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A new species of Rain Frog from Namaqualand, South Africa (Anura: Brevicipitidae: *Breviceps*)

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Abstract

Breviceps branchi **sp. nov**. is described from coastal Namaqualand, South Africa. It is most similar to *Breviceps namaquensis* in colour pattern and overall form, from which it differs by hand and foot morphology and 16S rRNA sequence.

Key words: *Breviceps*, new species, Namaqualand, 16S rRNA, South Africa

Introduction

The genus *Breviceps* is known from South Africa northwards to Kenya, and as far west as Angola, with the closely related *Balebreviceps* found in Ethiopia (IUCN 2011). There are presently 15 species recognised (Frost 2011).

The early taxonomy of the genus *Breviceps* was reviewed by Power (1926), by which time seven species were already known, including the Namaqualand endemics, *B. macrops* and *B. namaquensis*. Power (1926) discussed a number of characters that might be useful in separating species of rain frogs. On the basis of differences in 16S rRNA and morphology, I describe a new species of *Breviceps* from Namaqualand.

Material and methods

Sampling. A single specimen was collected in Namaqualand, South Africa. A small tissue sample was removed from thigh muscle, and the specimen was fixed in formalin for 24 h, then transferred to 70% ethanol for deposition in the herpetological collection of the Museum für Naturkunde, Leibniz Institute for Research on Evolution and Biodiversity at the Humboldt University, Berlin (ZMB). The specimen was compared to *B. macrops*, *B. gibbosus* and the types and additional material of *B. namaquensis*.

Measurements. The following measurements were taken and descriptors recorded: Snout-urostyle length SUL, head width at angle of mouth (HW), interorbital distance measured across the top of the head (IO), eyelid length (EL), distance between the anterior corners of the eyes (EE), internarial distance (NN), length of inner metatarsal tubercle (IMT), length of median flange on inner metatarsal tubercle (FGL), length of first toe from inner metatarsal tubercle (T1), length of foot from tip of fourth toe including the outer metatarsal tubercle (F), length of hand from tip of third finger including the palmar tubercle (H), number of tubercles under the third finger (F3T).

DNA extraction, amplification and sequencing. Tissues were digested using standard Proteinase-K protocol, and DNA was extracted using phenol-chloroform (Hillis *et al.* 1996). A 550 bp fragment of the mt 16S gene was amplified using the primers 16SaR-F and 16SbR-R of Kocher *et al.* (1989), as modified by Bossuyt & Milinkovitch (2000). Forward and reverse strands were sequenced. Purification and sequencing of both strands was carried out by the Central Analytical Facility of Stellenbosch University. Both sequences were checked against the chromatograms, trimmed, and combined into a single contig for each fragment using Sequencher 4.9 (GeneCodes Corporation). Sequences were checked using BLAST to confirm their placement in the genus (http://blast.ncbi.nlm.nih.gov/). The sequence is deposited in GenBank, accession number JQ965934. A comparative sequence from *B. namaquensis* was determined and deposited in GenBank, accession number JQ965933.

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