A New Species of the Atlantic Forest Endemic Genus *Paratelmatobius* (Anura: Leptodactylidae: Paratelmatobiinae) with a Reappraisal of the Advertisement Calls in the Genus

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ABSTRACT: The genus *Paratelmatobius* is endemic to the Atlantic Forest and comprises seven described species distributed across mountain ranges in southeastern and southern Brazil. An additional potentially new species was previously identified in a study addressing the phylogenetic relationships of the subfamily Paratelmatobiinae. To further investigate this lineage, we conducted field surveys to collect additional specimens and record its advertisement call. By integrating phylogenetic evidence with acoustic and morphological data, we confirmed the distinctiveness of this lineage and formally describe it here. We also reanalyzed the advertisement calls of six out of the seven congeners to enable direct acoustic comparisons. The new species is diagnosable from its congeners by a combination of characters, including a one-note advertisement call varying from 141 to 395 ms, formed by regular-spaced pulses produced at a repetition rate of 56 to 96 per second, and dominant frequency ranging from 3639 to 4113 Hz, the presence of vocal slits in males, nuptial pads in males that are not divided into two portions, and a belly coloration in life characterized by a gray or brown background with small white blotches and flecks. This species is currently known only from its type locality in the municipality of Salesópolis, state of São Paulo.

Key words: Acoustic characters; Amphibia; Endemism; Species description; Taxonomy

THE ATLANTIC Forest endemic genus *Paratelmatobius* Lutz and Carvalho 1958 (Anura: Leptodactylidae) currently comprises seven species distributed along the Serra do Mar and Serra da Mantiqueira mountain ranges in Brazil (Santos et al. 2020). The species of the genus, recognizable by having bright coloration on the venter, are divided into two morphological

groups (Pombal and Haddad 1999). The *P. lutzii* group, characterized by having a nuptial pad (in males) divided into two portions, males lacking vocal slits, first finger as long as or shorter than the second, medial margin of the first toe fringed or webbed, and head flattened, includes *P. gaigeae* (Cochran 1938), *P. lutzii* Lutz and Carvalho 1958, and *P. poecilogaster* Giaretta and Castanho 1990. The *P. cardosoi* group, diagnosed by having a nuptial pad (in males) not divided, males with vocal slits, first finger longer than second, medial margin of the first toe not fringed or webbed, and head not flattened, comprises *P. cardosoi* Pombal and Haddad 1999, *P. mantiqueira* Pombal and Haddad 1999, *P. yepiranga* Garcia, Berneck, and Costa 2009, and *P. segallai* Santos, Oliveira, Carvalho, Zaidan, Silva, Berneck, and Garcia 2019. These morphological groups are supported by DNA sequence data, although sequences from *P. lutzii* and *P. mantiqueira* are still unavailable (Lourenço et al. 2008; Santos et al. 2020).

In a recent study based on nuclear and mitochondrial markers, a putatively new species belonging to the *P. cardosoi* group was recovered, the *Paratelmatobius* sp. of Santos et al. (2020). During field surveys carried out in the Atlantic Forest of the state of São Paulo, we collected additional specimens and recorded the vocalizations of individuals assigned to this potentially new species, which we formally described in this study. Additionally, we provide a reanalysis of the advertisement calls in the genus to facilitate direct acoustic comparisons among species of *Paratelmatobius*.

MATERIALS AND METHODS

Field Data and Specimens Examined

We collected specimens during fieldwork in the Parque Estadual da Serra do Mar, Núcleo Padre Dória (Estação Biológica de Boraceia), a reserve in the Atlantic Forest of the Brazilian state of São Paulo (-23.654091°S, -45.889524°W, 847 m above sea level; all geographic

coordinates are in the system datum WGS84) from 15 to 19 December 2021. The collected specimens were euthanized in 5% lidocaine solution, fixed in 10% commercial grade formalin, preserved in 70% ethanol, and housed in the Célio F. B. Haddad Amphibian Collection, Rio Claro, São Paulo, Brazil (CFBH). For molecular analysis, we removed a small portion of the thigh muscle from the specimens immediately after euthanasia, before formalin fixation. The muscle tissue was stored in cryogenic vials with 100% ethanol in a -20ºC freezer. We also examined other specimens of the new species available in CFBH and the Herpetological Collection of Museu de Zoologia da Universidade de São Paulo, São Paulo, São Paulo, Brazil (MZUSP). For congeneric comparisons, we used information from original descriptions or redescriptions (i.e., Giaretta and Castanho 1990; Pombal and Haddad 1999; Zaher et al. 2005; Garcia et al. 2009; Santos et al. 2019) and specimens examined from herpetological collections (Appendix I). Museum acronyms follow Sabaj (2020), except UFMG-AMP, which stands for the Amphibian Collection of Centro de Coleções Taxonômicas, Universidade Federal de Minas Gerais (CCT/UFMG), Belo Horizonte, Minas Gerais, Brazil.

Molecular Phylogenetics and Genetic Distances

To confirm the identity of the newly collected specimens, we generated new DNA sequences. For this, we first extracted genomic DNA from three specimens using ethanol-preserved tissues and a standard ammonium acetate precipitation method (Maniatis et al. 1982). Then, we used Polymerase Chain Reaction (PCR) to amplify the same gene fragments as used in Santos et al. (2020): the mitochondrial cytochrome c oxidase subunit I (COI), cytochrome b (cyt-b), and the heavy strand transcription unit 1 (H1: 12S and 16S rRNA genes, plus the intervening $tRNA^{valine}$ gene); and the nuclear proopiomelanocortin A (POMC), recombination-activating protein 1 (RAG-1), rhodopsin (Rhod), tensin 3 (TNS3), and tyrosinase (Tyr). PCR primers,

reaction conditions, purification, and sequencing protocols follow Santos et al. (2020). We checked for quality and assembled the chromatograms using Geneious v.7 (Biomatters Ltd.).

To complement our sampling, we used sequences available from GenBank (Supplemental Table S1, available online). For *Paratelmatobius*, we selected two terminals per lineage, according to the phylogenetic hypothesis of Santos et al. (2020). Sequences were not available for *P. lutzii* and *P. mantiqueira*. As outgroups, we sampled the other genera of Paratelmatobiinae, including four of the seven described species of *Crossodactylodes*, and the monotypic genera *Rupirana* and *Scythrophrys*. We also included terminals of the other two subfamilies of Leptodactylidae and used the centrolenid *Vitreorana eurygnatha* to root the trees due to its close relationship with Leptodactylidae (Hime et al. 2021).

We performed sequence alignments for each marker using MAFFT v.7.49 (Katoh and Standley 2013). We used the E-INS-I algorithm for H1 and the G-INS-i algorithm for each of the coding gene fragments. Then, we concatenated the sequences of the eight aligned fragments using SequenceMatrix v.1.78 (Vaidya et al. 2011). We defined 22 a priori partitions, including the H1 and the three codon positions for each coding fragment, separately, to search for the best partition scheme and substitution models using the TESTMERGEONLY option in IQ-TREE v.2.1.2 (Minh et al. 2020) under the corrected Akaike information criterion (Hurvich and Tsai 1989) and restricting the search to models implemented on MrBayes. The best partition schemes and substitution models are given in Supplemental Table S2, available online.

