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Revised status of *Omolicna* subgenus *Agoo* (Hemiptera: Auchenorrhyncha: Fulgoroidea: Derbidae) with a new species from Costa Rica and new country records

BRIAN W. BAHDER[1], CHARLES R. BARTLETT[2],
ERICKA E. HELMICK[3], EDWIN A. BARRANTES BARRANTES[4],
MARCO A. ZUMBADO ECHAVARRIA[5], ERICA M. GOSS[6] & MARINA S. ASCUNCE[7]

[1]*University of Florida, Department of Entomology and Nematology—Fort Lauderdale Research and Education Center; 3205 College Ave., Davie, FL 33314-7719, USA. E-mail: bbahder@ufl.edu*
[2]*University of Delaware, Department of Entomology and Wildlife Ecology, 250 Townsend Hall, Newark, DE 19716-2160, USA E-mail: Bartlett@udel.edu*
[3]*University of Florida, Department of Entomology and Nematology—Fort Lauderdale Research and Education Center; 3205 College Ave., Davie, FL 33314-7719, USA. E-mail: ehelmick@ufl.edu*
[4]*Universidad of Costa Rica—Sede San Ramón, Departmento de Ciencias Naturales, de la Iglesia el Tremedal 400 mts al Oeste carretera hacia San Pedro, San Ramón, Alajuela, Costa Rica. E-mail: edwin.barrantes@ucr.ac.cr*
[5]*Universidad of Costa Rica—Sede San Ramón, Departmento de Ciencias Naturales, de la Iglesia el Tremedal 400 mts al Oeste carretera hacia San Pedro, San Ramón, Alajuela, Costa Rica. E-mail: marco.zumbado@ucr.ac.cr*
[6]*University of Florida, Department of Plant Pathology; 1453 Fifield Hall, Hull Rd., Gainesville, FL 32611-0680, USA E-mail: emgoss@ufl.edu*
[7]*University of Florida, Department of Plant Pathology; 1453 Fifield Hall, Hull Rd., Gainesville, FL 32611-0680, USA E-mail: ascunce@ufl.edu*

Abstract

An ongoing survey for novel phytoplasmas and viruses that affect palms (Arecaceae) and their potential vectors is being conducted in Costa Rica. During that survey, a new species of derbid planthopper (Hemiptera: Fulgoroidea) from the palm *Astrocaryum alatum* H.F. Loomis was found in Heredia State and is here described as *Agoo dahliana* **sp. n.** *Omolicna dubia* Caldwell and *O. latens* Fennah were also found on coconut palms (*Cocos nucifera* L.) and represent new country records. Sequence data for the cytochrome c oxidase subunit I (COI) were generated for 9 ingroup (*Omolicna* Fennah) and 1 outgroup (*Neocenchrea* Metcalf) taxa; and for 18S ribosomal RNA gene were generated for 8 ingroup plus 2 outgroup taxa (*Neocenchrea, Cenchrea* Westwood). These data were compiled with available data from GenBank and BOLD for maximum likelihood phylogenetic reconstruction for *Omolicna*. These results, plus morphological evidence, support changing the status of the genus-group name *Agoo* Bahder & Bartlett from subgenus within *Omolicna* to full genus, resulting in the new combination of *Agoo xavieri* Bahder & Bartlett. Based on the original description and illustration of the genitalia of *Omolicna rubrimarginata* Fennah (from Trinidad), we transfer this species to *Agoo*, creating the combination *Agoo rubrimarginata* (Fennah), and bringing the total number of species in this genus to three, with *A. dahliana* **sp. n.** and *A. xavieri* currently only known from Costa Rica. Based on both molecular and morphological evidence, *O dubia* is transferred to *Anchimothon* Fennah. A key to differentiate the species of *Agoo* is presented.

Key words: Derbidae, Cenchreini, new species, Costa Rica, planthopper, survey, genetic diversity

Resumen

En Costa Rica se está llevando a cabo actualmente una investigación sobre nuevos fitoplasmas y virus que afectan a las palmeras (Arecaceae) y sus potenciales vectores. Durante la presente investigación, se encontró una nueva especie de chicharrita de la familia Derbidae (Hemiptera: Fulgoroidea) en la palma *Astrocaryum alatum* H.F.Loomis en la provincia de Heredia y se describe aquí como *Agoo dahliana* **sp.n**. También se encontraron en cocoteros (*Cocos nucifera* L.) las especies *Omolicna dubia* Caldwell y *O. latens* Fennah, las cuales representan nuevos registros para el país. Los datos de secuencia para la subunidad I del citocromo c oxidasa (COI) se generaron de 9 taxones de grupo interno (*Omolicna*)

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y uno de grupo externo (*Neocenchrea*) y el gen de ARN ribosómico 18S se generó de 8 taxones de grupo interno y 2 de grupo externo (*Neocenchrea, Cenchre*a). Estos datos se compilaron con los datos disponibles de GenBank y BOLD con el fin de lograr la reconstrucción filogenética más probable para *Omolicna*. Estos resultados, más la evidencia morfológica, respaldan el cambio del subgénero dentro de *Omolicna* Fennah al nuevo género *Agoo* (Bahder & Bartlett), lo que resulta en la nueva nomenclatura *Agoo xavieri* (Bahder & Bartlett). Basados en la descripción original y la ilustración de los genitales de *Omolicna rubrimarginata* Fennah (de Trinidad), transferimos esta especie a *Agoo*, creando la nueva nomenclatura *Agoo rubrimarginata* (Fennah), e incrementando el número total de especies en este género a tres, con *A dahliana* **sp. n**. y *A. xavieri* actualmente solo registradas para Costa Rica. En base a evidencia molecular y morfologica, O. dubia se transfiere a Anchimothon Fennah. Se presenta una clave dicotómica para diferenciar las especies de *Agoo*.

Palabras clave: Derbidae, Cenchreini, especie nuevo, Costa Rica, chicharrita, encuesta, diversidad genética

Introduction

Derbids in the tribe Cenchreini Muir (within Derbinae Spinola) are recognized by a foliate paranotal region of the pronotum that partially subtend the antennae, pits on the postcubital vein of the clavus and lateral pits on the vertex (O'Brien 1982, Emeljanov 1995, Halbert *et al*. 2014). Keys to the tribes of Derbidae were presented by Fennah (1952) and Emeljanov (1995), although these sources differ in tribal composition and definition. Keys to genera within Cenchreini are found in Fennah (1952) and revised by O'Brien (1982) for New World genera. Both Fennah (1952) and O'Brien (1982) include taxa subsequently removed from Cenchreini by Emeljanov (1992, 1995). Recently, a genus in the tribe Cenchreini, *Omolicna* Fennah, has garnered new attention due to its potential as a vector of phytoplasmas in palms (Halbert *et al*. 2014, Silva *et al*. 2018).

The genus *Omolicna* consists of 22 species (Bourgoin 2019, Bahder *et al*. 2019). Halbert *et al*. (2014) provided a review of the genus including critical literature. The most recent species described in *Omolicna* was *O. xavieri* Bahder & Bartlett (Bahder *et al*. 2019), which was found on declining coconut palms (*Cocos nucifera* L.) in Costa Rica. Previously, the species *O. joi* Wilson, Halbert & Bextine was discovered in Florida on cabbage palm (*Sabal palmetto* (Walter) Lodd. ex Schult. & Schult. f.) and saw palmetto (*Serenoa repens* (W. Bartram) Small) (Halbert *et al*. 2014). *Omolicna joi* is considered a potential vector of the 16SrIV-D phytoplasma, the causal agent of lethal bronzing disease (LBD), as it was discovered investigating vectors for this disease (Harrison *et al*. 2008). Additionally, phytoplasmas belonging to the lethal yellowing group (16SrIV) were isolated from derbids in Jamaica (Brown *et al*. 2006). While evidence is lacking that derbids are competent vectors of 16SrIV phytoplasmas, finding this group of phytoplasmas in derbids from Jamaica has elicited concern over their potential to transmit these pathogens.

