



SHORT NOTE

New Record of *Platythyrea exigua* Kempf, 1964 (Hymenoptera: Ponerinae) and its Nuclear 1C Value: Insights into Biogeography and Genome Size

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Abstract

The ant tribe Platythyreini comprises a single genus, *Platythyrea* Roger, 1863, with 40 described species. *Platythyrea exigua* Kempf, 1964 is a Neotropical species and, in Brazil, had previously been recorded only in Mato Grosso and Rondônia (Amazon biome) and in Bahia (Atlantic Forest biome), the latter considered a possibly isolated population. Here, we report the first record of *P. exigua* from the Atlantic Forest of Minas Gerais State, based on specimens sampled in Mata do Paraíso, Viçosa, in 2022. This new record represents an important biogeographical link between previously disjunct populations in the Amazonian and Atlantic Forests. In addition, we provide the first nuclear genome size value for *P. exigua* ($1C = 0.266 \pm 0.01$ pg), which is markedly lower than values reported for other Ponerinae species. Together, these data highlight the importance of integrating faunal surveys with nuclear 1C values to improve our understanding of Neotropical ant diversity and distribution.

The ant tribe Platythyreini (Formicidae: Ponerinae) consists of a single genus, *Platythyrea* Roger, 1863, currently comprising 40 described extant species (Bolton, 2026). The genus has a pantropical distribution, occurring in tropical regions of Africa, Asia, Oceania, and the Americas. In Brazil, five species are recognized, including *Platythyrea exigua* Kempf, 1964 (Brown, 1975; Leyva, 2013). This species was originally described from a colony collected in Utariti, along the Papagaio River, Mato Grosso state, near the southern limit of the Amazon biome (Kempf, 1964). Subsequent records include an alate female from Parque Estadual Guajará-Mirim in Rondônia (Amazon biome), a worker from Ilhéus, Bahia (Atlantic Forest biome) (Delabie, 2001), and an additional record from Canindeyú, Paraguay (Wild, 2007). Thus, *P. exigua* may occur in both Amazonian and Atlantic Forest biomes.

The wide geographic separation between Amazonian and Atlantic Forest records (~2,000 km) led Delabie (2001) to propose that the Atlantic Forest population is disjunct and potentially isolated. Moreover, the species had not previously

been reported from intervening Brazilian states (such as Minas Gerais, Tocantins, or Goiás), raising questions about its true distribution and ecological requirements.

Beyond morphology and biogeography, genomic data can elucidate ant diversity and evolutionary patterns (Tsutsui et al., 2008). Genome size, expressed as nuclear 1C value, is a genomic attribute linked to karyotype organization and genome evolution (Gregory, 2005). In ants, nuclear 1C values have revealed substantial inter- and intraspecific variation, providing insights into hidden diversity, population structure, and evolutionary divergence. Associated with faunal surveys, nuclear 1C values allow more robust assessments of population continuity, genomic differentiation across biomes, and the extent to which geographically separated populations share conserved or divergent genomic profiles.

We report the first record of *P. exigua* from Minas Gerais (southeastern Brazil) and its first nuclear 1C value. Therefore, this finding fills a critical distributional gap between previously known Atlantic Forest and Amazonian records.



We also provide an essential genomic baseline for the species, highlighting the relevance of the integrative faunal and genomic approaches to advancing ecological, evolutionary, and conservation studies of Neotropical ants.

P. exigua samples were collected in Mata do Paraíso (20°41'20" S and 20°49'35" S, and 42°49'36" W and 42°54'27" W), located in Viçosa, Minas Gerais state, Brazil, in November 2022 (Figure 1). This area represents one of the largest remaining forest fragments in Viçosa, encompassing ~400 hectares at a mean elevation of 650 meters. The vegetation comprises hilltop, slope, and lowland forests and harbors several endangered fauna and flora species.

All foraging individuals were captured by active search, using tweezers, spoons, shovels, and brushes, and transferred to plastic vials. One specimen was dry-mounted under an Olympus SZ61 stereomicroscope using the taxonomic keys of Brown (1975) and Leyva (2013), and taxonomically identified by Dr. Júlio Cezar Mário Chaul and Dr. Lívia Pires do Prado.

