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Two new species of *Coccygidium* Saussure, 1892 from Australia, with notes on morphological and genetic variation amongst species.

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Abstract

Two new species of the cosmopolitan genus *Coccygidium* Sassure, 1892 (Hymenoptera: Braconidae: Agathidinae) are described from Australia. *Coccygidium fulguritum* Atkin-Zaldivar sp. nov. is described from Queensland based on the results of a citizen science study partnering with local schools, while *Coccygidium vittatum* Atkin-Zaldivar sp. nov. is described from South Australia. We also document morphological variation amongst specimens of *Coccygidium necatrix* Atkin-Zaldivar & Fagan-Jeffries, 2024 which have identical or very similar cytochome oxidase subunit 1 (COI) DNA barcodes to specimens in the type series. We outline the observed diversity in body and wing colour within *C. necatrix* and *C. mellosiheroine* Atkin-Zaldivar & Fagan-Jeffries, 2024 to aid identification of these agriculturally important species.

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Introduction

Coccygidium Saussure, 1892 is a genus of parasitoid wasp in the braconid subfamily Agathidinae. Species of *Coccygidium* are koinobiont endoparasitoids who use lepidopteran larvae in their first or second instar as their host (Stevens et al., 2010, 2011). All known hosts of *Coccygidium* are in the family Noctuidae (Sharkey et al., 2009). Several species of *Coccygidium* are parasitoids of *Spodoptera frugiperda* (J. E. Smith, 1797) (fall armyworm), an economically important, global pest of corn and maize crops (Agboyi et al., 2020; Koffi et al., 2020; Otim et al., 2021). There are 35 species of *Coccygidium*

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described globally from the Australasian, Afrotropical, Neotropical, Oriental and Palaearctic regions (Fagan-Jeffries et al. 2024; Yu et al., 2016; Ghramh, 2013). The genus was first recorded from Australia in 2010 (Stevens et al., 2010), yet the first formal descriptions of species did not occur until over a decade later. There are currently only two species of *Coccygidium* known from Australia, *C. mellosiheroine* Atkin Zaldivar & Fagan-Jeffries, 2024 and *C. necatrix* Atkin Zaldivar & Fagan-Jeffries, 2024, both of which have been reared from fall armyworm (Fagan-Jeffries et al., 2024). No other species have been described from Australasia. We here describe two new species of *Coccygidium*: one from Queensland that was named in collaboration with school students as part of the Insect Investigators program (Howe et al., 2025), and one from the Great Victoria Desert in South Australia.

Since the publication of the first two *Coccygidium* species for Australia (Fagan-Jeffries et al., 2024), additional specimens and sequence data have become available that broaden the known morphological variation within the described species *C. necatrix*, and also which increase the complexity of delimitation using molecular data. To better characterise all four known species, we here present new molecular data and comments on the observed patterns of morphological variation in the available specimens of *C. necatrix*. Although we were unable to reach definitive conclusions about the limits of morphological and molecular variation within the species, we consider presenting this data particularly important given the potential use of this species as a biological control agent of fall armyworm, and hope it will provide a solid foundation for a targeted project focussed on the systematics of the genus in a global context.

Methods

Specimen sources and DNA sequencing

Specimens used in this study were sourced from: 1) the *Insect Investigators* citizen science project (Howe et al., 2025); 2) the Wilinggin-West Kimberley Bush Blitz and the Jawoyn Bush Blitz expeditions (https://bushblitz.org.au/); 3) fall armyworm research projects in Queensland; 4) bulk and accessioned museum collections. Some specimens had already undergone DNA sequencing as part of other projects (Fagan-Jeffries et al., 2024). New sequences of the standard 658 bp barcoding region of cytochorome oxidase subunit one (COI) were generated either by extraction with Qiagen DNeasy Blood and Tissue kits, PCR amplification using the standard LCO1490 and HCO2198 Folmer primers (Folmer et al., 1994) and Sanger sequencing though the Australian Genome Research Facility, or alternatively through HotShot extraction (Lunt, 2017), PCR amplification with dual-indexed C_LepFolF/C_LepFolR primer cocktails (Hebert et al., 2025) and sequencing as a large pool of specimens on an Oxford Nanopore MinION flowcell, with bioinformatics performed following a slight modification of the pipeline in Hebert et al. (2025).

Morphological examination and species descriptions

Specimens were examined using an Olympus SZX16 microscope and were compared to keys focusing on Agathidinae of Australia and of Southeast Asia (Sharkey et al., 2009; Stevens et al., 2010; van Achterberg & Long, 2010). Morphological terms used follow the Hymenoptera Anatomy Ontology (Yoder et al., 2010) . The length of separate body sections (head, mesosoma, T1, remaining metasoma) are added to give an approximate total body length because of the curvature of many of the dried specimens. In concurrence with the mission statement of the Taxonomy Australia Decadal Plan (Taxonomy Decadal Plan Working Group, 2018), the species descriptions focussed on diagnostic characters that can be used to separate species and are supported by high-quality images and DNA data. Images of specimens were taken on a Canon 5DSR camera with a MPE 65 mm lens and stacked used the software Zerene Stacker. We diagnose the two new species against the other Australian taxa, but note that for practical reasons, we have assumed endemicity and have not diagnosed them against the other 33 described species from around the globe.

