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Why *Toxicocalamus longhagen* Roberts, Iova & Austin, 2022 (Serpentes, Elapidae) is a taxonomic *nomen dubium*

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Abstract

Roberts *et al*. (2022) presented a taxonomic decision, in which they proposed the species name *longhagen* for a single, poorly preserved specimen of elapid New Guinean snake in the species assemblage known as the *Toxicocalamus loriae* Group. Geographically widespread populations in this species group had long been united under a single name even though some character variation had been noted, and only a thorough morphological study by Kraus *et al*. (2022), published shortly after the description of *T. longhagen*, confirmed additional species-level diversity and the detail of character analysis needed to differentiate species in this group. Their work made clear that only examination of many specimens would allow an assessment of interspecific variation and species boundaries, and this had been explained to the authors of the Roberts *et al*. paper ahead of their manuscript submission. The authors of the Kraus *et al*. paper had examined the specimen used to diagnose *T. longhagen*, as well as a series of similar specimens, and found it impossible to make a reliable species-level determination. Our detailed evaluation of the taxon *longhagen* reveals that it is insufficiently differentiated from the now-known species of the *T. loriae* Group, that it cannot confidently be assigned to any of these species, and that none of the existing specimens of snakes in this group can be assigned to *T. longhagen*. It follows that *T. longhagen* as currently defined is a taxonomic *nomen dubium*. It will retain this status until such time when additional data or additional material can lead to a resolution of its taxonomy.

Key words

Code, taxonomic status, New Guinea, nomenclature, *mihi* itch, worm-eating snake, herpetology.

Introduction

The identification and delineation of new species is done by taxonomists, scientists who assemble observations about groups of organisms they hypothesize to be distinct evolutionary lineages. These facts are focused around examining patterns of geographic variation in phenotypic characters and determining if and where discontinuities and discrete, fixed differences appear in those distributional patterns. If the accumulated evidence from the specimens examined is conclusive, then taxonomists can propose a taxonomic decision, such as identifying clades and perhaps applying a scientific binomen to formally and permanently recognize new species. Upon publication, this new nomen enters the accounting system called nomenclature, a system subordinate and in service to taxonomic science, and the nomen's stability is maintained by the underpinning scientific evidence (Kaiser 2013). Although the level of evidence deemed conclusive for taxonomic decisions that lead to nomenclatural acts may vary based on the taxon under investigation or the specific preferences of the taxonomist(s), the decision must nevertheless be objectively verifiable using the evidence available, or no taxonomic stability can be attained.

If an attempt at objective verification of a taxonomic hypothesis is made and the data prove inconclusive, then this places the taxonomic decision in doubt or disqualifies it. Alas, while it may be straightforward to discredit a taxonomic decision, there is no direct recourse to disqualify a validly published taxon name once it has entered the realm of nomenclature. This is a critical defect of that system (Kaiser 2013; Kaiser *et al*. 2013). In addition, the bar for nomina to enter nomenclature is very low (nomina remain available whether or not their proposal was based on objective science), yet the options for removing doubtful or unstable nomina are few. The only recourses include relegating the nomen to the synonymy of an earlier, properly established nomen when clear character evidence allows, or to flag it by calling it a *nomen dubium* until such time as additional evidence emerges to satisfactorily support or refute the taxonomic decision.

A *nomen dubium* is "[t]he name of a nominal species for which available evidence is insufficient to permit recognition of the zoological species to which it was applied" (Mayr 1969: 407) or, put another way, "a name of unknown or doubtful application" (Glossary of the *International Code of Zoological Nomenclature*; Anonymous 1999). Alas, these definitions are inadequate since they do not differentiate between nomenclatural and taxonomic origins of the doubt (Dubois 2008, 2011). Issues producing a "nomenclatural *nomen dubium*" nowadays stem mostly from historic texts, such as when no type or type series was designated, or when type specimens were unknowingly distributed among multiple taxa (anaptonyms and synaptonyms, respectively; Dubois 2011). A nomen whose nomenclature is clear but that cannot be allocated taxonomically to a living population is a "taxonomic *nomen dubium*" (a nyctonym; Dubois 2011). The decision to consider a proposed taxon name as a nyctonym is a taxonomic one that must be objective and based on scientific evidence, just like the decision to propose the nomen in the first place was taxonomic. On the side of nomenclature, a nyctonym can subsequently be "rescued" from doubt via a taxonomic process: the presentation of additional, supportive evidence. Should any forthcoming evidence refute the decision to establish the taxon, then the name would be relegated to the synonymy of an existing taxon.

