analyzing approximately 490 bp of the mitochondrial 16S rRNA (see Rödel *et al.* 2009 for methods).