While *O. joi* adheres to the generic description of *Omolicna*, *O. xavieri* has substantial morphological differences from *Omolicna senso stricto* (Bahder *et al*. 2019). In addition to morphological discrepancies, significant differences were seen in both the 18S and COI gene, prompting the placement of *O. xavieri* into the subgenus *Agoo* Bahder & Bartlett (Bahder et al. 2019). While these differences were substantial, a more robust molecular analysis and further assessment of morphological features within *Omolicna* and related cenchreine genera is needed to provide support to establish a new genus.

While surveying palms in Costa Rica for planthoppers, specimens tentatively identified as *Omolicna* were found on *Astrocaryum alatum* H.F. Loomis at La Selva Biological Station in Costa Rica. Here they are described as a new species and two other *Omolicna* species (*Omolicna dubia* Caldwell and *O. latens* Fennah) are reported as new country records. Sequence data for cytochrome c oxidase subunit I (COI) and 18S ribosomal RNA gene were obtained for these and all other available taxa. These data were combined with available data from GenBank and BOLD for all available *Omolicna* species (8 taxa for CO1, 6 taxa for 18S, plus 2 outgroups) and used for maximum likelihood phylogenetic reconstruction to investigate taxon relationships and monophyly of the subgenera *Agoo* and *Omolicna sensu stricto*.

Materials and methods

Locality and Specimen Collection. Individuals of the novel taxon were aspirated from healthy appearing ex-

amples of the palm *A. alatum* and were immediately transferred to 95% ethanol. Specimens were collected (permit no. SINAC-ACTo-GASPPNI-016-2018) at La Selva Biological Station (Fig. 1), Heredia Province, Costa Rica (10.431269, -84.005961). In addition, two specimens of a derbid were collected from coconut palm in Gandoca Manzanillo National Wildlife Refuge (Fig. 1), Costa Rica (9.596208, -82.604283). Specimens were exported under permit number DGVS-256-2018 and imported into the U.S.A. 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 in Gainesville, FL, U.S.A..

FIGURE 1. Habitat and collection site of *Agoo dahliana* **sp. n.** and *Omolicna latens* at La Selva Biological Station (A) and for *Omolicna dubia* at Gandoca-Manzanillo Wildlife Refuge (B).

Morphological terminology. 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 attributed to Bahder and Bartlett.

Dissections and DNA Extraction. The genitalia that were dissected also served as the source of tissue for DNA extraction. The terminal end of the abdomens with genitalia 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 genitalia 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 genitalia 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 and Sequence Data Analysis. To obtain COI sequence data for the 5' barcoding region, a 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), 18S/Forward (5'-ACTGTCGATGGTAGGTTCTG-3') and 18S/Reverse (5'-GTCCGAAGACCTCACTAAA-3') were used. PCR reactions contained 5x GoTaq Flexi Buffer, 25 mM $MgCl_2$, 10 mM dNTP's, 10 mM of each primer (for both COI and 18S reactions), 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 55°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 59°C, 2 min extension at 72°C, followed by a 5 min extension at 72°C. All products were run on a 1.5% agarose gel stained with 1% GelRed (Biotium, Fremont, California, USA). PCR prod-

ucts 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 haplotypes were 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 for both COI and 18S analyses. Maximum Likelihood trees were generated using the Bootstrap method at 1,000 replicates based on the Tamura-Nei model for both COI and 18S gene sequences.

Taxon sampling. COI and 18S data from all other available species of *Omolicna*, plus 2 outgroups in the Cenchreini, were compiled for phylogenetic analyses (Tables 1, 2) and morphological comparison. These data include previously generated COI data by Bahder *et al*. (2019) for *Omolicna* (*Agoo*) *xavieri, O. brunnea* (McAtee), and *O. triata* (Caldwell) and data from the Barcode of Life Database (BOLD) for *Omolicna uhleri* (Table 2). The only Cenchreini 18S sequence data publicly available was from Bahder *et al.* (2019) and include *O.* (*Agoo*) *xavieri*, *O. brunnea* and *O. triata*. A total of 11 ingroup taxa were included for COI and 8 ingroup taxa for 18S.

TABLE 1. Cenchreini used for molecular extractions.

Species	Source	Collection Date	Locality
Agoo xavieri	FLREC	12-May-2018	Costa Rica
Anchimothon dubia	FLREC	14-May-2018	Costa Rica
Omolicna brunnea	FLREC	12-May-2018	Costa Rica
Omolicna dominicana	University of Delaware	20-June-2004	Dominica
Omolicna fulva	University of Delaware	August-2005	U.S.A., DE
Omolicna joi	FLREC	29-July-2018	U.S.A., FL
Omolicna latens	FLREC	22-May-2018	Costa Rica
Omolicna proxima	FDACS-DPI	18-July-1971	Trinidad
Omolicna puertana	University of Puerto Rico	23-March-2019	U.S.A., PR
Omolicna nero	University of Delaware	5-July-2003	Belize
Omolicna triata	FLREC	12-May-2018	Costa Rica
Cenchrea dorsalis	University of Delaware	29-August-1991	St. Vincent
Neocenchrea heidemanni	University of Delaware	2-September-2009	U.S.A., DE

TABLE 2. GenBank accession numbers for included Cenchreini.

	GenBank Accession No.	
Species	**COI**	**18S**
Agoo dahliana **sp. n.**	MN496467	MH472754
Agoo xavieri	MK443068	MK443073
Anchimothon dubia	MN496470	MN474755
Omolicna brunnea	MK443070	MK443071
Omolicna dominicana	MN496469	N/A
Omolicna joi	KF472312	MN472753
Omolicna latens	MN496472	MN472757
Omolicna puertana	MN496468	MN472751
Omolicna nero	MN496471	MN472752
Omolicna triata	MK443069	MK443072
Omolicna uhleri	CNCHG1197-12[1]	N/A
Neocenchrea heidemanni	MN496473	MN472758
Cenchrea dorsalis	N/A	MN472756

[1]Barcode of life (BOLD) accession number

Results and discussion

Sequence Data and Analysis. New sequence data were obtained for the COI gene (703 bp; 5') for six species of *Omolicna* and one species of *Neocenchrea* (Table 2) for this study in addition to the new species. New 18S gene sequences (1,493 bp) for the new species as well as five species of *Omolicna,* one *Neocenchrea*, and one *Cenchrea* (Table 2). Museum specimens did not consistently amplify for both loci, resulting in the lack of COI data for *Cenchrea dorsalis* McAtee and lack of 18S data for *O. dominicana* Fennah and *O. uhleri*.

