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A new species of planthopper in the genus *Haplaxius* (Hemiptera: Auchenorrhyncha: Fulgoroidea: Cixiidae) from coconut palm (*Cocos nucifera*) in Costa Rica

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Abstract

Haplaxius is a large genus of cixiid planthoppers that is widespread in the New World and economically important due to the role of *H. crudus* in transmitting palm lethal decline phytoplasmas. A new species of *Haplaxius*, here described as *Haplaxius pocococo* **sp. n.,** was discovered during survey work on palms in north-central Costa Rica. Placement in *Haplaxius* is supported by sequence analysis of the COI and 18S genes relative to congeners and by morphological characters.

Key words: planthopper, Cixiinae, Oecleini, biodiversity, palms, Costa Rica

Resumen

Haplaxius es un numeroso género de chicharritas de la familia Cixiidae; el cual se encuentra ampliamente distribuido en el Nuevo Mundo y es económicamente importante debido al papel de *H. crudus* en la transmisión de enfermedades fitoplasmáticas letales en las palmeras. Una nueva especie de *Haplaxius*, descrita en este documento como *Haplaxius pocococo* **sp. n**., fue descubierta durante un muestreo de palmeras localizadas en la región centro-norte de Costa Rica. La colocación de esta nueva especie bajo el género *Haplaxius* está respaldada por el análisis de secuencia de los genes COI y 18S en relación con los congéneres, así como por sus caracteres morfológicos.

Palabras clave: chicharrita, Cixiinae, Oecleini, biodiversidad, palmeras, Costa Rica

Introduction

The genus *Haplaxius* Fowler (Cixiidae: Cixiinae: Oecleini) is widespread in the New World, with 34 species reported from north of Mexico and 31 species from Mesoamerica, the Caribbean, and northern South America (Bartlett *et al.* 2014, Bourgoin 2020). While there are currently more described taxa from the Nearctic, there are likely many species remaining to be discovered in the Neotropics, such as the recently described *H. dougwalshi* Bahder & Bartlett (Bahder *et al.* 2020).

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Haplaxius is within the tribe Oecleini Muir, which is diagnosed by features of the forewing, face and hind leg; *viz*. the bases of the longitudinal veins Sc+R, and MP form a common stalk so that only two veins appear to arise from the basal cell (Muir 1922), front (metope) diamond-shaped with a median ocellus, an approximately straight frontoclypeal border, and the hind tibia lacks lateral teeth and bears a gap in the apical spinules (Emeljanov 2007). The genus *Haplaxius,* as currently circumscribed, is recognized by having evident tegulae, vertex compressed and lacking carina at midline and between eyes, mesonotum about twice as long as vertex or less, forecoxae lacking denticle, and carinae on pronotum terminating at the ventro-lateral apex. As currently defined, *Haplaxius* may be heterogeneous (Kramer 1979, Bahder *et al.* 2019) with significant variation in habitus and genitalia. The description of the related genus *Myxia* Bahder & Bartlett (Bahder *et al.* 2019), and the subsequent movement of *M. delta* Kramer from *Haplaxius* into *Myxia* (Echavarria *et al*. 2021), further suggests that the composition and limits of *Haplaxius* need review.

Haplaxius is of economic interest, because *H. crudus* (Van Duzee) is reported to transmit the lethal yellowing (LY) phytoplasma (16SrIV-A) in Florida (Howard & Thomas 1980). Additionally, *H. crudus* is also the putative vector of lethal bronzing (LB) phytoplasma (16SrIV-D) in Florida (Mou *et al*. 2020, Dzido *et al.* 2020). While the status of *H. crudus* on palms throughout Florida is well characterized (Humphries *et al.* 2021), the diversity of planthoppers on palms in the Neotropics is only beginning to be understood. The presence of described *Haplaxius* species on palms that resemble *H. crudus*, i.e. *H. skarphion* (Kramer), *H. jamaciae* (Kramer), plus undescribed taxa, provides challenges to vector ecology research in the Neotropics. Because of the complicated relationship and transmission pathway of 16SrIV phytoplasmas, the economic importance, and the high diversity of *Haplaxius* on palms, further survey and taxonomic work is imperative for understanding this group of planthoppers.

Herein we describe a new species of *Haplaxius* collected from coconut palms during survey work in Costa Rica. Sequence data for the barcoding region (5' region) of the cytochrome *c* oxidase subunit I gene (COI) and the 18S gene from the new species is used to evaluate genus level placement of the new species.

Materials and methods

Locality and Specimen Collection. Individuals of the novel taxon were collected from a coconut palm (*Cocos nucifera* L.) along a major highway (Fig. 1A) in the north-central region of Costa Rica, in Alajeula Province (Figure 1B). Specimens were aspirated directly from the palms and transferred to 95% ethanol in the field while still alive. Specimens were collected under permit no. SINAC-ACTo-GASPPNI-016-2018 and exported under permit number DGVS-256-2018 to the U.S.A. All specimens were 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 Kramer (1979) except with male terminalia nomenclature updated after Bourgoin (1988) and Bourgoin & Huang (1990) and forewing venation following Bourgoin *et al*. (2015). New taxa are to be attributed to Bahder and Bartlett.

