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A new species of planthopper in the genus *Agoo* Bahder & Bartlett (Hemiptera: Fulgoroidea: Derbidae) from coconut palm (*Cocos nucifera* L.) in Jamaica

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Abstract

A new species of the genus *Agoo* Bahder & Bartlett, *Agoo beani* **sp. n.** was found associated with coconut (*Cocos nucifera* L., Arecaceae) in Jamaica. This species was discovered as part of a survey of the Caribbean basin to document planthopper diversity on palms. Cytochrome c oxidase subunit I (COI) and 18S sequence data strongly support placement of the new species in *Agoo*. The morphological features of *Omolicna cocoana* Rodriguez-Leon & Hidalgo-Gato from Cuba are reviewed and this species transferred into the genus *Agoo*.

Key words: Jamaica, planthopper, biodiversity, taxonomy

Resumen

Una nueva especie del género *Agoo* Bahder & Bartlett, *Agoo beani* **sp. n.** fue encontrada en cocoteros (*Cocos nucifera* L., Arecaceae) en Jamaica. Esta especie fue descubierta mientras se llevaba a cabo una investigación para documentar la diversidad de chicharritas de las palmeras en la costa Caribeña. Los datos de la secuencia del citocromo c oxidasa subunidad I (COI) y de la secuencia 18S; respaldan firmemente la colocación de la nueva especie bajo el género *Agoo.* Además, se revisan las características morfológicas de *Omolicna cocoana* Rodríguez-León e Hidalgo-Gato de Cuba y esta especie se transfiere al género *Agoo.*

Palabras clave: Jamaica, chicharrita, biodiversidad, taxonomía

Introduction

Agoo Bahder & Bartlett (Derbidae: Derbinae: Cenchreini) is a recently described genus of planthopper discovered during survey work on palms in Costa Rica (Bahder *et al*. 2019). *Agoo* was at first established as a subgenus of *Omolicna* Fennah (Bahder *et al*. 2019), but was subsequently revised to full genus when *Agoo* and *Omolicna* were found to have large pairwise comparison sequence differences (18.7 –22.3% for COI, 9.6–10.0% for 18S) and *Agoo* clustered outside of *Omolicna* in maximum likelihood phylogenetic analyses based on 18S and COI gene sequences (Bahder *et al*. 2020a). This analysis also transferred *Omolicna rubrimarginata* Fennah to *Agoo* based on male ter-

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minalia. Additionally, the species *Agoo luzdenia* Bahder & Bartlett was discovered on coquito palms (*Astrocaryum alatum* Loomis) in Costa Rica (Bahder *et al.* 2020b), and two more species (*A. argutiola* Bahder & Bartlett and *A. spina* Bahder & Bartlett) have been described on coconut and oil palm (*Elaeis guineensis* Jacq.) in Brazil (Dollet *et al*. 2020), bringing the current number of species in the genus to six; viz. *A. dahliana*, *A. luzdenia*, *A. rubrimarginata*, *A. xavieri, A. argutiola* and *A. spina*.

The Cenchreini are a 'cixiid-like' tribe of Derbinae (Fennah 1952: 111) bearing foliate pronotal paranota forming fossae that partially subtend the antennae, pits on the postcubital vein of the clavus and lateral pits on the vertex (O'Brien 1982, Emeljanov 1996, Halbert *et al.* 2014). Emeljanov (1996) specifies that Cenchreini have a 'double apex' on the CuA forming an open marginal cell. The genus *Agoo* is currently recognized as moderate sized elongated planthoppers (including wings, males 4.7–7.3 mm, females 5.3–8.2 mm), with the head (in lateral view) smoothly rounded from the posterior vertex to the frontoclypeal suture (compared to *Omolicna* the frons is usually more narrowly compressed and the lateral carinae of the vertex and frons more strongly foliate), the medioventral process of the pygofer is subtriangular (lacking lateral processes), the aedeagus is nearly symmetrical with long, slender spines, and the endosoma is highly complex with many sclerotized spines. *Agoo* has a nearly symmetrical aedeagus whereas the aedeagus of *Omolicna* is noticeably asymmetrical. Another similar genus is *Cenanges* Fennah that was described from a single species, *C. spectralis* Fennah in Dominica (Fennah 1952). *Cenanges* can be separated from *Agoo* in the form of the aedeagus where the endosoma of *Cenanges* is large, simple with upward curving spines at apex whereas *Agoo* has a relatively smaller flagellum and a highly complex endosoma with spines arising from multiple locations that are angled in various directions. Further comparative study between *Cenanges* and similar Cenchreini is needed to more firmly establish generic limits.

