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Description of two new species of *Termes* (Isoptera: Termitidae) from Colombia and Venezuela using morphological and mitochondrial data

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Abstract

Two new species of the genus *Termes* Linnaeus are described through an integrative approach, combining whole mitogenome sequencing and comparative morphology across all neotropical congeneric species. Our maximum-likelihood phylogenetic reconstruction places the two new species in a clade sister to the *T. fatalis* species complex. *Termes chocoensis* **sp. nov.** was found along the Pacific coast of Colombia, and *Termes atlanticus* **sp. nov.** near the Atlantic coast and in Venezuela. Their soldiers differ from those of other *Termes* species in terms of head, pronotum, and mandible measurements. Workers exhibit a distinctive armature of the enteric valve, which is currently the only diagnostic character separating *T. fatalis* from *T. atlanticus* **sp. nov.** and *T. medioculatus* from *T. chocoensis* **sp. nov.**, highlighting the criticality of examining multiple castes when identifying *Termes* specimens.

Key words: Neotropical region, phylogeny, taxonomy, termite, Termitinae

Introduction

The number of termite species recorded in Colombia has been growing spectacularly in the past decade. In 2013, the catalogue from Krishna *et al.* reported 41 species, while the latest checklist (Pinzón Florián *et al.* 2025) listed up to 198. Despite this growth, the sampling effort remains unbalanced between regions, and some taxonomic groups are still challenging to identify at the species-level. The genus *Termes* Linnaeus is suffering from these problems, as it is composed of multiple species with similar-looking soldiers, the caste often used for species diagnosis, with few genetically identified specimens and unresolved geographic ranges (Fontaine *et al.* 2025).

Pinzón Florián *et al.* (2025) listed five species of the *Termes* genus in Colombia: *T. ayri* Bandeira & Cancello, *T. fatalis* Linnaeus, *T. hispaniolae* (Banks), *T. medioculatus* Emerson and *T. panamaensis* (Snyder), reported from the northern Atlantic coast to the southern Amazonian forest. The lack of reports along the Pacific coast and in the east of the country is likely due to the low number of surveys in those areas (Pinzón Florián *et al.* 2025). Identifications of *T. fatalis*, *T. panamaensis* and *T. medioculatus* should be taken with caution, as these species form a cryptic group whose soldiers are not easily distinguished (Fontaine *et al.* 2025). Additionally, *Termes nigritus*

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(Silvestri) is reported by Castro *et al.* (2021) from the Caquetá department, but was not included in Pinzón Florián *et al.* (2025) checklist. This record may be considered doubtful as the species was previously only reported from Argentina, Paraguay, and the south of Brazil (Krishna *et al.* 2013b). Two unidentified *Termes* are also mentioned by Pinzón Florián *et al.* (2017) and Casalla Daza & Korb (2019), both under the name *Termes* sp. 1. Records from the University of Florida Termite Collection (UFTC; https://www.termitediversity.org/) account mostly for *T. fatalis* and *T. hispaniolae* samples, all near the Atlantic coast.

We sequenced DNA from several Colombian samples. Our results indicated that two lineages proved to be different from the previously identified material (*i.e. T. fatalis*, *T. hispaniolae*, *T. panamaensis*, *T. medioculatus*, and the recently described *T. incognitus* Fontaine: Fontaine *et al.* 2025) and from the descriptions of the other neotropical *Termes* species: *T. ayri*, *T. bolivianus* (Snyder), *T. nigritus* and *T. riograndensis* Jhering. Herein, we describe them as two new species of the *Termes* genus, *T. atlanticus* **sp. nov.** Fontaine and *T. chocoensis* **sp. nov.** Fontaine & Roisin. We provide a comparison with all other neotropical species of *Termes* in order to facilitate their future identification, and to contribute at the necessary taxonomic revision of this genus.

Methods

Material used

The studied samples were collected in Colombia between 2015 and 2017 under permit no. 120 240,815, then stored at the Université Libre de Bruxelles (ULB), Belgium. For each colony, several soldiers and workers were collected in 100% ethanol for genetic analysis and in 80% ethanol for morphological analysis. We also studied two samples from the University of Florida Termite Collection (UFTC), preserved in 85% ethanol. One was collected in Colombia in 2008 under permit no. 2100-2-59891 (colony code CO785), the other in Venezuela in 2009 under permit no. 33793754 from the Venezuela Interior Department (colony code VZ0981). Overall, we examined four samples of *T. chocoensis* **sp. nov.** and three of *T. atlanticus* **sp. nov.** Details regarding their collect are given in the supplementary material in the Zenodo repository (DOI: 10.5281/zenodo.18837709). A map illustrating the distribution of the samples (Fig. 1) was created in QGIS v3.26.3 using Mapzen Global Terrain for elevation features and the standard Open Street Map background for zoomed-in sections.

Morphology

Soldiers and workers were measured using a Wild MMS 235 micrometer mounted on a stereomicroscope. We chose the same morphological parameters as in Fontaine *et al.* (2025) to allow comparison with *T. fatalis*, *T. incognitus*, *T. medioculatus* and *T. panamaensis*, and measurements were taken by the same operator as well. Abbreviations are indicated between brackets alongside the corresponding numbers of the parameters issued from Roonwal (1969). For the soldiers, we measured the head length to the tip of the frontal process (HLT, no.09), the head length to the antero-lateral corner of the genae (HLG), the head depth (HD, no.21), the head width (HW, no.17), the pronotum width (PW, no.68), the length of the left mandible (ML, no.36), the minimum width of the gula (GWmin, no.63), the maximum width of the gula (GWmax, no.62), and the length of the left hind tibia (TL, no.85). For the workers, we measured the head width (HW, no.17) and the length of the left hind tibia (TL, no.85). The range of the measurements for each species is given in Table 1. Pictures of soldiers and workers (Fig. 2 & 3) were taken with a Leica MZ6 stereomicroscope, using the Leica DFC295 camera operated by Leica Application Suite 4.6.1. Individuals were placed in 70% ethanol gel (hand sanitizer), and a mirror was placed under the dish to improve the visibility of the setae. Several pictures were taken at different depths and assembled using CombineZP (Hadley 2016).