Dissections and DNA Extraction. The terminalia that were dissected also served as the source of tissue for DNA extraction. The terminal end of the abdomen was removed and placed directly into a solution of tissue lysis buffer (buffer ATL) and proteinase K (180 µl ATL and 20 µl proteinase K) from the DNeasy® Blood and Tissue Kit (Qiagen). The abdomen was left to lyse for 24 hours at 56°C. Following lysis, 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. Primers to amplify COI and 18S loci are presented in Table 1. PCR reactions contained 5x GoTaq Flexi Buffer, 25 mM $MgCl_2$, 10 mM dNTP's, 10 mM of each primer, 10% PVP-40, and 2.5U GoTaq Flexi DNA Polymerase, 2 µl DNA template, and sterile dH_20 to a final volume of 25 µL. Thermal cycling conditions for 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 50°C, 2 min extension at 72°C, followed by a 5 min extension at 72°C. PCR products were run on a 1.5% agarose gel stained with GelRed to visualize amplification success. PCR products of the appropriate size were purified using the ExoSAP-IT™ Express PCR Product Cleanup Reagent per the manufacturers' protocol (ThermoFisher Scientific, Waltham, Massachusetts, USA). Purified PCR product was quantified using a NanoDrop Lite Spectrophotometer (ThermoFisher Scientific, Waltham, Massachusetts, USA) and sequenced using the SeqStudio Genetic Analyzer (Applied Biosystems). Contiguous files were assembled using DNA Baser (Version 4.36) (Heracle BioSoft SRL, Pitesti, Romania), aligned using ClustalW as part of the package MEGA7 (Kumar *et al.* 2016). 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 as well as the consensus tree with concatenated data for COI and 18S data.

FIGURE 1. Habitat and host plants (coconut palms, white arrow) where adults of *Haplaxius pocococo* **sp. n.** were collected.

TABLE 1. Primers used to obtain molecular sequence data for novel *Haplaxius.*

Name	Direction	Sequence (5'→3')	Amplicon Size	Reference
LCO1490	Forward	GGTCAACAAATCATAAAGATATTG	≈750 bp	Folmer *et al*. 1994
C1-J-2195RC	Reverse	ACTTCTGGATGACCAAAAAATCAA	≈750 bp	Bahder *et al*. 2021
18SFI	Forward	ACTGTCGATGGTAGGTTCTG	≈1,500 bp	Bahder *et al.* 2020
18SRI	Reverse	GTCCGAAGACCTCACTAAA	≈1,500 bp	Bahder *et al.* 2020

Taxon sampling. To assess the relationship of the novel taxon to other members of the Oecleini, four species of *Haplaxius,* three species of *Myxia* Bahder & Bartlett, plus *Nymphomyndus caribbea* (Fennah), and *Oecleus mackaspringi* Bahder & Bartlett were used (Table 2). All taxa used for phylogenetic placement were analyzed for both the COI and 18S genes.

TABLE 2. Taxa used as in-group and out-groups for molecular analysis of the COI and 18S genes for placement of the novel *Haplaxius*.

	GenBank Accession No.	
Species	COI	18S
Haplaxius dougwalshi	MT080284	MT002395
Haplaxius crudus	MT002393	MT002393
Haplaxius skarphion	MT900603	MT892907
Haplaxius pictifrons	MT946292	MN200098
Nymphomyndus caribbea	MT080286	MT002394
Oecleus mackaspringi	MN488999	MN422261
Myxia baynardi	MT900604	MT892909
Myxia belinda	MT900605	MN200096
Myxia delta	MT900602	MT892908

Systematics

Family Cixiidae Spinola 1839

Subfamily Spinola 1839

Tribe Oecleini Muir 1922

Genus *Haplaxius* Fowler 1904

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

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

Haplaxius pocococo Bahder & Bartlett, sp. n.

(Figures 2–7)

Type locality. 4.2 km SE of Santa Rosa de Pocosol (10˚ 35' 27.14" N, 84˚ 30' 28.83" W), Alajuela, Costa Rica.

Diagnosis. This species is recognized by a deep orange facial color traversed with a rough white arch, resulting in a bell-shaped orange patch along the frontoclypeal suture. Pygofer with triangular processes on the lateral margin of the opening and an ovoide medioventral process. Aedeagus with a large lateral process that is cupped and strongly curved inward, and a large swollen lobe on the opposite lateral margin of the aedeagus.

