



A new species of *Tachymenoides* (Serpentes: Dipsadidae: Tachymenini) from the puna of the Otishi National Park in Peru

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Abstract. We describe a new snake species of the genus *Tachymenoides* from the scientifically unexplored southern sector of the Otishi National Park in Peru (Region Junín). The single adult male specimen with a total length of 407 mm was obtained in the Pantano la Esperanza swamp of a puna valley at 3248 m a.s.l. The new species has smooth dorsal scales without apical pits in 19/17/15 series, 1 preocular, 2 postoculars, 1 loreal, undivided nasal scale, 2+3 temporals, 139 ventrals, 55 subcaudals, and a divided cloacal scale. In life, the dorsum is pale yellowish brown with scattered black blotches that form a paravertebral stripe (one scale wide) on each side at the posterior half of the body. The flanks are black ventrolaterally (2–3 scales high), followed at the posterior half of the body by a pale yellowish-brown longitudinal stripe of two scales width, bordered dorso-laterally by the black paravertebral stripe. The throat and first 60 mm of the ventral body are pale yellowish tan with black flecks, and a ventrolateral black stripe on each side of the same length, the remaining venter and tail entirely black. The head has dorsally a black stripe from the posterior margins of the postoculars extending over the outside margins of the rostrals over the head scales (2–3 scales in width) and narrowing to 1 scale width on the neck region before ending; laterally, the head has black flecks on the supralabials, and a black stripe extending from postoculars diagonally over parietals over posterior supralabials to the corner of the jaw. The iris is copper with a vertical pupil. The type locality of *Proctoporus titans* is corrected.

Key words. Squamata, reptiles, snakes, Andes, Region Cusco, Region Junín, protected areas.

Introduction

Otishi National Park (ONP) of the Avireri-Vraem Biosphere Reserve in Peru (regions Junín and Cusco) covers 305,973 ha between 750 and 4185 m encompassing five types of montane forests, and two different types of montane grasslands (SERNANP 2010). On its west side, the ONP is flanked by the Asháninka Communal Reserve and on its east side by the Machiguenga Communal Reserve (Fig. 1). ONP is located in the VRAEM (Valley of Rivers Apurímac, Ene, Mantaro) area, which is the center of Peru's coca production and narco-trafficking. Based on its remote location in a dangerous area and steep mountains of the Cordillera de Vilcabamba, the ONP is Peru's least scientifically surveyed national park.

A herpetological survey of the puna of the southern part of the ONP was conducted by four biologists (E. LEHR, J. C.

CUSI, M. I. FERNANDEZ, and R. J. VERA) and one national park guard (M. A. MAYTA) from May 16 to 30, 2022. The remote area was reached with a helicopter from Quillabamba (Fig. 2). Among the new species was the lizard *Proctoporus titans* (LEHR et al. 2022). Herein, we describe a new species of snake of the genus *Tachymenoides* based on molecular and morphological characters.

Materials and methods

Molecular genetics

We performed phylogenetic analyses to confirm generic placement of the new snake, and to examine its evolutionary relationships with other species of the Tachymenini (Dipsadidae). We obtained new sequences from our specimen MUSM 40925, and downloaded available sequences of species of Tachymenini from GenBank (Appendix 1).

We analyzed the fragment of the mitochondrial genes 12S rRNA with forward primer L1091mod (sequence: 5' CAA ACT AGG ATT AGA TAC CCT ACT AT 3'; modified from KOCHER et al. 1989) and reverse H1557mod (5' GTA CRC TTA CCW TGT TAC GAC TT 3'; modified from KNIGHT & MINDELL 1994), and cytochrome b with forward primer 703Botp.mod (5'-TCA AAY ATC TCA ACC TGA TGA AAY TTY GG-3') and reverse MVZ16p.mod (5'-GGC AAA TAG GAA GTA TCA YTC TGG YTT-3'; both primers from POOK et al. 2000). We used standard thermocycling conditions during the polymerase chain reaction (PCR) using a Proflex thermal cycler (Applied Biosystems), purified PCR products with Exosap-IT (ThermoFisher), and shipped PCR products to MCLAB (South San Francisco, CA, USA) for Sanger sequencing.

