Zootaxa 4975 (2): 357–368
https://www.mapress.com/j/zt/

Article

ISSN 1175-5326 (print edition)
ZOOTAXA
ISSN 1175-5334 (online edition)

https://doi.org/10.11646/zootaxa.4975.2.6
http://zoobank.org/urn:lsid:zoobank.org:pub:67697F85-7E5A-4CCC-AB1C-0343FE1E86C6

A new planthopper species in the genus *Omolicna* (Hemiptera: Auchenorrhyncha: Derbidae) from the Reserva Privada el Silencio de Los Angeles Cloud Forest in Costa Rica

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Abstract

Recent survey work on palms in Costa Rica has resulted in the discovery of several new species of Derbidae, especially in the Cenchreini. During a recent expedition, specimens collected by light trapping at the Hotel Villa Blanca (cloud forest) were determined to be a novel species of *Omolicna* Fennah. Sequence data was generated for the novel taxon for the cytochrome *c* oxidase subunit I (COI) and 18S loci. Pairwise analyses and phylogenetic analyses support placement of the novel taxon in *Omolicna.*

Key words: Derbidae, Costa Rica, planthopper, new species

Resumen

Un reciente trabajo de investigación en palmeras, llevado a cabo en Costa Rica, ha resultado en el descubrimiento de varias especies nuevas de la familia Derbidae, especialmente en la tribu Cenchreini. Durante un muestreo reciente; se determinó que los especímenes recolectados mediante trampa de luz en el Hotel Villa Blanca (bosque nuboso) pertenecían a una nueva especie del género *Omolicna* Fennah. Fueron generados, para esta nueva especie, datos de secuencia para la subunidad I de citocromo c oxidasa (COI) y para el loci 18S. Los análisis por pares y filogenéticos apoyan la colocación del nuevo taxón en el género Omolicna.

Palabras clave: Derbidae, Costa Rica, chicharrita, especies nueva

Introduction

The genus *Omolicna* Fennah is currently comprised of 19 species (Bourgoin 2020) distributed through eastern North America and the Neotropics (Bartlett *et al.* 2014). *Omolicna* is in the tribe Cenchreini Muir (within Derbinae Spinola). Cenchreini can be diagnosed as a 'less specialized' and 'cixiid-like' tribe of Derbinae (Fennah 1952: 111), bearing sensory pits on the vertex, frons and forewing (at least on the A1 vein in the clavus) and the lateral carinae of paranota foliate, forming fossae that surround the antennae. Emeljanov (1996) specified for Cenchreini that CuA has a 'double apex' forming an open marginal cell. In *Omolicna*, there is a robust overall body plan, an ornate medioventral process of pygofer that usually possesses lateral teeth, and the aedeagus is asymmetrical.

Accepted by A.-P. Liang: 14 Apr. 2021; published: 25 May 2021

Recent survey work on palms in Costa Rica and subsequent molecular analyses have resulted in the description of the closely allied genus *Agoo* Bahder & Bartlett (originally a subgenus of *Omolicna*, Bahder *et al.* 2019, 2020) and subsequent transfer of *O. rubrimarginata* Fennah to *Agoo* and *O. dubia* Caldwell to *Anchimothon* Fennah (Bahder *et al.* 2020). The most recently described *Omolicna* in the strict sense was *O. joi* Wilson, Halbert & Bextine, discovered during vector survey work for lethal bronzing (LB) disease of palms in Florida (Halbert *et al.* 2014), a lethal infection caused by the 16SrIV-D phytoplasma (Harrison *et al.* 2008). While derbids are not known as vectors of phytoplasmas, the introduction and spread of LB in Florida has renewed interest in the planthoppers associated with palms in both Florida and the Neotropics because of the putative ability of *Haplaxius crudus* to transmit the 16SrIV-A phytoplasma (causal agent of lethal yellowing) (Howard & Thomas 1980).

Herein we report a novel taxon in the genus *Omolicna* collected in Costa Rica. We provide DNA sequence data for the five-prime end of the cytochrome *c* oxidase subunit I gene (COI) and the 18S gene from the new taxon. A phylogenetic analysis is performed including the new taxon and available allied Cenchreini for both loci assessing the genus-level placement of the novel taxon among *Omolicna* and allied genera within the Cenchreini.

