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# A new species of planthopper in the genus *Jamaha* (Hemiptera: Fulgoroidea: Nogodinidae) from the Northeastern coast of Jamaica

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## Abstract

A new species of *Jamaha* Gnezdilov & O'Brien, 2008, is described from Jamaica and compared with other species in the genus. A key to the species of *Jamaha* is provided. Molecular data for the five-prime region of the cytochrome c oxidase subunit I (COI) gene and 18S rRNA gene is provided and compared to available Colpopterini, with other Nogodinidae as the outgroup, for a preliminary phylogenetic analysis. While the Colpopterini grouped with high support, these data remain too sparse to draw firm conclusions.

## Resumen

Se describe para Jamaica una nueva especie perteneciente al género Jamaha Gnezdilov & O'Brien 2008 y se compara con otras especies del mismo género. Además, se proporciona una clave para las especies de Jamaha. Para un análisis filogenético preliminar, se utilizan los datos moleculares para la región cinco-prima del gen de la subunidad I (COI) del citocromo *c* oxidasay para el gen 18S ARNr y se comparan con datos disponibles de la tribu Colpopterini y conespecies de la familia Nogodinidae como grupo externo. Si bien Colpopterini mostró unarelación altamente significativa con Jamaha, estos datos siguen siendo demasiado escasos para obtener conclusiones contundentes.

**Key words:** taxonomy, phylogenetics, biodiversity, survey, Colpopterinae

## Introduction

*Jamaha* Gnezdilov & O'Brien is a small Caribbean genus of planthopper in the family Nogodinidae (Colpopterinae: Colpopterini). It is currently comprised of two species; *J. chrysops* (Fennah, 1955) and *J. elevans* (Walker, 1858), both originally described from Jamaica (*J. elevans* was subsequently reported from Haiti by Melichar (1902) and Metcalf (1938) (Bourgoin, 2022). *Jamaha* is segregated from the genus *Colpoptera* Burmeister, 1835, diagnosed by the presence of an elongate lateral process on the opening of the pygofer (Gnezdilov & O'Brien, 2008; e.g.: Fennah 1955, Figs 1n, 2q). The family-level placement of *Colpoptera* has long been uncertain and the genus has been variously placed in the Flatidae (e.g., Walker 1858, Melichar 1902, 1923; Distant 1910), Ricaniidae (e.g., Van Duzee 1907) and Issidae (Fowler 1904, Metcalf 1938, 1958), before being moved to its current place in the

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Nogodinidae (Gnezdilov 2012). *Colpoptera* is the type genus of the Colpopterini established for *Colpoptera* and *Neocolpoptera* Dozier, 1931, (in the Issidae: Issinae) based on features of the wing (especially hind wing venation) and female gonoplacs (Gnezdilov 2003). The Colpopterini was upgraded in status to Colpopterinae and transferred to the Nogodinidae (with expanded genus composition) by Gnezdilov (2012) based primarily on the specialized 'beak-shaped' ovipositor and some characteristic venation patterns of both the fore- and hind wing. Subsequently, Szwedo *et al.* (2019) added the extinct genus *Niadrima* Szwedo to a new tribe Niadrimini in Colpopterinae. The Colpopterinae currently consists of 2 tribes (Colpopterini and Niadrimini), with 9 genera in the Colpopterini (1 African—the validity of which is currently in doubt, 2 Dominican amber—one recently (Szwedo *et al.* 2022), 6 Caribbean, Mesoamerican, and northern South American) and a total of 40 species (Niadrimini is monotypic). In the New World, the Colpopterini are distributed at least from Ecuador (noted in Barringer *et al.* 2019) north to northern Mexico (*C. albavenosa* Caldwell, 1945, was described from San Luis Potosí, and the type series of *C. bifurcata* Caldwell, 1945, included a specimen from Sonora; Caldwell, 1945), throughout the Caribbean, and with an undetermined species in southern Florida (Bartlett *et al.* 2014). As noted in Gnezdilov (2012: 350), it "is beyond doubt that further investigation" will increase the number of taxa in the Colpopterinae. Our review of undetermined Colpopterini suggests that there are many species in this tribe requiring description.

Recent vector survey work in Jamaica has focused on documenting Cixiidae in the region due to the ability of *Haplaxius crudus* Van Duzee to transmit the phytoplasma ('*Candidatus* Phytoplasma palmae') that causes lethal yellowing (LY) in coconut palms (*Cocos nucifera* L.) (Howard & Thomas 1980) and the discovery of a new species, *Oecleus mackaspringi* Bahder & Bartlett, 2019 that is a putative vector of LY (Myrie *et al.* 2019). During this survey, palms and surrounding vegetation have been sampled which also led to the discovery of a new species of derbid, *Agoo beani* Bahder & Bartlett, 2020 (Bahder *et al.* 2020).

As part of this survey work in February of 2022, a specimen of Colpopterini was collected by sweeping edge habitat on the beach on the northern coast of Jamaica. It was determined to belong to the genus *Jamaha* but not one of the described species. The known nogodinid fauna of Jamaica consists of both described species of *Jamaha*, plus *Colpoptera rugosa* Van Duzee, 1907 (described from Jamaica) and *Colpoptera sinuata* Burmeister, 1835 (described from Mexico, reported by Melichar 1923). Herein, the novel taxon is described, molecular data for the five-prime region of the cytochrome *c* oxidase subunit I (COI) gene and 18S rRNA gene is provided and compared to available members of Colpopterini, with other available taxa of Nogodinidae serving as outgroup, and a key to the species of *Jamaha* is provided.