Recently, survey work has commenced in coconut palm plots in Jamaica where the disease lethal yellowing (LY) is currently active to assess planthopper diversity and screen palm-feeding auchenorrhynchans for their ability to transmit the LY phytoplasma. Historically, the cixiid *Haplaxius crudus* has been implicated as the vector of LY (Howard & Thomas 1980); however, a new species of oecleine cixiid, *Oecleus mackaspringi* Bahder & Bartlett was described from LY infected plots in Jamaica (Myrie *et al*. 2019). While no derbids have been shown to transmit phytoplasmas, a wide variety of derbid planthoppers are known palm feeders (Lepesme 1947, Wilson *et al.* 1994, Howard 2001) and in the current survey derbids were the most abundant family encountered on coconut palms (W. Myrie, *unpublished data*). One planthopper found at multiple sites was identified in the field as a derbid in the Cenchreini, and subsequently determined to be a novel taxon in the genus *Agoo*. DNA sequence data was generated for the sew species for the barcoding region (5' of COI) and 18S. Herein, we describe the novel taxon, provide an updated key to the genus *Agoo*, and provide and updated phylogenetic analysis of *Agoo* relative to other cenchreines based on the COI and 18S loci.

Materials and methods

Locality and specimen collection. Specimens were collected between September 30th, 2019 and October 4th, 2019 in various coconut palm plots in Spring Garden (Portland Parish), Jamaica by sweep netting coconut palms where palm fronds were accessible from the ground (Fig. 1). Individuals were aspirated and stored in 95% ethanol and shipped to the University of Florida's Fort Lauderdale Research and Education Center (FLREC) (imported under permit P526-170201-001) for further processing. All specimens were collected from coconut palm (*Cocos nucifera* L).

Morphological terminology and identification. Morphological terminology generally follows that of Bartlett *et al.* (2014) with wing venation following Bourgoin *et al*. (2015). 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. Label information of type is quoted, with '/' indicating a new line and '//' indicating a new label. All specimens were measured and photographed using a Leica M205 C stereoscope. Images of specimens and all features photographed were generated using the LAS Core Software v4.12.

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 were 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 for the specimen used for molecular analysis 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 was then used for morphological characterization and photography.

FIGURE 1. Habitat in Spring Garden, Portland Parish, Jamaica where the holotype *of Agoo beani* **sp. n.** was collected.

PCR parameters, sequence data, and analysis. To obtain COI sequence data, DNA template from specimens was amplified using the primers LCO1490 (5'-GGTCAACAAATCATAAAGATATTG-3') (Folmer *et al*. 1994) and the reverse primer was HCO2198 (5'-TCAGGGTGACCAAAAAAATCA-3'). To obtain 18S sequence data, 18SF/Forward (5'-ACTGTCGATGGTAGGTTCTG-3') and 18SRII/Reverse (5'-AGCTTATGACTCGCGCTTACT-GGGAA -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: 5 min initial denaturation at 95°C, followed by 40 cycles of 1 min denaturation at 95°C, 30 sec annealing at 55°C, 1 min extension at 72°C, followed by a 5 min extension at 72°C. Thermal cycling conditions for 18S were as follows: 5 min initial denaturation at 95°C, followed by 35 cycles of 1 min 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 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 were sequenced using a 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). 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. Including the new species, 11 species representing 6 genera in the Cenchreini were used for

molecular and morphological comparison (Table 1)**.** DNA sequence data for COI was available for *Agoo dahliana*, *A. luzdenia*, and *A. xavieri.* For out-group comparisons *Anchimothon dubia*, *Neocenchrea heidemanni*, *Herpis* sp., *Omolicna triata*, *Omolicna brunnea*, *Omolicna cubana*, and *Cenchrea dorsalis* were used. For 18S, *Agoo dahliana*, *A. luzdenia*, and *A. xavieri* for in-group comparisons and *Anchimothon dubia*, *Omolicna triata*, *Omolicna brunnea*, *Omolicna cubana*, *Cenchrea dorsalis*, and *Herpis* sp. served as out-group comparisons.

TABLE 1. Cenchreini used for morphological and molecular comparisons (FLREC = University of Florida—Fort Lauderdale Research and Education Center; UDCC = University of Delaware Insect Research Collection, Newark, DE).

			GenBank Accession No.	
Species	**Source**	**Locality**	**COI**	**18S**
Agoo beani **sp. n.**	FLREC	Jamaica	MT413388	MT415403
Agoo dahliana	FLREC	Costa Rica	MN496467	MH472754
Agoo luzdenia	FLREC	Costa Rica	MT085818	MN999709
Agoo xavieri	FLREC	Costa Rica	MK443068	MK443073
Anchimothon dubia	FLREC	Costa Rica	MN496470	MN474755
Cenchrea dorsalis	UDCC	St. Vincent	MT413387	MN472756
Herpis sp.	FLREC	Costa Rica	MT085817	MT415406
Neocenchrea heidemanni	UDCC	U.S.A., DE	MN496473	MT415406
Omolicna brunnea	FLREC	Costa Rica	MK443070	MK443071
Omolicna cubana	FLREC	Jamaica	MT413386	MT415404
Omolicna triata	FLREC	Costa Rica	MK443069	MK443072

Systematics

Family Derbidae Spinola, 1839

Subfamily Derbinae Spinola, 1839

Tribe Cenchreini Muir, 1913

Type Genus: *Cenchrea* Westwood, 1840

Genus *Agoo* Bahder & Bartlett, 2019

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

Diagnosis. Head in lateral view smoothly rounded from posterior margin of vertex to frontoclypeal suture. Frons narrow, lacking median carina, lateral carinae foliate; transverse carina at fastigium absent. Paranota strongly foliate, forming fossae that partly surrounds antennae; folia exceeding scape and pedicle, quadrate to semiquadrate in frontal view. Aedeagus and endosoma nearly bilaterally symmetrical; aedeagus with pair of subapical cultrate processes and two pairs of elongate retrorse processes; endosoma with two pairs of elongate retrorse processes. Ventral lobe of pygofer (ventral view) broad, distally attenuating to rounded apex (subtriangular in form). Anal segment ventrally sinuate.