Materials and methods

Locality and Specimen Collection. Individuals of the novel taxon were collected from a mercury vapor light trap in the Reserva Privada el Silencio de Los Angeles Cloud Forest in Costa Rica at the Hotel Villa Blanca, Alajeula Province (120.03231, -84.485094). Specimens were aspirated from the light trapping cloth and transferred to 95% ethanol in the field while still alive. Specimens were collected (permit no. SINAC-ACTo-GASPPNI-016-2018) with permission of the Hotel Villa Blanca management and staff and exported under permit number DGVS-256-2018 to the U.S.A. and imported under permit number P526-170201-001. All specimens collected were measured, photographed and dissected using a Leica M205 C stereoscope. 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 that of Bartlett *et al*. (2014), except forewing venation following Bourgoin *et al*. (2015) and with male terminalia nomenclature modified after Bourgoin (1988) and Bourgoin & Huang (1990). New taxa are intended to be attributed to Bahder & 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 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, 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 sequence data, DNA template from specimens was amplified using the primers LCO1490 (5'-GGTCAACAAATCATAAAGATATTG-3') and HCO2198 (5'-TCAGGGTGACCAAAAAATCA-3') (Folmer *et al*. 1994). To obtain 18S sequence data, the primers developed by Bahder *et al.* (2019) were used and are as follows; forward primer 18SF (5'-ACTGTCGATGGTAGGTTCTG-3'), reverse primer 18SR (5'-GTCCGAAGACCTCACTAAA-3'). 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 COI were as follows: 2 min initial denaturation at 95°C, followed by 35 cycles of 30 sec denaturation at 95°C, 30 sec annealing at 40°C, 1 min 30 sec extension at 72°C, followed by a 5 min extension at 72°C. Thermal cycling conditions for 18S were as follows: 2 min initial denaturation at 95°C, followed by 35 cycles of 30 sec denaturation at 95°C, 30 sec annealing at 55°C, 2 min extension at 72°C, followed by a 5 min extension at 72°C. PCR products of the appropriate size were purified using the Exo-SAP-IT™ PCR Product Cleanup Reagent (ThermoFisher Scientific, Waltham, Massachusetts, USA). Purified PCR product was quantified using a NanoDropLite spectrophotometer (ThermoFisher Scientific, Waltham, Massachusetts, USA) and sent for sequencing at Eurofins Scientific (Louisville, KY, USA).

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). A matrix of pairwise differences using number of differences among COI and 18S 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. 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.

Taxon sampling. COI sequence data was used from species of *Omolicna* for in-group comparisons while *Anchimothon dubia* Caldwell, *Herpis metcalfi* O'Brien, *Neocenchrea heidemanni* Ball, *Cenchrea dorsalis* Westwood, and three species in the genus *Agoo* Bahder & Bartlett as out-group comparisons (Table 1). 18S sequence data was used from available species of *Omolicna* for in-group comparisons, three species of *Agoo*, *Anchimothon dubia*, and *Herpis metcalfi*, and *Cenchrea dorsalis* (Table 1). Taxon sampling and GenBank accession numbers are given in Table 1.

TABLE 1. Representative Cenchreini used for morphological and molecular comparisons.

			GenBank Accession No.	
Species	**Source**	**Locality**	**COI**	**18S**
Agoo xavieri	FLREC[1]	Costa Rica	MK443068	MK443073
Agoo dahliana	FLREC	Costa Rica	MN496467	MH472754
Agoo luzdenia	FLREC	Costa Rica	MT085818	MN999709
Omolicna brunnea	FLREC	Costa Rica	MK443070	MK443071
Omolicna mariajosae **sp. n.**	FLREC	Costa Rica	MT422534	MT424915
Omolicna cubana	FLREC	Jamaica	MT413386	MT415404
Omolicna dominicana	UD[2]	Dominica	MN496469	N/A
Omolicna joi	FLREC	U.S.A., FL	KF472312	MN472753
Omolicna latens	FLREC	Costa Rica	MN496472	MN472757
Omolicna puertana	UPR[3]	U.S.A., PR	MN496468	MN472751
Omolicna nero	UD	Belize	MN496471	N/A
Omolicna tarco	FLREC	Jamaica	MT422533	MT424914
Omolicna triata	FLREC	Costa Rica	MK443069	MK443072
Cenchrea dorsalis	UD	St. Vincent	MT413387	MN472756
Anchimothon dubia	FLREC	Costa Rica	MN496470	MN474755
Herpis sp.	FLREC	Costa Rica	MT085817	MT415406
Neocenchrea heidemanni	UD	U.S.A., DE	MN496473	MT415406

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Systematics

Family Derbidae Spinola 1839

Subfamily Derbinae Spinola 1839

Tribe Cenchreini Muir 1913

Genus *Omolicna* Fennah 1945

Type species: *Omolicna proxima* Fennah 1945

Amended diagnosis. Frons moderately broad (median carina absent), vertex and frons strongly keeled; transverse carina at fastigium sometimes present; profile of face (lateral view) not smoothly rounded but flattened on vertex

and face (in contrast with *Agoo*). Lateral carinae of paranota forming large foveae that subtend the basal antennal segment. Forewings with lateral, wax-producing pits and tubercles along costal, subcostal and Pcu veins. Terminalia bilaterally asymmetrical. Pygofer with ornate medioventral process with lateral teeth. Aedeagus strongly asymmetrical with longer processes laterad on right side. Anal tube usually with distal concavity between proximal ventral lobe and apical prolongation.