Description. *Color*. In life, adult males are generally pale green; in ethanol preserved specimens, green areas fade to stramineous yellow in males (Fig. 2A,B); females more strongly colored, reddish yellow (Fig. 2C,D). Males with vertex orangish anteriorly, paler posteriorly. Face orangish above frontoclypeal suture with rough white arc, resulting in bell-shaped orange patch below; clypeus and genae below antennae white; antennae orange. Pronotum anteriorly stramineous, posterior margin broadly white. Mesonotum orange-stramineous with irregular white patches along lateral carinae and posterior margin; mesonotum paler between lateral carinae forming weak median vitta; tegulae orangish, white patch on pleuron below tegulae; legs distally white. Wings clear with 2 diffuse dark patches on posterior margin, one near apex of clavus, one in cells formed by CuA (Fig. 4). Abdomen stramineous, dorsally darker. Females similar but more strongly patterned, red-orange.

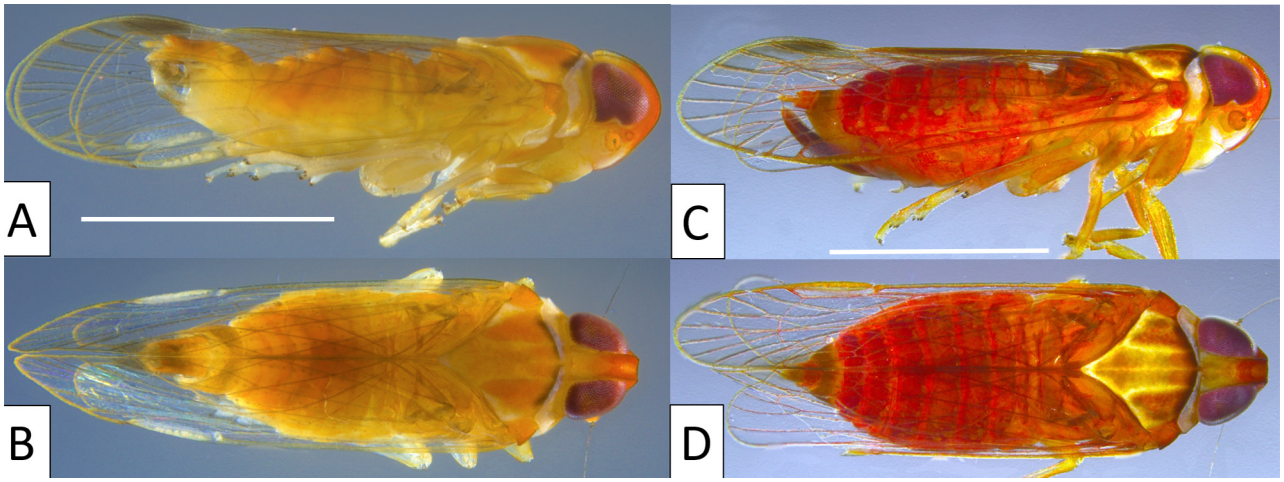

FIGURE 2. Adult habitus *Haplaxius pocococo* **sp. n.**; A) body lateral male, B) body dorsal male, C) body lateral female, and D) body dorsal female; scale = 1 mm.

Structure. Body length (including wings), males 2.58 mm, females 2.61 mm (Table 3). Head. Head with fastigium rounded in lateral view (Fig. 3A). Lateral carinae of vertex and frons keeled and foliaceous. Vertex with lateral margins subparallel, weakly converging anteriorly, posterior margin incised (Fig. 3B); posterior margin about level with posterior margin of compound eyes; disc concave. In frontal view, face ovoid, frons widest above frontoclypeal suture, strongly narrowing distally to fastigium, transverse carina present (Fig. 3C), median carina evident in ventral half of frons, obsolete dorsally, median ocellus present (Fig. 3C). Clypeus elongate-triangular. Antennae with scape very small, pedicel bulbous, about as wide as tall, bearing many irregularly placed sensory plaques. Lateral ocelli distinct, anterior to antennae, below compound eyes.