Is *Toxicocalamus longhagen* a nyctonym?

The nomen *Toxicocalamus longhagen* was recently introduced by Roberts *et al.* (2022) based on a single, discolored, adult male specimen of the "*T. loriae* Group" (*sensu* Kraus *et al.* 2022). Unfortunately, the evidence presented in its original description does not allow it to be either reliably

assigned to or reliably discriminated from any taxon (evolutionarily independent lineage) currently known to be a member of the species assemblage called the *T. loriae* Group. This group is defined as those species of *Toxicocalamus* having a combination of [1] paired subcaudals; [2] prefrontal not fused to internasal; [3] preocular not fused to prefrontal or internasal and typically in contact with nasal but not internasal; and [4] dorsum grey or brown and unspotted, with or without a dark vertebral stripe (Kraus *et al*. 2022). Snakes historically assigned to "*T. loriae*" have a confusing diversity of scale counts and color patterns but have been united by the otherwise conservative combination of these scale and color features.

We (Kraus *et al*. 2022) reviewed the systematics of the *T. loriae* Group and provided results from our analysis of 224 specimens, which included all specimens of "*T. loriae*" except for 97 of 118 specimens from a single population collected at Kundiawa, Chimbu Province, Papua New Guinea, for which we deemed analysis of 21 specimens to be sufficient (we did examine these additional 97 specimens to confirm their identity with the 21 specimens we used from Kundiawa, but we did not incorporate them into our taxonomic analyses). We concluded that this morphologically cohesive species complex included nine species: *T. loriae* (Boulenger, 1898); three nomina long synonymized under that name (*Apisthocalamus lamingtoni* Kinghorn, 1928; *Apisthocalamus loennbergii* Boulenger, 1908; *Pseudapistocalamus Nymani* Lönnberg, 1900); *T. nigrescens* Kraus, 2017; *T. mattisoni* Kraus, 2020; and three species we newly described (*T. atratus*, *T. spilorhynchus*, *T. vertebralis*). The clade to which *T. loriae* and its relatives belong was found to be monophyletic by Strickland *et al.* (2016), with inclusion of the morphologically divergent and readily diagnosed *T. pachysomus* Kraus, 2009 and *T. mintoni* Kraus, 2009, as well as the recently described *T. goodenoughensis* Roberts & Austin, 2020.

The sole specimen to which the name *T. longhagen* was assigned is clearly a member of the *T. loriae* Group on the basis of the unique character combination noted above, but it cannot be reliably diagnosed as a separate and valid taxon from the other nine members of this group because of three problems in the original description: [1] the presumptive new species was not compared to all then-known members of the *T. loriae* Group; [2] assessment of character variation within the *T. loriae* Group was made for only 12 of 321 available specimens (3.7 %); and [3] the putative taxon could not be differentiated using reliable color-pattern information, which is a critical diagnostic component for species in the *T. loriae* Group (Kraus *et al.* 2022). Consequently, it is unclear what taxon the sole specimen of *T. longhagen* represents.

Inadequate comparisons among species

As stated above, the *T. loriae* Group is morphologically conservative and in our own assessment of the group we could resolve species-level differences among *T. loriae*, its synonyms, and the newly recognized species only by examining all specimens of all populations available in museums (Kraus *et al*. 2022). Furthermore, we noted that there remained 19 specimens examined by us that we could not confidently assign to either a new or existing taxon due to preservation artefacts, primarily involving unreliable color-pattern information. Among those 19 specimens was the holotype of *T. longhagen*. Roberts *et al*. (2022) diagnosed their new species against only 12 specimens of the species complex: one of *T. loriae sensu stricto* (their "*T. loriae sensu* Kraus 2020"), two of *T. lamingtoni* (their "*T. loriae* clade 3 *sensu* Strickland *et al*. 2016"), and nine specimens of *T. atratus* (their "*T. loriae*" without further attribution), but they did not include types of any of the named forms. They also added some data obtained from post-description literature sources but not data from the original descriptions of *T. loriae* (Boulenger 1898), *T. lamingtoni*, *Apistocalamus Pratti* Boulenger, 1904, or *T. nymani*. Among the then-synonyms of *T. loriae*, Roberts *et al*. (2022) only included *T. loennbergii* in their comparisons, using data taken from Kraus (2020).