FIGURE 1. Habitat in Costa Rica at Hotel Villa Blanca where *Omolicna mariajosae* **sp. n.** holotype was collected.

Omolicna mariajosae Bahder & Bartlett sp. n.

(Figures 2–6)

Type locality. Costa Rica, Alajuela, Reserva Privada el Silencio de Los Angeles, Hotel Villa Blanca.

Diagnosis. Distinguished from congeners by the dark fuscous coloration, presence of tubercles on forewings along all major longitudinal veins and most branches, presence of a spurious vein (lacking tubercles) arising near fork of Sc and RA, the Pcu is fused with the CuP well in advance of the fusion of A1 with the composite vein; the medioventral process of pygofer with reduced lateral teeth, and endosoma with two strongly downcurved processes.

Description. *Color*. General body color dark fuscous, legs lighter brown, pronotum testaceous (yellowish in dried specimens). Wings uniformly light fuscous with reddish vein near wing apex (Fig. 2). Vertex lighter in color than frons.

Structure. Body length (all measurements averages, males $n = 2$): 2.91 mm with wings; 1.90 mm without wings. Head. In lateral view, rounded on anterior margin with dorsal margin planar (Fig. 3C). Frons relatively broad, widest at frontoclypeal suture, constricting just below ventral margin of eye, expanding slightly between eyes until reaching vertex, two rows of wax-producing pits on lateral margins running entire length of frons (Fig. 3A). Vertex relatively broad, approximately twice as wide at posterior margin as long at midline, posterior margin concave, anterior margin straight, two rows of wax-producing pits along lateral margins, median carina obsolete (Fig. 3B), transverse carina present at fastigium (Fig. 3B). Vertex length: 0.12 mm; width at hind margin: 0.23 mm; width at distal margin: 0.14 mm. Frons length: 0.69 mm; dorsal width: 0.30 mm; width frontoclypeal margin: 0.38 mm; width at narrowest point: 0.24 mm. Clypeus length: 0.26 mm.

FIGURE 2. Adult male habitus *Omolicna mariajosae* **sp. n.**; A. body lateral view and B. body dorsal view, scale = 1 mm.

Thorax. Pronotum with anterior margin convex, appearing angular, posterior margin smoothly concave, pronotal disk tricarinate, median carina distinct, lateral carinae closely following posterior margin of head (Fig. 3B). Paranota strongly foliately keeled and laterally projecting, lateral margin rounded from frontal view (Fig. 3A), nearly covering antennae in lateral view (Fig. 3C). Mesonotum tricarinate, lateral carinae sinuate, anteriorly distinct, converging and becoming obscure posteriorly; length at midline and width at tegulae approximately equal (Fig. 3B). Pronotum length at midline: 0.79 mm. Mesonotum length at midline: 0.49 mm, width: 0.61 mm. Spinulation of hind tibia, basitarsus, and second tarsomere 6-6-6.

FIGURE 3. Adult male *Omolicna mariajosae* **sp. n.**; A. head frontal view, B. head, pronotum and mesonotum dorsal view, C. head, pronotum and mesonotum lateral view, scale = 1mm.

Forewing (Fig. 4) with large tubercles along costal, Sc+R(+M) and A1 veins. Smaller tubercles along all major longitudinal veins and branches. 'Spurious' vein present between Sc and RA. Vein branching pattern (Fig. 4): RA two-branched, RP three-branched (RP_1 apically forked), MP five-branched, CuA two-branched. Unusually, CuP fused with Pcu in distal quarter, well prior to fusion with A1, which closely tracks wing trailing margin Fork of R (Sc+RA from RP) well proximad to fork of CuA, about at level of fusion of CuP with Pcu. Forewing length: 2.53 mm.

