Received: 3 October 2023 | Revised: 16 January 2024 | Accepted: 29 January 2024

DOI: 10.1111/aen.12682

TAXONOMIC ARTICLE

Austral Entomology WILEY

# Hymenopteran parasitoids of fall armyworm (*Spodoptera frugiperda* (J.E. Smith) (Lepidoptera: Noctuidae)) in Australia, with the description of five new species in the families Braconidae and Eulophidae

**Erinn P. Fagan-Jeffries**[1,2] | **Melina M. Miles**[3] | **Tareva-Chine C. Atkin-Zaldivar**[1] | **Andy G. Howe**[4] | **Siva Subramaniam**[3] | **Donna M. Chambers**[3] | **Frezzel Praise J. Tadle**[3] | **Saleh M. Adnan**[5] | **Verni Sivasubramaniam**[3] | **Alice Woodward**[6]

[1]School of Biological Sciences, The University of Adelaide, Adelaide, Australia

[2]South Australian Museum, Adelaide, Australia

[3]Department of Agriculture and Fisheries (DAF), Queensland, Australia

[4]Forest Research Institute, University of the Sunshine Coast, Sippy Downs, Australia

[5]New South Wales Department of Primary Industries, Wollongbar, Australia and Department of Primary Industries and Regional Development Western Australia, Australia

[6]Murraylands and Riverland Landscape Board, Murray Bridge, Australia

**Correspondence**
Erinn P. Fagan-Jeffries, School of Biological Sciences, The University of Adelaide, Adelaide, Australia.
Email: erinn.fagan-jeffries@adelaide.edu.au

**Funding information**
Australian Biological Resources Study Research Grant, Grant/Award Number: NTRGI000021; Australian Government Inspiring Australia Citizen Science Grants; Hort Innovation, Grant/Award Number: Project MT19015; Queensland Treasury through the 'Fall Armyworm Response' Project

## Abstract

Fall armyworm, *Spodoptera frugiperda* (J.E. Smith) is an invasive pest of agricultural crops including sweet corn and maize. The moth was first recorded in Australia in January 2020 and is now considered established in most states and territories, and research is underway to develop management strategies. Extensive rearing of *S. frugiperda* larvae and eggs occurred from March 2020 to April 2023 to understand the parasitoid complex present in Australia and identify potential biological control agents. We report here on the hymenopteran parasitoids reared during this period, which were identified using a combination of morphology and COI DNA barcoding, and provide images, a key to species, and contextual information to facilitate future research. Twelve species of parasitoids from five families of Hymenoptera are formally reported as parasitising *S. frugiperda* in Australia. Five species are here described as new: *Chelonus patbat* Fagan-Jeffries, **sp. nov.** (Braconidae), *Chelonus trojanus* Fagan-Jeffries, **sp. nov.** (Braconidae), *Coccygidium mellosiheroine* Atkin-Zaldivar & Fagan-Jeffries, **sp. nov.** (Braconidae), *Coccygidium necatrix* Atkin-Zaldivar & Fagan-Jeffries, **sp. nov.** (Braconidae), and *Euplectrus frugiperdata* Fagan-Jeffries, **sp. nov.** (Eulophidae).

**KEYWORDS**
biological control, *Chelonus*, *Coccygidium*, *Euplectrus*

Erinn P. Fagan-Jeffries: https://zoobank.org/urn:lsid:zoobank.org:author:C724E269-029E-49E8-8D95-6F5A5DA6BAAF

Tareva-Chine C. Atkin-Zaldivar: https://zoobank.org/urn:lsid:zoobank.org:author:A20374C5-7A3C-4411-BFBF-A4828DE9A1D2

This paper zoobank registration number: https://zoobank.org/urn:lsid:zoobank.org:pub:44BD3145-F5B7-43B9-97C5-C14A4E1DFEE1

*Version of record published on 29 May 2024*

## INTRODUCTION

Fall armyworm (*Spodoptera frugiperda* (J.E. Smith, 1797)) is a noctuid moth (Lepidoptera: Noctuidae) native to tropical regions of North and South America. The larvae of *S. frugiperda* have been reported as pests of corn and maize crops in the Western Hemisphere since the 1790s, with damaging outbreaks occurring throughout the following two centuries (Sparks 1979). By 2016, the moth had reached the African continent and was recorded feeding on economically important crops, including maize (Goergen et al. 2016). Soon afterwards, fall armyworm spread around the globe, including to India (Sharanabasappa et al. 2019), Indonesia (Sartiami et al. 2020) and China (Sun et al. 2021). *Spodoptera frugiperda* was detected in Australia in January 2020, with the introduction most likely originating from Indonesia (Qi et al. 2021).

There have been close to 100 hymenopteran parasitoid species reared from *S. frugiperda* across the globe, with high diversity from the families Braconidae and Ichneumonidae, and the superfamily Chalcidoidea (Agboyi et al. 2020; Ashley 1986; García-González, Rios-Velasco, & Iglesias-Pérez 2020; Gutiérrez-Ramírez et al. 2015; Li et al. 2023; Meagher et al. 2016; Molina-Ochoa et al. 2003, 2004; Murúa, Molina-Ochoa, & Fidalgo 2009; Otim et al. 2021; Sagar et al. 2022; Serrano-Domínguez et al. 2021; Youssef 2021). Of the species recorded overseas, only *Cotesia ruficrus* (Haliday), *Telenomus remus* Nixon, and *Trichogramma pretiosum* Riley are known to already occur in Australia. However, there is likely to be a diverse assemblage of native parasitoids associated with the seven species of *Spodoptera* and nearly 500 species of noctuid moths known from Australia, that potentially will parasitise *S. frugiperda* now that it has arrived on the continent.

In Australia, fall armyworm has been reported from all states and territories other than South Australia (Plant Health Australia 2023). Several surveys were undertaken to understand the parasitoid complex in Australia of the newly arrived *S. frugiperda*, including rearing studies with identification of parasitoids through both molecular and morphological methods. Whilst several dipteran parasitoids were recovered, we report only on the hymenopteran parasitoids in this publication, provide a key to species, and describe several of the species as new. It is intended that this initial summary of the hymenopteran parasitoid complex of *Spodoptera frugiperda* in Australia will facilitate ongoing work identifying potential biological control agents and designing integrated pest management practices.

## MATERIAL AND METHODS

### Collection and rearing protocols

*Spodoptera frugiperda* egg masses and larvae were collected from commercial crops, volunteer and cover crops, and field trials, in Queensland, New South Wales, Western Australia and the Northern Territory between January, 2020 and April, 2023. Material was collected from maize, sweet corn (*Zea mays* L.), sorghum (*Sorghum bicolor* L.), and capsicum (*Capsicum annuum* L.) at a range of crop stages, from seedling to reproductive, and at a range of infestation levels. Fields sampled were inclusive of unsprayed crops, organic crops, volunteer crops, trial plots, and commercial crops where insecticides were regularly applied. As the purpose of the collections was to screen for the presence of parasitoids only, no data were collected on the pest density. Consequently, no estimates of the percentage parasitism are attempted. Typically, *S. frugiperda* material was collected without evidence of parasitism, and it was retained in the laboratory until either parasitoid emergence, or *S. frugiperda* moth emergence. All rearing was undertaken at 25–28°C, 60%–80% relative humidity.

*Spodoptera frugiperda* egg masses were collected randomly from crops and retained on leaf material in individual vented, 25 mL glass vials in the laboratory. An initial assessment of parasitism was made at 2–4 days post collection, material was disposed of where *S. frugiperda* larvae had hatched from 100% of eggs. Unhatched egg masses, and egg masses that were showing signs of parasitism (blackened), were retained for final assessment at 10–14 days post collection. Only egg parasitoids were detected by this method. Egg-larval parasitoids, like *Chelonus* spp., were assessed by two methods. Egg masses that were attended by *Chelonus* females were collected and kept in individual vials in the laboratory for emergence. Between 25 and 50 neonate larvae hatched from the egg mass were randomly selected and transferred to individual Solo® cups with artificial diet. These cups were retained around 3 weeks for *Chelonus* emergence. Additionally, adults of *Chelonus* spp. that emerged from larvae collected in the field were used for identification.

Larvae, from first to 6th instar, were collected from crops in the field and transferred to artificial diet in the laboratory for rearing (General purpose Lepidoptera diet. Frontier Scientific Services, Delaware, US), other than the specimens collected in the Northern Territory, which were reared on leaves of the host plant from which they were collected. The artificial diet was a poor substrate for the successful pupation of some hymenopteran parasitoid species and resulted in the mortality of late instar parasitoid larvae and pre-pupae that attempted to burrow into the diet to pupate. Specimens of adult parasitoids were provided for taxonomic examination dry or in 70% ethanol, or collected live into 96% ethanol and stored at −18°C for molecular diagnostics.

The survey for egg parasitoids in Western Australia was undertaken by deploying a sentinel technique (mass exposure of eggs in the field) at the DPIRD Research Station site at Kununurra (Bezerra Dasilva et al. 2015). Fresh egg masses, used as sentinels, were sourced from the fall armyworm colony maintained at the Kununurra Research

Station. After collecting from rearing cages, eggs were attached to a paper card (4 cm × 4 cm). For this, no artificial glue was used, instead the paper card was moistened with water so that egg masses would stick to the card as the card dried. Approximately 40–50 eggs were placed in each card. The paper cards with the sentinel eggs were stapled individually on the underside of the whorl leaves and left for 24 hours. After 24 hours, they were recovered into a 65 mL diet container enclosed with lid and maintained in the laboratory at 24–26°C and a photoperiod of 12:12 (L:D). The sentinel egg masses were checked daily under a microscope to find any signs of parasitism. If any egg parasitoids were found, they were also preserved in 95% ethanol solution for morphological and molecular identification. Approximately 10 to 12 egg sentinel cards were placed in an unmanaged maize field at the DPIRD Kununurra research station twice per week from 2 September 2021 to 28 October 2021. A total of 144 egg cards were placed in the field over an 8-week period.

Several specimens of the *Chelonus* and *Coccygidium* species described here as new were collected in Malaise traps by regional school students as part of the *Insect Investigators* citizen science project (insectinvestigators.com.au). The project engaged 50 regional schools from 2022 to 2023 in three Australian states (Queensland, South Australia and Western Australia) in insect taxonomy and offered participants a chance to name new species. Students operated Malaise traps for 4 weeks in March 2022 and the network of traps in Queensland and South Australia contributed here to expanding the known distribution of several species. The authors guided students remotely through the naming process using online workshops, pictures, information on wasp biologies and so on. We adopted an iterative process whereby students and teachers brainstormed ideas using an electronic white board and Google Translate, on which we subsequently commented, before students sought a consensus name and etymology.

## DNA extraction, sequencing and phylogenetics

DNA was extracted from either whole specimens or single legs (for larger specimens) using a modified Gentra® Puregene® protocol for extraction from tissue. The cytochrome oxidase subunit 1 (COI) barcoding fragment was amplified using the standard LCO1490 and HCO2198 primer combination (Folmer et al. 1994) and Sanger sequenced at the Australian Genome Research Facility. Sequences for all specimens are available on the Barcode of Life Database (BOLD) (FAWAU001-23 to FAWAU096-23). Specimens from the *Insect Investigators* project were DNA extracted and sequenced by the Canadian Centre for DNA Barcoding at the Centre for Biodiversity Genomics in Guelph, Canada.