Molecular analyses

All public COI barcode sequences from specimens identified as *Coccygidium* were downloaded from the Barcode of Life Database (BOLD) on the 24 April 2026 using the search term 'Coccygidium' and removing sequences flagged as contaminants or misidentifications. Public data on Genbank was downloded using the search term 'Coccygidium' and selecting all sequences flagged as COI. There were no sequences on Genbank that were not also included in BOLD (identified by matching Genbank accession numbers to the relevant field in BOLD). One sequence from each BIN from outside Australia was selected to align with all available sequences from Australia, including newly sequenced material. A sequence of *Zelomorpha arizonensis* (BOLD Process ID: GBMIN142979-18) was used as an outgroup, as *Zelomorpha* is one of two genera in a clade that was recovered as sister to *Coccygidium* in a phylogenetic study of the subfamily (Sharkey & Chapman, 2017). Sequences from BOLD and newly sequenced barcodes were aligned using MAFFT v7.490 (Katoh et al., 2002; Katoh & Standley, 2013) in Geneious Prime 2023.0.4 and the alignment trimmed to 651 base pairs. Pairwise genetic distances among sequences in these alignments were visualised as a matrix in Geneious using the percent-identify calculation. Modelfinder (Kalyaanamoorthy et al., 2017) within IQ-TREE 3 (Wong et al., 2026) was used to select the bestfit model and partitioning for the three codon positions within the alignment and to construct a Maximum Likelihood tree. A second tree of only the clade containing *C. necatrix* and *C. mellosiheroine* was built using the

same methods, with an unidentified *Coccygidium* from Ghana (BOLD Process ID: TMGHA43414-24) used as an outgroup as the sequence consistently placed near the clade containing the two Australian species in every tree. IQ-TREE 3 was run three times on each alignment and the output with the lowest log likelihood was visualised. Trees were visualised using FigTree (http://tree.bio.ed.ac.uk/software/figtree/), and figures were edited using Adobe Photoshop Illustrator v.2023. Alignment files containing the list of BOLD accession numbers included in the two trees, and the uncollapsed trees with support values displayed on branches are available as supplementary files on Figshare (https://doi.org/10.25909/32566956).

Collaborative species naming

During the Insect Investigators citizen science project (2021–2023; Howe et al. 2025), numerous schools collected undescribed *Coccygidium* species in Malaise traps erected in or near school grounds during March 2022. We engaged Glendan State School to name *C. fulguritum* through an online meeting (40 minutes, May 2023) during which we provided background information on *Coccygidium*, discussed species description protocols and introduced the teacher and students to an online blackboard (Padlet, https://padlet.com/) where students could post name suggestions and etymologies. We subsequently facilitated the teacher to explore names with students and send a shortlist of three names, to which the lead author provided written feedback and candidate scientific names; the teacher engaged the whole school (in October 2023), including staff, to identify the consensus name.

Visualisation of distribution data

Identical COI sequences of *C. necatrix* were collapsed in Geneious Prime to identify the number of different haplotypes. Distribution data for all Australian specimens of *Coccygidium* were plotted using the Digital Atlas of Australia and exported as a svg file, which was manually edited in Adobe Illustrator to display the distribution of each species and each haplotype within *C. necatrix.*

Abbreviations

ANIC: Australian National Insect Collection, Canberra, Australia.

F1, F2: First (most proximal) flagellomere, second-most proximal flagellomere.

OD: Diameter of a posterior ocellus.

OOL: Minimum distance between a posterior ocellus and the eye margin.

POL: Distance between the posterior ocelli.

QM: Queensland Museum, Brisbane, Australia.

SAMA: South Australian Museum, Adelaide, Australia.

T1: First metasomal tergite.

Results

Australian *Coccygidium* in a global context

There is no evidence in the COI ML tree of global *Coccygidium* sequences (Fig. 1A) that the Australian species of *Coccygidium* are found elsewhere in the world, with all non-Australian COI sequences <96% similar to Australian representatives. However, more complete DNA reference databases for neighbouring countries will be needed to determine endemicity unequivocally. Unsuprisingly, given the use of a single mitochondrial gene, most nodes on the tree were poorly supported and multiple lineages, including *C. fulguritum*, changed position within the tree in each of the three iterations. See supplementary material for the full tree with branch support values displayed. However, *C. fulguritum* was always recovered clearly separated from the other two Australian species that have DNA barcode data available (*C. necatrix* and *C. mellosiheroine*).

The *C. necatrix complex*

At the time of the description of *C. necatrix* (Fagan-Jeffries et al., 2024) we had available a morphologically consistent set of specimens which became the type series, with multiple specimens reared from *Spodoptera frugiperda*, and others from recent Malaise traps. The species appeared easily distinguishable from a second morphospecies reared from the same host by the presence of a bright yellow area on the pterostigma, and bright yellow and brown alternating infuscation on the fore wing. We noted in the publication a few specimens, from a different geographic location to those of the type series, that appeared to have 'duller' colouration of the fore wing and body, with much paler T1 and T2 colouration, but which still possessed a lighter patch on the pterostigma. We excluded these from the type series, but assigned them to *C. necatrix* based on the extremely small COI divergences (one or two base pairs different in the 658 bp barcoding region) and the presumption this was an example of intraspecific colour variation. We now present further evidence that *C. necatrix* appears to be a morphologically variable complex and it will require more molecular evidence to establish if this morphological variation represents multiple species (Fig. 1B).