For the inference of phylogenetic relationships, we performed Bayesian inference (BI) and maximum likelihood (ML) analyses using the CIPRES Science gateway portal (Miller et al. 2010). The BI analysis was conducted in MrBayes v.3.2.7 (Ronquist et al. 2012) using two independent runs of 20 million generations, starting with random trees and four Markov chains (one cold), sampling every 1000 generations, and discarding the first 25% of generations and

118 trees as burn-in. We assessed the minimal effective sample sizes (ESS > 200) and the
119 convergence between the runs with Tracer v.1.7.2 (Rambaut et al. 2018). The ML analysis was
120 performed in RAxML v.8.2.12 (Stamatakis 2014), searching for the most likely tree 100 times.
121 We then computed node support using 1000 non-parametric bootstrap replicates. For this
122 analysis, we used the partition scheme recovered by IQ-TREE but applied the GTR + G model
123 for all partitions.

124 We estimated the uncorrected *p*-distances within and among species of *Paratelmatobius*
125 using the ~570 bp 16S rRNA gene fragment limited by the primers 16Sar-L and 16Sbr-H
126 (Palumbi et al. 1991). We chose this fragment, which is commonly used in anuran taxonomy
127 (Fouquet et al. 2007; Lyra et al. 2017), to obtain distances that are more comparable to those in
128 other studies. We calculated the distances with MEGA v.11.0.11 (Tamura et al. 2021), treating
129 gaps and missing data as pairwise deletions.

130

131 Sound Recording and Acoustic Analysis

132 We recorded one male at the Estação Biológica de Boraceia using a Marantz PMD 660
133 digital recorder and a Sennheiser ME66/K6 unidirectional microphone. Sound recordings are
134 housed in the Bioacoustic Collection of UFMG (CBUFMG), a repository of animal sounds of
135 CCT/UFMG. This male was recorded in the field on 18 December 2021 at 03:02 h, air
136 temperature of 18.1ºC (recordings CBUFMG 1148–1149, voucher CFBH 48142). A second male
137 (CFBH 48141) was recorded while calling from inside a plastic bag; however, we opted not to
138 analyze these ex-situ calls, as they were emitted in a different context. Nevertheless, it is
139 important to note that the calls were consistent with those recorded in the field and described
140 below (see Advertisement calls section in the Results).

141 For acoustic comparisons, we analyzed the calls of six out of the seven congeneric species

(*P. gaigeae*, *P. poecilogaster*, *P. cardosoi*, *P. segallai*, *P. mantiqueira*, and *P. yepiranga*). The exception is *P. lutzii*, as its call remains unknown. We focused the acoustic characterization only on reproductive calls (advertisement calls), even though the vocal repertoire of some species is composed of additional note types attributed to an aggressive category. Some species have a genetic structure delimited into lineages (sensu Santos et al. 2020). In those cases, we restricted our analysis to the lineages that contained the type localities, which are: *P. cardosoi* (lineage B) and *P. segallai* (lineage A). For *P. mantiqueira* and *P. yepiranga*, we reanalyzed calls previously described in Moroti et al. (2022) and Garcia et al. (2009), respectively; for *P. gaigeae*, we reanalyzed calls previously described in Giaretta and Magrini (2013) and additional calls recorded by us. Sound recordings are housed in CBUFMG, CFBH, Fonoteca Neotropical Jacques Vielliard, Museu de Diversidade Biológica, Universidade Estadual de Campinas, Campinas, São Paulo, Brazil (FNJV), and the Sound Repository of the Universidade Federal de Uberlândia, Ituiutaba, Minas Gerais, Brazil (AAG-UFU). Acoustic traits and sample sizes (recorded males and analyzed calls) are summarized in Table 1. Locality data and other metadata are provided in Supplemental Table S3, available online.

Before the analyses, we applied a 500-Hz high-pass (48 dB) to the sound recordings in Audacity v.3.3.3 (Audacity Team 2023). We analyzed the calls in Raven Pro v.1.6.5 (Bioacoustics Research Program 2024) using the following spectrogram parameters: window type = Hann, window size = 256 samples, 3dB filter bandwidth = 248 Hz, overlap = 90% (locked), hop size = 26 samples, DFT size = 1024 samples (locked), grid spacing = 43.1 Hz, and spectrogram color map = default. We quantified temporal and spectral traits of the call from oscillograms and spectrograms, respectively. From each call, we measured: note duration (s; delta time in Raven Pro), note rise time (%; peak time relative in Raven Pro), pulses per note, pulse repetition rate (pulses/s), note repetition rate (notes/min), and dominant frequency (Hz; peak

frequency in Raven Pro). We followed Köhler et al. (2017) for acoustic definitions and terminology (under a note-centered approach) and Cocroft and Ryan (1995) for the quantification of repetition rates. We produced sound figures using the packages seewave v.2.2.1 (Sueur et al. 2008) and tuneR v.1.4.5 (Ligges et al. 2017) in the R v.4.3.1 platform (R Core Team 2023), with the following settings: window = Hann, FFT overlap = 90%, FFT samples = 256 samples.

Morphological Analyses

Fingers are numbered preaxially to postaxially from I to IV. Terminology for nuptial pad follows Luna et al. (2018), and that for other morphological characters follows Duellman (1970), Heyer et al. (1990), Duellman and Lehr (2009), and Santos et al. (2019). Morphometric characters follow Duellman (1970) for snout-vent length (SVL), head length (HL), head width (HW), eye diameter (ED), tympanum diameter (TD), tibia length (TBL), and foot length (FL); Heyer et al. (1990) for hand length (HAL), thigh length (THL), and tarsal length (TAL); Napoli (2005) for eye-nostril distance (END), nostril to tip of snout distance (NSD), internarial distance (IND); Garcia et al. (2003) for distance between the anterior margins of eyes (AMD); Duellman et al. (1997) for forearm length (FAL); and Greene and Funk (2009) for arm length (AL), arm width (AW), and forearm width (FAW). Measurements were taken by M.T.T. Santos to the nearest 0.1 mm using digital calipers for SVL, HL, HW, AL, FAL, HAL, THL, TBL, TAL, and FL; and an ocular micrometer for ED, END, NSD, IND, AMD, TD, AW, and FAW. We determined the sex of the examined specimens based on the presence of vocal slits, nuptial pads, and forelimb hypertrophy in males, and the presence of mature oocytes in females. Descriptions of coloration in life are based on field observations and photographs.

RESULTS

Phylogenetic Analyses

The newly collected specimens were recovered nested with the specimens previously assigned to the putatively new species *Paratelmatobius* sp. (1.0 posterior probability and 100% maximum-likelihood bootstrap; Fig. 1). This clade, recovered as sister to *P. yepiranga*, was embedded within the species of the *P. cardosoi* group (all relationships among species with 1.0 posterior probability and 100% maximum-likelihood bootstrap). The uncorrected *p*-distances of the 16S fragment among *Paratelmatobius* sp. and congeners (Appendix II) ranged from 5.5% (*P. yepiranga*) to 10.0% (*P. gaigeae*).

Advertisement calls in *Paratelmatobius*

Paratelmatobius gaigeae.—The advertisement call consists of a single type of pulsed note that can be emitted isolated, in pairs, or series. Considering both single notes and note series, the note repetition rate varies from 18 to 190 (77.3 ± 51.3) per minute. The modal note (Fig. 2A) comprises regular-spaced pulses, except for (1) the first pulse, which is lower in amplitude and is isolated from the subsequent pulse (usually present in the analyzed notes), and (2) the last pulse, which is also isolated from the preceding pulse. Note duration varies from 32 to 87 (52.9 ± 4.8) ms, with rise time ranging from 18 to 74 (42.5 ± 7.4) % of note duration. Pulse number varies from 3 to 14 (7.7 ± 1.1), emitted at a rate of 70 to 256 (138.3 ± 13.2) per second. The note dominant frequency ranges from 2369 to 3488 (2835.4 ± 255.5) Hz (Table 1). There is no prominent frequency modulation. Our description matches well the previous description by Giaretta and Magrini (2013).