Sequences were aligned using MUSCLE (Edgar 2004) in Geneious Prime 2023.0.4 (https://www.geneious.com) and trees were constructed on the IQ-TREE webserver (Minh et al. 2020; Nguyen et al. 2015; Trifinopoulos et al. 2016) and edited in Figtree v1.4.4. Full specimen details for phylogenies are available in Data S1.

Sequences were uploaded to BOLD, and BOLD BINs are referenced under each species. BOLD groups sequences into Operational Taxonomic Units (OTUs) called Barcode Index Numbers (BINs), using the RESL algorithm (Ratnasingham & Hebert 2013). On the BOLD platform, a BIN page will list the specimens included in that OTU along with statistics including the maximum and minimum genetic distance amongst sequences included in that BIN.

## Morphology and imaging

Morphological terms follow the preferred labels and definitions in the Hymenoptera Anatomy Ontology (Yoder et al. 2010) and Eady (1968) for sculpturing terminology. Specimens were viewed using an Olympus SZX16 and the CellSens software was used for measurements. Images for figure plates were photographed using a Canon 5DS R camera with a MPE 65 mm lens and stacked using Zerene software.

## Acronyms

F1–3: Flagellomeres 1–3 (where flagellomere 1 is the closest flagellomere to the scape)
HE: Height of eye sensu Hansson et al. (2015)
HH: Head height sensu Hansson et al. (2015)
MS: Malar distance sensu 'malar space' Hansson et al. (2015)
OD: Posterior ocelli largest diameter
OOL: Ocular ocellar line (minimum distance between the outer margin of the ocelli and the inner margin of the eye)
POL: Posterior ocellar line (distance between inner margins of the posterior ocelli)
T1–3: Metasomal tergites 1–3.
WF: Width of face sensu Hansson et al. (2015)

## Institution Codes

QDPC: Queensland Primary Industries Insect Collection
QM: Queensland Museum, Brisbane, Australia
SAMA: South Australian Museum, Adelaide, Australia
WAM: Western Australian Museum, Perth, Australia
WINC: Waite Insect and Nematode Collection, The University of Adelaide, Australia

## RESULTS

After extensive field collections across four states and territories of Australia, there were 12 different hymenopteran parasitoids reared from *S. frugiperda* (Table 1). Five species were able to be identified using a combination of morphology and COI DNA barcodes (see specific details of identification methods under each species). Two species of ichneumonids were able to be identified as belonging to the genera *Eriborus* and *Temelucha*, but were not confidently identified to species level and will require further investigation.

Five species (one eulophid and four braconids) were diagnosed against known species from Australia, and from species documented parasitising *S. frugiperda* in other countries, and consequently were confirmed to be undescribed species. Four of these five species contain material collected concurrently through the *Insect Investigators* citizen science program and (in the case of *C. necatrix*) also through the Bush Blitz Wilinggin–West Kimberley expedition (Figure 1).

## TAXONOMY

### Key to the hymenopteran parasitoids known from fall armyworm in Australia:

1. Body size very small (< 2 mm), no closed cells in the fore wing (Chalcidoidea, Platygastroidea) ..... 2.
- Body size larger than 2 mm, multiple closed cells in the fore wing (Ichneumonoidea) ..... 4.

2. Body (including head and thorax) mostly pale brown/yellow, male antennae with very long setae ..... ***Trichogramma pretiosum***.
- At least head and thorax dark brown or black ..... 3.

3. Metasoma with pale centre dorsally and laterally (Figure 2b) [antennae with five flagellomeres] ..... ***Euplectrus frugiperdata*** sp. nov.
- Metasoma completely black (Figure 4c) [antennae with ..... >5 flagellomeres] ..... ***Telenomus remus*** (note that the hyperparasitoids reared from *Cotesia* spp. will also key here).

4. Dorsal metasoma completely fused, forming a sclerotised 'shield' or carapace (Figures 10a–c, 12a,b) [carapace black with either pale patches laterally or a single pale patch in the centre] (*Chelonus* spp.) ..... 5
- Dorsal metasoma not fused into a complete carapace, segments/tergites visible dorsally [dorsal metasoma brown, orange or dark] ..... 6.

5. Body length <4.5 mm, dorsal metasoma with continuous pale patch anteriorly (Figure 12b) ..... ***Chelonus patbat* sp. nov.**
- Body length >5 mm, dorsal metasoma with two pale sections near lateral margins, pale areas can vary in size (Figure 10b,c) and occasionally be very reduced, but species never with continuous white patch in centre of dorsal metasoma ..... ***Chelonus trojanus* sp. nov.**

6. Mesosoma mostly orange ..... 7
- Mesosoma mostly black ..... 9

**TABLE 1** A checklist of the hymenopteran parasitoids reared from *S. frugiperda* in Australia.

| Hymenopteran species | FAW life-stage attacked | Solitary/gregarious | Known distribution (in bold where parasitoid recorded attacking *S. frugiperda*) |
|---|---|---|---|
| **Eulophidae** | | | |
| *Euplectrus frugiperdata* sp. nov. | Larva | G | **WA** |
| **Scelionidae** | | | |
| *Telenomus remus* | Egg | G | **NT, QLD** |
| **Trichogrammatidae** | | | |
| *Trichogramma pretiosum* | Egg | G | **QLD, WA** |
| **Braconidae** | | | |
| *Coccygidium necatrix* sp. nov. | Larva | S | **QLD,** WA |
| *Coccygidium mellosiheroine* sp. nov. | Larva | S | **QLD, WA** |
| *Chelonus trojanus* sp. nov. | Egg | S | **NT, QLD** |
| *Chelonus patbat* sp. nov. | Unknown (assumed egg) | S | **QLD,** SA |
| *Cotesia icipe* | Larva | S | NT, **QLD,** SA |
| *Cotesia ruficrus* | Larva | G | **NSW, QLD,** SA, TAS, **WA** |
| *Microplitis abrs* | Larva | S | **QLD** |
| **Ichneumonidae** | | | |
| *Eriborus* sp. | Larva | S | **QLD** |
| *Temelucha* sp. | Larva | S | **QLD** |

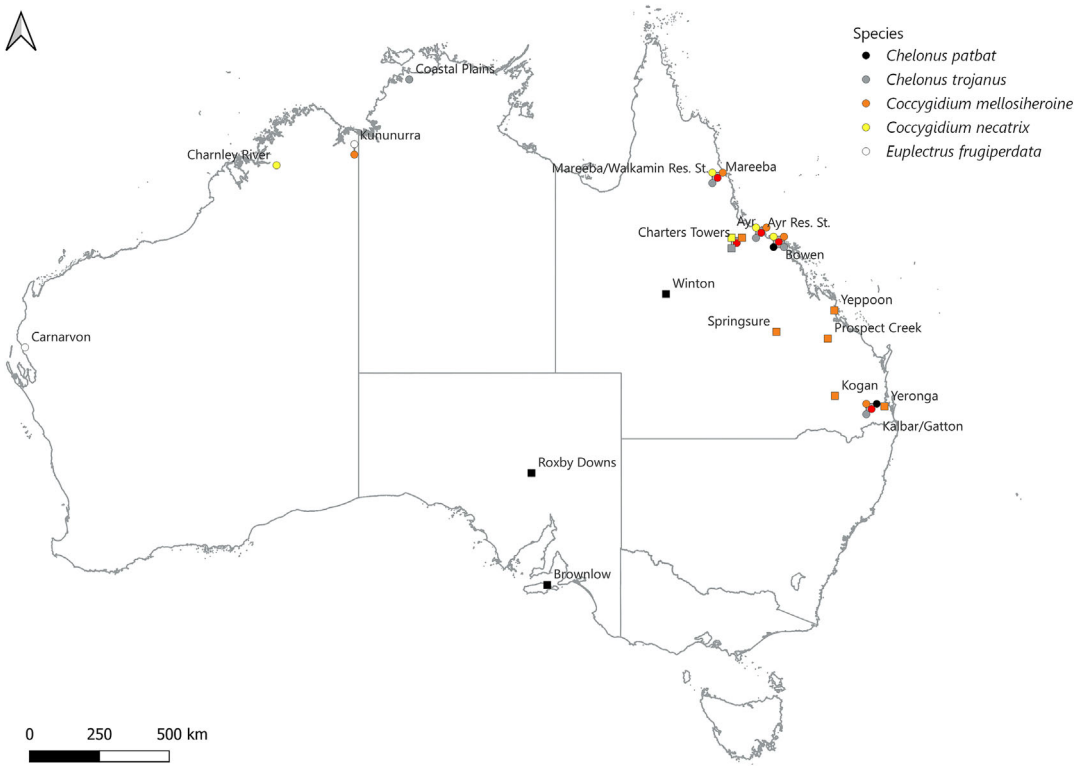


**FIGURE 1** Known distribution of the five newly described species. Colours indicate the species (see key in figure); circles represent locations where specimens were reared from, or collected as part of research relating to, *S. frugiperda* (other than the specimens collected on a bush blitz expedition at Charnley River, WA) whilst squares represent locations where specimens were collected by regional schools during the *Insect Investigators* citizen science project. Where multiple species were collected at the same (or nearby) sites, species markers are clustered around a red circle indicating the location.

7. Propodeum shorter than hind coxa length (Figures 5c and 7b), first metasomal segment not cylindrical (Figures 5a–c; 7a–c; 8b,e) [females: ovipositor shorter than hind tibia](*Coccygidium*) ……... 8
- Propodeum longer than hind coxa length, first metasomal segment thin and almost cylindrical forming a petiole (Figure 18a,c) [females: ovipositor longer than hind tibia] ……... …..... ***Telemucha* sp.**

8. Fore wing pterostigma with yellow or pale patch, fore wings with yellowish banding [fore wing r vein dark] (Figure 6a) …..... ***Coccygidium necatrix* sp. nov.**
- Fore wing pterostigma completely dark brown, fore wings without yellowish banding (Figure 8a) ……..... ***Coccygidium mellosiheroine* sp. nov.**

9. Body length >4 mm, fore wing venation as in Figures 17 a,c) ….... ***Eriborus* sp.**
- Body length <3 mm, fore wing venation as in Figures 4d, 14b or 15c,d (Microgastrinae) ……... 10

10. Fore wing with closed areolet (Figure 4d) ……..... ***Microplitis abrs***
- Fore wing with no areolet (Figures 14b and 15c,d (*Cotesia* spp.) …….. 11

11. The first tergite of the metasoma strongly broadening posteriorly (Figure 15a) …..... ***Cotesia ruficrus***
- The first tergite of the metasoma almost parallel sided, only broadening very slightly (Figure 14c) ……..... ***Cotesia icipe***

*Note: Cotesia can be a difficult genus to diagnose species morphologically, but COI DNA barcodes will clearly separate the two species.*

## HYMENOPTERA: CHALCIDOIDEA

## Eulophidae

### *Euplectrus* Westwood, 1832

See list of synonyms and general discussion of the genus in Hansson et al. (2015).

## Diagnosis

The new species below was keyed to genus using Bouček (1998).