Based on the analysis of the COI gene, *Agoo dahliana* **sp. n.** was on average, 20.3% different from members of the genus *Omolicna*, ranging from 18.4% to 22.3% (Table 3) and 14.7% different from *Agoo xavieri*. On average species within *Omolicna* differed by 15.7% from each other, ranging from 13.2% to 19.9% different for the region of COI analyzed (Table 3). The phylogenetic analysis resolved *Agoo dahliana* **sp. n.** near *Agoo xavieri* and distinct from *Omolicna senso stricto* as well as outgroup taxa (Fig. 2A). For the 18S gene, *Agoo dahliana* **sp. n.** differed by an average of 9.2% from members of the genus *Omolicna*, 6.7% from *Neocenchrea heidemanni* (Ball) 6.5% from *Cenchrea dorsalis* while only differing by 1.2% from *Agoo xavieri* (Table 4). With the exception of *O. dubia* (Caldwell) and *O. nero* Fennah variation among species in *Omolicna* was on average 0.75% (Table 4). Both *O. dubia* and *O. nero* differed by about 10% from other *Omolicna* and 2.3% from each other (Table 4). The phylogenetic analysis based on the COI revealed strong bootstrap support for *Agoo* as a distinct clade relative to *Neocenchrea* and *Omolicna senso stricto* (Fig. 2A). The phylogenetic analysis based on the 18S gene showed strong support for *Agoo dahliana* **sp. n.** as a distinct clade, resolving with *Agoo xavieri*, relative to *Omolicna senso stricto*, and *Cenchrea*, with strong bootstrap support (Fig. 2B). The *Agoo* clade also resolved distinct from the non-*Omolicna* outgroups. Maximum likelihood trees produced for both loci demonstrate strong support for *Agoo*, however, future efforts should seek to assess as many cenchreines as possible to understand the relationship among genera within the tribe.

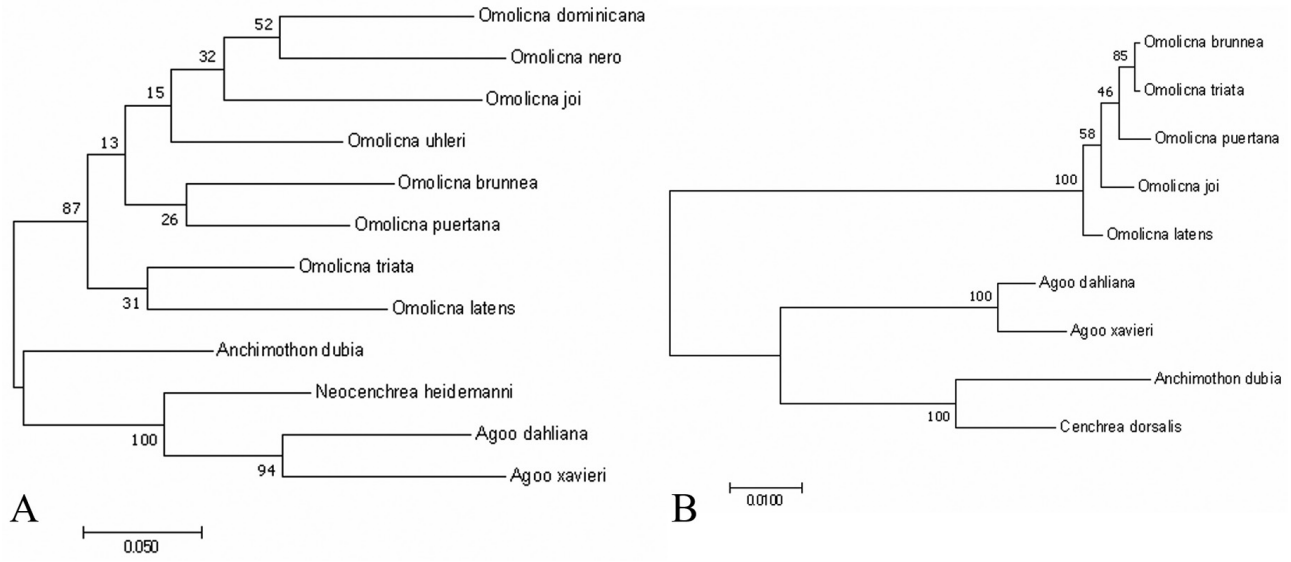

FIGURE 2. Maximum likelihood phylogenetic trees (1,000 replicates) based on the COI gene (A) and 18S gene (B) demonstrating the relationship of the novel taxon, *Agoo*, relative to other genera within the Cenchreini.

Morphological comparison. While the subgenera *Agoo* and *Omolicna* are similar, the medioventral process of the pygofer and the general morphology of the aedeagus correspond to differences observed in both the 18S and COI loci. All currently described *Omolicna* in the strict sense possess an ornate medioventral process on the pygofer that possess either lateral teeth/hooks, a multi-lobed apex, or a combination of these two features. Both *Agoo dahliana* **sp. n.** and *Agoo xavieri* possess a single, triangular lobe that lacks lateral teeth or hooks. In addition, *Omolicna* have an aedeagus that is strongly asymmetrical with processes that are rather short and stout whereas both *Agoo dahliana* **sp. n.** and *Agoo xavieri* possess an aedeagus with rather long and thin processes that are nearly symmetrical (not noticeably asymmetrical).

TABLE 3. Pairwise comparison for the COI gene based on 1,000 bootstrap replications using the *p*-distance method.

		1	2	3	4	5	6
1	*Agoo dahliana*		0.014	0.016	0.016	0.016	0.016
2	*Agoo xavieri*	0.147		0.015	0.015	0.015	0.016
3	*Omolicna puertana*	0.187	0.207		0.014	0.013	0.014
4	*Omolicna triata*	0.197	0.205	0.145		0.013	0.015
5	*Omolicna brunnea*	0.204	0.216	0.137	0.132		0.014
6	*Omolicna dominicana*	0.216	0.210	0.147	0.157	0.152	
7	*Anchimothon dubia*	0.184	0.197	0.149	0.144	0.165	0.165
8	*Omolicna nero*	0.223	0.226	0.160	0.163	0.187	0.152
9	*Omolicna joi*	0.221	0.246	0.165	0.157	0.166	0.165
10	*Omolicna uhleri*	0.189	0.192	0.131	0.132	0.157	0.149
11	*Omolicna latens*	0.204	0.233	0.158	0.137	0.150	0.160
12	*Neocenchrea heidemanni*	0.160	0.155	0.189	0.176	0.199	0.187
13	*Cedusa_inflata*	0.223	0.212	0.192	0.191	0.191	0.215

TABLE 3. (Continued)

		7	8	9	10	11	12	13
1	*Agoo dahliana*	0.015	0.016	0.016	0.015	0.016	0.015	0.017
2	*Agoo xavieri*	0.016	0.016	0.017	0.015	0.016	0.014	0.016
3	*Omolicna puertana*	0.014	0.014	0.015	0.013	0.014	0.015	0.015
4	*Omolicna triata*	0.014	0.015	0.014	0.013	0.014	0.015	0.015
5	*Omolicna brunnea*	0.015	0.016	0.015	0.014	0.014	0.016	0.015
6	*Omolicna dominicana*	0.015	0.014	0.015	0.015	0.014	0.015	0.016
7	*Anchimothon dubia*		0.015	0.016	0.015	0.015	0.015	0.015
8	*Omolicna nero*	0.171		0.015	0.014	0.015	0.016	0.016
9	*Omolicna joi*	0.187	0.174		0.014	0.015	0.017	0.016
10	*Omolicna uhleri*	0.163	0.152	0.152		0.014	0.016	0.016
11	*Omolicna latens*	0.158	0.184	0.178	0.139		0.016	0.016
12	*Neocenchrea heidemanni*	0.160	0.192	0.218	0.176	0.204		0.016
13	*Cedusa_inflata*	0.189	0.221	0.226	0.204	0.210	0.192	

TABLE 4. Pairwise comparison for the 18S gene based on 1,000 bootstrap replications using the p-distance method.

