European Journal of Taxonomy 1034: 31–57
https://doi.org/10.5852/ejt.2026.1034.3147

europeanjournaloftaxonomy.eu
ISSN 2118-9773
2026 · Ythier E. *et al.*

Received: 30 April 2024 • *Accepted: 18 November 2025* • *Published: 12 January 2026*

Topic editor: Magalie Castelin • *Section editor: Abel Pérez-González* • *Desk editor: Lizeth Alonso*

Research article

urn:lsid:zoobank.org:pub:EB344B7F-6B9B-4CEC-B48F-B0A71C43096F

A phylogenomic analysis of the genus *Auyantepuia* (Scorpiones: Chactidae) in French Guiana with the descriptions of two new species

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Abstract. A review of the scorpions of the genus *Auyantepuia* (Scorpiones, Chactidae) in French Guiana is conducted using an integrative taxonomic approach combining molecular analysis performed on the mitochondrial genome of most species occurring in the territory and more traditional morphological analyses, leading to the descriptions of two new species, *Auyantepuia kwata* sp. nov. and *Auyantepuia manmandinan* sp. nov. Diagnoses are presented for all *Auyantepuia* species occurring in French Guiana and an identification key is proposed. The total number of recognized species in the genus *Auyantepuia* species is raised to 15.

Keywords. Scorpion, integrative taxonomy, molecular, morphology, mitochondrial genome.

Ythier E., Chevalier J., Moreau L. & Murienne J. 2026. A phylogenomic analysis of the genus *Auyantepuia* (Scorpiones: Chactidae) in French Guiana with the descriptions of two new species. *European Journal of Taxonomy* 1034: 31–57. https://doi.org/10.5852/ejt.2026.1034.3147

Introduction

French Guiana, an overseas French territory spanning approximately 84 000 km² in South America, resides at the eastern fringe of the Guiana Shield, a mountainous expanse spanning Colombia, Venezuela, Guyana, Suriname, French Guiana, and Brazil. Encompassed predominantly by equatorial rainforest, its population is chiefly concentrated along the coastal regions. Over recent decades, extensive research has meticulously unraveled the biodiversity in French Guiana. Of notable recognition is its standing

as a biodiversity hub, particularly renowned for its remarkable richness and unique endemism among scorpions (Lourenço 2018).

The initial synthesis (Lourenco 1983) catalogued 18 species across eight genera and three families. Subsequent work (Ythier 2018b) provided a comprehensive overview, identifying 30 species spanning 12 genera and three families. Ongoing scrutiny has continued to reveal new dimensions of the scorpion fauna in French Guiana, with numerous new species reported since then (Lourenço 2018, 2021; Ythier & Chevalier 2020; Ythier *et al.* 2020; Lourenço & Chevalier 2022; Lourenço *et al.* 2022). These recent endeavors have expanded the known count to 40 species, a substantial 31 of which are possibly endemic to this territory.

The genus *Auyantepuia* González-Sponga, 1978 stands out as one of the most diverse genera within French Guiana, encompassing seven species. Beyond French Guiana, it extends its presence with one species documented in Venezuela (Bolivar), another in Suriname (Marowijne), and four in Brazil (Amapá, Amazonas, Pará). Recent explorations have unveiled promising discoveries, suggesting the existence of several potential new species within this genus. However, the taxonomic classification of this genus relies heavily on subtle morphological distinctions, often discerned from a limited number of specimens. This poses a significant challenge to affirming the validity of the current taxonomy and underscores the need for a more comprehensive evaluation of existing species.

Our primary objective is to conduct an extensive molecular analysis of the diverse *Auyantepuia* species inhabiting French Guiana. We employed a genome skimming methodology, proven to be highly efficient in sequencing complete mitochondrial genomes across various taxa. Mitochondrial genomes, often referred to as 'superbarcodes', circumvent limitations associated with singular short markers and can be efficiently used for species delimitation, phylogeographic of phylogenetic studies (Moreno-Carmona *et al.* 2023; Graham *et al.* 2024; Xu *et al.* 2025). In tandem with traditional morphological analyses, our study pursues three key objectives: (i) assessing the extent of genetic divergence among existing species, (ii) offering vital insights supportive of delineating new species, (iii) establishing a robust phylogenetic framework for genus-level investigations. Employing an integrative taxonomic approach, we lay the groundwork for describing two new species, employing this synthesized data as a cornerstone.

The two new species, *Auyantepuia kwata* sp. nov. and *Auyantepuia manmandinan* sp. nov., are morphologically described and extended diagnoses are presented for all other *Auyantepuia* species occurring in French Guiana. Distribution records are provided and an identification key to the nine *Auyantepuia* species reported from French Guiana is proposed. The total number of recognized species in the genus *Auyantepuia* species is raised to 15.

Material and methods

Molecular analysis

Taxon sampling

We included five out of the seven *Auyantepuia* species present in French Guiana as well as representatives of two potential new species. To test the validity of each species, we included as far as possible multiple specimens from the same species collected from various localities (four for *A. fravalae* Lourenço, 1983, two for *A. aurum* Ythier, 2018, two for *A. aluku* Ythier, 2018 and two for *A. laurae* Ythier, 2015). We also included the genus *Neochactas* Soleglad & Fet, 2003 as well as representatives of the genera *Brotheas* C.L. Koch, 1837 and *Hadrurochactas* González-Sponga, 1978. Following the recent revisions in the scorpion Tree of Life (Santibáñez-López *et al.* 2019, 2020, 2022, 2023), we rooted the tree with *Scorpiops tibetanus* (Iurida, Chactoidea - NC053569) as a near-outgroup and *Mesobuthus martensii* (Buthida, Buthoidea - NC009738) as a far-outgroup.

DNA extraction and sequencing

Total genomic DNA was extracted from leg muscle tissues using the DNeasy Blood and Tissue kit (Qiagen, Valencia, CA, USA), following the manufacturer's instructions. The quality and quantity of extracted genomic DNA was evaluated using a NanoDrop 2000 spectrophotometer (Thermo Fisher Scientific, Waltham, MA, USA) and a PicoGreen double-stranded DNA quantitation assay kit (Life Technologies, Carlsbad, CA, USA). The genomic DNA was sent for library construction and sequencing to the GeT-PlaGe core facilities of Genotoul (Toulouse, France). Library construction used the Illumina TruSeq Nano DNA Sample Prep Kit following the supplier's instructions (Illumina Inc., San Diego, CA, USA). After shearing by ultrasonication with a Covaris M220 (Covaris Inc., Woburn, MA, USA), purified fragments were A-tailed and ligated to sequencing indexed adapters. Fragments with an insert size of around 450 bp were selected with Agencourt Ampure XP beads (Beckman Coulter, Inc.), and enriched with 8 cycles of PCR before library quantification and validation. The libraries were multiplexed and the pool of libraries was then hybridized on one lane of NovaSeq flow cell using the Illumina TruSeq PE Cluster Kit ver. 3, and paired-end reads of 150 nucleotides were collected on the sequencer using the Illumina TruSeq SBS Kit ver. 3 (200 cycles). Quality filtering was performed by the Consensus Assessment of Sequence and Variation (CASAVA) pipeline. The paired-end reads were stored on the NG6 platform (Mariette *et al.* 2012).

Mitogenomes reconstruction and phylogeny

As recently performed for other arthropods (Cally *et al.* 2014; Kocher *et al.* 2014, 2015, 2016), the complete mitochondrial genomes were assembled de novo using NOVOplasty (Dierckxsens *et al.* 2016) and annotated using MITOS2 (Bernt *et al.* 2013; Fiedler *et al.* 2023) (Fig. 1). Coverage statistics were computed on the assembled genome with Geneious ver. 9 (Kearse *et al.* 2012), by mapping the reads using the following mapping parameter: a minimum overlap of 100 bp, a minimum overlap identity of 95%, a word length of 50 and a maximum mismatch per read of 5%.

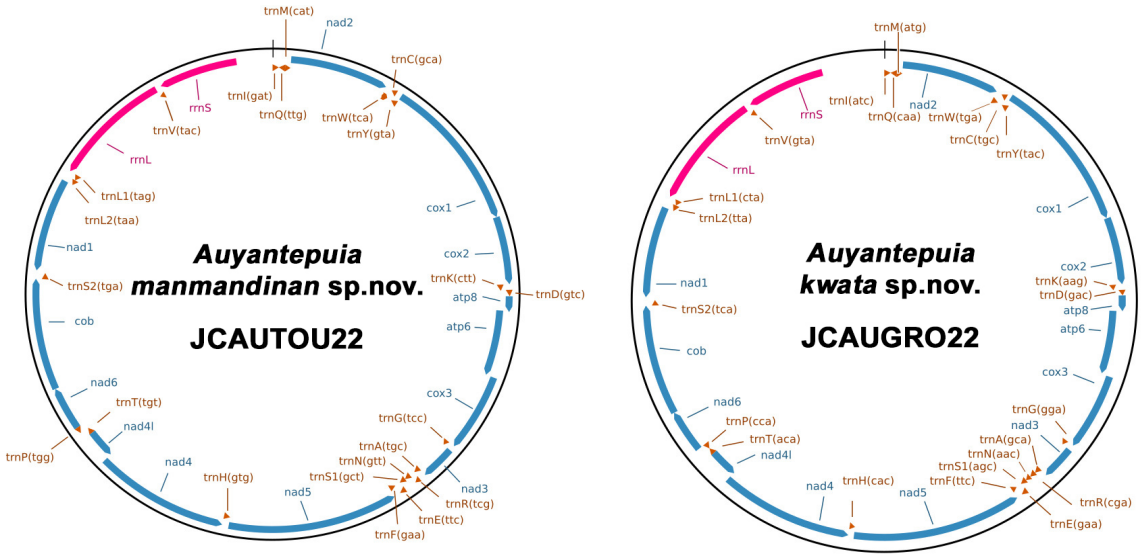

Fig. 1. Structure of the complete mitochondrial genomes of *Auyantepuia manmandinan* sp. nov. (JCAUTOU22) and *A. kwata* sp. nov. (JCAUGRO22). Ribosomal genes (pink), coding genes (blue) and transfer RNAs (brown) are depicted with arrows representing their position on the L or H strand.