Paratelmatobius poecilogaster.—The advertisement call consists of a single type of pulsed note that can be emitted isolated, in pairs or series. Considering both single notes and note series, the note repetition rate varies from 24 to 207 (81.2 ± 57.4) per minute. The modal note

214 comprises regular-spaced pulses except for (1) the first pulse, which is lower in amplitude and
215 isolated from the subsequent pulse (present in the majority of analyzed notes), and (2) the last
216 pulse, which is also isolated from the preceding pulse—note without isolated pulses in Fig. 2B.
217 Note duration varies from 29 to 77 (58.2 ± 5.9) ms, with rise time ranging from 3 to 86 (35.1 ±
218 5.9) % of note duration. Pulse number varies from 4 to 14 (9.5 ± 1.6), emitted at a rate of 100 to
219 228 (157.7 ± 20.4) per second. The note dominant frequency ranges from 2153 to 2929 (2467.9 ±
220 203.8) Hz (Table 1). There is no prominent frequency modulation. Our description generally
221 agrees with the original description by Giaretta and Castanho (1990).

222 ***Paratelmatobius cardosoi***.—The advertisement call consists of a single type of note that
223 can be emitted isolated or in series. The modal note is characterized by (1) a first portion with
224 lower amplitude, slightly lower frequency, and brief intervals between pulses and/or intervals
225 absent, followed by (2) a portion with higher amplitude, higher frequency, and amplitude
226 modulations with marked silence intervals between pulses (Figs. 2C, 3A). In cases where notes
227 are produced in long series, males can intercalate typical notes with shorter ones, characterized
228 by a reduction or complete absence of the first portion of the note (Fig. 3A). This pattern was
229 observed predominantly during antiphonal calling. Additionally, males can modulate the
230 amplitude of consecutive notes, creating a pattern of alternating lower and higher amplitudes
231 throughout the series. Considering both single notes and note series, the note repetition rate varies
232 from 35 to 81 (58.0 ± 31.9) per minute. Note duration varies from 80 to 177 (115.6 ± 15.1) ms,
233 with rise time ranging from 53 to 92 (71.6 ± 4.6) % of note duration. Pulse number varies from 7
234 to 25 (11.1 ± 1.8), emitted at a rate of 55 to 138 (97.9 ± 19.9) per second. The note dominant
235 frequency ranges from 3015 to 3876 (3205.6 ± 160.9) Hz (Table 1). Frequency modulation is
236 generally absent, except in the cases of notes emitted in antiphony. In those cases, one male emits
237 notes with a slight ascendent frequency modulation and the other emits notes with a slight

descendent frequency modulation. Our description generally agrees with the previous descriptions by Cardoso and Haddad (1990) [described as *P. gaigeae*] and Pombal and Haddad (1999).

Paratelmatobius mantiqueira.—The advertisement call consists of a single type of pulsed note (Fig. 2D) that are generally emitted in series, but the call may sometimes be emitted as isolated notes. Note series are characterized by a first note with lower amplitude, followed by notes that exhibit an increment in amplitude throughout the series. In some cases, isolated pulses appear in between pulsed notes (Fig. 3B). Considering both single notes and note series, the note repetition rate varies from 52 to 492 (340.6 ± 249.7) per minute. Note duration varies from 15 to 57 (30.4 ± 6.3) ms, with rise time ranging from 3 to 95 (38.6 ± 22.3) % of note duration. Pulse number varies from 2 to 13 (5.6 ± 1.7), emitted at a rate of 83 to 306 (161.6 ± 34.7) per second. One of the recorded males (recording FNJV 50514) produced calls with two, nonharmonic, frequency bands (Fig. 2D). The note dominant frequency ranges from 2498 to 3876 (2989.0 ± 520.1) Hz (Table 1). There is no prominent frequency modulation. Our description differs from that of Moroti et al. (2022), who interpreted the advertisement call as a note series. In contrast, we reinterpret the emission patterns and consider that the call consists of a single type of pulsed note, consistent with the calling patterns observed in most congeners.

Paratelmatobius yepiranga.—The advertisement call consists of a single type of pulsed note that is emitted isolated and in antiphonal calling (Fig. 4A). The note repetition rate varies from 15 to 17 (15.8 ± 1.5) per minute. Note duration varies from 489 to 710 (609.7 ± 22.1) ms, with rise time ranging from 4 to 85 (50.9 ± 8.1) % of note duration. Pulse number varies from 15 to 23 (19.1 ± 0.4), emitted at a rate of 24 to 39 (30.1 ± 1.8) per second. The dominant frequency ranges from 2089 to 2606 (2383.3 ± 97.9) Hz (Table 1). There is no prominent frequency modulation. Our description matches well the previous description by Garcia et al. (2009).

262 ***Paratelmatobius segallai***.—The advertisement call is composed of series of notes A and
263 B (Fig. 4C). These notes together can be emitted in different patterns, such as B + A, B + A + B,
264 B + A + A, and B + A + A + B. In long series, many consecutive notes B can be produced at the
265 end of note series. Note A has a higher amplitude and is composed of complete and incomplete
266 pulses. Note B has a lower amplitude and does not have well-marked amplitude modulations.
267 Considering both note types, the note repetition rate varies from 36 to 69 (52.6 ± 23.1) per
268 minute. Note A duration varies from 25 to 60 (45.0 ± 7.7) ms, with rise time ranging from 2 to 65
269 (33.3 ± 1.2) % of note duration. Pulse number varies from 4 to 9 (6.7 ± 1.1), emitted at a rate of
270 123 to 211 (148.3 ± 16.1) per second. Note A dominant frequency ranges from 2627 to 3230
271 (3035.8 ± 200.5) Hz. Note B duration varies from 24 to 54 (42.5 ± 9.1) ms, with rise time ranging
272 from 4 to 62 (38.2 ± 16.7) % per second. Note B dominant frequency ranges from 2326 to 3187
273 (2888.7 ± 354.8) Hz (Table 1). There is no prominent frequency modulation in either note A and
274 B of the call. Our analysis is consistent with the original description of Santos et al. (2019).

275 ***Paratelmatobius* sp**.—The advertisement call consists of a single type of pulsed note that
276 is emitted generally as single notes or sometimes as short note groups (Fig. 4B). The note
277 repetition rate was 10.5 per minute. Note duration varies from 141 to 395 (242.5 ± 53.0) ms, with
278 rise time ranging from 25 to 81 (56.6 ± 13.9) % of note duration. Notes are formed by complete
279 pulses (well-defined silent intervals), except during the attack phase, characterized by irregularly
280 distributed pulses. Pulse number varies from 13 to 25 (18.0 ± 2.7), emitted at a rate of 56 to 96
281 (73.4 ± 10.4) per second. The note dominant frequency ranges from 3639 to 4113 (3767.4 ±
282 128.9) Hz (Table 1). There is no prominent frequency modulation. On four occasions,
283 advertisement calls were followed by the emission of five-pulse notes with lower amplitude (Fig.
284 3C), though their function remains unclear. Note duration varies from 36 to 71 (58.0 ± 3.6) ms,
285 with rise time ranging from 6 to 80 (54.2 ± 5.6) % of note duration. The note dominant frequency

ranges from 2907 to 3639 (3186.9 ± 315.5) Hz. There is no prominent frequency modulation.

Taxonomic Account

By integrating phylogenetic evidence with bioacoustic and morphological data and following the unified species concept (de Queiroz 2007), we recognize *Paratelmatobius* sp. as a new species, which we formally name and describe as follows.

*Paratelmatobius **stellaris*** sp. nov.