We used Geneious R11, version 11.1.5 (Biomatters, <http://www.geneious.com/>) to align sequences with the MAFFT v7.017 alignment program (KATO & STANDLEY 2013), and trimmed sequences to a length of 472 bp for 12S and 735 bp for COI. We inferred the phylogeny using Maximum Likelihood with IQ-TREE v1.6.12 (NGUYEN et al. 2015) for phylogenetic inference of the concatenated sequence of the two gene fragments. We followed TREVINE et al. (2022) for partition and substitution models, i.e., the model GTR+G

for all subsets: subset 1 for gene 12S, subset 2 for COI1, subset 3 for COI2, and subset 4 for COI3. Our phylogenetic analysis included 20 terminals and a 1208-bp alignment for the partitioned dataset, branch length was unlinked among the partitions. In IQ-TREE, we used the ultrafast bootstrap method (10000 bootstrap alignments).

We also estimated uncorrected p-distances (i.e., the proportion of nucleotide sites at which any two sequences are different) for 12S and cytb sequences in MEGA X (TAMURA et al. 2007, KUMAR et al. 2018), and uploaded the table to Figshare (DOI: 10.6084/m9.figshare.22693447). The most commonly sequenced genes for Tachymenini snakes are 12S and cytb (Appendix 1).

Morphology

The specimen was fixed in 10% formol and stored in 70% ethanol. Tissue samples (liver) were taken before preservation and stored in 96%-proof ethanol. Taxonomy follows TREVINE et al. (2022). The format of the description and terminology of the morphological characters follow mostly BAILEY et al. (2005), FRANCO et al. (2017), and TREVINE et al. (2022). Terminology of head scales follows DIXON et al. (1993). We recorded number of supralabials and noted which of those are in contact with the eye, number of loreals, pre and postoculars, temporals (distinguished as primary temporals in touch with the rear of the postoculars, and secondary temporals in touch with the rear of the primaries; primary temporals separated by a plus sign from secondary temporals), and infralabials, noting how many touch the primary and secondary genials. Dorsal

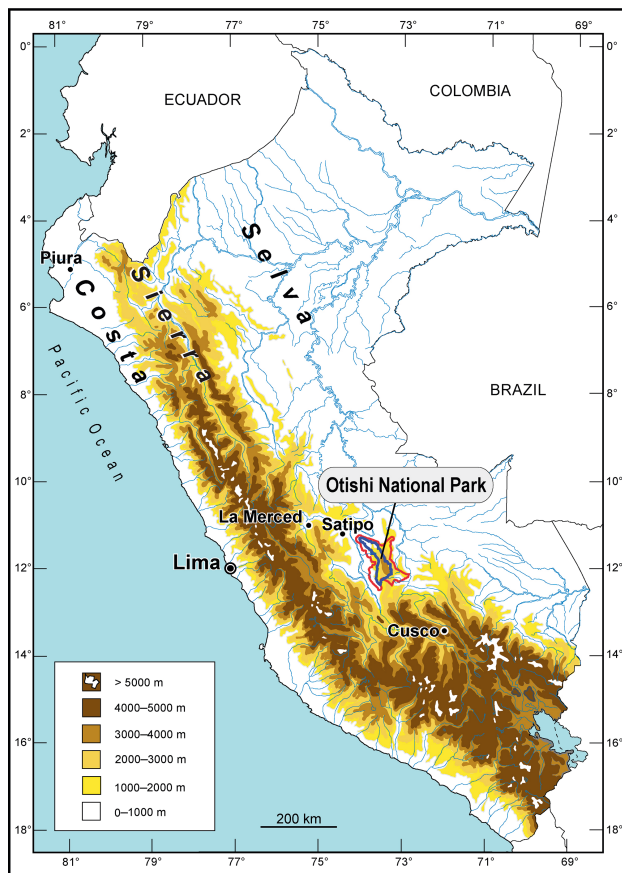


Figure 1. Map of Peru with the Otishi National Park outlined in blue, the Asháninka Communal Reserve on its west side, and the Machiguenga Communal Reserve on its east side outlined in red.

