

# A window to Central African forest history: distribution of the *Xenopus fraseri* subgroup south of the Congo Basin, including a first country record of *Xenopus andrei* from Angola

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**Abstract.** The *Xenopus fraseri* subgroup contains several morphologically very similar, small- to medium-sized species that mainly occur in Central Africa. Only two species, *X. pygmaeus* and *X. fraseri*, have previously been reported from south of the Congo Basin. The latter has frequently been confused with *X. andrei*, a closely related species reported to be restricted to Cameroon, Gabon, and the Central African Republic. The actual distribution of *X. fraseri* is therefore in need of a critical revision, and southern Central African records are to be reassessed. Here we report the first confirmed record of *Xenopus andrei* from the Serra do Pingano, Uíge Province, Angola. The presence of the species in northern Angola sheds light on the palaeoclimatic history of the region and supports a hypothesized link between Central African forest biomes and the disconnected forest fragments of northern Angola.

**Key words.** Amphibia, Anura, Pipidae, Angola, biogeography, forest remnants, new country record, *Xenopus fraseri*, *Xenopus andrei*.

## Introduction

Despite the fact that members of the genus *Xenopus* WAGLER, 1827 have advanced to become a number-one vertebrate model organism in genome biology (e.g., HELLSTEN et al. 2010) and biomedicine (CANNATELLA & DE SÁ 1993), the taxonomy of this genus has remained far from being resolved. Almost all extant species have been confused with one another for varying periods, and literature records are thus to be used with caution. Many species belong to diploid-polyploid cryptic species groups that presumably are the result of hybridisation processes, thus making the correct identification of museum specimens and the reconstruction of particular species' distributions difficult. The fact that large parts of the core native distributional range (sub-Saharan Africa) have historically been undersampled, due to limited access to remote areas or political instability in several countries, complicates the situ-

ation even further. For all these reasons, published distributions of nominal taxa are therefore considerably flawed in many cases.

The so-called *Xenopus fraseri* subgroup is a particularly troublesome example, as it is subject to all of these shortcomings and problems. There is considerable confusion as to the actual composition of the subgroup, which is reflected by controversial phylogenetic arrangements. LOUMONT & KOBEL (1991) recognized six species with different ploidy levels ( $2n = 4x = 36$ : *X. fraseri* BOULENGER, 1905, *X. pygmaeus* LOUMONT, 1986;  $2n = 8x = 72$ : *X. amieti*, KOBEL, DU PASQUIER, FISCHBERG & GLOOR, 1980; *X. andrei* LOUMONT, 1983; *X. boumbaensis* LOUMONT, 1983;  $2n = 12x = 108$ : *X. ruwenzoriensis* TYMOWSKA & FISCHBERG, 1973), whereas in the original description of *X. pygmaeus*, LOUMONT (1986) additionally included *X. vestitus* LAURENT, 1972 and *X. wittei* TINSLEY, KOBEL & FISCHBERG, 1979 (both  $2n = 72$  and suggested to be either octoploid or allotetraploid, de-

pending on reference), which are now widely considered to form a separate subgroup (*X. vestitus-wittei* subgroup). In a recent contribution, WAGNER et al. (2013) suggested an inclusive subgroup delineation and additionally included *X. longipes* LOUMONT & KOBEL, 1991 (2n = 6x = 108), the more recently described *X. lenduensis* EVANS, GREENBAUM, KUSAMBA, CARTER, TOBIAS, MENDEL & KELLEY, 2011 (2n = 8x = 72), and *X. itombwensis* EVANS, CARTER, TOBIAS, KELLEY, HANNER & TINSLEY, 2008 (2n = 8x = 72). However, in the original descriptions the latter two were assigned to the *X. vestitus-wittei* subgroup (EVANS et al. 2008, 2011). *Xenopus longipes* on the other hand, had traditionally been regarded as representing a separate subgroup with a sole representative. While further tentative new species are continuously discovered (e.g., EVANS et al. 2011) and additional distributional records are established (e.g., ZIMKUS & LARSON 2012, WAGNER et al. 2013), the actual subgroup delineation needs urgent revision to avoid further confusion.

Until the phylogenetic structure has been comprehensively clarified, we maintain the inclusive perspective proposed by WAGNER et al. (2013) and refer to this subgroup as *X. fraseri* subgroup sensu lato. Given the complex phylogenetic relationships among the various *Xenopus* taxa (e.g., assuming a recent speciation through hybridisation) and the patchy distributional records, clarity can only be achieved by adopting an integrative taxonomic approach (i.e., combining morphological, bioacoustic, molecular, ecological, and biogeographical data).