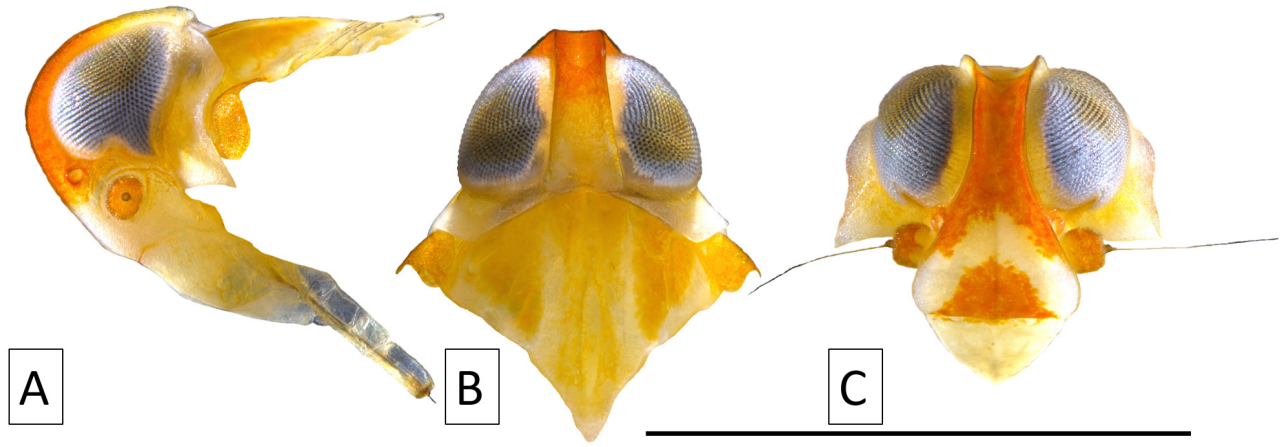

FIGURE 3. Adult *Haplaxius pocococo* **sp. n.**; A) head, pronotum, and mesonotum lateral view, B) head, pronotum, and mesonotum dorsal view, and C) head and pronotum frontal view; scale = 1 mm.

TABLE 3. Biometric data for adult males and females of *Haplaxius pocococo* **sp. n.**

	Male (*n*=2)		Female (*n*=2)	
Metric	Range	Avg.±SE	Range	Avg.±SE
Body length, with wings	2.58	2.58±0.00	2.61	2.61±0.00
Body length, without wings	2.05	2.05±0.00	2.07	2.07±0.00
Forewing length	2.06	2.06±0.00	2.05	2.05±0.00
Vertex length, midline	0.30	0.30±0.00	0.30	0.30±0.00
Vertex width, basal margin	0.16	0.16±0.00	0.20	0.20±0.00
Vertex width, distal margin	0.10	0.10±0.00	0.10	0.10±0.00
Frons length, midline	0.69	0.69±0.00	0.69	0.69±0.00
Frons width, dorsal margin	0.16	0.16±0.00	0.16	0.16±0.00
Frons width, frontoclypeal suture	0.40	0.40±0.00	0.40	0.40±0.00
Frons width, narrowest point	0.16	0.16±0.00	0.16	0.16±0.00
Frons width, widest point	0.49	0.49±0.00	0.49	0.49±0.00
Clypeus length	0.16	0.16±0.00	0.16	0.16±0.00
Pronotum length, midline	0.01	0.01±0.00	0.01	0.01±0.00
Mesonotum length, midline	0.50	0.50±0.00	0.50	0.50±0.00
Mesonotum width	0.53	0.53±0.00	0.53	0.53±0.00

Thorax. Pronotum short, in dorsal view narrowest medially, wider laterally; posterior margin concave; in lateral view, paradiscal region widest near dorsal margin of tegulae, posterior margin concave, ventral margin extended to a rounded point. Pronotal carinae following posterior contour of eyes, turning posterior just above ventral margin of eye, terminating at ventro-lateral margin of prothorax (Figs. 3A, C). Mesonotum tricarinate, lateral carinae subparallel, curved laterally to reach posterior margin (Fig. 3B). Forewings transparent, with diffuse dark markings along trailing margin near apex of clavus and CuA (cell C5', Fig. 4), with setal pits present along main veins. Claval apex near wing midlength, about parallel to ScP reaching wing margin; fusion of PCu and A1 about in basal third of wing, with PCu+A1 reaching wing margin before claval apex (i.e., clavus closed). Fork of CuA proximad of RA+ScP from RP fork, with both of these proximad of claval apex (Fig. 4); forewing branching pattern: RA 1-branched, RP 2-branched, MP 5-branched, CuA 2-branched with CuA connected with CuP by icu crossvein (Fig. 4).

