



## A new species of planthopper in the genus *Haplaxius* (Hemiptera: Fulgoroidea: Cixiidae) from disturbed submontane rainforest in Jamaica

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### Abstract

*Haplaxius* is a large genus of cixiid planthopper found in the New World. The genus is of particular interest due to the ability of *H. crudus* to transmit the phytoplasmas for lethal decline in various palm species, primarily in the Caribbean and Florida, U.S.A. During recent vector survey work in Jamaica, a specimen was collected at Castleton Botanic Garden and determined to be a new species of *Haplaxius*. The novel taxon is herein described, *Haplaxius fornicus* **sp. n.**, and corresponding DNA sequence data is provided for the barcoding region of the cytochrome *c* oxidase subunit I (COI) gene, 18S rRNA gene, and histone 3 (H3) gene. An updated phylogeny of the genus is provided with currently available taxa demonstrating additional support for the placement of *H. fornicus* **sp. n.** in *Haplaxius*.

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

### Resumen

*Haplaxius* es un numeroso género de chicharritas de la familia cixiidae que se distribuye en el Nuevo Mundo. Este género es de particular interés debido a la capacidad de *H. crudus* para transmitir los fitoplasmas que causan una enfermedad letal en varias especies de palmeras, principalmente en el Caribe y en Florida, EE. UU. Durante un reciente muestreo de vectores en Jamaica, se recolectó un espécimen en el Jardín Botánico de Castleton y se clasificó como una nueva especie de *Haplaxius*. En el presente documento se describe el nuevo taxón, *Haplaxius fornicus* **sp. n.** y se proporcionan los datos de secuencia de ADN para la región del código de barras genético del citocromo *c* oxidasa subunidad I (COI), del gen 18S ARNr y para el gen de la histona 3 (H3). Además, se proporciona la filogenia actualizada del género con los taxones actualmente disponibles que provee evidencia adicional para la ubicación de *H. fornicus* **sp. n.** en *Haplaxius*.

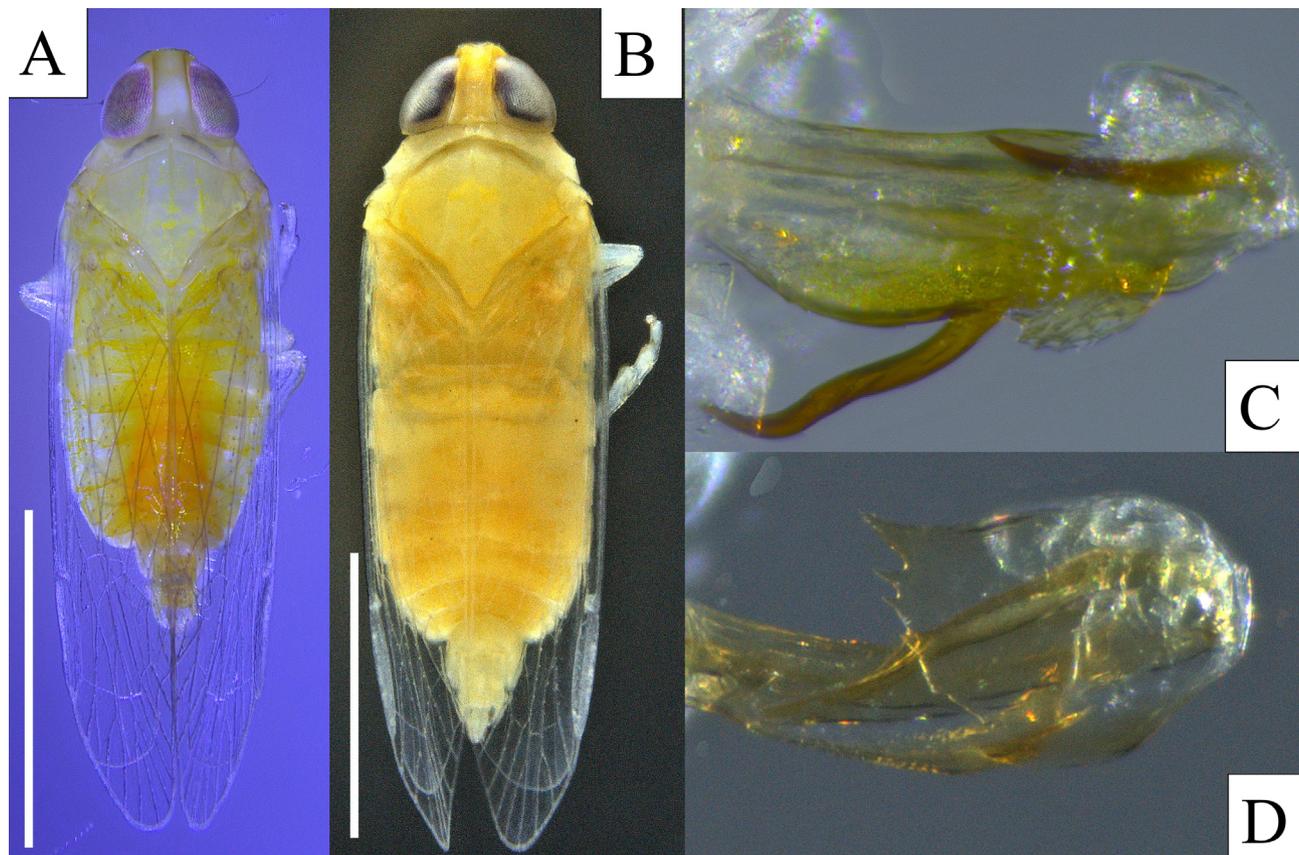
**Palabras clave:** taxonomía, filogenética, Caribe, muestreo, biodiversidad

### Introduction

*Haplaxius* Fowler (Cixiidae: Cixiinae: Oecleini) is a large genus (67 species) of New World planthoppers found from southern Canada to northern South America, including the Caribbean (Barrantes *et al.* 2021, Bourgoin 2022, Echavarría *et al.* 2022). The genus is of interest because *H. crudus* is a vector of the lethal yellowing (LY) phytoplasma, ‘*Candidatus* Phytoplasma palmae’ (Howard & Thomas 1980) and lethal bronzing (LB) phytoplasma, ‘*Ca. P. aculeata*’ (Mou *et al.* 2022). While other species of *Haplaxius* are known to feed on palms (Bahder *et al.* 2020, Barrantes *et al.* 2021), their role in the epidemiology of palm lethal decline has not been established. Survey efforts in Jamaica seeking to understand vector ecology resulted in the discovery of a new species, *Oecleus mackaspringi* Bahder & Bartlett (Myrie *et al.* 2019), currently a suspected vector of LY.

