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Availability of Recently Described *Ptychadena* (Anura: Ptychadenidae) Nomina from Ethiopia

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Frogs of the genus *Ptychadena* (Boulenger, 1917) have long been identified as harboring cryptic diversity and comprising numerous species-complexes (Largen 1997; Zimkus *et al.* 2017), and many authors have recognized the particularly high hidden richness in the Ethiopian highlands (Largen 1997; see Largen & Spawls 2010 and refs. within). This cryptic diversity was confirmed by recent molecular studies (Freilich *et al.* 2014; Smith *et al.* 2017a, Reyes-Velasco *et al.* 2018). Those authors identified a congruent set of evolutionarily distinct candidate species using both mitochondrial and nuclear DNA, and described the geographic and ecological isolation of these species in detail (Freilich *et al.* 2014; Smith *et al.* 2017a).

Smith *et al.* (2017a,b; SEA hereafter) in particular performed Bayesian species delimitation and validation analyses, revised the taxonomy of the *Ptychadena neumanni* species group, and named a total of 5 new species of *Ptychadena* based on morphological and molecular characters. In an effort to adhere to the spirit of good taxonomic practices (Kaiser *et al.* 2013; Renner 2016), SEA used a multilocus dataset and multiple species discovery approaches that require no *a priori* assignment of individuals to species groups and tested the valididty of their findings with rigorous Bayesian species validation. Subsequently they applied a phylogenetic species criterion (as an extension of the biological species concept and contained within the general linage concept of de Queiroz 2007) for a conservative approach to naming identified species. The new taxa named by SEA were based on type specimens, and these were adequately described and diagnosed, as required by the ICZN (1999). Importantly, the descriptions included morphological characters that vary between taxa, and appear to be diagnostic in combination, without reference to the molecular data. Finally, the characters listed in the description in combination with distribution (elevation and geographic) and ecology (described by SEA 2017a) are sufficient for proper identification. While the *Code* does not place restrictions on what constitutes a character (ICZN 1999), or whether diagnosis or description are both required in taxonomic actions (Renner 2016), SEA included morphological, molecular, and spatial data in their species descriptions which in combination are both diagnostic and descriptive.

Recently, a paper by Reyes-Velasco *et al.* (2018), hereafter REA, questioned the validity of taxonomic actions made by SEA and the authors' use of Bayesian species delimitation to erect formal taxa. REA performed further phylogenetic and population-genetic analyses of the *P. neumanni* speces complex using mitochondrial DNA and genome-wide SNPs. While acknowledging the existence of the candidate species identified by SEA, REA chose not to use the revised taxonomy provided in SEA, apparently on the basis that REA disagreed with the methods and conclusions of SEA. REA incorrectly stated that the taxonomy proposed by SEA did not conform to Article 13 and should be considered *nomina nuda* and thus unavailable under the rules of the Code (ICZN 1999). REA subsequently disregared the taxonomy of SEA.

While it is outside the scope of this commentary to critique the use of one species-delimitation method or another (see Carstens *et al.* 2013), we here focus on the purely nomenclatural aspects and show that the arguments against the availability of the proposed nomina of SEA set forth by REA are flawed. We demonstrate that REA misinterpret the language of the *International Code of Zoological Nomenclature* (ICZN 1999), hereafter the *Code,* and that REA' arguments are also philosophically flawed by conflating species delimitation with species description (the naming of species and designation of type specimens). The rules of taxonomy are relatively clear and while mistakes will and have been made, the *Code* al-

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lows for corrections to be made (see Dubois *et al.* 2015). In the original study, Smith et al. (2017a) failed to recognize that Zoobank registration numbers were not included in the formal descriptions in their original publication (a requirement of the *Code* for online only publications (IUZN 1999; 2012 amendment), necessitating the publication of a correction (Smith et al. 2017b). Here, we aim to correct the record regarding the taxonomic actions interpreted by REA.

The argument used by REA for declaring the species of SEA *nomina nuda*; lacking "appropriate [morphological] diagnostic characters is incorrect. Article 13 of the ICZN states: "13.1.1. [A name must be] be accompanied by a description or definition that states in words characters that are purported to differentiate the taxon (ICZN 1999). The *Code* does not require a specific level of distinctiveness to differentiate species, nor does it place any restriction on what those characters may be (thoroughly reviewed in Cook *et al.* 2010; Renner 2016). According to the *Code* there is no actual requirement for a character to be demonstrated as diagnostic in any way, as the *Code* allows for diagnoses or descriptions as alternative choices in taxonomic actions (Renner 2016). This is a critical detail which ads to the scientific rigor of the taxonomic process, as the diagnostic capacity of characters is a hypothesis which can then be tested and refined by future studies (Gaston and Mound 1993; Kaiser *et al.* 2013). SEA included morphological descriptions and putatively diagnostic characters related to both color pattern and gross morphological variation. The requirement here is only that the names be associated with a description, reference or indication. The names of SEA unambiguously possess a description, and thus are categorically not *nomina nuda.*

