

# HOLOTIPUS

HOLOTIPUS  
ONLINE

## MAGAZINE



Holotipus (online)



Received on

20 November 2021 / Accepted on

2 March 2021 / Published on

4 October 2021

Research Article

# A new species of *Homonota* (Squamata: Gekkota: Phyllodactylidae) from Paraguay

HUGO CABRAL<sup>1,2,3</sup> & PIER CACCIALI<sup>2,3</sup>

[HTTP://ZOOBANK.ORG/URN:LSID:ZOOBANK.ORG:PUB:CF1D469D-1CDC-4053-BA2F-E618E416BA55](http://zoobank.org/urn:lsid:zoobank.org:pub:CF1D469D-1CDC-4053-BA2F-E618E416BA55)  
[HTTPS://DOI.ORG/10.53561/KAYV6367](https://doi.org/10.53561/KAYV6367)

<sup>1</sup>PROGRAMA DE PÓS-GRADUAÇÃO EM BIOLOGIA ANIMAL, UNIVERSIDADE ESTADUAL PAULISTA, SÃO JOSÉ DO RIO PRETO, SP, BRAZIL.

<sup>2</sup>INSTITUTO DE INVESTIGACIÓN BIOLÓGICA DEL PARAGUAY. DEL ESCUDO 1607, ASUNCIÓN, PARAGUAY.

<sup>3</sup>ASOCIACIÓN GUYRA PARAGUAY, AV. CNEL. CARLOS BÓVEDA, PARQUE ASUNCIÓN VERDE, VIÑAS CUÉ, PARAGUAY.

CORRESPONDING AUTHOR: HUGUITOCABRAL@GMAIL.COM

### Abstract.

The 12 recognized species of the genus *Homonota* are geographically restricted to central and southern South America in Argentina, Brazil, Uruguay, Bolivia, and Paraguay. The phylogenetic relationships within the genus are well known where three groups are identified, each of them containing four species: the *whitii* group (*Homonota darwinii*, *H. williamsii*, *H. whitii*, and *H. andicola*), the *borellii* group (*H. borellii*, *H. taragui*, *H. rupicola*, and *H. uruguayensis*) and the *horrida* group (*H. horrida*, *H. underwoodi*, *H. septentrionalis*, and *H. marthae*). During fieldwork in Paraguay, we found a specimen of *Homonota* with unique morphological and geographical traits. Thus, we performed a comparative morphological analysis against specimens housed in different Paraguayan collections. Additionally, we performed a DNA analysis of our specimen to assess its relationships within the genus. Results suggest that this specimen represents a new species of the *Homonota horrida* group based on molecular and morphological evidence. The new species is characterized by a robust body, 10 longitudinal rows of strongly keeled scales separated by one or two granular scales, square-shaped mental scales, small postmental scales, one or two rows of rectangular scales in the upper eye scales, rostral scale divided, edge of auditory meatus serrated posteriorly, and black and brown background coloration with one white vertebral line and seven white transverse bands. The new species is restricted to Paraguari Department, characterized by herbaceous grasslands with rocky outcrops.

**KEYWORDS:** GECKOS, *HOMONOTA*, GRASSLANDS, PHYLOGENY, TAXONOMY, SOUTH AMERICA

## Introduction

Geckos of the genus *Homonota* Gray 1845 are known from central and southern South America (Kluge 1964; Cajade et al. 2013; Morando et al. 2014) in Argentina (Avila et al. 2012; Cajade et al. 2013; Morando et al. 2014), Brazil (Vaz-Ferreira & Sierra de Soriano 1961), Uruguay (Carreira et al. 2005), Bolivia (Langstroth 2005), and Paraguay (Cacciali et al. 2007; 2017), and currently 12 species are recognized (Avila et al. 2012; Cajade et al. 2013; Morando et al. 2014; Cacciali et al. 2018). The genus is in the Phyllodactylidae family with the genera *Garthia* Donoso-Barros & Vanzolini, 1965, *Gymnodactylus* Spix, 1825, *Phyllodactylus* Gray, 1928, *Phyllopezus* Peters, 1978, and *Thecadactylus* Goldfuss, 1820 (Gamble et al. 2011).

The phylogenetic relationships within the genus are well known (Morando et al. 2014) with three groups recognized, the *whitii* group with four species (*Homonota darwinii* Boulenger, 1885, *H. williamsii* Avila, Perez, Minoli & Morando, 2012, *H. whitii* Boulenger, 1885 and *H. andicola* Cei, 1978) with the most austral distribution in the genus (Morando et al. 2014), the *borellii* group (*H. borellii* (Peracca, 1897), *H. taragui* Cajade, Etchepare, Falcione, Barraso & Alvarez, 2013, *H. rupicola* Cacciali, Ávila & Bauer, 2007, and *H. uruguayensis* (Vaz-Ferreira & Sierra de Soriano, 1961)) and the *horrida* group (*H. horrida* (Burmeister, 1861), *H. underwoodi* Kluge, 1964, *H. septentrionalis* Cacciali, Morando, Medina, Kölher, Motte & Avila, 2017 and *H. marthae* Cacciali, Morando, Avila & Kölher, 2018) (Morando et al. 2014; Cacciali et al. 2018). Cacciali et al. (2017) consider *Homonota fasciata* a species inquirenda and until new works appear, we would agree with this taxonomic arrangement.

Between geckos in the genus *Homonota* there is a great diversity and degree of speciation; this is demonstrated by later works describing new species using molecular and morphological data (Cacciali et al. 2007; 2017; 2018; Avila et al. 2012; Cajade et al. 2013). In Paraguay, three species of *Homonota* are recorded: *H. rupicola* in the department of Cordillera and apparently endemic to the Cerro Pedregal (Cacciali et al. 2007), *H. septentrionalis* in the western part of the Dry Chaco ecoregion (Cacciali et al. 2017), and *H. marthae* distributed in the central area of the Dry Chaco ecoregion (Cacciali et al. 2018). In December 2016, we carried out an expedition in the Department of Paraguairí, near the city of Caapucu where an unusual specimen of *Homonota* was collected, and after further examination using morphological and molecular analyses we found the specimen to belong to an undescribed species which we describe below as a new species from Paraguay.

## Material and Methods

We analysed specimens from the following collections: Museo Nacional de Historia Natural del Paraguay (MNHNP) and Instituto de Investigación Biológica del Paraguay (IIBP), and data from a recent publication (Cacciali et al. 2017; 2018) of the genus in Paraguay were compared to have a more precise description. When paired structures exist, data are presented in left/right orientation. We evaluated characters normally used in the taxonomy of the genus following recent works (Avila et al. 2012; Cacciali et al. 2017; 2018).

### Morphological analysis

We include the following meristic data: SAM (scales around midbody), DS (dorsal scales), VS (ventral scales), DT (number of keeled dorsal tubercles from occipital area to cloaca level), TVS (number of transversal rows of ventral scales, counted longitudinally at midline from the chest (shoulder level) to inguinal level), LVS (number of longitudinal rows of ventral scales, counted transversally at midbody), SL (number of supralabial scales), IL (number of infralabials scales), 4TL (number of lamellae under the fourth toe), 3FL (number of lamellae under the third finger).