Ribosomal genes were aligned using MAFFT ver. 7 (Katoh & Standley 2013) and the Iterative refinement method with local pairwise alignment information, with subsequent trimming using trimal 1.4 (Capella-Gutiérrez *et al.* 2009) with the automated option. Coding genes were aligned using TranslatorX (Abascal *et al.* 2010) to consider the amino-acid sequence. Individual genes were concatenated using FasconcatG (Kück & Meusemann 2010; Kück & Longo 2014). We also used ModelFinder (Kalyaanamoorthy *et al.* 2017) as implemented in IQ-TREE 2.4.0 (Minh *et al.* 2020) to evaluate the best partition scheme as well as the optimal model for each partition. Coding genes were treated either as nucleotide sequences or as amino-acid sequences. Optimization was followed by Maximum Likelihood tree search with partition models (Chernomor *et al.* 2016) and support was assessed using the ultrafast bootstrap approximation (Hoang *et al.* 2018).

In order to provide some practical recommendations, we amplified in silico several short molecular markers to evaluate their ability for species identification / discovery. We used the classical 658 base pair [bp] fragment of the cox1 gene as amplified by the primers LCO1490 5'-GGTCAACAAATCATAAAGATATTGG-3′ and HCO2198 5′-TAAACTTCAGGGTGACCAAAAAATCA-3′ (Folmer *et al.* 1994), a 490 bp fragment of the 12S gene as amplified by Sc-12F 5′-AGAGTGACGGGCAATATGTG-3′ and Sc-12R 5′- CAGCGGCTGCGGTTATAC-3′ and a 399 bp fragment of the 16S gene as amplified by Sc-16F 5′-CGATTTGAACTCAGATCA-3′ and Sc-16R 5′- GTGCAAAGGTAGCATAAT-3′ (Soltan-Alinejad *et al.* 2021). In silico amplification was performed in Geneious followed by a distance analysis using the Neighbor Joining algorithm.

Morphological analysis

Illustrations and measurements were made with the aid of a Motic SMZ-1713 digital stereo microscope with an ocular micrometer, together with digital camera Tucsen HD Lite and a Canon EOS 7D camera. Maps were built using maps-for-free.com and Photoshop software. Measurements follow Stahnke (1970) and are given in mm. Trichobothrial notations are those developed by Vachon (1974), morphological terminology mostly follows Hjelle (1990) and chelicerae dentition follows Vachon (1963). Type material studied herein is deposited in the following collections: MNHN, Muséum national d'Histoire naturelle, Paris, France; EYPC, Éric Ythier private collection, Romanèche-Thorins, France; JCPC, Johan Chevalier private collection, Awala-Yalimapo, French Guiana, France.

Results

Molecular analysis

Mitogenomes organization

The newly sequenced mitochondrial genomes of the genera *Auyantepuia*, *Neochactas*, *Brotheas*, and *Hadrurochactas* exhibit a genomic organization consistent with that of previously published scorpion mitogenomes, including *Scorpiops tibetanus*, which was used as an outgroup.

Molecular analyses

The final molecular matrix of the 14 *Auyantepuia* mitochondrial genomes contained 12 970 sites and 5171 patterns with 15 partitions corresponding to the 13 coding genes and two ribosomal genes. ModelFinder indicated an optimal set of eight partitions for the nucleotide dataset: nad6+nad3+nad2+atp8+atp6, nad4+nad5, nad4L, nad1, cytb, cox3, cox2+cox1, 12S+16S and a set of six partitions for the amino-acid dataset: cytb+nad1+cox3, nad5+atp6+nad4+nad4L, nad2+nad3+nad6, cox1+cox2, atp8, 12S+16S. The phylogenetic analysis based on nucleotide sequences provided a robust phylogenetic tree with a Log Likelihood of -95 961 and high support values (Fig. 2). The topology shows *A. kelleri* as sister to all the species followed by *A. fravalae* as sister to the remaining species. When several specimens were included for the same species, the species was always found monophyletic with 100% support values.

The two new species form clear distinct lineages with substantial genetic divergence compared to their closest relatives. When the coding genes were analyzed using amino-acids, the Log-likelihood of the tree was -47 665 and the topology was very similar to the previous tree. The topology differed mainly in the position of *Auyantepuia aurum* which is sister to *Auyantepuia kwata* in the "nucleotide dataset" and sister to *A. manmandinan* + *A. kwata* + *A. aluku* + *A. laurae* in the "amino-acid dataset".

When comparing the 1530 base pairs alignment of the complete cox1 gene, *A. kwata* sp. nov. (JCAUGRO22) shows a similarity of 92.3% to its closest relative (*A. laurae* JCAUJAV22) while *A. manmandinan* sp. nov. (JCAUTOU22 and JCAUSIN22) shows a similarity of 91.4% to its closest relatives (*A. laurae* JCAUJAV22 and *A. aluku* JCAUCRE17) (Table 1). When analysed separately, the short barcode fragments of the cox1, 12S and 16S genes showed that they all provide sufficient discriminatory power for species identification (data not shown).

Taxonomy

Phylum Arthropoda Von Siebold, 1848
Class Arachnida Lamarck, 1801
Order Scorpiones Koch, 1837
Family Chactidae Pocock, 1893

Genus ***Auyantepuia*** Gonzalez-Sponga, 1978

Diagnosis (emended from Ythier & Chevalier 2020)

Scorpions of small size with a total length of 14 to 34 mm. General coloration reddish yellow to reddish brown. Tegument smooth overall. Trichobothrial pattern of type C; neobothriotaxic '*majorante*' (Vachon 1974). Pedipalp chelal fingers very short compared to chelal length, with trichobothria *db* and *esb* frequently at the same level; in some species these can be basal to trichobothrium Et_5. Ventral

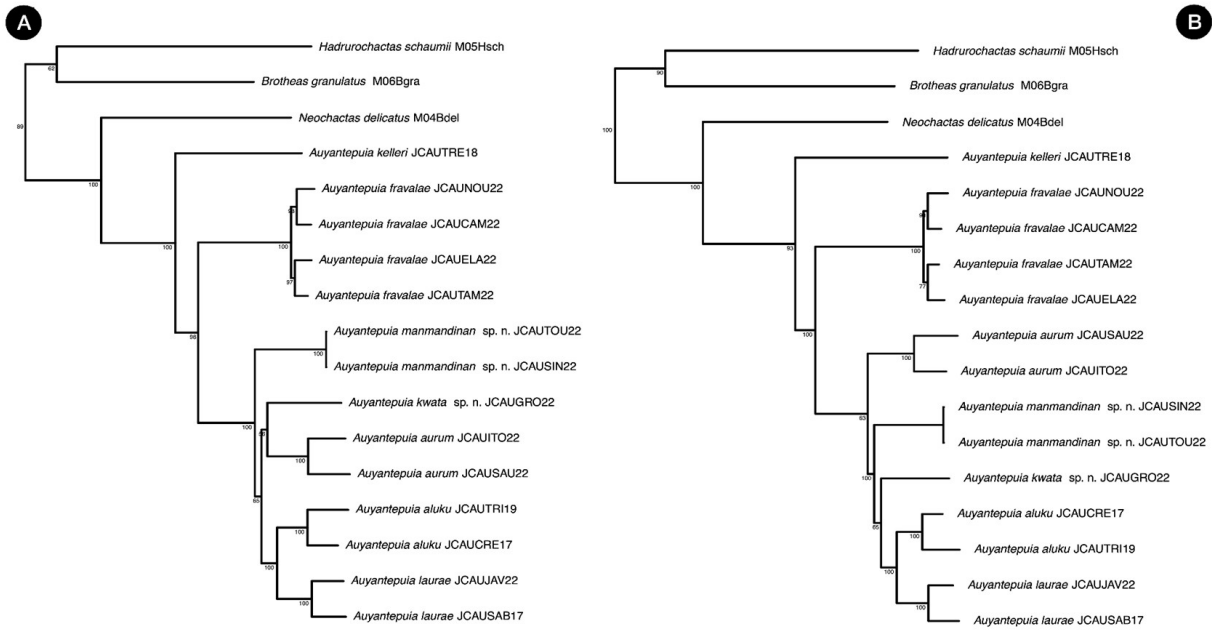

Fig. 2. Maximum Likelihood phylogenies of the complete mitochondrial genome inferred using IQ-TREE2 with coding genes treated as nucleotide sequences (panel A) or as amino-acid sequences (panel B).

Table 1. Percentage identity matrix (in percent) of the complete COI gene.

	JCAUCRE 17	JCAUTRI 19	JCAUITO 22	JCAUSAU 22	JCAUCAM 22	JCAUELA 22	JCAUNOU 22	JCAUTAM 22	JCAUTRE 18	JCAUJAV 22	JCAUSAB 17	JCAUGRO 22	JCAUSIN 22	JCAUTOU 22
JCAUCRE 17		93.7	91.0	92.1	90.0	89.9	89.5	89.5	88.6	93.1	91.9	91.0	91.3	91.4
JCAUTRI 19	93.7		90.3	90.6	89.8	89.5	89.0	89.2	87.8	92.0	91.7	91.4	90.6	90.7
JCAUITO 22	91.0	90.3		92.9	89.0	89.0	89.0	88.8	88.2	91.4	91.7	91.3	90.4	90.5
JCAUSAU 22	92.1	90.6	92.9		89.3	89.4	88.6	89.0	88.6	91.8	92.0	92.2	90.6	90.7
JCAUCAM 22	90.0	89.8	89.0	89.3		96.7	97.6	96.2	89.8	90.3	90.8	89.8	89.6	89.6
JCAUELA 22	89.9	89.5	89.0	89.4	96.7		96.1	96.4	89.0	90.0	90.4	89.9	89.2	89.2
JCAUNOU 22	89.5	89.0	89.0	88.6	97.6	96.1		95.9	89.3	90.1	90.7	89.2	89.3	89.3
JCAUTAM 22	89.5	89.2	88.8	89.0	96.2	96.4	95.9		89.0	89.8	89.9	89.4	89.1	89.2
JCAUTRE 18	88.6	87.8	88.2	88.6	89.8	89.0	89.3	89.0		89.3	89.1	88.5	88.8	88.8
JCAUJAV 22	93.1	92.0	91.4	91.8	90.3	90.0	90.1	89.8	89.3		94.1	92.3	91.4	91.4
JCAUSAB 17	91.9	91.7	91.7	92.0	90.8	90.4	90.7	89.9	89.1	94.1		91.8	91.2	91.1
JCAUGRO 22	91.0	91.4	91.3	92.2	89.8	89.9	89.2	89.4	88.5	92.3	91.8		90.5	90.6
JCAUSIN 22	91.3	90.6	90.4	90.6	89.6	89.2	89.3	89.1	88.8	91.4	91.2	90.5		99.9
JCAUTOU 22	91.4	90.7	90.5	90.7	89.6	89.2	89.3	89.2	88.8	91.4	91.1	90.6	99.9	

surface of metasomal segment V with large spiniform granules which form an arc in the posterior region. Pectines with 5 to 8 teeth.