*Haplaxius* is defined by features of the forewing, face, and hind leg; the bases of longitudinal veins Sc+R and MP form a common stalk so that only two veins appear to arise from the basal cell (a tribal feature, Muir 1922), frontal view of frons diamond-shaped with median ocellus, nearly straight frontoclypeal border, and lacking lateral teeth on the hind tibia (Emeljanov 2007). *Haplaxius* may be heterogenous as the genus is currently understood (viz. Kramer 1979). Recently, the genus *Myxia* Bahder & Bartlett was described as similar to *Haplaxius* but differing based on molecular data and morphology (especially the male terminalia, most notably the medioventral lobe of the pygofer triangular, the phallobase prolonged into projection ventrad of the aedeagus, and the anal tube short, stout and distally downcurved) (Bahder *et al.* 2019, Echavarría *et al.* 2021a, b).

During an expedition in Jamaica in February of 2022, a small planthopper was collected at the Castleton Botanic Garden by sweeping foliage of palms and other broadleaf monocots. In the field, it was tentatively identified as a cixiid and appeared to belong to the genus *Haplaxius* based on superficial observations and behavior. The species of *Haplaxius* previously reported from Jamaica are *H. crudus* and *H. jamaicae* (Kramer) (Kramer 1979) (Fig. 1). After close examination, it was confirmed to belong to the genus *Haplaxius* and determined to be a new species. Herein, the novel taxon is described and sequence data is provided for the cytochrome *c* oxidase subunit I (COI) barcoding region, 18S rRNA gene, and histone 3 (H3) gene along with an updated phylogeny.



**FIGURE 1.** *Haplaxius* species of Jamaica; (A) habitus *Haplaxius crudus* (male); (B) habitus *Haplaxius jamaicae* (male); (C) left lateral view of aedeagus for *H. crudus* and (D) *H. jamaicae*; scale = 1 mm”

## Materials and methods

**Locality and specimen collection.** Individuals of the novel taxon were collected by sweeping vegetation, aspirated, and immediately transferred to 95% ethanol. Specimens were collected at the Castleton Botanic Garden (Fig. 2) on 16-II-2021, Saint Mary Parish, Jamaica (18.170892, -76.823239), and imported to the U.S.A. under permit number P526-170201-001. All specimens collected were measured, photographed, and dissected using a Leica M205 C stereoscope and Leica DFC25 camera. Images of specimens and all features photographed were generated using the LAS Core Software v4.12. Voucher specimens, including primary types, are stored at the University of Florida—Fort Lauderdale Research and Education Center (FLREC) in Davie, FL, U.S.A, and the Florida State Collection of Arthropods (FSCA) in Gainesville, FL, U.S.A.

**Morphological terminology and identification.** Morphological terminology generally follows Kramer (1979) except with male terminalia nomenclature updated after Bourgoïn (1988) and Bourgoïn & Huang (1990) and forewing venation following Bourgoïn *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 abdomen 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 terminalia were then used for morphological characterization and photography.

**PCR parameters, sequence data, and analysis.** To obtain COI, 18S, and H3 sequence data, previously published primers were used in all PCR reactions (Table 1). PCR reactions contained 5x GoTaq Flexi Buffer, 25 mM MgCl<sub>2</sub>, 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<sub>2</sub>O 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 annealings, 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 manufacturers' 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), 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, 18S and H3 loci as well as the consensus tree with concatenated data for COI, 18S and H3 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 placement of novel taxon and PCR parameters for each locus.

Locus	Primer	Direction	Sequence (5' →3')	Annealing	Extension	Reference
COI	COI_D1_F	Forward	GGAACWATAAGAAGWATAATYATY-	40°C	1 min. 30 sec.	Humphries <i>et al.</i> 2021
	C1-J-2195RC	Reverse	CG ACTTCTGGATGACCAAAAAATCAA			
18S	18SF	Forward	ACTGTCGATGGTAGGTTCTG	50°C	2 min.	Bahder <i>et al.</i> 2019
	18SR	Reverse	GTCCGAAGACCTCACTAAA			
H3	H3F	Forward	CAGACGGCBMGKAARTCSACC	55°C	30 sec.	Echavarría <i>et al.</i> 2021b
	H3R	Reverse	GTKACHCKCTTRGCGTGRAT			

**Taxon sampling.** For molecular comparisons, *Haplaxius cotinga* Bahder & Bartlett, *H. crudus* (Van Duzee), *H. dougwalshi* Bahder & Bartlett, *H. skarphion* (Kramer), *H. pocococo* Bahder & Bartlett, *H. pictifrons* (Stål), *H. lunatus* (Van Duzee) were used for in-group comparisons and *Oecleus borealis* Van Duzee, *O. dormido* Bahder & Bartlett, *O. mackaspringi* Bahder & Bartlett, *Myxia belinda* Bahder & Bartlett, *M. delta* (Kramer), *M. hernandezii* Bahder & Bartlett, *M. baynardi* Bahder & Bartlett, *Nymphocixia unipunctata* Van Duzee, *N. caribbea* Fennah, and *Melanoliarius chuliotus* (Ball) were used as outgroups. GenBank Accession numbers for all included taxa are provided in Table 2.