We also include the following metric characters: snout-vent length (SVL) from tip of the snout to vent, trunk length (TrL) distance from axilla to groin from posterior edge of forelimb insertion to anterior edge of hindlimb insertion; foot length (FL) from tip of claws of the 4th toe to heel, tibial length (TL) greatest length of tibia, from knee to heel; arm length (AL) from tip of claws of the 3rd finger to elbow, head length (HL) distance between anterior edge of auditory meatus and snout tip, head width (HW) taken at level of the temporal region, head height (HH) maximum height of head, measure at parietal level area, the eye-nostril distance (END) from anterior edge to the posterior edge of nostril, eye-snout distance (ESD) from the anterior edge of the eye to the tip of the snout, eye-meatus distance (EMD) from the posterior edge of the eye to the anterior border of the ear opening, interorbital distance (ID), and internostril distance (IND).

### DNA analysis

Based on morphological examination, we allocated the new taxon in the *Homonota horrida* group, sensu Cacciali et al. (2017; 2018). We then carried out a genetic analysis using sequences of the mtDNA 16S gene as it has proved to be useful for taxonomic identification (Batista et al. 2014; Kölher et al. 2014).

## Results

### Phylogenetic inference

Our final alignment of 16S consisted of 271 bp, and the best substitution model was HKY+I. Sequence divergence between the new species and the other species in our analysis range between 4.1% and 4.8% for 16S (Table 2). The ML and BI tree (Figure 1) using 16S recognized 4 clusters, both showing the new species as a sister clade to specimens of *H. horrida* from southern Argentina with strong support (bootstrap value = 82%, and posterior probability = 0.89). Both trees (ML and BI) have the same topology, with *H. septentrionalis* as a sister clade of *H. marthae*, *H. horrida* and the new species. Analysis of intraspecific divergence with ABGD found two groups (Table 3), with *H. horrida*, *H. marthae* and *H. septentrionalis* in group one, and the new species in group 2, this is congruent with our previous ML and BI trees, providing strong evidence for the recognition of a new taxon. In addition to the morphological support, the molecular analysis also provided strong support for the hypothesis that our sample represents an undescribed taxon, which we here formerly describe and name.

### *Homonota itambere* sp. nov.

**Etymology:** the epithet is combination of two Guaraní words, ita = rock, ambere = lizard, a lizard who lives in the rocks. The species name is an allusion of the habitat where the species was found, as a lizard that lives in the rocks. The name is used here as a noun in apposition.

**Holotype:** IIBP 4437, an adult female from Estancia Guajho, Departamento of Paraguairí (26°14'55.81"S, 57°17'48.03"W, 143 m) (Figure 2), collected by Hugo Cabral, 14 December 2016. Collecting permits were provided by the Ministerio del Ambiente y Desarrollo Sostenible, MADES 126/2016 and 258/2016.

### Diagnosis

A species of *Homonota* assigned to the *horrida* group (sensu Cacciali et al. 2018) based on molecular evidence and by the color pattern composed of a white vertebral line and five to seven transverse white lines appearing as banded, similar to *H. horrida*, *H. septentrionalis* and *H. marthae*. A large species of *Homonota* (SVL= 56 mm) with robust body, with 10 longitudinal rows of strongly keeled scales separated by one or two granular scales, a square shape mental scale, small postmental scales

Accession number and localities are presented in Table 1. We used three sequences of *H. septentrionalis*, one of *H. marthae* from Paraguay and three of *H. horrida* from Argentina, using *Phyllopezus przewalskii* as the outgroup, and since no 16S sequence of *H. underwoodi* were available, we did not include it in this analysis.

Alignment was performed using MAFFT 7 (Katoh & Standley 2013) to automatically align sequences through its webserver. We included the Q-INS-I search strategy for corrections with the secondary structure for 16S, then we used Gblocks 0.91b (Castresana 2000) to eliminate poorly aligned positions and divergent regions of DNA through its online server. MSA viewer (Yachdav et al. 2016) were used to visualize and export the alignment to fasta format. The best substitution model for the gene was perform with jModelTest 2.1.10 (Darriba et al. 2012), lower value of delta Akaike Information Criterion ( $\Delta$ AIC) were used to select the best model.

We preformed two phylogenetic analyses, first a Maximum Likelihood (ML) approach, and then a Bayesian inference (BI). We estimated the uncorrected genetic pairwise distance of our dataset in MEGA10.0.5, for ML analysis we used IQ-Tree (Nguyen et al. 2015) through its webserver (Trifinopoulos et al. 2016) using 10,000 non-parametric bootstrap replicates plus 10,000 replicates of Shimodaira-Hasegawa approximate likelihood ratio (Sh-aLRT) (Anisimova et al. 2011) and 10,000 ultrafast bootstrap (UFBoot) approximation replicates (Minh et al. 2013). For BI we convert the alignment to be used in MrBayes v3.2 in Mesquite 3.6 (Maddison & Maddison 2017). For this we ran the analysis in independent duplicates, with 40,000,000 generations for MCMC with a sampling frequency of 1,000 generations. Trees were visualized and exported then using FigTree v1.4.4 (available at <http://tree.bio.ed.ac.uk/software/figtree/>). We considered convergence when the standard deviation of split frequencies was 0.015 or less and when Potential Scale Reduction Factor approached 1.0 (Gelman & Rubin 1992).

The degree of intraspecific divergence within the alignment (removing the outgroup) were performed with the species delimitation test ABCD (Puillandre et al. 2012) through its webserver (<https://bioinfo.mnhn.fr/abi/public/abgd/abgdweb.html>), using 10 steps of prior minimum and maximum simple genetic distance from 0.001 to 0.1 (default), and 0.5 of relative gap width, since higher (default) values tend to exceedingly split clades (Kekkonen et al. 2015; Yang et al. 2016).