The presumptive new species was based on only a single specimen even though in prior correspondence we had cautioned against this approach. To wit, just after the manuscript of Kraus *et al.* (2022) had been submitted for review, the first author received a draft of the description of *T. longhagen* from the first and third authors of Roberts *et al.* (2022) with the request for a review. On 30 June 2022 he responded, explaining:

> I would also note that the taxon you are describing has eight available specimens, not one. Why did you not include the others? They are all at UPNG [University of Papua New Guinea]—one more from Dobel, six from Wonenara, EHP [Eastern Highlands Province, Papua New Guinea]. Any description of a new form should include them all so as to provide the best assessment currently available of variation. This is especially important because two of the systematically important features in this group, which you use to diagnose your new species, are problematic in this PNGNM [Papua New Guinea National Museum and Art Gallery] specimen.

This advice was not heeded, even though the office of the second author of Roberts *et al.* (2022) lies just 3 km from those specimens.

Inadequate assessment of character variation

The diagnosis of *T. longhagen* is based on 16 characters. Of these, most only serve to distinguish members of the *T. loriae* Group from other, quite divergent, species in the genus and are irrelevant to the present discussion. Only the following were of potential value to provide a differential diagnosis against members of the *T. loriae* Group: [1] preocular not in contact with nasal; [2] presence of two postoculars; [3] presence of one large posterior temporal; [4] 200 ventral scales; and [5] 43 subcaudal scales. These five characters were used to compare the holotype of *T. longhagen* to four members of the *T. loriae* Group (a composite "*T. loriae*", *T. loennbergii*, *T. mattisoni* and *T. nigrescens*), relying on published data without the benefit of a specimen-based assessment of intraspecific variation in these features within this complex. While this approach was adequate for comparisons with *T. mattisoni* and *T. nigrescens*—species well characterized in their original descriptions (Kraus 2017, 2020)—it was inadequate for synonyms and taxonomically unassigned populations. Considering that these synonymies were established (McDowell 1967, 1969) because the dearth of specimens many decades ago limited understanding of variation within the group, the current availability of more than 300 specimens from this complex provides a definitive remedy.

It had repeatedly been stated in the literature (e.g., Kraus 2009, 2017, 2020; O'Shea *et al.* 2018) that the *T. loriae* Group comprised several species, so a limited diagnostic approach was clearly inadvisable. Furthermore, another seven UPNG specimens (referred to in the quote above) seemed likely to be conspecifics of the purported new species but were not included in the assessment. The determination of possible conspecificity was based on two lines of reasoning: [1] the sole other topotypic specimen (UPNG 3992) has a yellow venter irregularly dusted with brown, placing it at variance from the other species recognized by Kraus *et al.* (2022) but suggesting that the holotype of *T. longhagen* originally had the same pattern; and [2] six specimens from Wonenara, Eastern Highlands Province, Papua New Guinea, exhibit a similar ventral pattern to UPNG 3992, though discoloration makes this match less certain for some specimens. As a consequence, possible intraspecific variation of potentially diagnostic features within *T. longhagen* went unassessed, and no determination of how such variation might compare to that in the other species of the complex was made. In fact, our own research showed that the five listed diagnostic features of *T. longhagen* do not serve to unambiguously diagnose a new taxon within the *T. loriae* Group and we determined that any taxonomic decision

or even reliable species assignment of these specimens was impossible (Kraus *et al.* 2022). In the following paragraphs, we consider the problems with each character in more detail.

Preocular contact with the nasal

These scales may be in contact, or they may be separated from each other by contact between the prefrontal and the second supralabial. Roberts *et al.* (2022) used preocular-nasal separation as a distinguishing feature of *T. longhagen*. However, in the taxa now recognized as members of the *T. loriae* Group this character cannot be diagnostic when assessed in only a single specimen because it is intraspecifically variable in *T. loriae*, *T. loennbergii*, *T. nymani*, *T. atratus*, *T. spilorhynchus* and *T. vertebralis*. More problematic is that it also varies among the seven UPNG specimens that may belong to the same taxon as the holotype of *T. longhagen* (see above). Consequently, observation of lack of contact between the preocular and nasal in a single specimen cannot be viewed as having diagnostic value in determining whether *T. longhagen* is a valid taxon within this species complex. Roberts *et al.* (2022) missed this fact because they based their analysis on a single specimen and did not assess the broader variation of this character, contrary to the advice provided them.

Number of postoculars

There is a single postocular scale in *T. loennbergii* and *T. mattisoni*. Roberts *et al.* (2022) sought to distinguish *T. longhagen* from these two species by the presence of two postoculars. This is correct. However, this character also serves to distinguish *T. longhagen* from *T. lamingtoni* and *T. nigrescens* (unremarked by Roberts *et al.* 2022) but not from *T. loriae*, *T. nymani*, *T. vertebralis*, *T. spilorhynchus* or *T. atratus*, all of which show intraspecific variation in this character. All but *T. loriae* show a strong tendency towards the presence of two postoculars (Kraus *et al.* 2022), the character state in the *T. longhagen* holotype.