Notes on the genus *Auyantepuia*

Despite some early debates on the validity of the genus *Auyantepuia* (Soleglad & Fet 2003; Fet & Soleglad 2005) we here follow (Prendini & Wheeler 2005) along with (Lourenço & Qi 2007; Lourenço & Duhem 2010; Ythier 2015, 2018a, 2018b) in considering *Auyantepuia* as a valid genus. With the two new species described in this work, the total number of *Auyantepuia* species is raised to 15. The genus seems to have a disrupted and relictual pattern of geographical distribution, with a strong concentration of species in the Guayana floristic province (Mori 1991) (Fig. 3).

Composition of the genus *Auyantepuia* (in chronological order of description)

Auyantepuia parvulus (Pocock, 1897) (Brazil)
Auyantepuia scorzai (Dagert, 1957) (Venezuela)
Auyantepuia fravalae Lourenço, 1983 (French Guiana)
Auyantepuia gaillardi Lourenço, 1983 (French Guiana)
Auyantepuia sissomi Lourenço, 1983 (French Guiana)
Auyantepuia kelleri (Lourenço, 1997) (French Guiana)
Auyantepuia mottai Lourenço & Araujo, 2004 (Brazil)
Auyantepuia amapaensis Lourenço & Qi, 2007 (Brazil)
Auyantepuia surinamensis Lourenço & Duhem, 2010 (Suriname)
Auyantepuia laurae Ythier, 2015 (French Guiana)
Auyantepuia aluku Ythier, 2018 (French Guiana)
Auyantepuia aurum Ythier, 2018 (French Guiana)
Auyantepuia royi Ythier, 2018 (Brazil)
Auyantepuia kwata sp. nov. (French Guiana)
Auyantepuia manmandinan sp. nov. (French Guiana)

Auyantepuia fravalae Lourenço, 1983

Diagnosis (Ythier 2018a)

Species of large size when compared with the average size of the other species of the genus, with a total length ranging from 26–34 mm in males and 29 mm in females. General coloration reddish brown. Carapace dark reddish brown with blackish spots around the ocular tubercle and on lateral edges of the carapace; ocular tubercle dark, almost black. Tergites reddish with several confluent lighter zones. Venter greyish yellow, the sternite VII darker; pectines and genital operculum yellow ochre. All metasomal segments reddish, slightly darker than the mesosoma; several reticular blackish spots on the ventral and lateral sides of segments I to V. Vesicle reddish yellow with several darker spots corresponding to granules; basis of aculeus reddish and tip of aculeus reddish black. Chelicerae dark yellowish with blackish spots starting at the basis of fingers and spreading along the chelicerae; fingers reddish. Pedipalps reddish with several longitudinal blackish spots on the three segments (femur, patella and chela). Legs light yellow with several diffuse light brown spots. Carapace with a fine granulation with bigger granules on the anterior part; anterior edge very slightly concave, almost straight. Tergites with medium size granulation, especially on the posterior part. Pectinal tooth count ranging 8–9 in males and 8–8 in females. Sternites smooth with spiracles rounded in shape. Ventral side of metasomal segments IV and V with medium size granulation on IV, important and spinoid on V; dorsal lateral carinae weakly marked on segments I to IV; lateral supramedian carinae well-marked on segments I to IV and weakly marked on V; other carinae absent. Pedipalp femur with four almost complete carinae; patella and chela with all carinae vestigial; dorsal and internal sides of femur granular; chela strongly granulated dorsally,

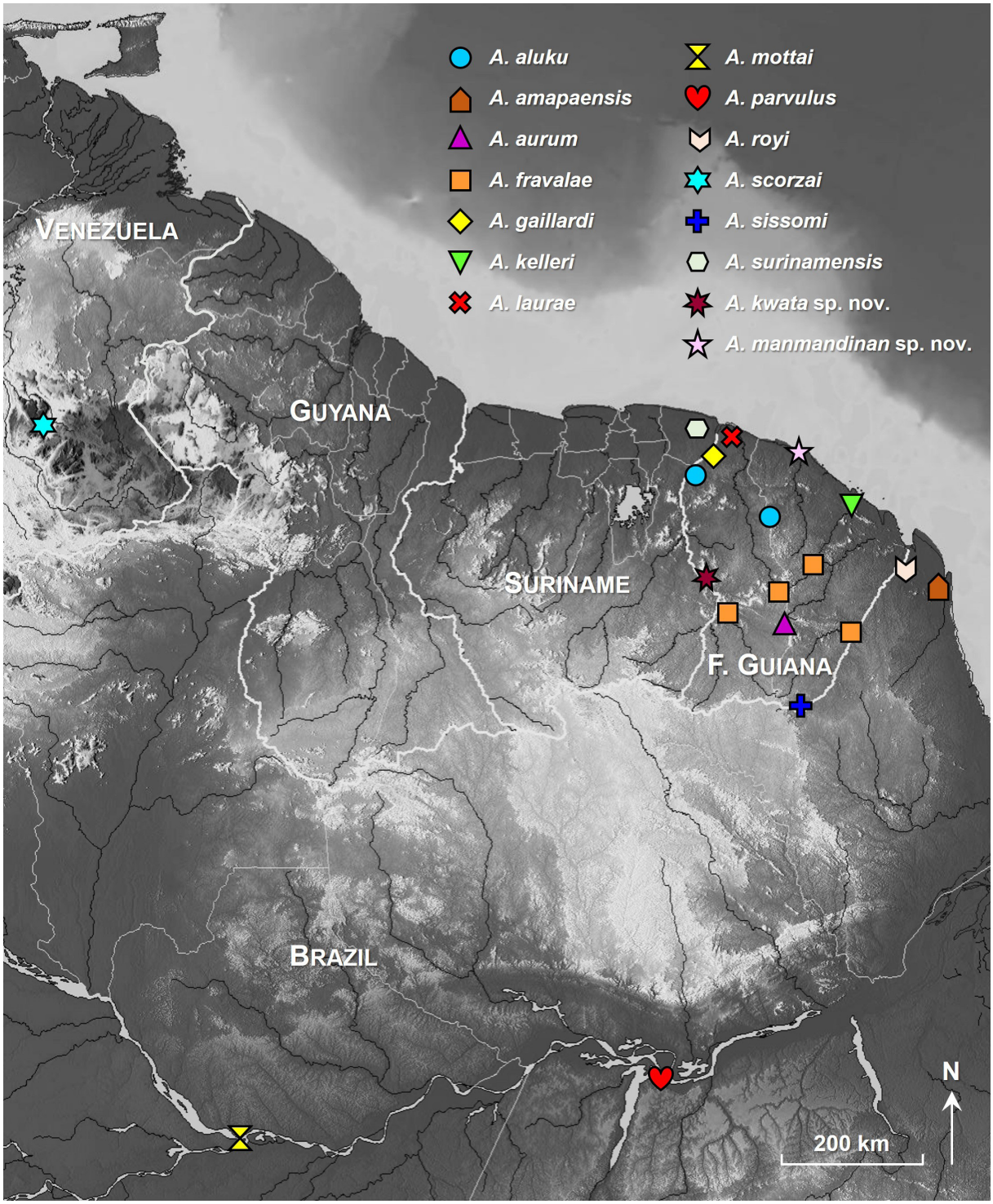

Fig. 3. Map of northern South America showing the approximate known distribution of *Auyantepuia* species.

only few scattered granules internally; dentate margins on movable fingers with six rows of granules separated by bigger granules.

Material examined

FRENCH GUIANA • 1 ♂; Nouragues Reserve; 19–20 Apr. 2022; J. Chevalier leg.; JCAUNOU22; EYPC, EY0408 • 1 ♂; Saut Tampok; 20–30 Jul. 2022; J. Chevalier leg.; JCAUTAM22; EYPC, EY0402 • 1 ♂; Elahé; 17 May 2022; J. Chevalier leg.; JCAUELA22; EYPC, EY0409 • 2 ♂♂; Camopi; 08 Mar. 2022; J. Chevalier leg.; JCAUCAM22; EYPC, EY0400.

Distribution

Auyantepuia fravalae is distributed in central French Guiana and has been reported from the Nouragues Reserve (type locality), Saül, Elahé, Tampok and Camopi (Fig. 4).

Auyantepuia gaillardi Lourenço, 1983

Diagnosis (Ythier, 2018a)

Species of medium to large size when compared with the average size of the other species of the genus, with a total length of 25 mm in males and 27 mm in females. General coloration reddish yellow. Carapace light reddish with yellowish spots on the posterior and lateral edges; ocular tubercle blackish. Tergites yellowish with several confluent darker spots, greyish. Venter pale yellow, the sternite VII darker; pectines and genital operculum yellow ochre. All metasomal segments uniformly reddish, slightly darker than the prosoma. Vesicle of same coloration as metasomal segment V; aculeus dark reddish. Chelicerae uniformly yellowish; tip of fingers reddish. Pedipalps reddish, the femur slightly yellowish. Legs uniformly pale yellow. Carapace with a fine granulation in males, smooth in female; anterior edge very slightly concave, almost straight. Tergites with a fine granulation similar to the one on carapace in males, smooth in females. Pectinal tooth count 7–8 in males and 6–7 in females. Sternites smooth with spiracles rounded in shape. Metasomal segment V with spinoid granulation ventrally; dorsal lateral and lateral supramedian carinae on segments I to V weakly marked; other carinae absent. Pedipalp femur with dorsal internal, dorsal external and ventral internal carinae well-marked; internal side granular; patella and chela with all carinae vestigial; chela weakly granular dorsally; dentate margins on movable fingers with six rows of granules separated by bigger granules.

Distribution

Auyantepuia gaillardi is known only from its type locality in Saint-Jean-du-Maroni, in northwestern French Guiana (Fig. 4).