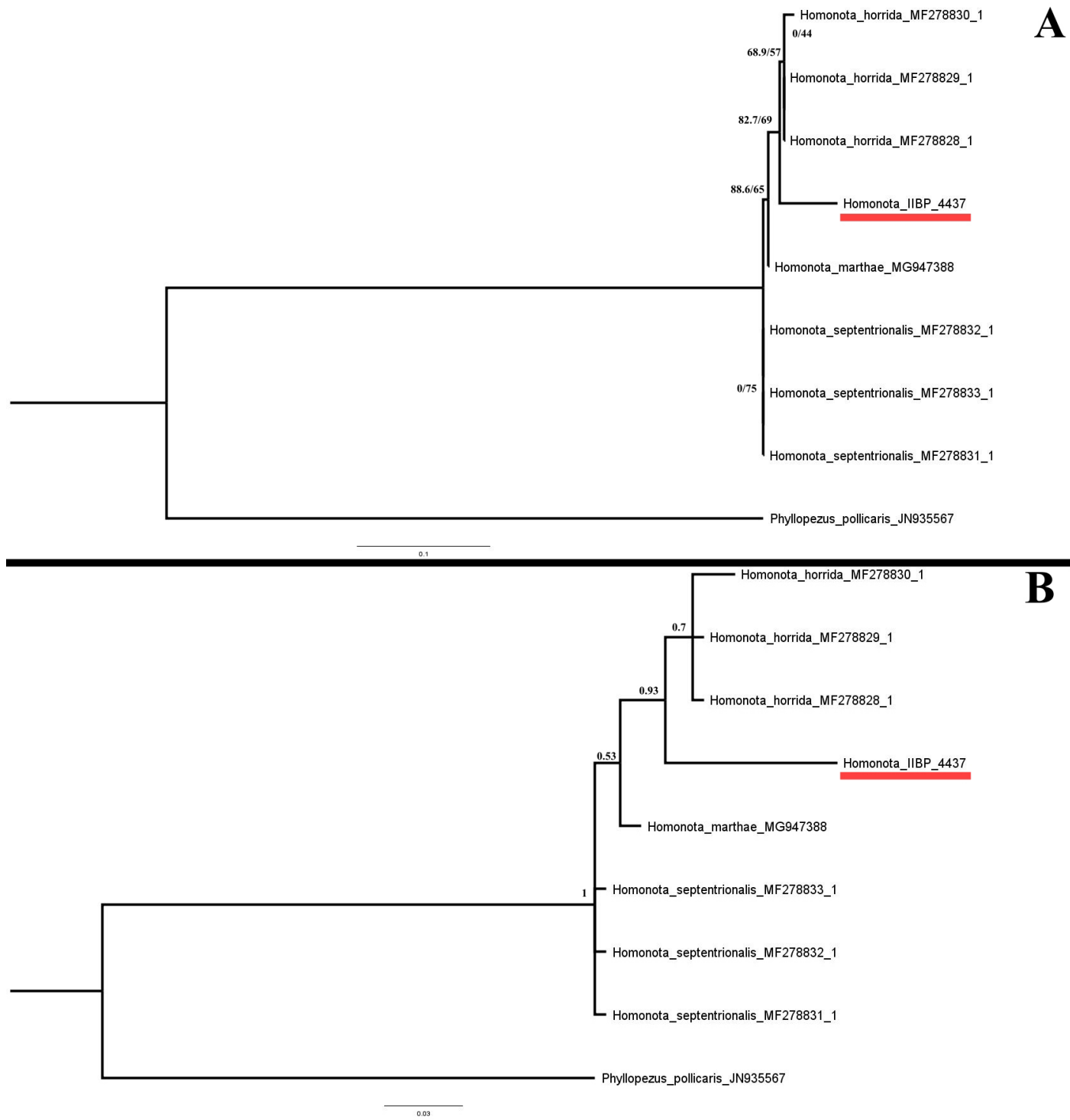


Figure 1.  
Species tree of *Homonota horrida* group with related species showing the positions of the new specie A) Maximum likelihood inference B) Bayesian inference. Bars represent substitution per site. Support values are shown at the beginning of each clade.

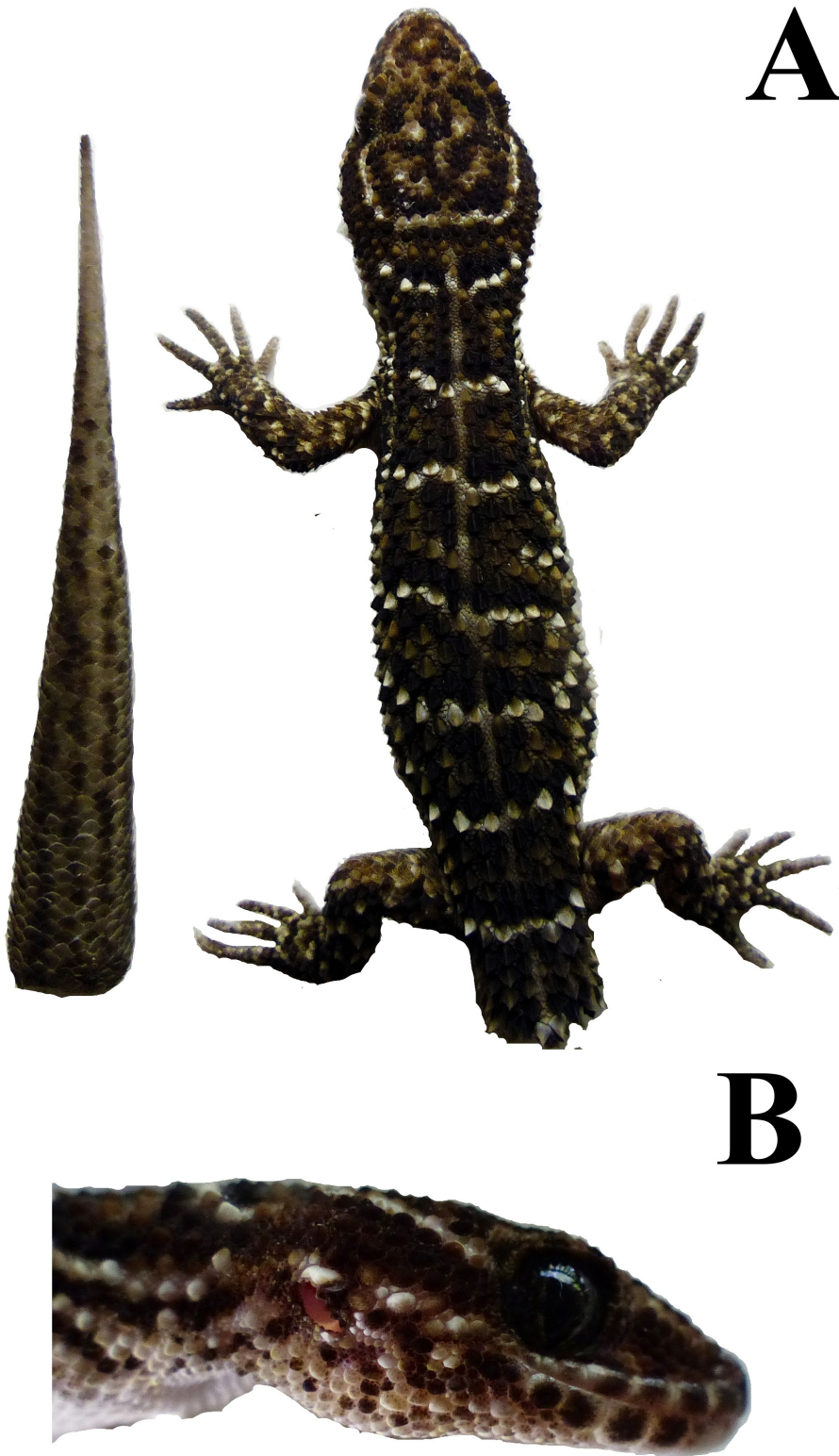


Figure 2.  
Photograph of the holotype of *Homonota itambere* sp. nov. minutes after euthanasia. A) Dorsal coloration, and B) lateral view of the head, note the enlarged white tubercle at the edge of the auditory meatus.