(Figs. 5, 6; Table 2)

Holotype.—CFBH 48141 (field number MTTS 635), adult male, collected at Parque Estadual da Serra do Mar (núcleo Padre Dória; Estação Biológica de Boraceia), municipality of Salesópolis, state of São Paulo, southeastern Brazil (-23.654770°, -45.887620°; 868 m above sea level), on 16 December 2021, by M.T.T. Santos, B.S. Carvalho, P.D.P. Pinheiro, and P.P.G. Taucce.

Paratypes.—Five specimens (all from the same locality as the holotype). CFBH 48142 (adult male), collected on 18 December 2021 by M.T.T. Santos and B.S. Carvalho. CFBH 48143 (adult female), collected on 20 January 2022 by R.A. Martins. MZUSP 160821 (adult female), 160822 (juvenile), collected on 15 September 2013 by F. Dal Vechio, R. Recoder, and M. Teixeira Jr. MZUSP 160823 (adult male), collected on 9–13 December 2017 by T. Grant.

Diagnosis.—*Paratelmatobius stellaris* is diagnosable from its congeners by the following combination of characters: (1) advertisement call with note duration of 141–395 ms; (2) note dominant frequency of 3639–4113 Hz; (3) note structure formed by regular-spaced pulses; (4) call with a single type of note; (5) pulse repetition rate of 56–96 per second; (6) tympanic annulus visible through the skin; (7) males with vocal slits; (8) presence of a poorly-developed

mandibular tubercle; (9) nuptial pads in males not divided; (10) adult males with finger I longer than II; (11) in life, belly coloration consisting of a gray or brown background with small white blotches and flecks; (12) foot fringed, not webbed; (13) toe tips not expanded; (14) presence of tubercles on upper eyelid; (15) dorsolateral fold well-developed; (16) in life, external margins of throat lacking orange blotches; (17) adult males SVL 17.4–18.4 mm.

Comparisons.—*Paratelmatobius stellaris* is distinguished from its congeners (characters in parentheses) by having advertisement call with a note duration of 141–395 ms (32–87 ms in *P. gaigeae*; 29–77 ms in *P. poecilogaster*; 15–57 ms in *P. mantiqueira*; and 489–710 ms in *P. yepiranga*; Table 1); a higher dominant frequency, ranging from 3639–4113 Hz (2369–3488 Hz in *P. gaigeae*; 2153–2929 Hz in *P. poecilogaster*; 2627–3230 Hz in *P. segallai*; and 2089–2606 Hz in *P. yepiranga*); a note structure formed essentially by regular-spaced pulses (note structure formed by two distinct portions in *P. cardosoi*); call with a single type of note (two-note call in *P. segallai*); a higher pulse repetition rate, varying from 56–96 per second (24–39 in *P. yepiranga*).

Paratelmatobius stellaris is morphologically distinguished from species of the *P. lutzii* group (*P. lutzii*, *P. gaigeae*, and *P. poecilogaster*) by having tympanic annulus visible through the skin (not visible); presence of vocal slits in males (absence); presence of mandibular tubercle (absence); nuptial pads in males not divided (divided in two portions); adult males with finger I longer than II (finger I shorter than or as long as finger II); belly coloration in life consisting of a gray or brown background with small white blotches and flecks; Fig. 7A (black or reddish background with a few large white blotches in *P. lutzii*, Fig. 7F; reddish background bordered or not by several white blotches in *P. gaigeae*, Fig. 7G; varying from orange background with dark brown or blackish blotches with or without white borders to dark brown or blackish background with large orange blotches with or without white borders or with large whitish blotches in *P. poecilogaster*, Fig. 7H). *Paratelmatobius stellaris* further differs from *P. lutzii* by having a

fringed foot (webbed foot); and smaller males, SVL 17.4–18.4 mm (SVL 19.3–23.5 mm) and from *P. poecilogaster* by having toe tips not expanded (expanded).

Regarding congeners of the *P. cardosoi* group (*P. cardosoi*, *P. mantiqueira*, *P. segallai*, and *P. yepiranga*), *P. stellaris* is distinguished from *P. cardosoi* by the presence of tubercles on the upper eyelid (absence); and a well-developed dorsolateral fold (poorly developed). From *P. mantiqueira* and *P. yepiranga*, the new species can be distinguished by its belly coloration in life consisting of a gray or brown background with small white blotches and flecks (gray or brown background with large orange blotches; Fig. 7B, C). It also differs from *P. mantiqueira* by having larger males, SVL 17.4–18.4 mm (SVL 14.4–16.8 mm) and from *P. yepiranga* by having a poorly developed mandibular tubercle; Fig. 8A (well-developed; Fig. 8B); absence of orange blotches on external margins of throat in life; Fig. 7A (presence; Fig. 7B); and smaller males, SVL 17.4–18.4 mm (SVL 20.7–22.1 mm). Apart from the advertisement calls (see above) and phylogenetic position (Fig. 1), no other characters allow us to distinguish *P. stellaris* from *P. segallai*.

Description of holotype.—Adult male, SVL 17.6 mm; body robust; head slightly wider than long (HW/HL 1.02); head width 0.40 SVL; head length 0.39 SVL; snout not flattened, rounded in dorsal and lateral views; END shorter than ED (END/ED 0.83); canthus rostralis slightly curved in dorsal view and rounded in cross-section; loreal region slightly concave; nostrils slightly protuberant, elliptical, dorsolaterally directed; interorbital area flat, more than twice as long as ED (AMD/ED 2.38). Eyes large and protuberant (ED/HL 0.27; ED/HW 0.26), laterally oriented; upper eyelid margin with small, scattered tubercles and a prominent tubercle in its medial region. Tympanic membrane undifferentiated; tympanic annulus medium-sized (TD/ED 0.69), visible through the skin; supratympanic fold poorly developed, from posterior edge of eye curving downward to arm insertion. Poorly-developed mandibular tubercle present

on the posterior edge of the lower jaw. Dorsolateral fold well-developed, extending from the posterior corner of the eye to the inguinal region.

Choanae small, oval, spaced 1.9 mm from each other. Vomerine odontophores present, positioned posterior to the level of the choanae. Tongue ovoid, not notched, free behind for about one-third of its length. Vocal slits short, located at the level of the posterior third of the tongue; vocal sac externally indistinct. Single, small tooth-like process present anteriorly on the lower jaw, fitting to a socket between premaxillae.

Forelimb robust, hypertrophied, lacking fold or fringe, poorly-developed tubercle present on the anterior surface of arm; forearm slightly more robust than arm (FAW/AW 1.08); fingers short, robust, with rounded tips; relative length of fingers II < I < IV < III; Finger I broadly widened, bearing a nuptial pad formed by numerous dark colored spicule-shaped papillae covering dorsomedially the skin of Metacarpus I and prepollex; subarticular tubercles large, flat, oval in ventral view on Finger I, and round in ventral view on Fingers II–IV; supernumerary tubercles absent; inner metacarpal tubercle flat, elliptical; outer metacarpal tubercle large, flat, and nearly round in ventral view.

Hindlimb medium-sized and moderately robust (THL/SVL 0.47; TBL/SVL 0.44), bearing two transverse irregular dermal crests on dorsal surfaces of thigh and tibia; tarsal fold absent; toes medium-sized, robust, with narrow and rounded tips; relative length of toes I < II < V < III < IV; toes not webbed, bearing flexible lateral fringes, except in medial margin of Toe I; fringes joined between Toes II and III, III and IV, and IV and V; subarticular tubercles flat, oval in ventral view on toe I, and rounded in ventral view on Toes II–V; supernumerary tubercles absent; inner metatarsal tubercle large, flat, and elliptical in ventral view; outer metatarsal tubercle small, nearly rounded in ventral view, conical in profile.