Some workers were dissected to extract their mandibles and enteric valve (*i.e.* the second part of the proctodeum), which were mounted on microscope slides in a polyvinyl alcohol-based mounting medium (CMCP-9, Polysciences Inc.). They were photographed with a 5MP ToupCam E3ISPM camera (ToupTek Photonics) mounted on a Leitz Laborlux D microscope (Fig. 4). Pictures of the left mandibles were imported in ImageJ (Schneider *et al.* 2012) to measure their mandibular index (abbreviated MI), as defined by Emerson (1960): the distance between the tip of the apical tooth and the tip of the first marginal tooth divided by the distance between the tips of the first and the third marginal teeth. All raw measurements are available in the supplementary material on the Zenodo repository.

FIGURE 1. Geographic distribution of the two new *Termes* species: *T. atlanticus* **sp. nov.** in red and *T. chocoensis* **sp. nov.** in green. Type localities are indicated by a star symbol. The area with overlapping symbols is magnified a first time in the lower left section, then enlarged further in the lower right section.

TABLE 1. range of soldiers and workers measurements, by species. Data of *T. fatalis, T. incognitus, T. medioculatus* and *T. panamaensis* (soldiers) are from Fontaine *et al.* (2025). Abbreviations: "*n* =" is the number of measured individuals of each species; HLT = head length to the tip of the frontal process; HLG = head length to the antero-lateral corner of the genae; HD = head depth; HW = head width; PW = pronotum width; ML = length of the left mandible; GWmin = minimum width of the gula; GWmax = maximum width of the gula; TL = length of the left hind tibia; MI = mandibular index.

Species	***Termes atlanticus* sp. nov.**	***Termes chocoensis* sp. nov.**	***Termes fatalis***	***Termes incognitus***	***Termes medioculatus***	***Termes panamaensis***
Soldiers						
***n* =**	*5*	*19*	*60*	*53*	*61*	*5*
HLT	1.61–1.75	1.16–1.40	1.47–1.92	1.12–1.68	1.27–1.77	1.43–1.54
HLG	1.61–1.73	1.20–1.44	1.42–1.81	1.21–1.67	1.32–1.73	1.50–1.62
HD	0.74–0.79	0.57–0.76	0.66–0.87	0.63–0.81	0.64–0.8	0.77–0.82
HW	0.97–1.00	0.81–0.91	0.81–0.98	0.73–0.93	0.78–0.94	0.93–0.97
PW	0.58–0.62	0.49–0.56	0.52–0.66	0.50–0.63	0.49–0.66	0.60–0.63
ML	1.80–1.84	1.54–1.74	1.75–2.04	1.51–1.85	1.65–1.97	1.82–1.86
GWmin	0.17–0.19	0.17–0.22	0.10–0.19	0.17–0.22	0.11–0.21	0.16–0.21
GWmax	0.34–0.37	0.26–0.33	0.29–0.37	0.27–0.4	0.26–0.38	0.29–0.34
TL	0.87–0.89	0.73–0.83	0.75–0.91	0.64–0.87	0.70–0.90	0.88–0.91
Workers						
***n* =**	*8*	*12*	*18*	*16*	*21*	*4*
HW	0.81–0.93	0.65–0.88	0.74–0.84	0.71–0.8	0.7–0.85	0.79–0.82
TL	0.61–0.78	0.57–0.76	0.61–0.84	0.57–0.71	0.53–0.77	0.67–0.77
MI	1.06 (*n*=1)	1.47–1.92 (*n*=7)	1.08–1.52	1.24–1.85	1.35–2.03	1.36 (*n*=1)

The diagnosis against other neotropical species is based on the measurements from Bandeira & Cancello (1992) for *T. ayri*, Snyder (1926) for *T. bolivianus*, Banks (1919) and Emerson (1925) for *T. hispaniolae*, Silvestri (1903) for *T. nigritus* and *T. riograndensis*, Fontaine *et al.* (2025) for *T. fatalis*, *T. incognitus*, *T. medioculatus* and *T. panamaensis*. The measurement range for these last four species is shown next to that of the new species in Table 1. The measurements of *T. panamaensis* workers are new and were taken on four individuals of the type colony (accession USNM003075 from the US National Museum, Washington DC). Comparisons with *T. bolivianus*, *T. nigritus* and *T. riograndensis* should be taken with caution as they rely only on the measurement of one specimen, which may not be representative of the species' intraspecific variability.

Mitochondrial genome sequencing

We performed whole genomic DNA extractions on one individual of each colony using the DNeasy Blood & Tissue extraction kit (Qiagen). Tissues were broken down in 2 mL microtubes with two 3 mm steel beads and TissueLyser II (Qiagen). Libraries were prepared with the NEBNext Ultra™ II FS DNA Library Preparation Kit (New England Biolabs) and the Unique Dual Indexing Kit (New England Biolabs). We reduced reagent volumes down to 1/15th of the manufacturer's recommendation. One nanogram of DNA was used as input. The fragmentation step was limited to 5 minutes of incubation at 37 °C to avoid over-fragmentation. Libraries were pooled in equimolar concentrations and sequenced using either the Novaseq platform or Illumina HiSeq X, producing 150 base-pairs reads. We used fastp v0.20.1 (Chen *et al.* 2018) to trim adapters and low-quality bases from raw reads, metaSPAdes v3.13 (Nurk *et al.* 2017) to assemble the trimmed reads, and MitoFinder v1.4 to identify mitogenomic fragments (Allio *et al.* 2020) for mitogenome annotation. Sequences are deposited in GenBank under accessions PX717463 to PX717467 (details in Supplementary material).