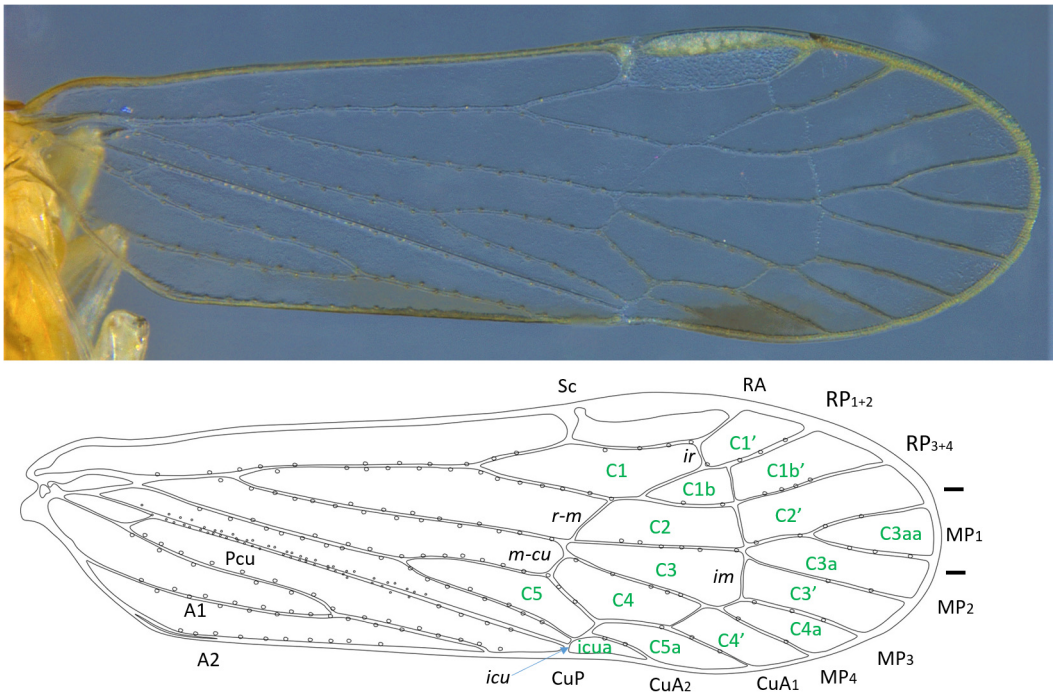

FIGURE 4. Forewing venation of *Haplaxius pocococo* **sp. n.**: black = vein, green = cell, italics = crossvein.

Terminalia. Pygofer in lateral view broad, irregular in outline but approximately quadrate with ventral anterior process and large triangular median processes on lateral portion of pygofer opening (Fig. 5A). In ventral view, medioventral lobe elongate and ovoid, approximately 1.5x long as wide (Fig. 5B). Gonostyli in lateral view distally expanded and angled dorsad with rounded apex, strongly sinuate on dorsal margin with strong basal curve, resulting in constriction of gonostyli, appearing spear-like (Fig. 5A); in ventral view, appearing clubbed, inner margin strongly sinuate, outer margin strongly curved distad (Fig. 5B). Aedeagus asymmetrical and complex (Figs 6 & 7); aedeagal shaft with large, cupped process (near midlength) on right lateral margin (A1), curving anterio-dorsad (Figs 6A-C & 7A-C), large, bulbous projection, angled dorsad, on left lateral side of shaft (A2) (Fig. 6 & 7); two elongate retrorse processes arising at dorsum of shaft apex, both strongly sinuate, angled anterio-dorsad, one (A3) more robust and angled to right lateral side, second (A4) slender angled to left lateral side (Figs. 6 & 7); flagellum with two large processes, one (F1) on right lateral side, nearly reaching A1, smaller process (F2) on left lateral side, surrounding A4. Anal tube in lateral view elongate, dorsal and ventral margins subparallel in basal 2/3, ventral margin projected in distal 1/3 (giving ventral margin a concave appearance), to elongate acute apex; ventral surface with large subapical median ventral process, irregularly triangular, angled ventrad (Fig. 5A); in dorsal view, lateral margins slightly sinuate, extending half beyond apex of pygofer lateral processes (Fig. 6C); anal column (paraproct, anal style) elongate, much longer than remainder of 11th segment.