We have sequenced seven different COI haplotypes all within ~2.2% divergence of the type series (haplotype 1; Fig1B–C). One haplotype is only represented by a short (326 bp) sequence from a specimen from South Australia, significantly outside the general distribution of *C. necatrix,* and is probably a distinct species (haplotype 6, Fig1B–C). However, the other six haplotypes overlap in distribution, and display varying morphology. The "type series" morphology, specimens with bright orange/yellow T1 and T2, bright patterns of yellow and dark infuscation on the wing and a clear yellow patch on the pterostigma (Fig 2B), appears in haplotypes 1, 4, 5 and 7. The "muted" morphology, where there is a distinct pale patch on the pterostigma but the fore wing has a con-

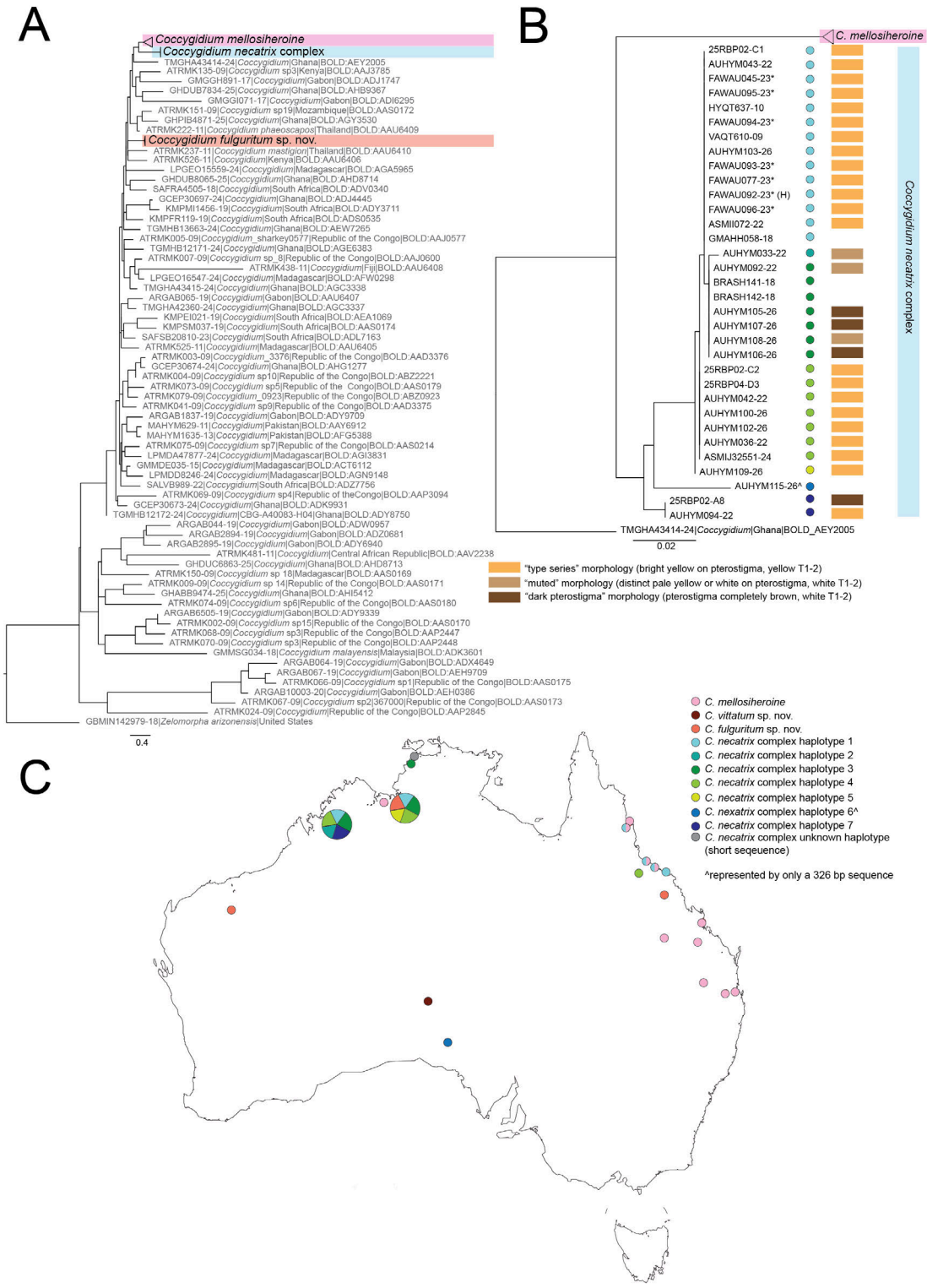


Figure 1. A) Maximum Likelihood tree built using an alignment of COI showing the relationship of the Australian species with the publicly available sequences of *Coccygidium* from around the world. B) Maximum Likelihood tree of the clade containing *C. necatrix*; tip labels display BOLD Process ID codes, whilst coloured circles after each tip label indicate the haplotype (1–7) and correspond to the coloured circles on the distribution map (Fig. 1C). The symbol (H) indicates the holotype of *C. necatrix*, (*) indicates the specimen was reared from *S. frugiperda*, (^) indicates a 326 bp sequence that should be treated with caution. The three coloured rectangles (orange, light brown and dark brown) indicate the three observed morphotypes within the clade. C) Distribution map of the DNA barcoded specimens of all four species of *Coccygidium* described from Australia, created using the Digital Atlas of Australia (sources: Esri, TomTom, Garmin, FAO, NOAA, USGS, © OpenStreetMap contributors, and the GIS User Community, Esri, USGS).