Skin shagreen except on the belly (smooth) and posterior surface of the thigh around the

cloaca (coarsely granular). Cloacal opening directed posteriorly at the upper level of thighs, covered above by a poorly developed cloacal flap.

Measurements of holotype (in mm).—SVL 17.6; HL 6.9; HW 7.0; ED 1.9; TD 1.3; END 1.5; NSD 1.2; IND 2.0; AMD 4.4; AL 4.7; AW 2.0; FAL 4.2; FAW 2.1; HAL 3.9; THL 8.3; TBL 7.7; TAL 4.4; FL 8.0.

Coloration.—In life, dorsum brown with scattered whitish and greenish flecks (Fig. 5A). Dorsal surface between the orbits dark brown. A dark brown, somewhat triangular blotch is present in the scapular region. A cream middorsal stripe extends from the medial third of the body to the cloacal region, which is fragmented anteriorly and continuous posteriorly. Loreal region light brown. A small dark brown blotch in the inguinal region. A fragmented whitish line from behind the eye to the inguinal region, delimiting dorsally the dorsolateral fold. Flank with a dark-brown band dorsally delimited by the dorsolateral fold, expanded after arm insertion. Ventral to the dark-brown band the flank is brown with several whitish flecks. Tubercles on eyelids, posterior third of mandible, and proximal third of arm whitish. Limbs brown dorsally with scattered whitish tubercles and flecks. A dark brown bar in the wrist. Spicules on nuptial pad black. Dermal crests on thighs and tibia cream. Toes light brown. Heel and anterior surface of the thigh dark brown. Outer surface of tibia with dark brown transverse bars. A thin dark-brown band extends from the cloacal region to the posterior surfaces of thighs. Ventral surfaces of fingers and toes light brown. Ventral surfaces of the throat, chest, belly, hindlimbs, and distal third of forearms varying from dark grey to dark brown with scattered small whitish blotches and flecks, more numerous on belly and thigh. Ventral surfaces of arms and the proximal half of forearms orange (Fig. 5B). Iris copper-colored with dark brown reticulations and a thin vertical stripe.

In preservative, the colors fade, turning into pale tones. Dorsal blotches become less distinct. The cream colors of the middorsal stripe and dermal crests of the thighs and tibia

become whitish. The orange colors of the ventral surfaces of the forelimbs become cream (Fig. 6).

Variation.—Snout in lateral view varies from rounded (CFBH 48141, MZUSP 160821–23) to slightly sloping (CFBH 48142–43). The shape of the Finger I tip can be rounded (CFBH 48141, MZUSP 160823), slightly pointed (CFBH 48142, 48143, MZUSP 160821), or pointed (MZUSP 160822). The blotch in the scapular region varies in shape and is somewhat rounded in the specimens MZUSP 160821–23. In two specimens (CFBH 48143 and MZUSP 160823), the middorsal stripe is smaller and covers just the posterior third of the body. The number and size of blotches on the belly show some variation. The specimens CFBH 48143 and MZUSP 160821–23 have larger blotches and a few flecks, whereas the specimens CFBH 48141–42 exhibit smaller blotches and numerous flecks. One specimen (MZUSP 160822; juvenile) has a dark brown labial bar as well as a cream coloration on the external margins of the throat.

Males can be distinguished from females by the presence of vocal slits, nuptial pads, and hypertrophy of forelimbs (males AW/AL 0.41–0.47; females AW/AL 0.30–0.33; and males FAW/FAL 0.43–0.50; females FAW/FAL 0.31–0.34). Additionally, males possess wider thumbs and are slightly smaller than females (males SVL 17.4–18.4; females SVL 18.5–19.1).

Etymology.—The specific epithet *stellaris* is derived from Latin and means “of or pertaining to a star; stellar, starry”. This name refers to the ventral coloration pattern of the new species in life, which resembles a starry sky (Fig. 5B). The name is an adjective in the nominative singular.

Distribution.—*Paratelmatobius stellaris* is known only from its type locality at Parque Estadual da Serra do Mar, Núcleo Padre Dória, Estação Biológica de Boraceia (-23.65477°, -45.88762°W; 868 m above sea level), municipality of Salesópolis in the state of São Paulo (Fig. 9).

Natural history.—*Paratelmatobius stellaris* occurs in a montane dense ombrophilous forest within one of the ten administrative centers of Parque Estadual da Serra do Mar, the largest continuous section of Atlantic Forest in Brazil (Secretaria de Meio Ambiente, Infraestrutura e Logística 2024). The type locality is considered one of the wettest areas in southeastern Brazil, with an average annual rainfall exceeding 3,300 mm (Departamento de Águas e Energia Elétrica 2024). In December 2021, we visited the area during periods of intense rainfall (the rain paused only briefly throughout our fieldwork). We explored several locations around the lodging of Estação Biológica de Boraceia but found two male specimens of *P. stellaris* at a single site. Both male individuals were vocalizing in the leaf litter and were not inside or on the edges of any streams or temporary ponds (though ponds likely formed as the rain persisted). Notably, one of the specimens (CFBH 48141; holotype) vocalized inside the collection bag for several moments.

Another species of *Paratelmatobius*, *P. cardosoi*, was sympatric with *P. stellaris* at the type locality. *Paratelmatobius cardosoi* was observed at higher abundance, with males actively calling in temporary ponds less than 100 meters from where the males of *P. stellaris* were vocalizing. A third species, *P. poecilogaster*, is also found within the reserve but occupies a different type of microenvironment, specifically small puddles in the beds of streams (Pombal and Haddad 1999). This species was not encountered during our fieldwork.

Conservation.—*Paratelmatobius stellaris* is known to occur only at Parque Estadual da Serra do Mar, Núcleo Padre Dória, a strictly protected area (International Union for Conservation of Nature [IUCN] Category II; Dudley 2008) of 26,154.02 ha. During our fieldwork we heard vocalizations from only two individuals, both of which were collected. Additionally, only three other specimens have been deposited in zoological collections (CFBH, MZUSP), despite the type locality being a well-sampled area for anurans (Heyer et al. 1990). In contrast, we recorded numerous individuals of *P. cardosoi* across various locations, and the species is well-represented

in zoological collections. Therefore, *P. stellaris* appears to be a rare species. Alternatively, other possibilities include: (1) we may have sampled isolated individuals and failed to locate the preferred species' reproductive microhabitat, or (2) the species exhibits explosive breeding, and neither our fieldwork nor historical surveys coincided with its peak reproductive period. Despite the species being found in a strictly protected area, the available information on its geographic distribution, ecological requirements, and potential threats is insufficient to assign it to a specific threat category. Therefore, *P. stellaris* may appropriately fall under the Data Deficient category given the current knowledge gaps.

Remarks.—There are other characters that are useful to distinguish *P. stellaris* from congeners but exhibit a degree of variation and overlap. Males of *P. stellaris* (SVL 17.4–18.4 mm; Table 2) are generally smaller than males of *P. poecilogaster* (18.4–26.0; Pombal and Haddad 1999; Appendix I). The belly coloration in life, with small white blotches and flecks in *P. stellaris* (Fig. 7A), tends to distinguish it from *P. cardosoi* and *P. segallai*, which generally exhibit orange blotches (Figs. 7D-1–3 and 7E-1–3, respectively). However, these species may also have white blotches and flecks (Figs. 7D-4 and 7E-4), a pattern similar to that of *P. stellaris*.