Presence of one large posterior temporal

Toxicocalamus mattisoni has two posterior temporals touching the anterior temporal, and Roberts *et al.* (2022) used the fact that a single large posterior temporal touches the anterior temporal in the *T. longhagen* holotype as a character (their figure 4) to distinguish it from *T. mattisoni*. This is correct when using the restrictive novel definition of posterior temporal scales provided by those authors. However, the arrangement of scales on the posterior part of the head of the *T. longhagen* holotype includes two scales, one behind the other, on both the right and left sides of the holotype, but not both touch the anterior temporal. During our examination of this specimen, we did not consider the number of posterior temporals diagnostic in the *T. loriae* Group because we followed a more inclusive definition of what should be considered a posterior temporal (e.g., Boulenger 1893; Peters 1964; Malnate & Underwood 1988; Lillywhite 2008). This broader definition, which considers those scales behind the anterior temporal(s) and lying between the parietals and the last supralabial, but not with the requirement of touching the anterior temporal(s), was apparently also used in the description of *T. goodenoughensis* (Roberts & Austin 2020). Coded according to the more restrictive definition of Roberts *et al.* (2022), the other seven specimens possibly representing this same taxon (including the topotypic specimen) all have two posterior temporals (by our definition two or three), with only one (UPNG 1214) possessing a single posterior temporal touching the anterior temporal on one

side of the head. Furthermore, the pattern of having two or three posterior temporals by the broader definition we used characterizes every specimen of *T. loriae* Group snakes, except for one side of one specimen of *T. nymani*, which has a single scale due to an obvious fusion (Kraus *et al.* 2022). Given the positional variability of the posterior temporal scales in these snakes and the variation in how many are in contact with the anterior temporal, this character clearly lacks diagnostic value for determining species boundaries within the *T. loriae* Group.

Number of ventral scales

This feature was used to distinguish *T. longhagen* from *T. loennbergii* and *T. mattisoni*, and whereas the first had 200 ventral scales (we counted 199), data taken from Kraus (2020) showed *T. loennbergii* with 213–218 and *T. mattisoni* with 170–181 ventrals. Although these contrasts used by Roberts *et al.* (2022) are correct, the number of ventrals does not distinguish *T. longhagen* from *T. nymani*, *T. vertebralis* or *T. atratus*, and it is only marginally higher than in *T. loriae* (162–197), *T. lamingtoni* (160–195) or *T. spilorhynchus* (172–197), and of questionable distinction from them. We found that the seven other specimens possibly conspecific with the holotype of *T. longhagen* have a ventral number ranging from 182–213, with the specimen from the type locality of *T. longhagen* having 213. Such variation indicates that this feature appears to be of no diagnostic value against the other seven members of the *T. loriae* Group.

Number of subcaudal scales

This feature was used to distinguish *T. longhagen* (43 subcaudals) from *T. loennbergii* (22–32 subcaudals). However, subcaudal scale number is a sexually dimorphic character in all species of the *T. loriae* Group (Kraus *et al*. 2022); whereas the holotype of *T. longhagen* is a male, *T. loennbergii* is only known from four females. Subcaudal values for the five UPNG females that we presume likely to be conspecific with the *T. longhagen* holotype have a range of 29–36, which would make this feature of no diagnostic value vis-à-vis *T. loennbergii*. Subcaudal number of the holotype is also not diagnostic against males of any other species of the *T. loriae* Group (Kraus *et al*. 2022: Table 1).

Summary

Of the five characters used to diagnose the holotype of *T. longhagen* from other members of the *T. loriae* Group, one used female-specific values to compare with a male, three have no diagnostic value among *T. loriae* Group species, and one has diagnostic value when populational trends are examined but not for single individuals. These problems could have been avoided since the first and third authors of Roberts *et al.* (2022) had been informed that an exhaustive study of the *T. loriae* Group (Kraus *et al.* 2022) was under review and that

> I would suggest that your ms. would benefit from waiting until ours is published because it will give you a much better indication of the range of morphological variation in the complex and especially in those characters that are of taxonomic reliability across the complex (and which you emphasize in your ms.). Plus, of course, it will make clearer how this specimen differs from all of the already-existing names.

We also stated our decision not to apply any name to specimens too poorly preserved for adequate analysis, including the holotype of *T. longhagen*.