## Materials and Methods

**Locality and specimen collection.** The specimen was collected by sweeping vegetation on the beach underneath a coconut palm (Fig. 1), aspirating then transferring directly to 95% ethanol. The specimen was collected near Snow Hill, Portland Parish, Jamaica (18.197197, -76.525658) and exported to the U.S.A. under permit number P526-170201-001. The specimen collected was measured, photographed, and dissected using a Leica M205 C stereoscope and Leica DFC25 camera. Images of the specimen and all features photographed were generated using the LAS Core Software v4.12. The holotype is deposited at the University of Florida – Fort Lauderdale Research and Education Center (FLREC) in Davie, FL, U.S.A.

**Morphological terminology and identification**. Morphological terminology generally follows Gnezdilov (2012) except for the use of the traditional terms frons and vertex for metope and coryphe, and male terminalia nomenclature updated after Bourgoin (1988) and Bourgoin & Huang (1990) and forewing venation following Bourgoin *et al.* (2015). New taxa are to be attributed to Bahder and Bartlett.

**Dissections and DNA extraction.** The terminalia that were dissected also served as the source of tissue for DNA extraction. The terminal end of the abdomens was removed and placed directly into a solution of tissue lysis buffer (buffer ATL) and proteinase K (180 µl ATL and 20 µl proteinase K) from the DNeasy® Blood and Tissue Kit (Qiagen). The abdomen was left to lyse for 24 hours at 56°C. Following lysis, the eluate was transferred to a new 1.5 ml microcentrifuge tube and DNA extraction proceeded as per the manufacturer's instructions. The terminalia were then immersed in 200 µl of buffer ATL and 200 µl of buffer AL from the same kit and placed at 95°C for 24 hours to remove fat, wax, and residual tissue. The cleared genitalia were then used for morphological characterization and photography.

**PCR parameters, sequence data, and analysis.** To obtain COI and 18S sequence data, previously published primers were used in all PCR reactions (Table 1). PCR reactions contained 5x GoTaq Flexi Buffer, 25 mM $MgCl_2$, 10 mM dNTP's, 10 mM of each primer, 10% PVP-40, and 2.5U GoTaq Flexi DNA Polymerase, 2 µl DNA template, and sterile $dH_20$ to a final volume of 25 µL. Thermal cycling conditions for all loci involved were as follows: 2 min initial denaturation at 95°C, followed by 35 cycles of 30-sec denaturations at 95°C, 30-sec annealing, and extension at 72°C. Specific annealing temperatures and extension times for respective loci are presented in Table 1. Products were visualized on a 1.5% agarose gel stained with GelRed (Biotium). PCR products of the appropriate size were purified using the ExoSAP-IT™ Express PCR Product Cleanup Reagent per the manufacturer's protocol (ThermoFisher Scientific, Waltham, Massachusetts, USA). The purified PCR product was quantified using a NanoDrop Lite Spectrophotometer (ThermoFisher Scientific, Waltham, Massachusetts, USA) and sequenced using the SeqStudio Genetic Analyzer (Applied Biosystems). Contiguous files were assembled using DNA Baser (Version 4.36) (Heracle BioSoft SRL, Pitesti, Romania), and aligned using ClustalW as part of the package MEGA7 (Kumar *et al.* 2016). Maximum Likelihood trees were generated using the Bootstrap method at 1,000 replicates based on the Tamura-Nei model for both the COI and 18S loci as well as the consensus tree with concatenated data for COI and 18S data. A matrix of pairwise differences using the number of differences among 18S for a subset of taxa within each genus was calculated with MEGA7 (Kumar *et al.* 2016). The bootstrap method was used for variance estimation at 1,000 replicates and using the p-distance model.

**TABLE 1.** Primers used to amplify corresponding gene regions used to assess the placement of novel taxon and PCR parameters for each locus.

| Locus | Primer | Direction | Sequence (5' -3') | Annealing | Extension | Reference |
|---|---|---|---|---|---|---|
| COI | COI_D1_F<br>C1-J-2195RC | Forward<br>Reverse | GGAACWATAAGAAGWATAATYATYCG<br>ACTTCTGGATGACCAAAAAATCAA | 40˚C | 1 min. 30 sec. | Humphries *et al.* 2021 |
| 18S | 18SF<br>18SR | Forward<br>Reverse | ACTGTCGATGGTAGGTTCTG<br>GTCCGAAGACCTCACTAAA | 50˚C | 2 min. | Bahder *et al.* 2019 |