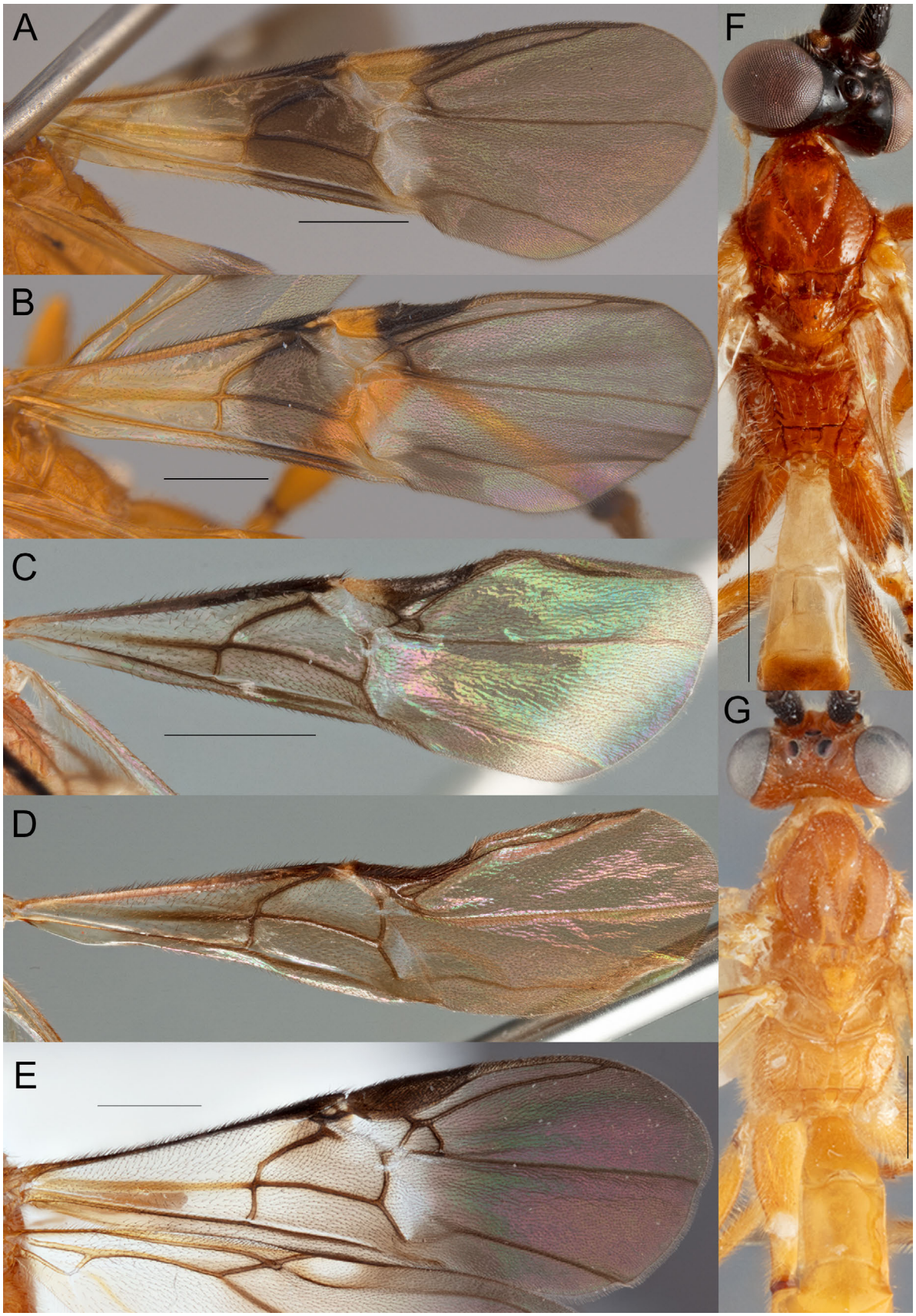


Figure 2. Wing colouration variation in Australian *Coccygidium* specimens. A) *C. fulguritum* sp. nov., female holotype. B) *C. necatrix* 'type series' morphology, BOLD process ID 25RBP02-C2. C) *C. necatrix*, female BOLD process ID: AUHYM033-22, 'muted' morphology. D) *C. necatrix,* female BOLD process ID: AUHYM106-26, 'dark pterostigma' morphology. E) *C. mellosiheroine*, female holotype. F) *C. necatrix* female BOLD process ID: AUHYM033-22, 'muted' morphology. G) *C. necatrix* female holotype.

tiguous brown infuscation (Fig. 2C), the body colouration is often duller with a darker head, and T1–2 is white, occurs in haplotypes 2 and 3. Four specimens, in haplotypes 3 and 7, display the "muted" morphology but with the pale section of the pterostigma virtually indistinguishable (Fig. 2D).

Concerningly, the two specimens with a dark pterostigma would run to *C. mellosiheroine* (Fig. 2E) in the key to hymenopteran parasitoids of *S. frugiperda* (Fagan-Jeffries et al., 2024) and despite further examination of additional specimens, we have not found a consistent morphological character to separate *C. mellosiheroine* and *C. necatrix* if we exclude the colouration of the fore wing. To ensure this was not due to a specimen mix-up or mislabeled vial, we reextracted and sequenced the specimen falling inside haplotype 3 that has a completely dark pterostigma, and confirmed the same COI sequence was recovered from the new extraction.

Despite the morphological complexity, members of the *Coccygidium necatrix* complex appear to be distinguishable from *C. mellosiheroine* using DNA barcoding (interspecific distances of 3.8–5.6% amongst full-length COI sequences). Available sequences of *Coccygidium mellosiheroine* had intraspecific distances of <0.4%. Sequences of the newly described species *C. fulguritum* Atkin-Zaldivar sp. nov. had intraspecific distances of <0.8%, with interspecific COI distances of >3% to *C. necatrix* and *C. mellosiheroine*.