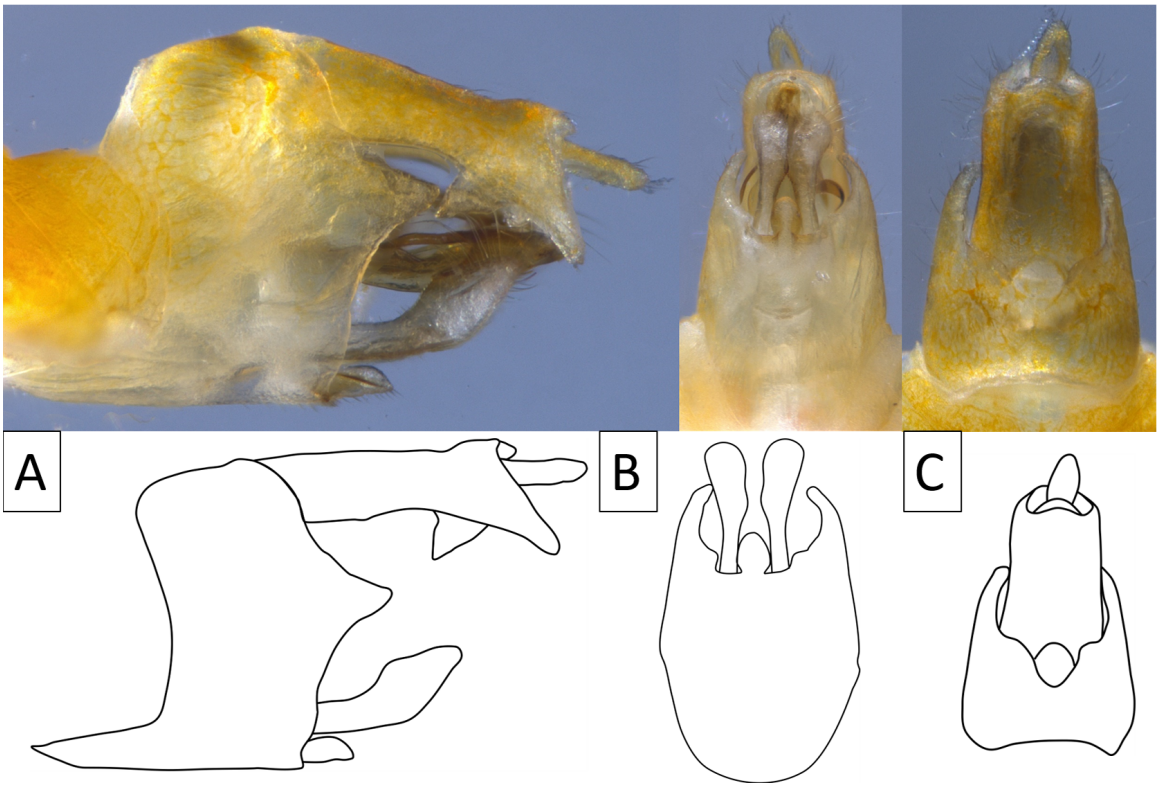

FIGURE 5. Male terminalia of *Haplaxius pocococo* **sp. n.**; A) lateral view, B) ventral view, and C) dorsal view.

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

Distribution. Costa Rica (Alajuela)

Etymology. The specific name given is an amalgamation of the name of the nearest town, Pocosol and Spanish word for coconut—"coco", the host of the new taxon, resulting in pocococo.

Material examined. Holotype male "Costa Rica, Alajuela / Santa Rosa de Pocosol / 16.VI.2019 / Sweeping *Cocos nucifera* / Coll.: B.W.Bahder // Holotype / *Haplaxius pocococo* /" (FLREC); Paratypes, Santa Rosa de Pocosol [16.VI.2019] (1 male, 1 female—FSCA, 1female—FLREC).

Sequence Data. For *Haplaxius pocococo* **sp. n.** a 677 bp product was obtained for the COI gene (GenBank Accession No. MW086873). On average *H. pocococo* **sp. n.** differed by 10.2% (SE±0.01) from other species of *Haplaxius* (with *H. dougwalshi* being most similar, 9.2% different) (Table 4) and the average variability among species of *Haplaxius* for COI was 13.49% (SE±0.01). Furthermore, *Haplaxius pocococo* **sp. n.** differed from *Nymphomyndus*, *Oecleus*, and *Myxia* by 16.9%, 16.8% and approximately 19.0%, respectively (Table 4). While *Haplaxius*

pocococo **sp. n.** resolved within *Haplaxius* in the phylogenetic analysis for COI, there in general was weak support for *Haplaxius* (Fig. 8A). However, there was strong support (90) for *Haplaxius pocococo* **sp. n.** resolving next to *H. dougwalshi* (Fig. 8A).

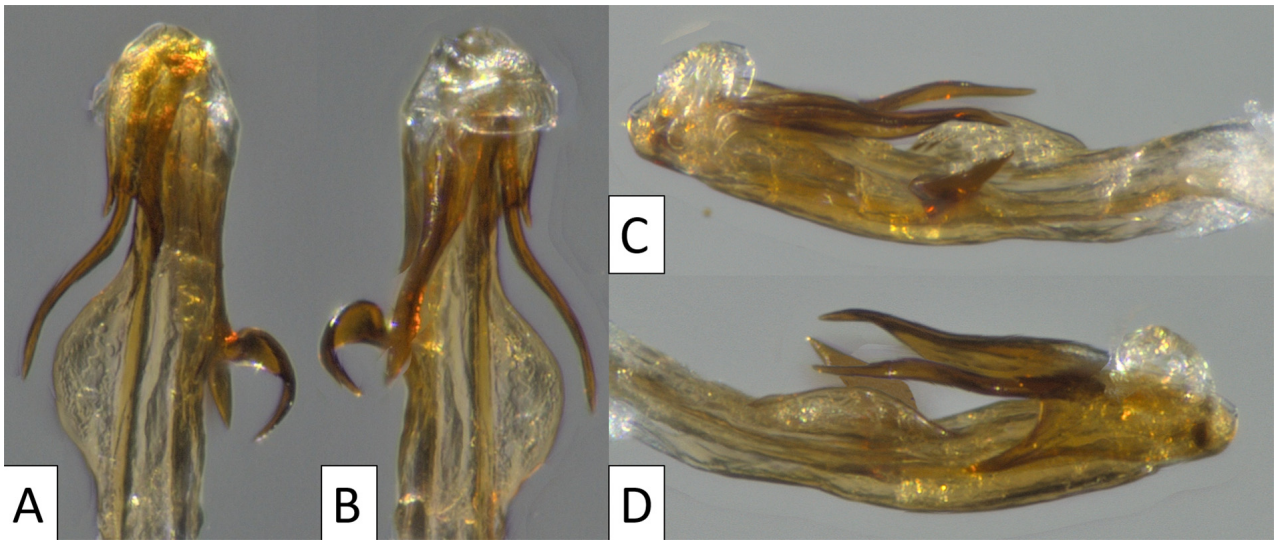

FIGURE 6. Aedeagus of *Haplaxius pocococo* **sp. n.**; A) ventral view, B) dorsal view, C) right lateral view, and D) left lateral view.