		1	2	3	4	5	6	7	8	9	10	11
1	*Agoo dahliana*		0.003	0.008	0.008	0.008	0.007	0.008	0.008	0.008	0.007	0.007
2	*Agoo xavieri*	0.012		0.008	0.008	0.008	0.007	0.007	0.008	0.008	0.007	0.007
3	*Omolicna latens*	0.097	0.098		0.003	0.003	0.008	0.008	0.003	0.003	0.008	0.008
4	*Omolicna brunnea*	0.096	0.097	0.009		0.002	0.008	0.008	0.001	0.002	0.008	0.008
5	*Omolicna puertana*	0.099	0.100	0.011	0.006		0.008	0.008	0.002	0.003	0.008	0.008
6	*Anchimothon dubia*	0.075	0.076	0.103	0.103	0.102		0.004	0.008	0.009	0.006	0.005
7	*Omolicna nero*	0.079	0.075	0.100	0.103	0.100	0.023		0.008	0.009	0.006	0.006
8	*Omolicna triata*	0.098	0.099	0.009	0.002	0.006	0.103	0.103		0.002	0.008	0.008
9	*Omolicna joi*	0.098	0.099	0.009	0.006	0.009	0.105	0.104	0.008		0.008	0.008
10	*Neocenchrea heidemanni*	0.067	0.068	0.100	0.100	0.098	0.041	0.047	0.100	0.102		0.001
11	*Cenchrea dorsalis*	0.065	0.067	0.099	0.098	0.096	0.040	0.045	0.099	0.100	0.053	

Remarks. The morphological differences are supported by these molecular data. The differences in variance for 18S observed between generic outgroups further support revising the status of *Agoo* to full genus status. The approximate 10% difference between *Agoo* and *Omolicna* is much larger that the difference observed between *Neocenchrea* and *Cenchrea* (5.3%). The difference between both *Cenchrea* and *Neocenchrea* and *Omolicna* was

approximately 10%, similar to that between *Agoo* and *Omolicna*, further supporting generic level status for *Agoo.* The revised status for *Agoo* results in the new status for *Agoo xavieri* (Bahder & Bartlett).

For phylogenetic tree construction, COI and 18S had to be analyzed separately due to the inability to amplify both loci for all taxa examined due to primer mismatch, template degradation of museum specimens, or both. Furthermore, a large sampling of outgroup taxa is generally desired but because most of the non-*Omolicna* Cenchreini available were older museum specimens, amplification success was difficult and achieved only for *Cenchrea dorsalis* and *Neocenchrea heidemanni.*

One species in the genus *Omolicna*, *O. rubrimarginata* Fennah, appears to conform to the features listed as belonging to *Agoo*. The description and illustration by Fennah (1945) demonstrate a single, triangular medioventral process on the pygofer and the illustration (Fennah 1945, Plate 10, Fig. 161–168) and description also highlights that the processes on the aedeagus are slender. Based on the description of the medioventral process and aedeagus of *O. rubrimarginata* in Fennah (1952), we propose moving *O. rubrimarginata* from *Omolicna* to *Agoo.* This move would result in the newly described genus, *Agoo*, containing three valid, distinct species; *Agoo xavieri*, *Agoo dahliana* **sp. n.**, and *Agoo rubrimarginata*.

Unfortunately, specimens of all known species of *Omolicna* were not available for morphological evaluation and molecular characterization. Specimens of *O. brunnea* and *O. triata* from Bahder et al. (2019) were included for morphological comparisons (Fig. 3) as were *O. dubia* and *O. latens* (this study). Specimens of *O. proxima* Fennah, *O. puertana* Caldwell, *O. dominicana*, *O. fulva* (Van Duzee), *O. nero*, and *O. joi* were also obtained for morphological comparison (Fig. 3). Of all species of *Omolicna* examined, all possessed a multilobed medioventral process (Fig. 4) and an asymmetrical aedeagus (Fig. 5). It is interesting to note the distinct structure of the aedeagus and anal tube in *O. dubia* relative to other congeners. These differences with the significant difference in both COI and 18S sequence data with other *Omolicna* merit the movement of *O. dubia* to a different genus.

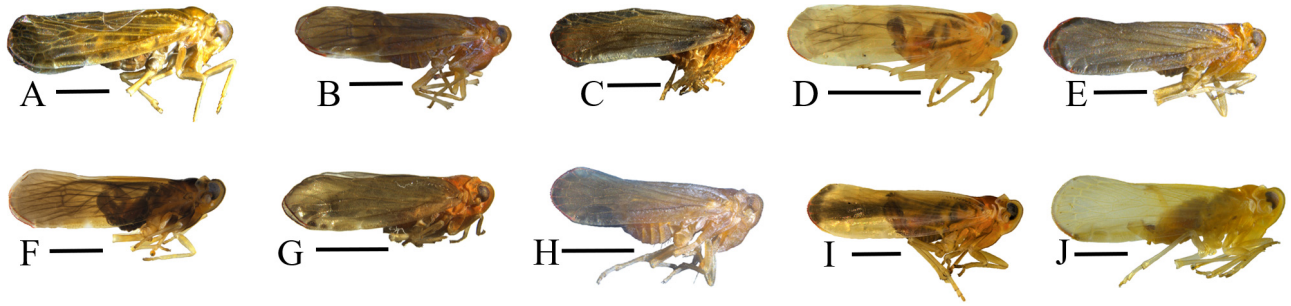

FIGURE 3. Species of the genus *Omolicna* used in this study for molecular work and morphological comparisons; A. *O. proxima*, B. *O. puertana*, C. *O. dominicana*, D. *O. latens*, E. *O. fulva*, F. *O. brunnea*, G. *O. nero*, H. *O. joi*, I. *O. triata*, J. *O. dubia*.

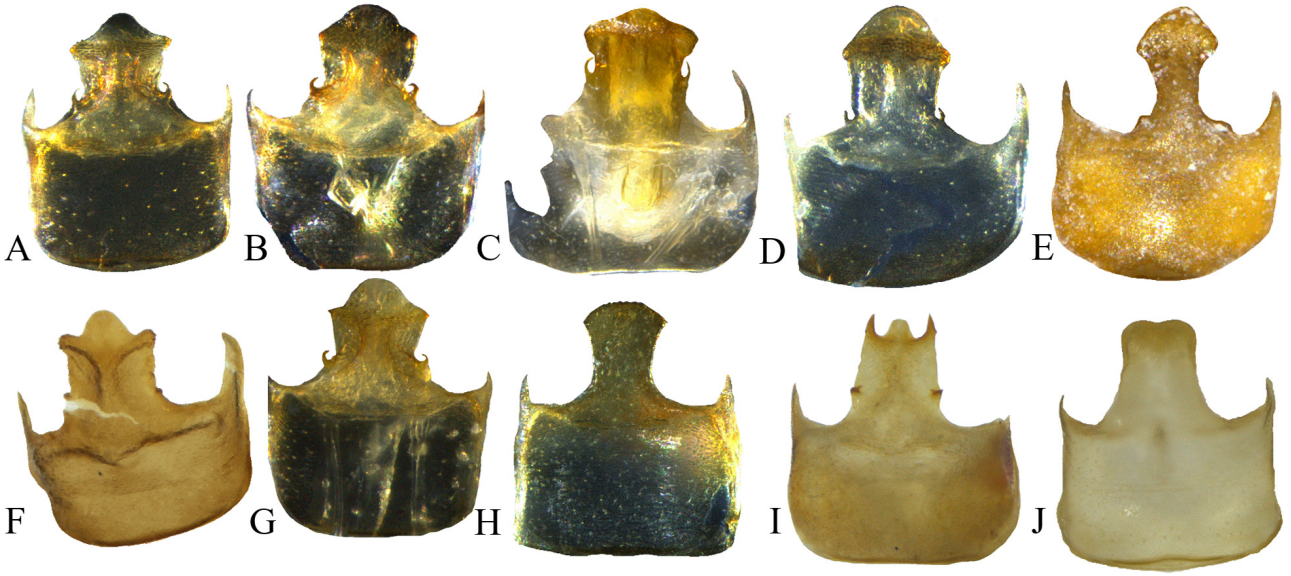

FIGURE 4. Ventral view of the medioventral process of the pygofer for species of the genus *Omolicna* used in this study for molecular work and morphological comparisons; A. *O. proxima*, B. *O. puertana*, C. *O. dominicana*, D. *O. latens*, E. *O. fulva*, F. *O. brunnea*, G. *O. nero*, H. *O. joi*, I. *O. triata*, J. *O. dubia*.