**TABLE 2.** Molecular taxon sampling and GenBank accession numbers

| Taxon | COI | 18S | Reference |
|---|---|---|---|
| *Bibilicallia* sp. (Lipocalliini) | KF226803 | n/a | Gopurneko *et al.* 2013 |
| *Biolleyana costalis* (Nogodinini) | n/a | DQ532558 | Urban & Cryan 2007 |
| *Bladina* sp. 1 (Bladinini) | n/a | KX761570 | Wang *et al.* 2016 |
| *Bladina* sp. 2 (Bladinini) | n/a | DQ532560 | Urban & Cryan 2007 |
| *Bladina* sp. (Bladinini) | KX702953 | n/a | Wang *et al.* 2016 |
| *Colpoptera* sp. 1 (Colpopterini) | MN344434 | n/a | GenBank direct submission |
| *Colpoptera* sp. 2 (Colpopterini) | MN345333 | n/a | GenBank direct submission |
| *Colpoptera* n. sp. (Jamaica) | n/a | n/a | n/a |
| *Danepteryx* sp. | n/a | DQ532547 | Urban & Cryan 2007 |
| *Dictyssa* sp. | n/a | DQ532548 | Urban & Cryan 2007 |
| *Goniopsara* sp. (Pisachini) | MN344913 | n/a | GenBank direct submission |
| *Goniopsara* sp. | MN345874 | n/a | GenBank direct submission |
| Lipocalliini sp. | n/a | DQ532550 | Urban & Cryan 2007 |
| *Lipocallia* sp. 1 (Lipocalliini) | KF227123 | n/a | Gopurneko *et al.* 2013 |
| *Lipocallia* sp. 2 (Lipocalliini) | KF227120 | n/a | Gopurneko *et al.* 2013 |
| *Lipocallia* sp. 3 (Lipocalliini) | KF227121 | n/a | Gopurneko *et al.* 2013 |
| *Paradetya* sp. (Varcini) | n/a | DQ532559 | Urban & Cryan 2007 |
| *Paravarcia* sp. (Varcini) | n/a | JX556769 | Song & Liang 2013 |
| *Pisacha naga* (Pisachini) | n/a | JX556770 | Song & Liang 2013 |
| *Pisacha* sp. (Pisachini) | n/a | JX556771 | Song & Liang 2013 |

**Taxon sampling.** For molecular comparisons, an unidentified species of *Colpoptera* collected during the same survey/collecting event is included in the analysis. Other available Nogodinidae on GenBank with data for COI and 18S, accession numbers, and references are presented in Table 2. Available data included 2 undetermined *Colpoptera* (Colpopterinae: Colpopterini), 3 undetermined *Bladina* species (Bladininae: Bladinini); 1 *Goniopsara,* and 2 *Pisacha* species (Nogodininae: Pisachini), 1 *Paradetya* and 1 *Paravarcia* (Nogodininae: Varciini); 1 *Bibilicallia*, 3 *Lipocallia* and 1 Lipocalliini (Nogodininae: Lipocalliini); 1 *Biolleyana* (Nogodininae: Nogodinini); and 1 *Danepteryx* and 1 *Dictyssa* (Tropiduchidae: Elicinae: Elicini). The last two taxa were included since they had formerly been placed in Nogodinidae (e.g., Fennah 1984).

**FIGURE 1.** Habitat and locality of *Jamaha playa* **sp. nov.**

## Systematics

### Family Nogodinidae Melichar, 1898

### Subfamily Colpopterinae Gnezdilov, 2003

### Tribe Colpopterini Gnezdilov, 2003

### *Jamaha* Gnezdilov & O'Brien, 2008

**Type species.** *Poeciloptera elevans* Walker, 1858; by original designation.

**Emended diagnosis** (modified from Gnezdilov & O'Brien 2008). Body elongate, forewings narrow, nearly parallel-sided. Vertex quadrate, just wider than long, medially concave, apex weakly convex, posterior margin strongly concave. Frons roughly rhomboid, widest near level of antennae, median carina present, frontoclypeal suture sinuate or convex. Pronotum short, mesonotum about 4x length of pronotum along midline. Forewings widely rounded apically, Sc+RA, MP, and CuA all originating near apex of basal cell. Hind tibia with single lateral tooth. Male pygofer with hind margin bearing long process medially. Aedeagus without ventral hooks, with multiple branched dorsolateral phallobase lobes (which may be bilaterally asymmetric). Anal tube varied. Female (Gnezdilov & O'Brien 2008, Figs 70-71) with gonoplacs rounded, not fused medially. Median field of posterior connective lamina of gonapophyses IX comprised of two areas that bear median denticles accompanied by larger lateral teeth. Lateral fields of the laminae without processes. Gonocoxa VIII with weakly convex hind margin. Endogonocoxal process narrowing apically. Anterior connective lamina of gonapophysis VIII with 3 teeth in apical group and 3 keeled teeth in lateral group.

**Remarks**. The elongated posterior projection on the lateral margins of the male pygofer is a diagnostic feature of the genus. Gnezdilov & O'Brien (2008: 23) also specified that the genus is distinguished from *Colpoptera* "by the narrow and elongated parts of the ovipositor which probably represents a different manner of oviposition – the elongated and fused gonoplacs are probably used as a directing case for the narrow and pointed endogonocoxal processes and anterior connective laminae in oviposition." Gnezdilov & O'Brien (2008) made comparisons between species in *Jamaha* and *Colpoptera sinuata* Burmeister, 1835, the type species of *Colpoptera*, including a male and female syntype from the Museum für Naturkunde der Humboldt-Universität, Berlin, Germany. This is significant because the monophyly of *Colpoptera* as currently comprised has yet to be assessed. At present, there have been no external features proposed that serve to distinguish among the genera *Colpoptera*, *Jamaha,* and *Caudibeccus*.

### *Jamaha playa* Bahder & Bartlett sp. nov.

(Figures 2–9)

**Type locality.** Snow Hill, Portland Parish, Jamaica (18.197197, -76.525658) (Fig. 1).

**Etymology.** The specific epithet '*playa*' is the Spanish word for beach, based on the habitat where the specimen was collected. The specific name is intended to be indeclinable.