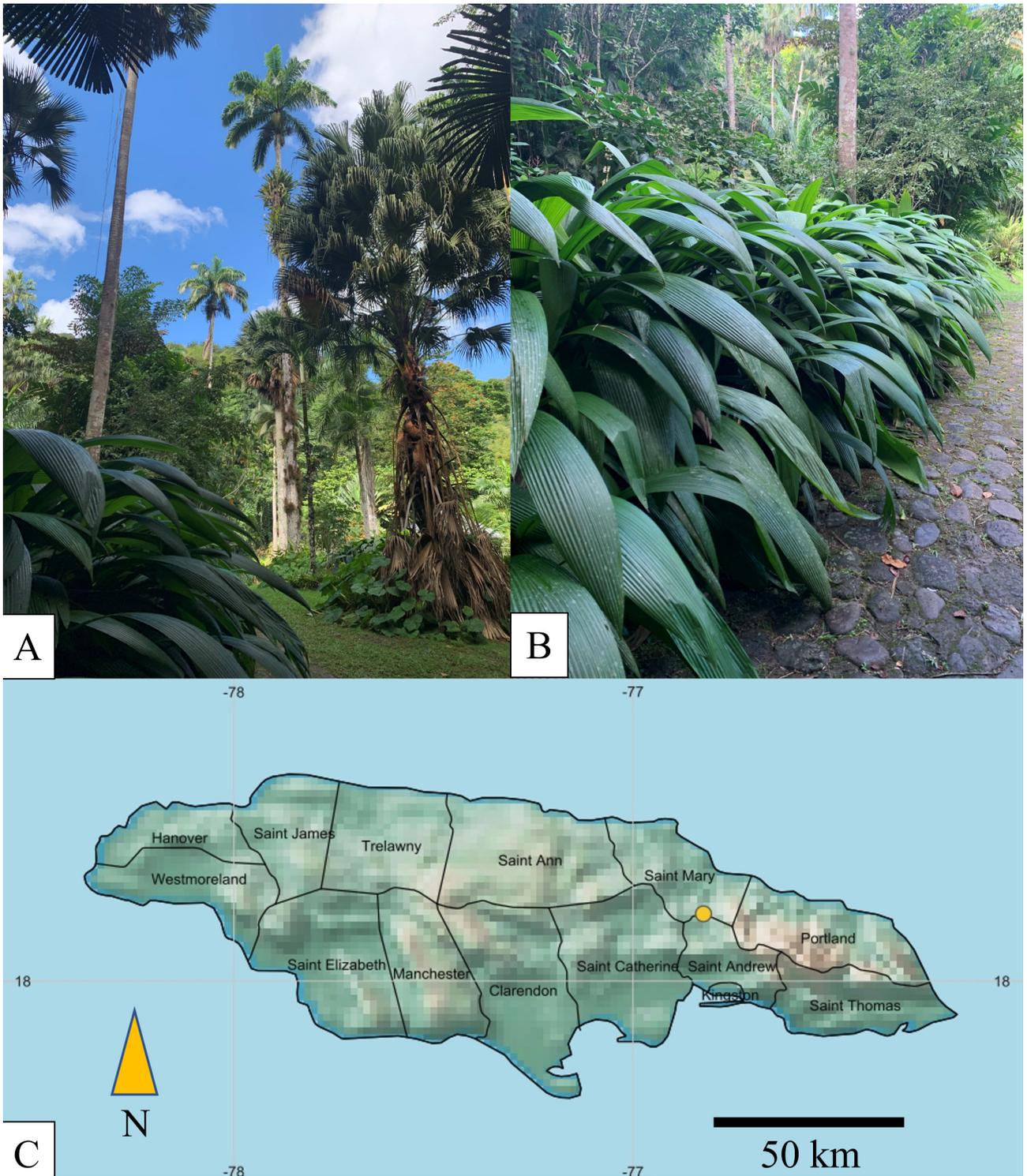


FIGURE 2. Habitat and type locality of *Haplaxius fornicus* sp. n.; (A, B) habitat, and (C) location of Castleton Botanic Garden.

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

Taxon	Locality	GenBank Accession No.			Collection
		COI	18S	H3	
<i>Haplaxius crudus</i>	Costa Rica	MT080284	MT002393	MZ274037	FLREC
<i>Haplaxius cotinga</i>	Costa Rica	ON763279	ON758370	ON755134	FLREC
<i>Haplaxius dougwalshi</i>	Costa Rica	MT080284	MT002395	MZ297815	FLREC
<i>Haplaxius lunatus</i>	Florida, U.S.A.	OM264285	OM258692	OM262388	FLREC
<i>Haplaxius skarphion</i>	Costa Rica	MT900603	MT892907	MZ274039	FLREC
<i>Haplaxius pocococo</i>	Costa Rica	MW086873	MW086509	OM262387	FLREC
<i>Haplaxius pictifrons</i>	Delaware, U.S.A.	MT946292	MN200098	MZ274038	FLREC
<i>Myxia belinda</i>	Costa Rica	MT900605	MN200095	MZ274041	FLREC
<i>Myxia delta</i>	Costa Rica	MT900602	MT892907	MZ274042	FLREC
<i>Myxia hernandezi</i>	Costa Rica	MZ234085	MZ262449	MZ274043	FLREC
<i>Myxia baynardi</i>	Costa Rica	MT900604	MT892909	MZ274040	FLREC
<i>Nymphocixia unipunctata</i>	Florida, U.S.A.	OM264284	OM258690	OM262389	FLREC
<i>Nymphocixia caribbea</i>	Jamaica	MT080286	MT002394	MZ274044	FLREC
<i>Oecleus borealis</i>	Florida, U.S.A.	OM264286	OM258691	OM262390	FLREC
<i>Oecleus dormido</i>	Costa Rica	OM264283	OM258693	OM262392	FLREC
<i>Oecleus mackaspringi</i>	Jamaica	MN488999	MN422261	MZ274045	FLREC
<i>Melanoliarus chuliotus</i>	Florida, U.S.A.	OM264287	OM258689	OM262392	FLREC

## Systematics

### Family Cixiidae Spinola, 1839

#### Subfamily Cixiinae Spinola, 1839

#### Tribe Oecleini Muir, 1922

#### Genus *Haplaxius* Fowler, 1904

**Type species:** *Haplaxius laevis* Fowler, 1904 (type species designation by Caldwell 1946: 203)

**Diagnosis** (modified from Bahder *et al.* 2020). Small to average size cixiids (3.2–6.4 mm); head (dorsal view) narrower than pronotum, eyes large (elongate-oval, diagonally truncate posteriorly, usually with ventral emargination at antennae); vertex elongate, moderately broad (among Oecleini), vertex disc slightly concave, sides and apex carinate, median carina usually absent, apex variably produced beyond eyes (usually weakly projected). In lateral view, apex of head bluntly angled, ocellus beneath eye (anterior to antenna). In facial view, sides of frons concave (“flared”) and carinate, midline of frons carinate, interrupted near frontoclypeal suture by ocellus (ocellus sometimes obsolete), clypeus subtriangular with lateral margins and midline carinate. Antennal scape reduced, pedicel robust, flagellum beadlike basally and filamentous distally. Pronotum narrow, with irregular ridges and distinct paranotal region, length shortest on midline, posterior margin indented; tegulae evident. Mesonotum tricarinate; longitudinal midlength of mesonotum about 2× or less that of vertex. Hind tibiae without lateral spines. Forewings tectiform, usually hyaline or transparent, but sometimes infuscated or patterned, veins usually with small setae-bearing pustules (tubercles). Male pygofer usually longest on ventral margin, hind lateral margin of opening variably produced, medioventral lobe of pygofer well-developed. Aedeagus asymmetrical and elaborated with projections and processes, vertical connective articulating base of aedeagus with gonostyli (genital styles). Gonostyli symmetrical and usually simple. Anal tube symmetrical or asymmetrical, with processes from one or both ventral margins and sometimes with median ventral projections.