DISCUSSION

The phylogenetic topologies are consistent with those of Santos et al. (2020), which used a similar data matrix and analytic parameters. The analyses strongly support *P. stellaris* as the sister species to *P. yepiranga* and as part of the *P. cardosoi* group (Fig. 1). The uncorrected *p*-distances for the 16S mitochondrial fragment between *P. stellaris* and *P. yepiranga* (5.5%) fall within the range observed among other species of *Paratelmatobius* within the same morphological species group (e.g., *P. cardosoi* and *P. segallai*, 4.8–7.0%; *P. gaigeae* and *P. poecilogaster*, 4.5–5.7%). Although *P. stellaris* is morphologically cryptic with respect to *P.*

segallai, they are highly distinct genetically (*p*-distance: 6.8–7.7%; Appendix II), and acoustically (Table 1). Moreover, based on current knowledge, their geographic ranges do not overlap (Fig. 9), which may assist in species identification when calls are unavailable.

Some morphological traits historically used to distinguish between species and the groups *P. cardosoi* and *P. lutzii* show variation and should be interpreted cautiously. The medial margin of the first toe was traditionally described as fringed or webbed in species of the *P. lutzii* group (fringed in *P. gaigeae* and *P. poecilogaster*; webbed in *P. lutzii*) and as unfringed in species of the *P. cardosoi* group (*P. cardosoi*, *P. segallai*, *P. mantiqueira*, and *P. yepiranga*; e.g., Pombal and Haddad 1999; Garcia et al. 2009; Santos et al. 2019). However, our examination of specimens (Appendix I) indicates that while *P. gaigeae* and *P. poecilogaster* generally have more developed fringes compared to species of the *P. cardosoi* group, fringes in medial margin of Toe I can be absent or present in the latter group. When present, they vary from narrow to well-developed. The relative lengths of fingers I and II is also historically used as a diagnostic trait for distinguishing between species groups, with species of the *P. cardosoi* group having first finger longer than second, while first finger is reported to be as long as or shorter than second in species of the *P. lutzii* group. However, our review (Appendix I) indicates that this diagnosis is only valid for male specimens.

The shape of finger III was previously used to distinguish *P. cardosoi*, *P. yepiranga*, and *P. segallai*—characterized by a pointed tip—from congeners with a rounded tip (Pombal and Haddad 1999; Garcia et al. 2009; Santos et al. 2019). In *P. stellaris*, the shape varies from rounded to slightly pointed or pointed, rendering this character unreliable for distinguishing it from congeners. Furthermore, our examination of specimens (Appendix I) shows that although finger III is typically pointed in *P. cardosoi* and *P. segallai*, it can be rounded in a small number of specimens across different lineages of both species, further limiting its diagnostic value.

Finally, the absence of spicules on nuptial pads is usually used to distinguish *P. lutzii* from congeners (e.g., Pombal and Haddad 1999; Garcia et al. 2009; Santos et al. 2019), but during our analyses (Appendix II) we observed one specimen of *P. lutzii* with spicules (MZUSP 137902).

Our analyses indicate that the emission patterns of advertisement calls in *Paratelmatobius* are much more variable than previously reported. Behavioral and social contexts of vocal signaling, such as whether males are calling isolated or engaging in antiphonal calling, influence the predominance of single notes versus note series (e.g., Cardoso and Haddad 1990; Giaretta and Castanho 1990; Moroti et al. 2022). Even so, certain species appear more capable of sustaining very high repetition rates, exceeding 490 notes per minute (e.g., *P. mantiqueira*; Table 1), whereas *P. stellaris* and *P. yepiranga* seem unable to maintain such high calling rhythms (<20 notes per minute), even during antiphonal interactions observed in *P. yepiranga* (Table 1). These differences in signaling strategies prevent us from distinguishing species based on note repetition rates. Notably, *P. stellaris* exhibits the lowest note repetition rate (10.5 per minute) based on an isolated calling male; however, antiphonal calling has not yet been documented for this species.

The vocal repertoire of different genera of Paratelmatobiinae has been described over the past years (e.g., Juncá and Lugli 2009; Giaretta and Magrini 2013; Santos et al. 2021; Moser and Lingnau 2021). However, a relevant portion of the call variation observed in *Paratelmatobius* remains undescribed and unassigned to specific communication roles. Two phenomena can be observed concomitantly: (1) abrupt changes in call structure, with different note types produced in combination, and (2) continuous variation in note duration, pulse repetition rate, and sound amplitude. The latter, although more subtle, suggests that minor changes in vocal signals may mediate reproductive and/or aggressive intraspecific interactions. Patterns of acoustic variation in *Paratelmatobius* remain understudied, providing an open venue for future research on the vocal communication system of these elusive leaf-litter frogs.

Although some species of *Paratelmatobius* have a typical structure in their advertisement calls, the temporal and spectral variation is often high enough to cause overlap in call traits among species. Closely related species tend to have more similar calls, such as the cases of *P. gaigeae* and *P. poecilogaster*, and *P. stellaris* and *P. yepiranga*. The call of *P. mantiqueira* stands out for its short duration and high repetition rate, whereas *P. gaigeae* and *P. poecilogaster* produce calls of short duration but at much lower repetition rates. The call of *P. segallai* is unique by being formed by two different note types, namely note A and note B. By contrast, the calls of *P. stellaris* and *P. yepiranga* have the longest durations, the greatest pulse numbers, and the lowest pulse repetition rates within the genus, but differ from each other by remarkable differences in note duration, dominant frequency, and pulse repetition rate. Meanwhile, the call of *P. cardosoi* exhibits high levels of variation, which overlap in most traits with those of congeners, but its note structure is generally formed by two portions with different sound amplitudes and amplitude modulation patterns.

In a previous study, the analysis of museum voucher specimens of *Paratelmatobius* from Boraceia revealed two individuals with distinct morphological traits compared to the abundant *P. cardosoi*. These specimens exhibited a general similarity to *P. segallai*, which is distributed further south in the states of São Paulo and Paraná, and to *P. yepiranga*, known only from a single locality relatively close to Boraceia (Fig. 9). Genetic sequencing and phylogenetic analyses confirmed that these two individuals did not cluster with *P. cardosoi* from the same locality and exhibited high genetic divergence from both *P. segallai* and *P. yepiranga* (Santos et al. 2020). This preliminary evidence prompted a targeted field expedition, resulting in the collection of additional specimens and the recording of its advertisement call, which ultimately confirmed the lineage as a new species. Consequently, the prior availability of specimens and tissue samples in zoological collections was a key factor in the successful description of *P. stellaris*. This case

highlights the critical importance of sustained funding for taxonomic research and the maintenance of natural history museum collections, especially in a period marked by widespread resource shortages (Britz et al. 2020; Engel et al. 2021; Löbl et al. 2023).

Acknowledgments.—We are indebted to P.D.P. Pinheiro, P.P.G. Taucce, and R.A. Martins for their assistance with fieldwork. R.S. Recoder provided important information about specimens collected in 2013. We thank A. Benetti, T. Grant and H. Zaher (MZUSP) for a loan of specimens. We thank the manager A.M. Vasques and the staff of Estação Biológica de Boraceia as well as the manager A.L.A.M. Wuo and the staff of Parque Estadual da Serra do Mar Núcleo Padre Dória for logistical support. Field collection permits provided by Instituto Chico Mendes de Conservação da Biodiversidade (ICMBio-SISBIO #59179-4) and the Comissão Técnico-Científica do Instituto Florestal (COTEC-SP #260108-007.622/2017). Financial support was received from Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq PROTAX #441497/2020-9) and Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG #APQ-03369-21). This research benefited from resources of the Centro de Estudos de Insetos Sociais (CEIS) of the Universidade Estadual Paulista (UNESP), Rio Claro, São Paulo. São Paulo Research Foundation (FAPESP #2021/06575-1, #2024/03528-0) and CNPq (PROTAX #151193/2021-5) provided postdoctoral fellowships to MTTS. CAPES provided a Master's fellowship for L. Vilela (88887.838734/2023-00). CNPq provided a Master's fellowship to B.S. Carvalho (PROTAX #130863/2021-1), and an undergraduate research scholarship to I.E.C. Silva (PROTAX # 120040/2021-2, #117541/2022-2). MTR thanks CNPq (#302864/2020-2) and FAPESP (#2011/50146-6) for funding, and students of his lab for help in the field. PCAG thanks CNPq (PROTAX #441497/2020-9 and research fellowship #310301/2018-1). CFBH thanks CNPq for a research fellowship (#304713/2023-6) and FAPESP (#2021/10639-5) for financial

574 support.