Whilst we are not able to definitively determine the species limits of *C. necatrix* here, we take this opportunity to present the evidence of morphological variability in the species due to the economic importance of it as a parasitoid of *S. frugiperda.* We describe two new species that are morphologically distinguishable from *C. mellosiheroine* and from all morphotypes of *C. necatrix*, to ensure all four species are available to be included in future phylogenomic studies. We recommend the genus is subject to a global taxonomic revision using genome-level molecular information, which will hopefully resolve these issues and provide stronger species boundary resolution to aid research into their use as biological control agents.

Key to the described species of *Coccygidium* found in Australia

No males are currently known for two of the four species of Australian *Coccygidium*, therefore this key has only been tested on female specimens.

We are aware of at least one specimen of *C. necatrix* which has the yellow pterostigma patch extremely indistinct (Fig. 2D) and would likely key to *C. mellosiheroine* in the key below. We recommend confirming identifications with DNA barcoding.

1 Anterior central area of the propodeal areola broad, with a maximum length/maximum width ratio of <2 (Fig. 6D); propodeum dark, much darker than mesoscutum (Fig. 6E) ***C. vittatum* sp. nov.**

1 Anterior central area of the propodeal areola narrow, with a maximum length/maximum width ratio of 2–3 (e.g. Fig. 2F, 2G, 3D) propodeum yellow or orange, similar in colour to mesoscutum (e.g. Fig. 2F, 2G, 3E) **2**

2 Fore wing r vein yellow; proximal yellow patch on pterostigma covers >50% of pterostima (Fig. 3G) ***C. fulguritum* sp. nov.**

2 Fore wing r vein dark; pterostigma either completely dark, or if with proximal yellow patch, patch covers ≤50% of pterostigma (Fig. 2B–E) **3**

3 Fore wing with proximal yellow patch, generally quite distinct (Fig. 2B–C) ***C. necatrix***

3 Fore wing completely dark, with no pale or yellow patches (Fig. 2E) ***C. mellosiheroine***

Taxonomy

Genus *Coggygidium* Saussure, 1892

https://www.zoobank.org/NomenclaturalActs/018e0893-e782-49b1-a76c-9ec896dfe68d

Coccygidium Saussure, 1892: 15. Type species: *Coccygidium luteum* (Brullé, 1846).

Brachyrhopalum Kriechbaumer, 1894: 312. Type species: *Brachyrhopalum pallidum* Kriechbaumer, 1894.

Neophylax Ashmead, 1900: 119. Type species: *Neophylax snyderi* Ashmead, 1900.

Ahngeria Kokujev, 1902: 6. Type species: *Ahngeria transcaspica* Kokujev, 1902.

Dichelosus Szépligeti, 1902: 71. Type species: *Dichelosus fuscipennis* Szépligeti, 1902.

Lisitheria Cameron, 1904: 306. Type species: *Lisitheria nigricornis* Cameron, 1904.

Spilomicrodus Cameron, 1904: 323. Type species: *Spilomicrodus nigriceps* Cameron, 1904.

Xanthomicrodus Cameron, 1904: 157. Type species: *Xanthomicrodus iridipennis* Cameron, 1904.

Caenophylax Schulz, 1911: 88. Type species: *Neophylax snyderi* Ashmead, 1900.

Amputostypos Sharkey, 2009: 30. Type species: *Disophrys concolor* Szépligeti, 1908.

Coccygidium can be separated from the other genera of Agathidinae known from Australia by the following characters in combination: fore tarsal claws cleft, base of fore tarsal claw without spines forming comb (= not pectinate); fore tibial spur long, equal to or greater than 0.8× length of basitarsus, aristate and sinuate; preapical spines not present on anterior surface of mid tibia; frons with lateral carinae present; fore wing cell 1–RS triangular, posterior margin longer than anterior margin; fore wing vein 2–RS2 absent; ovipositor short, length much less than 0.5× length of metasoma, curved ventrally (Stevens et al., 2010).

For a key to the Agathidinae genera of Australia, see Stevens et al. (2010).

Coccygidium fulguritum Atkin-Zaldivar sp. nov.

Figures 2A, 3–4.

urn:lsid:zoobank.org:act:913BF55A-5A91-4677-BCC0-FDA1F5DBC51A

Holotype: ♀; Queensland; Glenden; -21.35, 148.12; 15–22 March 2022; Glenden State School students; Malaise trap; BOLD ASMII6781-22; QM: T265053.

Paratypes: ♀; Queensland; Glenden; -21.35, 148.12; 15–22 March 2022; Glenden State School students; Malaise trap; BOLD ASMII6887-22; QM T265055. ♀; Queensland; Charters Towers; -20.06, 146.28; 15–22 March 2022; Columba Catholic College students; Malaise trap; BOLD ASMII061-22; QM T265054. ♀; Northern Territory, Gregory National Park; Station Creek; 0.2 km NNW Bullita Camp Ground; 16°06'42"S, 130°25'23"E; 12–16 June 2001; Malaise Trap; ME Irwin, FD Parker, C Lambkin; DNA exAga12; BOLD AUHYM101-26; ANIC ANIC00029065. ♀; Northern Territory; Victoria Hwy, 38.5 km SW Timber Creek, 15°42'40"S, 130°07'48"E; 6–13 June 2001; Malaise Trap; ME Irwin, FD Parker, C Lambkin; DNA exAga21; BOLD AUHYM110-26; ANIC ANIC00029059. ♀; Western Australia; Karijini Natl Park, Weano Gorge Rd; 22°23'18"S, 118°15'23"E; 711 m; 24 April–14 May 2003; Malaise Trap; [collector(s) unknown]; DNA exAga15; BOLD AUHYM104-26; ANIC ANIC00029069.