While we admit that the diagnosis of SEA may seem scanty or inadequate to some, they contain both diagnostic characters and descriptions in conformance with the Code, and are not unusual for cryptic amphibian species such as *Ptychadena*. For example, the original diagnosis for *P. harenna* in Largen (1997) is: " Diagnosis. A *Ptychadena* of moderate size and proportions (snout-vent length of adult males about 38 mm, tibia about 57% of snout-vent length) and with the foot moderately webbed (2⅓–2½ phalanges free on the fourth toe, 1–1½ on the fifth); in which the skin folds on the back are extensively and irregularly fragmented, the median pair at least being conspicuously feeble and scarcely extending anterior to the shoulder region; there is a pale triangle on top of the snout; a marked tendency towards reduction or almost complete loss of dark markings on the back, at least in the mid-dorsal region and sometimes overall; a very obscure pattern of sparse, irregularly distributed, pale freckles or mottling on the back of the thigh; and an extensive suffusion of dark pigment on the ventrum. No pale line on the tibia and no supernumerary metatarsal tubercles." Correspondingly, the description of *P. baroensis* Smith *et al.* 2017a provides the diagnosis: "... *P. baroensis* is a moderately large *Ptychadena* with males known to reach an s.v.l. of 47.8mm. The dorsum is brown to tannish red, may have spots and is covered by a series of longitudinal skin ridges that are often indistinct or broken. The triangular patch on the snout is less pronounced than that of *P. anchieta* sensu stricto, which in Ethiopia is only known from lowlands east of the GRV. Webbing on the hind feet is extensive with usually only two phalanges free on the longest toe. The back of the thigh is often marked with yellow and black longitudinal bands and the ventral side of the body is white to pale yellow."

As systematists, we support the view that diagnoses are most helpful when they contain multiple characters that are quantitatively distinct between taxa. However, this is a matter not only of the *existence* of such characters (which may not be the case for cryptic species), but also of the amount of *time* and *effor*t placed into describing the taxa. Such effort must be balanced against the need for speedy recognition of species which might be of conservation concern. Putatively diagnostic characters (and thus, by implication, hypotheses about species-level variation among populations in external morphology) have been provided, and can be tested, rejected, or modified in the future (Gaston and Mound 1993; Kaiser *et al.* 2013. Similarly, informal comments received by the authors of SEA (*pers. comm.* and from anonymous peer reviewers of the present manuscript) have suggested that characters reported are not useful to biologists in the field. While we feel that in combination the charcters reported by SEA are diagnostic, their utility in the field is not a requirement of the *Code,* nor is it a reasonable expectation for many such cryptic taxa*.* Field identifcation is often impossible in many taxa (e.g. pediculid lice, Hymenoptera, Coleoptera, or even vertebrates such as sphenomorphine skinks or tyrannid flycatchers) and proper identification takes both technical expertise, training and often additional tools such as molecular methods. Lastly, the diagnostic characters reported and level of detail provided in the descriptions by SEA are not uncommon for cryptic amphibian species.

Informal criticisms have also been made (https://amphibiaweb.org/species/8790; accessed 18 April 2019) that this paper [Smith *et al*. 2017b] fails to state in which permanent collection the types are deposited, as required by Code, although this information was included in the first paper, raising the unresolved technical question of legality of the names. The critique here refers to Articles 16.4.1 and 16.4.2, requiring explicit fixation of a holotype and a statement of intent that they will be (or are) deposited in a collection and a statement indicating the name and location of that collection. As noted in the critique, Smith *et al*. (2017a) stated that the type specimens in the TJC and XF field series were deposited at the Zoological Museum of Natural History (ZMNH), Addis Ababa University in Addis Ababa, Ethiopia where they await accessioning. The citation of Smith *et al*. (2017a) by Smith *et al*. (2017b) and the listing of the same field series numbers provides clear continuity for the statement of accessioning and does not affect availability of the names.