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Published on XX Month 20XX

APPENDIX I

Additional specimens examined (all from Brazil)

Paratelmatobius cardosoi.—SÃO PAULO: municipality of Bertioga, Parque das Neblinas (CFBH 38980, 38982, 38989–38990, UFMG-AMP 3237); municipality of Itanhaém, Parque Estadual da Serra do Mar, Núcleo Curucutu (CFBH 16770, 16780, 22130, 27718); municipality of Santo André, Paranapiacaba (CFBH 862–865, MZUSP 65374–65375 [paratypes], CFBH 37757 [topotype]).

Paratelmatobius gaigeae.—SÃO PAULO: municipality of Bananal, Estação Ecológica do Bananal (CFBH 7156); municipality of São José do Barreiro, Parque Nacional da Serra da Bocaina (CFBH 36069–36070, 36079, 48465–48466, 48469, UFMG-AMP 15004–15008 [topotypes]).

Paratelmatobius lutzii.—MINAS GERAIS: municipality of Itamonte, Parque Nacional de Itatiaia (CFBH 295, MZUSP 52878–52880, 94621, 137901–137903 [topotypes]).

Paratelmatobius mantiqueira.—MINAS GERAIS: municipality of Sapucaí-Mirim (MZUSP 15133 [holotype], 15128–15132, 15134–15142 [paratypes]).

Paratelmatobius poecilogaster.—SÃO PAULO: municipality of Bertioga, Parque das Neblinas (CFBH 48467, 48470, UFMG-AMP 3238–3240, 20711, 21316–21317, 21319–21321); municipality of Cunha, Parque Estadual da Serra do Mar, Núcleo Cunha (CFBH 23892); municipality of Santo André, Paranapiacaba (MZUSP 65372 [holotype], CFBH 6266, MZUSP 65373 [paratypes], CFBH 866, 3251–3253, 12004, 12005, 28959, 28960, 28983 [topotypes]); municipality of São Luiz do Paraitinga, Parque Estadual da Serra do Mar, Núcleo Santa Virgínia (CFBH 7730–7733, 7935–7939, 9594–9595, 9878, 9880–9883).

Paratelmatobius segallai.—PARANÁ: municipality of Piraquara, Parque Estadual Pico do Marumbi, Mananciais da Serra (CFBH 43545 [holotype], CFBH 43546–43557 [paratypes]). SÃO

PAULO: municipality of Piedade (MZUSP 136422–136425); municipality of Pilar do Sul (CFBH 8366–8367, 8370); municipality of São Miguel Arcanjo (CFBH 36009, 36011, 40681, 48462–48463); municipality of Tapiraí (CFBH 16535–16537).

Paratelmatobius yepiranga.—SÃO PAULO: municipality of Bertioga, Parque das Neblinas (MZUSP 137563 [holotype], 136696–136698 [paratypes]).

790 APPENDIX II

791 Uncorrected *p*-distances (percentage) of mitochondrial 16S rRNA fragment (ca. 570 bp)
792 within (diagonals) and among species of *Paratelmatobius*. Data are shown as range (mean) when
793 appropriate.

Species	*P. stellaris*	*P. yepiranga*	*P. cardosoi*	*P. segallai*	*P. gaigeae*	*P. poecilogaster*
P. stellaris	0.0 (n = 6)					
P. yepiranga	5.5	0.0 (n = 2)				
P. cardosoi	7.3–8.6 (8.0)	7.3–8.8 (8.0)	0.0–2.2 (1.7, n = 8)			
P. segallai	6.8–7.7 (7.4)	5.7–7.7 (6.9)	4.8–7.0 (5.8)	0.0–5.3 (2.9, n = 8)		
P. gaigeae	9.6–10.0 (9.8)	9.5–9.9 (9.7)	8.6–9.3 (9.0)	8.6–10.2 (9.5)	1.1 (n = 2)	
P. poecilogaster	8.9–9.8 (9.3)	9.1–10.2 (9.8)	7.7–9.4 (8.7)	8.1–10.3 (9.3)	4.5–5.7 (4.9)	0.2–3.2 (1.7, n = 8)

794 TABLE 1.—Summary of advertisement call traits of species of *Paratelmatobius*. Data are presented as mean ± standard deviation
795 (minimum–maximum). Sample sizes are number of recorded males / analyzed calls.

Species	Pulse number	Note rise time (%)	Note duration (ms)	Note repetition rate (per min)	Pulse repetition rate (per s)	Dominant Frequency (Hz)
P. cardosoi (2/97)	11.1 ± 1.8 (7–25)	71.6 ± 4.6 (53–92)	115.6 ± 15.1 (80–177)	58.0 ± 31.9 (35–81)	97.9 ± 19.9 (55–138)	3205.6 ± 160.9 (3015–3876)
P. gaigeae (12/169)	7.7 ± 1.1 (3–14)	42.5 ± 7.4 (18–74)	52.9 ± 4.8 (32–87)	77.3 ± 51.3 (18–190)	138.3 ± 13.2 (70–256)	2835.4 ± 255.5 (2369–3488)
P. mantiqueira (3/43)	5.6 ± 1.7 (2–13)	38.6 ± 22.3 (3–95)	30.4 ± 6.3 (15–57)	340.6 ± 249.7 (52–492)	161.6 ± 34.7 (83–306)	2989.0 ± 520.1 (2498–3876)
P. poecilogaster (9/135)	9.5 ± 1.6 (4–14)	35.1 ± 5.9 (3–86)	58.2 ± 5.9 (29–77)	81.2 ± 57.4 (24–207)	157.7 ± 20.4 (100–228)	2467.9 ± 203.8 (2153–2929)
P. segallai note A (2/48)	6.7 ± 1.1 (4–9)	33.3 ± 1.2 (2–65)	45.0 ± 7.7 (25–60)	52.6 ± 23.1 (36–69)	148.3 ± 16.1 (123–211)	3035.8 ± 200.5 (2627–3230)
P. segallai note B	—	38.2 ± 16.7	42.5 ± 9.1		—	2888.7 ± 354.8

(2/30)		(4–62)	(24–54)			(2326–3187)
P. stellaris sp. nov.	18.0 ± 2.7	56.6 ± 13.9	242.5 ± 53.0	10.5	73.4 ± 10.4	3767.4 ± 128.9
(1/50)	(13–25)	(25–81)	(141–395)		(56–96)	(3639–4113)
P. yepiranga (3/41)	19.1 ± 0.4	50.9 ± 8.1	609.7 ± 22.1	15.8 ± 1.5	30.1 ± 1.8	2383.3 ± 97.9
	(15–23)	(4–85)	(489–710)	(15–17)	(24–39)	(2089–2606)

807 TABLE 2.—Measurements and proportions for the adult specimens of the type series of *Paratelmatobius stellaris*. Values (mm) are
808 reported as ranges (mean ± SD) where appropriate. See text for measurement abbreviations.