The voucher specimen was deposited in the Entomological Collection of the Coleoptera Laboratory at the Federal University of Viçosa (CELC) under the identifier number ANTWEB104 7054. The specimen was photographed using a Leica M205A stereomicroscope coupled with an MC170 HD digital camera, and the images were stacked and edited in Zerene and GIMP softwares, respectively. Full-resolution images have been uploaded to the website AntWeb.org. The distribution map was generated using QGIS (Version 3.40.9).

P. exigua individuals were fixed in methanol: acetic acid solution (3:1), which was replaced twice after 10 min each. After 24 h at -20 °C, this solution was replaced with absolute ethanol, which was also replaced twice after 10 min intervals, and the samples were maintained in absolute ethanol at -20 °C. This fixative procedure was adopted because, compared with absolute ethanol or 70% ethanol, it resulted in flow cytometry histograms with G_0/G_1 peaks with a coefficient of variation below 5%. Therefore, the suspensions had a higher



Fig 1. Map of South America showing the known distribution of the ant *Platythyrea exigua*, including previously reported localities in Paraguay and in the Brazilian states of Bahia (BA), Rondônia (RO), and Mato Grosso (MT), as well as the new record from Minas Gerais (MG), Brazil, documented in the present study.

number of intact, well-preserved, and stoichiometrically stained nuclei, resulting in reproducible and accurate flow cytometry measurements.

The nuclear 1C value was measured for five *P. exigua* adult individuals, which were processed individually and simultaneously with the internal standard, *Drosophila melanogaster* (Meigen, 1830) (1C = 0.18 pg – Bennett et al., 2003). Cerebral ganglia were dissected in physiological solution (0.155 mM NaCl) and transferred to 100 µL OTTO-I lysis buffer (Otto, 1990). The ganglia were macerated 10 times using a pestle in a 1.5 mL microtube. The suspensions were increased to 1.0 mL with the same buffer, filtered through a 30 µm nylon mesh, and centrifuged at 100 ×g for 5 min. The pellet was incubated for 10 min in 100 µL of OTTO-I lysis buffer and stained with 300 µL of OTTO-II buffer (Otto, 1990) supplemented with 75 µM propidium iodide and 50 µg mL⁻¹ RNase (Tavares et al., 2010). The nuclear suspensions were analyzed on a BD Accuri C6 flow cytometer (BD Accuri C6 flow cytometer, Accuri cytometers, Belgium) equipped with a laser source (488 nm) to promote emission through FL2 (615 – 670 nm) and FL3 (>670 nm) filters. More than 10,000 nuclei were analyzed for each repetition. The mean 1C value was presented here in pg and Mbp (1C pg = 978 Mbp, Doležal et al., 2003).

Based on a combination of diagnostic morphological traits (Brown, 1975; Leyva, 2013), the *P. exigua* classification was confirmed. The individuals exhibited a relatively small body size, a long and narrow head (head width including eyes less than 0.9 mm; excluding eyes less than 0.8 mm), a swollen and convex clypeus in the middle; a posterior margin of

petiolar node that, in dorsal view, has lateral corners extending posterad as short, blunt teeth or angles; and mandibles with 6–11 teeth (Figure 2).

High-quality flow cytometry histograms were obtained, with coefficients of variation ranging from 4.4 to 4.8%, confirming the robustness of the methodology. The mean 1C value for *P. exigua* was 0.266 ± 0.01 pg (260.15 Mbp) (Figure 3).