**Diagnosis.** Vertex (dorsal view) parallel-sided and medially concave, apex weakly convex, posterior margin deeply concave. Frons elongate, bearing median carina, roughly rhomboid, widest dorsad of frontoclypeal suture. Forewings with Sc+RA, MP and CuA all originating near apex of basal cell. Hind tibiae with a lateral spine. Each lateral margin of pygofer opening bearing 2 large posterior processes, a large dorsal spatulate process and an elongate ventral process. Aedeagus bearing multiply branched subapical lateral processes (left side with 4 apices, right side with 3). Anal tube in lateral view with apex downcurved and broadly expanded into large truncate apices.

**Description.** Elongate (6.94 mm with wings, Table 3), entire body stramineous with fuscous wash over entire body, abdominal tergites orange/rust colored, wings generally fuscous with costal region transparent and anal region mottled, fuscous patch near apex on posterior margin.

**TABLE 3.** Biometric data for *Jamaha playa* **sp. nov.**; measurements in mm.

| Character | Measurement (*n*=1) |
|---|---|
| Body length, with wings | 6.94 |
| Body length, no wings | 4.33 |
| Forewing length | 5.98 |
| Vertex length | 0.32 |
| Vertex width, basal margin | 0.53 |
| Vertex width, distal margin | 0.45 |
| Pronotum length, midline | 0.30 |
| Mesonotum length, midline | 1.21 |
| Mesonotum width | 1.38 |
| Frons width, dorsal margin | 0.45 |
| Frons width, clypeal suture | 0.51 |
| Frons width, widest | 0.92 |
| Frons width, narrowest | 0.45 |
| Frons length, midline | 1.02 |
| Clypeus length | 0.75 |

**FIGURE 2.** Adult habitus *Jamaha playa* **sp. nov.** (A) male lateral view and (B) male dorsal view; white arrow indicates lateral spine.

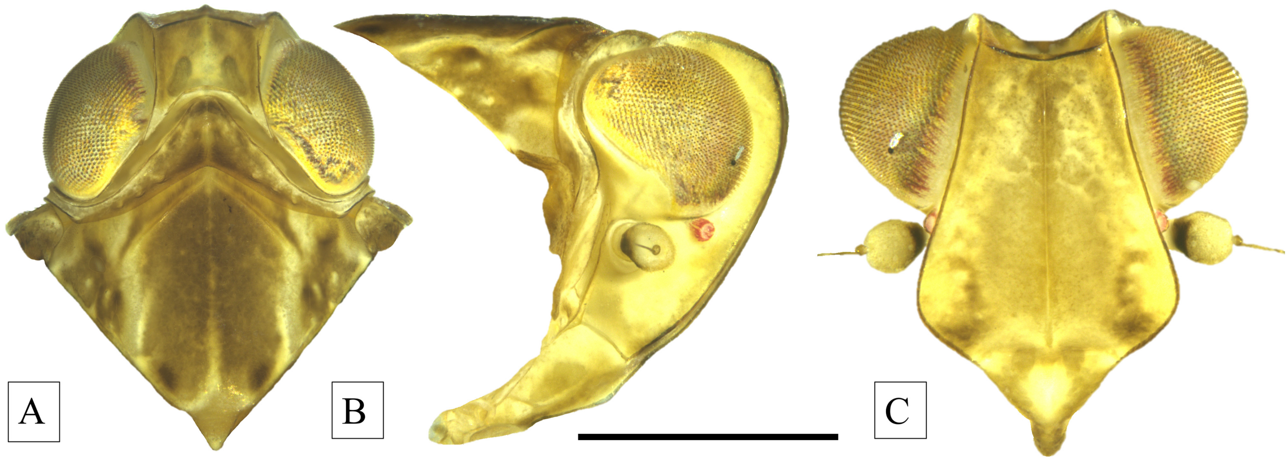

**FIGURE 3.** Adult *Jamaha playa* **sp. nov.** (A) head, pronotum, mesonotum dorsal view, (B) head and pronotum lateral view, and (C) head frontal view; scale = 1 mm.

**Head**. In dorsal view, head (including eyes) just wider than pronotum. Vertex quadrate, wider than long at midline, lateral margins subparallel, raised (medially depressed), median carina evident, anterior margin convex, transverse carina at fastigium, posterior margin, strongly concave (Fig. 3A). In lateral view, head weakly projected in front of eyes, dorsum roundly declinate to fastigium, angled at transverse carina, face weakly convex (Fig. 3B). In frontal view, vertex concave, transverse carina at fastigium weakly concave, face (including clypeus) pentagonal, lateral margins of frons keeled, expanding from fastigium approximately to level of antennae, then constricted to frontoclypeal suture; median carina distinct to frontoclypeal suture. Frontoclypeal suture sinuate, medially with concave dimple, laterally convex to margin; clypeus triangular (Fig. 3C). Compound eyes oval, ventrocaudal margin flattened (weakly concave near antenna), lateral ocelli distinct beneath eyes. Antennae below eyes and caudad of lateral ocelli, scape very short and ring-like, pedicel ovoid, bearing many sensory plaques, flagellum bristle-like with bulbous base.