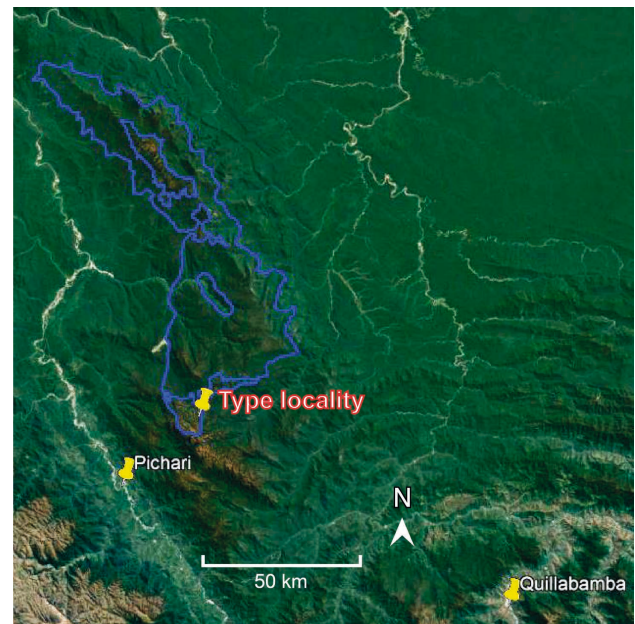


Figure 2. Google Earth image with the border of the Otishi National Park in blue and the type locality of *Tachymenoides harisonfordi* sp. n. indicated by a yellow pin.

scales were counted in three different portions of the body (separated by a slash): one head length before the head, at the middle of the body, and one head length before the cloaca. We follow DOWLING (1951) for counting ventrals and subcaudals (excluding the spine). A slash separates character counts taken on opposite sides of the head, with the left side indicated first. The number of maxillary and dentary teeth on the left side was counted. Sex was determined by the presence or absence of inverted hemipenes by making a small incision on the base of the tail following DOWLING & SAVAGE (1960). All measurements are in mm. Snout–vent length (SVL, distance from the snout tip to the posterior end of the cloaca) and tail length (TL, distance from the posterior end of the cloaca to the tip of the tail) were taken to the nearest millimeter from the specimen straightened against a meter stick. Other measurements taken with digital calipers to the nearest 0.1 mm include: eye to nostril distance (straight line distance between anterior corner of orbita and posterior margin of external nares), snout length (straight line distance from tip of snout to posterior end of interprefrontal suture), head length (distance from tip of snout to posterior margin of jaw), head width (distance between lateral margins of supraoculars), head height (at tallest point), distance between nostrils, eye height, and eye width. Greatest length and greatest width of the following head scales (left if applicable) were measured with a digital caliper to the nearest 0.1 mm: internasal, loreal, prefrontal, frontal, and parietal. Photographs of snakes by E. LEHR. The holotype was photographed immersed in ethanol to avoid reflections. All maps were prepared by E. LEHR. Notes on the coloration in life were taken from field notes and photographs. Comparative data were taken from original species descriptions and the specimens examined (Appendix 2). Collection acronyms are: MUSM = Museo de Historia Natural Universidad Nacional Mayor de San Marcos, Lima, Peru. NZCS = National Zoological Collection of Suriname, Paramaribo, Suriname. Field number code is: IWU = Illinois Wesleyan University. Threat status was evaluated using the IUCN criteria (2013). Google Earth was accessed on 4 September 2022 to design the map.

Nomenclatural acts

The electronic edition of this article conforms to the requirements of the amended International Code of Zoological Nomenclature (ICZN), and hence the new names contained herein are available under that Code from the electronic edition of this article. This published work and the nomenclatural acts it contains have been registered in ZooBank, the online registration system for the ICZN. The LSID (Life Science Identifier) for this publication is: urn:lsid:zoobank.org:pub:CE499640-F22F-4E76-9BBo-FC6F7EE7268D. The electronic edition of this work was published in a journal with an ISSN, and has been archived and is available from the following digital repositories: zenodo.org, salamandrajournal.com.

Results

Molecular genetics

Our phylogeny (Fig. 3) recovered a new species as sister taxon of *Tachymenoides affinis*, with strong bootstrap support (0.99) at the node of their most recent common ancestor. The overall topology was largely congruent with the topology obtained by TREVINE et al. (2022) with a larger number of genes and terminals, and we followed their proposed taxonomic changes here. One interesting difference is that in our phylogeny *Mesotes* is recovered as the sister genus of *Tachymenoides*, and this clade of two genera is sister clade to *Dryophylax*, whereas in TREVINE et al. (2022), *Mesotes* is basal to the clade composed of *Dryophylax* and *Tachymenoides*. Genetic distances further support the close relationship between *T. affinis* and the new species of *Tachymenoides*, because for both 12S and cytb, the estimates of p-distances are lowest for this pair (2.1% for 12S and 5.8% for cytb) than for all pairwise comparisons with the new species (see Table at Figshare, DOI: 10.6084/m9.figshare.22693447).

Systematics

We place the new species in the genus *Tachymenoides* of the family Dipsadidae following TREVINE et al. (2022) and our molecular phylogeny (Fig. 3).