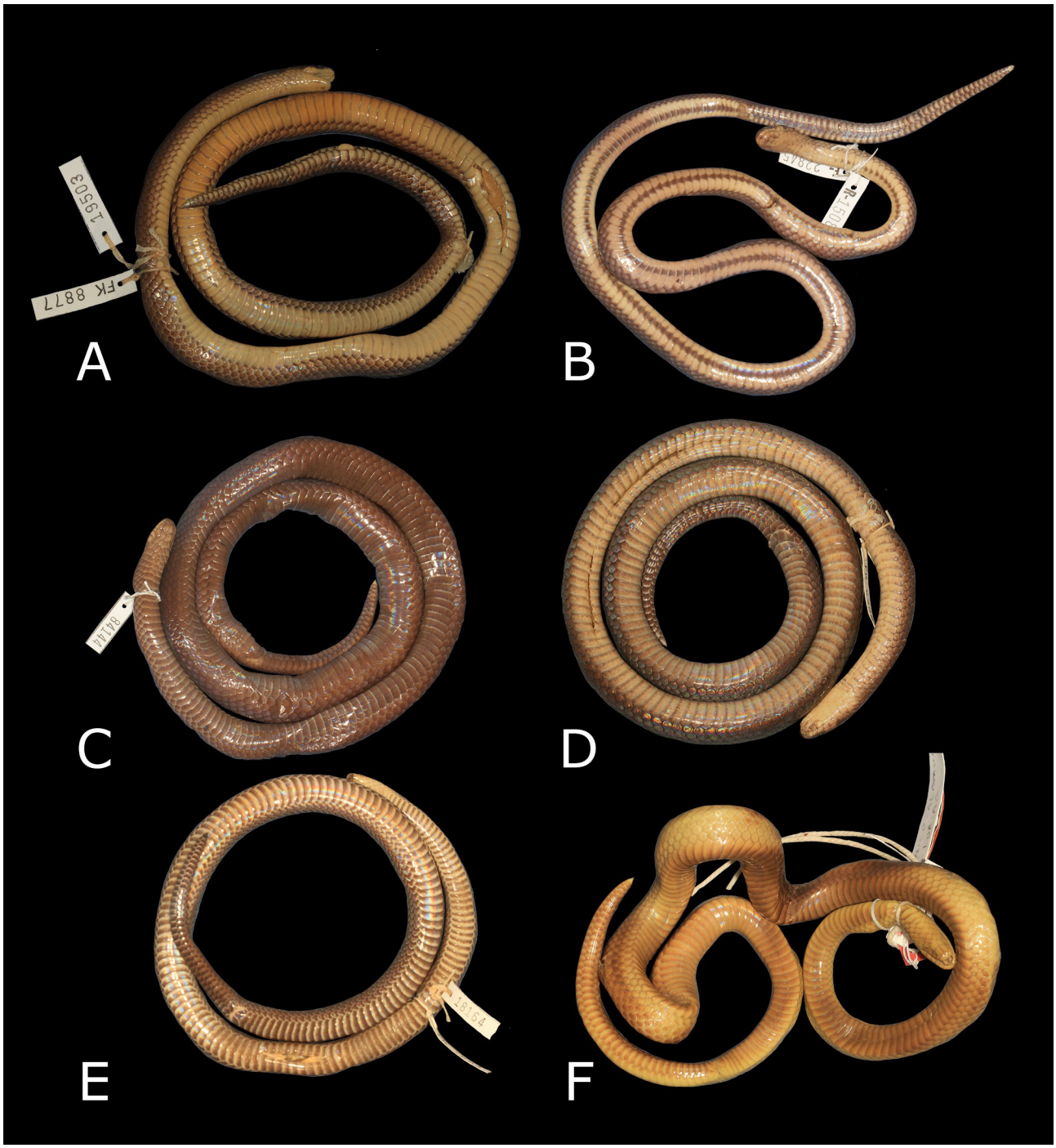

FIGURE 1. Documented variation in ventral color patterns in members of the *Toxicocalamus loriae* Group in contrast to that of *T. longhagen*. [A] Color pattern 1 (*T. loriae*, BPBM 19503). [B] Color pattern 2 (*T. loriae*, MCZ R150803). [C] Color pattern 3 (*T. atratus* holotype, MCZ 84144). [D] Color pattern 4 (*T. nigrescens* holotype, BPBM 16545). [E] Color pattern 5 (*T. mattisoni* paratype, BPBM 18164). [F] No discernable color pattern (*T. longhagen* holotype, PNGNM 22160).