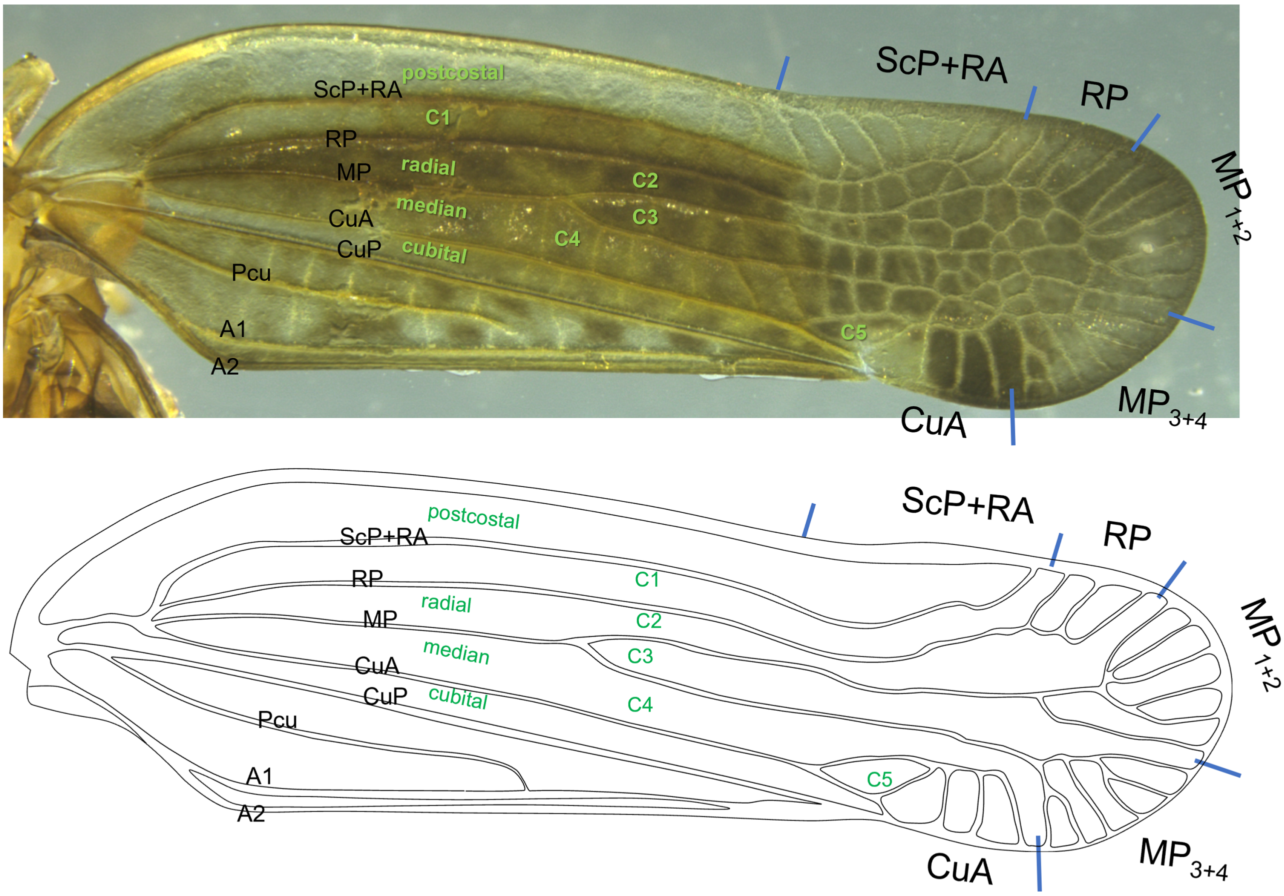

**FIGURE 4.** Forewing venation of *Jamaha playa* **sp. nov.** (black = veins, green = cells, terminology following Bourgoin *et al.* 2015).

**Thorax**. Pronotum in dorsal view widest at midline, strongly narrowing laterally, anterior and posterior margins keeled, anterior margin strongly convex, posterior margin strongly concave, median carina present, disc bearing 3 indistinct tubercles along posterior margin on each side of midline (Fig. 3A); in lateral view, paradiscal region narrow, strongly sinuate on anterior and posterior margin anterior margin keeled (Fig. 3B). Mesonotum tricarinate, median carina reaching scutellum, lateral carinae strongly diverging from median carina near anterior margin, then abruptly much weaker, angled parallel to median carina to hind margin (Fig. 3A). Fore and mid tibia approximately 2/3 length of hind tibia, both lacking lateral spines, hind tibiae with single lateral spine and apical spinulation of tibiae and tarsal segments 8-8-2.

**Forewing**. Forewing thickened, elongate, leading margin sinuate, weakly convex to weak inflection at stigmatal region, costal margin straight from scutellar margin to apex of clavus (Fig. 4); wing apex rounded, slightly projected in region of $MP_{1+2}$. Vein reticulations throughout forewing (including clavus), strongest in distal third. Apex of clavus in distal ¾ of forewing, fusion of Pcu and $A_1$ in distal third of clavus, composite vein reaching wing margin at claval apex. Sc+RA, MP and CuA all originate near apex of basal cell. Postcostal cell with 7 faint costal crossveins to subcostal posterior region, then 7 stronger crossveins in subcostal posterior region. RP ending with 3 terminals. MP forked near wing midlength (forming cell C3), apical region bearing 12 apical veins (between last RP vein and postclaval margin). CuA bearing 3 terminals.