Members of the *X. fraseri* subgroup sensu stricto (LOUMONT & KOBEL 1991) are considered to be forest-bound and restricted to the lowland rainforests of the Congo Basin (but see LAURENT 1950, 1954, RUAS, 1996, WAGNER et al. 2013 for records from south of the Congo Basin). Moreover, this subgroup has been regarded to contain a number of cryptic (FAIN & TINSLEY 1993) and morphologically hardly distinguishable taxa. Two species in particular, the name-bearing *X. fraseri* and the closely related *X. andrei*, have frequently been confused on grounds of their similar morphology. The reported distributions of these two species should therefore be viewed with the necessary precaution and likely need reassessment. This is particularly true for historic *X. fraseri* records from outside its Central African range (LAURENT 1950, 1954, RUAS, 1996).

The recent discovery of a small *Xenopus* in northern Angola that clearly belongs to the *X. fraseri* subgroup prompted us to further investigate the status of the subgroup south of the Congo Basin. The purpose of this contribution is therefore to clarify the taxonomic status of the Angolan specimen and critically review the distributional patterns of *X. fraseri* in its reported Central African range. The results are discussed in the light of a previously hypothesised link between Central African rainforest biomes (Lower Guinea Rain Forest Block sensu WHITE 1997) and disconnected rainforest patches in northern Angola that are thought to have historically been part of the larger Guineo-Congolian tropical forest phytogeographic region.

## Material and methods

### Specimen data

A single subadult male (22.2 mm SVL) of a hitherto unidentified *Xenopus* species tentatively assigned to *X. andrei* on grounds of external morphology was collected at the beginning of the rainy season on 3 October 2013 at around 15:30 h at the foot of the Serra do Pingano (7°40'22.7" S, 14°56'17.7" E, 604 m a.s.l.), northern Angola. The discovery was made during a short survey of the herpetofauna of two cordilleras (Serra do Uíge and Serra do Pingano) located in Angola's northwestern province of Uíge. These cordilleras contain the last forested patches situated in an otherwise fully deforested and anthropogenically severely degraded surrounding matrix (Fig. 1). The specimen was retrieved from a small and shallow section of a stream locally known as Mbalage, approximately 100 m away from its confluence with the Rio Loge. It was found at the stream's edge, submerged in water. This section is located in a closed-canopy forest patch covered with thick, wet leaf litter. The specimen was subsequently euthanised using commercially available toothache pain relief gel containing 20% Benzocaine and subsequently preserved in 70% ethanol. It is now stored in the herpetological collection of the Museum für Tierkunde, Senckenberg Natural History Collections Dresden (MTD), under collection number MTD 48661. Tissue samples in 99.9% ethanol are stored in the tissue bank of the MTD.

### Morphological comparison

To clarify the taxonomic identity of the new specimen from Angola we compared morphometric data obtained from the newly recorded specimen and *X. andrei* material deposited at the Natural History Museum of Geneva (MHNG), including the holotype of *X. andrei* (MHNG 2088.32) and a topotypic series (MHNG 2644.51; 2645.70–72), as well as a series of *X. andrei* (MHNG 2196.1–3; MHNG 2238.30–37) from Bouchia, Central African Republic (a total of six adult females and nine adult males, excluding the newly recorded Angolan voucher; compare Tab. 1).

As there are no written records for this material at the MHNG, it is impossible to clarify whether the comparative material contains the six paratypes mentioned by LOUMONT (1983) as part of a live breeding stock kept at the "Station de Zoologie expérimentale de Genève". We quantified morphological differences using a metric multidimensional scaling approach (PCoA = Principal coordinate analysis) with a posteriori validation of identified groupings using a similarity profile permutation test (SIMPROF, CLARKE, SOMERFIELD & GORLEY 2008). All statistical analyses were performed using the packages *vegan* (OKSANEN et al. 2012) and *clustsig* (WHITAKER & CHRISTMAN 2010) in the R statistical software, version 2.14.2 (R Development Core Team 2012). Morphometric measurements are compiled in Table 1 and include the following 13 parameters: BW – body width; ED – eye diameter; FL – femur length; HL – head



length; HW – head width; IND – internasal distance; IOD – interorbital distance; LA – length from foreleg angle to hind leg angle; PF – No. of periocular folds; SoT – length of subocular tentacle; SVL – snout–vent length; TaL – tarsus length; TiL – tibia length. To account for allometric relations in measured characters, measurements were corrected for body size, measured as snout–vent-length (SVL) prior to analysis. Data entering the analyses included the following parameters and ratios: ED, FL, IND, IOD, TaL, TiL, SoT, as well as HW/HL and BW/LA.