Lack of color-pattern information

Kraus *et al.* (2022) documented that few single unique character states could be used to diagnose the nine members of the *T. loriae* Group from one another. Instead, unique combinations of characters

exist and can be reliably used to support taxonomic decisions. As we noted then, and as can be seen from the comments above, most scalational features of diagnostic use vary intraspecifically to one degree or another (though a few exceptions exist), requiring assessments of central tendencies and statistics at the population level to prove any diagnostic value. In contrast, we showed that color-pattern features and, in some cases, ontogenetic shifts in color pattern are of critical importance for diagnosing species in this group. This proved particularly true for the ventral color pattern of these animals as well as the patterns of yellow markings on the head and nape. Unfortunately, those data are not reliably available for the holotype of *T. longhagen*, which is clearly bleached but also seemingly discolored otherwise due to its time in preservative. This was also explained in the same email:

> PNGNM 22160 is sun bleached, and current color pattern cannot be relied on to reflect what the taxon looks like in life... This is especially important for the ventral color pattern, which I am not able to confidently determine as either naturally yellow or brown faded to yellow, in either case clouded with brown. Either of these are options in this group and either would be taxonomically diagnostic, so it is important to know what the natural state is. The other seven specimens suggest that yellow clouded with brown may be the correct description for this form, but, again, all are compromised by years of light exposure.

Options for ventral color pattern in adults of the known taxa of the *T. loriae* Group are: [1] uniformly yellow (typically pale yellow in preservative), found in *T. lamingtoni*, *T. loennbergii*, *T. spilorhynchus* (the sole large adult has a yellow venter with the anterior portion of each ventral dusted with pale brown), *T. vertebralis* and some *T. loriae* (Fig. 1A); [2] yellow with a mid-ventral row of brown spots or scattered spots, found only in some *T. loriae* (Fig. 1B); [3] black in life, turning in preservative to uniformly dark brown or with each ventral dark brown anteriorly and fading to pale brown or dark yellow posteriorly, found in *T. nymani* and *T. atratus* (Fig. 1C); [4] gray, with each ventral darker gray anteriorly, found in *T. nigrescens* (Fig. 1D); and [5] gray or yellow clouded or banded with darker gray, found in *T. mattisoni* (Fig. 1E). The holotype of *T. longhagen*, as well as the other seven specimens that appear to represent the same taxon, cannot be reliably assigned to any of these pattern classes, and PNGNM 22160, the *T. longhagen* holotype, has by far the most distorted color pattern (Fig. 1F). In fact, that specimen is so bleached that the pattern of yellow markings on the head and nape—or even whether such markings are present—cannot be reliably determined. In the absence of reliable information on color pattern in these specimens, we chose to forego guessing whether they represented a valid new taxon or were merely anomalous, poorly preserved representatives of a species we had already diagnosed based on reliably characterized specimens.

Discussion

None of the characters presented as diagnostic in the original description of *T. longhagen* allows for unambiguous diagnosis against any of the members of the *T. loriae* Group, but two (preocular contact with nasal, number of postoculars) are potentially useful against one or more species. Other diagnostically useful characters, unmentioned in the description of *T. longhagen*, include that the cloaca is covered by two scales, distinguishing the *T. longhagen* holotype from *T. lamingtoni*, and the presence of a single intergenial, distinguishing it from *T. loriae sensu stricto*. *Toxicocalamus longhagen* may also differ from *T. loennbergii* by having two postoculars, but sample sizes of both taxa are small. Left uncertain is whether or how *T. longhagen* differs from *T. nymani*, *T. atratus*, *T. spilorhynchus* and *T. vertebralis* or, if different, how the taxon may be reliably diagnosed. The underlying taxon to which the name *T. longhagen* has been applied may possibly be different from

all other members of the *T. loriae* Group. However, it cannot be credibly diagnosed based on the substandard holotype and additional presumptive specimens of *T. longhagen* at hand, which is why we chose to not apply a name to any of those specimens. All are distorted to some degree by long exposure to light or strong chemicals. Consequently, it is impossible to know what the true color pattern of those specimens was, and this casts doubt on any attempt to diagnose them taxonomically. In the absence of reliable information on ventral color pattern and the pattern of yellow markings on the head and nape it is impossible to determine whether *T. longhagen* represents one of the well-characterized taxa of the *T. loriae* Group treated by us or a novel taxon.