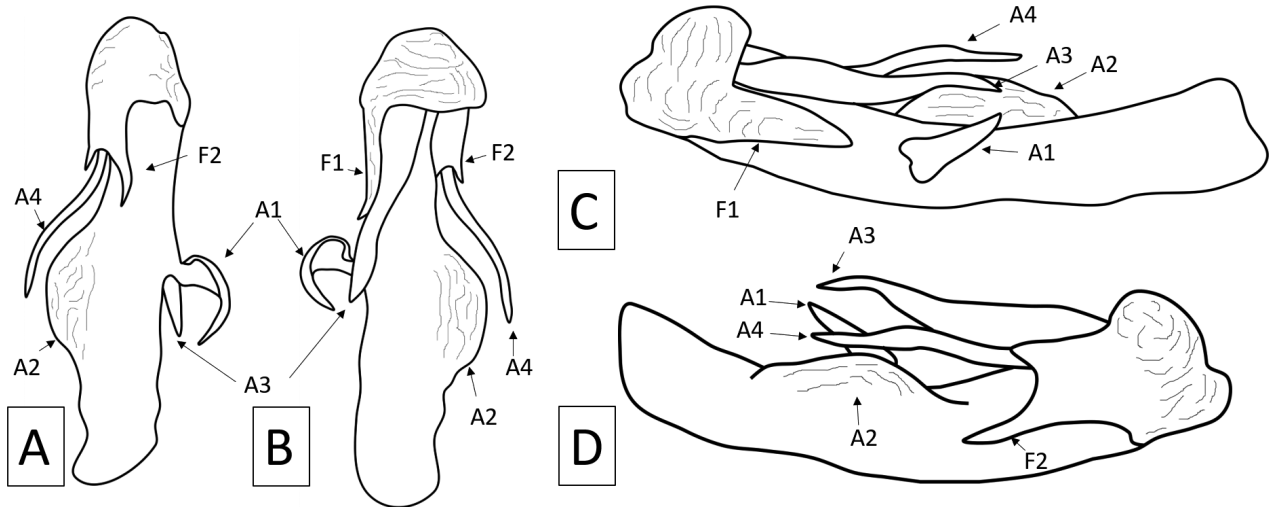

FIGURE 7. Illustration of edeagusof *Haplaxius pocococo* **sp. n.**; A) ventral view, B) dorsal view, C) right lateral view, and D) left lateral view.

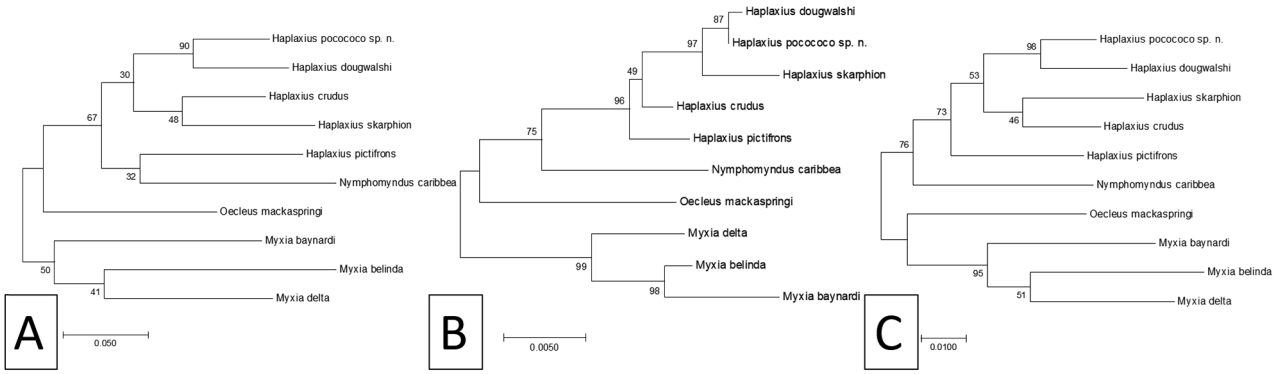

FIGURE 8. Maximum likelihood phylogenetic trees (1,000 replicates) giving phylogenetic position of *Haplaxius pocococo* **sp. n.** relative to related taxa in Oecleinibased on the; A) COI gene, B) 18S gene and C) a consensus tree based on concatenated COI and 18S data.