Auyantepuia sissomi Lourenço, 1983

Diagnosis (Ythier 2018a)

Species of medium to large size when compared with the average size of the other species of the genus, with a total length of 26 mm in females. General coloration yellowish. Carapace yellowish with light brown spots around the ocular tubercle and on the lateral edges of the carapace; posterior part and furrows lighter; ocular tubercle dark, almost black. Tergites greyish with several confluent lighter spots, yellowish, forming a longitudinal stripe. Venter yellow ochre. All metasomal segments reddish yellow, with greyish spots on lateral sides of I to V and on ventral side of III to V; ventral side of segments I and II without pigmentation. Vesicle reddish yellow; basis of aculeus reddish and tip of aculeus reddish black. Chelicerae yellowish with greyish spots; fingers yellowish with reddish teeth. Pedipalps reddish yellow with longitudinal light brown spots on the patella and chela, the dorsal side of the femur almost entirely covered with light brown spots; chela reddish. Legs pale yellow with several diffuse greyish spots. Carapace without granules, almost smooth; anterior edge very slightly concave. Tergites with few

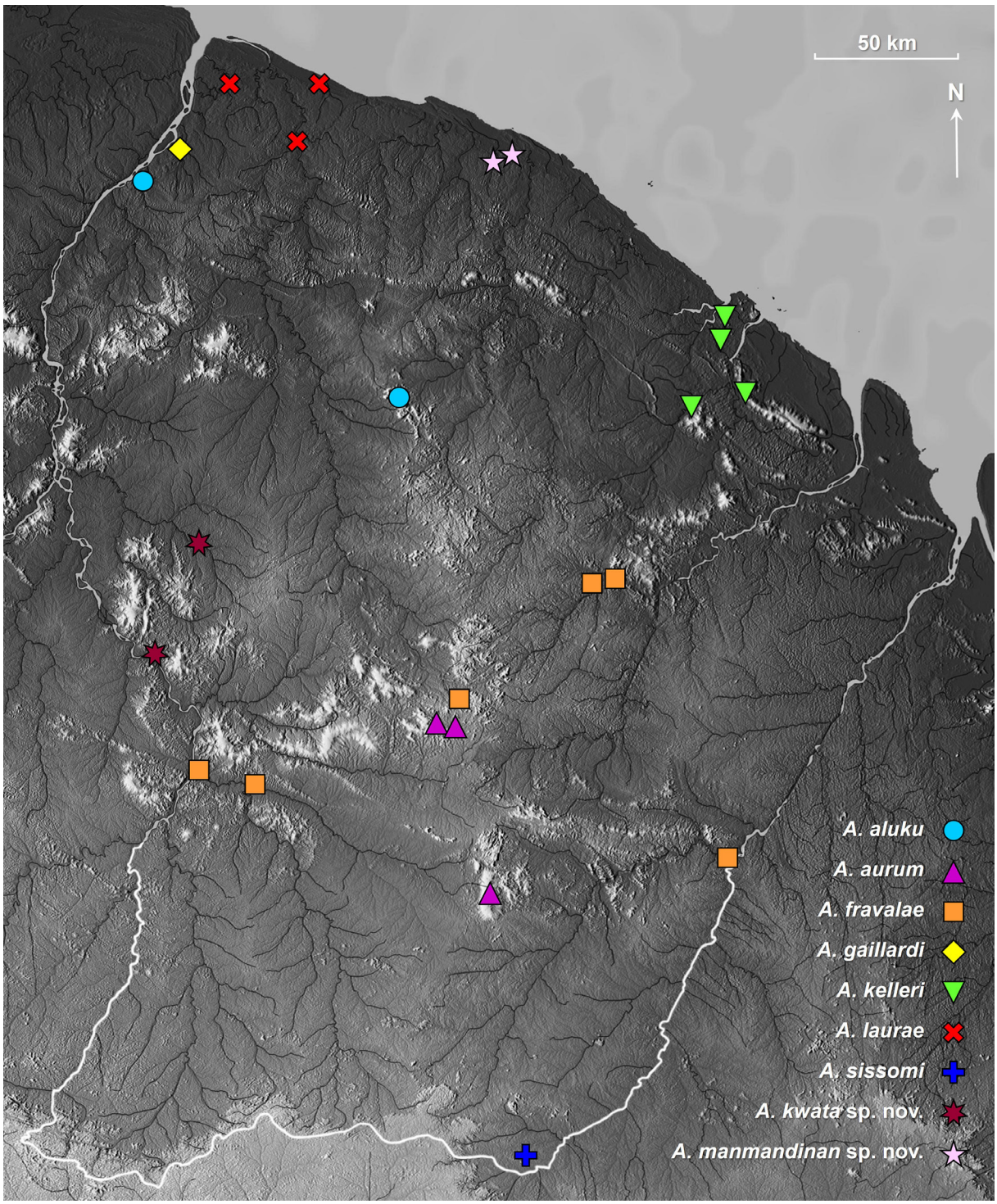

Fig. 4. Map of French Guiana showing the known distribution of *Auyantepuia* species.

scattered fine granules. Pectinal tooth count 6–7 in females. Sternites smooth with spiracles rounded in shape. Metasomal segment V with spinoid granulation ventrally; dorsal lateral carinae weakly marked on segments I to IV; lateral supramedian carinae well-marked but incomplete on segments I to IV; other carinae absent. Pedipalp femur with three carinae well-marked and almost complete; patella and chela with all carinae vestigial; dorsal and internal sides of femur granular; dorsal side of chela granular, internal side with few scattered granules; dentate margins on movable fingers with six rows of granules separated by bigger granules.

Distribution

Auyantepuia sissomi is known only from its type locality in the upper Oyapock, in southeastern French Guiana (Fig. 4).

Auyantepuia kelleri (Lourenço, 1997)

Diagnosis (Ythier & Chevalier 2020)

Species of small size when compared with the average size of the other species of the genus, with a total length ranging from 14–18 mm in males and 17–22 mm in females. General coloration brownish to reddish brown. Carapace reddish brown to reddish yellow, intensely marked with brownish variegated spots around the ocular tubercle and on the anterior edge of the carapace; posterior part and furrows lighter; ocular tubercle darker. Tergites brownish with confluent yellowish spots. Venter yellowish to yellowish brown. Metasomal segments reddish brown, marked with variegated brownish spots on lateral and dorsal sides of segments I to V; ventral side of all segments reddish brown, without spots. Vesicle reddish brown with basis of aculeus reddish brown and tip of aculeus reddish black. Chelicerae yellowish with variegated dark brown spots anteriorly, at the base of fingers; fingers yellowish with reddish teeth. Pedipalps reddish brown with longitudinal dark brown spots, chela reddish. Legs yellowish with brownish spots. Carapace lustrous and acarinate, with some minute punctations; furrows shallow; anterior edge emarginated. Tergites acarinate, almost smooth and shiny. Pectinal tooth count ranging 6–8 in males and 5–6 in females. Sternites smooth with spiracles rounded in shape. Metasomal tegument almost lustrous, without granulation, and with a few punctations; segment V with spinoid granulation ventrally, moderately marked; carinae on segments I to V vestigial or absent; only lateral supramedian carinae are weakly marked on segments I to IV. Pedipalp femur with dorsal internal, dorsal external and ventral internal carinae well-marked; internal face weakly granular, other faces smooth; patella and chela with all carinae vestigial; chela weakly granulated dorsally, almost smooth, with few scattered granules internally, dorso-internal carina weakly marked; dentate margins on fixed and movable fingers with 6 rows of granules.

Material examined

FRENCH GUIANA • 1 ♂; Matoury, Désirée path; 2 Oct. 2018; J. Chevalier, E. Dewynter and M. Dewynter leg.; EYPC, EY0165 • 2 ♂♂, 1 ♀; Kaw mountain, Regional Natural Reserve Trésor, between camp Favard and camp Savane; 22 Nov. 2018; J. Chevalier and J.-F. Szpigel leg.; JCPC • 2 ♂♂, 2 ♀♀; same collection data as for preceding; 23 Nov. 2018; EYPC, EY0166 • 14 ♂♂; Kaw mountain, Regional Natural Reserve Trésor, on the path of the reserve; 21 Nov. 2018; J. Chevalier and J.-F. Szpigel leg.; JCPC • 1 ♂, 3 ♀♀, 1 juvenile ♀; Mount Grand Matoury, Antenna; 3 Mar. 2021; J. Chevalier leg.; JCAUGRA22; EYCP, EY0407.

Distribution

Auyantepuia kelleri is distributed in northeastern French Guiana and has been reported from Cacao (type locality), Kaw mountain and Mount Grand Matoury (Fig. 4).

Auyantepuia laurae Ythier, 2015

Diagnosis (Ythier & Chevalier 2020)

Species of medium to large size when compared with the average size of the other species of the genus, with a total length of 21 mm in males and ranging from 22–28 mm in females. General coloration reddish brown. Carapace reddish yellow, intensely marked with brownish variegated spots around the ocular tubercle and on the anterior and posterior edges of the carapace; ocular tubercle darker, almost black. Tergites reddish brown with reddish yellow spots. Venter yellowish to reddish yellow. Metasomal segments reddish yellow, marked with variegated brownish spots on lateral and dorsal sides of segments I to V; ventral side with intensely marked variegated brownish spots on segments IV and V and weakly marked variegated brownish spots on segment III, other segments without spots. Vesicle reddish yellow with basis of aculeus brownish and tip of aculeus reddish. Chelicerae yellowish with variegated dark brown spots; fingers reddish yellow with dark brown spots, teeth reddish. Pedipalps reddish brown, with longitudinal dark brown spots. Legs yellowish, intensely marked with brownish spots. Carapace lustrous and acarinate, with some minute punctations; furrows shallow; anterior edge emarginated. Tergites acarinate, almost smooth and shiny. Pectinal tooth count 7–7 in males and 5–6 in females. Sternites smooth and shiny, VII acarinate; spiracles rounded in shape. Only metasomal segments IV and V longer than wide; metasomal tegument almost lustrous, without granulation, and with a few punctations; segment V with spinoid granulation ventrally, weakly to moderately marked; carinae on segments I to V vestigial or absent; only lateral supramedian carinae are weakly marked on segments I to IV. Pedipalp femur with dorsal internal, dorsal external and ventral internal carinae moderately marked, internal face weakly granular, other sides smooth; patella smooth, with all carinae vestigial; chela manus dorsal surface weakly granulated on distal half in both sexes, internal surface almost smooth, with few scattered granules in male and smooth in female, dorso-internal carina weakly marked; dentate margins on fixed and movable fingers with six rows of granules.

Material examined

Holoype

FRENCH GUIANA • 1 ♀ near Saut Sabbat, 50 km south of Mana and 50 km east of Saint-Laurent-du-Maroni; under wood log; Jan. 2015; E. Ythier and G. Roy leg.; MNHN.

Paratypes

FRENCH GUIANA • 2 ♀♀; same data as for holotype; MNHN.