Tachymenoides harrisonfordi sp. n. (Figs 4–6)

English Common Name: Harrison Ford's Slender Snake
LSID: urn:lsid:zoobank.org:act:C9970EA1-02FF-480A-8B71-731E26BD482A

Holotype (Figs 4–6): MUSM 40925 (field number IWU 404), a male from the puna of the Otishi National Park (12°19'23.10" S, 73°35'43.54" W; WGS84), 3248 m a.s.l., Distrito Río Tambo, Provincia Satipo, Region Junín, Peru, collected on 22 May 2022 by E. LEHR, J. C. CUSI, M. I. FERNANDEZ, and R. J. VERA.

Definition: One preocular, 10 maxillary teeth; 11 dentary teeth; dorsal scale rows smooth in 19/17/15 series; dorsal scales lacking apical pits; ventrals 139; subcaudals 54; venter entirely black except for the anterior 60 mm that are pale yellowish-tan scattered with black flecks, distinguishing a ventrolateral black stripe on each side of the same length; irregular scattered black blotches forming a dorsal longitudinal stripe on the posterior half of the body; flanks ventrolaterally black about 2–3 scales high, posterior third of the body with three longitudinal skin folds (one middorsal, two paravertebral).

Diagnosis: *Tachymenoides harrisonfordi* sp. n. can be distinguished from *T. affinis* (Fig. 7), the single species currently

in *Tachymenoides*, as follows: *Tachymenoides harrisonfordi* sp. n. has dorsal scale rows in 19/17/15 series (17/17/15 in *T. affinis*), cloacal scale undivided (usually divided), longitudinal body folds (absent), dorsum in life pale yellowish brown with scattered black blotches that form a paravertebral stripe on each side at the posterior half of the body (less patterned dorsal coloration of reddish brown, WALKER 1946), and the ventral coloration is predominately black with two ventrolateral stripes of 60 mm length posterior to jaws (two to five non-continuous longitudinal ventral stripes in a few specimens, forming a dark band in each ventral scale, with a general darkening tendency towards the tail; some specimens have an overall dark venter, with no discernible stripes, TREVINE et al. 2022). *Tachymenoides harrisonfordi* sp. n. and *T. affinis* have similar dentition numbers (10 maxillary teeth and 11 dentary teeth in *T. harrisonfordi* sp. n. vs 6–13 maxillary teeth and 10–16 dentary teeth in *T. affinis*, TREVINE et al. 2022). Both *T. affinis* and *T. harrisonfordi* sp. n. lack apical pits (TREVINE et al. 2022, this paper) and are immediately separated from all 15 *Dryophylax* spp. which have apical pits (TREVINE et al. 2022, UETZ et al. 2023).

Description of the holotype: Adult male with inverted hemipenes and a body opening on its left side resulting from tissue removal (Fig. 5); SVL 315 mm, TL 92 mm. Dorsal scales smooth in 19/17/15 rows, without apical pits; 139 ventral scales; 54 paired subcaudals; cloacal scale divided; usual complement of head scales present (Fig. 6);

7/8 supralabials, 3rd + 4th/3rd to 5th contacting the orbit; 8/9 infralabials, 1st to 4th contacting first pair of chin shields, 4th/5th contacting second pair of chin shields; two pairs of chin shields; temporals 2+3/2+3; nasal undivided; 1/1 preocular, 2/2 postoculars; right maxilla with eight pre-diastemal teeth and two grooved and enlarged post-diastemal teeth; 11 dentary teeth. Head length 14.7 mm; head width 6.1 mm; head height 5.6 mm; snout length 3.1 mm; distance between nostrils 2.6 mm; eye height 2.3 mm; eye width 2.7 mm; distance between eyes 5.8 mm; eye–nostril distance 2.6 mm; internasal scale (left) wider than long (length 1.1 mm, width 1.6 mm); loreal scale longer than wide (length 1.0 mm, width 0.8 mm); prefrontal scale wider than longer (length 1.8 mm, width 2.0 mm); frontal scale longer than wide (length 4.6 mm, width 2.0 mm); parietal scale longer than wide (length 5.3 mm, width 3.3 mm).