We do not alter the diagnosis or description of the genus given in Hansson et al. (2015), other than noting that whilst they state in the diagnosis for *Euplectrus* 'Mesoscutum … midlobe with a complete median carina and with three pairs of setae', we note that this is not always a completely raised median carina for the whole length of the mesoscutum. This is also case for the new species described here, which has a raised median carina only in the posterior third or half of the mesoscutum.

## Biology and distribution

There are 19 species of *Euplectrus* known from Australia, most described before 1940. Members of the genus are generally ectoparasitoids of lepidopteran larva (Hansson et al. 2015), and several species have been reared from fall armyworm in other countries (Murúa, Molina-Ochoa, & Fidalgo 2009; Ogunfunmilayo et al. 2021; Sturza et al. 2013).

## *Euplectrus frugiperdata* Fagan-Jeffries, sp. nov

(Figures 2 and 3)

https://zoobank.org/urn:lsid:zoobank.org:act:991981BF-EDC6-416D-A989-8CB1E34D0B72

## Material examined

### *Holotype*

♀; Western Australia; Kununarra; 15°39′06.4″S 128°42′47.4″E; 22 September 2021; S. Adnan; reared from larva of *S. frugiperda*; field code: 112; BOLD: FAW-CR112-112; WAM: 116188.

### *Paratypes*

**Western Australia:** 3♀; collection data as holotype; WAM: 116190-92; ♀; collection data as holotype except: 15°52′50.4″S, 128°43′47.0″E; 17 September 2021; field code: 110; BOLD: FAW-CR110-110; WAM: 116187. ♀; collection data as previous; WAM: 116193. ♀; collection data as holotype except: 5°37′20.6″S, 128°45′35.6″E; 1 October 2021; field code: 106; BOLD: FAW-CR106-106; WAM: 116186. ♀; collection data as previous; WAM: 116194. ♀; collection data as holotype except: 15°28′01.1″S, 128°51′01.2″E; 26 July 2021; field code: 107; WAM: 116195. ♂; collection data as previous; WAM: 116196. ♂; Carnarvon; 24°49′30.0″S, 113°45′37.9″E; 29 August 2021; S. Adnan; reared from larva of *S. frugiperda* in sweet corn; field code: 117; BOLD: FAW-CR117-117; WAM: 116189. ♂; collection data as previous; WAM: 116197. 2♀; collection data as previous except: 24°51′31.9″S, 113°42′37.6″E; field code: 120; WAM: 116198, 116 199. ♂; collection data as previous; WAM: 116200.

## Diagnosis

Only two of the species known from Australia have verified COI DNA barcodes. The specimen reared from *S. frugiperda* is >10% divergent from the available COI DNA barcodes of *E. flavipes* (Fonscolombe) (e.g., BOLD BC-ZSM-HYM-23871-E10) and *E. bicolor* (Swederus) (e.g., BOLD BCHYM12720-15).

*Euplectrus frugiperdata* can be diagnosed against the other species known from Australia as follows:

- from *Epiactis australiensis* Ashmead, 1900, *E. melanocephalus* Girault, 1913, and *E. seminigrifemur* Girault, 1924 by having the hind coxa yellowish, not black or dark brown.
- from *E. kurandaensis* Girault, 1913 by having a pale hind coxa (*E. kurandaensis* has a dark hind coxa) and by only having the median carina on the mesoscutellum raised in only the posterior third to half (*E. kurandaensis* has a strong median carina for the whole length of the mesoscutum)
- from *E. agaristae* Crawford, 1911, *E. cariniscutum* Girault, 1915, *E. migneti* Girault, 1936 and *E. scotti* Girault, 1913 by having the median carina on the mesoscutum raised only in the posterior half (the listed species have a strong median carina for the whole length of the mesoscutum). Additionally, *E. frugiperdata* can be diagnosed from *E. agaristae* by having the first flagellomere of similar length to the pedicel (*E. agaristae* has the first flagellomere distinctly longer than the pedicel); from *E. cariniscutum* by having much weaker sculpturing on the mesoscutum and mesoscutellum.
- from *E. acutigaster* Zhu & Huang 2003 by having the first metasomal segment almost as long as wide (*E. acutigaster* has the first metasomal segment 1.8–2× longer than broad).
- from *E. cairnsensis* Girault, 1913 by having the first metasomal segment almost as long as broad (*E. cairnsensis* has the first metasomal segment clearly longer than broad [exact measurements not taken]). Additionally, whilst the head is missing on the syntype of *E. cairnsensis* as it is crushed on a slide, the other material identified by Girault has larger eyes and a smaller malar distance than *E. frugiperdata*.
- from *E. immargiventris* Girault, 1915 by having the mesoscutum with a medial carina visible in the posterior third (*E. immargiventris* has no trace of a

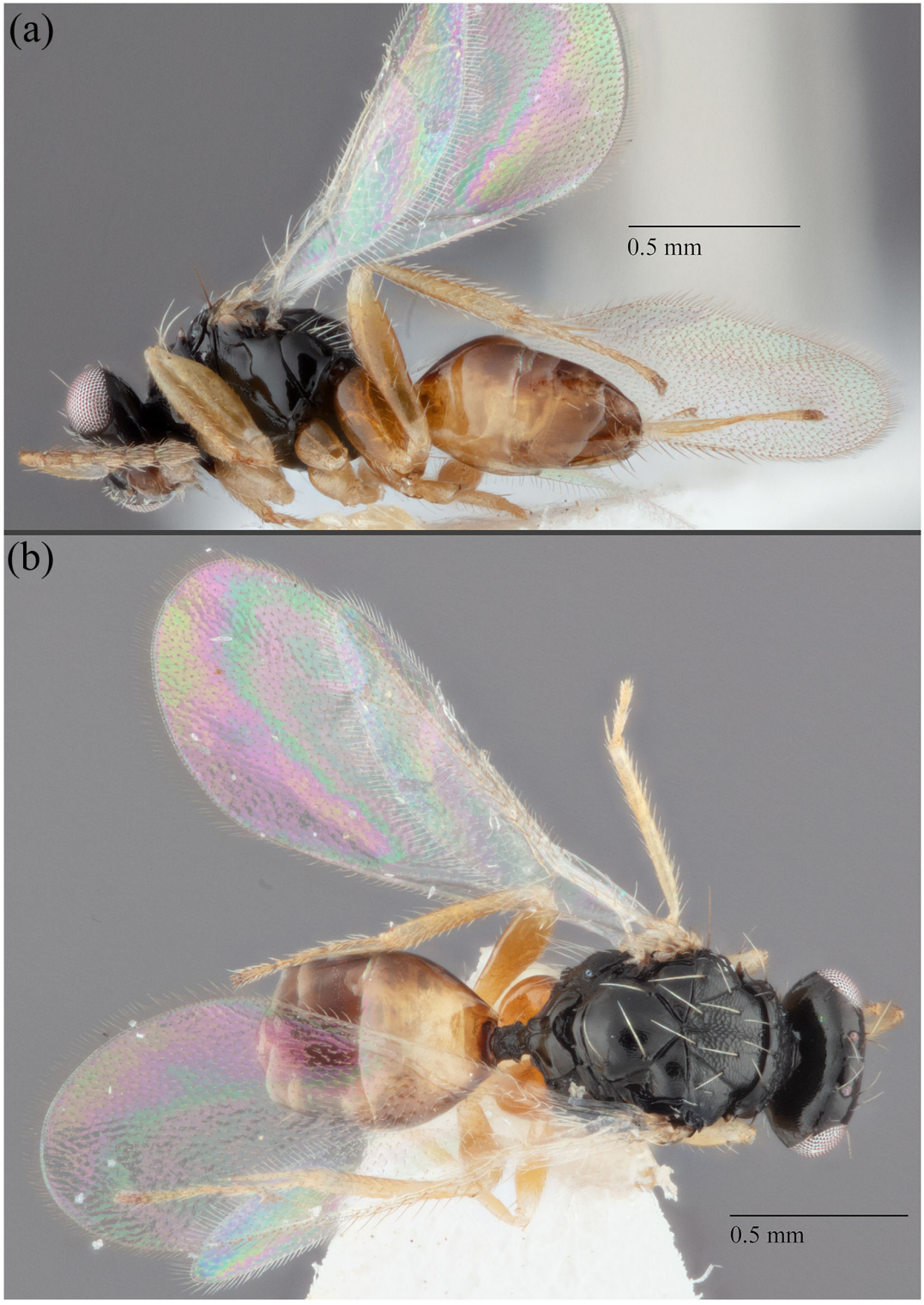


**FIGURE 2** *Euplectrus frugiperdata* sp. nov. holotype. (a) Lateral habitus. (b) Dorsal habitus.

medial carina on the mesoscutum). Additionally, *E. immargiventris* has the mesoscutum and mesoscutellum much more strongly sculptured.

- from *E. laeviscutellum* Zhu & Huang 2003 by having the first metasomal segment almost as long as wide (*E. laeviscutellum* has the first metasomal segment 1.5–1.6× longer than broad). Additionally, based on the illustration of this species (figure 23 [Zhu & Huang 2003]), the malar distance of *E. laeviscutellum* is much shorter than in *E. frugiperdata*.
- from *E. manilae* Ashmead, 1904 by having the malar distance larger than the eye length when the head is