Other material

FRENCH GUIANA • 1 ♂; Mana, Camp Angoulème; 3. Mar. 2018; J. Chevalier and B. Tan leg.; JCAUANG19; EYPC, EY0169 • 1 ♀; Mana, path of the Forêt des Sables Blancs; 21 Jan. 2017; J. Chevalier and B. Tan leg.; JCPC • 1 ♀; same collection data as for preceding; 8 Jul. 2017; EYPC, EY0097 • 2 ♀♀; same collection data as for preceding; 24 Nov. 2018; JCPC • 1 ♀; Saint-Laurent-du-Maroni, ADNG path; 11 Jul. 2018; J. Chevalier and B. Tan leg.; JCAUADN18; EYPC, EY0168.

Distribution

Auyantepuia laurae is distributed in northwestern French Guiana and has been reported from Saut Sabbat (type locality), Mana and Saint-Laurent-du-Maroni (Fig. 4).

Auyantepuia aluku Ythier, 2018

Diagnosis (Ythier & Chevalier 2020)

Species of medium size when compared with the average size of the other species of the genus, with a total length ranging from 20–26 mm in males and 20–23 mm in females. General coloration reddish brown. Carapace reddish yellow, intensely marked with brownish variegated spots around the ocular tubercle and on the anterior and posterior edges of the carapace; ocular tubercle darker, almost black. Tergites reddish brown with confluent reddish yellow spots on the sides and the middle of tergites. Venter yellowish to reddish yellow. Metasomal segments reddish yellow, marked with variegated brownish spots on lateral and dorsal sides of segments I to V; ventral side with weakly marked variegated brownish spots on segments IV and V, other segments without spots. Vesicle reddish yellow with basis of aculeus brownish and tip of aculeus reddish. Chelicerae yellowish with variegated dark brown spots; fingers reddish yellow with dark brown spots, teeth reddish. Pedipalps reddish brown, with longitudinal dark brown spots. Legs yellowish, marked with brownish spots. Carapace lustrous and acarinate, with some minute punctations; furrows shallow; anterior edge emarginated. Tergites acarinate, almost smooth and shiny. Pectinal tooth count ranging from 7–7 in males and 5–6 in females. Sternites smooth and shiny, VII acarinate; spiracles rounded in shape. Only metasomal segments IV and V longer than wide; metasomal tegument almost lustrous, with lateral sizes covered with medium size granulation on all segments in male, smooth in female; medium size granulation on ventral side of segments III to V in male, only on segment V in female, these granules are spinoid on segment V; carinae on segments I–V vestigial or absent; only lateral supramedian carinae are weakly marked on segments I to IV. Pedipalp femur with dorsal internal, dorsal external and ventral internal carinae moderately marked; internal face weakly granular, other faces smooth; patella smooth, with all carinae vestigial; chela manus dorsal surface weakly granulated on distal half in both sexes, internal surface almost smooth, with few scattered granules in male and smooth in female, dorso-internal carina weakly marked; dentate margins on fixed and movable fingers with six rows of granules.

Material examined

Holotype

FRENCH GUIANA • ♀; Apatou, Crevette River; 30 Jun. 2017; J. Chevalier and P. Gallier leg.; JCAUCRE17; MNHN

Paratypes

FRENCH GUIANA • 4 ♀♀; same data as for holotype; EYPC, EY0094.

Other material

FRENCH GUIANA • 3 ♂♂, 3 ♀♀; Natural Reserve La Trinité; Oct. 2018; J. Chevalier leg.; JCPC • 1 ♂, 1 ♀, 2 immature ♂♂, 3 immature ♀♀; Natural Reserve La Trinité; Apr. 2019; J. Chevalier leg.; JCPC • 2 ♂♂, 1 ♀; same collection data as for preceding; EYPC, EY0171 • 1 ♂, 1 juvenile ♂; Natural Reserve La Trinité, at the top of the inselberg; 13 Apr. 2019; J. Chevalier leg.; EYPC, EY0172 • 5 ♂♂, 1 ♀; Natural Reserve La Trinité, Aya; Oct. 2010; C. Courtial leg.; EYPC, EY0496.

Distribution

Auyantepuia aluku is distributed in northwestern French Guiana and has been reported from Apatou (type locality) and the Natural Reserve La Trinité (Fig. 4).

Auyantepuia aurum Ythier, 2018

Diagnosis (Ythier 2018a)

Species of large size when compared with the average size of the other species of the genus, with a total length ranging from 25–30 mm in males and 26–29 mm in females. General coloration reddish brown. Carapace reddish yellow, marked with brownish variegated spots around the ocular tubercle and on the anterior and posterior edges of the carapace; ocular tubercle darker, almost black. Tergites brownish with confluent yellowish spots on the sides and the middle of tergites, forming a longitudinal median stripe. Venter yellowish. Metasomal segments reddish yellow, marked with variegated brownish spots on lateral and dorsal sides of segments I to V and on ventral side of segments III, IV and V; ventral side of segments I and II yellowish, without spots. Vesicle reddish yellow with basis of aculeus blackish and tip of aculeus reddish. Chelicerae yellowish with variegated dark brown spots; fingers reddish yellow with dark brown spots at their basis, teeth reddish. Pedipalps reddish yellow, with longitudinal dark brown spots. Legs yellowish, intensely marked with brownish spots. Carapace acarinate, with some fine granulations on central, lateral and posterior parts; furrows shallow; anterior edge emarginated. Tergites acarinate, with some fine granulations, stronger on their posterior edges. Pectinal tooth count ranging from 5–7 in males and 6–6 in females. Sternites smooth and shiny, VII acarinate; spiracles rounded in shape. Metasomal segments III, IV and V longer than wide; metasomal tegument with medium size granulation on lateral sides of all segments and on ventral side of segments III to V, granules spinoid on segment V; carinae on segments I–V vestigial, only lateral supramedian carinae are weakly marked on all segments. Pedipalp femur with dorsal internal, dorsal external and ventral internal carinae moderately marked, internal face weakly granular, other faces smooth; patella smooth, with all carinae vestigial; chela moderately granulated, with dorso-internal carina weakly marked; dentate margins on fixed and movable fingers with six rows of granules.

Material examined

Holotype

FRENCH GUIANA • ♂; Saül, Gros arbres trail; 21–22 Aug. 2017; J. Chevalier, B. Tan and R. Legallic leg.; MNHN.

Paratype

FRENCH GUIANA • 1 ♂; same data as for holotype; EYPC, EY0095.

Other material

FRENCH GUIANA • 1 ♂, 3 ♀♀, 1 immature ♂; Saül; 2022; J. Chevalier leg.; JCAUSAU22; EYCP, EY0406 • 1 ♂; Mount Itoupé, Montagne couronnée; 12–22 Nov. 2018; E. Courtois and M. Dewynter leg.; JCAUITO22; EYCP, EY0403.

Distribution

Auyantepuia aurum is distributed in central French Guiana and has been reported from Saül (type locality) and Mount Itoupé (Fig. 4).

Auyantepuia kwata sp. nov.

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Figs 5–14

Diagnosis

Species of small to medium size when compared with the average size of the other species of the genus, with a total length ranging from 18–25 mm in males (n = 5) and 22–25 mm in females (n = 8) (see

morphometric values in the description). General coloration reddish brown, with carapace, chelicerae, pedipalps and legs marked with darker spots. Tergites brownish with yellowish confluent spots on the sides and the middle of tergites, but not forming a longitudinal median stripe. Ventral side of metasomal segments I and II yellowish, without spots. Body and appendages weakly to moderately granulated; metasomal tegument with lateral sizes covered with medium size granulation on all segments in male, almost smooth in female; medium size granulation on ventral side of segments III to V in both sexes, spinoid on V; chela manus dorsal surface well granulated on entire surface in male, weakly granulated on distal half in female, internal surface weakly granulated on distal half in male, smooth in female, dorso–internal carina weakly marked. Pectinal tooth count ranging from 7–7 in males (n = 7) and 5–7 in females (n = 9; mean 6). Trichobothrial pattern of type C neobothriotaxic 'majorante'.

Etymology

The specific name is a noun placed in apposition to the generic name and refers to the French Guianese creole name for the red-faced spider monkey, *Ateles paniscus* (Linnaeus, 1758). The specific name also honors the Association Kwata, acting for nature conservation in French Guiana.

Material examined

Holotype

FRENCH GUIANA • ♂; Abounami River, Gros Saut; 4.162734° N, 53.999708° W; under wood log on the ground; 17–28 Nov. 2020; J. Chevalier leg.; MNHN, JCAUGRO22.