Remarks. The species *Omolicna cocoana* Rodriguez-Leon & Hidalgo-Gato was described from Cuba (Merino & González 2005). Photographs of this species were solicited but due to the closure of many public institutions globally due to SARS-CoV-2 pandemic, these resources are not available. Based on the description, this species has similarities with *A. beani* **sp. n.**. However, some aspects of the wing coloration and armature of the aedeagus appear distinct among the two taxa. Based on the marked similarities, *O. cocoana* appears to belong in the genus *Agoo*. The general form of the aedeagus is more similar to that of *Agoo* by having long, slender processes as well as possessing a subapical tooth on the aedeagus (a feature not present in all species of *Agoo* but it is shared with *A. beani* **sp. n.**

as well as *A. xavieri* and absent in all currently described species of *Omolicna*). In addition, the anal segment in *O. cocoana* lacks the strong ventral lobe commonly seen in *Omolicna*, the general form of the gonostyli is that of *Agoo* where the expansion in ventral view is a rather large lobe rather than the well-defined hook-like projection seen in *Omolicna*. Finally, the medioventral process of the pygofer in *O. cocoana* is a small, subtriangular process that is not ornate, very similar to *A. beani* **sp. n.** and lacks the lateral teeth or ornate form that is observed in *Omolicna*. Because of these morphological similarities as well as salient features being more similar to described taxa in *Agoo*, we herein move *O. cocoana* to the genus *Agoo* (as *Agoo cocoana* (Rodriguez-Leon & Hidalgo-Gato), **new combination**), bringing the number of species in the genus to seven; *A. beani* **sp. n.**, *A. cocoana*, *A. dahliana*, *A. luzdenia*, *A. rubrimarginata, A. spina*, and *A. argutiola*.

Key to the species of *Agoo*

1.	Wings lacking distinct markings	2
-	Wings with spots, longitudinal bands, or both	5
2.	Aedeagal shaft with pair of spines on dorsolateral margin about 2/3 from base	3
-	Aedeagul shaft without pair of spines on dorsolateral margin	4
3.	Apical margin of forewing pink; anal segment long, tubular, and pointing downward at apex; Trinidad	*A. rubrimarginata*
-	Aprical margin of forewing not pink; anal segment short and stout, not angled downward at apex; Jamaica	*A. beani* **sp. n.**
4.	Lateral margin of pygofer opening with acuminate medially directed lobed	*Agoo spina*
-	Lateral margin of pygofer opening lacking acuminate medially directed lobe	*A. argutiola*
5.	Wings with black spots (lacking distinct stripe), dorsal surface of parameres bearing large lobe with a median invagination resulting in two processes	*A. dahliana*
-	Wings with distinct longitudinal stripe(s)	6
-	Single stripe present on forewing, basal process of aedeagus absent or if present, angled posterior	7
7.	Stripe of forewing terminating in red with distal black spot, parameres with sclerotized ridge on outer lateral margin near midlength bearing sharp projections	*A. luzdenia*
-	Stripe on forewing fuscous, parameres lacking lateral ridge	*A. xavieri*

Agoo beani sp. n. Bahder & Bartlett

(Figures 2–6)

Type locality. Spring Garden, Portland Parish, Jamaica

Diagnosis. A moderate sized, pale species; body and legs stramineous, forewings weakly fuscous on apical and trailing veins and cells, anterior cells and veins whitish except diffuse patch in costal cell; apical margin red. Genitalia approximately bilaterally symmetrical. Gonostyli spatulate in lateral view, dorsal process with two converging sclerotized projections and one membranous dorsally directed lobe; in ventral view gonostyli with large inner lobe at midlength with pointed, weakly sclerotized apex. Aedeagus approximately symmetrical with 3 pair of projections including 2 pair of elongate subapical retrorse spines and 1 pair of short subapical cultrate spines. Endosoma robust with 2 pair of robust elongate spines, ventral pair dorsally curved, reaching base of aedeagus; dorsal pair shorter, curved mediodorsad.

Description. *Color*. General body color stramineous (Fig. 2) with subtle markings. Head with carinae and sensory pits of vertex and frons darker, lateral ocelli whitish. Pronotum with lateral margins of paranotal fovea darker. Mesonotum slightly embrowned laterally, medially paler; carinae pale. Forewing with trailing and apical veins and cells of weakly darkened; veins and cells of leading margin whitish except diffuse dark marking costal cell. Abdominal tergites medially orangish.