No genomic data were recovered for one sample (colony code COL17-15). Therefore, Sanger sequencing was used to obtain individual mitochondrial gene sequences. We ended up sequencing only the 12S rRNA and the cytochrome oxidase subunit II (COII) gene, as these markers were sufficient for sample identification. We extracted genomic DNA from the head of a soldier using the NucleoSpin Tissue kit (Macherey-Nagel). PCR amplification of the COII gene was performed using the primers ModAtLeu (Miura *et al.* 2000) and B-tLys (Simon *et al.* 1994), while the 12S rRNA was amplified using primers 12Sai and 12Sbi (Simon *et al.* 1994). Reactions were carried out in a total volume of 25 µL, containing 1.5 µL of template DNA, 0.5 µL of MyTaq DNA polymerase (2.5 U; Bioline), 0.5 µL of each primer (20 µM), 5 µL of MyTaq Reaction Buffer, and 17 µL of PCR-grade water. Thermal cycling conditions followed those described in Fontaine *et al.* (2025). Sequencing reactions were prepared using the BigDye Terminator v3.1 kit (Applied Biosystems) in a final volume of 11.2 µL, comprising 1.0 µL of BigDye, 2.1 µL of 5x sequencing buffer, 0.1 µL of primer (20 µM), 3 µL of PCR product, and 5 µL of PCR-grade water. The sequencing program consisted of an initial denaturation at 96 °C for 1 minute, followed by 25 cycles of denaturation at 96 °C for 10 seconds, annealing at 50 °C for 5 seconds, and extension at 60 °C for 4 minutes. Capillary electrophoresis was performed on an ABI 3730 sequencer (Applied Biosystems), and resulting chromatograms were manually edited using CodonCodeAlinger 8.0.2 (CodonCode Corporation). The two resulting sequences are deposited in GenBank under accessions PX680676 (COII) and PX684446 (12S).

Mitochondrial genomes and individual sequences were compared to the GenBank database using the megablast algorithm from the NCBI BLAST tool (https://blast.ncbi.nlm.nih.gov/) to check if sequences of the new species had already been published.

Phylogenetic reconstruction

We used a maximum likelihood approach to infer the phylogenetic position of the sequenced samples. Newly obtained sequences and mitochondrial genomes were aligned with Termitinae sequences from Bourguignon *et al.* (2017) and Fontaine *et al.* (2025). The mitochondrial genome of colony CO785 was published by Hellemans *et al.* (2026) under accession PX592414. The 37 mitochondrial genes—*i.e.* 13 protein-coding, two rRNA, and 22 tRNA genes—were aligned using MAFFT v7.305 (Katoh & Standley 2013). Protein-coding nucleotide sequences were translated into their amino acid sequences using the transeq function from EMBOSS v6.6.0 (Rice *et al.* 2000), then aligned with MAFFT. Protein alignments were back-translated into codon alignments using PAL2NAL v14 (Suyama *et al.* 2006). All alignments were concatenated using FASconCAT-G_v1.04.pl (Kück & Longo 2014).

We used IQTREE v1.6.12 (Nguyen *et al.* 2015) for tree reconstruction, using the best-fit substitution model as determined by ModelFinder (TVM+F+R3 according to the Bayesian information criterion). Branch support was assessed using ultrafast bootstrap (Minh *et al.* 2013) with 1,000 replicates. The obtained values were corrected with the nearest neighbour interchange search included in IQTREE (option -bnni) to reduce the risk of overestimating branch supports. *Tuberculitermes bycanistes* was used to root the tree.

Results

Taxonomy

Termes atlanticus Fontaine, sp. nov.

Material examined

Holotype: soldier, COLOMBIA: La Guajira: Palomino El Matuy, 11.24608°N -73.54622°E, 2016.VII.10, coll. Y. Roisin (accession COL16-04). **Paratypes**: soldiers and workers from type colony. **Other material**: CO785, COLOMBIA: Atlántico: Puerto Colombia (Barranquilla outskirts), 10.98511°N -74.94283°E, 2009.VI.07, coll. R. Scheffrahn & J. A. Chase (workers); VZ0981, VENEZUELA: Falcón: east of Churaguara, 10.79181°N -69.42545°E, 2008.V.28, coll. R. Scheffrahn & J. R. Mangold (soldiers, workers). Holotype and paratypes from colony COL16-04 are deposited in the Royal Belgian Institute for Natural Sciences (RBINS), Brussels, Belgium. Other paratype soldiers and workers are stored at the Université Libre de Bruxelles (ULB), Brussels, Belgium, and samples will be sent to the American Museum of Natural History (AMNH), New York, United States of America, and the Universidad del Valle, Cali, Colombia.

Description

Soldier (Fig. 2A–C): head rectangular with slightly rounded posterior edges, relatively short, with sparse fine setae. Head color uniformly pale yellow. Frontal process forming an acute triangle, with an almost straight dorsal margin. Setae more numerous on the tip of the frontal process and on its anterior side. Antennae longer than the mandibles, composed of 14 articles (including the scape as the first article), with $4^{th} < 3^{rd} < 2^{nd} = 5^{th}$. Labrum translucent, rectangular, ending in two very fine lateral points. Mandibles rod-shaped, nearly symmetrical and dark, slightly enlarged towards the end where the two mandibles press against each other, and ending in a hook-like tip. Postmentum constricted posteriorly about half of its maximal width. Pronotum saddle shaped.