#### Molecular analysis

In addition to the morphological analysis we used sequences of the mitochondrial 16S rRNA gene employing a DNA barcoding approach. This approach has proven to be a comparatively robust and reliable tool in amphibian taxonomy (VENCES et al. 2005). Molecular comparisons included the single new Angolan voucher and previously published sequences for *Xenopus* spp. including

that of the holotype of *X. andrei* (e.g., EVANS et al. 2004, 2011, WAGNER et al. 2013) most of which are accessible through GenBank (BENSON et al. 2013). DNA of the new *Xenopus* voucher (MTD 48661; GenBank sequence accession number: LN679997) was extracted from a fresh tissue sample using the peqGold Tissue DNA Mini Kit (PEQLAB Biotechnologie GmbH). We used the primers 16sar-L and 16sbr-H of PALUMBI et al. (1991). PCR cycling procedure followed SCHMITZ et al. (2005). The PCR product was purified using QIAquick purification kits (Qiagen). The new sequence was initially aligned to the existing 16S GenBank sequences (553 bp) using ClustalX (THOMPSON et al. 1997; default parameters) and the resulting alignment was corrected manually with BioEdit (HALL 1999). Direct comparisons of the sequence of the new Angolan voucher with published sequences were also conducted in BioEdit. To visualize the phylogenetic position of the new Angolan voucher, three well-established techniques for phylogenetic estimation were applied: (1) Neighbour-joining (NJ), (2) Bayesian Inference (BI; MrBayes, version 3.22; HUELSENBECK & RONQUIST, 2001; RONQUIST et al., 2012)



Figure 1. Study area, Uíge province, northern Angola. A) Montane forest remnants in the Serra do Uíge ecosystem, Uíge Province, northwestern Angola; B) Access road at the foot of the Serra do Pingano cordillera, parallel to Mbalage creek; C) Main river course of Rio Loge; D) Mbalage creek, capture site of *X. andrei* (MTD 48661), near the confluence with the Rio Loge.

Table 1. Meristic data of *Xenopus andrei*. All measurements in mm. <sup>a</sup> – Holotype, <sup>b</sup> – Angola specimen. \* – deviations from the original description by LOUMONT (1983) are likely caused by preservation artefacts and/or observer bias.

Coll. No.	Sex	BW	ED	FL	HL	HW	IND	IOD	LA	PF	SoT	SVL	TaL	TiL
<b>MTD 48661<sup>a</sup></b>	<b>m</b>	<b>10.9</b>	<b>2.1</b>	<b>9.0</b>	<b>8.1</b>	<b>8.4</b>	<b>1.2</b>	<b>2.3</b>	<b>8.6</b>	<b>12</b>	<b>0.9</b>	<b>22.2</b>	<b>9.2</b>	<b>14.0</b>
<b>MHNG 2088.32<sup>b</sup></b>	<b>f</b>	<b>15.6</b>	<b>2.4</b>	<b>14.2</b>	<b>11.4</b>	<b>11.1</b>	<b>1.9</b>	<b>3.8</b>	<b>16.9</b>	<b>8*</b>	<b>1.3</b>	<b>36.1*</b>	<b>18.6</b>	<b>15.0</b>
MHNG 2644.51	m	11.8	2.6	14.9	11.1	10.0	2.1	3.1	13.3	9	1.2	32.0	13.6	20.3
MHNG 2645.70	f	24.8	3.5	20.4	15.2	14.0	1.9	4.5	20.4	10	1.6	47.8	17.8	26.2
MHNG 2645.71	m	17.1	2.7	13.8	10.4	10.6	1.6	3.2	12.7	9	1.4	30.2	13.2	18.4
MHNG 2645.72	f	28.7	3.2	18.8	13.6	12.8	2.3	3.7	21.9	12	1.5	45.7	16.3	24.3
MHNG 2196.1	f	14.7	3.4	15.6	12.3	13.6	2.2	4.0	14.2	10	1.4	39.6	17.7	25.0
MHNG 2196.2	f	14.8	3.5	17.5	13.4	13.9	2.3	3.9	16.8	12	1.3	41.3	19.0	28.6
MHNG 2196.3	f	11.8	3.0	11.4	10.3	10.2	2.3	3.2	9.1	12	1.3	28.2	12.6	18.3
MHNG 2238.30	m	13.0	3.2	13.8	11.8	11.0	2.4	3.2	9.8	11	1.3	30.1	13.7	20.0
MHNG 2238.31	m	14.6	2.6	13.5	11.3	10.9	2.2	3.3	13.3	10	1.2	32.7	15.1	19.3
MHNG 2238.32	m	13.5	3.2	12.5	11.3	11.2	2.0	3.4	9.9	10	1.1	29.5	15.0	20.4
MHNG 2238.33	m	14.2	2.8	13.2	11.4	11.3	2.3	3.7	11.2	10	0.7	29.6	14.7	19.7
MHNG 2238.34	m	11.7	3.3	12.2	10.1	9.9	2.4	3.0	8.2	10	1.3	27.1	13.1	18.5
MHNG 2238.35	m	12.2	2.8	12.6	11.3	10.9	2.4	3.6	9.8	9	1.3	31.6	14.1	20.1
MHNG 2238.36	m	14.0	3.5	14.0	11.8	11.6	2.5	3.5	11.4	9	1.1	31.3	14.8	20.9