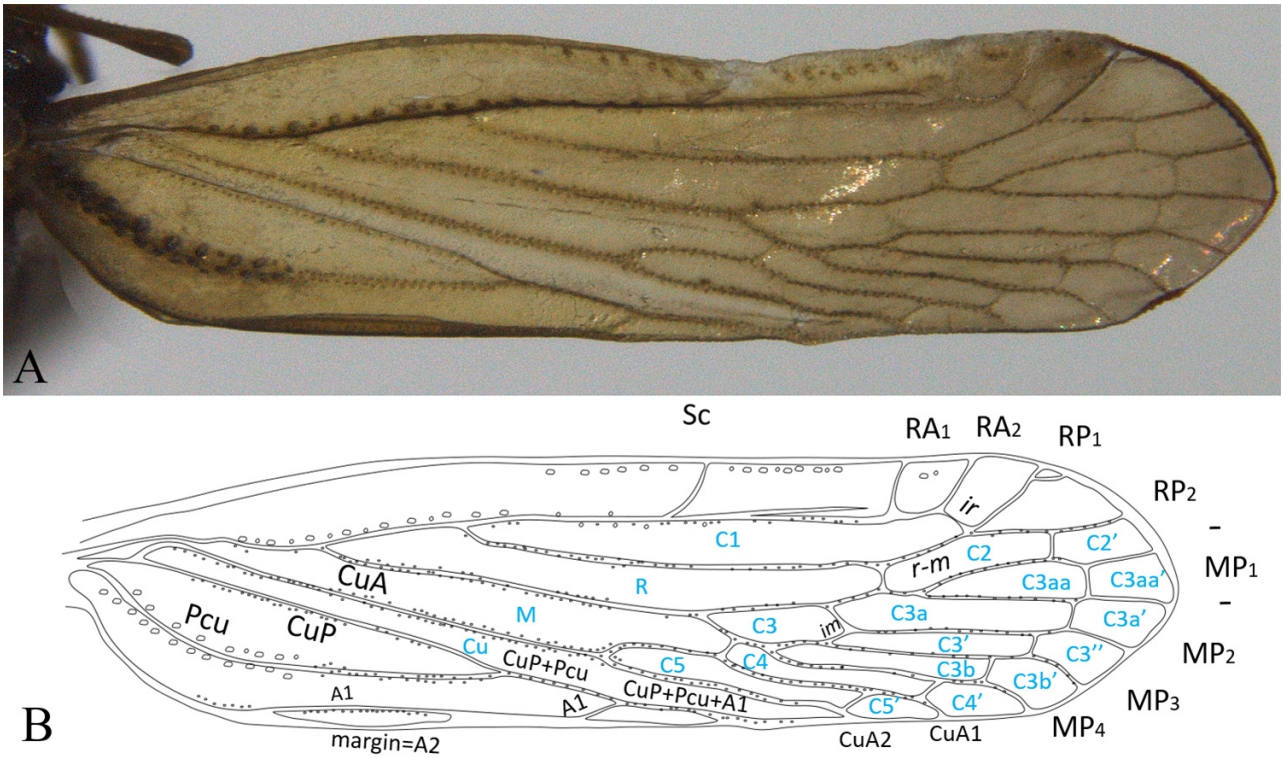

FIGURE 4. *Omolicna mariajosae* **sp. n.**, forewing venation; A. photograph and B. line art; black=vein, blue=associated cell.

Terminalia. Pygofer in lateral view narrow, with irregularly sinuate margins; narrowest dorsally, abruptly enlarged ventrally (Fig. 5A); median process in ventral view ornate with apex rounded, subapical teeth and small lateral basal teeth (Fig. 5B). Parameres in lateral view becoming wider distally, rounded ventrally, distal margin truncate, distal half of dorsal margin straight to dorsal process then strongly sloped ventrad; dorsal process with rounded apex, weakly sclerotized, angled anteriodorsad with smaller sclerotized process on lateral margin (Fig. 5A). Parameres in ventral view spatulate, narrow proximally, with pair of medially directed teeth, proximal tooth small bifurcated, distal very large and cultrate, curved basad; distal margin straight (Fig. 5B).

Aedeagus asymmetrical, all processes associated with aedeagal apex (A1–A3 on right side and A4–6 on left side) and endosoma (E1 on right side and E2 and E3 on left side); right side of aedeagus with three robust processes, approximately equal in length (A1–A3), right side of endosoma with single dorsal process (E1) strongly downcurved at apex (Fig. 6A), aedeagus left lateral side with three processes (Fig. 6B, A4–A6), all more slender than processes on right lateral side, ventral two processes (A5, A6) significantly more slender and shorter, ventral-most process smallest (Fig. 6B). Endosoma left lateral with dorsal process (E2) moderately downcurved, equal in length to the first endosomal process, third process on left side longer than all other processes, curved dorsad (E3) (Fig. 6C). Anal tube in lateral view robust, with large, irregularly sinuate ventral lobe setting off strong distal concavity; apex elongate, and projecting to pointed apices (Fig. 5A); dorsal margin straight. In dorsal view, lateral margins subparallel with ventral lobes visible past midlength, anal column short, nipple-like (Fig. 5C).

Plant associations. Unknown. Collected at light trap in primary growth cloud forest at an elevation of approximately 1,100 meters.

Distribution. Costa Rica (Alajuela)

Etymology. The specific name is given in honor of the lead author's daughter, Maria Jose.