Structure. Body length males: 5.76–5.78 mm (*n*=7) with wings; 3.59–3.61 mm without wings, body length females (*n*=7): 5.77–5.79 mm with wings; 3.60–3.62 mm. Head. In lateral view, anterior margin of head smoothly rounded from posterior margin of vertex to frontoclypeal suture (Figs. 3C). Rostrum exceeding hind coxae (Fig. 2B). In frontal view (Fig. 3A), lateral carinae of head foliately keeled, keel bearing a row of sensory pits for entire length of vertex and frons. Frons narrow (median carina absent), narrowest near middle of compound eyes, becoming gradually wider both dorsally and ventrally (to frontoclypeal suture). Vertex triangular, broadest near base, deeply and truncately concave at posterior margin (Fig. 3B), anteriorly notched. Vertex length males: 0.25–0.26 mm; females: 0.26–0.26 mm. Vertex width at hind margin males: 0.16–0.17 mm; females: 0.17 mm. Vertex width at

distal margin males: 0.05–0.06 mm; females: 0.06 mm. Frons length males: 0.55–0.56 mm; females 0.56–0.56 mm. Frons dorsal width males: 0.13–0.14 mm; females; 0.15 mm. Frons frontoclypeal margin width males: 0.21–0.22 mm; females: 0.23 mm. Clypeus length males: 0.75–0.76 mm; females: 0.77 mm.

FIGURE 2. *Agoo beani* **sp. n.**, male adult habitus; A. body lateral view and B. body dorsal view, scale bar = 1 mm.

Thorax. Pronotum relatively wide at midline (about half length of frons), anterior margin convexly arched behind vertex, following posterior margin of head around eyes (Fig. 3B), median carina obsolete, lateral carinae tracing head outline; paranota strongly foliate (exceeding antennal pedicle), projecting above and beneath antennae, paranotal foveae semiquadrate in frontal view (Fig. 3A). Pronotum length at midline, males: 0.24–0.25 mm; females: 0.25 mm. Mesonotum approximately as wide as long at midlength, tricarinate, lateral carinae subparallel (Fig. 3B). Mesonotum length at midline males: 0.80–0.81 mm; females: 0.81 mm. Mesonotum width males: 0.94–0.95 mm; females: 0.95–0.96 mm. Spinulation of hindleg; 7-6-5.

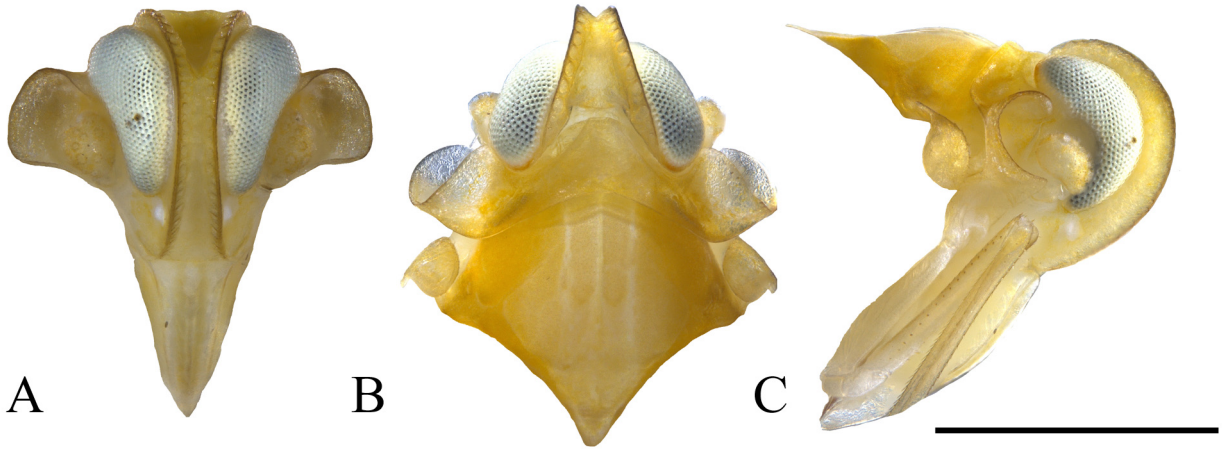

FIGURE 3. *Agoo beani* **sp. n.**, male adult; A. head frontal view, B. head, pronotum and mesonotum dorsal view, C. head, pronotum and mesonotum lateral view, scale bar = 1mm.