***Haplaxius fornicus* Bahder & Bartlett sp. n.**

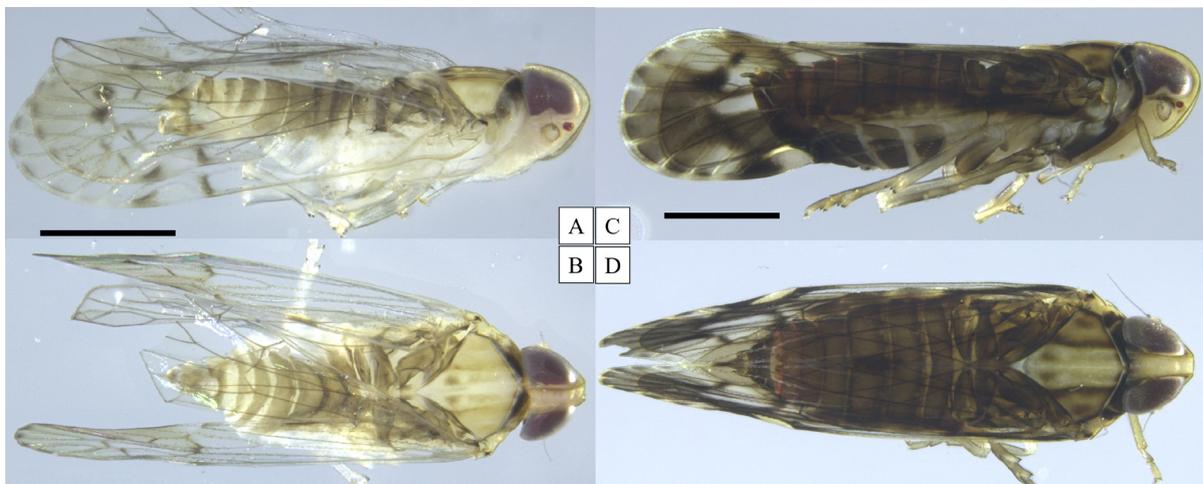
(Figures 3–10)

**Type locality.** Castleton Botanic Garden (18.170892, -76.823239), Saint Mary Parish, Jamaica (Fig. 1).

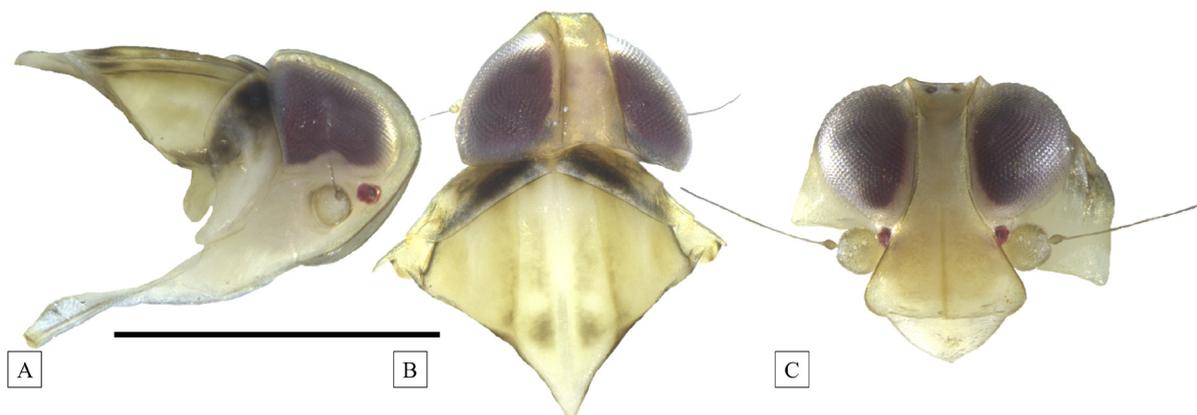
**Diagnosis.** Strongly sexually dimorphic; males pale yellow with fuscous wash over dorsal surface, forewings clear. females heavily infuscate over entire body, forewings mostly infuscate. Aedeagus with two large, serrated flanges near apex connecting to flagellum and a row of small spines on right-ventral margin.

**Description.** *Color.* Body generally pale gray-yellow, head of uniform coloration (ocellus red), face unmarked. Males pale yellow on dorsum (dorsally washed with fuscous posterior to mesonotum, slightly paler between lateral carinae of mesonotum), ivory white on venter; disc of pronotum with irregular nearly black marking; wings mostly clear, tinged with fuscous in distal third past nodal line; crossveins tinged fuscous, a strong spot at im-crossvein, additional markings tracing Sc vein, at apex of pterostigma, at the apices of marginal cells and on the marginal vein of the clavus ( $A_2$ ) proximad of composite  $Pcu+A_1$  vein reaching wing margin. Females with same base color and pattern as males, except more strongly infuscate over entire body including venter and wings (Fig. 3).

*Structure.* Body length (including wings), males: 4.32 mm ( $n = 1$ ), females 5.05–5.06 mm ( $n = 3$ ). Body weakly compressed.



**FIGURE 3.** Adult habitus of *Haplaxius fornicus* sp. n.; (A) male lateral view, (B) male dorsal view, (C) female lateral view and (D) female dorsal view; scale = 1 mm.