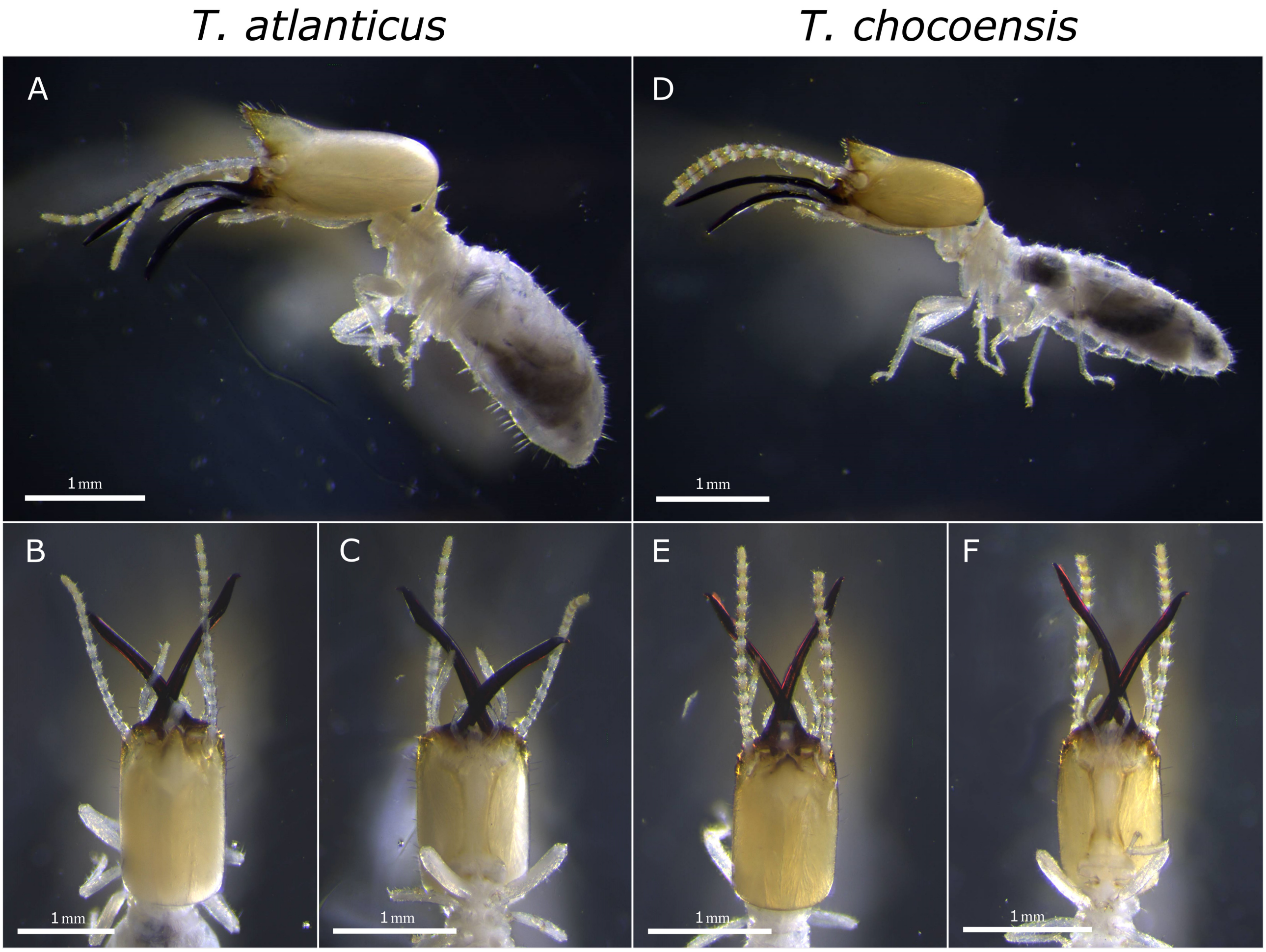

FIGURE 2. Holotypes of *T. atlanticus* **sp. nov.** (A–C) and *T. chocoensis* **sp. nov.** (D–F). A and D, habitus; B and E, dorsal view of the head capsule; C and F, ventral view of the head capsule.

Worker (Fig. 3A–D):): head rounded dorsally, flattened laterally. Head yellow to pale yellow. Clypeus bulging dorsally, divided into two lateral bulges visible in frontal view. Pronotum saddle-shaped, much narrower than the head. Antennae with 14 articles. Abdomen rounded in lateral view, not elongated. Digestive tube (Fig. 4A–D) with a round crop leading to the funnel-shaped proventriculus. The midgut is long and well-developed, initiating with a well-marked bulging pocket on the left. The midgut looping towards the right side of the body and continues ventrally under the gizzard. The mixed segment is ventral, and gives way to the proctodeum on the right side. The first segment (P1), dorsal, is enlarged and ends with a thinner section looping clockwise, where the enteric valve (P2) is inserted on the paunch (P3). The enteric valve bears 6 cushions, alternating between bigger (25–30 spines) and smaller (15–25 spines) ones. The spines are almost not sclerified, with a large, flattened base, often crescent-shaped, and a very short tip (Fig. 4D). The fourth proctodeal segment (P4) starts dorsally in a thin loop before going down on the right side of the body and leading onto the rectum.