In life (Fig. 4), the dorsum is pale yellowish brown with scattered black blotches that form a paravertebral stripe (one scale wide) on each side at the posterior half of the body. The flanks are black ventrolaterally (2–3 scales high), followed at the posterior half of the body by a pale yellowish-brown longitudinal stripe of two scales width, bordered dorsolaterally by the black paravertebral stripe. The throat and first 60 mm of the ventral body are pale yellowish tan with black flecks, and a ventrolateral black stripe on each side of the same length, the remaining venter and tail entirely black. The head has dorsally a black stripe from the posterior margins of the postoculars extending over the

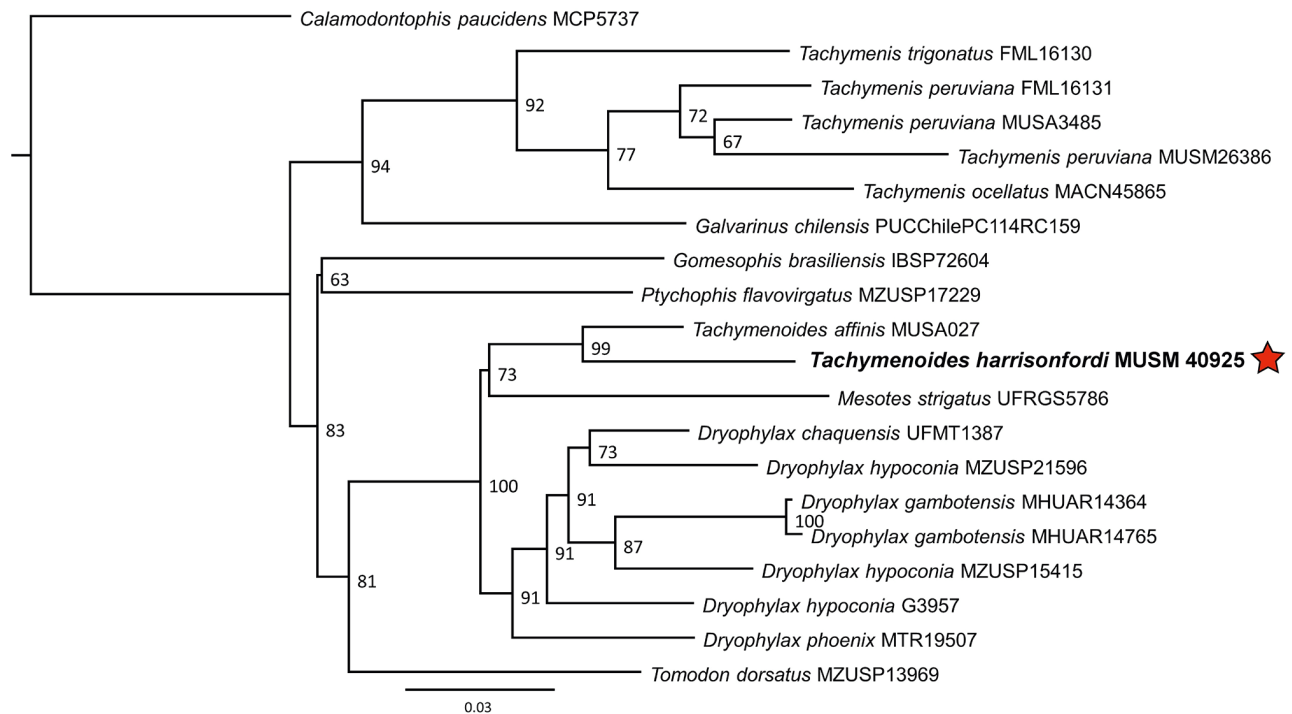


Figure 3. Phylogenetic analysis of 12S rRNA and cytochrome b gene fragments by using Maximum Likelihood. Maximum likelihood optimal tree with bootstrap node values from the analysis of a concatenated dataset of 472 bp (12S) and 735 bp (cytb) of 20 species aligned by MAFFT based on the GTR+G model, and node support assessed using 10,000 replicates in IQTREE.

outside margins of the rostrals over the head scales (2–3 scales in width) and narrowing to 1 scale width on the neck region before ending; laterally, the head has black flecks on

the supralabials, and a black stripe extending from postoculars diagonally over parietals over posterior supralabials to the corner of the jaw. The iris is copper with a vertical pupil.

After 10 months in preservative (Fig. 5), the coloration is nearly identical as described for the live holotype, except that the coloration is slightly paler, and the iris is gray.

Etymology: We dedicate this species to HARRISON FORD, actor and conservationist, in recognition of his work for Conservation International and his voice for nature (e.g., “Nature is speaking – Harrison Ford is The Ocean”).