Measurement			Body ratios		
	Males (n = 3)	Females (n = 2)		Males (n = 3)	Females (n = 2)
SVL	17.4–18.4 (17.8 ± 0.5)	18.5–19.1	HW / HL	1.01–1.02	1.01–1.02
HL	6.6–7.1 (6.9 ± 0.3)	7.2–7.5	HL / SVL	0.38–0.39	0.39
HW	6.6–7.2 (6.9 ± 0.3)	7.4–7.6	HW / SVL	0.38–0.40	0.40
ED	1.7–2.0 (1.8 ± 0.1)	1.9–2.0	END / ED	0.76–0.83	0.76–0.77
END	1.4–1.5 (1.5 ± 0.1)	1.4–1.5	AMD / ED	2.22–2.44	2.29–2.33
NSD	1.2–1.2 (1.2 ± 0.0)	1.2	AMD /HL	0.61–0.64	0.59–0.61
IND	1.9–2.1 (2.0 ± 0.1)	2.3	AMD / HW	0.60–0.63	0.58–0.60
AMD	4.2–4.4 (4.3 ± 0.1)	4.2–4.6	ED / HL	0.26–0.27	0.26
TD	1.2–1.3 (1.3 ± 0.0)	1.2–1.4	ED / HW	0.26–0.27	0.25–0.26

AL	4.7–4.9 (4.8 ± 0.1)	4.7–4.9	TD / ED	0.68–0.73	0.65–0.74
AW	1.9–2.3 (2.0 ± 0.2)	1.4–1.6	TD / HL	0.19	0.17–0.19
FAL	4.2–4.4 (4.3 ± 0.1)	4.4–4.5	AW / AL	0.41–0.47	0.30–0.33
FAW	1.8–2.1 (2.0 ± 0.2)	1.4–1.5	FAW / FAL	0.43–0.50	0.31–0.34
HAL	3.8–3.9 (3.9 ± 0.1)	4.1	FAW / AW	0.90–1.08	0.94–0.96
THL	8.1–8.4 (8.3 ± 0.1)	8.3–8.4	AL / SVL	0.26–0.27	0.25–0.26
TBL	7.6–8.0 (7.8 ± 0.2)	7.9	FAL / SVL	0.24	0.24
TAL	4.3–4.6 (4.5 ± 0.2)	4.4–4.6	HAL / SVL	0.21–0.22	0.22
FL	8.0–8.0 (8.0 ± 0.0)	7.9–8.1	THL / SVL	0.45–0.47	0.44–0.45
			TBL / SVL	0.43–0.44	0.41–0.43
			TAL / SVL	0.25	0.24
			FL / SVL	0.44–0.46	0.42–0.43

Figure captions:

FIG. 1.—The 50% majority-rule consensus tree from Bayesian phylogenetic inference, showing the relationships of the new species of *Paratelmatobius*. Newly collected specimens are highlighted in gray. The analysis was based on a dataset comprising three mitochondrial (heavy strand transcription unit 1, including 12S and 16S rRNA along with the intervening $tRNA^{valine}$; cytochrome c oxidase subunit I; and cytochrome b) and five nuclear (proopiomelanocortin A; recombination-activating protein 1; rhodopsin; tensin 3; and tyrosinase) gene fragments. Numbers at the nodes represent posterior probabilities / bootstrap support values, with asterisks (*) denoting 1.0 posterior probability / 100% bootstrap support. The small dashed rectangle highlights the two nodes not recovered in the maximum likelihood analysis. The corresponding topology and support values for these nodes from the maximum likelihood analysis are shown within the large dashed rectangle.

FIG. 2.—Advertisement calls of (A) *Paratelmatobius gaigeae* (isolated pulse at the beginning of the note), (B) *P. poecilogaster* (isolated pulses absent), (C) *P. cardosoi*, and (D) *P. mantiqueira*. Sound recordings: (A) CBUFMG 1129, (B) CBUFMG 1133, (C) CBUFMG 1143, (D) FNJV 50514.

FIG. 3.—Additional note types in the vocal repertoires of (A) *Paratelmatobius cardosoi* (typical note followed by a short note), (B) *P. mantiqueira* (first note with lower amplitude, followed by typical notes, including an isolated pulse), (C) *P. stellaris* sp. nov. (typical note followed by a short note). Sound recordings: (A) CBUFMG 1142, (B) FNJV 50521, and (C)

CBUFMG 1148.

FIG. 4.—Advertisement calls of (A) *Paratelmatobius yepiranga*, (B) *P. stellaris* sp. nov., and (C) *P. segallai* (note B followed by note A). Sound recordings: (A) CBUFMG 1146, (B) CFUFMG 1149, and (C) CBUFMG 1144.

FIG. 5.—*Paratelmatobius stellaris*, holotype in life (CFBH 48141, male, SVL 17.6 mm) in dorsal (A) and ventral (B) views.

FIG. 6.—*Paratelmatobius stellaris*, holotype in preservative (CFBH 48141). (A) Dorsal view, (B) ventral view; scale bar = 5 mm. (C) Head in dorsal view and (D) in lateral view, (E) right hand and (F) right foot in ventral view; scale bars = 1 mm.

FIG. 7.—Ventral coloration patterns of *Paratelmatobius stellaris* and congeners. (A) *P. stellaris* CFBH 48142; (B) *P. yepiranga* MZUSP 137563; (C) *P. mantiqueira* unvouchered; (D) *P. cardosoi* CFBH 48461 (1), UFMG-AMP 20710 (2), UFMG-AMP 21326 (3), UFMG-AMP 21325 (4); (E) *P. segallai* UFMG-AMP 20773 (1), CFBH 48464 (2), CFBH 48462 (3), CFBH 48463 (4); (F) *P. lutzii* unvouchered; (G) *P. gaigeae* CFBH 48466 (1), CFBH 48465 (2), unvouchered (3); (H) *P. poecilogaster* CFBH 48467 (1), UFMG-AMP 21316 (2), CFBH 44868 (3), CFBH 48468 (4). Note the similarity between *P. stellaris* (A) and one of the patterns

858 recorded for *P. cardosoi* (D4) and *P. segallai* (E4). Photos credits: (B) M. Segalla, (C) E. Muscat,
859 (F) I. Sazima, and (G3) E. Domenico.
860
861
862 FIG. 8.—One of the diagnostic characters of *Paratelmatobius stellaris* in comparison with
863 its sister species *P. yepiranga*. Head in ventrolateral view of (A) *P. stellaris* (MZUSP 160821),
864 showing a poorly-developed mandibular tubercle (arrow head) and of (B) *P. yepiranga* (MZUSP
865 136698) showing a well-developed mandibular tubercle (arrow head). Scale bar = 1mm.
866
867
868 FIG. 9.—Geographic distribution of *Paratelmatobius stellaris* and its congeners in
869 southeastern and southern Brazil. Occurrence records for congeneric species were obtained from
870 Santos et al. (2019, 2020); Rotenberg et al. (2020); Vrcibradic et al. (2010); Pombal and Haddad
871 (1999); Garcia et al. (2009); Zaher et al. (2005); and amphibian collections (CFBH, MNRJ, and
872 MZUSP). For *Paratelmatobius poecilogaster*, we added two records from iNaturalist
873 (observations #91110048 and #91110681) after verifying identification through specimens
874 photographs and confirming the geographic coordinates with the author. Abbreviations for
875 Brazilian states: MG (Minas Gerais), PR (Paraná), RJ (Rio de Janeiro), SC (Santa Catarina), SP
876 (São Paulo).