Of the other genera within the Cenchreini, *Anchimothon* Fennah, 1952 seems to be the most appropriate genus to place *O. dubia*. *Anchimothon* is diagnosed by males possessing an elongate and narrow anal segment, the apex of parameres strongly hooked inwards, and a semi-rounded medio-ventral lobe lacking lateral teeth. The only described species of *Anchimothon* is *A. parishi* Muir, 1918 (Fig. 6). While sequence data could not be obtained for *A. parishi* the general form of the terminalia and aedeagus closely resemble those of *O. dubia* and with the significant deviation that *O. dubia* presents relative to *Omolicna* at the molecular level supports the movement of *O. dubia* to *Anchimothon*, bringing the current species count of the genus to two, *A. dubia* and *A. parishi*.

FIGURE 5. Dorsal view of the aedeagus for species of the genus *Omolicna* used in this study for molecular work and morphological comparisons; A. *O. proxima*, B. *O. puertana*, C. *O. dominicana*, D. *O. latens*, E. *O. fulva*, F. *O. brunnea*, G. *O. nero*, H. *O. joi*, I. *O. triata*, J. *O. dubia*.

Systematics

Family Derbidae Spinola 1839

Subfamily Derbinae Spinola 1839

Tribe Cenchreini Muir 1913

Type Genus: *Cenchrea* Westwood 1840

Genus *Agoo* Bahder & Bartlett 2019, new status

Type species: *Agoo xavieri* Bahder & Bartlett, 2019

Amended diagnosis. Frons narrower and paranota more strongly foliate than genus *Omolicna*. Transverse carina at fastigium lacking. Paranotal folia quadrate to semiquadrate in frontal view. Ventral lobe of pygofer (ventral view) broad, distally attenuating to rounded apex. Aedeagus and endosoma nearly bilaterally symmetrical. Segment X ventrally sinuate (lacking convexity found in most *Omolicna*).

FIGURE 6. Adult male *Anchimothon parishi*; A. lateral habitus, B. dorsal habitus.

Key to the species of *Agoo*

1. Process present on dorsal surface of paramere (Fig. 9), sclerotized points on parameres; pair of processes on aedeagus situated posterior, wings with distinct black spots. . . . . *dahliana* **sp. n.**
1'. Process absent on dorsal surface of paramere, no sclerotization on parts of parameres; all processes on aedeagus situated anterior; wings immaculate. 2
2. Body yellow, wings with fuscous stripe on forewing, orange pattern on frons, aedeagus with lateral pair of large sub-basal acuminate teeth. . . . . *xavieri*
2'. Body fuscous, wings hyaline, aedeagus lacking sub-basal acuminate teeth . . . . . *rubrimarginata*

Agoo dahliana Bahder & Bartlett sp. n.

(Figures 7–11)

Type locality. La Selva Biological Station, Heredia, Costa Rica

Diagnosis. Body overall testaceous with darker areas. Orange patches on dorsal portion of clypeus and genae. Dark patch on venter of abdomen and fuscous bands on pronotal foveae. Forewings with many dark spots in cells. Male pygofer with median ventral process wider than long; broad near base, attenuating distally to broadly rounded

apex (lateral teeth lacking). Parameres, in lateral view, possess a single, large ventral lobe; dorsal surface bearing large lobe with two weakly sclerotized processes; basal process angled posteriorly; in ventral view parameres possess large, hooked lobes with acute sclerotized apices; paramere apices rounded with distinct, anterior facing, sclerotized spine. Aedeagal apex with two elongate processes on each side, one pair at apex, one pair subapical, in addition to complex endosoma bearing additional processes. Segment X (= "anal tube") in lateral view robust, caudal portion stout, and ventrally sinuate, apex acute and moderately downcurved; in dorsal view deeply notched in caudal aspect.

Description. *Color*. General body color yellowish-brown (Fig. 7); face deep orange on dorsal third of clypeus, frons above frontoclypeal suture, and genae below antennae (Fig. 8A); lateral carinae of front and vertex darkened. Paranotal folia with dark spots on inner surface. Mesonotum diffusely infuscate with orange, medially pale (giving appearance of weakly contrasted median vitta); lateral-most portion of mesonotum and tegulae pale. Forewings faintly yellowish, veins white (distally) to clouded (basally); distal cells with diffuse dark spots. Basal cells also possessing orange shading. Dorsum of abdomen orangish; aedeagus appearing dark brown within paler terminalia.

FIGURE 7. Adult male habitus *Agoo dahliana* **sp. n.**; A. body lateral view and B. body dorsal view (B), scale = 1 mm.

Structure. Body length males (*n* =5): 7.11–7.32 mm with wings; 4.52–4.54 mm without wings; females (*n*=10): 7.41–7.70 mm with wings; 4.55–4.57 mm without wings. Head. In lateral view, anterior margin of head smoothly rounded (Fig. 8C). Vertex deeply concave posteriorly, notched distally (Fig. 8B), broadest near base, tapering distally; lateral margins decidedly keeled, bearing two (somewhat irregular) rows of sensorial pits, disc depressed, without distinct carinae. Transverse apical carina separating vertex from frons absent. Vertex length males: 0.30–0.31 mm; females: 0.32–0.33 mm. Vertex width at hind margin males: 0.37–0.38 mm; females: 0.38–0.39 mm. Vertex width at distal margin males: 0.15–0.17 mm; females: 0.17–0.20 mm. Frons with lateral carinae strongly keeled, narrowest between compound eyes, diverging slightly ventrad until reaching the frontoclypeal suture (Fig. 8A); sensorial pits next to each carina for entire length, carinae absent on disc of frons. Frons length males: 0.861–0.863 mm; females: 0.870–0.890 mm. Frons dorsal width males: 0.11–0.13 mm; females: 0.12–0.14 mm. Frons frontoclypeal margin width, males: 0.28–0.29 mm; females: 0.29–0.30 mm. Clypeus with lateral carinae keeled, sensorial pits absent, converging near midlength to labrum. Clypeus length males: 0.70–0.73 mm; females: 0.75–0.78 mm.

Thorax. Pronotum short, anterior margin following contours of posterior margin of head (Fig. 8B); convex, anteriorly truncate behind vertex, narrowed behind eyes; posterior margin moderately concave; paranotal regions moderately foliate, partially subtending antennae in lateral view, forming fossae (Figs. 8A-C). Pronotum length at midline males: 0.30–0.30 mm; females: 0.31–0.33 mm. Mesonotum appearing slightly elevated in lateral view (Figs. 8B, 8C); in dorsal view, with three subparallel longitudinal carinae, indistinctly reaching posterior margin. Mesonotum length at midline males: 1.01–1.02 mm; females: 1.04–1.05 mm. Mesonotum width males: 1.22–1.24 mm; females: 1.26–1.29 mm.