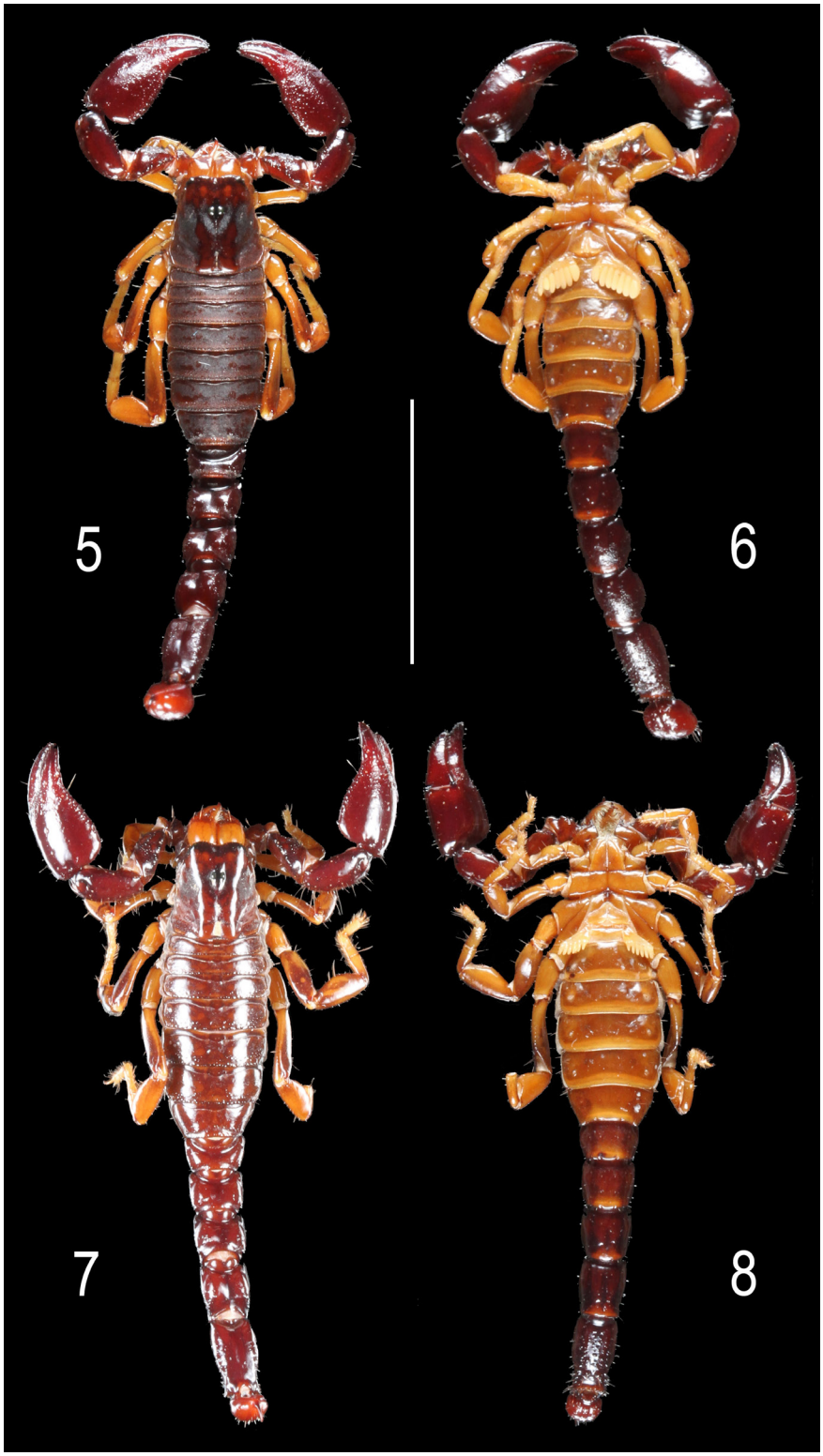
Paratypes

FRENCH GUIANA • 1 ♀; Abounami River, Gros Saut; 4.162734° N, 53.999708° W; under wood log on the ground; 17–28 Nov. 2020; J. Chevalier leg.; MNHN, JCAUGRO22 • 1 ♂, 1 ♀; same data as for preceding; JCPC • 1 ♂, 1 ♀, 1 immature ♀; same data as for preceding; EYCP, EY0401 • 1 ♂, 1 ♀; Papaïchton; 3.80810° N, 54.15022° W; under wood log on the ground; 19–20 May 2022; J. Chevalier leg.; MNHN • 2 immature ♂♂, 2 ♀♀; same data as for preceding; JCPC • 1 ♂; 2 ♀♀; same data as for preceding; EYCP, EY0405.

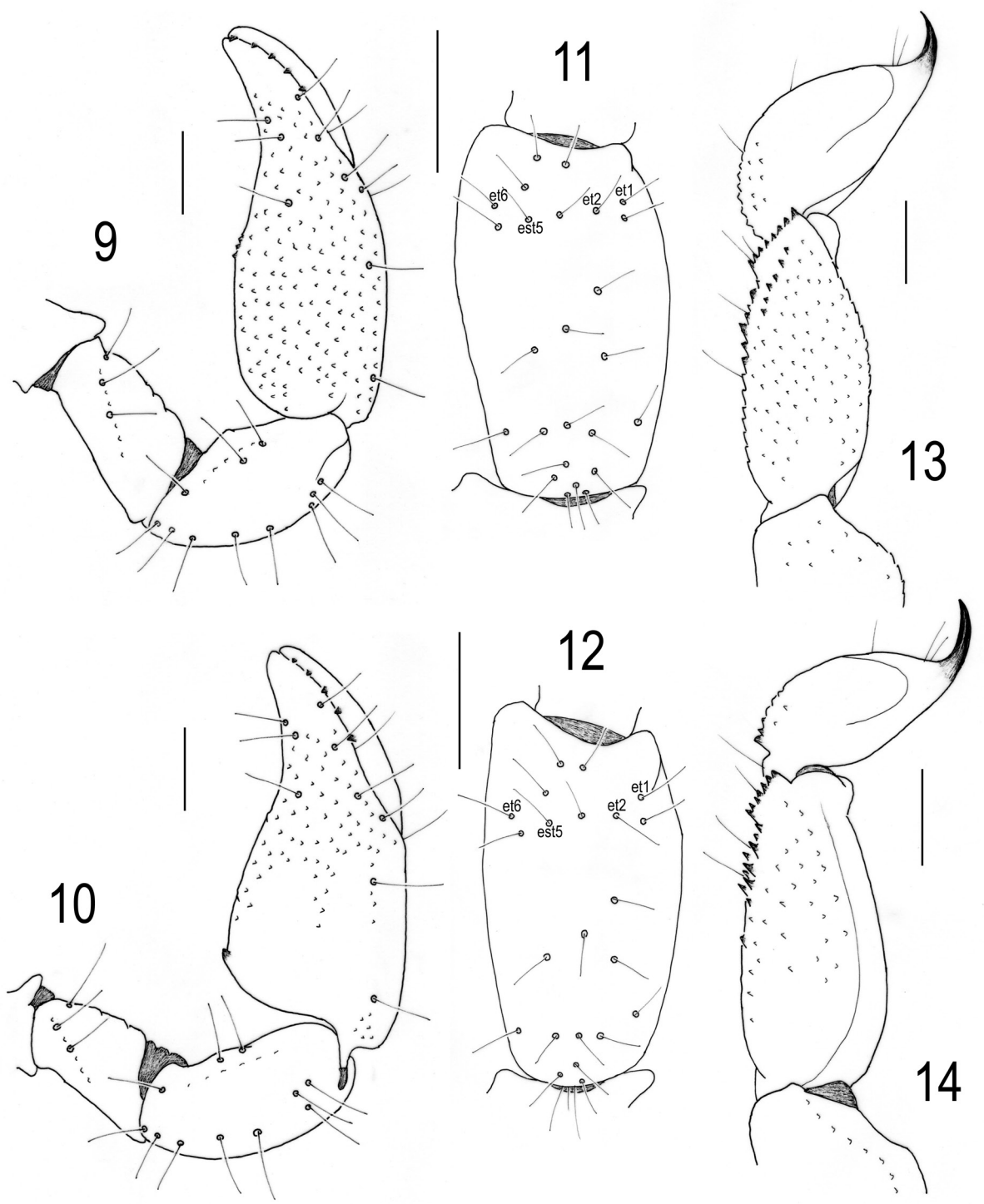
Description (based on male holotype and adult males and females paratypes)

Coloration. General coloration reddish brown. Carapace reddish yellow, marked with brownish variegated spots around the ocular tubercle and on the anterior and posterior edges of the carapace; ocular tubercle darker, almost black. Tergites brownish with confluent yellowish spots on the sides and the middle of tergites, but not forming a longitudinal median stripe. Venter yellowish. Metasomal segments reddish yellow, marked with variegated brownish spots on lateral and dorsal sides of segments I to V and on ventral side of segments III, IV and V; ventral side of segments I and II yellowish, without spots. Vesicle reddish yellow with basis of aculeus blackish and tip of aculeus reddish. Chelicerae yellowish with variegated dark brown spots; fingers yellowish with dark brown spots at their basis, teeth reddish. Pedipalps reddish yellow, with longitudinal dark brown spots. Legs yellowish, intensely marked with brownish spots.

Morphology. Carapace acarinate, with some fine granulations on central, lateral and posterior parts; furrows shallow; anterior edge emarginated. Tergites acarinate, with some fine granulations over the entire surface in male, smooth with few scattered granules on their posterior edge in female. Sternum pentagonal, wider than long. Pectinal tooth count ranging from 7–7 in males (n = 7) and 5–7 in females (n = 9; mean 6), fulcra absent. Sternites smooth and shiny, VII acarinate; spiracles rounded in shape. Only metasomal segments IV and V longer than wide; metasomal tegument with lateral sides covered with medium size granulation on all segments in male, almost smooth in female; medium size granulation on ventral side of segments IV–V in male, only on segment V in female, these granules are spinoid on



Figs 5–8. *Auyantepuia kwata* sp. nov., habitus, male holotype and female paratype from Abounami River (MNHN). **5–6**. Male holotype, dorsal (5) and ventral (6) aspects. **7–8**. Female paratype, dorsal (7) and ventral (8) aspects. Scale bar = 1 cm.



Figs 9–14. *Auyantepuia kwata* sp. nov., male holotype and female paratype from Abounami River (MNHN). **9–12**. Trichobothrial pattern. **9–10**. Pedipalp, dorso–external aspects, male holotype (9) and female paratype (10). **11–12**. Pedipalp patella, external aspect, male holotype (11) and female paratype (12). **13–14**. Metasomal segment V and telson, lateral aspect, male holotype (13) and female paratype (14). Scale bars = 1 mm.

segment V; carinae on segments I–V vestigial, only lateral supramedian carinae are weakly marked on all segments. Pedipalp femur with dorsal internal, dorsal external and ventral internal carinae moderately marked, internal face weakly granular, other faces smooth; patella smooth, with all carinae vestigial; chela manus dorsal surface well granulated on entire surface in male, weakly granulated on distal half in female, internal surface weakly granulated on distal half in male, smooth in female, ventral surface smooth in both sexes; dorso-internal carina weakly marked; dentate margins on fixed and movable fingers with six rows of granules. Trichobothrial pattern of type C neobothriotaxic 'majorante'; patella with external trichobothrium et_2 proximal to et_1 and est_5 proximal to et_6. Chelicerae with dentition typical of the family Chactidae (Vachon, 1963), and with dense setation ventrally and internally.

Morphometric values (in mm) of the male holotype and one female paratype. Total length including telson, 23.81/23.25. Carapace: length, 3.58/3.58; anterior width, 1.58/1.58; posterior width, 3.53/3.63. Mesosoma length, 6.28/7.30. Metasomal segments: I: length, 1.40/1.26; width, 2.33/2.19; II: length, 1.67/1.58; width, 2.09/1.95; III: length, 1.86/1.77; width, 2.05/1.86; IV: length, 2.23/2.09; width, 1.95/1.72; V: length, 3.53/3.16; width, 1.81/1.58; depth, 1.49/1.35. Telson: length, 3.26/2.51; width, 1.72/1.30; depth, 1.30/0.98. Pedipalp: femur length, 2.14/2.09, width, 1.12/1.07; patella length, 2.56/2.74, width, 1.26/1.26; chela length, 4.98/5.07, width, 1.77/1.81, depth, 2.51/2.56; movable finger length, 2.70/2.33.