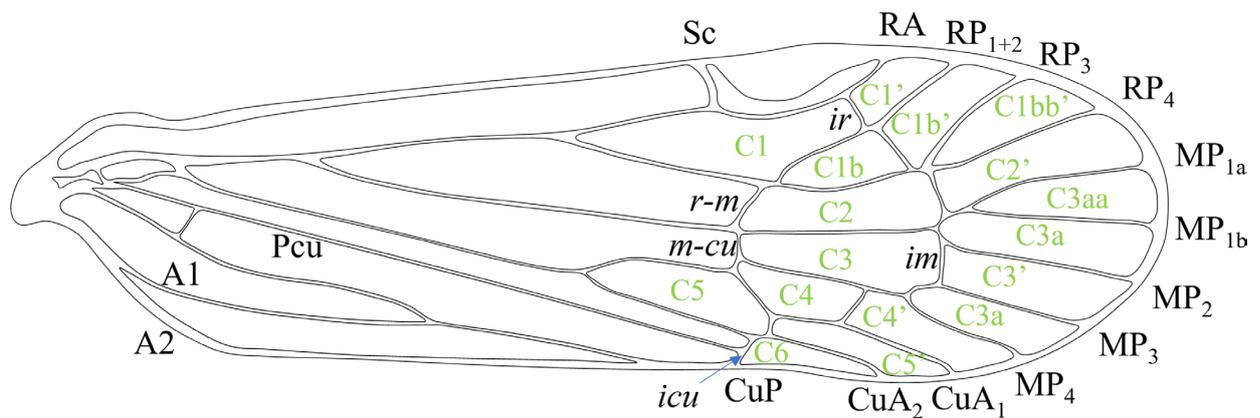
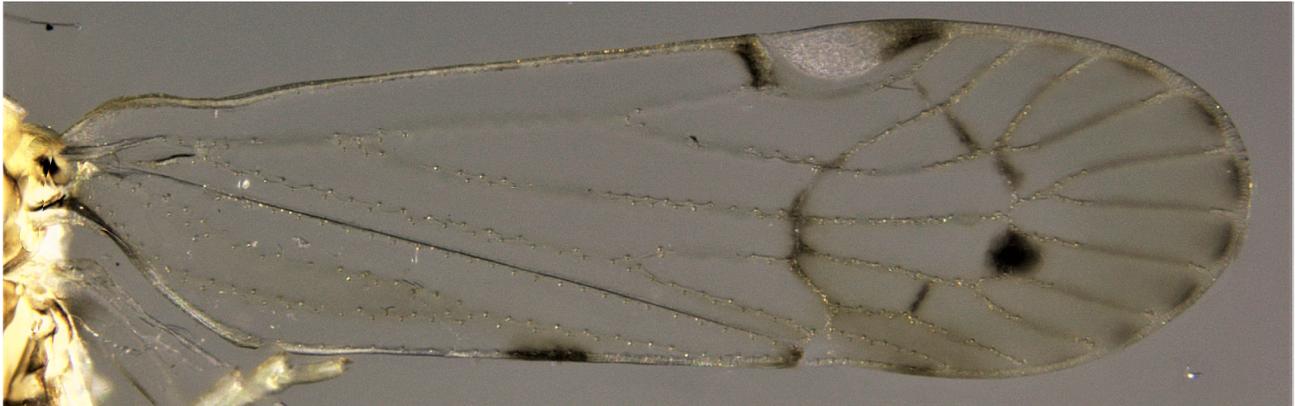
**FIGURE 4.** Adult male *Haplaxius fornicus* sp. n.; (A) head, pronotum and mesonotum lateral view, (B) head, pronotum, and mesonotum dorsal view, and (C) head and pronotum frontal view; scale = 1 mm.

**Head.** Head in dorsal view narrower than pronotum; in lateral view, evenly rounded from back of head to frontoclypeal suture, head weakly projected in front of eyes (Fig. 4A). In dorsal view (Fig. 4B), vertex nearly parallel-sided, widest at posterior margin, narrowing slightly to anterior margin; posterior margin slightly concave, anterior margin truncate at fastigium, transverse carinae present at fastigium; vertex approximately twice as long as

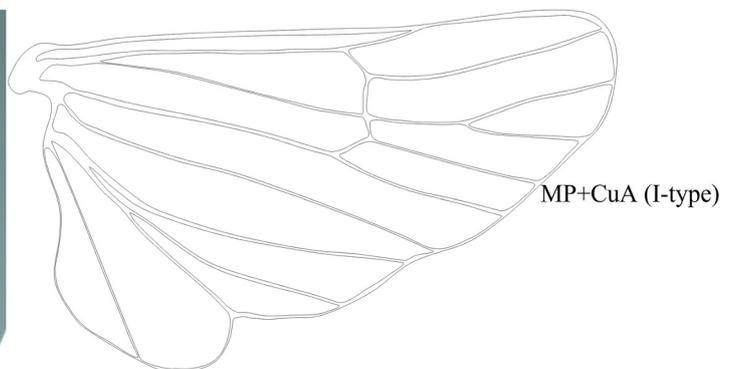
wide (at posterior margin). In frontal view (Fig. 4C), face (frons plus clypeus) rhomboid, frons narrowest at dorsal margin, expanding ventrad to about lower level of antennae before constricting to frontoclypeal suture, median carina evident, reaching transverse suture at fastigium, median ocellus obsolete; frontoclypeus straight, clypeus inverse triangular.

**Thorax.** Pronotum narrow in dorsal view, convex on anterior margin, concave on posterior margin, median carina complete, lateral (postocular) carinae evident, terminating at ventrolateral apex (Fig. 4B). Mesonotum longer at midline than vertex plus pronotum, tricarinate, lateral carinae subparallel, weakly diverging posteriorly (Fig. 4B).

Forewing elongate oval, weakly expanding distad, apex rounded; apex of clavus just beyond midlength, fork of MP from ScP+R in proximal quarter of wing, fusion of Pcu+A<sub>1</sub> distad of branching of MP near midlength of clavus, branching of RP from ScP+RA (forming cell C1) and branching of CuA (forming cell C5) at same level, preceding apex of clavus. Vein branching pattern RA unbranched, RP 3-branched, MP 5-branched and CuA 2-branched (Fig. 5). Hindwing with I-type connection between MP and CuA veins (Fig. 6).