Nomina dubia are understandably a part of vertebrate paleontological science, where only partial specimens may be available for species descriptions, and where these may not be directly comparable to species described based on other partial specimens from different anatomical regions. It is disappointing to see questionable names created in modern systematics for neontological specimens. As shown in the present case, a typological reliance on examination of only a smattering of specimens and partial comparison with relevant literature is a poor substitute for directly examining comprehensive series of specimens when these are available, especially in taxa having a number of synonyms and a diversity of phenotypes placed under a single name, as was long known for *T. loriae sensu lato* at the time *T. longhagen* was described. While clearly divergent diagnostic features may certainly result in a strongly supported taxonomic decision based on use of only a single specimen—as shown in other species of *Toxicocalamus* (e.g., *T. ernstmayri* O'Shea, Parker & Kaiser, 2015; *T. holopelturus* McDowell, 1969; *T. pachysomus*)—questionable single specimens in poor condition, demonstrably discolored artificially, and lacking in critical diagnostic features, are never sensible choices for evidence-based work.

Based on the evidence, the holotype of *T. longhagen* cannot be diagnosed from known, demonstrably valid *T. loriae* Group taxa. Since this name-bearing type is the only certainly known representative to anchor the nomen in nomenclature, it "is insufficient to permit recognition of the zoological species to which it was applied" (Mayr 1969: 407). This unfortunately renders *T. longhagen* a taxonomic *nomen dubium*, "a name of unknown or doubtful application" (Glossary of the *International Code of Zoological Nomenclature*; Anonymous 1999), and specifically a nyctonym (Dubois 2011). The situation can only be remedied by a comprehensive comparative study of new character information for the *T. longhagen* holotype (since it is the only specimen certainly of that species) and all *T. loriae* Group taxa, which would need to include a set of specimens large enough to allow for an assessment of variation and to allow for assignment of the seven specimens that might be *T. longhagen* conspecifics. Given the limited utility of external morphology to the definition of *T. longhagen*, these data would have to be molecular or osteological (with the need to generate a suitably large data set of multiple characters and multiple individuals in either case). This analysis might then form the basis for an expanded, definitive diagnosis of *T. longhagen* to rescue the name from its doubtful application.

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References

Anonymous [International Commission on Zoological Nomenclature] (1999) *International code of zoological nomenclature*. Fourth edition. London (The International Trust for Zoological Nomenclature): i–xxix + 1–306. <https://doi.org/10.1046/j.1365-3113.2000.252107.x>.

Boulenger, G. A. (1893) *Catalogue of the snakes in the British Museum (Nat. Hist.).* Volume **1**. *Containing the families Typhlopidæ, Glauconiidæ, Boidæ, Ilysiidæ, Uropeltidæ, Xenopeltidæ, and Colubridæ Aglyphæ, part.* London (Taylor & Francis): i–xiii + 1–448. <https://doi.org/10.5962/bhl.title.8316>.

Boulenger, G. A. (1898) An account of the Reptiles and Batrachians collected by Dr. L. Loria in British New Guinea. *Annali del Museo civico di Storia naturale di Genova*, (2), **18**: 694–710.

Boulenger, G. A. (1904) Descriptions of three new snakes. *Annals and Magazine of natural History*, (7), **13**: 450–452. <https://doi.org/10.1080/00222930408562477>.

Boulenger, G. A. (1908) Description of a new elapine snake of the genus *Apisthocalamus*, Blgr., from New Guinea. *Annals and Magazine of natural History*, (8), **1**: 248–249. <https://doi.org/10.1080/00222930808692393>.

Dubois, A. (2008) Le *Code International de Nomenclature Zoologique*: présentation, philosophie, règles majeures, problèmes actuels. *In*: D. Prat, A. Raynal-Roques & A. Roguenant (ed.), *Peut-on classer le vivant? Linné et la systématique aujourd'hui*, Paris (Éditions Belin): 355–402.

Dubois, A. (2011) The *International Code of Zoological Nomenclature* must be drastically improved before it is too late. *Bionomina*, **2**: 1–104. <https://doi.org/10.11646/bionomina.2.1.1>.

Kaiser, H. (2013) The Taxon Filter, a novel mechanism designed to facilitate the relationship between taxonomy and nomenclature, vis-à-vis the utility of the Code's Article 81 (the Commission's plenary power). *Bulletin of zoological Nomenclature*, **70**: 293–302. <https://doi.org/10.21805/bzn.v70i4.a17>.

Kaiser, H., Crother, B. I., Kelly, C. M. R., Luiselli, L., O'Shea, M., Ota, H., Passos, P., Schleip, W. D. & Wüster, W. (2013) Best practices: in the 21st century, taxonomic decisions in herpetology are acceptable only when supported by a body of evidence and published via peer-review. *Herpetological Review*, **44**: 8–23.