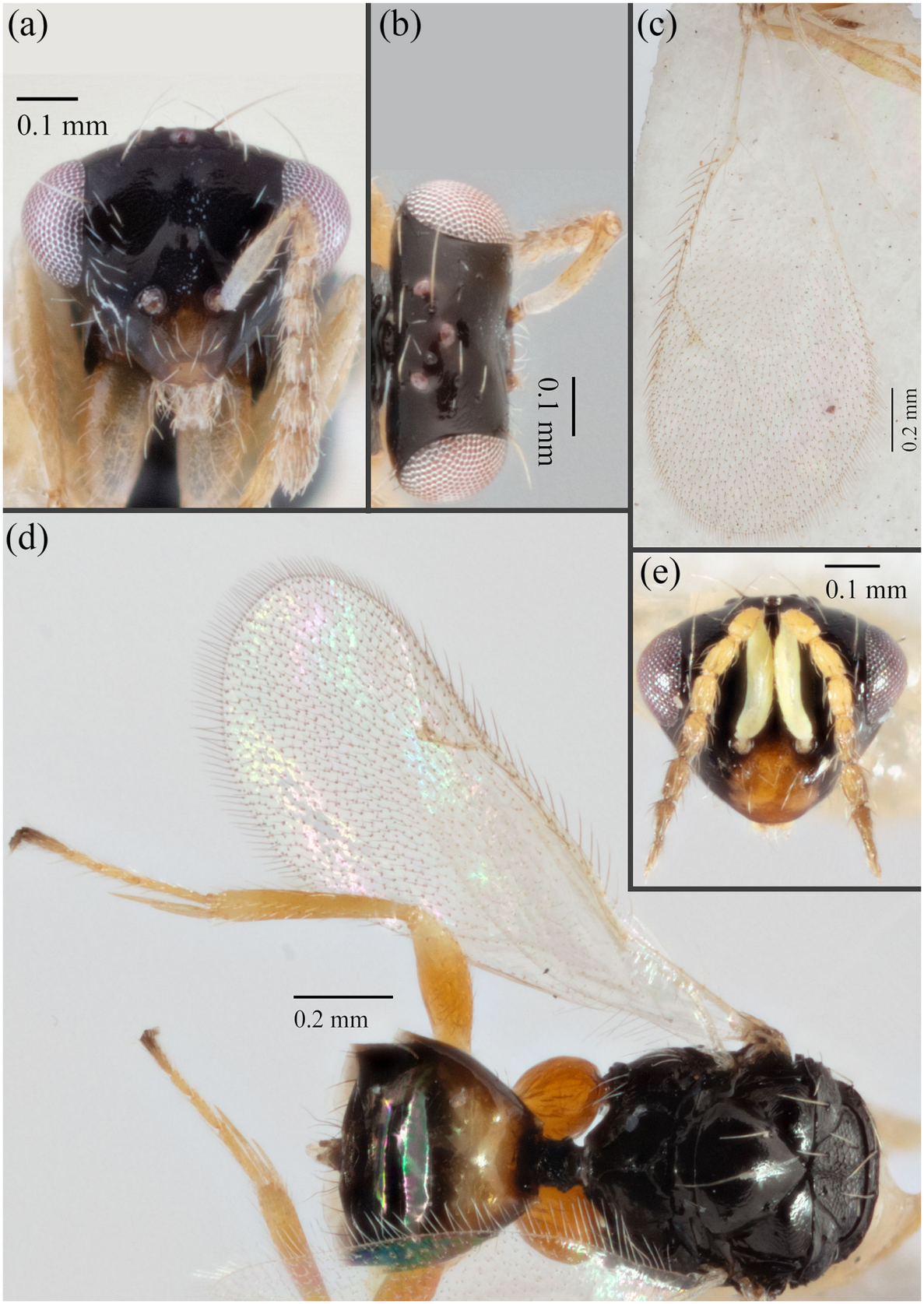


**FIGURE 3** *Euplectrus frugiperdata* sp. nov. (a) Holotype female anterior head. (b) Holotype female dorsal head. (c) Female (WAM: 116186) fore wing. (d) Male (WAM: 116197) dorsal habitus. (e) Male (WAM: 116197) anterior head.

viewed laterally (*E. manilae* has the eye length larger than the malar distance in the lateral head view).
- from *E. paribus* Zhu & Huang 2003 by having the gena black (*E. paribus* has the gena yellow).
- from *E. pullipes* Girault, 1915 by having the hind coxa honey-yellow (*E. pullipes* has the hind coxa darker, a mid-to-dark brown), and by having the median carina on the mesoscutum visible in the posterior third to half (*E. pullipes* does not have any trace of a median carina on the mesoscutum).
- from *E. xanthocephalus* Girault, 1913 by having the head mostly black (*E. xanthocephalus* has the head yellowish).
- *Euplectrus lutheri* Girault, 1924 appears to be the most superficially morphologically similar species amongst the currently described Australian species. From our examination of the syntype (which is missing a head), *Enchytraeina lutheri* has the abdomen darker than in *E. frugiperdata*. Whilst slight colour variation on the metasoma is not a particularly reliable character, without the head available of *E. lutheri* for morphological comparison, we believe it is justifiable to describe *E. frugiperdata* as a novel species with the understanding that future work (include the ability to extract genetic data from the syntype) may result in a synonymisation.

*Euplectrus frugiperdata* can be diagnosed from the other species of *Euplectrus* known from fall armyworm outside Australia as follows:

- from *E. laphygmae* Ferriere, 1941, reported from fall armyworm in Nigeria (Ogunfunmilayo et al. 2021) by having the gena black (*E. laphygmae* has the gena yellow).
- from *E. platyhypenae* Howard, 1885 reported from fall armyworm in Argentina (Murúa, Molina-Ochoa, & Fidalgo 2009) by having the median carina on the mesoscutum only strongly raised in the posterior third to half, the hind coxa yellowish and the clypeus with at least some yellow to reddish colouration (*E. platyhypenae* has the mesoscutum with the median carina strongly raised for the whole length, the hind coxa dark at base, and the head completely black).
- from *E. furnius* Walker, 1843 reported from fall armyworm in Brazil (Sturza et al. 2013) by the clypeus with at least some yellow or reddish colouration (*E. furnius* has the 'lower face black').
- *Euplectrus frugiperdata* appears to be morphologically similar to *E. comstockii*, reported to parasitise fall armyworm in laboratory experiments (Bultman et al., 1997) but (using the characters and measurements given in Hansson et al. (2015) and the images in Shauff & Janzen (2001)) *E. frugiperdata* has a much thinner groove anteriorly on the metascutellum (referred to as the dorsellum in the abovementioned studies).

## Description

Based on holotype female.

### *Female*

***Colour.*** Antennal scape white, rest of antenna pale yellow/brown (Figure 3a), head black other than clypeus and supraclypeal area which is yellowish brown (Figure 3a). Mesosoma black. Legs (including fore- and mid-coxae) pale yellowish, similar colour to antennae. Hind coxae only slightly darker, 'honey-yellow'. Metasoma dark brown posteriorly, anteriorly with paler, yellowish area dorsally (Figure 2b), darker around edges. Metasoma laterally and ventrally lightening from dark brown to yellowish (Figure 2a).

***Body length (not including head).*** 1.6 mm.

***Head.*** Triangular in anterior view; very smooth; POL = 0.14 mm; OOL = 0.09 mm; OD = 0.03 mm; HH = 0.45 mm; HE = 0.23 mm; MS = 0.23 mm; WF = 0.34 mm; scape length = 0.28 mm; scape width at widest point = 0.05 mm; pedicel length = 0.09 mm; F1 length = 0.09 mm; F2 length = 0.09 mm; F2 length / F2 width = 1.8; F3 length = 0.10 mm; F3 length/F3 width = 2.1.

***Mesosoma.*** Pronotum with strigose sculpturing. Mesoscutum with fine reticulate sculpturing (Figure 2b), median carina clear and raised in posterior third, only faintly visible as an indentation and slight change in sculpturing pattern (not a raised carina) on the anterior half of the mesoscutum. Mesoscutellar-axillar complex smoother than mesoscutum, lateral lobes with fine reticulate sculpturing, middle lobe with extremely fine reticulate sculpturing. Metanotum smooth with thin crenulate furrow between the mesoscutellar-axillar complex and the metanotum (~10 'pits'). Propodeum smooth with strong median carina, anteromedially with triangular 'cup' sensu Hansson et al. (2015). Hind tarsus (not including tarsal claws) 0.49 mm; longest hind tibial spur 0.26 mm.

***Metasoma.*** First metasomal tergite (petiole) length: 0.12 mm if measured from edge of propodeum, 0.10 mm if only sculptured area measured; first metasomal tergite width at widest point (i.e., from point to point of the flanges) = 0.12 mm; first metasoma tergite width at posterior margin = 0.10 mm. First metasomal tergite with a distinctive shape with flange-like broadened section anteriorly, irregularly but strongly sculptured. Remaining tergites smooth and shiny.

***Variation.*** Paler area on metasoma varying in size and shape. Paler area on clypeus and supraclypeal area

varying from almost non-existent (face almost completely black) to extensive yellowish to reddish-brown area (but never extending to gena or above the antennal foramen). Distinctiveness of median carina on the anterior half of the mesoscutum varying from non-existent to clearly visible due to changes in sculpturing or an indistinct line (but never a raised carina in the anterior half).

### *Male*

Scape broader than in female, and coloured supraclypeal area a brighter yellow, with edges more clearly defined.

## Remarks

No attempt has been made to diagnose the species against the fauna of other countries other than those listed above (where they are known from fall armyworm in other countries). Whilst this means there is a small chance of a synonymy being required in the future if the species is discovered to be cosmopolitan rather than endemic, we consider it critical to make a scientific name and sequence data available for the Australian fauna so that further biocontrol studies can be conducted. We examined the type material of the eleven Australian species described by Girault that are held in the QM, but for other species found in Australia we relied on the original descriptions, redescriptions and high-resolution images (Hansson et al. 2015; Zhu & Huang 2003) and images of the type specimens in the USNM (in the case of *Euplectrus manilae*). We compared the COI DNA barcodes to those available on BOLD, and the barcodes of *E. frugiperdata* are >10% divergent from any described species where DNA is available.

## Etymology

The species epithet relates to the known host, *S. frugiperda*.

## Distribution

Northern and central Western Australia, from maize crops in the Kununurra and Carnarvon regions. Despite rearing of *S. frugiperda* in other parts of the country, *E. frugiperdata* has not yet, to the best of our knowledge, been reared outside of Western Australia.

## Biology

Reared from larva of *S. frugiperda*. We have no evidence of *E. frugiperdata* being con-specific with *Euplectrus* from overseas, as it appears to be distinct from species reported from the host in other countries. As we are therefore assuming it is an endemic species that has been able to switch onto fall armyworm since its introduction, the host range of *E. frugiperdata* is likely to be broader than only *S. frugiperda*.

# Trichogrammatidae

## *Trichogramma pretiosum* Riley, 1879

(Figures 4a,b)

## Material examined

**Queensland:** bulk vial (>40 specimens); Gatton, −27.54 S, 152.33 E; 8 December 2020; M. Miles; reared from eggs of *S. frugiperda* on *Brassica* sp.; field code: FAW-39; BOLD (single specimen from bulk vial): FAW-CR19-FAW-39; QDPC: 0-178 517. Bulk vial (five specimens); Ayr Research Station, −19.61 S, 147.37 E; 21 December 2020; M. Miles; reared from eggs of *S. frugiperda* on maize; field code: FAW-52; BOLD (single specimen from bulk vial): FAW-CR30-FAW-52; QDPC: 0-178 518. Bulk vial (>20 specimens); collection data as previous; 17 December 2020; field code: FAW-54; BOLD (single specimen from bulk vial): FAW-CR32-FAW-54; QDPC: 0-178 519. **Western Australia:** bulk vial (originally two specimens, one destroyed for DNA extraction); Kununurra −15.65178, 128.71317; 7 September 2021; S. Adnan; reared from eggs of *S. frugiperda* on maize; field code: 101; BOLD (single specimen from bulk vial): FAW-CR101-101; QDPC: 0-178 515. bulk vial (originally two specimens, one damaged for DNA extraction); collection data as previous; field code: 102; BOLD (single specimen from bulk vial): FAW-CR102-102; QDPC: 0-178 516.

## Remarks

COI DNA barcodes of the specimens listed above are extremely similar (identical or <1% divergent) from sequences identified as *T. pretiosum* on BOLD, including specimens from the United States, Mexico and Brazil. The sequences of specimens from Australia fall into the BIN BOLD:ADY5798.