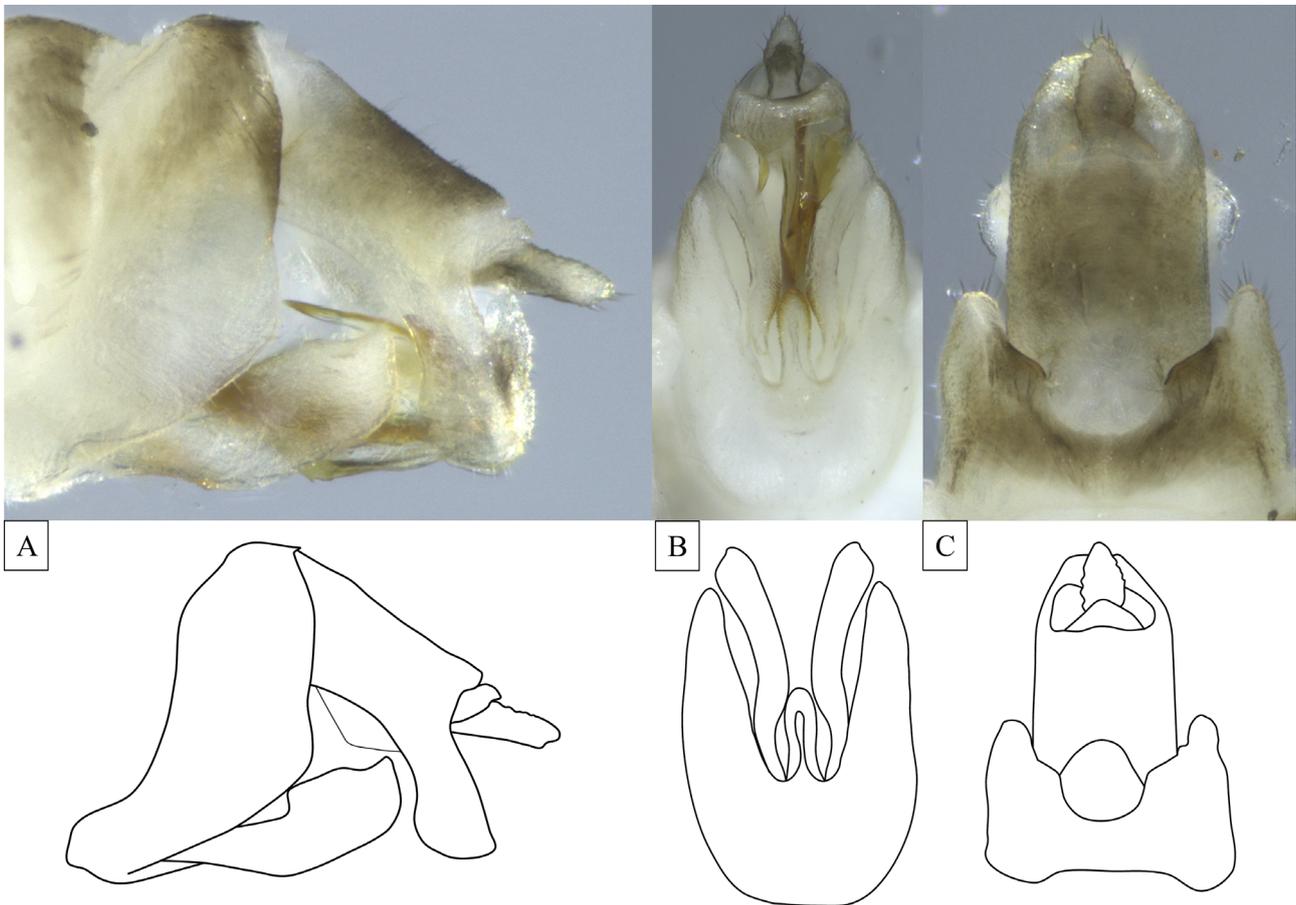
**FIGURE 5.** Forewing venation of *Haplaxius fornicus* sp. n.; black = vein, italics = crossvein, green = cell (interpretation following Bourgoin *et al.* 2015).



**FIGURE 6.** Hindwing venation of *Haplaxius fornicus* sp. n. displaying I-type connection between MP and CuA veins.

Spinulation of hind tibiae and tarsomeres is 6-7-8.

**Terminalia.** Pygofer irregular in lateral view, concavely sinuate on anterior margin, convexly sinuate on posterior margin, widest near midlength, narrowest at dorsal and ventral margins (Fig. 7A). In ventral view, medioventral process elongate, approximately 3X long as wide at base; weakly oblanceolate, apex rounded, slightly constricted below midlength, bearing a ventral median ridge (Fig. 7B). Gonostyli in lateral view “scoop-like”, dorsal and ventral margins irregularly sinuate, narrowest at base, expanding distad to midlength, then dorsally expanded to semiquadrate region on dorsal margin before apex, ventral margin convex (Fig. 7A). In ventral view, “paddle-like”, elongate, narrowest at base, curved lateral, strongly sinuate on outer and inner margins, sub-quadrate at apex, widest supapically (Fig. 7B). Aedeagus tubular, in lateral view shaft upcurved, with midventral row of teeth and large diagonally oriented serrated flange on ventral margin (A1, Figs 8 and 9), a second (A2) large serrate flange on right side; A1 arising subapically on ventral margin, left side, curving diagonally distad to base of endosoma; A2 arising on right lateral side extending distally to base of endosoma, endosoma comprised of an elongate tubular membranous tube and three sclerotized processes (F1, F2, and F3), endosoma with dorsal longitudinal concavity; F1 and F2 arising near dorsal of endosomal base, F1 angled to left lateral side, slightly sinuate; F2 angled to right lateral side, approximately twice as long and more slender than F1; F3 similar in length and shape to F1, arising on left lateral side of flagellum at midpoint in basal half (Figs 8 and 9). Anal tube in lateral view relatively short and stout with broad, downcurved apex; dorsal and ventral margins subparallel nearly to paraproct, apex broad, curved ventrad, to broadly rounded apex; bearing subtriangular process near midpoint on inner ventral margin, in ventral view, asymmetrical, left lateral side with protrusion on anterior margin (Fig. 7C); paraproct short and conical.



**FIGURE 7.** Male *Haplaxius fornicus* sp. n. terminalia; (A) lateral view, (B) ventral view, and (C) dorsal view.

**Plant associations.** Unidentified palms (Arecaceae) and unidentified monocot (Fig. 1).

**Distribution.** Jamaica (Saint Mary Parish).

**Etymology.** The specific name refers to the serrated flanges that resemble the head of Fornicus, a villain in the film “Cabin in the Woods”. The name is intended to be indeclinable.