Diagnosis:

Coccygidium fulguritum can be diagnosed from the three species of *Coccygidium* known from Australia by the presence of a yellow area on the pterostigma reaching past the r vein, and the r vein yellow. Other Australian species either have a completely dark pterostigma, or if with a yellow area on the pterostigma, the yellow area does not extend to the r vein.

Description (based on female holotype):

Female.

Colour: Head dark yellow, with darker area around the occiput, antenna uniformly dark brown; mesosoma dark yellow; fore and mid legs dark yellow, hind leg dark yellow with distal third of hind tibia and hind tarsi dark brown; fore wing with yellow infuscation proximally and on pterostigma and r vein, with pale band continuing from pterostigma (as in Fig. 4G), rest of wing infuscation and veins dark; metasoma dark yellow; ovipositor sheaths dark brown.

Body length: ~6.2 mm; head length in lateral view: 0.7 mm; mesosoma length in lateral view: 2.3 mm; T1 length in lateral view: 0.9 mm; metasoma from proximal margin of T2 to end of hypopygium in lateral view: 2.3 mm.

Head: head width in anterior view: 1.4 mm; minimum distance between eyes in anterior view (face width): 0.7 mm; eye height in anterior view: 0.7; malar space (measured as the minimum distance between eye and mandible): 0.2 mm; POL: 0.15 mm; OOL: 0.17 mm; OD: 0.16 mm; face reasonably smooth, evenly setose; number of flagellomeres: 40; F1 length/width ratio (l/w): 2.7; F2 l/w: 2.2.

Mesosoma: Mesoscutum maximum length / maximum width in dorsal view: 1.2; mesoscutum punctate with setae, notauli complete, area of the mesoscutum between the notauli with a central longitudinal ridge created by two parallel longitudinal indentations (but see variation section); central area of the propodeal areola (area superomedia), with a maximum length/maximum width ratio of 2.1. Fore wing length: 5.9 mm. Hind tibia length: 1.9 mm; longest hind tibial spur length: 0.8 mm; hind basitarsus length: 1.2 mm.

Metasoma: T1 length in dorsal view 0.96 mm; maximum width of scleratised area of T1 (near posterior margin): 0.47 mm; T1 with lateral projections near base then widening towards posterior margin, smooth and setose along margins but glabrous on dorsal surface; extruded part of ovipositor sheath length (measured in lateral view from apex of hypopygium): 0.5 mm; ovipositor sheaths densely setose for entire length.

Variation: Measurement variation measured on two paratypes (BOLD sample ID: BIOUG71215-F01 and BOLD sample ID: ExAga12). Body length: 6.5–7.1 mm; head length in lateral view: 0.9; number of flagellomeres: 40–41; mesosoma length: 2.5–2.6 mm; fore wing length: 5.6–6.0 mm; metasoma length: 3.1–3.6 mm; T1 length in dorsal view: 0.93–1.1 mm; T1 width at posterior margin: 0.4–0.5 mm.

Male. Unknown.

Etymology: Named, in collaboration, by students from Glenden State School during 2023; the yellow wing infuscation and yellow patch on the pterostigma reminded students of "a cartoon character who has been electrocuted or struck by lightning, along with the "charred" black marks on its wings". To reflect this, the species name is a Latin adjective meaning 'struck by lightning'.

Remarks: Sequences for the type series currently constitute BOLD BIN:AEU2745. *Coccygidium fulguritum* has not been reared from *Spodoptera frugiperda* as far as we are aware.

Distribution: Known from northern Australia, across Western Australia, Northern Territory and Queensland.

Coccygidium vittatum Atkin-Zaldivar sp. nov.

Figures 5–6.

urn:lsid:zoobank.org:act:1BBE5364-3D1F-4FA4-AD27-12C0ECD0F309

Holotype: ♀; South Australia; 10 km NW Emu Junc., Great Victoria Desert; 10 October 1976; J.A. Herridge and G.F. Gross; at light; SAMA 32-035981.



Figure 3. *Coccygidium fulguritum* sp. nov., lateral habitus. Scale bar 1 mm.

Diagnosis:

Coccygidium vittatum can be diagnosed from the three other species found in Australia by a much broader anterior central area of the propodeal areola (Fig. 6D), with a maximum length/maximum width ratio of 1.3 (compared to 2–3 in other Australian species), and a dark propodeum (pale/yellow in the other species).

Description (based on female holotype):

Female.

Colour: Head dark yellow; scape and first three flagellomeres dark brown (remaining flagellomeres broken in holotype); mesosoma dark yellow except for propodeum, propodeum dark brown; fore, mid and hind coxa and femur dark brown, fore and mid tibia and tarsus dark yellow similar to mesosoma; hind tibia dark brown distally and dark yellow proximally (hind tarsi missing in holotype); fore wing hyaline with a uniform brown tinge, veins dark brown, pterostigma primarily dark brown but with a yellow spot proximally; T1 and T2 on metasoma yellow and lighter than mesosoma, dorsal metasoma from T3 onwards (distally) dark brown; ovipositor sheaths dark brown.

Body length: ~8.8 mm; head length in lateral view: 1.0 mm; mesosoma length in lateral view: 3.4 mm; T1 length in lateral view: 1.5 mm; metasoma from proximal margin of T2 to end of hypopygium in lateral view: 2.9 mm.

Head: maximum head width in anterior view: 1.8 mm; minimum distance between eyes in anterior view (face width): 1.0 mm; eye height in anterior view: 1.0 mm; malar space (measured as the minimum distance between eye and mandible): 0.3 mm; POL: 0.13 mm; OOL: 0.24 mm; OD: 0.20 mm; F1 length/central width ratio (l/w): 2.5; F2 l/w: 2.0; face reasonably smooth, evenly setose across face.