## Biology and distribution

*Trichogramma pretiosum* has been reared from eggs of *S. frugiperda* in *Brassica* spp., corn and maize crops in both northern and southern Queensland and northern Western Australia. *Trichogramma pretiosum* was originally described from specimens reared from cotton worm, *Alabama argillacea* (Hübner), in the USA, but is now widespread across the globe. The species has been used as a commercial

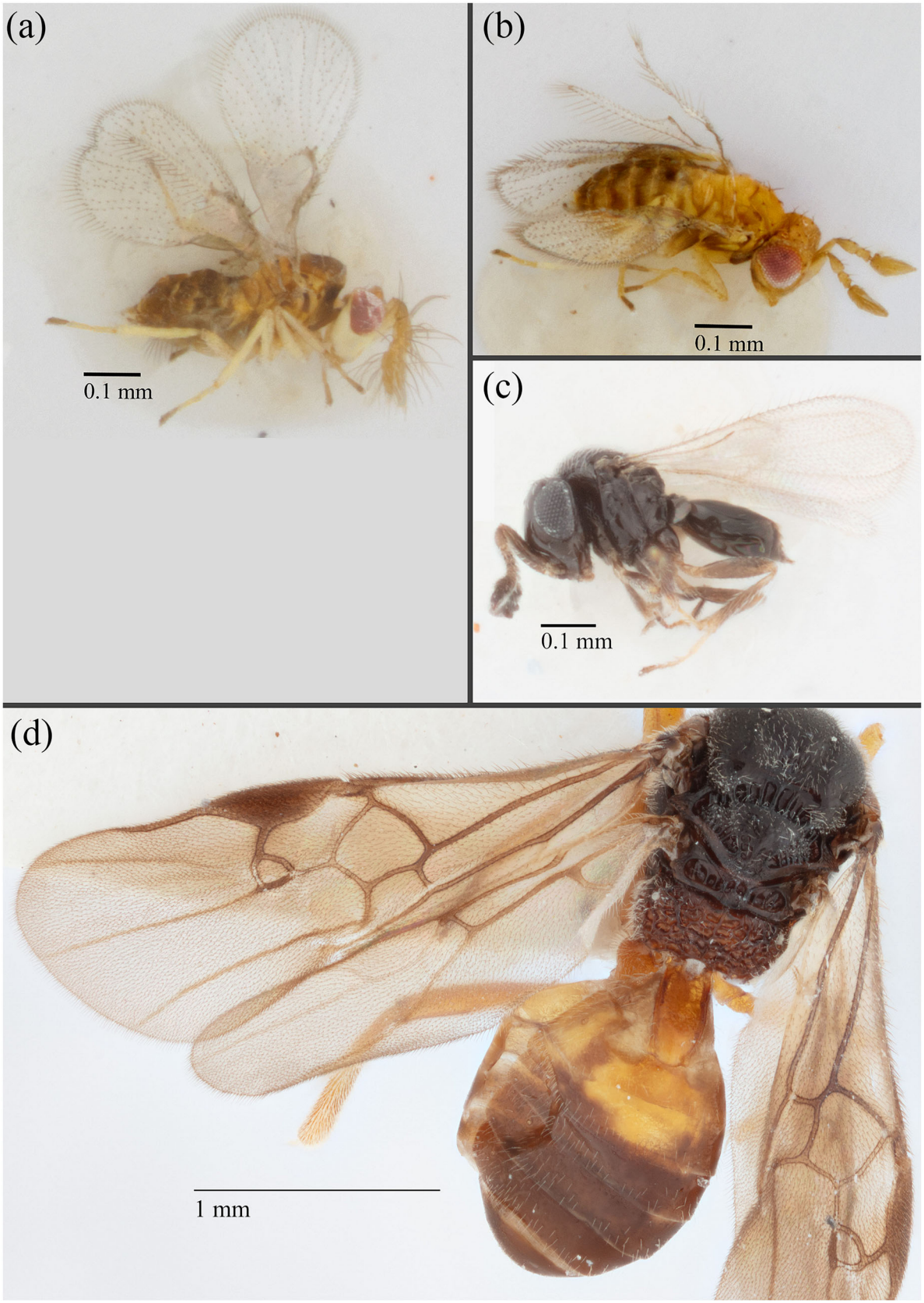


**FIGURE 4** (a) *Trichogramma pretiosum* male lateral habitus. (b) *Trichogramma pretiosum* female habitus. (c) *Telenomus remus* lateral habitus. (d) *Microplitis abrs* (FAW-1) dorsal habitus and wings.

biological control agent for many lepidopteran species and has been reared from *S. frugiperda* in several countries including Brazil (de Lourdes Corrêa Figueiredo et al. 2015), Mexico (Jaraleño-Teniente et al. 2020) and several countries in Africa (Kenis et al. 2019). *Trichogramma pretiosum* was introduced to northern Western Australia in the 1970s (Michael & Woods 1978, 1980, cited in Davies & Zalucki 2008) but is now found throughout northern Australia (Davies & Zalucki 2008) and is sold by Australian integrated pest management companies for use against noctuid, pyralid and plutellid moth pests.

## Hymenoptera: Platygastroidea

## Scelionidae

### *Telenomus remus* (Nixon, 1937)

(Figure 4c)

## Material examined

**Northern Territory:** 2♀; Coastal Plains; −12.58769, 131.31275; 23–24 June 2021; F. P. Tadle; reared from *S. frugiperda* eggs in sweet corn; sentinel eggs deployed in organic farm; field code: DITT-NT 04; BOLD: FAW-CR72-DITT-NT-04 (from co-reared specimen); QDPC: 0-178 510, 0-178 511.

## Identification

COI DNA barcodes of a specimen co-reared with that listed above are <1% divergent from specimens identified as *T. remus* on BOLD (e.g., GBAH9862-15 from Ecuador and GBAH9861-15 from the USA). Specimens were also compared with the images of the holotype of *T. remus* available in Liao et al. (2019) and the images of specimens reared from *S. frugiperda* in Brazil available in Wengrat et al. (2021).

## Biology and distribution

*Telenomus remus* has been reared from eggs of *S. frugiperda* in the Northern Territory. Specimens of *Telenomus* (not identified to species level) have also been reared from *S. frugiperda* in southern Queensland. *Telenomus remus* was originally described from specimens reared from *Spodoptera* spp. in Malaysia (Nixon 1937), and was introduced to Australia for use against noctuid pests (Michael et al. 1984). The species is either being used or investigated as a control agent of *S. frugiperda* in many other parts of the world (Coromoto Colmenarez et al. 2022; Pomari et al. 2013).

## Hymenoptera: Ichneumonoidea

## Braconidae: Agathidinae

### *Coccygidium* Saussure, 1892

*Coccygidium* Saussure, 1892: 15.

**Type species:** *Coccygidium luteum* (Brullé, 1846), by monotypy.

For full list of synonymies and references, see detailed list in Stevens, Austin, & Jennings (2010).

### *Coccygidium necatrix* Atkin-Zaldivar & Fagan-Jeffries, sp. nov.

(Figures 5 and 6)
https://zoobank.org/urn:lsid:zoobank.org:act:4B7BCC7F-05CF-47EB-9711-2B174C488A87

## Material examined

### *Holotype*

♀; Queensland; Ayr Research Station; −19.61, 147.37; 30 November 2020; M. Miles; reared from larva of *S. frugiperda* on sorghum; unsprayed trial plot; field code: FAW-48; BOLD: FAW-FAW48A-FAW48; QM: T260055.

### *Paratypes*

**Queensland:** ♀; same collection data as holotype; BOLD: FAW-CR27-FAW48; QM: T260053. ♀; as previous; BOLD: FAW-FAW48B-FAW48; QM: T260056. ♀; as previous; BOLD: FAW-FAW48C-FAW48; QM: T260057. ♂; as previous; BOLD: FAW-FAW48D-FAW48; QM: T260058. ♂; Bowen; −20.007, 148.194; 3 January 2021; S. Subramaniam; reared from *S. frugiperda* larva on sorghum; unsprayed blocks; field code: BO-08-2022; BOLD: FAW-CR97-BO-08-2022; QM: T260054. ♂; collection data as previous; field code: BO-09-2022; QM: T260059. ♀; as previous; field code: BO-10-2022; QM: T260060. ♀; collection data as previous except 14 October 2021; sweetcorn; sprayed blocks; field code BO-31-2022; QM T260063. ♀; collection data as previous except 17 May 2021; field code BO-33-2022; QM T260062. ♀; as previous except 14 October 2021; field code BO-50-2022; QM T260061. ♂; Charters Towers; −20.05764, 146.27211; 22–29 March 2022; Columba Catholic College students; Malaise trap; BOLD: ASMII072-22; QM: T260064. ♀; Lockwood Rd, Mareeba; −17.06, 145.46; 24 August 2021; C. MacDonald; reared from *S. frugiperda* larva on maize; volunteer plants after harvest; field code: T1D4; QDPC: 0-178 484.

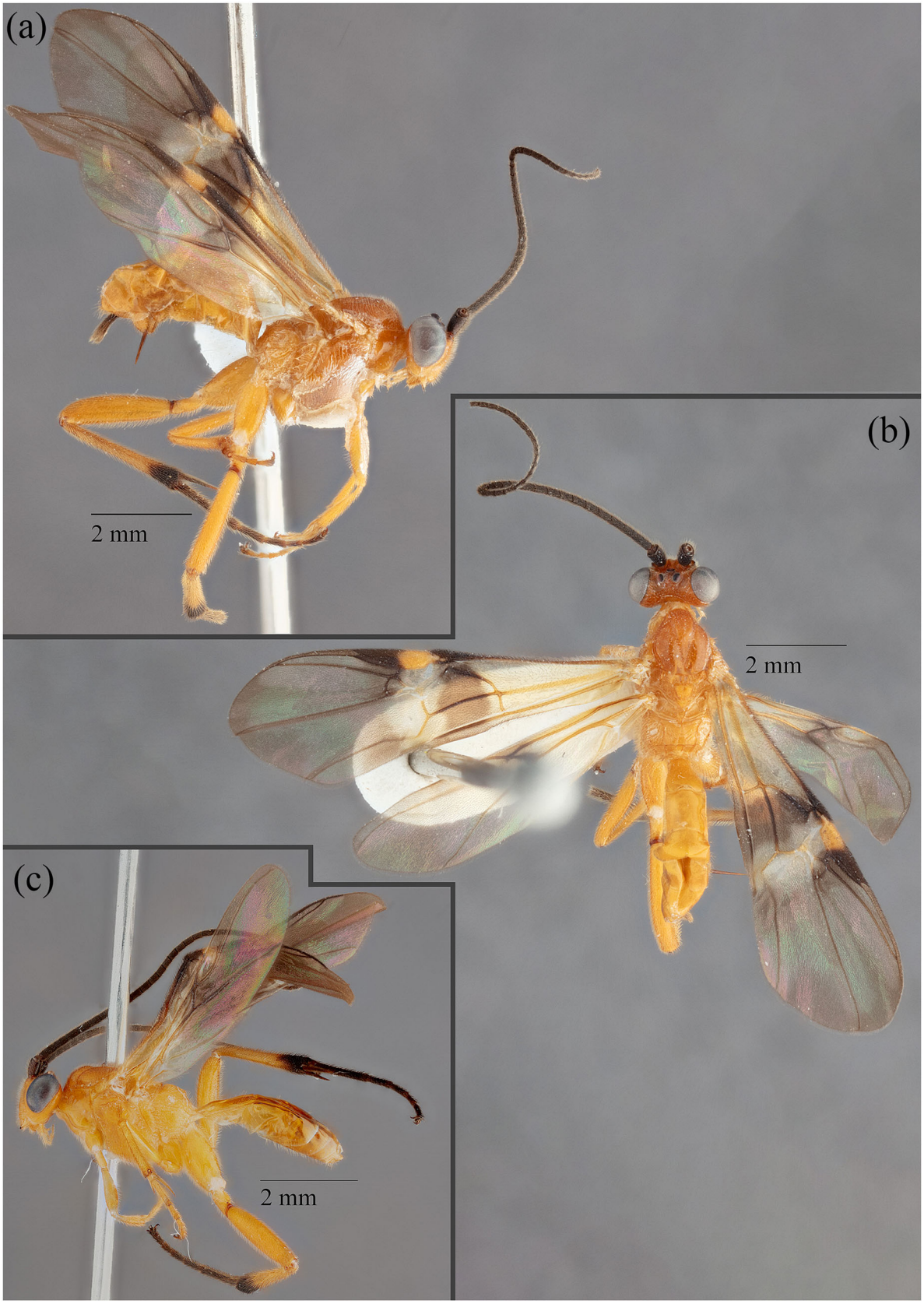


**FIGURE 5** *Coccygidium necatrix* sp. nov. (a) Holotype, lateral habitus. (b) Holotype, dorsal habitus. (c) Male (QM: T260058) lateral habitus.