and (3) Maximum Likelihood (ML; RAxML version 7.0.4; STAMATAKIS, 2006, using the rapid hill-climbing algorithm following STAMATAKIS et al., 2007 and the GTR+G model).

#### Distribution records

Due to a lack of available museum vouchers with known locality data, we conducted literature as well as electronic data base searches to compile known locality data for the *Xenopus fraseri* subgroup sensu lato with a particular focus on members known or suspected to occur south of the Congo Basin (*X. andrei*, *X. fraseri*, *X. pygmaeus*). Spatial data used to create a distributional map in the freely available software QGIS 2.2.0-Valmiera (QGIS Development Team 2014) were derived from the VertNet data portal (CONSTABLE et al. 2010), MEASEY, J. & R. TINSLEY (2013), and this study.

### Results

#### Morphological comparison

The general morphology of the Angolan specimen corresponds with that of the holotype of *X. andrei* as well as the series investigated for comparison (Fig. 2). All specimens included in the PCoA fall into a single SIMPROF-validated cluster. Nonetheless, there are subtle, yet non-significant differences among specimens that result in separated positions in multivariate morphospace (Fig. 3, PCoA-biplot centroids and SIMPROF sub-cluster structure). These differences may be the result of intraspecific or inter-population variability, but given the comparatively small sample

size (N = 17), we cannot provide a conclusive answer to this question until additional vouchers become available.

In the brief original description that is based on seven individuals (two males, five females) from Longyi, Cameroon, LOUMONT (1983) provides only very limited morphological data and states that there are only few morphological characters that can be used to distinguish *X. andrei* from *X. fraseri*. In fact, the only distinguishing feature given is the number of “stitches” (epidermal mechanoreceptors) in the lateral line system. This is somewhat misleading as there is no clear difference in this character in the corresponding table that summarizes the morphological data (mean 16 in *X. andrei* vs. mean 16–19 in *X. fraseri* depending on locality). However, there is a slight but consistent difference in the number of periocular stitches (higher in *X. andrei*). Our own data show that the number of periocular stitches varies within the same range given in the original description of *X. andrei* (9–12; 12 in the Angolan specimen).

#### Molecular phylogenetic analysis

Morphological results are reflected by molecular data. The barcoding analysis placed the new Angolan specimen in the extended *X. fraseri* subgroup as defined by WAGNER et al. (2013). The 16S sequence of the *Xenopus* voucher from Angola clustered right next to *X. andrei* from GenBank (AY581627) and showed a very strong genetic similarity to the latter (uncorrected p-distances of 0.6%). The genetic distances to all other described species of the *X. fraseri* subgroup are much larger (uncorrected p-distances between 2.2% [to *X. longipes*] and 6.7% [to *X. vestitus*]). A preliminary phylogenetic tree (Fig. 4), including the ma-



jority of members of the subgroup *sensu lato* and based on 16S sequences only, while lacking any basal resolution, corroborates our identification of the Angolan voucher as *X. andrei*, as it is placed in a fully-supported clade together with the sequence of a previously published Cameroonian *X. andrei* specimen. Additionally, the Bayesian analysis also weakly supports a sister relationship with *X. itombwensis*, but this relationship is not supported in either the NJ or the ML trees. The latter results are in accordance with the phylogenetic tree published by EVANS et al. (2011) in which *X. itombwensis* was found to be the sister taxon of *X. wittei*.