Distribution, natural history, and threat status: The holotype is only known from the type locality (Fig. 8), which is a humid puna (Holdridge life zone “tropical subalpine pluvial páramo,” HOLDRIDGE [1967], INRENA [2003]) valley in the southern sector of the ONP, an area that is in a strict protection zone (Zona de Protección Estricta, INRENA [2003]). The valley has several shallow ponds that hold temporary water forming the extended Pantano la Esperanza swamp (Fig. 8A). The vegetation consists of tall Peruvian feather grass (Figs 8B, C), mosses, bushes, small scattered trees, and dense *Polylepis* forests, and bamboo patches along the mountain slopes. The holotype was found at 10:30 AM sunbasking on moss between Peruvian feather grass in the swamp (Fig. 8C). We consider *T. harrisonfordi* sp. n. a potential predator for *Proctoporus titans*, the other reptile species found at the type locality. LEHR et al. (2022, p. 15) de-



Figure 4. Living holotype of *Tachymenoides harrisonfordi* sp. n. (MUSM 40925) in dorsolateral (A), dorsal (B), and ventral views (C). The red arrows point to the skin folds. Total length of the snake is 407 mm.

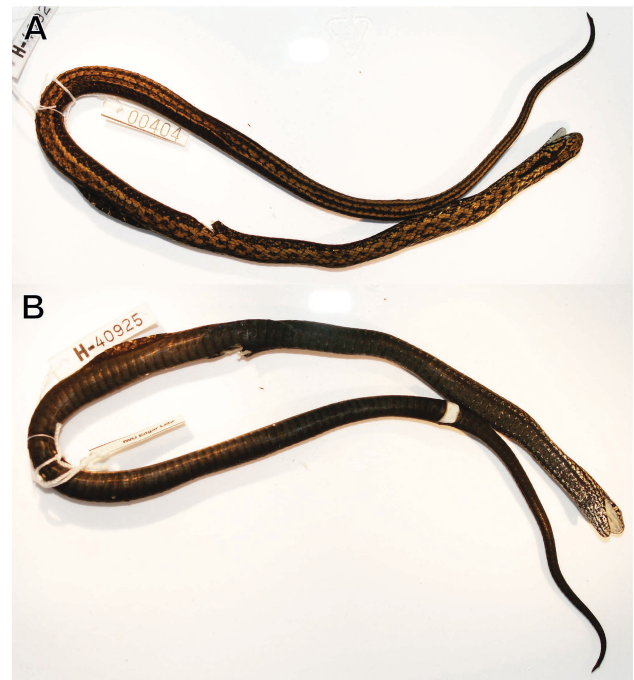


Figure 5. Preserved holotype of *Tachymenoides harrisonfordi* sp. n. (MUSM 40925) in dorsal (A) and ventral (B) views. Total length of the snake is 407 mm.

scribed the type locality for *P. titans* incorrectly as “Distrito Echarate, Provincia La Convención, Region Cusco,” which is corrected here as “Distrito Río Tambo, Provincia Satipo, Region Junín.” No frogs have been discovered at the type locality or its proximate surroundings. The activities of narco-traffickers in the ONP impact the biodiversity but it is unknown to what degree. We suggest classifying *T. harrisonfordi* sp. n. as “Data Deficient” according to the IUCN red list criteria (IUCN 2013).

Discussion

The recent comprehensive phylogenetic analysis of Tachymenini snakes using molecular and morphological characters by TREVINE et al. (2022) resulted in four new genera (*Apograpton*, *Galvarinus*, *Tachymenoides*, and *Zonateres*),

three revalidated genera, and many new combinations of snakes formerly incorrectly assigned to *Tachymenis* or *Thamnodynastes*.

TREVINE et al. (2022) revealed a close phylogenetical relationship between *Tachymenoides* and *Dryophylax* which also is confirmed in our phylogeny (Fig. 3).

An unusual snake character that *Tachymenoides harrisonfordi* sp. n. displays, are the three longitudinal skin folds on the posterior dorsal/dorsolateral body that look like keels (Figs 4A, B, 5A). Whereas skin folds in snakes can be the outcome of malnutrition, after having given birth or after oviposition, the presence of the folds in the male specimen does not seem to be the result of malnutrition. At least the snake behaved normally and was not weak in any way. In preservative, the skin folds are present and overlap and slightly cover scales. TREVINE et al. (2022) provide detailed descriptions and morphological variation in Appendix 3 for *T. affinis* in which two out of 16 examined specimens have dorsal scales in 19/17/15 series, and a few specimens have the venter entirely black. Both species seem to occupy different habitats; *T. affinis* inhabits Andean grasslands and montane forests in northern and central Peru (regions of Amazonas and Huánuco, UETZ et al. 2023), whereas



Figure 6. Head of the living holotype of *Tachymenoides harrisonfordi* sp. n. (MUSM 40925) in lateral (A), dorsal (B), and ventral (C) views. The head length is 14.7 mm.