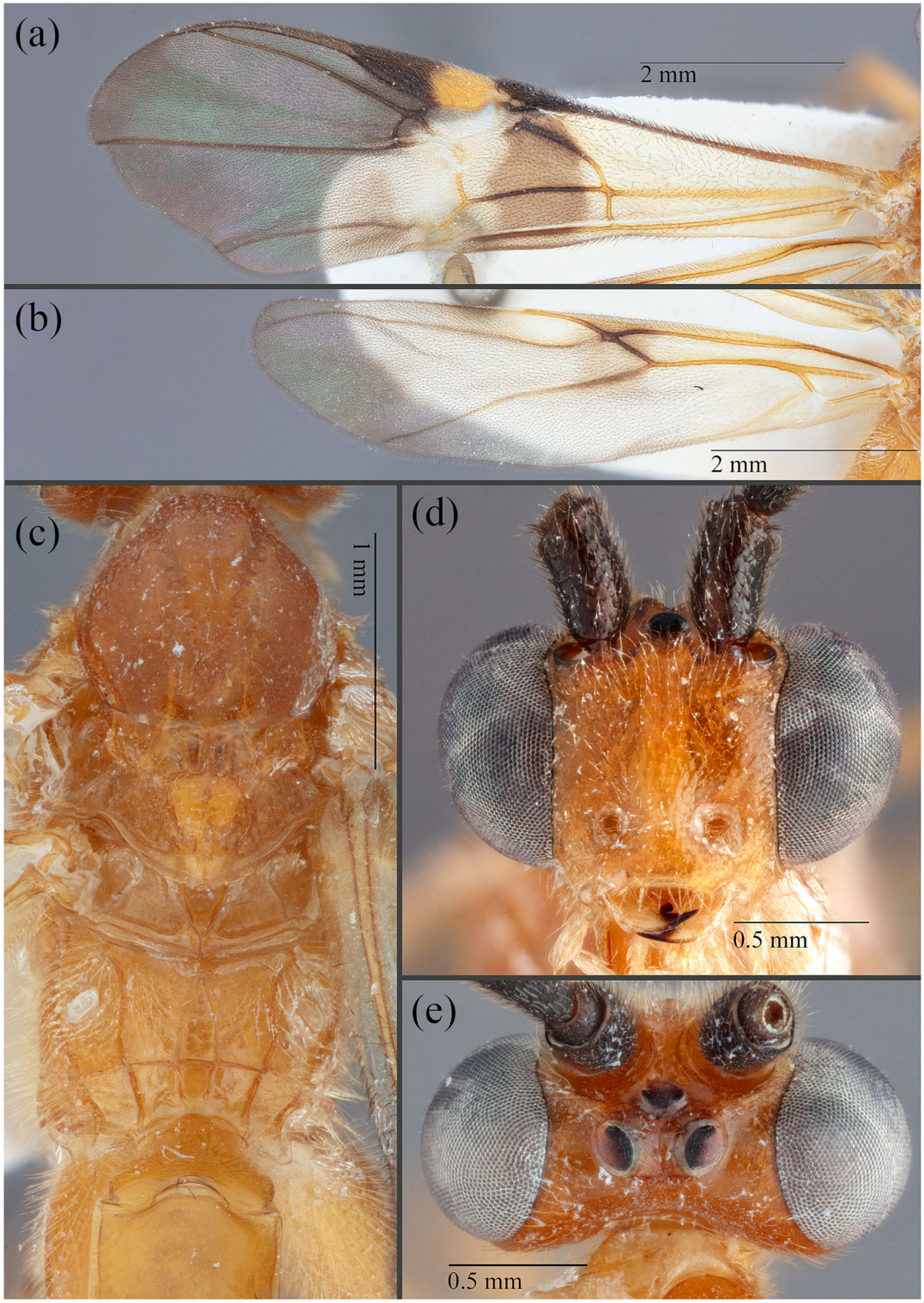


**FIGURE 6** Coccygidium necatrix sp. nov. holotype. (a) Fore wing. (b) Hind wing. (c) Dorsal mesosoma. (d) Anterior head. (e) Dorsal head.

## *Other material*

We include the following specimens in *C. necatrix* as they have COI barcodes 0%–2% divergent from the barcode of the holotype, and agree in coarse morphology. However, the pale area on the pterostigma is much lighter, sometimes pure white, and in some specimens the lateral metasoma and dorsal T1–2 are also bright white. We believe these are likely to be population level colour differences, but do not include the specimens in the

paratype series and recommend further genomic and morphological studies are conducted to confirm the species boundaries within *Coccygidium*.

**Western Australia:** ♀; Charnley River Artesian Range Wildlife Sanctuary, Wilinggin Country, edge of Lake Doherty; −16.5084, 125.2508; 454 m; 25 July 2022; 9:40 am; E.P. Fagan-Jeffries; Swept vegetation; Bush Blitz West Kimberley; BOLD: AUHYM033-22; WAM: 116173. ♀; collection data as previous; BOLD: AUHYM036-22; WAM: 116174. ♀; Charnley River Artesian Range Wildlife Sanctuary, Wilinggin Country, near homestead; −16.7165, 125.4607; 404 m; 26 July 2022; 9:00 pm; E.P. Fagan-Jeffries; LepiLED (to light sheet); Bush Blitz West Kimberley; BOLD: AUHYM042-22; WAM: 116175. ♀; collection data as previous except: 22 July 2022; 6:10 pm; BOLD: AUHYM043-22; WAM: 116176. ♀; Charnley River Artesian Range Wildlife Sanctuary, Wilinggin Country, near homestead; −16.7168, 125.4604; 403 m; 20–27 July 2022; E.P. Fagan-Jeffries, M.S. Harvey, J.D. Wilson, Malaise trap over water; Bush Blitz West Kimberley; BOLD: AUHYM092-22; WAM: 116177.

## Diagnosis

*Coccygidium necatrix* can be easily separated from the three species of *Coccygidium* reared from *S. frugiperda* around the globe (*C. transcaspicum* Kokujev, 1902, *C. melleum* (Roman, 1910) and *C. luteum* (Brullé, 1846)) and from *C. mellosiheroine* sp. nov. by the yellow markings on the pterostigma and fore wing, which are not present in any of the four species listed above. *Coccygidium necatrix* can be separated from an undescribed morphologically similar species of *Coccygidium* that overlaps in distribution, but has not yet been reared from *S. frugiperda*, by the fore wing r vein dark (the fore wing r vein is yellow in the three specimens available of the undescribed species).

## Description

Based on female holotype.

### *Female*

***Colour.*** Head honey-yellow, antennae uniformly dark brown; mesosoma honey-yellow; fore and mid legs honey-yellow, hind legs honey-yellow with distal third of hind tibia and hind tarsus dark brown (Figure 5a); fore wing with alternating dark and yellowish banding as in Figure 6a; metasoma honey-yellow; proximal end of ovipositor sheaths dark brown, distal end of sheaths honey-yellow.

***Body length.*** 8.4 mm.

***Head length in lateral view.*** 1.0 mm; head width in anterior view: 1.8 mm; minimum distance between eyes in anterior view: 0.8 mm; malar distance: 0.20 mm; POL: 0.13 mm; OOL: 0.19 mm; OD: 0.16 mm; number of flagellomeres: 39; F1 length/width ratio (l/w): 2.4; F3 l/w: 1.9; F4 l/w: 2.2; penultimate flagellomere 1/w: 1.8; apical flagellomere length: 0.16 mm. Face reasonably smooth, evenly setose.

***Mesosoma length.*** 2.7 mm. Fore wing length: 7.4 mm. Hind tibia length: 2.3 mm; longest hind tibial spur length: 1.0 mm; hind basitarsus length: 1.4. Mesoscutum smooth, setose with complete notauli.

***Metasoma length.*** 4.7 mm; T1 length in dorsal view: 1.0 mm; T1 width at the posterior margin: 0.6 mm; T1 widening significantly towards posterior margin, smooth and densely setose along margins but very sparsely setose on dorsal surface; extruded part of ovipositor sheath length (measured in lateral view from apex of hypopygium): 0.70 mm; ovipositor sheaths densely setose for the entire length.

***Variation.*** All paratypes except one have a fully honey-yellow metasoma, the metasoma on one paratype (QDPC: 0-178 484) is honey-yellow proximally but becomes dark brown distally. In two female specimens (that do not have COI DNA barcodes) the head is much darker, almost black. Measurement variation (only these characters measured on three female paratypes [QDPC: 0-178 484, QM: T260056, QM: T260053, QM: T260058], other characters in description not measured on paratypes): body length: 7.1–7.6 mm; head length in lateral view: 0.8 mm; number of flagellomeres 42–45; mesosoma length: 2.6–2.8 mm; fore wing length: 6.5–7.1 mm; metasoma length: 3.6–4.7 mm; T1 length in dorsal view: 1.0–1.3 mm; T1 width at posterior margin: 0.5–0.6 mm.

### *Male*

As female, with both colour and measurement variation within the range of female variation.

## Remarks

At the time of writing, this species forms the BIN BOLD:AAH2023. Along with the specimens listed in the material examined, this BIN includes two specimens from the Northern Territory collected in 1997 and 2001, and two specimens from Queensland collected in 2009 and 2010. Whilst we have not examined these specimens, the COI barcodes only differ by 1–3 base pairs. As these specimens predate the entry of *S. frugiperda* into Australia, it strengthens the hypothesis that *C. necatrix* is native and has been able to broaden its host range to fall armyworm.

We have documented a morphologically similar species in Queensland through the *Insect Investigators* project (BIN BOLD:AEU2745) which is currently only known from three specimens collected in Malaise traps by Columba

Catholic College students and Glenden State School students. This undescribed species has a very distinct COI DNA barcode to *C. necatrix*, but as we have not yet studied the species in depth, we do not describe it here. We only include mention of it to note that there is more than one species of *Coccygidium* in Australia with yellow and dark wing banding, and that the species collected in *Insect Investigators* can be diagnosed from *C. necatrix* by the colour of the fore wing r vein.

## Etymology

During the collaborative naming process of *C. mellosiheroine* with the schools who collected specimens during the citizen science project *Insect Investigators* (see etymology section of *C. mellosiheroine*), the idea of the wasp being an 'assassin' of fall armyworm was a common theme. The species epithet chosen by the authors for this species, *necatrix*, is based on the Latin word for slayer or murderess and was inspired by the suggestions from the school students during this collaborative naming process.

## Distribution

*Coccygidium necatrix* is known from Queensland, northern Western Australia and (based currently only on COI DNA sequences) from the Northern Territory.