### Distribution

*Xenopus fraseri* has been reported from southwestern Cameroon to the eastern Democratic Republic of the Congo (DRC), and south to northern Angola, as well as from the island of Bioko (formerly Fernando Poo), Equatorial Guinea (TINSLEY et al. 2004, FRETEY et al. 2011). Additional records from the northeastern DRC, up to the border with Uganda are considered to represent *X. pygmaeus* (compare WAGNER et al. 2013). LAURENT (1950, 1954) reported on 132 *X. fraseri* specimens collected in the Dundo Region of northeastern Angola, an area bordering the DRC. Whether

these specimens still exist is unclear as collections in Angola are still not fully accessible. Accounts on the populations of *X. fraseri* in the northeastern part of the country (Muíta, Luachimo, and Dundo) provided in RUAS (1996) refer to these previously published records, while no information is given on the additional records from central and southern Angola depicted in the accompanying map (RUAS, 1996, p. 33, Fig. 1).

We are aware of a single *X. fraseri* voucher from Angola (no precise locality information given) that is included in the collection of the Redpath Museum, McGill University, under collection number RMMU 2253, although its taxonomic identity needs to be confirmed.

Apart from the type locality at Longyi, Cameroon (LOUMONT 1983), *X. andrei* has only been reported with certainty from two additional localities in Gabon (Mekambo, north-central Gabon and Makokou, northeastern Gabon) and one in the Central African Republic (Bouchia, type locality of *X. pygmaeus*), but has been suggested to be more widespread (MEASEY & TINSLEY 2013) and extending into neighbouring regions of Equatorial Guinea, the Congo and the DRC. Our record from Angola represents the first confirmed record of *X. andrei* from this country and extends the known distributional range of the species considerably (Fig. 5).

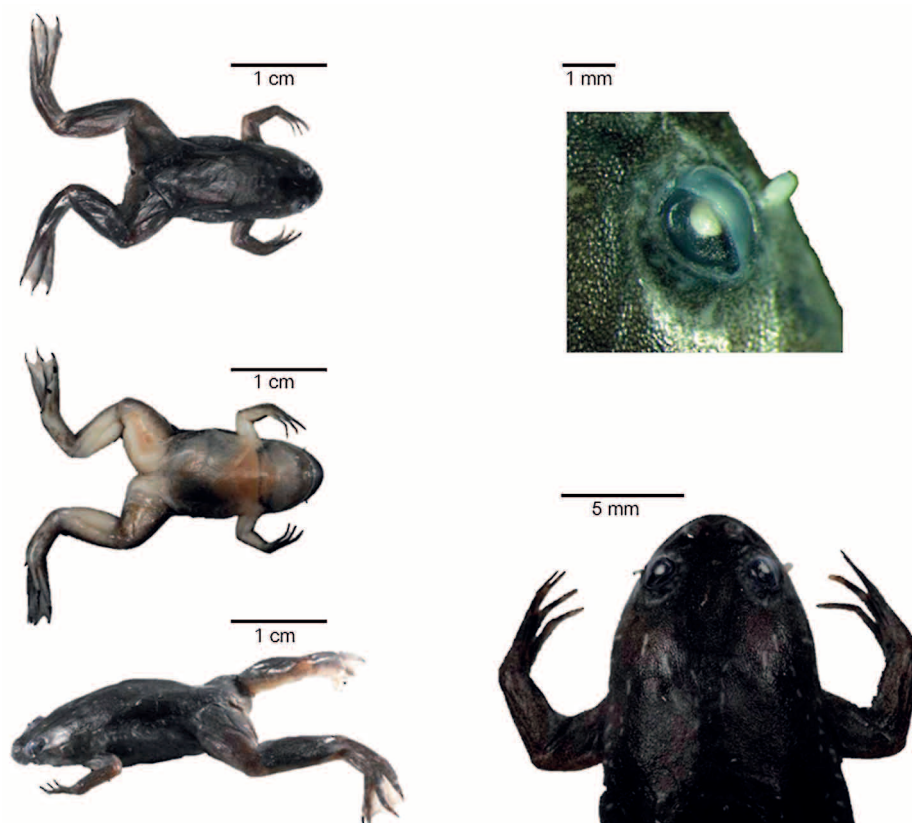


Figure 2. The newly collected specimen of *Xenopus andrei* (MTD 48661) from Angola after preservation. Left column top to bottom: dorsal, ventral, and dorsolateral views. Right column: close-up of periocular stitches and eyelid coverage, as well as subocular tentacle (top) and anterior body portion showing arrangement of subocular tentacles and periocular, as well as lateral side organ stitches.