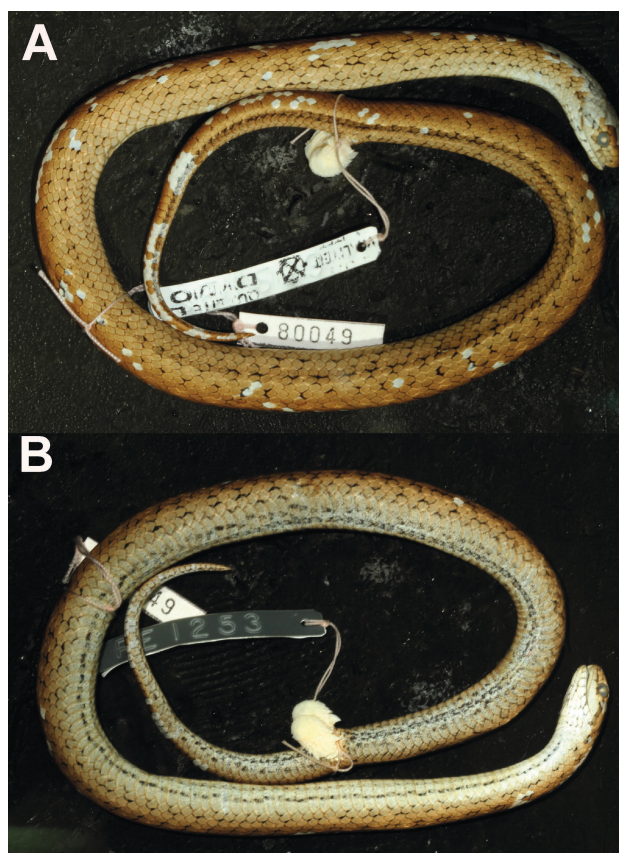


Figure 7. Preserved male specimen of *Tachymenoides affinis* (SMF 80049) from Region Huánuco (Conchamarca, ca. 2900 m a.s.l.) in dorsal (A) and ventral (B) views. Total length of the snake is 404 mm. Photos by G. KÖHLER.

T. harrisonfordi sp. n. inhabits high-elevational wetlands in southern Peru (Region Junín, and likely Cusco). Hopefully, more specimens of *T. harrisonfordi* sp. n. will be discovered, including females and juveniles, to describe its variation. However, its type locality in the VRAEM makes biodiversity research dangerous. CHABANI (2023) discussed the impact of narco-trafficking on biodiversity and biodiversity research; also see LEHR et al. (2022).