## *Coccygidium mellosiheroine* Atkin-Zaldivar & Fagan-Jeffries, sp. nov.

(Figures 7 and 8)
https://zoobank.org/urn:lsid:zoobank.org:act: E82C1A03-5936-4229-87B3-F03FE3EAC7E1.

## Material examined

### *Holotype*

♀; Queensland; Lockwood Rd, Mareeba; −17.06, 145.46; 24 August 2021; C. MacDonald; reared from *S. frugiperda* larva on maize; volunteer plants after harvest; field code: T2D2; BOLD: FAW-CR86-T2D2; QM: T260032.

### *Paratypes*

**Queensland:** ♀; collection data as holotype; field code: T3B2; BOLD: FAW-CR83-T3B2; QM: T260030. ♂; collection data as previous; field code: T2B5; BOLD: FAW-CR84-T2B5; QM: T260031. ♂; collection data as previous; field code: T1A8; BOLD: FAW-CR85-T1A8; QDPC: 0-178 478. ♀; collection data as previous; field code: T3D1; QDPC: 0-178 480. ♀; collection data as previous; field code: T1D8; QDPC: 0-178 481. ♀; collection data as previous; field code: T2A2; QDPC: 0-178 482. ♀; collection data as previous; field code: T2A7; QDPC: 0-178 483. ♀; collection data as previous; field code: T2C6; QM: T260034. ♀; collection data as previous; field code: T1A4; QM: T260035. ♀; collection data as previous; field code: T2A4; QM: T260036. ♂; collection data as previous; field code: T1B1; QM: T260037. ♀; Ayr Research Station; −19.61, 147.37; 22 December 2020; A. Quade; reared from *S. frugiperda* larva on corn; unsprayed trial plot; field code FAW-53; BOLD: FAW-CR31-FAW53; QM: T260029. ♀; Gatton; 3 March 2023; M. Miles; reared from *S. frugiperda* larva on maize; trial plot; field code: FAW2241; BOLD: FAW-CRM15-FAW2241; QM: T260033. ♀; collection data as previous; BOLD: FAW-CRM16-FAW2241; QDPC: 0-178 479. ♀; Bowen; −20.007, 148.194; 4 May 2021; S. Subramaniam; reared from *S. frugiperda* in sweetcorn on sprayed blocks; field code: BO-34-2022; QM: T260038 (in ethanol). ♂; collection data as previous except 14 October 2021; field code: BO-35-2022; QM: T260039 (in ethanol). ♂; collection data as previous except 23 June 2021; V. Sivasubramaniam; field code: BO-32-2022; QM: T260040 (in ethanol). ♂; Charters Towers; −20.05764, 146.27211; 1–8 March 2022; Columba Catholic College students; Malaise trap; BOLD ASMII015-22; QM: T260041. ♂; collection data as previous except: dates 8–15 March 2022, BOLD: ASMII048-22; QM: T260042. ♂; as previous except: dates 22–29 March 2022; BOLD ASMII074-22; QM: T260043. ♂; Springsure; −24.11508, 148.08658; 15–22 March 2022; Springsure State School students; Malaise trap; BOLD ASMII132-22; QM: T260044. ♂; Yeppoon; −23.13496, 150.73139; 1–8 March 2022; Yeppoon State High School students; Malaise trap; BOLD ASMII1371-22; QM: T260045. ♀; Yeronga; −27.5192027, 153.0218222; 22–29 March 2022; Yeronga State School students; Malaise trap; BOLD: ASMII2311-22; QM: T260046. ♂, collection data as previous except: dates 1–8 March 2022; BOLD ASMII2325-22; QM: T260047. ♂, Kogan; −27.03796, 150.75682; 22–29 March 2022; Kogan State School students; Malaise trap; BOLD ASMII4409-22; QM: T260048. ♂, collection data as previous; BOLD: ASMII4410-22; QM: T260049. ♂; collection data as previous; BOLD ASMII4417-22; QM: T260050. ♂; Prospect, −24.41964, 150.43007; 22 March - 1 April 2022; Prospect Creek State School students; Malaise trap; BOLD ASMII7392-22; QM: T260051. ♂; collection data as previous; BOLD ASMII7393-22; QM: T260052. **Western Australia:** ♀; Kununarra; 15°28′01.1″S 128°51′01.2″E; 8 October 2021; S. Adnan; reared from *S. frugiperda* on maize; field code: 114; BOLD: FAW-CR114-114; QM: T260028 (in ethanol – specimen broken).

## Diagnosis

*Coccygidium mellosiheroine* can be diagnosed from *C. necatrix* by the absence of a yellow or pale patch on the pterostigma, and the absence of yellow/pale fore

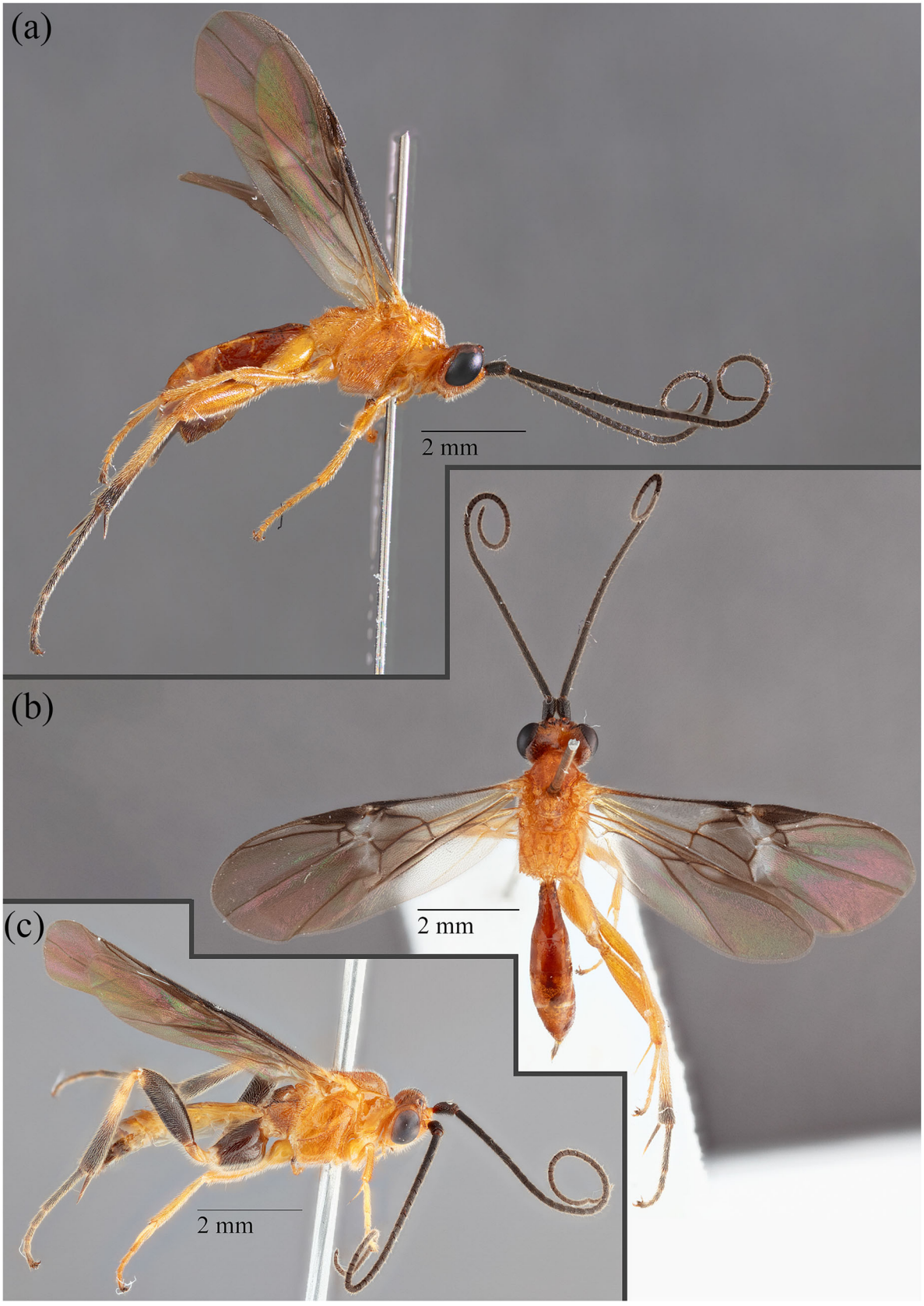


**FIGURE 7** *Coccygidium mellosiheroine* sp. nov. (a) Holotype, lateral habitus. (b) Holotype, dorsal habitus. (c) Male (QM: T260041) lateral habitus.

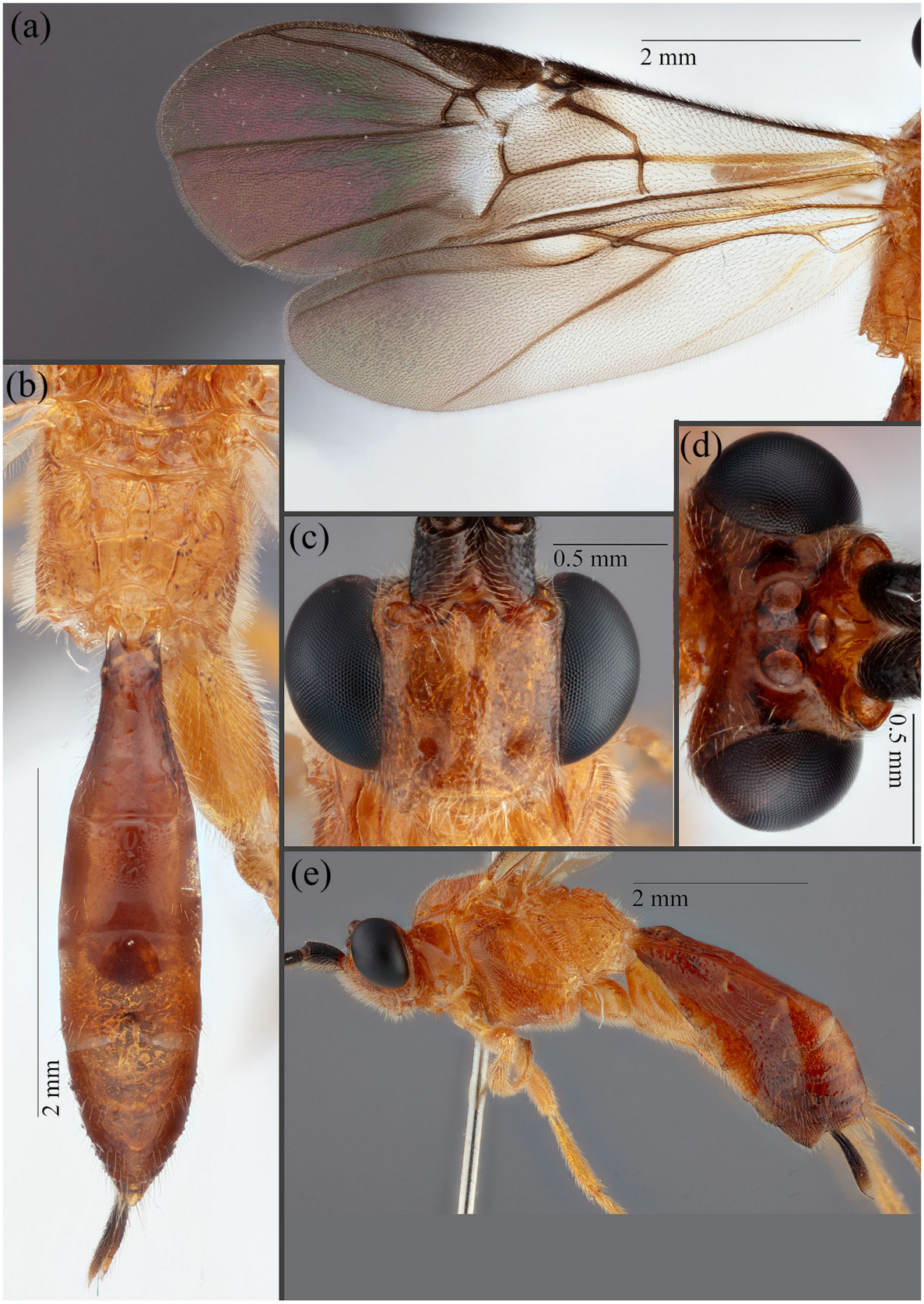


**FIGURE 8** *Coccygidium mellosiheroine* sp. nov. holotype. (a) Fore wing and hind wing. (b) Dorsal mesosoma. (c) Anterior head. (d) Dorsal head. (e) Lateral habitus.