Comparisons

Auyantepuia kwata sp. nov. is morphologically more similar to *A. aluku* reported from Crevette River (Apatou) and the Natural Reserve La Trinité and with *A. manmandinan* sp. nov. described from Toussaint River (Sinnamary). These two species can however be distinguished from *A. kwata* by the following main features:

- *Auyantepuia aluku*: (i) ventral side of metasomal segments I–II yellowish, without spots (segments I to III without spots in *A. aluku*), (ii) medium size granulation on ventral side of metasomal segments IV-V in male (granulation on segments III to V in *A. aluku*), (iii) male chela manus dorsal surface well granulated on entire surface (weakly granulated on distal half in *A. aluku*) and internal surface weakly granulated on distal half (almost smooth, with few scattered granules in *A. aluku*).

- *Auyantepuia manmandinan* sp. nov.: (i) chela manus dorsal surface well granulated on entire surface in male, weakly granulated on distal half in female, internal surface weakly granulated on distal half in male, smooth in female (dorsal and internal surfaces smooth in both sexes in *A. manmandinan*), (ii) tergites with confluent yellowish spots on the sides and the middle of tergites, but not forming a yellowish longitudinal median stripe (longitudinal stripe in *A. manmandinan*), (iii) patella with external trichobothrium et_2 proximal to et_1 (et_2 distal or at same level to et_1 in *A. manmandinan*) and est_5 proximal to et_6 (est_5 distal to et_6 in *A. manmandinan*).

Moreover, the molecular analysis performed on the mitochondrial genome of the new species shows substantial genetic divergence compared to *A. aluku* and *A. manmandinan* sp. nov.

Distribution

Auyantepuia kwata sp. nov is known only from its type localities in Abounami River (Gros Saut) and Papaïchton, in western French Guiana (Fig. 4).

Auyantepuia manmandinan sp. nov.
urn:lsid:zoobank.org:act:6E965380-4431-446E-A520-BFA04F32E815
Figs 15–24

Diagnosis

Species of medium size when compared with the average size of the other species of the genus, with a total length ranging from 21–23 mm in males (n=2) and 21–25 mm in females (n=2) (see morphometric values in the description). General coloration reddish brown, with carapace, chelicerae, pedipalps and legs marked with darker spots. Tergites brownish with confluent yellowish spots on the sides and the middle of tergites, forming a longitudinal median stripe. Ventral side of metasomal segments I and II yellowish, without spots. Body and appendages weakly to moderately granulated; metasomal tegument with lateral sizes covered with medium size granulation on segments III to V in male, smooth in female; medium size granulation on ventral side of segments III to V in both sexes, spinoid on V; chela manus dorsal and internal surfaces smooth in both sexes, dorso-internal carina weakly marked. Pectinal tooth count ranging from 7–7 in males (n=2) and 6–7 in females (n=2; mean=6). Trichobothrial pattern of type C neobothriotaxic 'majorante'.

Etymology

The specific name is a noun placed in apposition to the generic name and refers to the French Guianese creole name for the white-faced saki monkey, *Pithecia pithecia* (Linnaeus, 1766). The specific name also refers to the Manmandinan Lodge, where the new species was collected.

Material examined

Holotype

FRENCH GUIANA • ♂; Toussaint River, Manmandinan Lodge; 5.35482° N, 53.00532° W; under wood log on the ground; 10 Aug. 2021; J. Chevalier leg.; MNHN, JCAUTOU22.

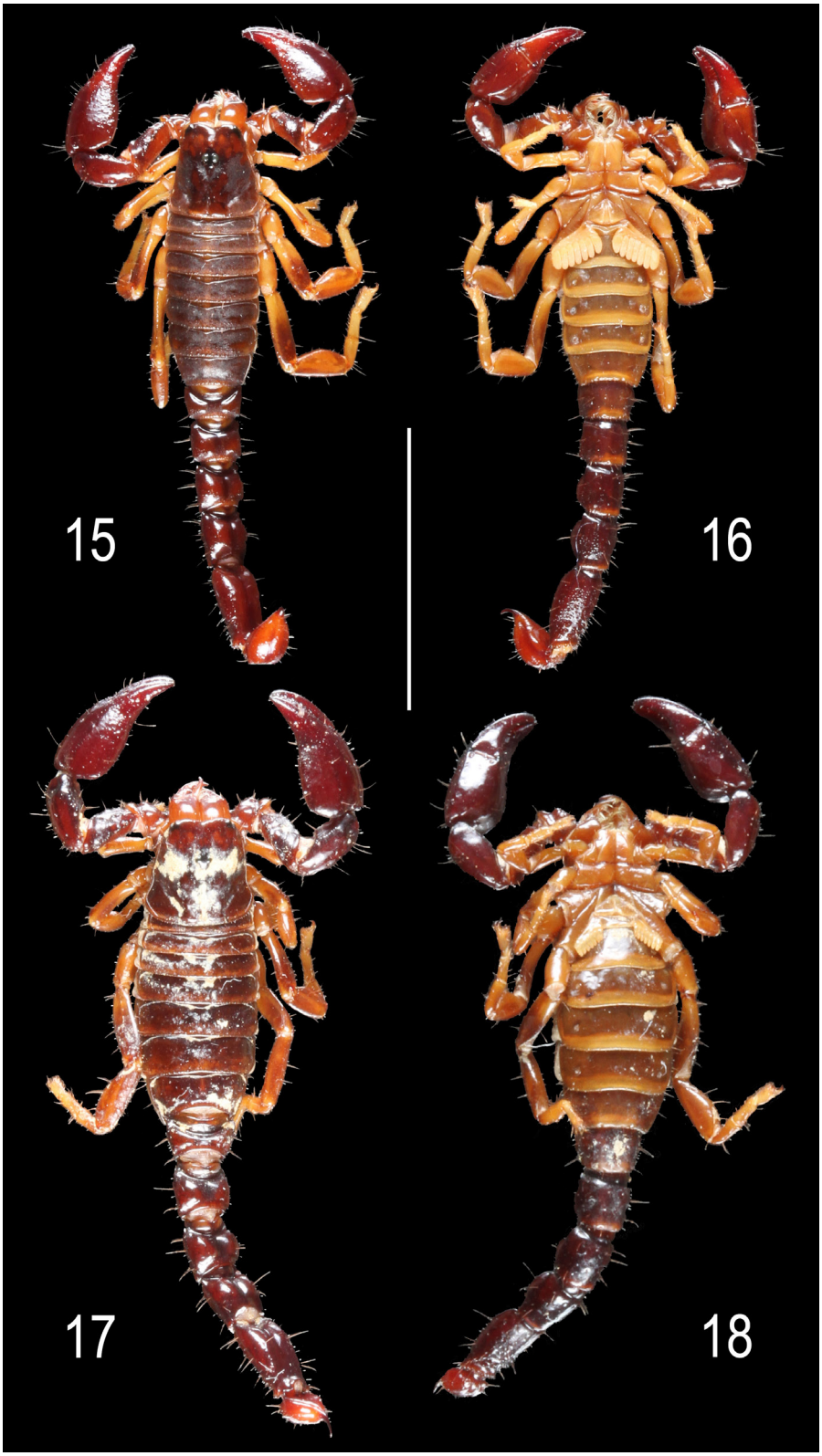
Paratypes

FRENCH GUIANA • 1 ♀; Toussaint River, Manmandinan Lodge; 5.35482° N, 53.00532° W; under wood log on the ground; 10 Aug. 2021; J. Chevalier leg.; MNHN, JCAUTOU22 • 1 ♀; same data as for preceding; JCPC • 1 ♂; same data as for preceding; EYCP, EY0404.

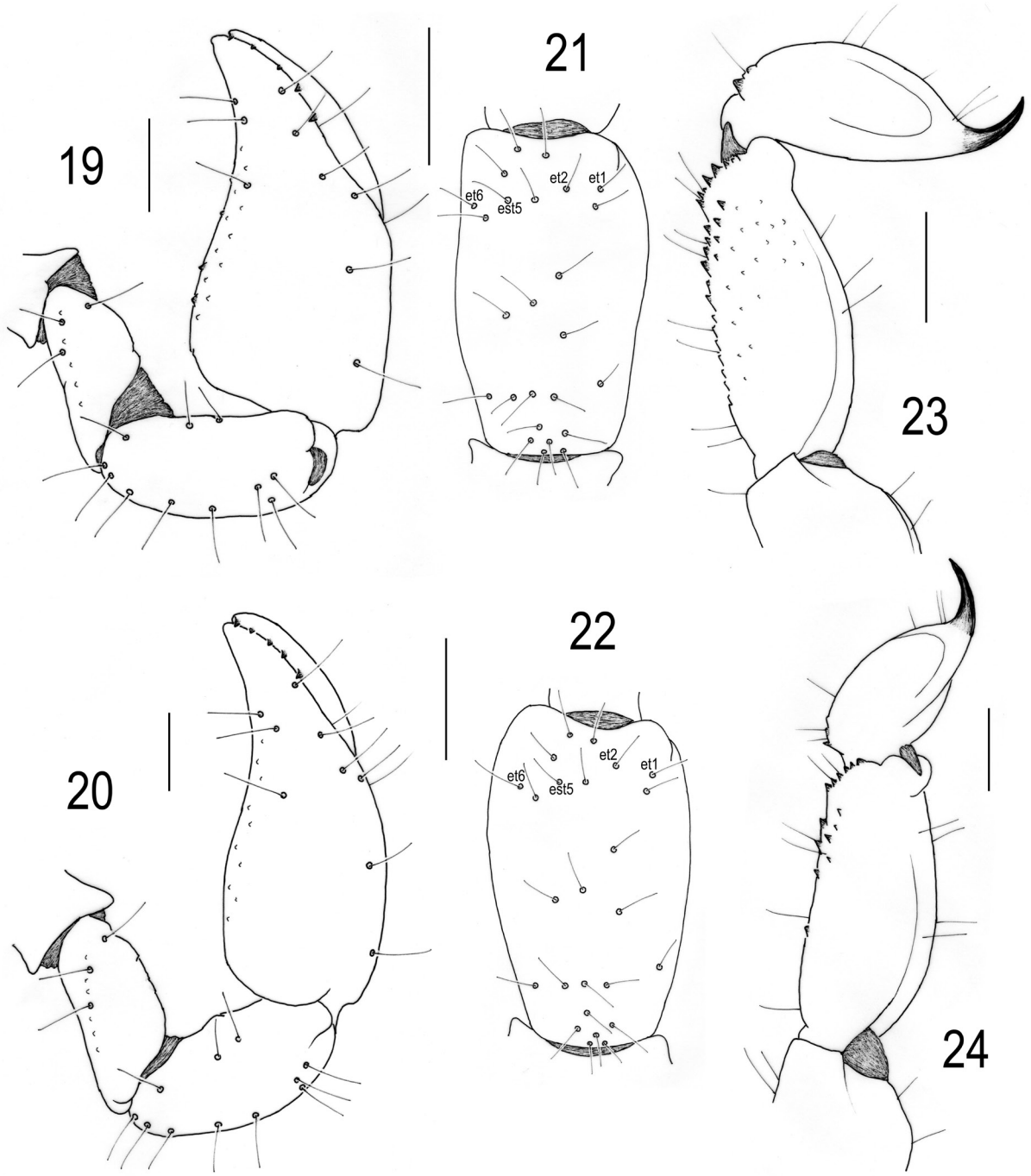
Description (based on male holotype and adult males and females paratypes)