TABLE 4. 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
1	*Haplaxius pocococo* **sp. n.**		0.012	0.015	0.014	0.014	0.015	0.015	0.016	0.017	0.016
2	*Haplaxius dougwalshi*	0.092		0.015	0.013	0.014	0.016	0.015	0.016	0.017	0.016
3	*Haplaxius skarphion*	0.140	0.155		0.013	0.015	0.015	0.016	0.016	0.016	0.017
4	*Haplaxius crudus*	0.134	0.120	0.112		0.015	0.016	0.016	0.017	0.017	0.017
5	*Haplaxius pictifrons*	0.144	0.155	0.157	0.140		0.016	0.017	0.017	0.017	0.017
6	*Nymphomyndus caribbea*	0.169	0.182	0.168	0.171	0.175		0.016	0.017	0.017	0.017
7	*Oecleus mackaspringi*	0.168	0.164	0.179	0.177	0.199	0.190		0.017	0.016	0.016
8	*Myxia belinda*	0.193	0.199	0.186	0.203	0.215	0.214	0.199		0.017	0.017
9	*Myxia delta*	0.192	0.197	0.182	0.190	0.184	0.204	0.192	0.193		0.017
10	*Myxia baynardi*	0.184	0.192	0.206	0.195	0.199	0.212	0.175	0.221	0.182	

A 1,396 bp product was obtained for the 18S gene (GenBank Accession No. MW086509). On average *Haplaxius pocococo* **sp. n.** differed by an average of 0.48% (SE±0.02) from other species of *Haplaxius* (with *H. dougwalshi* being most similar, 0.1% different) (Table 5) and the average variability among species of *Haplaxius* for 18S was 0.6% (SE±0.00). Furthermore, *Haplaxius pocococo* **sp. n.** differed from *Nymphomyndus*, *Oecleus*, and *Myxia* by 2.3%, 1.6%, and approximately 2.4% respectively (Table 5). Based on the phylogenetic analysis for 18S, *Haplaxius pocococo* **sp. n.** resolved within the *Haplaxius* clade adjacent to *H. dougwalshi* with moderate support (87). However, there was strong support for *Haplaxius* (97) based solely on 18S (Fig. 8B). The consensus tree utilizing both COI and 18S data also showed *Haplaxius pocococo* **sp. n.** within *Haplaxius* with strong support in its placement adjacent to *H. dougwalshi* (Fig. 8C).

TABLE 5. 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
1	*Haplaxius pocococo* **sp. n.**		0.001	0.002	0.002	0.003	0.004	0.003	0.004	0.005	0.004
2	*Haplaxius dougwalshi*	0.001		0.002	0.002	0.003	0.004	0.004	0.004	0.005	0.004
3	*Haplaxius skarphion*	0.005	0.006		0.002	0.003	0.004	0.004	0.004	0.005	0.004
4	*Haplaxius crudus*	0.005	0.005	0.009		0.002	0.003	0.003	0.004	0.004	0.004
5	*Haplaxius pictifrons*	0.008	0.009	0.012	0.005		0.004	0.003	0.004	0.004	0.004
6	*Oecleus mackaspringi*	0.023	0.022	0.027	0.020	0.020		0.004	0.004	0.005	0.004
7	*Nymphomyndus caribbea*	0.016	0.016	0.018	0.013	0.014	0.022		0.004	0.004	0.004
8	*Myxia belinda*	0.023	0.022	0.027	0.019	0.020	0.024	0.022		0.003	0.003
9	*Myxia baynardi*	0.027	0.026	0.031	0.023	0.024	0.028	0.026	0.009		0.003
10	*Myxia delta*	0.021	0.020	0.025	0.019	0.021	0.024	0.022	0.009	0.014	

Remarks. Based on morphological characters and available molecular data *Haplaxius pocococo* **sp. n.** is placed in *Haplaxius* as currently comprised. *Haplaxius dougwalshi* is closely related to *Haplaxius pocococo* **sp. n.** based on both morphology (see below) and molecular data that suggest that *Haplaxius pocococo* **sp. n.** and *H. dougwalshi* form a clade within available *Haplaxius* species. There is also less variability in the sequence data between these two species compared to other *Haplaxius* for both loci. Furthermore, both species have a large, curved process near the midlength of the aedeagal shaft that is not present in the other species in this study. While other species of *Haplaxius* possess a process at the mid-point (viz. *H. flocki* (Kramer), *H. viridis* (Ball), *H. ovatus* (Ball) and *H. simplicatus* Caldwell), the strongly curved process is similar between *H. dougwalshi* and *Haplaxius pocococo* **sp. n.**, and they have similar facial color patterns, lateral processes of the pygofer opening, and comparable gonostyli and medioventral process of the pygofer.

Discussion

The discovery of *Haplaxius pocococo* **sp. n.** on coconut palm highlights the untapped diversity of planthoppers on palms in the Neotropics. Because *Haplaxius* is known to be involved in the transmission of palm lethal decline phytoplasmas, this finding is of particular interest with respect to palm phytoplasma vector research. Specimens of the novel taxon represented about 3% of the specimens collected from coconut palms at this sample site in Costa Rica, with the remainder being identified as *H. crudus* (10%), and *H. skarphion* (87%). This observation highlights the care needed in vector research when mass collecting of cixiids from coconut palms for transmission assays. Because of the role of *Haplaxius crudus*, and potentially *Haplaxius* in general, in the epidemiology of palm lethal decline phytoplasmas, an in-depth understanding of the diversity of the group is essential. Further work on palms in the Neotropics is needed. In addition, the genus *Haplaxius*, as currently defined, appears to be heterogeneous, and a genus-level revision of *Haplaxius* is needed.

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