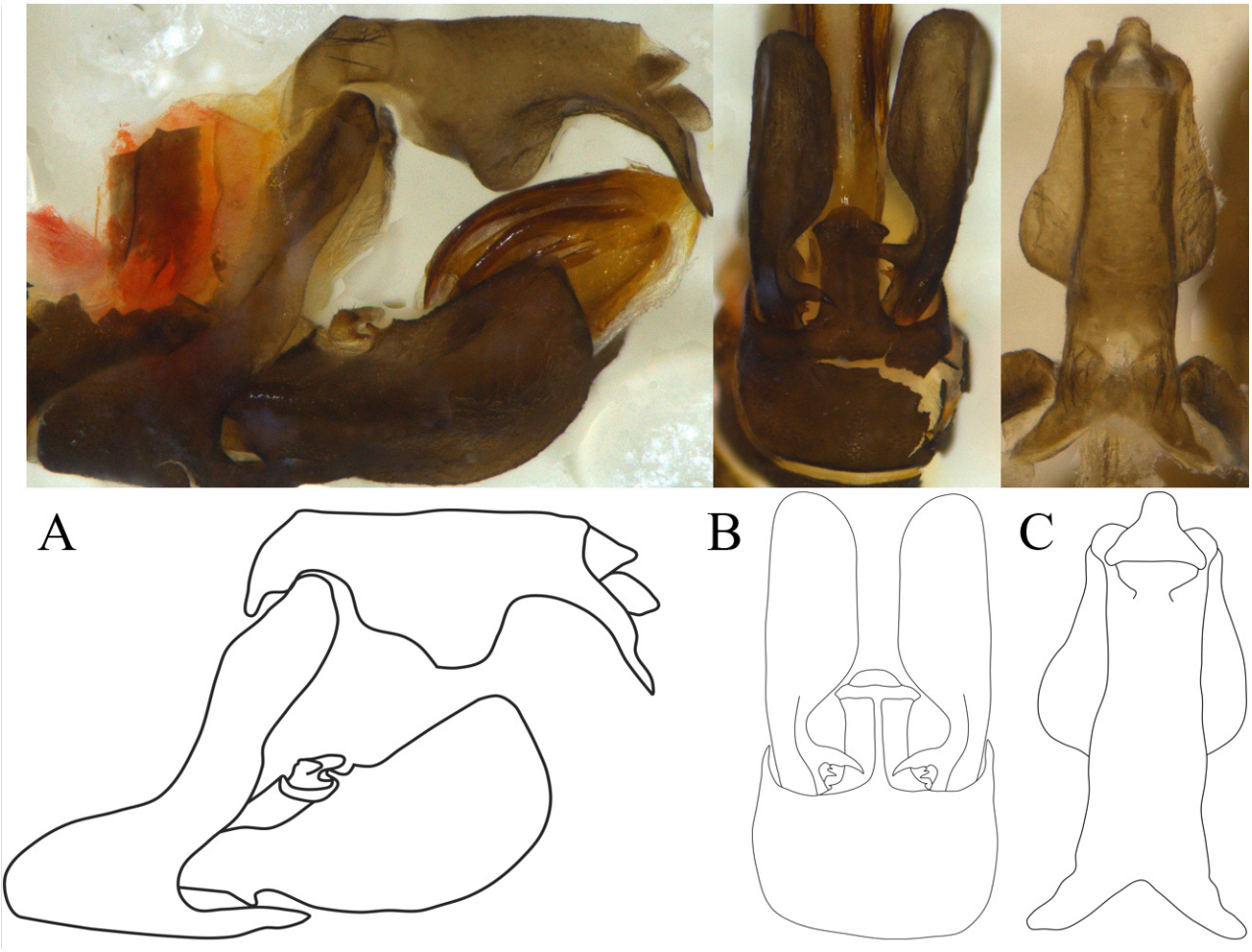

FIGURE 5. Male terminalia of *Omolicna mariajosae* **sp. n.**; A. lateral view, B. ventral view, and C. dorsal view.