As of December 26th 2019, the specimens deposited at ZMNH by TJC have been accessioned (Table 1**)**. This process took some time as the ZMNH was shortstaffed due to recent political and economic difficulties in Ethiopia. The specimens deposited by XF and SB (coauthors on REA) could not be located by TJC in a 2017 trip to Ethiopia or subsequently by ZMNH staff. These specimens are presumed to still be at ZMNH but are in long term storage as the museum transitions to a newly rennovated facility. Furthermore, it should be noted that attempts were made by TJC to contact XF and SB regarding the status of these specimens in 2017 and 2018 without response. Any researcher who has worked with facilities in the developing world is familiar with the myriad difficulties that can hinder the timely and accurate curation of biodiversity resources and natural-history collections. This should never be an impediment to taxonomic progress, particularly given its crucial importance for conservation management. Here, we provide photographs (Figure 1) showing the labeled jars that have been accessioned in the ZMNH, offering definitive proof that the specimens exist, are labeled properly, have now been accessioned, and in all other aspects generally conform to Recommendations 16C and 72F.

TABLE 1. List of specimens, TJC field series and ZMNH accession numbers for available types provided in Smith *et al.* (2017a; 2017b).

Species	**Field Series**	**Accession Number**	**Type**
Ptychadena baronensis	TJC318	H2019,2182	Holotype
Ptychadena baronensis	TJC319	H2019,2183	Paratype
Ptychadena baronensis	TJC343	H2019,2184	Paratype
Ptychadena baronensis	TJC344	H2019,2185	Paratype
Ptychadena nuerensis	TJC455	H2019,2188	Holotype
Ptychadena nuerensis	TJC410	H2019,2186	Paratype
Ptychadena nuerensis	TJC451	H2019,2187	Paratype
Ptychadena levenorum	TJC219	H2019,2180	Holotype
Ptychadena goweri	TJC224	H2019,2181	Holotype

Finally, informal comments received by the authors of SEA (*pers. comm.* and from anonymous peer reviewers of the present manuscript) have suggested a similarity between this case and that of the unavailable names proposed for some *Hemidactylus* species by Leach and Fujita (2010), as discussed by Bauer *et al*. (2011). Those names entirely lacked diagnoses and in some cases type localities. In contrast, we have demonstrated that the names of SEA clearly and unambiguously contained diagnoses, type specimens, and type localities. The only issue affecting availability and validity in Smith *et al*. (2017a) was the issue of ZooBank registration, and the publication of Smith *et al*. (2017b) rectified this in all respects.

The scientific method applied by SEA is both in adherence with the *Code* and in the spirit of best practices for publishing taxonomic decisions as outlined by Kaiser *et al.* (2013), which states that taxonomic changes should: 1) adhere to the governance and spirit of the *Code*, 2) preserve stability in nomenclature when possible, and 3) be based upon evidence and a biologically meaningful species concept. Addtionally, Kaiser *et al.* (2013) propose that 21st century taxonomists should generate hypotheses of group membership based upon primary sources (in the case of SEA these were whole specimens, ecological data, DNA sequences and the available literature), test these hypotheses rigorously (what is considered rigorous is outside the scope of this commentary), and submit proposed taxonomic decisions to peer-reviewed journals with accompanying rationale. All were carried out by SEA.

REA also claim that SEA were unjustified in describing taxa without including topotypic material in their molecular analyses, while acknowledging that topotypic material is unavailable, and in some cases the type material is presumed lost. SEA included samples that were ecologically aligned (geographic and elevational distribution) with topotypic material and used this criteria in ascribing molecular candidate species to existing species names. This practice is not without precident, particularly in geographic regions where type descriptions are often vague and type material often misplaced/presumed lost (see Medina *et al.* 2016). No taxonomy is perfect (indeed species are continuously evolving biological entities and taxa are hypotheses to be tested (Gaston and Mound 1993; Kaiser *et al.* 2013), but it is clear that the taxonomy of SEA is valid under the rules of the *Code,* and the species limits of the *P. neumanni* species complex delineated in Smith *et al.* (2017a) are testable hypotheses. Finally, REA attempt to discredit the validity of two lowland taxa described by SEA without performing any analyses of lowland *Ptychadena* in their study.