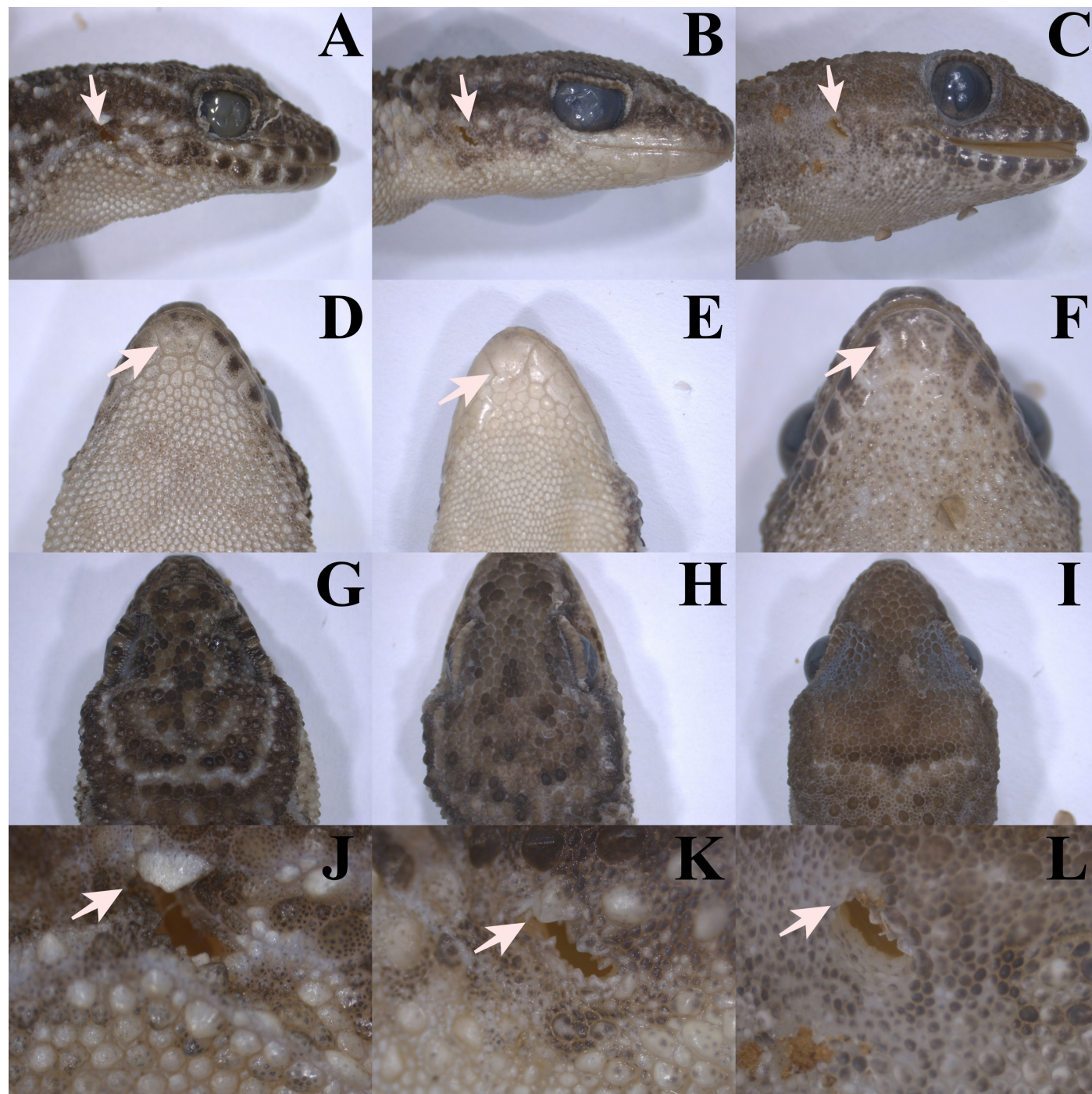


Figure 3.

Lateral, ventral, dorsal and auditory meatus view of the holotype of *Homonota itambere* **sp. nov.** (A, D, G, J) and comparisons with *H. marthae* (B, E, H, K) and *H. septentrionalis* (C, F, I, L). A-C) white arrow indicating the position of the auditory meatus in relation with to the commissure of the mouth, D-F) Detail of the mental region, showing the size and shape of mental and postmental scales, G-I) Dorsal view of the head showing the coloration pattern of *H. itambere* **sp. nov.**, *H. marthae* and *H. septentrionalis*, J-L) The white arrow indicates the sizes and shape of the enlarged tubercle and the edge of the auditory meatus of *H. itambere* **sp. nov.**, *H. marthae* and *H. septentrionalis*.

### Description of the holotype

Adult female, SVL= 56 mm, TrL= 26.2 mm, tail broken near the base, FL= 10 mm, TL= 9.3, AL= 24 mm, HL= 13.1 mm, HW=11.3, HH= 8.5 mm, END= 5.6 mm, EMD= 4.2 mm, ESD= 6.1 mm, ID= 5.79 mm, IND= 2.39 mm. Rostral wider with a groove complete in the middle of the scales, nares surrounded and contacting the rostral, supranasal and first SL contacting the rostral and nares, two postnasal contacting the nares, not the rostral; (left first) SL 8/8, IL 5/5.

Three tubercular scales on the mouth commissure; upper region of the muzzle and head slightly convex covered by large and small heterogeneous juxtaposed and granular scales; superciliary scales imbricated forming a serrated edge, associated to spiny-like scales on the posterior half of the orbit; lateral sides of the head covered with large, keeled tubercles and small, granular scales (Figure 3A, G); auditory meatus oblique with serrated edge posteriorly (Figure 3J), one large scale in the upper border; IL 5/5; mental quadrangular, postmental circular and small, almost the same size of the following posterior scales, first IL contacting the mental twice as large than postmental scales; scales under the head small with black dots, becoming less notable reaching the commissure of the mouth; dorsolateral of the neck with granular, juxtaposed scales mixed with keeled scales; throat region covered by imbricate cycloid scales; dorsum covered with 10 longitudinal strongly keeled scales separated by one or two granular scales, except on the vertebral, where the keeled scales are separated by three or four granular ones; ventral scales cycloid and imbricate with 17 longitudinal rows at midbody; suprascapular and axillary region surrounded by small, imbricate scales, inguinal region and cloacal opening surrounded by smooth scales, anterior and dorsal surfaces of forelimbs covered by large imbricate and keeled scales; posterior region and ventral surface of forelimbs covered by small, juxtaposed granules; ventral surface of hind limbs covered by large, imbricate scales; subdigital lamellae of hands, counting from the pollex first are: (left first) 7/7, 11/11, 15/13, 13/14, 11/9; and subdigital lamellae of feet, starting from hallux were recorded as follows: 14/14, 17/15, 15/15, 13/11, 8/7; scales at the base of the tail (regenerated stump) imbricate and weekly to moderately keeled on dorsal region of the tail.