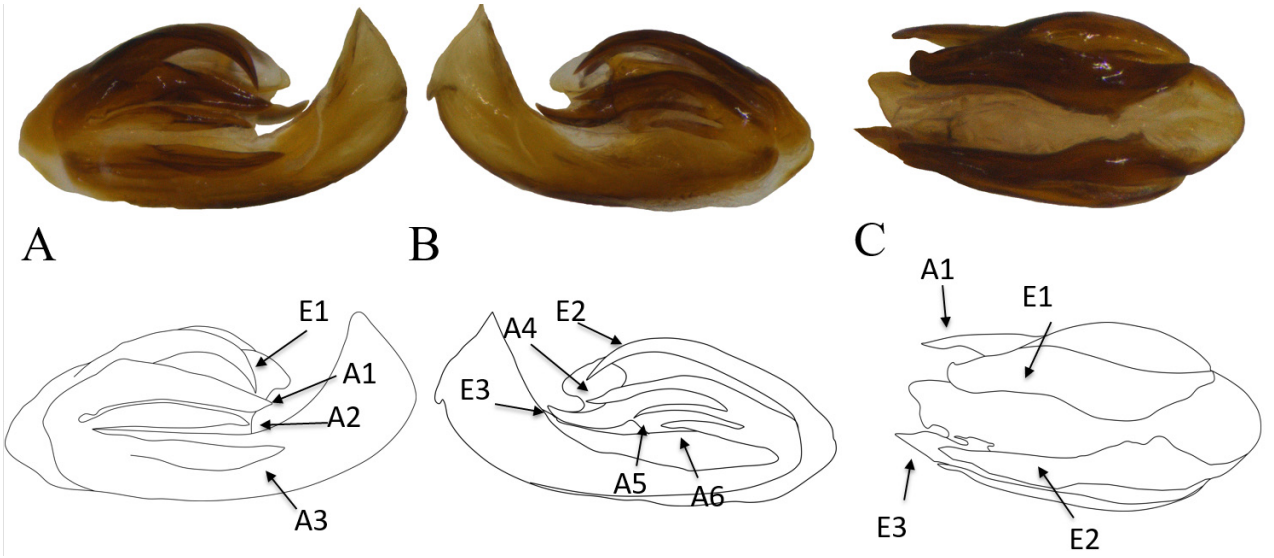

FIGURE 6. Aedeagus of adult male *Omolicna mariajosae* **sp. n.**; A. right lateral view, B. left lateral view, and C. dorsal view.

Material examined. Holotype male "Costa Rica, Alajuela / Los Angeles Cloud Forest / 15.V.2018 / Coll.: B.W. Bahder, light trap / Holotype *Omolicna mariajosae* ♂" (FLREC); Paratype: 1 male, same data as holotype (FLREC).

Sequence Data and Analysis. For *Omolicna mariajosae* **sp. n.**, a 761 bp product was generated for the COI locus (GenBank Accession No. MT422534). Based on the pairwise comparison of the COI loci for all taxa sampled,

Omolicna mariajosae **sp. n.** is on average 15.4% (±0.005) different from other members of *Omolicna*, 17% different from *Anchimothon dubia*, 21% (±0.004) different from the genus *Agoo*, 19% different from *Neocenchrea heidemanni*, 20% different from *Herpis metcalfi*, and 23% different from *Cenchrea dorsalis* (Table 2). Based on the phylogenetic analysis using the COI locus, *Omolicna mariajosae* **sp. n.** resolved well within the genus *Omolicna* (Fig. 7A).

For the 18S locus, a 1,395 bp product was generated for *Omolicna mariajosae* **sp. n.** (GenBank Accession No. MT424915). Based on the pairwise comparison of 18S, *Omolicna mariajosae* **sp. n.** differed, on average, by 3.3% (±0.0008) from other species of *Omolicna*, whereas excluding the novel taxon, the average variability among species with *Omolicna* was on average 0.7% (±0.001) (Table 3). *Omolicna mariajosae* **sp. n.** differed from the genus *Agoo* by an average of 11.7% (±0.0009), 12.2% from *Anchimothon dubia*, 11.8% from *Cenchrea dorsalis*, and 13.5% from *Herpis metcalfi* (Table 3). The phylogenetic analysis demonstrated *Omolicna mariajosae* **sp. n.** resolves within the genus *Omolicna* and that there is relatively strong support at the genus level for the cenchreine genera sampled in this study (Fig. 7B).