Coloration. General coloration reddish brown. Carapace reddish yellow, marked with brownish variegated spots around the ocular tubercle and on the anterior and posterior edges of the carapace; ocular tubercle darker, almost black. Tergites brownish with confluent yellowish spots on the sides and the middle of tergites, forming a longitudinal median stripe. Venter yellowish. Metasomal segments reddish yellow, marked with variegated brownish spots on lateral and dorsal sides of segments I to V and on ventral side of segments III, IV and V; ventral side of segments I and II yellowish, without spots. Vesicle reddish yellow with basis of aculeus blackish and tip of aculeus reddish. Chelicerae yellowish with variegated dark brown spots; fingers yellowish with dark brown spots at their basis, teeth reddish. Pedipalps reddish yellow, with longitudinal dark brown spots. Legs yellowish, intensely marked with brownish spots.

Morphology. Carapace acarinate, with some fine granulations on central, lateral and posterior parts; furrows shallow; anterior edge emarginated. Tergites acarinate, with some fine granulations over the entire surface in male, smooth with few scattered granules on their posterior edge in female. Sternum pentagonal, wider than long. Pectinal tooth count ranging from 7–7 in males (n=2) and 6–7 in females (n=2; mean 6), fulcra absent. Sternites smooth and shiny, VII acarinate; spiracles rounded in shape.



Figs 15–18. *Auyantepuia manmandinan* sp. nov., habitus, male holotype and female paratype from Toussaint River (MNHN). **15–16**. Male holotype, dorsal (15) and ventral (16) aspects. **17–18**. Female paratype, dorsal (17) and ventral (18) aspects. Scale bar = 1 cm.



Figs 19–24. *Auyantepuia manmandinan* sp. nov. male holotype and female paratype from Toussaint River (MNHN). **19–22.** Trichobothrial pattern. **19–20**. Pedipalp, dorso–external aspects, male holotype (19) and female paratype (20). **21–22**. Pedipalp patella, external aspect, male holotype (21) and female paratype (22). **23–24**. Metasomal segment V and telson, lateral aspect, male holotype (23) and female paratype (24). Scale bars = 1 mm.

Only metasomal segments IV and V longer than wide; metasomal tegument with lateral sides covered with medium size granulation on all segments in male, smooth in female; medium size granulation on ventral side of segments IV–V in male, only on segment V in female, these granules are spinoid on segment V; carinae on segments I–V vestigial, only lateral supramedian carinae are weakly marked on all segments. Pedipalp femur with dorsal internal, dorsal external and ventral internal carinae moderately marked, internal face weakly granular, other faces smooth; patella smooth, with all carinae vestigial; chela manus dorsal, internal and ventral surfaces smooth in both sexes; dorso-internal carina weakly marked; dentate margins on fixed and movable fingers with six rows of granules. Trichobothrial pattern of type C neobothriotaxic 'majorante'; patella with external trichobothrium et_2 distal or at same level to et_1 and est_5 distal to et_6. Chelicerae with dentition typical of the family Chactidae (Vachon 1963), and with dense setation ventrally and internally.

Morphometric values (in mm) of the male holotype and one female paratype. Total length including telson, 20.69/22.56. Carapace: length, 3.16/3.72; anterior width, 1.63/1.63; posterior width, 3.12/3.77. Mesosoma length, 6.05/6.28. Metasomal segments: I: length, 1.12/1.35; width, 2.00/2.33; II: length, 1.35/1.63; width, 1.77/1.95; III: length, 1.53/1.81; width, 1.72/1.95; IV: length, 1.81/2.09; width, 1.67/1.86; V: length, 2.79/3.26; width, 1.58/1.67; depth, 1.30/1.30. Telson: length, 2.88/2.42; width, 1.44/1.40; depth, 1.16/0.98. Pedipalp: femur length, 1.86/2.33, width, 0.88/1.07; patella length, 2.33/2.79, width, 1.12/1.30; chela length, 4.42/5.12, width, 1.58/1.91, depth, 1.81/2.51; movable finger length, 2.37/2.79.

Comparisons

Auyantepuia manmandinan sp. nov. is morphologically more similar to *A. aluku* reported from Crevette River (Apatou) and the Natural Reserve La Trinité and with *A. kwata* sp. nov. described from Abounami River (Gros Saut) and Papaïchton. These two species can however be distinguished from *A. kwata* by the following main features:

- *Auyantepuia aluku*: (i) ventral side of metasomal segments I–II yellowish, without spots (segments I to III without spots in *A. aluku*), (ii) medium size granulation on ventral side of metasomal segments IV–V in male (granulation on segments III to V in *A. aluku*), (iii) both sexes with chela manus dorsal surface smooth (weakly granulated on distal half in *A. aluku*) and internal surface smooth (almost smooth, with few scattered granules in male *A. aluku*).

- *Auyantepuia kwata* sp. nov.: see comparisons in description of *A. kwata.*

Moreover, the molecular analysis performed on the mitochondrial genome of the new species shows substantial genetic divergence compared to *A. aluku* and *A. kwata* sp. nov.

Distribution

Auyantepuia manmandinan sp. nov. is known from its type locality in Toussaint River and has also been reported from a close site in Sinnamary, in northern French Guiana (Fig. 4).

Key to the species of Auyantepuia from French Guiana

The following key is proposed for the seven species of *Auyantepuia* described from French Guiana. This key is based on the previous key proposed by Ythier & Chevalier (2020), taking into consideration the new material analysed in the present note. This key must be considered as imperfect, provisional and susceptible to possible exceptions, hence it is to be used with caution and should not be the only tool for identifying a specimen. If there is any doubt, original descriptions should also be consulted.

1. Pedipalp chela weakly to moderately granulated..... 2
– Pedipalp chela moderately to strongly granulated..... 7

2. Ventral side of several metasomal segments without darker variegated spots……..... 3
– Ventral side of all metasomal segments without darker variegated spots..... 6

3. Chela manus dorsal surface smooth in both sexes..... ***A. manmandinan*** sp. nov.
– Chela manus dorsal surface granulated in both sexes..... 4

4. Male chela manus well granulated on entire surface dorsally and weakly granulated on distal half internally..... ***A. kwata*** sp. nov.
– Male chela manus weakly granulated on distal half dorsally and almost smooth internally..... 5

5. Ventral side of metasoma with weakly marked spots on segments IV and V, other segments reddish yellow, without spots..... ***A. aluku*** Ythier, 2018
– Ventral side of metasoma with intensely marked spots on segments IV and V and weakly marked spots on segment III, other segments yellowish, without spots ..... ***A. laurae*** Ythier, 2015

6. Body, pedipalps, legs and chelicerae marked with darker variegated spots; small species (14–22 mm)..... ***A. kelleri*** (Lourenço, 1997)
– Body, pedipalps, legs and chelicerae without darker variegated spots; larger species (25–27 mm). ..... ***A. gaillardi*** Lourenço, 1983

7. Ventral side of metasoma with darker variegated spots on all segments ……
……..…. ..... ***A. fravalae*** Lourenço, 1983
– Ventral side of metasoma with darker variegated spots on segments III to V, other segments without spots 8

8. General coloration reddish brown..... ***A. aurum*** Ythier, 2018
– General coloration yellowish..... ***A. sissomi*** Lourenço, 1983

Discussion

Our integrative taxonomic approach has laid the groundwork for a comprehensive analysis of the *Auyantepuia* species found in French Guiana. Specifically, we present compelling evidence for the existence of two new species. It is noteworthy that the genus exhibits subtle morphological differences, with species sometimes distinguished mainly by size and coloration. While these differences may suffice for species identification when large sets of individuals are available, they can pose challenges when dealing with isolated specimens, particularly juveniles. Hence, we strongly advocate an integrative approach combining morphology and molecular markers.

In this study, we employed a genome skimming strategy targeting the mitochondrial genome. This approach is relatively straightforward from a molecular biology standpoint, requiring no amplification. Since the library preparation involves short fragments (typically 400 base pairs or shorter), it can accommodate specimens with degraded DNA, where traditional Sanger sequencing targeting longer fragments would fail. However, we acknowledge that the higher cost associated with this approach may remain prohibitive compared to Sanger sequencing, particularly when a large number of specimens need to be analyzed. In our investigation, we assessed the performance of three fragments in the cox1, 12S, and 16S genes for species identification and discovery. Despite their varying sizes, ranging from 399 to 658 base pairs, all three markers demonstrated sufficient divergence to complement morphological analyses effectively.

While molecular data offer an additional layer of evidence to aid morphological analyses, they do not singularly resolve all taxonomic issues. In our study, we only assigned species-level status when it was supported by both significant genetic divergence and clear morphological characters. Thus, we adopted a conservative approach, maintaining specimens within the same species despite high genetic divergence when no discernible morphological differences were observed. This was exemplified in cases such as *A. aluku* (93.3% genetic similarity), *A. aurum* (92.9% genetic similarity), and *A. laurae* (94.1% genetic similarity).

We acknowledge that approaches employing algorithms such as AGBD (Puillandre *et al.* 2012) or mPTP (Kapli *et al.* 2017) might provide more objective results about species delimitations. Whether based on direct measures of genetic distance, or on differences in phylogenetic tree branch lengths, all these methods are based on the assumption that intra-specific genetic distances are different from inter-specific distances. As such, they all require a good sampling of the different populations within species in order to provide good estimates of the intra-specific variability. Further studies would thus need to include a better sampling of the different populations within each species in order to provide more objective estimates of species boundaries.

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