Coloration in life (minutes after euthanasia).

Dorsal surface of the head with small white and brown blotches irregularly mixed with black marks and a thin occipital white band from eye to eye, this occipital band is followed posteriorly by a dark brown coloration, dorsal surface of the neck with a black

(Figure 3D), one or two rows of rectangular scales in the upper eye scales, rostral scale divided, edge of auditory meatus serrated posteriorly with an enlarged tubercle, and black and brown background coloration with one white vertebral line with seven transverse white bands (Figure 3A). It can be distinguished from *H. andinicola*, *H. whitii* and *H. underwoodi*, *H. darwini* by the presence of longitudinal rows of dorsal keeled scales (smooth dorsal scales in *H. andinicola*, *H. whitii* and *H. underwoodi*, keeled scales restricted to the posterior part of the dorsum in *H. darwini*), also from *H. underwoodi* by the low number of 4TL (17) (vs 20-25 4TL in *H. underwoodi*), also from *H. rupicola* by the high number of 4TL (17) (vs 14-15 in *H. rupicola*), differs from *H. rupicola*, *H. taragui*, *H. williamsi*, *H. borelli*, *H. andinicola* and *H. whitii* by the higher number of 3FL (15) (vs 10-12 in *H. rupicola*, 11-13 in *H. taragui*, 11-14 in *H. williamsi*, 10-13 in *H. borelli*, 13-14 in *H. andinicola* and 12-14 in *H. whitii*), from *H. borelli* and *H. rupicola* by the oblique shape of the auditory meatus (rounded in *H. borelli* and *H. rupicola*), from *H. rupicola*, *H. taragui*, *H. borelli* and *H. uruguayensis* by serrated edge of the auditory meatus (smooth in *H. rupicola*, *H. taragui*, *H. borelli* and *H. uruguayensis*) from *H. septentrionalis*, *H. marthae* and *H. horrida* by the number of keeled longitudinal dorsal scales (10) (vs. 4-8 in *H. septentrionalis* and *H. marthae* and 16 in *H. horrida*) from *H. horrida* and *H. rupicola* by the relative high position of the auditory meatus to the mouth commissure (lower position in *H. horrida* and *H. rupicola*). Differs from *H. rupicola*, *H. taragui*, *H. williamsi* by the well-developed tubercles, some with keeled scales on the side of the head, from the eye to the neck (vs. less developed tubercles or moderate keeled in *H. rupicola*, *H. taragui*, *H. williamsi*), from *H. rupicola*, *H. taragui*, *H. williamsi*, *H. uruguayensis* by the dorsal coloration of the head and body consisting of transverse clear bands on a darker dorsum (vs. reticulate pattern, resembling a salt and pepper pattern), also differs from *H. marthae*, *H. septentrionalis* and *H. horrida* by the tail's poorly developed keeled scales, (strongly keeled scales especially at the base of the tail in *H. marthae*, *H. septentrionalis* and *H. horrida*), *H. marthae* by the presence of a thin white occipital band (lack of a white band in *H. marthae*), also from *H. septentrionalis* and *H. horrida* by the thin white occipital band (vs. wider white occipital band), from *H. septentrionalis* by the shape of the mental scales, with a more quadrangular shape (vs. mental scales with a triangular shape, longer then wider in *H. septentrionalis* and finally from *H. horrida* by the small size of the postmental scales, about the same size of posterior scales (moderately enlarged postmental scales, about twice the size of corresponding scales in *H. horrida*).



band separated with a white transverse band (Figure 2). Supralabials, infralabials and rostral dark brown with white on the suture of scales, upper lateral view of the head dark brown from nostril to eyes, and from eyes to auditory meatus, covered by thin light brown line and white scales from the commissure of the mouth to the suprascapular region. Dorsal coloration is black and brown bands separated by a transvers white band and a vertebral white stripe from the neck to the first four scales of the tail. Dorsal surface of the limb, forelimb, fingers and toes with a salt and pepper coloration with brown, black and very conspicuous white marks, dorsal coloration of the tail with brown and black incomplete and diffused stripes. Ventral coloration is immaculate white from mental scale to cloaca region, with the presence of black chromatophores in all the ventral scales, not visible with the naked eye, tail with grey coloration. Only the ventral region of the arms and finger lamellae have a brown coloration.

Color in preservative

Dorsal coloration of the head with white and dark brown small blotches irregularly mixed, and a brown and a thin occipital white band from eye to eye, this occipital band is followed posteriorly by a dark brown coloration, dorsal surface of the neck with a brown band separated with a white transverse band. Supralabials, infralabials and rostral brown with white on the suture of scales, upper lateral view of the head brown from nostril to eyes, and from eyes to auditory meatus, covered by a thin light brown and white scales from the commissure of the mouth to the suprascapular region. Dorsal coloration with dark brown bands separated by transverse white lines and a vertebral white stripe from the neck to the first four scales of the tail. Dorsal surface of the limb, forelimb, fingers and toes with a salt and pepper coloration of brown, and very conspicuous white marks, dorsal coloration of the tail with brown and black incomplete and diffused stripes. Ventral coloration immaculate white from mental scale to cloaca region, with the presence of black chromatophores in all the ventral scales, not visible with the naked eye, tail with grey coloration. Only the ventral region of the arms and finger lamellae have a brown coloration.

Distribution and habitat

*Homonota itambere* **sp. nov.** is restricted to grasslands of the Paraguari Department (Figure 4), the environment inhabited by *H. itambere* **sp. nov.** is characterized by grasslands with rocky outcrops (Cartes et al. 2016), hydromorphic soil and a slight wavy topography (Fretes et al. 1970). The locality is a transition area between the Humid Chaco and Atlantic Forest and it is known for the presence of the Caacupe Craton

(Fúlfaro 1996), with a complex geological history (Nuñez 1999; Cubas et al. 1998) (Figure 5). This species does not appear to be abundant as we carried out six additional expeditions in the area to locate more specimens with unsuccessful results.

Discussion

The description of this new species elevated to five the number of taxa in the *Homonota horrida* group, being the most diverse species group of the genus so far. As stated by Cacciali et al. (2018), the taxonomy of the *H. horrida* group was ignored for many years, and the latest described new species demonstrates that this group had been overlooked for quite some time. The phylogenetic relations of the genus were studied in detail by Morando et al. (2014) and then updated by Cacciali et al. (2018) with all the new species described until that date. We are aware that describing a new species based on a single specimen, is not the best practice for taxonomy, but after six unsuccessful trips aimed to find additional specimens, and given that our data are supported by molecular, morphological, and chorological analyses, we decided to describe the species to provide a name to the new taxon, with the intention of carrying out additional expeditions to the type locality and surrounding areas in order to have a better understanding of the population and conservation status of *Homonota itambere* **sp. nov.** It is important to note that *Homonota* species are usually easy to find, however, this is not the case for the new species, and we believe that this is a new cryptic species with a presumably restricted distribution, like other related species such *H. rupicola*, and *H. taragui* (Cacciali et al. 2007; Cajade 2013).