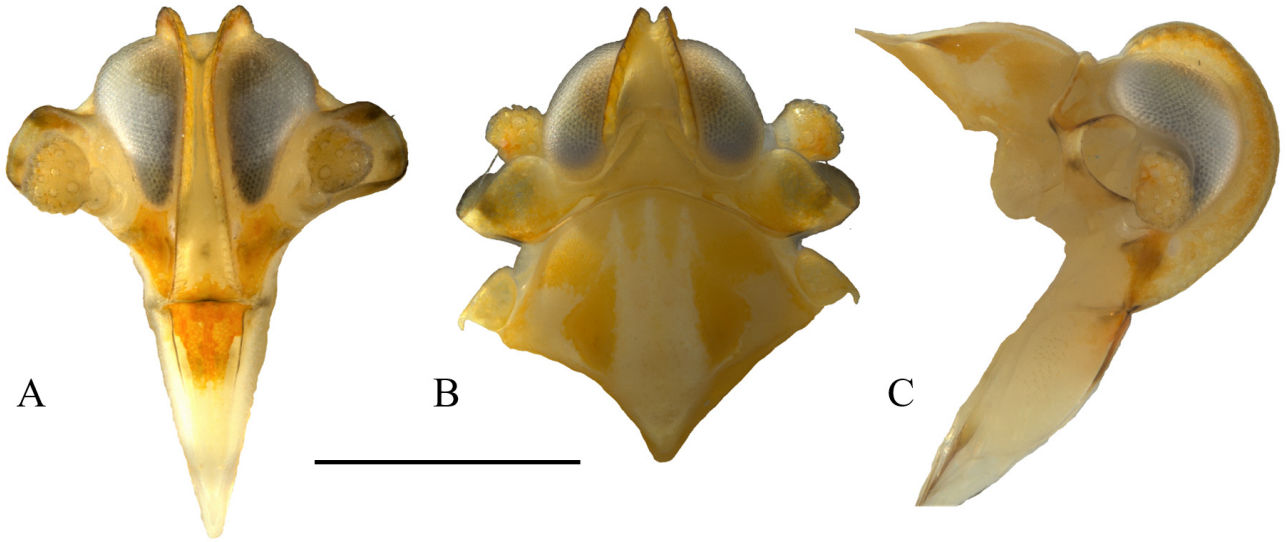

FIGURE 8. Adult male *Agoo dahliana* **sp. n.**; A. head frontal view, B. head, pronotum and mesonotum dorsal view, C. head, pronotum and mesonotum lateral view, scale=1mm.

Forewing (Fig. 9) with row of sensory pits along costal vein, reaching fork of ScP, second row along basal 2/3rd of ScP+R (nearly to fork of ScP) and third row along basal half of postcubitus. Forks of R and CuA veins approximately at the same level, both well proximad of claval apex. Claval apex just beyond midpoint of wing, fork of MP just distad of claval apex; RA 1-branched, RP 1-branched, MP 4-branched and CuA 3-branched. Junction of Pcu+A1 in basal half of wing. Forewing length males: 6.27–6.30 mm; females: 6.70–7.00 mm.

Terminalia. Pygofer, in lateral view, narrow, distal and proximal margins sinuate (Fig. 10A), broadest ventrally; in ventral view, ventral opening of pygofer bearing rounded lobe (Fig. 10B), widest at base and attenuating distally to rounded apex, lobe at base wider than long. Parameres, in ventral view, broadest ventrally with margins running parallel until expanding into a large, rounded tooth at midlength, strongly hooked with sclerotized apex pointing anteriorly; portion distal to hooked tooth of uniform width, narrower than basal portion until expanding slightly at terminus which possesses an anteriorly facing sclerotized spine (Figure 10B); in lateral view possessing a single, large ventral lobe; dorsal surface bearing large lobe with an invagination on posterior aspect, resulting in two lightly sclerotized processes, with posterior process pointing dorsally and anterior process angled posteriorly. Aedeagus with four elongate processes, one shorter pair at apex, one large pair subapical, all angled ventrad and pointing anteriorly. Complex endosoma with large retrorse median process, medium sized pair of retrorse lateral processes, and dorsal pair of posteriorly facing processes (Fig. 11). Endosoma complex, retrorse, bearing additional projections and asymmetrical 3-dimensional structures, but appearing to have two lateral processes, one medial process and a pair of dorsal processes (Fig.11). Segment X (= "anal tube"), in lateral view, robust, caudal portion stout, and ventrally sinuate, apex acute and moderately downcurved; in dorsal view, deeply notched on caudal aspect (Fig. 10).

Plant associations. Coquito (*Astrocaryum alatum* H.F. Loomis), Arecaceae.

Distribution. Costa Rica (Heredia).

Etymology. The specific name is an honorarium for the lead author's daughter, Dahliana Lucía Bahder.

Material examined. Holotype male "Costa Rica, Heredia / La Selva Biological Station / Brian W. Bahder; 22 May 2018 / aspirated from coquito // Holotype/*Agoo*/*dahliana*" (FLREC). Paratypes, same data as holotype (11 males, 18 females, FLREC).

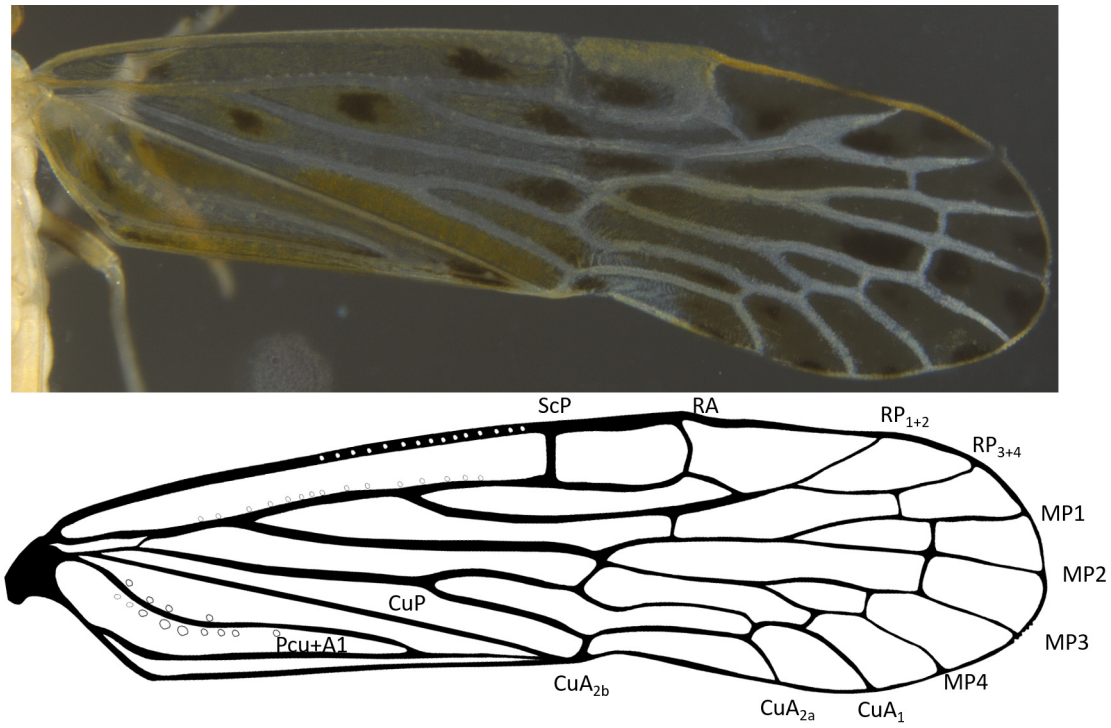

FIGURE 9. *Agoo dahliana* **sp. n.**, forewing venation.