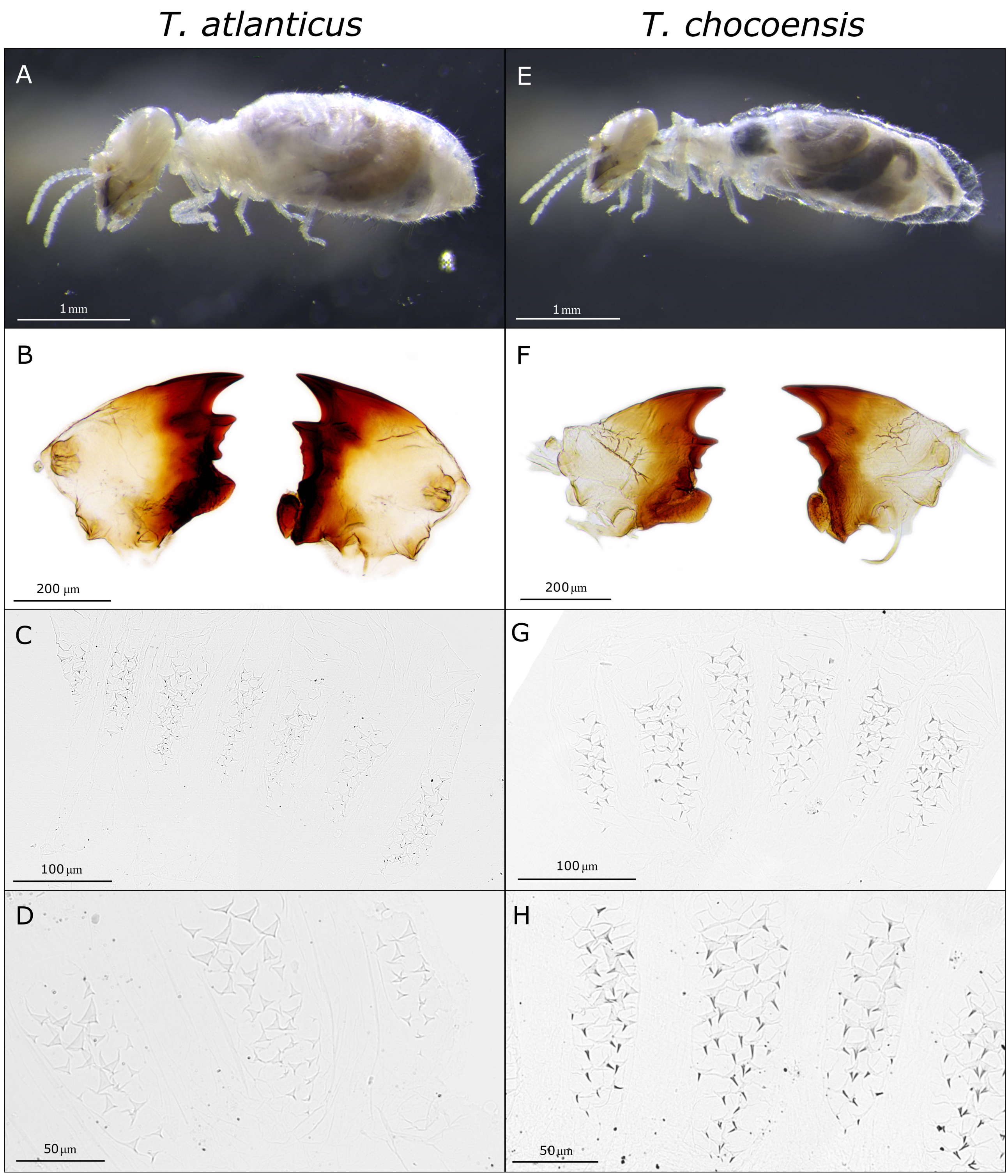

FIGURE 3. Paratype workers of *T. atlanticus* **sp. nov.** (A–D) and *T. chocoensis* **sp. nov.** (E–H). A and E, habitus; B and F, mandibles; C and G, general view of the enteric valve; D and H detail of the enteric valve. All from type colonies except D (VZ0981) and G (COL15-19).

Diagnosis

Termes atlanticus **sp. nov.** is best distinguished by the enteric valve armature of the workers. It bears about half as much spines than in the *T. fatalis* species complex (*sensu* Fontaine *et al.* 2025, *i.e. T. fatalis*, *T. incognitus*, *T. medioculatus* and *T. panamaensis*), and lacks the heavily sclerified spines and the sclerotized cushions of *T. hispaniolae*. According to drawings from Godoy & Torales (1993), *T. nigritus* and *T. riograndensis* seem to have a similar enteric valve as *T. atlanticus* **sp. nov.**. They can nonetheless by distinguished from *T. atlanticus* **sp. nov.** by measurements on the soldier (detailed below). The soldiers resemble those of the *T. fatalis* species complex, although the frontal process has a straighter dorsal edge, with the tip never bent upwards in our specimens. The head width of the soldier is also greater than that of most individuals of these species, and the head of the soldier and the worker are lighter-colored. Soldiers of *T. atlanticus* **sp. nov.** differ from other species by the following measurements:

- *T. ayri* has a shorter head (1.33–1.39 mm), a narrower pronotum (0.48–0.51) and shorter mandibles (1.47–1.56 mm, Bandeira & Cancello 1992).
- *T. bolivianus* has a narrower pronotum (0.55 mm) according to one measurement from Snyder (1926), and a shorter frontal processes when compared to the drawing from Mathews (1977: fig. 77). Mathews is however unsure of its identification.
- *T. hispaniolae* has a longer and larger head (HLT: 1.54–1.70 mm, HW: 1.09–1.16 mm), a larger pronotum (0.73 mm) and longer mandibles (2.15 mm, Emerson 1925), and a longer head (1.90 mm, Banks 1919).
- *T. incognitus* has a shorter and narrower head (HLT, HW).
- *T. medioculatus* has a narrower head (HW).
- *T. nigritus* has a shorter head (1.46 mm) and shorter mandibles (1.5 mm, Silvestri 1903).
- *T. panamaensis* has a shorter head (HLT).
- *T. riograndensis* has a larger head (1.10 mm, Silvestri 1903).
- *T. chocoensis* **sp. nov.** has a shorter and narrower head (HLT, HLG, HW), a narrower pronotum (PW), shorter mandibles (ML), a narrower gula (GWmax) and shorter hind tibia (TL).

Soldiers' measurements do not differ from those of *T. fatalis*.

Ecology

The type colony was collected in a small stump in a shadowed pasture, a picture of which is included in the supplementary material on the Zenodo repository.

Etymology

The name *atlanticus* refers to the Atlantic coast of Colombia and Venezuela, near which the samples were found.

Termes chocoensis **Fontaine & Roisin, sp. nov.**

Material examined

Holotype: soldier, COLOMBIA: Chocó: Arusi: Choiba ecolodge, 5.56932°N -77.50415°E, 2017.VII.31, coll. Y. Roisin, D. Sillam-Dussès & R. Fougeyrollas, (accession COL17-27). **Paratypes**: soldiers and workers from type colony. **Other material**: COL15-19, COLOMBIA, Chocó: Nuquí: El Cantil ecolodge, 5.61972°N -77.42147°E, 2015.VII.28, coll. Y. Roisin (soldiers, workers); COL17-15, COLOMBIA, Chocó: Nuquí: Guachalito, 5.62183°N -77.42035°E, 2017.VII.29, coll. Y. Roisin, D. Sillam-Dussès & R. Fougeyrollas (soldiers, workers); COL17-20, COLOMBIA, Chocó: Nuquí: Guachalito, 5.62°N -77.42°E, 2017.VII.29, coll. Y. Roisin, D. Sillam-Dussès & R. Fougeyrollas (soldiers, workers). Holotype and paratypes from colony COL17-27 are deposited in the Royal Belgian Institute for Natural Sciences (RBINS), Brussels, Belgium. Other paratype soldiers and workers are stored at the Université Libre de Bruxelles (ULB), Brussels, Belgium, and samples will be sent to the American Museum of Natural History (AMNH), New York, United States of America, and the Universidad del Valle, Cali, Colombia.