Mesosoma: Mesoscutum maximum length / maximum width in dorsal view: 1.1 mm. Mesoscutum punctate with setae, punctures smaller and shallower in the central area between noutauli. Central area of the propodeal areola (area superomedia), with a maximum length/maximum width ratio of 1.3. Fore wing length: 8.2 mm. Maximum hind tibia length: 2.6 mm; longest hind tibial spur length: 1.1 mm.

Metasoma: T1 length in dorsal view: 1.7 mm; maximum width of scleratised area of T1 (near posterior margin): 0.7 mm; T1 with lateral projections then widening

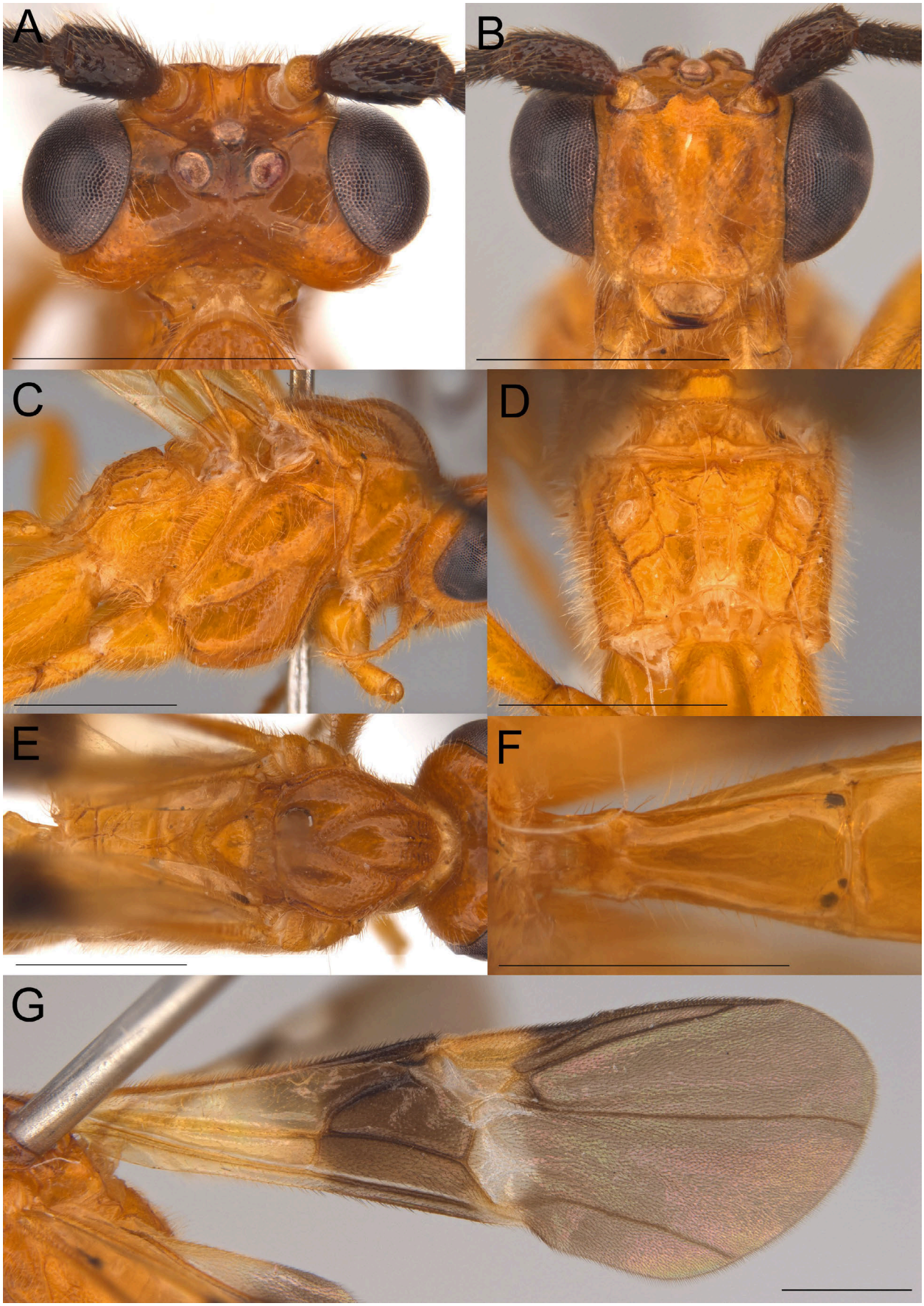


Figure 4. *Coccygidium fulguritum* sp. nov. female holotype, A) dorsal head, B) frontal head, C) lateral mesosoma. D) propodeum, E) dorsal mesosoma, F) dorsal metasomal tergite 1, G) fore wing. Scale bars 1 mm.



Figure 5. *Coccygidium vittatum* sp. nov., female holotype, lateral habitus. Scale bar 1 mm.

towards posterior margin, smooth and setose along margins but glabrous on dorsal surface; extruded part of ovipositor sheath length (measured in lateral view from apex of hypopygium): 0.7 mm; ovipositor sheaths densely setose for entire length, ovipositor evenly and distinctly curved.

Male. Unknown.

Etymology: The species epithet *vittatum* is from the Latin vittatus, in this context meaning 'decorated or bound with a ribbon' and refers to the diagnostic dark propodeum situated between the paler mesoscutum and metasomal tergites. The epithet is a neuter adjective.