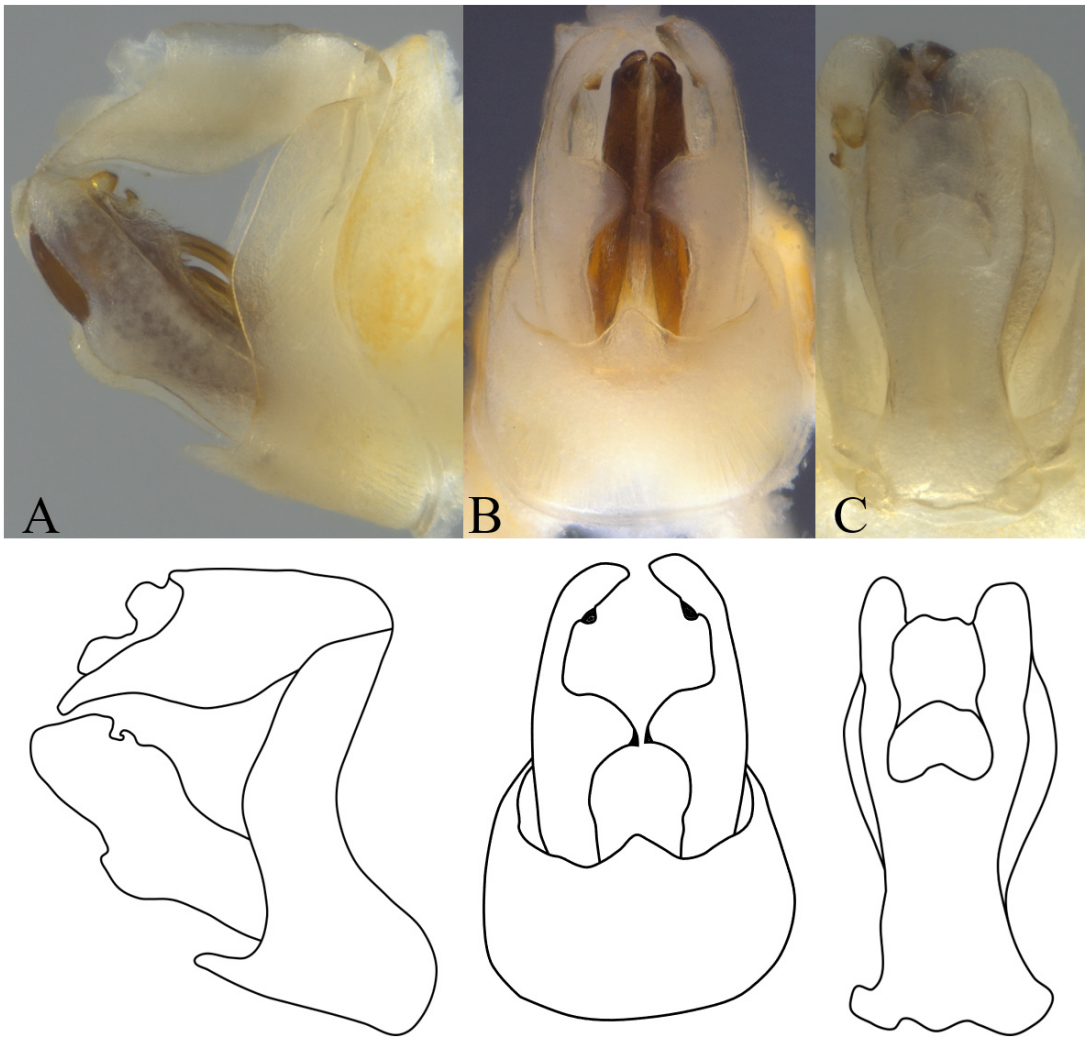

FIGURE 10. Male terminalia of *Agoo dahliana* **sp. n.**; A. lateral view, B. ventral view, and C. dorsal view.

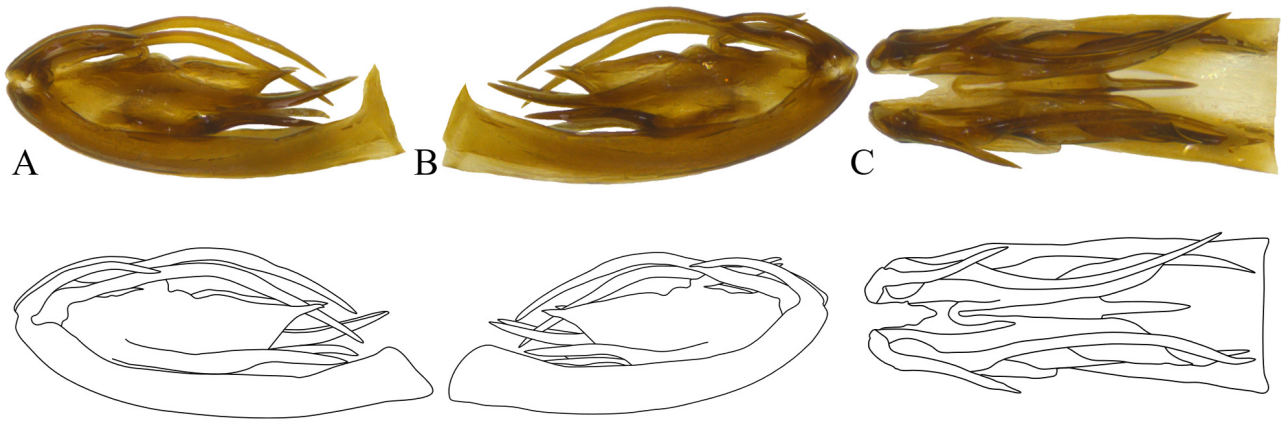

FIGURE 11. Aedeagus of adult male *Agoo dahliana* **sp. n.**; A. right lateral view, B. left lateral view, and C. dorsal view.

Other specimens collected and reported:

Anchimothon dubia (McAtee) (Figure 12)—Costa Rica, Limón, Manzanillo National Wildlife Refuge, Brian W. Bahder; 18 May 2018, aspirated from coconut (2 males, 1 female). Previously reported from Chiapas, Mexico as *Omolicna dubia* (Caldwell 1944).

Omolicna latens Fennah (Figure 13)—Costa Rica, Heredia / La Selva Biological Station / Brian W. Bahder; 21 May 2018 / light trap (3 males, 10 females). Previously reported from Trinidad (Fennah 1952).