**Male terminalia**. Pygofer in lateral view irregular, narrowest dorsally (Fig. 5), posterior margin convex bearing two large processes; dorsal process broadly spatulate with rounded apex, taller than wide; ventral process (the genus-level diagnostic feature) elongate, narrow, apex bluntly pointed. Gonostyli broad, rounded at apex, exceeding both processes of pygofer, capitulum short and broad, lateral tooth a subapical ridge (Fig. 5). Aedeagus bilaterally asymmetrical, shaft simple, terete, weakly upcurved bearing multiply branched subapical lateral processes (dorsolateral phallobase lobes, ventral hooks absent); apical processes (A1 & A2) hooked cephalad, short; middorsal processes (A3 & A4) elongate, slender, curved dorsad, irregularly sinuate; basal processes on left lateral side apically bifurcated (A5 & A7) into robust processes similar in length to A1 and A2; basal process on right lateral side (A6) lacking ventral bifurcation (Fig. 6). Anal tube in lateral view narrow basally, subparallel on dorsal and ventral margins, downcurved ventrally past midpoint, constricting then expanded to very broad truncate apices (Fig. 5). Paraproct thin and elongate.

**Female**. Unknown.

**Type material.** Holotype, ♂: “Jamaica, Portland Parish / nr. Snow Hill (restaurant) / 15. II.2022 / sweeping weeds on beach / Coll.: B.W.Bahder // Holotype / *Jamaha playa* ♂” (FLREC).

**Plant associations.** Unknown, collected sweeping herbaceous weeds on the beach.

**Distribution.** Jamaica (Portland Parish), near Snow Hill.

**FIGURE 5.** Adult male *Jamaha playa* **sp. nov.** terminalia in left lateral view.

**Sequence data.** For *J. playa* **sp. nov.**, a 531 bp product was generated for the COI gene (GenBank Accession No. OQ120945) and a 1,402 bp product for the 18S gene (GenBank Accession No. OQ116784). Based on data available for other taxa within Nogodinidae for the COI and 18S gene, *J. playa* **sp. nov.** resolves adjacent to *Goniospara* spp. with weak bootstrap support (56) (Fig. 7A). For the 18S gene, of the available taxa, *J. playa* **sp. nov.** resolved closest to the *Colpoptera* sp. (from this study) with strong bootstrap support (100). The pairwise comparison generated based on 18S data demonstrates that *J. playa* **sp. nov.** differs from *Colpoptera* sp. by 4.3% and on average, differs by 5.1% (±0.1) from other genera within the Nogodinidae.

**Remarks.** The elongate projection on the lateral margin of the pygofer opening places *J. playa* **sp. nov.** in the genus *Jamaha*. Features of the male terminalia seem to offer the clearest features for species recognition. The terminalia of *J. elevans* and *J. chrysops* were both illustrated (as *Colpoptera*) in Fennah (1955). *Jamaha chrysops* lacks the dorsal spatulate process of the pygofer found in *J. playa* **sp. nov.** and differs in the form of the subapical lateral processes of the aedeagus and the form of the anal tube (viz. Fennah 1955, Figs 1n, 1o). *Jamaha elevans* is more similar to *J. playa* **sp. nov.** in that both possess a rounded lobe near the dorsal margin of the pygofer in lateral view, however, this lobe appears larger and constricted at the base in *J. playa* **sp. nov.** compared to *J. elevans* (Fennah 1955, fig 2q). Also, *J. elevans* has fewer branches of the subapical lateral processes (2 apices on the right side, 3 on left, versus 3 on right, 4 on the left in *J. playa* **sp. nov.**). Distant (1910) considered *C. rugosa* and *J.*

*elevans* synonyms, however, this was not supported in later works. We examined syntypes of *Colpoptera rugosa* from the California Academy of Sciences collection to determine whether our new species might be attributed to that taxon. While we were able to exclude *C. rugosa*, we discovered that the syntype series were of mixed identity, which invoked a cascade of issues that we felt were better contended with in a separate manuscript.