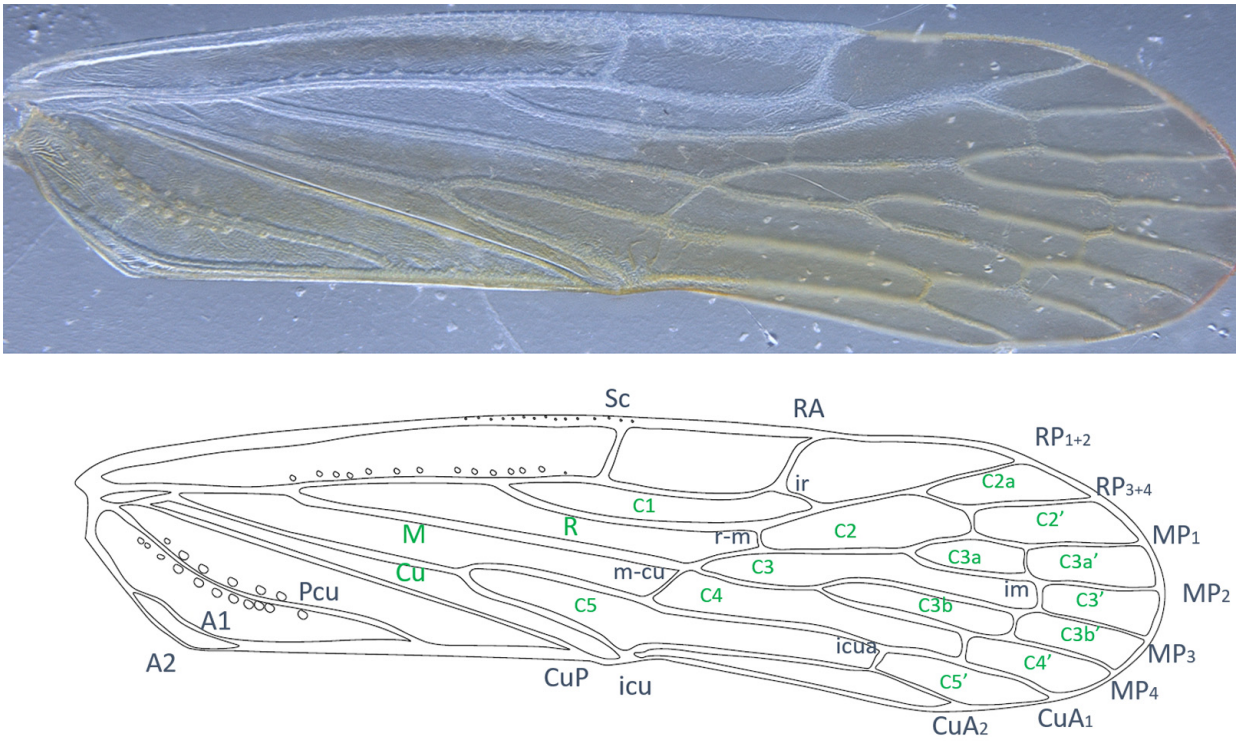

FIGURE 4. *Agoo beani* **sp. n.**, forewing venation.

Tegminal branching pattern RA 1 branched, RP 2 branched, MP 4 branched (M basally fused with Sc+R forming long stem from basal cell), CuA 2 branched (appearing 3 branched with icu); fork of Sc+RA and RP slightly distad of CuA fork, the latter just anterior to fusion of Pcu and A1 in clavus (A1 closely tracing trailing margin for most of length); claval apex at about tegmen midlength. Forewing length males: 5.26–5.27 mm; females: 5.27–5.27 mm.

Terminalia. Pygofer in lateral view narrow, posterior and anterior margin sinuate (Fig. 5A), widest ventrally (very narrow dorsally); medioventral process in ventral view subtriangular, wider than long (Fig. 5B). Gonostyli in lateral view spatulate, ventral margin strongly sinuate, dorsal margin linear, small lobe near midlength, unsclerotized, two converging sclerotized processes, similar in size, distad of lobe (Fig. 5A). Aedeagus approximately bilaterally symmetrical bearing three pairs of processes (Fig. 6), one pair (Figs. 6A, B; A1, A2), subapical, short and cultrate, apex sharp, directed caudad; 2 pair of elongate retrose process arising approximately apically, median pair (Fig. 6C, A3, A4), angled anteriorly, curved ventrad, extending to midlength of aedeagus (Fig. 6A, B); lateral pair (Fig. 6C, A5, A6) nearly straight with apex slightly curved dorsad (Fig. 6A, B). Endosoma complex bearing four large, robust sclerotized processes from apex (Fig. 6, E1-E4), curved dorsad; larger pair (E1, E2) reaching aedeagal base, appearing distad to shorter pair (E3, E4) in dorsal view. Anal tube stout and short (exceeded by gonostyli) in lateral view (Fig. 5A), anterior and posterior margins parallel, ventral margin straight, forming parallelogram.

Plant associations. Coconut (*Cocos nucifera* L.), Arecaceae.

Distribution. Jamaica (Portland Parish, St. Elizabeth Parish).

Etymology. The specific name is in honor of Mr. Basil Bean, former director of the Coconut Industry Board in Kingston, Jamaica.

Material examined. Holotype male "Jamaica, Portland Parish / Spring Garden, CIB Plot / 01.X.2019 / Coll.: B.W.Bahder / Host: *Cocos nucifera* // Holotype/ *Agoo beani*" (FLREC). Paratypes, same as holotype (17 males, 6 females, FLREC and FSCA).