Morphologically, the new species belongs to the *H. horrida* group due to the presence of keeled dorsal scales, a white vertebral stripe, and other similar coloration features. According to our molecular data, *Homonota itambere* **sp. nov.** is most closely related to specimens of *H. horrida (fasciata)* from Mendoza, Argentina. The distance between these two species is more than 1,000 km. This may also be due to the lack of available samples within those 1,000 km. However, it is surprising that the species is more closely related to southern populations, more than *H. septentrionalis* and *H. marthae* due to the proximity in the distribution of both species on the other side of the Paraguayan River. Also, this represents the first species of the *horrida* group on the other side of the Paraguayan River, and the locality where the species was found is part of the Caacupe Craton (Fúlfaro 1996) and the Alto Asunción (Hernandez et al. 2005), which may act as a barrier for the isolation of the new species. All these questions could be tested as new data become available and test the diversification

Table 1. Specimen vouchers and GenBank accession numbers of samples used in this study.

Species	Voucher	16S
<i>Homonota septentrionalis</i>	MNHNP 11873	MF278833
	MNHNP 12238	MF278832
	SMF 101984	MF278831
<i>Homonota horrida</i>	LJAMM-CNP 10576	MF278830
	LJAMM-CNP 10495	MF278829
	BYU 47941	MF278828
<i>Homonota marthae</i>	SMF 101438	MG947388
<i>Homonota</i> <b>sp. nov</b>	IIBP 4437	MZ098621
<i>Phyllopezus przewalskii</i>	LG 1093	JN935567

Table 2. Uncorrected pairwise genetic distance (in percentages) based on 16S mtDNA among *H. septentrionalis*, *H. horrida*, *H. marthae* and the new taxon (grey cells). Minimum and maximum values between species in bold. Accession and voucher numbers are provided in Table 1.

	MNHNP 11873	MNHNP 12238	SMF 101984	LJAMM-CNP 10576	LJAMM-CNP 10495	BYU 47941	SMF 101438	IIBP 4437
<i>Homonota septentrionalis</i>	-							
<i>Homonota septentrionalis</i>	0.0	-						
<i>Homonota septentrionalis</i>	0.0	0.0	-					
<i>Homonota horrida</i>	1.9	1.9	1.9	-				
<i>Homonota horrida</i>	1.1	1.1	1.1	0.7	-			
<i>Homonota horrida</i>	1.1	1.1	1.1	0.7	0.0	-		
<i>Homonota marthae</i>	0.4	0.4	0.4	1.9	1.1	1.1	-	
<i>Homonota</i> <b>sp.nov.</b>	4.4	4.4	4.4	4.8	4.1	4.1	4.5	-

Table 3. Intraspecific divergence.

	Prior maximal distance
Partition 1 found 2 groups	P= 0.001000
Partition 2 found 2 groups	P= 0.001668
Partition 3 found 2 groups	P= 0.002783
Partition 4 found 2 groups	P= 0.004642
Partition 5 found 2 groups	P= 0.007743
Partition 6 found 1 groups	P= 0.012915



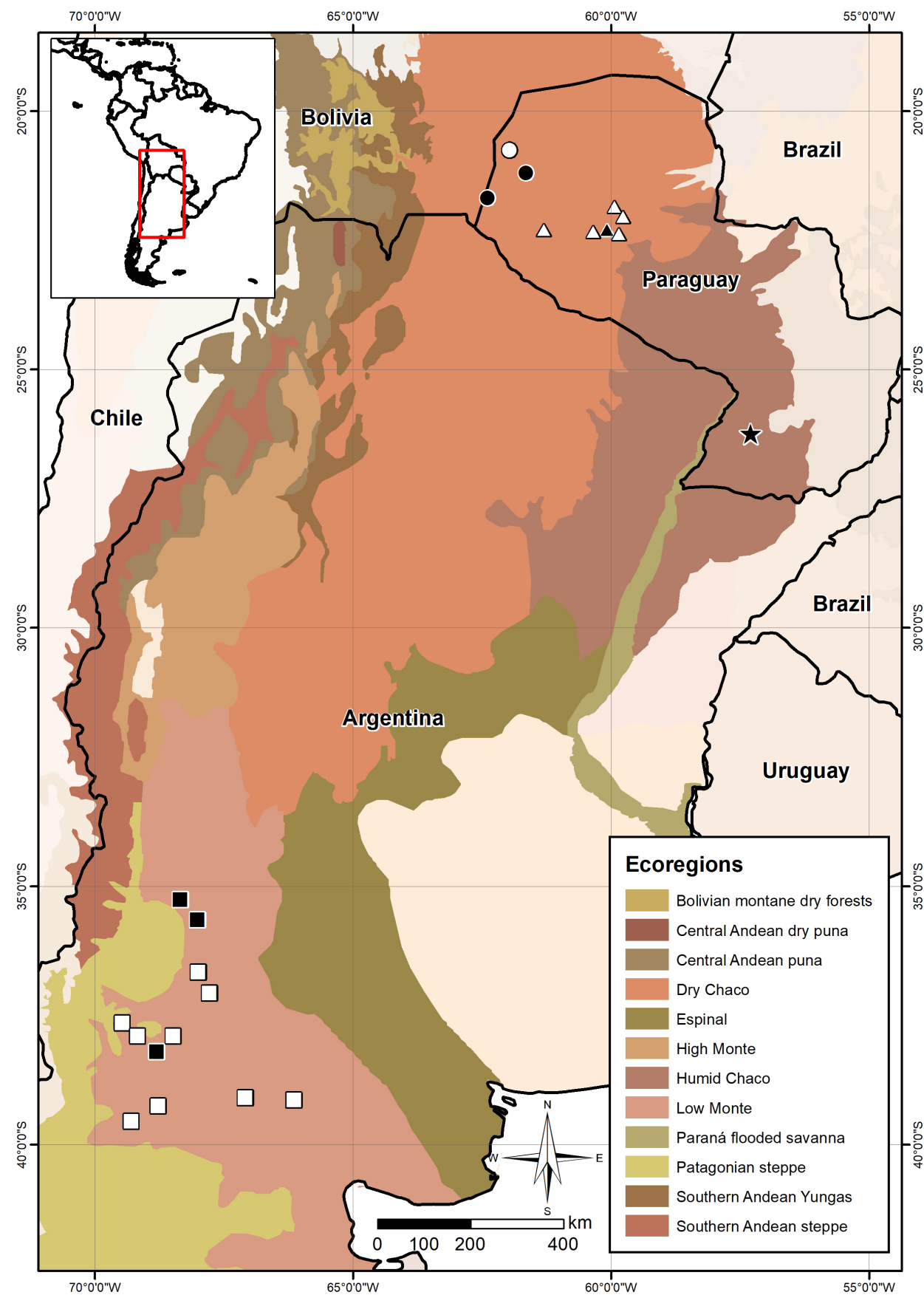


Figure 4.  
Distribution map of *Homonota itambere* **sp. nov.** showing the type locality (black star) and *H. septentrionalis* (circle), *H. marthae* (triangles) and *H. horrida* (squares). Black symbols represent molecular material used in or study.