### Discussion and synthesis

Because of the difficulties with unambiguously identifying particular species in the *X. fraseri* subgroup, it is likely that several records of *X. fraseri* actually refer to other species, including *X. andrei*. This may particularly be the case in historic *X. fraseri* records from Angola.

We cannot rule out the possibility that specimens referred to as *X. fraseri* in LAURENT (1950, 1954) and additional records from central and southern Angola in RUAS (1996) are in fact conspecific with *X. andrei*, as these were recorded prior to the revision of the *X. fraseri* subgroup, in which *X. andrei* was described as a new species. However, due to the absence of corresponding vouchers, this cannot at present be resolved conclusively. Until these records are either confirmed or disproved by unambiguously assigned vouchers, we suggest restricting the known range of *X. fraseri* to previously reported Central African localities. Our *X. andrei* record from the Serra do Pingano must therefore be considered the first confirmed country record of a member of the *X. fraseri* subgroup for Angola that can unambiguously be assigned to an identified voucher. This emphasizes the urgent need for a critical revision of the

distributional data of *X. fraseri*, as this will ultimately also help to clarify the species' conservation status and thus its IUCN Red List categorisation. This is likewise true for other members of the subgroup, including, among others, *X. andrei* or *X. pygmaeus* (see WAGNER et al. 2013).

The presence of *X. andrei* in the Uíge Province is particularly surprising because this locality is situated approximately 2,400 km south of the previously confirmed southernmost locality at Makokou, northeastern Gabon.

Together with the recent discovery of *X. pygmaeus*-like specimens in Zambia (app. 1,300 km south of the southernmost distribution of *X. pygmaeus* reported so far, WAGNER et al. 2013), this casts serious doubt on whether the Congo Basin (in its current extent) really represents the general southern distributional boundary for members of the *X. fraseri* subgroup. Evidence that comes from other

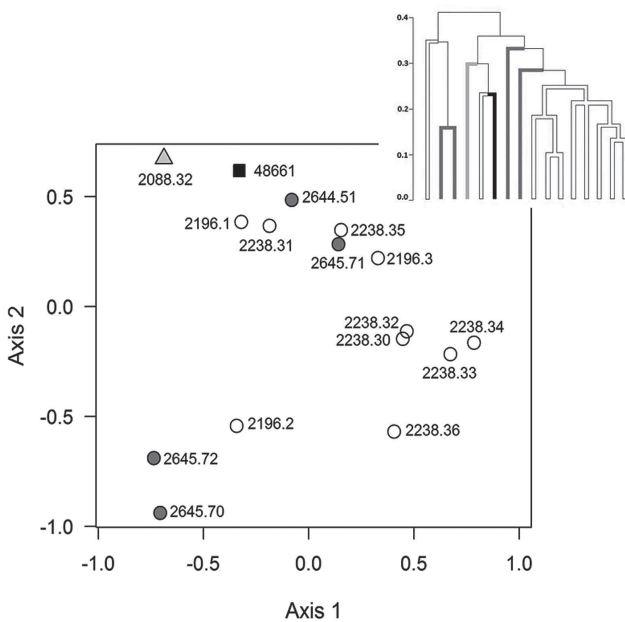


Figure 3. Morphometric analyses of compared *Xenopus andrei* material. Results of principal coordinate analysis (PCoA) based on Gower distances depicting *X. andrei* specimen in morphospace (biplot). Triangle – *X. andrei* holotype (MHNG 2088.32); square – Angolan specimen (MTD 48661); grey circles – topotypic series (MHNG 2644.51, MHNG 2645.70–72); white circles – *X. andrei* series (MHNG 2196.1–3, MHNG 2238.30–37) from Bouchia, Central African Republic. Inset figure: Results of SIMPROF analysis, based on 10,000 generated similarity profiles, 9,999 permutations. All specimens included in the PCoA fall into a single SIMPROF-validated cluster ( $P = 0.001$ ). Colour coding corresponds to coding in PCoA biplot.