Description

Soldier (Fig. 2D–F): head rectangular with posterior edges slightly rounded, not very long, covered in sparse fine setae. Head color is uniform, but variable across colonies between deep orange and yellow. Frontal process relatively short (rarely goes farther than the anterior part of the genae), with a slight dorsal bulge and a pointy tip turned upwards. Pilosity more abundant on the tip and the anterior part of the frontal process. Antennae with 14 antennomeres (including the scape as the first article), longer than the mandibles. Relative size of antennomeres: $4^{th} < 3^{rd} < 2^{nd} = 5^{th}$. Labrum translucent, ending in two very short lateral points. Maxillary palps of 4 articles. Mandibles are long, slender, almost symmetrical and dark colored. The distal quarter of the mandibles is slightly enlarged, and ends with a fine tip bent like a hook towards the interior (*i.e.*, it appears towards the exterior when the mandibles are snapped). Postmentum outlined by dark edges, constricted posteriorly about two thirds to three quarters of its maximal width. Pronotum saddle-shaped. Abdomen variably elongated, digestive tube visible through the transparent cuticle.

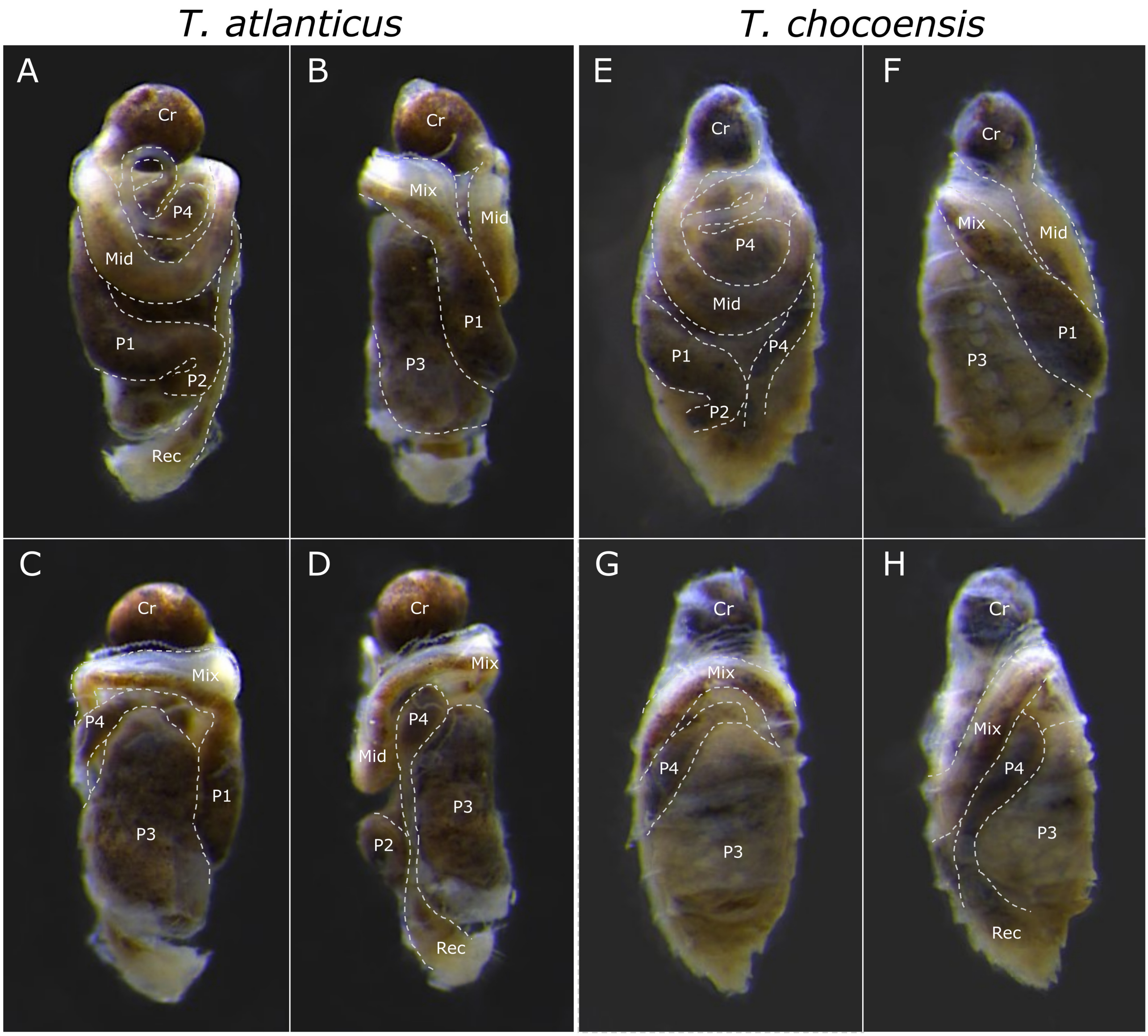

FIGURE 4. Digestive tube of paratype workers from type colonies of *T. atlanticus* (A–D) and *T. chocoensis* (E–H). A and E, dorsal view; B and F, left view; C and G, ventral view; D and H, right view. Abbreviations: Cr = crop, Mid = midgut, Mix = mixe segment, P1 to P4: segments of the proctodeum, Rec = rectum.