Remarks: As only one specimen is known, no information on the male or intraspecies variation could be gathered. The specimen does not have full antennae with flagellomeres broken off, all tarsi not intact, mid-leg was removed during DNA extractions. Despite the incompleteness of the specimen, and the lack of additional material and DNA sequences, we felt it was justified to describe this species as it is one of the only records of *Coccygidium* currently known from South Australia, and dramatically expands the known distribution of the genus.

Distribution: South Australia, Great Victorian Desert.

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Author Contributions:

Tareva-Chine C. Atkin-Zaldivar: Conceptualisation (equal), data curation (lead), formal analysis (equal), investigation (lead), resources (equal), visualisation (supporting), writing – original draft preparation (equal), writing – review & editing (equal). **Ben A. Parslow:** resources (equal), supervision (supporting), visualisation (equal), writing – review & editing (equal). **Andy G. Howe:** project administration (Insect Investigators), resources (equal), writing – original draft preparation

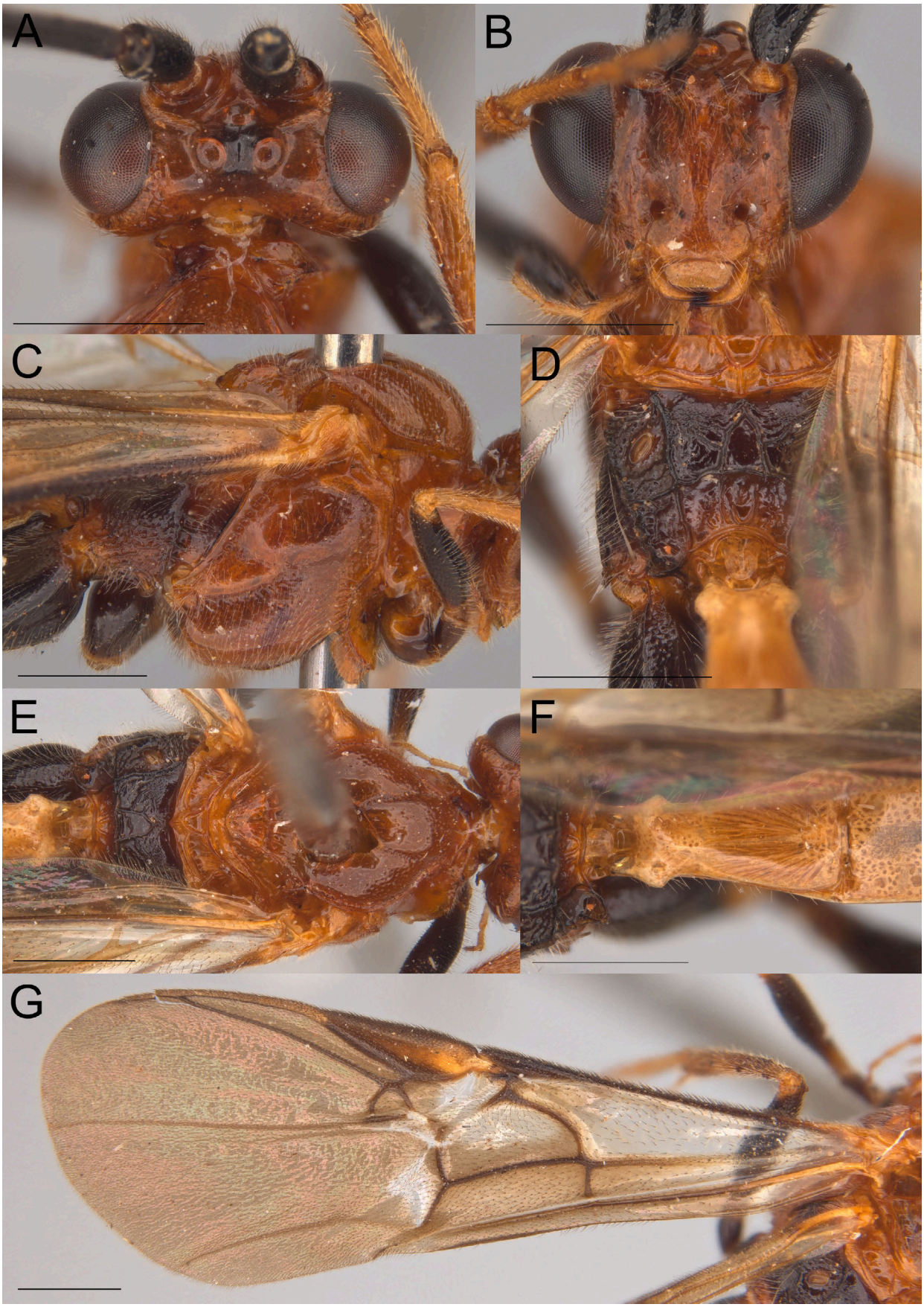


Figure 6. *Coccygidium vittatum* sp. nov, female holotype, A) dorsal head, B) frontal head, C) lateral mesosoma, D) propodeum, E) dorsal mesosoma, F) dorsal metasomal tergite 1, G) fore wing. Scale bars 1 mm.

(supporting), writing – review & editing (equal). **Vian L. Pettit:** data curation (supporting), visualisation (supporting), writing – review & editing (supporting). **Erinn P. Fagan-Jeffries:** conceptualisation (equal), data curation (supporting), formal analysis (equal), funding acquisition, investigation (supporting), project administration, resources (equal), supervision (lead), visualisation (equal), writing – original draft preparation (equal), writing – review & editing (equal).

Supplementary Data

Alignment files containing the list of BOLD accession numbers included in the two trees, and the uncollapsed trees with support values displayed on branches are available as supplementary files on Figshare (https://doi.org/10.25909/32566956).

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