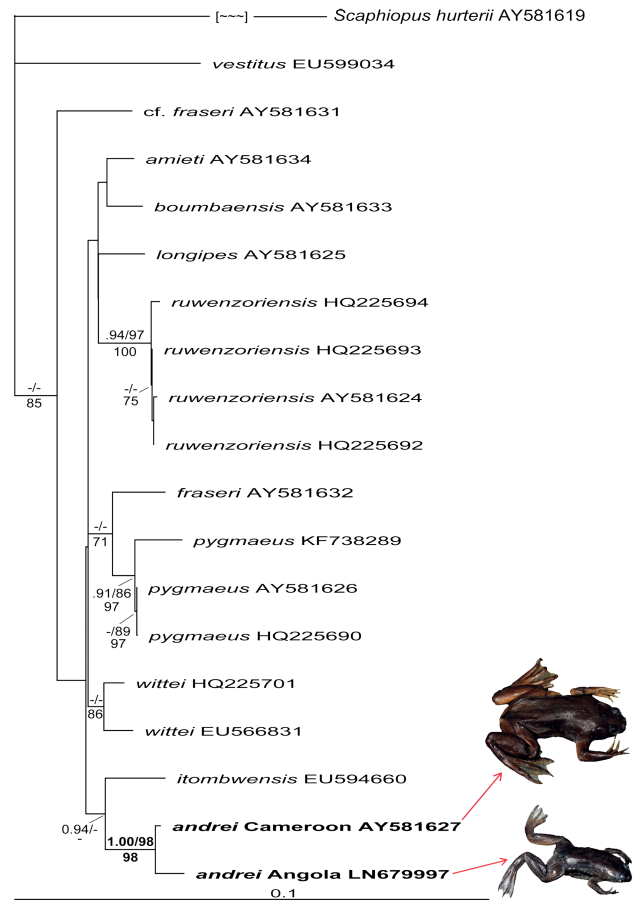


Figure 4. Phylogeny of African clawed frogs based on the 16S mitochondrial gene (553 bp), highlighting the position of the new Angolan record of *X. andrei*. Numbers above branches indicate Bayesian posterior probabilities and Maximum-Likelihood bootstraps, numbers below branches are Neighbour-joining bootstrap values. Only highly significant values (ML: > 70 / PP: > 0.90 / NJ: > 70) are shown. Specimens depicted represent *X. andrei* from Cameroon (top), MHNG 2644.51 (GenBank AY581627) and *X. andrei* from Angola (bottom), MTD 48661 (GenBank LN679997).

remarkable amphibian discoveries recently made in the largely underrepresented southern Central African forest biomes indeed seems to challenge this assumption for amphibians in general (ERNST et al. 2014) and this is also reflected in reptile distribution patterns (e.g., WAGNER et al. 2008, WAGNER et al. 2009).

The observation that an increasing number of species turns up well outside their previously reported ranges, also highlights the fact that current biogeographical delimitations may, to a considerable extent, simply reflect sampling gaps and taxonomic misidentifications rather than true biogeographical patterns. Moreover, these newly established faunal data shed light on the forest history of the region as a whole. If included in larger biogeographical models, they may contribute to solving open questions concerning early Pleistocene glaciation dynamics assumed to

have affected the recent and historic extent of the Guineo-Congolian tropical forest phytogeographic region.

A late Quaternary connection among central African rainforest patches has previously been hypothesized based on palaeoenvironmental reconstructions (MALEY 1991). These analyses have also clearly shown extensions of montane vegetation to low altitudes, particularly in northern Angola and the southern DRC (MALEY 1987), making a previous link between central African forest biomes as far apart as Cameroon and the forest remnants of northern Angola likely (see also WAGNER et al. 2008). This seems to be supported by the occurrence of forest-bound amphibian species with a suggested distributional centre in Central Africa.

Without doubt, the palaeoenvironmental history of the region is much more complex than previously assumed, and the debate on the precise location of potential late Pleistocene forest refuges has not yet been convincingly settled (compare COLYN et al. 1991). In the particular case of Angola, we even lack more recent accounts of forest dynamics and fragmentation, which poses an additional challenge on disentangling recent and historic drivers of biogeographical patterns. Data derived from different taxonomic groups are thus badly needed to narrow existing knowledge gaps.