Figure 5.  
General view of the habitat of *Homonota itambere* **sp. nov.**, showing the rocky formations and grasslands habitats.



hypothesis made by Morando et al. (2014). The new species can be easily differentiated from the congeners in the *H. horrida* group by their robust body, with 10 longitudinal rows of strongly keeled scales separated by one or two granular scales, a square-shaped mental scale, small postmental scales, one or two rows of rectangular scales in the upper eye scales, rostral scale divided, edge of auditory meatus serrated posteriorly and black and brown background coloration with a white vertebral line with seven transverse white bands.

The locality where the new species is found presents a mix of open grassland vegetation and rocky outcrops. We believe that this species may well be found in other similar rocky outcrops in southern Paraguay and additional expeditions are needed to understand better the distribution and habitat use of this cryptic species. Nevertheless, we propose that this new species can be considered as Data Deficient until new populations or specimens are found.

According to Morando et al. (2014) the ancestor of the *horrida* group (referred as *fasciata* group in Morando et al. 2014) was isolated in emergent areas of southern Bolivia and northern Argentina and dispersed later to the south and east. While our new species is far from these areas, the ancestor of *horrida* may have reached the other side of the Paraguay River before the river formerly appeared or reached the other side of the river by crossing on debris or aquatic vegetation during flood events. Or, perhaps it occurred another way; the ancestor of the *horrida* group originated in central Paraguay, and from there the dispersion to the south and west began. This may explain why the new species is more related to the Mendoza clade of *H. horrida*, and not to those in the Chaco of Paraguay. However, future studies and analyses of the phylogeographics of the genus are necessary to elucidate these theories.

## Acknowledgments

We would like to thank to Francisco Parcerisa the owner of Guajho Farm for access and accommodation during fieldwork, also to Lorena Sforza for contacting the owner of Guajho. To Viviana Rojas, Tatiana Galluppi, Marcos Baez, Edder Ortiz, Walter Cabral for help during fieldwork. We thank anonymous peer reviewers for suggestions to improve the quality of our manuscript. We thank the Ministerio del Ambiente y Desarrollo Sostenible (MADES) for collection permits. The authors also thank CONACYT for financial support through the PRONII program. Also, thanks to Francisco Brusquetti for allowing access to specimens under his care. HC would like to thank Coordenação de Aperfeiçoamento Pessoal de Nível Superior (CAPES, Brazil), Programa de Estudantes-Convênio de Pós-Graduação (PEC-PG),

for their fellowship. This specimen was found in the framework of the project CONACYT 14 INV 063 “Visión de Biodiversidad Nacional y Evaluación Ecorregional: La ecología al servicio de las decisiones de conservación y análisis de la fragmentación de los hábitats” led by Guyra Paraguay.

## Literature cited

- Avila, L., Perez, C., Minoli, I. & Morando, M. (2012) A new species of *Homonota* (Reptilia: Squamata: Gekkota: Phyllodactylidae) from the Ventania mountain range, Southeastern Pampas, Buenos Aires Province, Argentina. *Zootaxa* 3431: 19-36. <https://doi.org/10.11646/zootaxa.3431.1.2>.
- Batista, A., Köhler, G., Mebert, K. & Vasely, M. (2014) A new species of *Bolitoglossa* (Amphibia: Plethodontidae) from eastern Panama, with comments on other members of the adspersa species group from eastern Panama. *Mesoamerican Herpetology* 1(1): 97-121.
- Carreira, S., Achaval, F. & Meneghel, M. (2005) *Reptiles de Uruguay*. Universidad de la República, Facultad de Ciencias, Montevideo, Uruguay, 640.
- Cacciali, P., Ávila, L. & Bauer, F. (2007) A new species of *Homonota* (Squamata, Gekkonidae) from Paraguay, with a key to the genus. *Phyllomedusa* 6(2): 137-146. <https://doi.org/10.11606/issn.2316-9079.v6i2p137-146>.
- Cacciali, P., Morando, M., Medina, C., Köhler, G., Motte, M. & Avila, L. (2017) Taxonomic analysis of Paraguayan samples of *Homonota fasciata* Duméril & Bibron (1836) with the revalidation of *Homonota horrida* Burmeister (1861) (Reptilia: Squamata: Phyllodactylidae) and the description of new species. *PeerJ* 5, e3523. <https://doi.org/10.7717/peerj.3523>.
- Cacciali, P., Morando, M., Avila, L. & Köhler, G. (2018) Taxonomic analysis of Paraguayan samples of *Homonota* (Reptilia, Squamata, Phyllodactylidae) from the central region of northern Paraguay. *Zoosystematics and Evolution* 94(1): 147-161. <https://doi.org/10.3897/zse.94.21754>.
- Cajade, R., Etchepare, E., Falcione, C., Barraso, D. & Alvarez, B. (2013) A new species of *Homonota* (Reptilia: Squamata: Gekkota: Phyllodactylidae) endemic to the hills of Paraje Tres Cerros, Corrientes Province, Argentina. *Zootaxa* 3709: 162-176. <http://doi.org/10.11646/zootaxa.3709.2.4>.
- Cartes, J., Fontana, J. & Yanosky, A. (2016) Una aproximación hacia las definiciones eco-regionales del sur de la Región Oriental del Paraguay. *Extensionismo, innovación y transferencia tecnológica* 3: 13-20. <http://doi.org/10.30972/eitt.302769>.