Worker (Fig. 3E–H): head round dorsally, of variable color (dark to pale yellow). Clypeus forming a clear bulge, visible laterally. Antennae with 14 articles. Abdomen very elongated, with a transparent cuticle. Digestive tube (Fig. 4E–H): gizzard in dorsal position, spherical when filled. Proventriculus small, opening at the left side of the body. Midgut initiating with a small bulging pocket on the left, then elongated and forming a loop towards the right, ending ventrally under the gizzard. Mixed segment ventral. First part of the proctodeum (P1) widening on the left side and going up dorsally, ending with a 180° elbow plunging towards the ventral side where the enteric valve (P2) opens onto the paunch (P3). Enteric valve with six cushions, alternating between bigger (with ca. 25–30 spines) and smaller (15–20 spines) ones; spines with dark sclerified tips (Fig. 4H). Paunch very wide, occupying almost half of the abdomen when viewed from the ventral side. Fourth proctodeal segment (P4) opening dorsally, anterior to the P3, forming a complete anticlockwise loop around its emergence from the P3, of quite narrow diameter and contained within the space delimited by the dorsal loop of the midgut. P4 then goes ventrally and to the right, descending posteriorly below the beginning of the mixed segment, and reaching the centre of the dorsal side. Rectum pear-shaped, distinctly located below the P3.

Diagnosis

T. chocoensis **sp. nov.** is easily distinguished from other neotropical *Termes* species by the unique enteric valve of the workers, bearing characteristic spines ending in a dark sclerotized tip. These spines are similar to those of *Inquilinitermes inquilinus* (Emerson), but they are less numerous and not as long. The enteric valve also differs from *T. hispaniolae*—which is the only other neotropical *Termes* with sclerotized spines—in having more spines, always very pointy, never blunt, and the cushions are never sclerotized. The enteric valve has about half less spines than in the *T. fatalis* species complex, spines being more spaced and with a better-defined outline. Soldiers of *T. chocoensis* **sp. nov.** are among the smallest of the genus, along those of *T. incognitus* and *T. ayri*. The frontal process is shorter than in the *T. fatalis* species complex, but with a similar dorsal curvature. Soldiers of *T. chocoensis* **sp. nov.** differ from other species by the following measurements:

- *T. ayri* has shorter hind tibia (0.62–0.65 mm, Bandeira & Cancello 1992).
- *T. bolivianus* has a longer head (1.70 mm, Snyder 1926).
- *T. hispaniolae* has a longer and larger head (HLT: 1.54–1.70 mm, HW: 1.09–1.16 mm), a larger pronotum (0.73 mm), longer mandibles (2.15 mm) and longer hind tibia (0.97–1.00 mm, Emerson 1925) and a longer head (1.90 mm, Banks 1919).
- *T. fatalis* has a longer head (HLT, HLG) and longer mandibles (ML).
- *T. nigritus* has a larger head (1.00 mm, Silvestri 1903).
- *T. panamaensis* has a slightly larger head (HW) and longer hind tibia (TL)
- *T. riograndensis* has a longer and larger head (HLG: 1.60 mm; HW: 1.10 mm), and longer mandibles (1.80 mm, Silvestri 1903).
- *T. atlanticus* **sp. nov.** has a longer and larger head (HLT, HLG, HW), a larger pronotum (PW), longer mandibles (ML), a larger gula (GWmax) and longer hind tibia (TL).

Soldiers' measurements do not differ from those of *T. incognitus* and *T. medioculatus*.

Ecology

Collected in rotten wood and in constructions at the base of a tree.

Etymology

The biogeographical region of Chocó, Colombia, in which the samples were found.

Phylogeny

The maximum likelihood phylogeny inferred from mitochondrial genomes (Fig. 5) places *T. atlanticus* **sp. nov.** and *T. chocoensis* **sp. nov.** in a monophyletic clade, grouped together and distinct from previously sequenced *Termes* species. They are placed as the sister-clade of the *T. fatalis* species complex sensu Fontaine *et al.* 2025 (*T. fatalis* + *T. panamaensis* + *T. medioculatus* + *T. incognitus*), with maximum branch support.