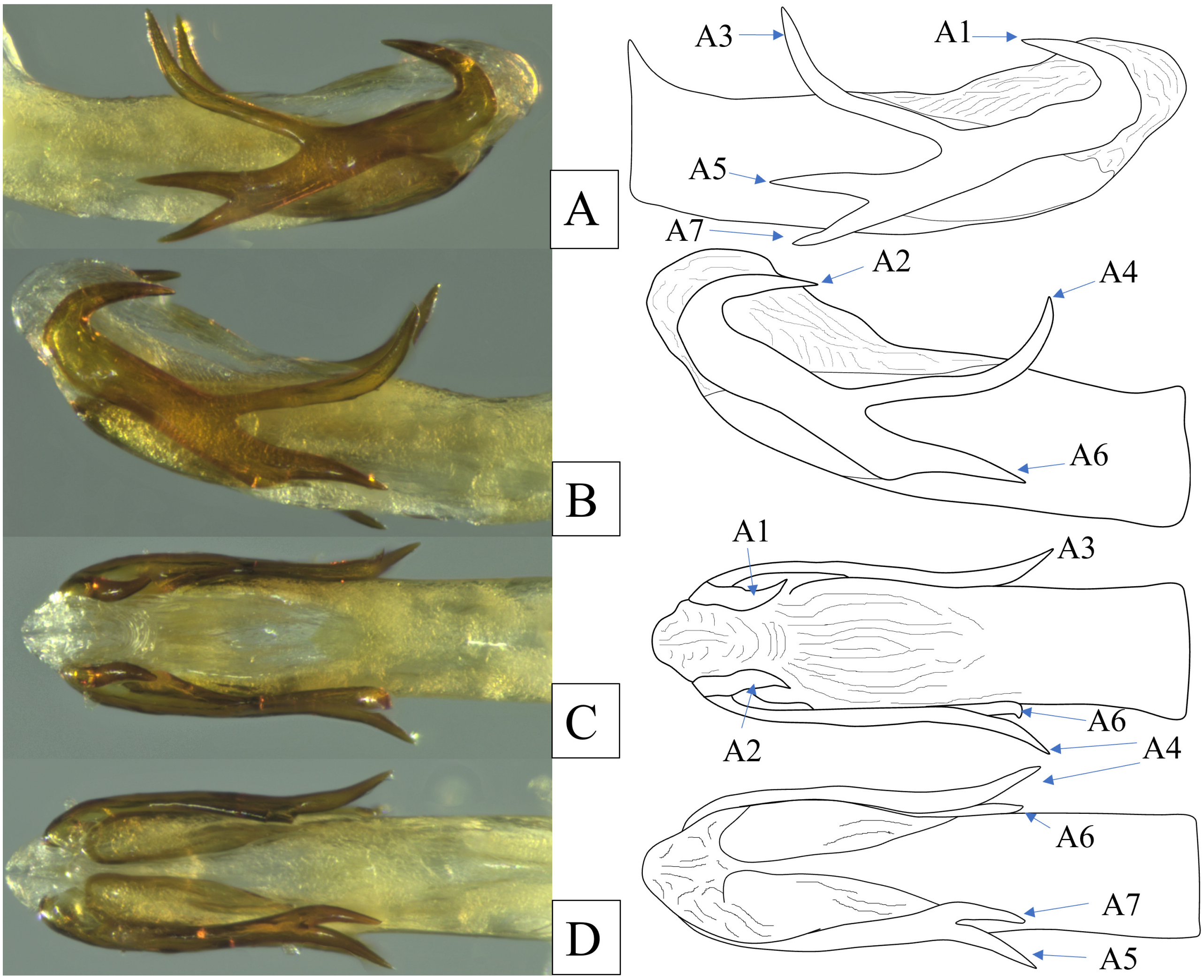

**FIGURE 6.** Aedeagus of *Jamaha playa* **sp. nov.** (A) left lateral view, (B) right lateral view, (C) dorsal view, and (D) ventral view.

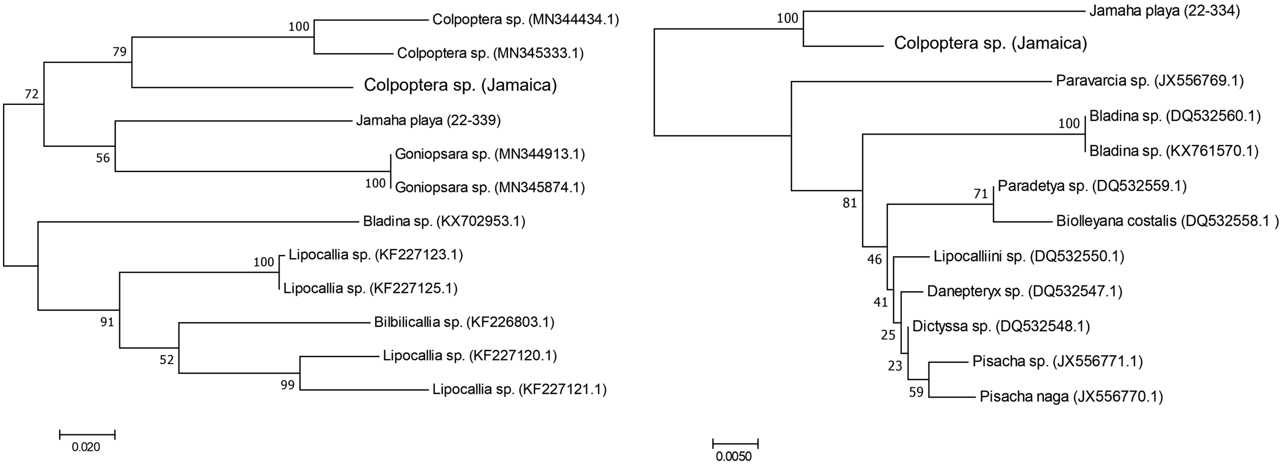

**FIGURE 7.** Maximum Likelihood trees (1,000 replicates) exhibiting relationship of *Jamaha playa* **sp. nov**. to available nogodinid taxa. (A) COI, (B)18S, scale bar = percent nucleotide difference.

Based on the pairwise comparison, the level of variability between *Jamaha* and *Colpoptera* is consistent with intergenic levels of variability (based on 18S) based on the taxa available for analysis. Molecular resources for the group are limited so no definitive conclusions can be drawn from the analysis performed, however, these data were intended as preliminary, and as new species are discovered, new molecular data are generated, and previously described taxa are analyzed, a clearer assessment of the relationships of species and genera in the Nogonidinidae will be possible.

Some of the values presented as intergeneric differences are low and likely more indicative of intrageneric levels of variability. It is unclear if this is due to errors in the taxonomy of the groups or errors in the identification of the specimens uploaded to GenBank, or both.