- Castresana, J. (2000) Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. *Molecular Biology and Evolution* 17: 540-552. <https://doi.org/10.1093/oxfordjournals.molbev.a026334>.
- Cubas, N., Garcete, A., Meinhold, K., de Figueredo, L., Benítez, J., González, M., Burgath, K. & Höhndorf, A. (1998) *Mapa geológico de la República del Paraguay. Hoja Villa Florida. Texto explicativo*. MOPC-BGR, Asunción, 74 p.
- Darriba, D., Taboada, G.L., Doallo, R. & Posada, D. (2012) jModelTest 2: more models, new heuristic and parallel computing. *Nature Methods*: 9(8): 772. <https://doi.org/10.1038/nmeth.2109>.
- Fretes, R., Samudio, R. & Gay, C. (1970) *Las Praderas Naturales del Paraguay, I: Clasificación y descripción*. Programa Nacional de Investigación y Extensión Ganadera, Ministerio de Agricultura y Ganadería. Publicación Miscelánea N° 5. Asunción, 86 p.
- Fúlfaro, V. (1996) Geology of Eastern Paraguay. Alkaline Magmatism. In: Comin-Ciaramonti, P & Gomes, C. (Eds), *Central Eastern Paraguay. Relationships with Coeval Magmatism in Brazil*. Edusp/Fapesp, Sao Paulo, 17-29 p.
- Gamble, T., Bauer, A., Colli, G., Greenbaum, E., Jackman, T., Vitt, L. & Simons, M. (2011) Coming to America: multiple origins of New World geckos. *Journal of Evolutionary Biology* 24: 231-244. <https://doi.org/10.1111/j.1420-9101.2010.02184.x>.
- Gelman, A. & Rubin, D. (1992) Inference from Iterative Simulation Using Multiple Sequences. *Statistical Science* 7: 457-511. <https://doi.org/10.1214/ss/1177011136>.
- Hernández, R., Jordan, T., Farjat, A., Echavarría, L., Idelman, B. & Reynolds, J. (2005) Age, distribution, tectonics, and eusttic controls of the Paranense and Caribbean marine transgressions in southern Bolivia and Argentina. *Journal of South American Earth Sciences* 19: 495-512. <https://doi.org/10.1016/j.jsames.2005.06.007>
- Katoh, K. & Stanley, D.M. (2013) MAFFT multiple sequences alignment software version 7: improvements in performance and usability. *Molecular Biology and Evolution* 30(4): 772-780. <https://doi.org/10.1093/molbev/mst010>.
- Kekkonen, M., Mutanen, M., Kaila, K., Nieminen, M. & Hebert, P. (2015) Delineating species with DNA barcodes: a case of taxon dependent method performance in moths. *PLoS ONE* 10: e0122481. <https://doi.org/10.1371/journal.pone.0122481>.
- Kluge, A. (1964), A revision of the South American gekkonid lizard genus *Homonota* Gray. *American Museum Novitates* 2193: 1-41.

- Köhler, G., Vargas, J. & Lotzkat, S. (2014) Two new species of the *Norops pachypus* complex (Squamata, Dactyloidae) from Costa Rica. *Mesoamerican Herpetology* 1(2): 254-280. <https://doi.org/10.11646/zootaxa.3125.1.1>.
- Langstroth, R.P. (2005) Adiciones confirmadas y probables para la saurofauna boliviana. *Kempffiana* 1(1): 101-128.
- Madison, W.P. & Madison, D.R. (2017) Mesquite: a modular system for evolutionary analysis. Version 3.6. Available at: <http://www.mesquiteproject.org> (accessed on 11 September 2021).
- Minh, B.Q., Thi Nguyen, M.A. & von Haeseler, A. (2013) Ultrafast approximation for phylogenetic bootstrap. *Molecular Biology and Evolution* 30(5): 1188-1195. <https://doi.org/10.1093/molbev/mst024>.
- Morando, M., Medina, C., Avila, L., Perez, C., Buxton, A. & Sites, J. (2014) Molecular phylogeny of the New World gecko genus *Homonota* (Squamata: Phyllodactylidae). *Zoologia Scripta* 43(3): 249-260. <https://doi.org/10.1111/zsc.12052>.
- Nuñez, M. (1999) Mapa geológico de la República del Paraguay. Hoja Coronel Oviedo 5670. Texto Explicativo. MOPC-BGR, Asunción, 30 p.
- Puillandre, N., Lambert, A., Brouillet, S. & Achaz, G. (2012) ABGD, Automatic Barcode Gap Discovery for primary species delimitation. *Molecular Ecology* 21(8): 1864-1877. <https://doi.org/10.1111/j.1365-294X.2011.05239.x>.
- Trifinopoulos, J., Nguyen, L.T., von Haeseler, A. & Minh, B.Q. (2016) W-IQ-TREE: a fast-online phylogenetic tool for Maximum Likelihood analysis. *Nucleic Acid Research* 44: 232–235. <https://doi.org/10.1093/nar/gkw256>.
- Vaz-Ferreira, R. & Sierra de Soriano, B. (1961) Um nuevo gekkonidae del Uruguay. *Comunicaciones Zoológicas del Museo de História Natural de Montevideo* 91(5): 1-14.
- Yachdav, G., Wilzbach, S., Rauscher, B., Sheridan, R., Sillitoe, I., Protector, J., Lewis, S.E., Rost, B. & Golberg, T. (2016) MSASviewer: interactive JavaScript visualization of multiple sequence alignments. *Bioinformatics* 32(22): 3501-3503. <https://doi.org/10.1093/bioinformatics/btw474>.
- Yang, Z., Landry, J.H. & Hebert, P. (2016) A DNA Barcode Library for North American Pyraustinae (Lepidoptera: Pyraloidea: Crambidae). *PLoS ONE* 11: e0161449. <https://doi.org/10.1371/journal.pone.0161449>.



*Holotipus*  
is an open access, peer-reviewed scientific journal  
devoted to Zoology, Systematics and Taxonomy.  
Special issues are dedicated to editorials and  
scientific papers focused on Art and Biology.

Submitting papers should be addressed to  
Publisher, Chief Editor or Managing Editor:  
[holotipus@holotipus.it](mailto:holotipus@holotipus.it)

Designed, published and printed in Italy by  
Holotipus publisher & ActionKlavier studio,  
Corso Peschiera 315/A, 10141 Torino.

Holotipus rivista di zoologia sistematica e  
tassonomia ISSN 2704-7547

**Publisher**  
Matteo Grasso

**Founder & Co-Editor-in-Chief**  
Carlo Arrigo Casadio

**Co-Editors-in-Chief**  
Francesco Vitali  
Marco Scotini

**Managing Editor**  
Pier Cacciali Sosa

**Complete editors list on**  
<https://www.holotipus.it/>

We permanently archive all published articles on  
LOCKSS, Biotaxa and Zenodo. However, you can find  
the latest volume available on [holotipus.it/archive/](https://www.holotipus.it/archive/).

We would love to receive your manuscript.  
You can find all the related guidelines on  
[holotipus.it/publication-norms/](https://www.holotipus.it/publication-norms/).  
Please do not forget to have a look at our Editorial policy.

Photographs  
© Hugo Cabral & Pier Cacciali (Figs. 1-5).



Front cover image  
General view of the habitat of *Homonota itambere* **sp. nov.**, showing the  
rocky formations and grasslands habitats.

Every effort has been made to trace copyright holders and to obtain  
their permission for the use of copyright material. The publisher apologizes  
for any errors or omissions in the above list and would be grateful if notified  
of any corrections that should be incorporated in future.

Cite as Cabral, H. & Cacciali, P. (2021) A new species of *Homonota* (Squamata:  
Gekkota: Phyllodactylidae) from Paraguay. *Holotipus rivista di zoologia  
sistematica e tassonomia* 11(2): 93-108. <https://doi.org/10.53561/KAYV6367>.