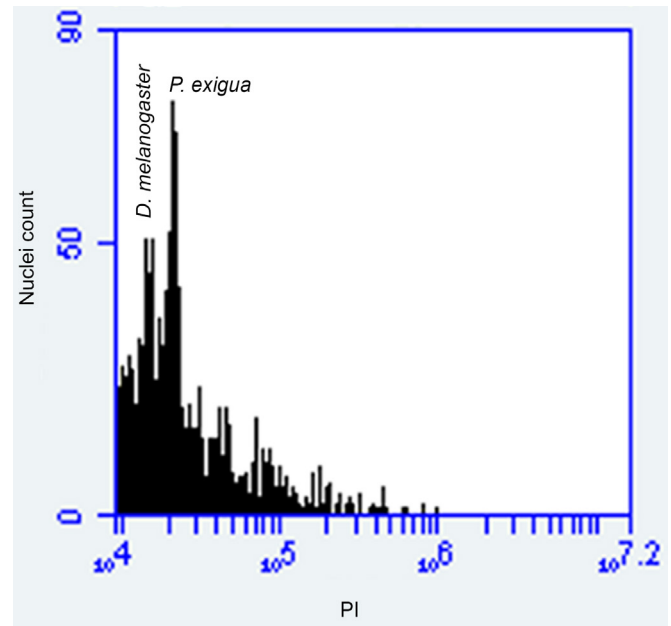


Fig 3. Representative flow cytometry histogram obtained for the DNA content measurement of *Platythyrea exigua*. G_0/G_1 nuclei peak of female *Drosophila melanogaster* (internal standard 2C = 0.36 pg) and G_0/G_1 nuclei peak of female *P. exigua* (2C = 0.532 pg).