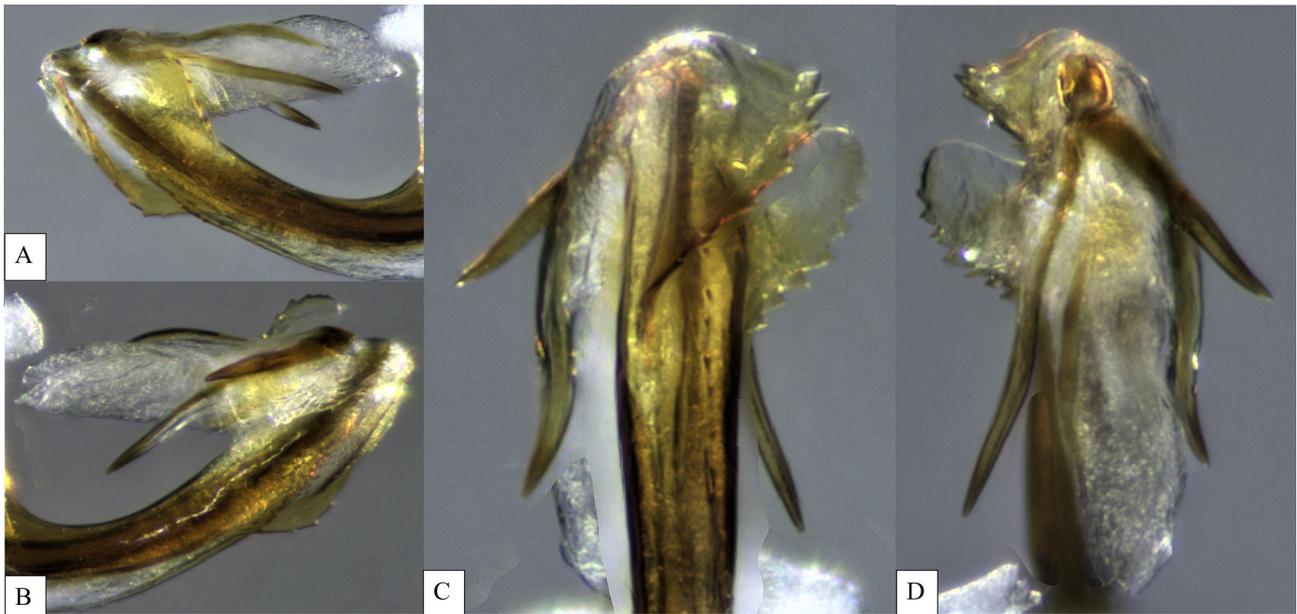


FIGURE 8. Aedeagus of *Haplaxius fornicus* sp. n.; (A) right lateral view, (B) left lateral view, (C) ventral view, and (D) dorsal view.

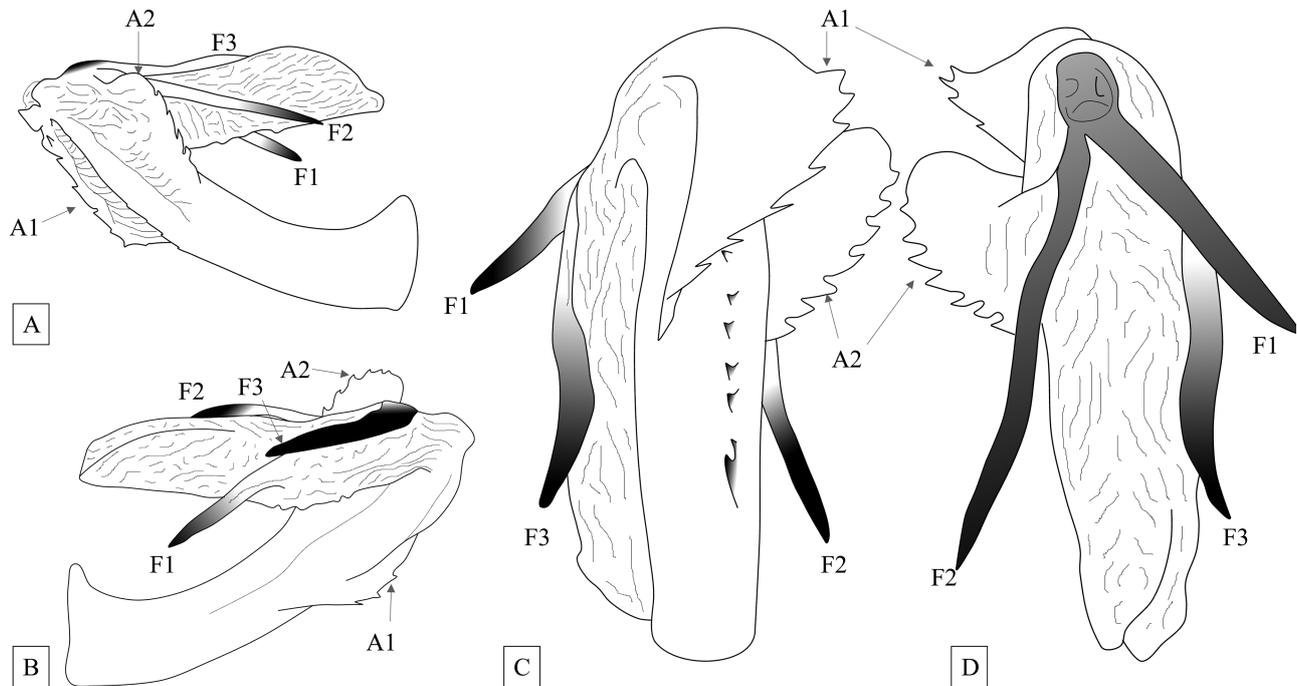


FIGURE 9. Aedeagus line-art for *Haplaxius fornicus* sp. n.; (A) right lateral view, (B) left lateral view, (C) ventral view, and (D) dorsal view.

**Material examined.** Holotype male “Jamaica, Saint Mary Parish / Castleton Botanic Garden / 16. II.2022 / Sweeping vegetation / Coll.: B.W.Bahder // Holotype / *Haplaxius fornicus* ♂” (FLREC); Paratypes, Castleton Botanic Garden [16. II.2022] (1 female—FSCA, 2 females—FLREC). Genitalia of female paratype presented in Figure 10.

**Sequence data.** For the COI gene, a 548 bp sequence was generated (GenBank Accession No. OP160200), for 18S a 1,360 bp sequence was generated (GenBank Accession No. OP158203), and for H3 a 321 bp sequence was generated (GenBank Accession No. OP179300). Based on independent analyses for each locus, *Haplaxius fornicus* sp. n. resolved within *Haplaxius* for all three genes. For COI there is weak bootstrap support (11 to 58) for all branches except for the closely related taxa (*H. pocococo*/*H. dougwalshi*, *H. crudus*/*H. lunatus*, and *M. delta*/*M. hernandezi*). While phylogenetic relationships were stronger based on H3, bootstrap support is still