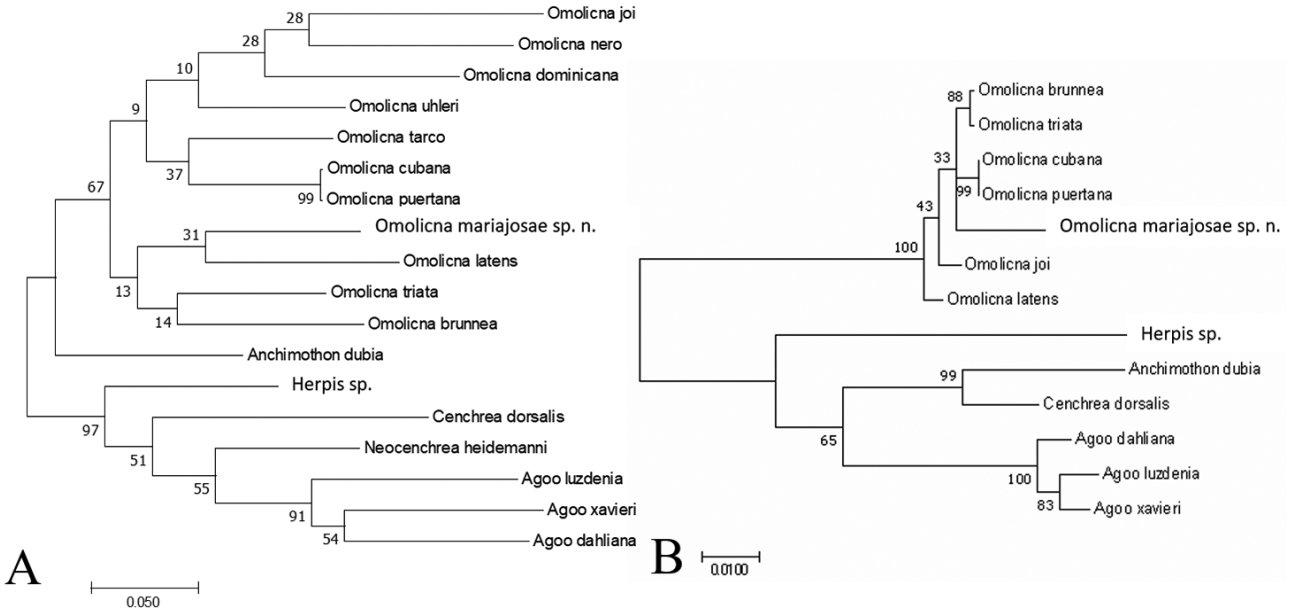

FIGURE 7. Maximum likelihood phylogenetic trees (1,000 replicates) demonstrating the relationship of the novel taxon, *Omolicna mariajosae* **sp. n.** relative to other species in *Omolicna* and other genera within the Cenchreini based on the; A. COI gene and B. 18S gene.

Remarks. While the novel taxon generally exhibits the morphological features observed in many species of *Omolicna*, there are significant deviations that make *O. mariajosae* **sp. n.** unique among *Omolicna*. A striking feature, relative to other *Omolicna*, is the asymmetry of the aedeagus. Bahder *et al.* (2020) found that in dorsal view, the longest process was on the right side of all taxa studied whereas the longest aedeagal process in *O. mariajosae* **sp. n.** is on the left side. Furthermore, the forewing of *O. mariajosae* **sp. n.** appears unusual among *Omolicna* by the presence small tubercles along most veins, a spurious vein in the subcostal cell, and the fusion of the Pcu with CuP before the A1 in the forewing. The combination of molecular data and morphological characters confirm the placement of this new species in the genus *Omolicna*.

Interestingly, available sequence data for both 18S and COI show *O. cubana* (from Jamaica) and *O. puertana* (from Puerto Rico) to be the same—100% identical for 18S and 99.8% for COI. Similarities in the aedeagus and terminalia (viz. Caldwell & Martorell 1951: 202, plate 24), Fennah 1952:135, figs. 13G, L,M,N) alongside the genetic evidence, seem to support that the taxa may be the same; however, we have not yet examined type material which is needed to confirm or refute the synonymy.

TABLE 2. Pairwise comparison for the COI gene based on 1,000 bootstrap replications using the p-distance method; numbers on bottom left=percent difference, numbers in upper right=standard error.

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	Omolicna_mariajosae_sp._n.		0.01	0.01	0.01	0.02	0.01	0.01	0.01	0.01	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
2	Omolicna_uhleri	14.0		0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.02	0.02	0.02	0.02	0.01	0.02
3	Omolicna_triata	14.0	14.0		0.01	0.02	0.01	0.01	0.01	0.01	0.02	0.02	0.01	0.02	0.02	0.02	0.02	0.02	0.02
4	Omolicna_latens	15.0	14.0	14.0		0.02	0.01	0.01	0.01	0.01	0.02	0.01	0.01	0.02	0.02	0.02	0.02	0.01	0.02
5	Omolicna_joi	18.0	15.0	16.0	18.0		0.02	0.01	0.02	0.02	0.02	0.01	0.02	0.02	0.02	0.02	0.02	0.02	0.02
6	Omolicna_cubana	15.0	13.0	14.0	16.0	17.0		0.01	0.01	0.00	0.02	0.01	0.01	0.02	0.02	0.02	0.02	0.02	0.02
7	Omolicna_brunnea	15.0	16.0	14.0	15.0	17.0	14.0		0.01	0.01	0.02	0.01	0.02	0.02	0.02	0.02	0.02	0.02	0.02
8	Omolicna_tarco	15.0	14.0	13.0	15.0	18.0	0.11	14.0		0.01	0.01	0.01	0.01	0.02	0.02	0.02	0.02	0.02	0.02
9	Omolicna_puertana	15.0	13.0	14.0	16.0	17.0	0.00	14.0	0.11		0.02	0.01	0.01	0.02	0.02	0.02	0.02	0.02	0.02
10	Omolicna_nero	17.0	16.0	16.0	19.0	18.0	16.0	19.0	16.0	16.0		0.01	0.01	0.02	0.02	0.02	0.02	0.02	0.02
11	Omolicna_dominicana	17.0	15.0	16.0	17.0	17.0	15.0	16.0	14.0	15.0	16.0		0.02	0.02	0.02	0.02	0.02	0.02	0.02
12	Anchimothon_dubia	17.0	17.0	15.0	16.0	20.0	15.0	17.0	14.0	15.0	18.0	17.0		0.02	0.02	0.02	0.01	0.02	0.02
13	Agoo_dahliana	21.0	19.0	20.0	21.0	22.0	19.0	21.0	20.0	19.0	23.0	22.0	18.0		0.01	0.01	0.01	0.02	0.02
14	Agoo_luzdenia	22.0	18.0	20.0	22.0	23.0	19.0	20.0	21.0	19.0	20.0	20.0	19.0	16.0		0.02	0.02	0.02	0.02
15	Agoo_xavieri	21.0	20.0	21.0	24.0	26.0	21.0	23.0	20.0	21.0	24.0	22.0	20.0	15.0	16.0		0.01	0.02	0.02
16	Neocenchrea_heidemanni	19.0	18.0	18.0	21.0	22.0	20.0	20.0	18.0	20.0	20.0	19.0	16.0	16.0	16.0	16.0		0.01	0.02
17	Herpis_metcalfi	19.0	18.0	18.0	18.0	22.0	18.0	17.0	18.0	18.0	22.0	18.0	18.0	18.0	19.0	20.0	15.0		0.02
18	Cenchrea_dorsalis	23.0	20.0	20.0	24.0	24.0	20.0	23.0	23.0	20.0	21.0	23.0	22.0	21.0	20.0	20.0	17.0	18.0	