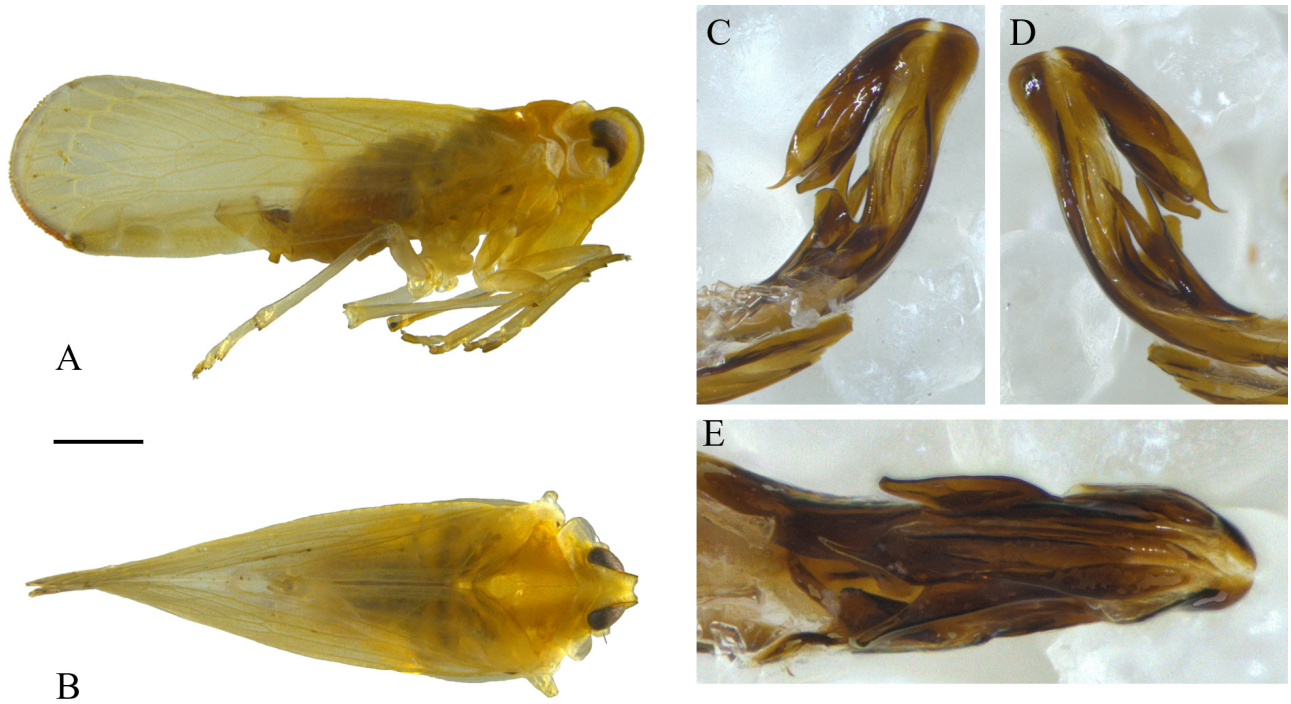

FIGURE 12. Adult male of *Anchimothon dubia*, A. lateral habitus, B. dorsal habitus, C. left lateral view of aedeagus, D. right lateral view of aedeagus, E. dorsal view of aedeagus, and F. right lateral of terminalia; scale = 1 mm.

Remarks. *Agoo dahliana* **sp. n.** is a fascinating species that shares many similarities with *Agoo xavieri*, including a similarity in appearance to *Omolicna*. *Agoo dahliana* **sp. n.** is similar to *Agoo xavieri* in possessing a single, triangular medioventral process, a subtriangular lobe on the ventral portion of the parameres, and a near-symmetrical aedeagus. The species differ in that *Agoo dahliana* **sp. n.** possesses sclerotized tips on the inner lateral lobes of the parameres (lacking in *Agoo xavieri*), processes on the aedeagus in a different orientation (oriented ventrad in *Agoo dahliana* **sp. n.**, dorsad in *Agoo xavieri*), possession of a pair of distally facing processes on the dorsal surface of the endosoma (lacking in *Agoo xavieri*) and a noticeable stouter medioventral process of the pygofer (elongated in *Agoo xavieri*). In addition, *Agoo dahliana* **sp. n.** has many black spots on the wings whereas *Agoo xavieri* lacks

spots and instead has a single, fuscous longitudinal band. These morphological differences, when considered with the COI and 18S data, indicate that *Agoo dahliana* **sp. n.** and *Agoo xavieri* are distinct species.

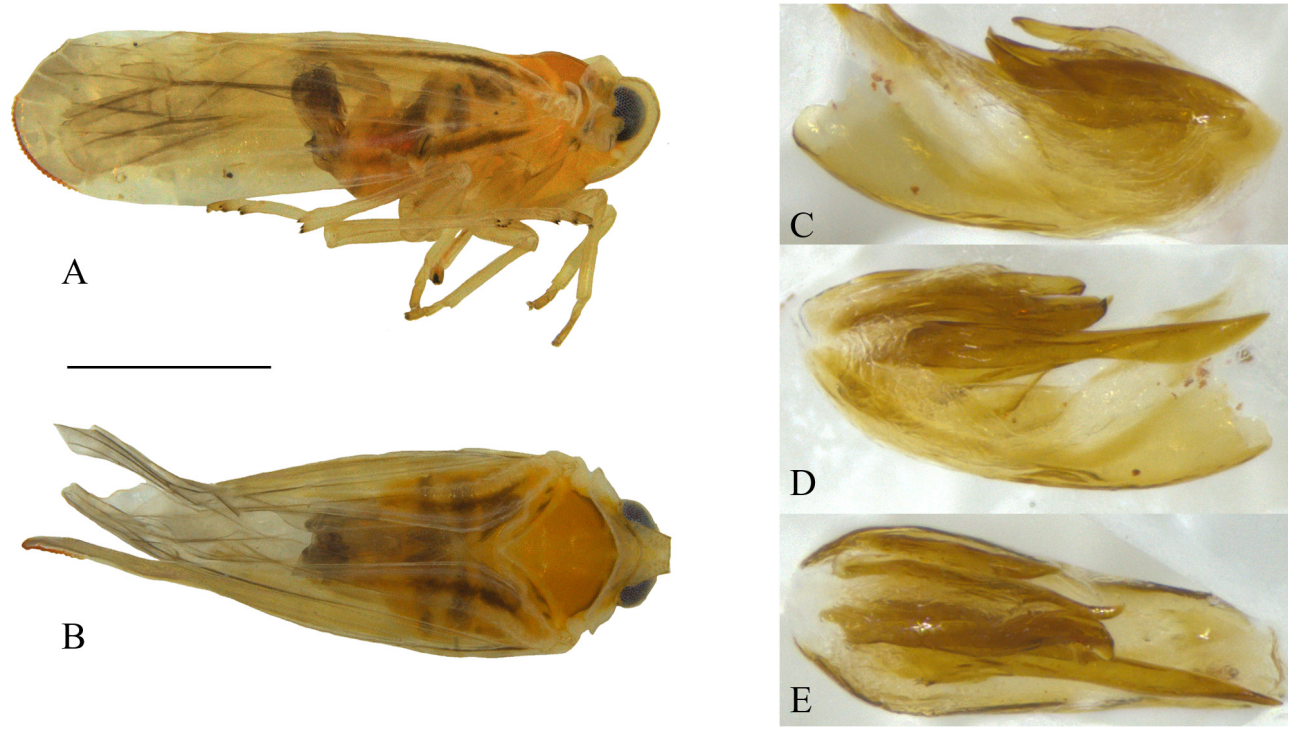

FIGURE 13. Adult male of *Omolicna latens*, A. lateral habitus, B. dorsal habitus, C. left lateral view of aedeagus, D. right lateral view of aedeagus, and E. dorsal view of aedeagus, scale = 1 mm.

Discussion

The documentation of *A. dubia* and *O. latens* in Costa Rica as well as the discovery and description of a novel species that supports the establishment of the genus *Agoo* highlights the unknown diversity of Cenchreini and the potential for further species discovery in the region. Another area of interest is to document the microbial diversity associated with cenchreines because of their potential to harbor phytoplasmas that pose a risk to economically important crops (Brown *et al*. 2006, Halbert *et al*. 2014). This justifies conducting survey work and describing novel taxa.

Acknowledgments

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