Sequence data. A total of 641 bp for the COI locus were sequenced for *Agoo beani* **sp. n.** (GenBank Accession No. MT413388). On average, *A. beani* **sp. n.** differed by 15.9% from other members of *Agoo* (Table 1) while differing 20.5% in average to other genera within the Cenchreini for the COI locus based on the pairwise comparison (Table 1). The maximum likelihood analysis demonstrated strong bootstrap support (93) for the genus *Agoo* relative to other taxa within the Cenchreini (Fig. 7) with *A. beani* **sp. n.** resolving within the *Agoo* clade.

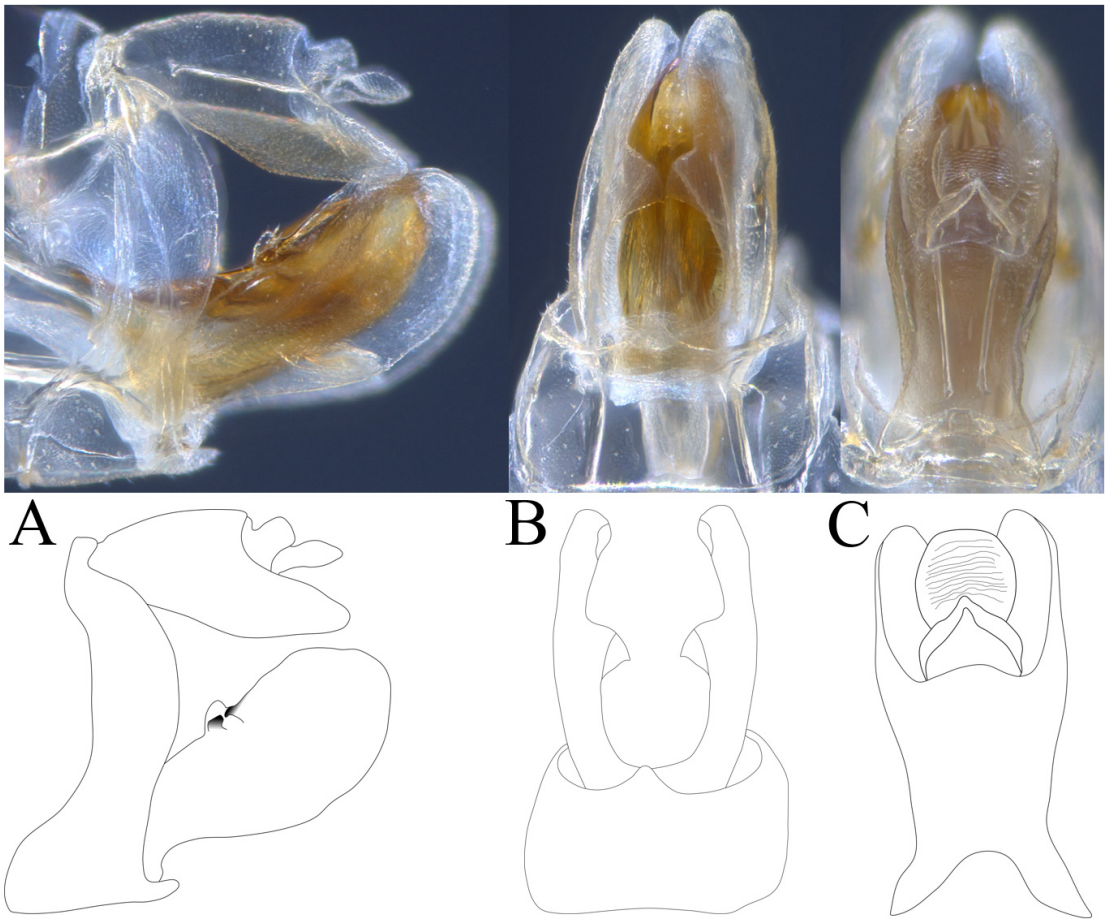

FIGURE 5. Male terminalia of *Agoo beani* **sp. n.**; A. lateral view, B. ventral view, and C. dorsal view.

A 1,380 bp product was sequenced for the 18S locus for *A. beani* **sp. n.** (GenBank Accession No. MT415403). Based on the pairwise comparison, on average, *A. beani* **sp. n.** differed by 1.0% on average from other members of *Agoo* (Table 2), while other members of *Agoo* differed by about 1% from each other (Table 2). On average, *A. beani* **sp. n.** differed by 14.1% from the other genera within the Cenchreini that were analyzed (Table 2). The maximum likelihood analysis based on 18S demonstrated even higher bootstrap support for the genus *Agoo* (100) and *A. beani* **sp. n.** resolved in the *Agoo* clade (Fig. 7). The consensus tree generated between COI and 18S also provides strong bootstrap support for *Agoo* as a clade but also the placement of *A. beani* **sp. n.** within the genus.