It may seem surprising that these data are largely lacking despite an otherwise long history of natural exploration on the African continent. But this simply reflects the difficulties associated with biodiversity research in the region. Due to the protracted civil war in Angola (1975–2002), opportunities for scientific research in the region were limited and as a consequence biodiversity research advanced little. Today's knowledge of Angola's national biodiversity remains poor compared to that of many other sub-Saharan countries. This is particularly true for herpetofaunal diversity (CONRADIE et al. 2012a). Despite its large size (1.25 million km<sup>2</sup>) and exceptional habitat diversity (BURGESS et al. 2004), ranging from desert in the south to lowland rainforest in the north, the known amphibian and reptile diversity ranks well below that of neighbouring countries, e.g., the DRC (Angola: 101 amphibian species, of which 11 are considered endemic vs. DRC: 224 amphibian species, of which 48 are considered endemic, compare FRÉTEY et al. 2011) or countries of similar size, e.g., South Africa (Angola: 257 reptile species vs. South Africa: 381 reptile species, of which app. 45 % are endemic, compare CONRADIE et al. 2012b). Recent surveys, and the few available new studies that resulted in the description of new taxa (CONRADIE et al. 2012a, b; 2013) indicate that the diversity, distribution and relationships of the Angolan herpetofauna are poorly understood and that herpetofaunal diversity is largely underestimated due to a lack of systematic sampling in the past. While the aforementioned studies mainly focused on (montane) grasslands, savannahs, and shrublands in the west-central highland and southwestern provinces, surveys have largely neglected the last remaining lowland rainforest patches of northern Angola. However, due to their assumed link with the large Congolese Forest bioregion and unique position within the range of Angolan ecosystems they promise to harbour an exceptionally rich herpetofau-

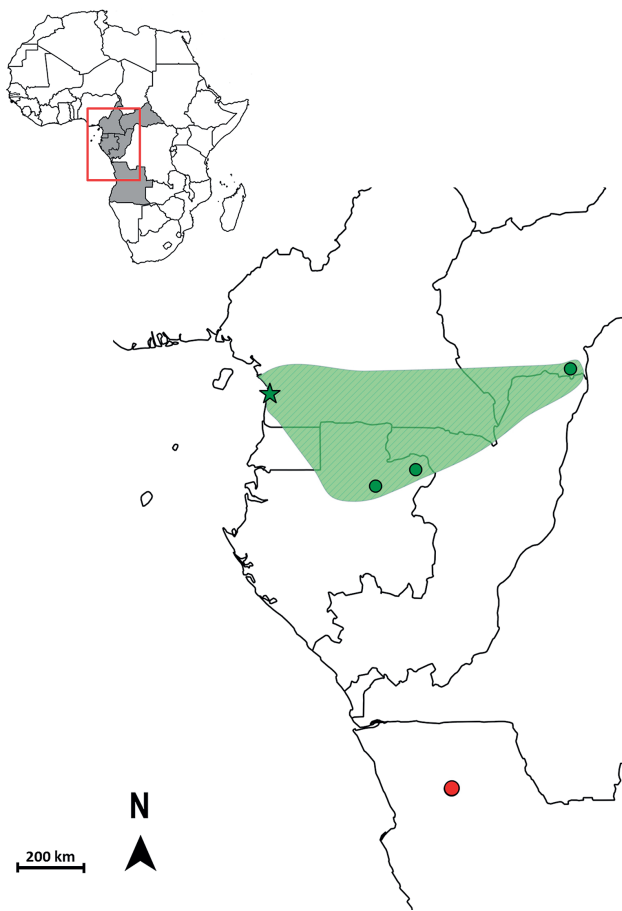


Figure 5. Map showing the known distribution of *Xenopus andrei* (green polygon) and the new record in Angola. The green star marks the type locality at Longyi, Cameroon. Green circles indicate confirmed records from Gabon (Mekambo, north-central Gabon and Makokou, northeastern Gabon) and the Central African Republic (Bouchia). The red circle marks the new record (MTD 48661) from the Serra do Pingano, Uíge Province, Angola. Spatial data derived from VertNet data portal (CONSTABLE et al. 2010), last accessed 17 February 2014, MEASEY, J. & R. TINSLEY (2013), and this study.

na. At the same time, they are facing immense pressures from increasing deforestation and fragmentation. The survey that resulted in the discovery of *Xenopus andrei* and the hairy frog (ERNST et al. 2014.) in Angola was one of the first systematic surveys conducted in this previously neglected yet very promising region.

Findings such as ours open a path to reconstructing the phylogenetic history of selected taxa and may help to uncover the poorly understood biogeographical and anthropogenic history of the region as a whole. This is particularly important as evidence accumulates that northern Angolan rainforests may have served as a refugial area for rainforest taxa during periods of dramatic climatic fluctuations (compare, e.g., WAGNER et al. 2008). It also highlights today's paramount importance of the remaining forest fragments in the larger geographical context.

Rapid biodiversity surveys in combination with modern scientific techniques and long-term monitoring routines are therefore urgently needed to obtain a better understanding of the largely underappreciated herpetofauna persisting in these fragile forest remnants and to resolve both taxonomical and biogeographical questions. This will provide the basis for a more comprehensive assessment of Angola's biodiversity in general and is a prerequisite for the development of sound and sustainable conservation strategies of its most precious and unique ecosystems.

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