Kinghorn, J. R. (1928) Notes on some reptiles and batrachians from the Northern Division of Papua, with descriptions of new species of *Apisthocalamus* and *Lygosoma*. *Records of the Australian Museum*, **16**: 289–293. <https://doi.org/10.3853/j.0067-1975.16.1928.790>.

Kraus, F. (2009) New species of *Toxicocalamus* (Squamata: Elapidae) from Papua New Guinea. *Herpetologica*, **65**: 460–467. <https://doi.org/10.1655/09-002.1>.

Kraus, F. (2017) Two new species of *Toxicocalamus* (Squamata: Elapidae) from Papua New Guinea. *Journal of Herpetology*, **51**: 574–581. <https://doi.org/10.1670/17-035>.

Kraus, F. (2020) A new species of *Toxicocalamus* (Squamata: Elapidae) from Papua New Guinea. *Zootaxa*, **4859**: 127–137. <https://doi.org/10.11646/zootaxa.4859.1.5>.

Kraus, F., Kaiser, H. & O'Shea, M. (2022) Hidden diversity in semi-fossorial Melanesian forest snakes: a revision of the *Toxicocalamus loriae* complex (Squamata, Elapidae) from New Guinea. *Vertebrate Zoology*, **72**: 997–1034. <https://doi.org/10.3897/vz.72.e89647>.

Lillywhite, H. B. (2008) *Dictionary of herpetology*. Malabar (Krieger): 1–384.

Lönnberg, E. (1900) Reptiles and batrachians collected in German New Guinea by the late Dr Erik Nyman. *Annals and Magazine of natural History*, (7), **6**: 574–582. <https://doi.org/10.1080/00222930008678427>.

Malnate, E. V. & Underwood, G. (1988) Australasian natricine snakes of the genus *Tropidonophis*. *Proceedings of the Academy of natural Sciences of Philadelphia*, **140**: 59–201

Mayr, E. (1969) *Principles of systematic zoology*. New York (McGraw Hill): i–xi + 1–428.

McDowell, S. B. (1967) *Aspidomorphus*, a genus of New Guinea snakes of the family Elapidae, with notes on related genera. *Journal of Zoology*, London, **151**: 497–543. <https://doi.org/10.1111/j.1469-7998.1967.tb02130.x>.

McDowell, S. B. (1969) *Toxicocalamus*, a New Guinea genus of snakes of the family Elapidae. *Journal of Zoology*, London, **159**: 443–511. <https://doi.org/10.1111/j.1469-7998.1969.tb03900.x>.

Mones, A. (1989) *Nomen dubium* vs. *nomen vanum*. *Journal of Vertebrate Paleontology*, **9**: 232–234. <https://doi.org/10.1080/02724634.1989.10011757>.

O'Shea, M., Allison, A. & Kaiser, H. (2018) The taxonomic history of the enigmatic Papuan snake genus *Toxicocalamus* (Elapidae: Hydrophiinae), with the description of a new species from the Managalas Plateau of Oro Province, Papua New Guinea, and a revised dichotomous key. *Amphibia-Reptilia*, **39**: 403–433. <https://doi.org/10.1163/15685381-20181052>.

Peters, J. A. (1964) *Dictionary of herpetology. A brief and meaningful definition of words and terms used in herpetology*. New York (Hafner Publishing): 1–392.

Roberts, J. R. & Austin, C. C. (2020) A new species of New Guinea worm-eating snake (Elapidae: *Toxicocalamus* Boulenger, 1896), with comments on postfrontal bone variation based on micro-computed tomography. *Journal of Herpetology*, **54**: 446–459. <https://doi.org/10.1670/20-043>.

Roberts, J. R., Iova, B. & Austin, C. C. (2022) A new species of New Guinea worm-eating snake (Serpentes, Elapidae, *Toxicocalamus* Boulenger, 1896) from Western Highlands Province, Papua New Guinea. *Zoosystematics and Evolution*,

98: 399–409. <https://doi.org/10.3897/zse.98.90520>.

Strickland, J. L., Carter, S., Kraus, F. & Parkinson, C. (2016) Snake evolution in Melanesia: origin of the Hydrophiinae (Serpentes, Elapidae) and the evolutionary history of the enigmatic New Guinean elapid *Toxicocalamus*. *Zoological Journal of the Linnean Society*, **178**: 663–678. <https://doi: 10.1111/zoj.12423>.

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