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
1	*Agoo beani* **sp. n.**		0.02	0.01	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
2	*Agoo dahliana*	16.0		0.01	0.01	0.02	0.02	0.02	0.01	0.02	0.02	0.02
3	*Agoo luzdenia*	14.9	16.3		0.01	0.02	0.02	0.02	0.02	0.02	0.02	0.02
4	*Agoo xavieri*	17.1	15.3	16.2		0.02	0.02	0.02	0.01	0.02	0.02	0.02
5	*Anchimothon dubia*	21.2	19.2	20.0	20.8		0.02	0.02	0.02	0.01	0.01	0.01
6	*Cenchrea dorsalis*	21.3	21.6	19.5	20.0	21.3		0.02	0.02	0.02	0.02	0.02
7	*Herpis* sp.	20.7	18.7	19.1	20.4	17.9	18.3		0.01	0.01	0.01	0.01
8	*Neocenchrea heidemanni*	19.9	16.5	16.0	15.2	17.1	17.4	15.7		0.02	0.02	0.02
9	*Omolicna triata*	18.6	20.8	19.5	20.7	15.2	20.2	16.8	18.3		0.01	0.01
10	*Omolicna cubana*	20.2	20.4	18.1	21.2	15.2	20.7	17.9	19.9	14.1		0.01
11	*Omolicna brunnea*	21.0	22.0	19.7	21.8	17.1	22.8	16.3	20.5	13.1	13.4	

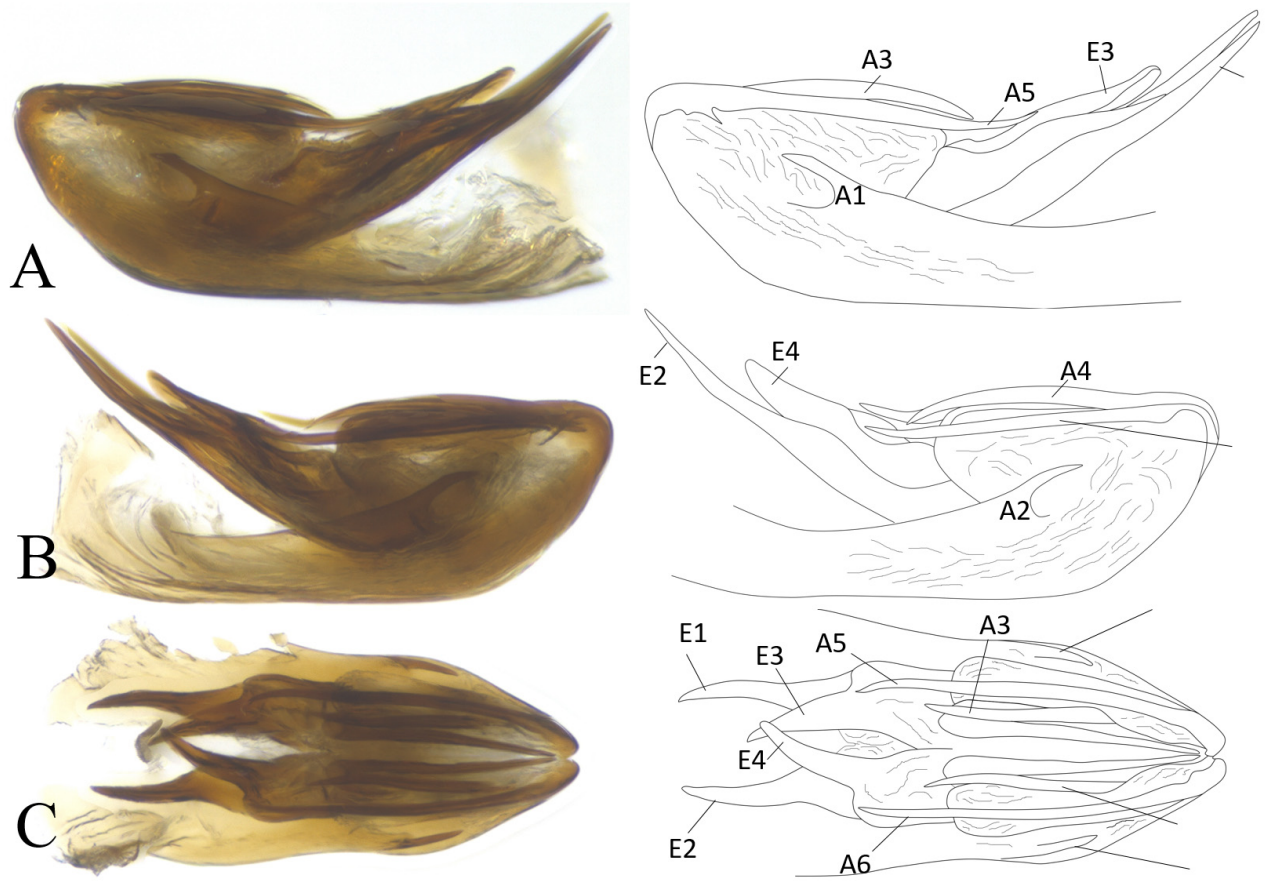

FIGURE 6. Aedeagus of *Agoo beani* **sp. n.**; A. right lateral view, B. left lateral view, and C. dorsal view.