## Key to species of *Jamaha* (based on male terminalia)

1\. Male pygofer in lateral view bearing a large spatulate process dorsad of the elongate process on the lateral margin of the pygofer opening (Fig. 5); anal tube greatly expanded at apex . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 2

–. Male pygofer in lateral view bearing only an elongate process on the lateral margin of the pygofer opening; anal tube in lateral view bearing a large ventral tooth, but not particularly expanded apically . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . *J. chrysops*

2\. Large dorsal spatulate process of the lateral margin of the pale pygofer constricted near the base (Fig. 5); anal tube apically truncate; dorsolateral phallobase lobes 4-branched on the left side, 3 branched on the right (Fig. 6) . . . . . . . . . . . . . . . *J. playa* **sp. nov.**

–. Large dorsal spatulate process of the lateral margin of the pale pygofer not constricted near the base; anal tube apically concave (Fennah 1955, fig. 2q); dorsolateral phallobase lobes 2-branched on the left side, 3 branched on the right (Fennah 1955, Figs 2r, 2s) . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . *J. elevans*

**TABLE 4.** Pairwise comparison showing estimates of evolutionary divergence between sequences based on the 18S rRNA gene for *Jamaha playa* **sp. nov.** demonstrating intrageneric and intergeneric variability; the percent differences per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal and were obtained by a bootstrap procedure (1000 replicates).

| | | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *Jamaha playa* **sp. nov.** | | 0.006 | 0.006 | 0.007 | 0.007 | 0.006 | 0.006 | 0.006 | 0.008 | 0.006 | 0.007 | 0.006 |
| 2 | *Colpoptera* sp. | 0.043 | | 0.005 | 0.006 | 0.006 | 0.005 | 0.005 | 0.005 | 0.006 | 0.005 | 0.005 | 0.005 |
| 3 | *Biolleyana costalis* | 0.049 | 0.029 | | 0.005 | 0.005 | 0.002 | 0.002 | 0.002 | 0.005 | 0.001 | 0.002 | 0.002 |
| 4 | *Bladina* sp. 1 | 0.057 | 0.042 | 0.024 | | 0.000 | 0.004 | 0.004 | 0.004 | 0.007 | 0.004 | 0.004 | 0.004 |
| 5 | *Bladina* sp. 2 | 0.057 | 0.042 | 0.024 | 0.000 | | 0.004 | 0.004 | 0.004 | 0.007 | 0.004 | 0.004 | 0.004 |
| 6 | *Dictyssa* sp. | 0.047 | 0.026 | 0.003 | 0.021 | 0.021 | | 0.000 | 0.000 | 0.005 | 0.001 | 0.001 | 0.000 |
| 7 | *Danepteryx* sp. | 0.047 | 0.026 | 0.003 | 0.021 | 0.021 | 0.000 | | 0.000 | 0.005 | 0.001 | 0.001 | 0.000 |
| 8 | Lipocalliini sp. | 0.047 | 0.026 | 0.003 | 0.021 | 0.021 | 0.000 | 0.000 | | 0.005 | 0.001 | 0.001 | 0.000 |
| 9 | *Paravarcia* sp. | 0.063 | 0.042 | 0.028 | 0.041 | 0.041 | 0.028 | 0.028 | 0.028 | | 0.005 | 0.005 | 0.005 |
| 10 | *Paradetya* sp. | 0.048 | 0.027 | 0.002 | 0.022 | 0.022 | 0.001 | 0.001 | 0.001 | 0.027 | | 0.001 | 0.001 |
| 11 | *Pisacha naga* | 0.048 | 0.027 | 0.004 | 0.022 | 0.022 | 0.001 | 0.001 | 0.001 | 0.029 | 0.002 | | 0.001 |
| 12 | *Pisacha* sp. | 0.047 | 0.026 | 0.003 | 0.021 | 0.021 | 0.000 | 0.000 | 0.000 | 0.028 | 0.001 | 0.001 | |

## Discussion

All three species of *Jamaha* were originally described from Jamaica. Only *J. elevans* has been reported outside of Jamaica (from Haiti by Melichar 1902: 65). This report should be verified as it may be a misidentification (or lapsus); however, we can confirm the presence of *Jamaha* on Hispaniola from an undescribed species from Pedernales province of the Dominican Republic discovered while exploring museum specimens (University of Delaware Reference Collection) of undetermined Colpopterini. Also, it is not clear that all the species currently in *Colpoptera* are correctly placed since some of the diagnostic features among New World Colpopterini genera (viz. *Colpoptera* from *Jamaha* and *Caudibeccus*) are based on features of male and female terminalia, which have not been described for all *Colpoptera*, most notably *C. marginalis* Burmeister, 1835 and *C. rustica* (Fabricius, 1803). Museum collections include many specimens that appear to be undescribed species in the Colpopterini.

The discovery of *J. playa* **sp. nov.** in Jamaica further highlights the need for continued survey work of planthoppers in the region. Thus far, all species of *Jamaha* are known from Jamaica. Only *J. elevans* is known from outside of Jamaica (reported from Haiti, Melichar 1902, Metcalf 1938). The true distribution of *Jamaha* in the Caribbean is unknown but seems likely that both known species and undescribed species are also present on nearby islands. Further survey work of the surrounding islands is needed.

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