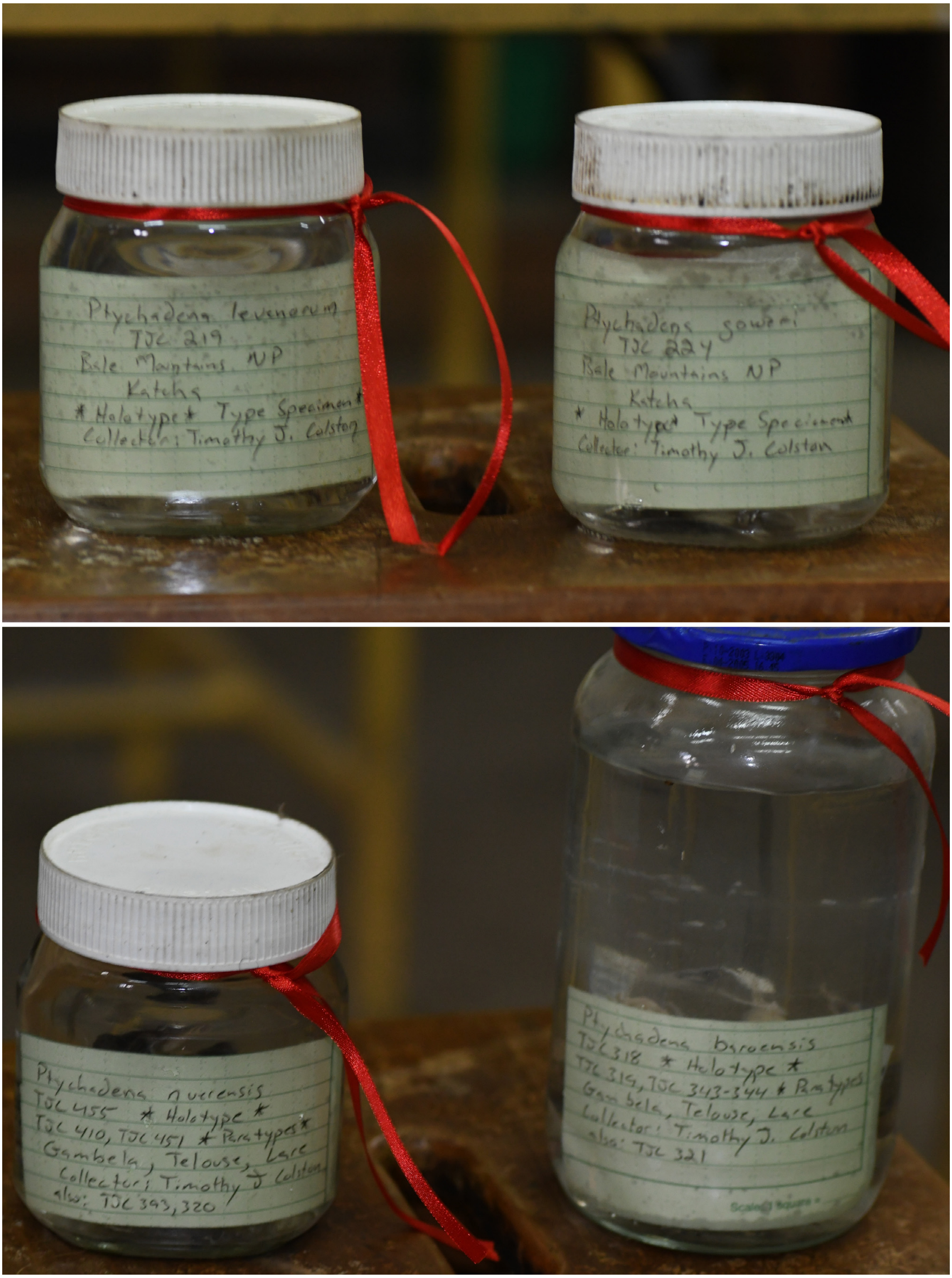

FIGURE 1. Photographs of available type specimens from Smith *et al.* (2017a; 2017b) jarred and deposited at ZMNH, Addis Ababa, Ethiopia. Photos were taken by TJC in October of 2017. Accession numbers provided in Table 1.

Ultimately, REA claim that the taxonomy of SEA should be ignored, as they feel the species descriptions do not contain (morphological) characters that are sufficiently diagnostic (*pers comm.* & REA). We have already addressed how this is incorrect by the rules of nomenclature, but it is also a philosophically unwarranted practice. By applying a stringent morphological species concept in taxonomy whilst primarily accepting an evolutionary or phylogenetic species concept in species delimitation, there is a fundamental disconnect between theory and practice (Cook *et al*. 2010; Carstens *et al.* 2013; de Queiroz 2007).

No *Codes* (Bacterial, Botanical, Zoological) address what constitutes a species, a purposeful omission reflecting the lack of a universally accepted species concept (de Queiroz 2007; Mallet 2013). The *Codes* of taxonomy only address *how* to name a species, and make no claims on what is a minimally diagnostic character (Renner 2016). What is fundamentally important is that any data used in descriptions be linked to types and therefore testable in an integrative taxonomic framework (Cook *et al.* 2010; Renner 2016). In their species descriptions SEA unambiguously designate types, along with diagnostic characters for the taxa they describe. Under the rules of the *Code* and recent guidelines of best practices in taxonomy, the names established by SEA are indeed valid and available.

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