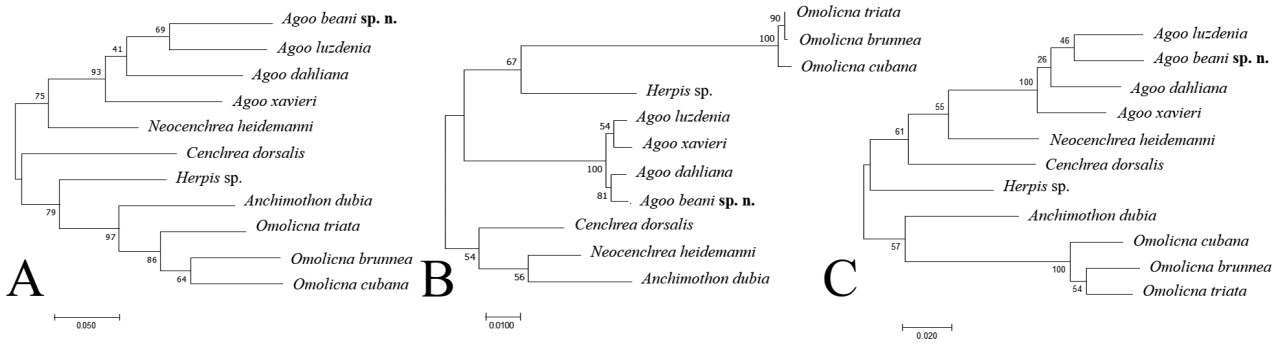

FIGURE 7. Maximum likelihood phylogenetic trees (1,000 replicates) demonstrating the relationship of the novel taxon, *Agoo beani* **sp. n.** relative to other species in *Agoo* and other genera within the Cenchreini based on the: A. COI gene, B. 18S gene, and C. consensus tree utilizing both the COI and 18S loci.

Remarks. The overall structure of the terminalia and aedeagus and strong molecular evidence supports *Agoo beani* **sp. n.** as distinct from all currently described species of *Agoo*. Initially, the wing coloration in the field appeared similar to that of *A. xavieri*; however, the fuscous stripe in *A. beani* **sp. n.** is not as pronounced as in *A. xavieri* and the general color of *A. xavieri* is a more brilliant yellow. The two species also differ in features of the terminalia, but perhaps may be most easily diagnosed by *A. beani* **sp. n.** with the ventral lobe of the pygofer wider than long (longer than wide in *A. xavieri*) and the parallelogram-shaped ventral margin of the anal tube (sinuate with apex elongated in *A. xavieri*).

Other features observed in the genus, such as an elongate and narrow frons, subquadrate projections of paranota in frontal view, and nearly symmetrical aedeagus with complex endosoma are present in *A. beani* **sp. n.** and because of these features along with strong molecular evidence for both the COI and 18S loci, the placement of the novel taxon in *Agoo* is strongly supported.

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
1	*Agoo beani* **sp. n.**		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
2	*Agoo dahliana*	5.8		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
3	*Agoo luzdenia*	6.2	1.0		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
4	*Agoo xavieri*	6.3	1.0	0.8		0.0	0.0	0.0	0.0	0.0	0.0	0.0
5	*Anchimothon dubia*	11.8	6.9	6.9	7.3		0.0	0.0	0.0	0.0	0.0	0.0
6	*Cenchrea dorsalis*	11.2	6.2	6.2	6.6	3.4		0.0	0.0	0.0	0.0	0.0
7	*Herpis* sp.	14.9	10.1	9.8	10.0	10.2	9.3		0.0	0.0	0.0	0.0
8	*Omolicna triata*	14.3	9.4	9.5	9.5	9.9	9.8	10.9		0.0	0.0	0.0
9	*Omolicna cubana*	14.6	9.7	9.8	9.7	9.8	9.7	11.3	0.7		0.0	0.0
10	*Omolicna brunnea*	14.5	9.5	9.6	9.6	10.0	9.8	11.1	0.2	0.7		0.0
11	*Neocenchrea heidemanni*	17.5	13.0	12.7	13.2	8.2	10.3	15.8	15.2	15.1	15.2	

Discussion

The strong support based on the morphology, COI sequence data and 18S data establish the new taxon as a member of the genus *Agoo*. Furthermore, this molecular data strongly supports *Agoo* as monophyletic within the Cenchreini based on the COI and 18S loci as well as the consensus between the two loci.

The discovery of another new species in the genus *Agoo* from coconut palms is significant in that it adds to this recently discovered taxon but also highlights the seemingly largely unexplored diversity of planthoppers the feed on palms in the neotropics. Furthermore, undiscovered taxa are also important in the context of their role, if any, pathogen transmission. The novel taxon was discovered during survey work of LY infected palms in Jamaica and while derbids are not known vectors of palm infecting phytoplasmas (16SrIV), still needs to be screened for the presence of phytoplasma.

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