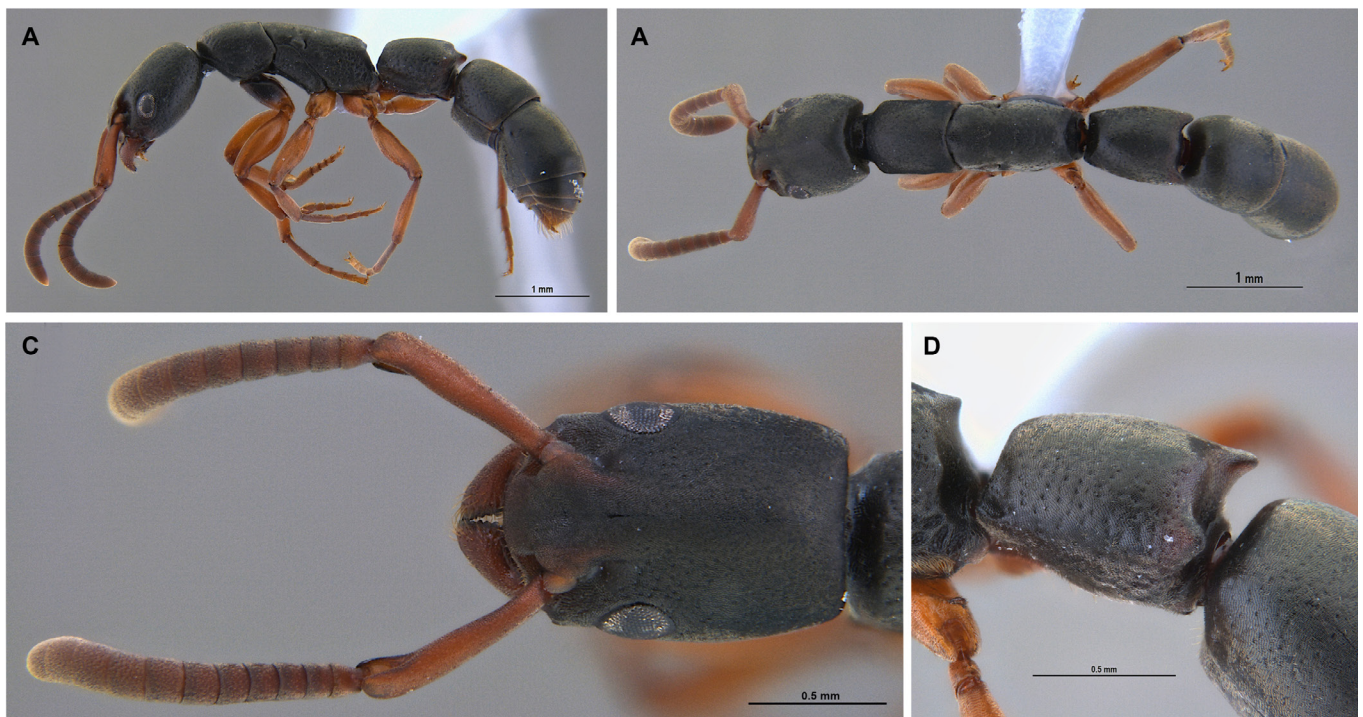


Fig 2. *Platythyrea exigua* worker from Viçosa, Minas Gerais, Brazil. A. lateral view; B. dorsal view; C. full-face view of head; D. petiole in dorsolateral oblique view showing posterolateral protuberances.

Despite significant advances in the knowledge of Neotropical ant diversity (Lattke, 2003; Economo et al., 2018; reviewed in Feitosa et al., 2022), the geographic distributions of many taxa remain poorly resolved (Schmidt et al., 2022; Feitosa et al., 2022; Costa et al., 2025). This gap largely reflects uneven sampling efforts, habitat heterogeneity, and the cryptic or inconspicuous habits of several ant taxa.

The occurrence of *P. exigua* in Minas Gerais demonstrates that targeted and active sampling strategies are essential to prospect cryptic taxa that are frequently overlooked by conventional methods, such as pitfall trapping. This record provides evidence that even well-sampled regions may harbor undocumented species occurrences. Although the Atlantic Forest is one of the most intensively surveyed biomes for ants (Feitosa et al., 2022), *Platythyrea* species, despite their broad tropical distribution, are notoriously underrepresented in inventories, likely due to their inconspicuous behavior and cryptic nesting habitats, ranging from arboreal to ground-nesting strategies (Schmidt & Shattuck, 2014; Delabie et al., 2015).

This new record represents the first occurrence of *P. exigua* in southeastern Brazil and bridges a major distributional gap between Amazonian and Atlantic Forest populations. Combined with previous records from northern Brazil and Paraguay, our data indicate a disjunct distribution spanning Amazonian and Atlantic Forest biomes. Such a disjunct pattern is consistent with historical connections between these regions, potentially facilitated by dispersal corridors during the Miocene, Pliocene, and Pleistocene (Prates et al., 2017; Castro-Astor et al., 2024).

In addition to its biogeographic significance, we provide the first nuclear 1C value for *P. exigua*, which is considerably lower than values reported for other Ponerinae taxa (0.47–0.50 pg; Tsutsui et al., 2008; Moura et al., 2021), revealing pronounced genomic variation in this subfamily. The interspecific variation in nuclear 1C values mirrors the extensive genome size diversity documented across Formicidae, including Myrmicinae, Formicinae, and Dolichoderinae, with values ranging from below 0.30 pg to above 0.60 pg. Such variation supports the view that genome size evolution in ants is characterized by repeated, independent expansions and contractions (Moura et al., 2021).

For species with disjunct or poorly documented distributions, such as *P. exigua*, genome size data offer a complementary framework for evaluating population continuity and potential evolutionary divergence. Similarities or differences in nuclear DNA content among geographically distant populations may help distinguish between a single cohesive taxon and differentiated evolutionary units (Cardoso et al., 2018; Moura et al., 2021).

In conclusion, the discovery of *P. exigua* in the Brazilian State of Minas Gerais not only fills a key distributional gap but also provides the first genomic characterization of the species. Together, these findings reinforce the importance of integrating biodiversity inventories with nuclear 1C value

analysis to better understand the ecological and evolutionary complexity of Neotropical ants.

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Authors' Contributions

M.G.T.: Conceptualization; methodology; investigation; formal analysis; writing-original draft; writing-review & editing; visualization; supervision; project administration.

G.A.T.: Conceptualization; methodology; investigation; formal analysis; writing-review & editing; visualization.

P.O.M.P.: Conceptualization; methodology; investigation; formal analysis; writing-review & editing; visualization.

W.R.C.: Conceptualization; methodology; investigation; formal analysis; investigation; writing-review & editing; visualization.

Conflict of Interest

The authors declare there are no conflicts of interest.

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