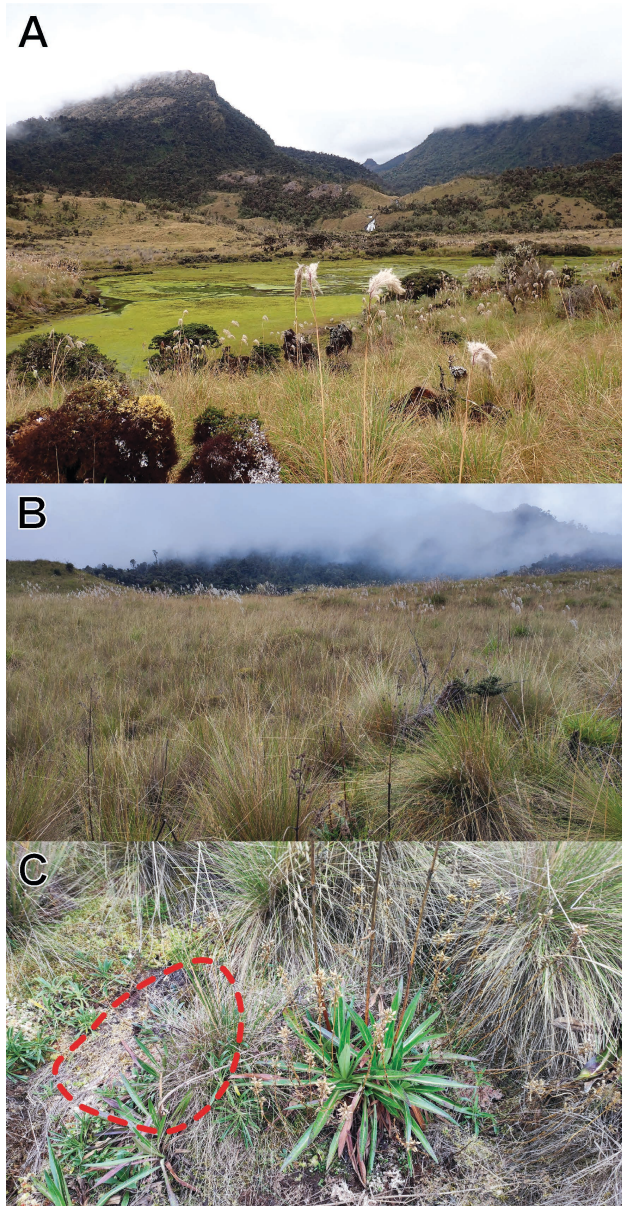


Figure 8. Habitat of *Tachymenoides harrisonfordi* sp. n. (A) Overview of the type locality of *T. harrisonfordi* sp. n. with the Pantano la Esperanza swamp and the Kitamarapo waterfall in the south, photographed 25 May 2022 at 11:22 AM by M. FERNÁNDEZ. (B) Proximity of the type locality with Peruvian feathergrass photographed on 22 May 2022 at 3:27 PM by J. C. CUSI. (C) Sun-basking site (indicated by a red dashed line) of *T. harrisonfordi* sp. n., photographed on 22 May 2022 at 3:27 PM by J. C. CUSI.

We expect that more new species of *Tachymenoides* unknown to science will be discovered when preserved tachymenins are re-examined and reviewed. This of course requires unhindered access to the specimens stored in public herpetological collections. We urge any curator to grant access for unhindered scientific research to progress.

Acknowledgments

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Appendix 1

Genbank accession numbers for the taxa and genes sampled in this study.

Species	Voucher	12S	cytb
<i>Calamodontophis paucidens</i>	MCP5737	OP024352	OP036772
<i>Dryophylax chaquensis</i>	UFMT1387	OP024305	OP036793
<i>Dryophylax gambotensis</i>	MHUAR14765	OP024322	OP036806
<i>Dryophylax gambotensis</i>	MHUAR14364	OP024321	OP036805
<i>Dryophylax hypoconia</i>	G3957	OP024317	OP036790
<i>Dryophylax hypoconia</i>	MZUSP15415	OP024310	OP036797
<i>Dryophylax hypoconia</i>	MZUSP21596	OP024315	OP036804
<i>Dryophylax phoenix</i>	MTR19507	OP024348	OP036788
<i>Galvarinus chilensis</i>	PUCCh PC114/RC159	OP024298	OP036831
<i>Gomesophis brasiliensis</i>	IBSP72604	OP024287	OP036773
<i>Pseudotomodon trigonatus</i>	FML16130	OP024329	OP036833
<i>Ptychophis flavovirgatus</i>	MZUSP17229	OP024290	OP036774
<i>Tachymenis ocellatus</i>	MACN45865	OP024288	OP036835
<i>Tachymenis peruviana</i>	FML16131	OP024294	OP036834
<i>Tachymenis peruviana</i>	MUSA3485	OP024295	NA
<i>Tachymenis peruviana</i>	MUSM26386	OP024296	NA
<i>Tachymenoides affinis</i>	MUSA027	OP024304	OP036775
<i>Tachymenoides harrisonfordi</i>	MUSM40925	OQ883945	OQ870342
<i>Thamnodynastes strigatus</i>	UFRGS5786	OP024328	OP036815
<i>Tomodon dorsatus</i>	MZUSP13969	OP024300	OP036808

Appendix 2

Comparative material examined.

Tachymenoides affinis: Peru: Region Huánuco: Ambo: Conchamarca, 2800 m: MUSM 38744, Region Huánuco: Acomayo, 3000 m: MUSM 2723–25, Region Huánuco: Conchamarca (Santa Rosa), ca. 2900 m: SMF 80049; *Tachymenis peruviana*: Peru: Region Huánuco: Chaglla: MUSM 20062–64; *Thamnodynastes pallidus*: Suriname, unknown location: NZCS R129; Indira Gandhiweg km 14: NZCS R283.