TABLE 3. Pairwise comparison for the 18S gene based on 1,000 bootstrap replications using the p-distance method; numbers on bottom left=percent difference, numbers in upper right=standard error.

		1	2	3	4	5	6	7	8	9	10	11	12	13
1	Agoo_dahliana		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
2	Agoo_luzdenia	1.4		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
3	Agoo_xavieri	1.2	0.9		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
4	Anchimothon_dubia	7.3	6.9	7.5		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
5	Cenchrea_dorsalis	6.3	6.0	6.4	3.7		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
6	Herpis_metcalfi	9.4	9.0	9.0	9.6	8.3		0.0	0.0	0.0	0.0	0.0	0.0	0.0
7	Omolicna_brunnea	9.6	9.7	9.6	10.0	9.6	11.5		0.0	0.0	0.0	0.0	0.0	0.0
8	Omolicna_cubana	9.7	9.9	9.7	9.9	9.4	11.7	0.7		0.0	0.0	0.0	0.0	0.0
9	Omolicna_joi	9.6	9.8	9.6	10.2	9.8	11.3	0.8	1.0		0.0	0.0	0.0	0.0
10	Omolicna_latens	9.6	9.7	9.6	10.0	9.6	11.5	0.9	1.0	0.9		0.0	0.0	0.0
11	Omolicna_mariajosae_sp._n.	11.6	11.8	11.5	12.2	11.8	13.1	3.2	3.3	3.2	3.7		0.0	0.0
12	Omolicna_puertana	9.7	9.9	9.7	9.9	9.4	11.7	0.7	0.00	1.0	1.0	3.3		0.0
13	Omolicna_triata	9.6	9.8	9.6	10.1	9.6	11.6	0.2	0.7	0.9	0.9	3.2	0.7	

Discussion

With the description of *O. mariajosae* **sp. n.** there are now 20 species in *Omolicna*, but the status of *O. puertana* and *O. cubana* needs to be investigated by examination of type material. The discovery and description of *O. mariajosae* **sp. n.** further underscores the undiscovered diversity of planthoppers within the Caribbean basin. While the host association of *O. mariajosae* **sp. n.** in unknown, many species of *Omolicna* are documented from palm hosts including: *O. brunnea* and *O. triata* (Bahder *et al.* 2019), *O. cocoana* (Rodriguez-Leon & Hidalgo-Gato 2005), *Omolicna joi* (Halbert *et al.* 2014), and *O. tarco* (Bahder, *unpublished data*). While current survey work is in the context of vector relationships with palm lethal decline phytoplasma, other novel taxa will inevitably be discovered and help elucidate relationship of derbids to host and habitat preferences. While *O. mariajosae* **sp. n.** has unknown host affinities, its discovery is important to further knowledge of the diversity of this fascinating genus of planthoppers.

Acknowledgements

The authors are grateful to staff and management at Hotel Villa Blanca for their ongoing support of this research. The authors are grateful to Luz Bahder for translating the abstract into Spanish. Funding for this research was provided University of Florida—Institute of Food and Agricultural Sciences and Emerging Pathogens Institute for providing seed grant funding to support survey work in Costa Rica. We thank Thierry Bourgoin (Muséum national d'histoire naturelle, Paris) for assistance with interpreting the forewing.

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