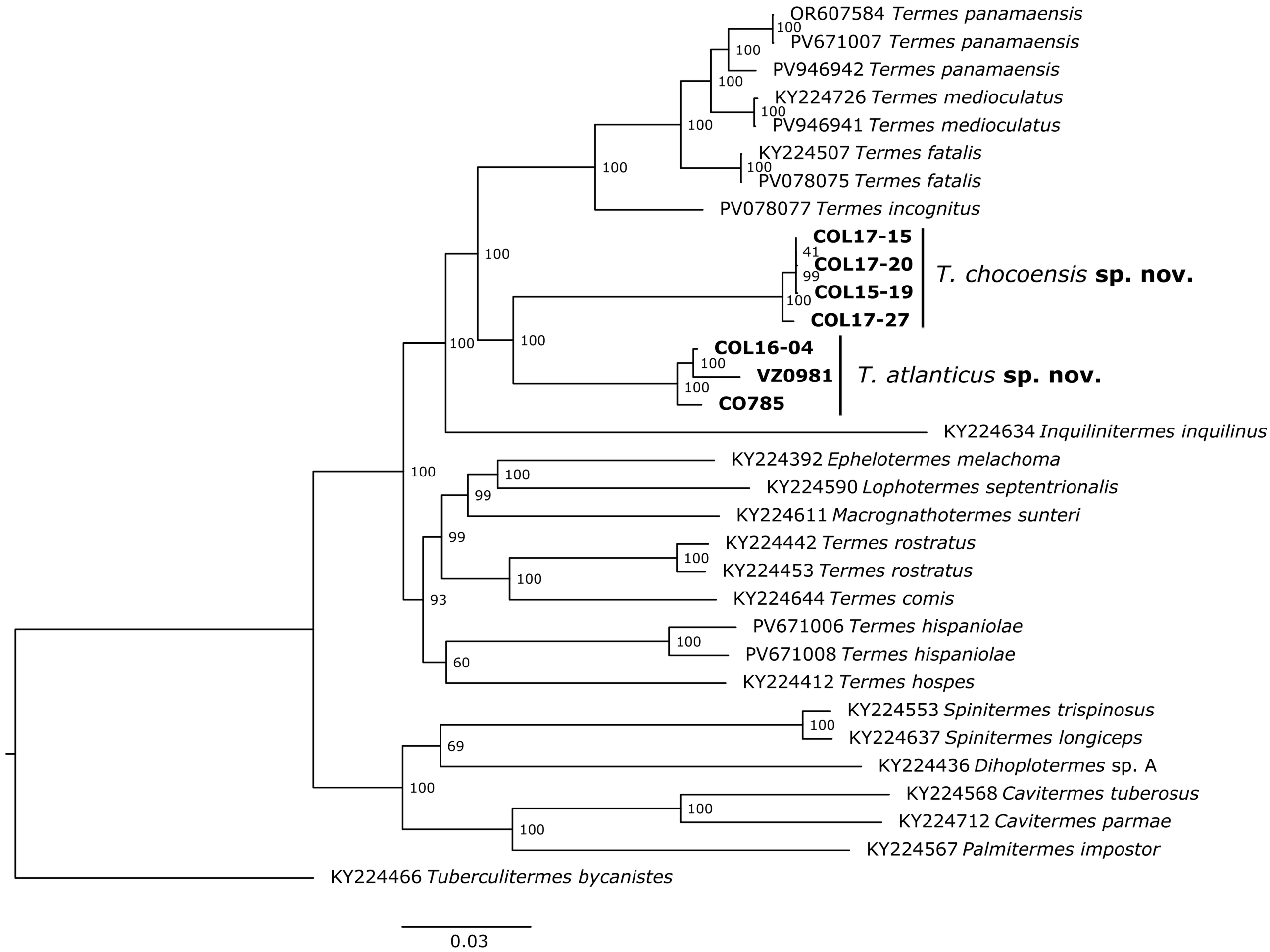

FIGURE 5. Maximum likelihood phylogeny based on whole mitochondrial genomes, with ultrafast bootstrap branch supports as node values. Sequences retrieved from GenBank are named with their accession first, and new sequences are indicated in bold.

Comparison of the complete mitochondrial genomes with the GenBank nucleotide database showed that both clades have 90 to 91% similarity with sequences KY224507 (*T. fatalis*), KY224464 (*Inquilinitermes* sp.), KY224611 (*Macrognathotermes sunteri*), and OQ555373 (*Quasitermes incisus*) from Bourguignon *et al.* (2017) and Wang *et al.* (2023). Blast results of the COII gene revealed that sequences from *T. atlanticus* **sp. nov.** have over 99% similarity with sequence MH090853, the *Termes* sp. 1 from Casalla Daza & Korb (2019). In *T. chocoensis* **sp. nov.**, COII sequences matches only up to 91 to 92% of sequence OR509620 (*Termes fatalis*) from Paulino Monteiro *et al.* (2025).

Discussion

Our mitogenome-based phylogeny provides evidence for two new *Termes* species from Colombia. *T. chocoensis* **sp. nov.** is the second *Termes* species reported in the Pacific region of Colombia after *T. hispaniolae* (Pinzón Florián *et al.* 2025). *T. atlanticus* **sp. nov.** matches one unidentified sequence previously deposited in GenBank, also collected near the Atlantic coast of Colombia (Casalla Daza & Korb 2019).

The two new species present a high number of morphological differences between their soldiers (seven out of nine parameters measured), although they are sister species. This is contrasting with the situation in the *T. fatalis* species complex, where soldiers are much more similar (Fontaine *et al.* 2025). The absence of difference in soldiers' measurements between *T. fatalis* and *T. atlanticus* **sp. nov.**, and between *T. medioculatus* and *T. chocoensis* **sp. nov.** implies that these species cannot reliably be distinguished without examining the workers' enteric valve. It also highlights the need to use castes other than soldiers for the identification of *Termes* species, as in the close genus *Palmitermes* Hellemans & Roisin (Hellemans *et al.* 2017), and in the species of the Cubitermitinae genus *Isognathotermes* Sjöstedt (Josens *et al.* 2025).

Previous reports of *T. fatalis* and *T. medioculatus* should thus be taken with caution if they are not verified against the new species proposed here. Their presence in Colombia, as well as that of *T. ayri* and *T. nigritus*, should be confirmed through DNA barcoding to avoid any doubt. On the other hand, the presence of *T. hispaniolae* and *T. panamaensis* is expected in Colombia since they are widely reported in the Caribbean region (Krishna *et al.* 2013b; Scheffrahn 2020).

Our results show the need for a larger barcoding effort of Colombian samples to assess which of the reported species are truly present in the country. Currently most neotropical *Termes* records are based on morphological identification only, which can be misleading in the light of our results and those of Fontaine *et al.* (2025). Geographic distributions inferred from those records may therefore be unreliable. A large-scale biogeographic study based on molecular data, as recently done on *Heterotermes* (Carrijo *et al.* 2020) and *Labiotermes* (Pontes-Nogueira *et al.* 2026), would be useful to circumscribe the distribution area of *Termes* species. It would then facilitate their identification by allowing researchers to rule out possible species identification based on known geographic range. A complete identification key of neotropical *Termes* species based on type or genetically identified material is needed to enable termitologists to correctly identify members of this genus down to the species level.

Contributions

NF, formal analysis and first draft; SH, data processing; EK, lab work; RHS, DSD, YR, field work; TB, DSD, IA, funding. All authors commented and edited the draft, then approved the final version.

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Data Availability

The five new mitogenome sequences produced for this study are available on GenBank under accession numbers PX717463 to PX717467. The two mitochondrial gene sequences of sample COL17-15 obtained with Sanger sequencing were deposited under accession numbers PX680676 (COII) and PX684446 (12S). The supplementary material, containing raw measurements and sample collection information, is available in the following Zenodo repository: https://doi.org/10.5281/zenodo.18837709.

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