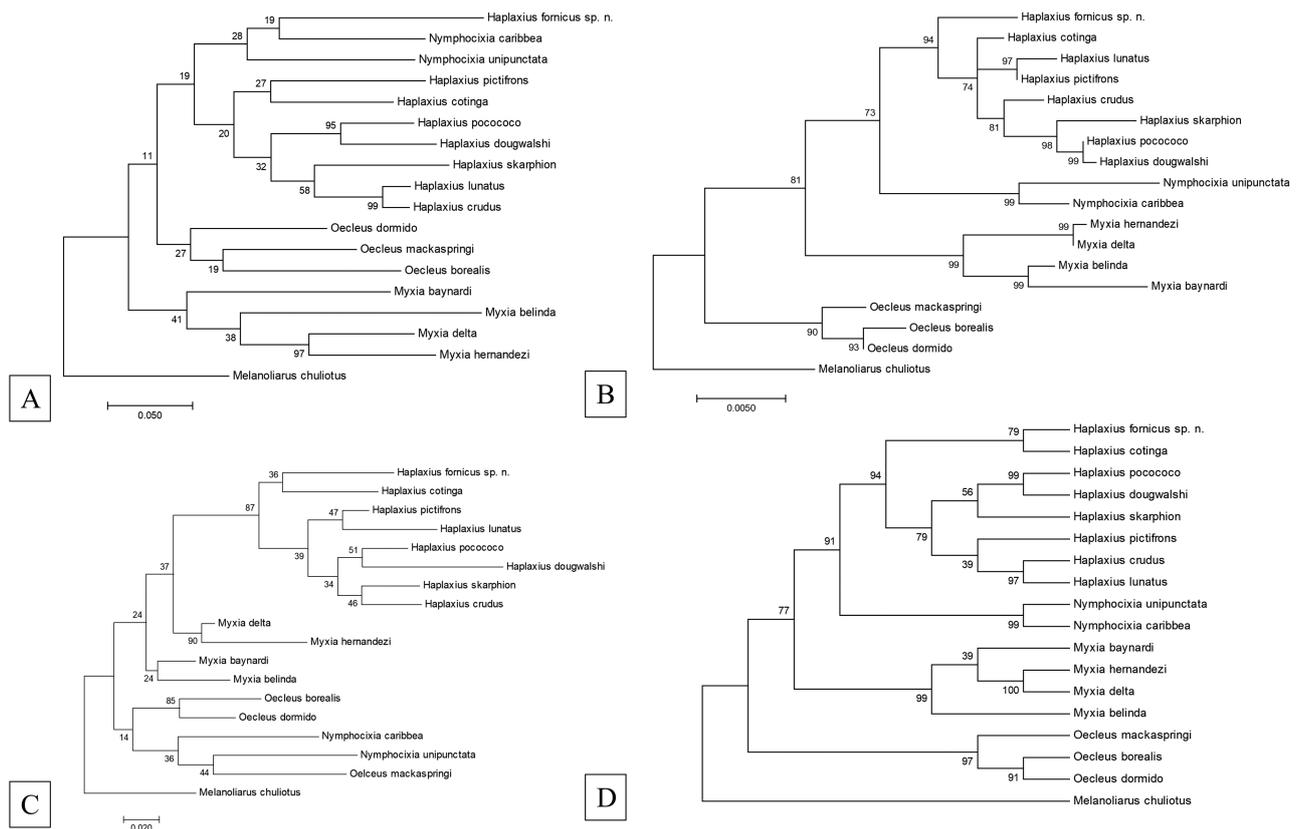
generally weak (<80), except for *Haplaxius* as a genus (87 bootstrap support), *M. delta*/*M. hernandezi* (90), and *O. borealis*/*O. dormido* (85). The strongest bootstrap support (94) observed for placement of *Haplaxius fornicus* sp. n. in *Haplaxius* was for the 18S locus (Fig. 11). The consensus tree generated from all three loci (concatenated) also shows strong support (94) for placement of *Haplaxius fornicus* sp. n. in *Haplaxius*.



**FIGURE 10.** Female genitalia of *Haplaxius fornicus* sp. n.: (A) right lateral view, (B) dorsal view and (C) ventral.

**Remarks.** Morphological characters and molecular data support the placement of *Haplaxius fornicus* sp. n. in *Haplaxius*. Among *Haplaxius* known from Jamaica (currently *H. jamaicae* and *H. crudus*), *H. fornicus* sp. n. differs in general coloration (the fuscous wash of *H. fornicus* sp. n. males is absent in both *H. jamaicae* and *H. crudus* adult males), and the shape of the male terminalia (anal tube downcurved to broad apex in *H. fornicus* sp. n. not downcurved in *H. jamaicae* and *H. crudus*; the aedeagus of *H. fornicus* sp. n. bear two large serrate flanges, absent in both *H. jamaicae* and *H. crudus*; and the elongate shape of the midventral process of the pygofer). In the key to Mexican and Neotropical species presented by Kramer (1979: 352), *H. fornicus* sp. n. keys in the first couplet as having a ventral lobelike extension on the anal tube in the first couplet, and aedeagus bearing three processes in the second couplet which leads to a choice between *H. jamaicae* and *H. meadi* Kramer (presumed Mexican, but taken with banana cargo in Philadelphia). *Haplaxius fornicus* sp. n. differs from both of these species by the fuscous coloration, the downcurved anal tube, and the presence of the serrate flanges on the aedeagus.

While the lack of a diamond-shaped C5 cell and open C5' cell observed in the novel taxon is somewhat unique in the Oecleini, the general form of these cells is similar to other species of *Haplaxius* recently discovered in the Neotropics (*H. pocococo*, *H. dougwalshi*, *H. cotinga*). Conversely, recently examined species in *Oecleus* (*O. domido*, *O. mackaspringi*) and *Myxia* appear to possess the characters of the C5 cell outlined by Le Cesne *et al.* (2021). Recently, the monophyly of the Oecleini has been called into question and the discrepancy in wing patterns observed may further indicate that the tribe as a taxon needs to be reassessed as new species are discovered and compared to previously described taxa.



**FIGURE 11.** Maximum likelihood phylogenetic tree based on 1,000 replicates; (A) COI gene, (B) 18S rRNA gene, (C) H3 gene, and (D) consensus tree of concatenated COI, 18S, and H3 sequences; scale bar = percent nucleotide difference.

## Discussion

*Haplaxius formicus* sp. n. is the third known species of *Haplaxius* from Jamaica. *Haplaxius formicus* sp. n. does not appear to be closely allied with the other Jamaican species in general appearance, details of the terminalia, or based on available molecular data. Among species with molecular data, *H. formicus* sp. n. appears most closely related to *H. cotinga* Bahder & Bartlett, a species recently described from Costa Rica (Echavarría *et al.* 2022), although it bears few obvious morphological similarities to this species. Additional study is needed to better understand the phylogeny of *Haplaxius* and determine whether the genus is heterogeneous as appears to be the case based on the overall habitus of species and the morphological details of the terminalia.

The discovery of another species of *Haplaxius* further aids in understanding the diversity and phylogeny of this group of planthoppers. While it is not established if species other than *H. crudus* can transmit palm lethal decline phytoplasmas, other species of *Haplaxius* are of interest, especially in Jamaica, where there is active LY spread. Future research efforts will seek to assess this species and other *Haplaxius* species for their ability to acquire and transmit LY.

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