wing banding. *Coccygidium mellosiheroine* can be diagnosed from the described species of *Coccygidium* that are known from *S. frugiperda* outside of Australia as follows:

- From *C. transcaspicum* Kokujev, 1902 and *C. melleum* (Roman, 1910) known from fall armyworm in India (Gupta et al. 2020; Sharanabasappa et al. 2019) by a very clearly differentiated dark area on the apical half of the hind tibia (both species listed above have at most a slightly different colour on the apical half of the hind tibia). Description and images in Gupta et al. (2020) used as reference for *C. transcaspicum*, and image of reared specimen provided in Sharanabasappa et al. (2019) used as reference for *C. melleum*.
- From *C. luteum* (Brullé, 1846) reared from fall armyworm throughout Africa (Agboyi et al. 2020; Otim et al. 2021) most easily by COI DNA barcodes, which differ by >4% and form distinctly different clades on a phylogeny (Figure S1).

## Description

### *Female*

***Colour.*** Head honey-yellow with darker area posteriorly; antennae uniformly dark brown; mesosoma honey-yellow; fore- and mid- legs completely honey-yellow, similar colour to mesosoma, hind legs honey-yellow other than distal end of hind tibia and all of the hind tarsus which is significantly darker (dark brown) than the rest of the tibia; fore wing tinged dark brown particularly at distal end, fore wing veins in proximal third of wing yellowish but transitioning to dark brown (Figure 8a), with most of the wing veins and the pterostigma uniformly dark brown; metasoma darker than mesosoma, light brown; ovipositor sheaths dark brown.

***Body length.*** 6.6 mm.

***Head length in lateral view.*** 0.8 mm; head width in anterior view: 1.6 mm; minimum distance between eyes in anterior view: 0.8 mm; eye height in anterior view: 0.8 mm; malar distance: 0.21 mm; POL: 0.14; OOL: 0.18; OD: 0.19; number of flagellomeres: 41; F1 length/width ratio (l/w): 2.5; F3 l/w: 2.5; F4 l/w: 2.3: penultimate flagellomere l/w: 1.3; apical flagellomere length: 0.14 mm. Face reasonably smooth, evenly setose.

***Mesosoma length.*** 2.5 mm. Fore wing length: 6.4 mm. Hind tibia length: 2.2 mm; longest hind tibial spur length: 0.8 mm; hind basitarsus length: 1.3 mm. Mesoscutum smooth, setose with complete notauli; propodeum smooth with raised pattern of carina (Figure 8b).

***Metasoma length.*** 3.3 mm; T1 length in dorsal view 1.2 mm; T1 width at posterior margin 0.6 mm; T1 widening significantly towards posterior margin, smooth, setose along margins but less so on dorsal surface; extruded part of ovipositor sheath length (measured in lateral view from apex of hypopygium): 0.82 mm; ovipositor sheaths densely setose for entire length.

***Variation.*** Many paratypes have the metasoma the same colour as the mesosoma anteriorly and then darkening towards the posterior apex. One paratype (FAW-53) has metasoma the same colour as mesosoma for the entire length. Measurement variation (only these characters measured on three female paratypes [FAW-53, T3B2, FAW2241(CRM15)], other characters in description not measured on paratypes): body length 6.3–6.7 mm; head length in lateral view: 0.7–0.8 mm; number of flagellomeres 40–41 (two paratypes with 40, one with 41); mesosoma length 2.3–2.6 mm; fore wing length: 4.9–6.4 mm; metasoma length 2.3–3.0 mm; T1 length in dorsal view 1.0 mm; T1 width at posterior margin: 0.4–0.6 mm.

### *Male*

As female except three of the four specimens where we have DNA barcoding data (and all of the males for which we do not) have the hind coxa and hind femur entirely dark brown and a larger proportion of the hind tibia dark brown (e.g., Figure 7c).

## Remarks

This species currently forms the BIN BOLD:ADT0259. The most closely related species with molecular data available on BOLD is *C. necatrix*, also known from *S. frugiperda* in Australia and with overlapping distributions, however the two species are easily morphologically identifiable by the wing banding patterns.

## Etymology

This species was named in collaboration with four of the schools who collected specimens in their Malaise trap during the citizen science project *Insect Investigators:* Prospect Creek State School, Kogan State School, Yeppoon State High School, and Yeronga State School. The school students were invited to suggest potential species names, and two of the common ideas concerned the wasp being 'honey-coloured' and the species being a 'knight/hero' for helping to fight fall armyworm. The species epithet *mellosiheroine* references the Latin mellosus (honey coloured) and heroine (female hero) and is a noun in apposition.

## Distribution

This species is broadly distributed across Queensland, and also known from a single specimen from northern Western Australia.

## Braconidae: Cheloninae

### *Chelonus* Panzer, 1806

*Chelonus* Panzer, 1806: 164.

**Type species:** *Ichneumon oculator* Fabricius, 1775 (by subsequent designation).

For treatment of the Australian taxa and relevant synonyms, see Kittel & Austin (2014).

### *Chelonus trojanus* Fagan-Jeffries, sp. nov.

(Figures 10 and 11)
https://zoobank.org/urn:lsid:zoobank.org:act:168290C1-3717-4390-A6F9-62BE707C3562

## Material examined

### *Holotype*

♀; Queensland; Bowen; −20.007, 148.194; 14 September 2021; V. Sivasubramaniam; reared from *S. frugiperda* larva on sweetcorn; spray blocks; field code: BO-21-2022; BOLD: FAW-CR123-BO-21-2022; QM: T260014.

### *Paratypes*

**Northern Territory:** ♂; Coastal Plains; 12°35′15.7″S 131°18′45.9″E; 11 August 2022; F.P. Tadle; reared from *S. frugiperda* larva on organically grown sweet corn plants; field code: DITT-NT-02; BOLD: FAW-CR72-DITT-NT-02; QM: T260018. ♀; collection data as previous except: field code: DITT-NT-03; BOLD: FAW-CR74-DITT-NT-03; QM: T260019. ♀; collection data as previous except: field code: DITT-NT-05; BOLD: FAW-CR75-DITT-NT-05; QM: T260020. **Queensland:** ♀; Charters Towers; −20.05764, 146.27211; 1–8 March 2022; Columba Catholic College students; Malaise trap; BOLD ASMII018-22; QM: T260024. ♀; collection data as previous; BOLD: ASMII017-22; QM: T260025. ♀; collection data as holotype except: 22 October 2021; field code: BO-15-2022; BOLD: FAW-CR111_22-BO-15-2022; QM: T260011. ♀; collection data as holotype except: 17 May 2021; field code: BO-16-2022; BOLD: FAW-CR118_22-BO-16-2022; QM: T260013 (in ethanol). ♂; collection data as previous except field code: BO-17-2022; BOLD: FAW-CR104_22-BO-17-2022; QM: T260008. ♂; collection data as holotype except 15 July 2021; field code: BO-19-2022; BOLD: FAW-CR115_22-BO-19-2022; QM: T260012 (in ethanol). ♀; collection data as holotype except 6 July 2021; field code: BO-20-2022; BOLD: FAW-CR129-BO-20-2022; QM: T260015 (in ethanol). ♂; collection data as holotype except 14 October 2021; field code: BO-23-2022; BOLD: FAW-CR110_22-BO-23-2022; QDPC: 0-178 475. ♂; collection data as holotype except 23 March 2021; field code: BO-24-2022; BOLD: FAW-CR108_22-BO-24-2022; QM: T260009 (ethanol). ♀; collection data as holotype except: 22 September 2021; reared from *S. frugiperda* larva collected as egg mass that was attended by *Chelonus* sp.; field code: BO-22-2022; QM: T260026. ♀; collection data as holotype except 23 March 2021; S. Subramaniam; field code: BO-01-2021; BOLD: FAW-CR66-BO-01-2021; QDPC: 0-178 476. ♀; collection data as holotype except: 4 August 2021; S. Subramaniam; adult wasp collected will attending egg mass of *S. frugiperda*; field code: BO-26-2022; BOLD: FAW-CR109_22-BO-26-2022; QM: T260010. ♀; collection data as previous except: −19.985, 148.227; 19 February 2021; adult wasp collected whilst attending *S. litura* eggs in moringa; field code: BO-04-2021; BOLD: FAW-CR64-BO-04-2021; QM: T260017. ♀; collection data as holotype except: 14 January 2022; J. Stanley; reared from *S. frugiperda* larva on sorghum; unsprayed cover crop; field code: BO-53-2022; QM T260027. ♀; collection data as holotype except: 7 December 2021; volunteer corn; field code: BO-06-2022; BOLD: FAW-CR95-BO-06-2022; QDPC: 0-178 477. ♂; collection data as previous except: 20 December 2021; reared from *S. frugiperda* larva, collected as egg mass; field code: BO-07-2022; BOLD: FAW-CR96-BO-07-2022; QM: T260023. ♂; Ayr; −19.55, 147.43; 28 June 2021; V. Sivasubramaniam; reared from *S. frugiperda* larva on sweet corn; sprayed crops; field code: BU-01-2022; BOLD: FAW-CR139-BU-01-2022; QM: T260016 (ethanol). ♂; Gatton; −27.54, 152.33; 25 January 2022; J. Duff; reared from *S. frugiperda* larva in sweet corn; field code: LV-03-2022; BOLD: FAW-CR93-LV-03-2022; QM: T260022. ♂; Kalbar; −27.84, 152.63; 12 February 2021; A. Quade; reared from larva of *S. frugiperda* on maize; field survey; field code: FAW-32; BOLD: FAW-CR03-FAW-32; QDPC 0-178 474. ♀; Walkamin Research Station; −17.13, 145.27; 26 August 2021; C. MacDonald; reared from *S. frugiperda* larva on maize; field code: T1D5; BOLD: FAW-CR82-T1D5; QM: T260021.

### *Other material*

The below specimen was a larva that was destructively sampled for DNA but is included as it broadens the distribution of the species and is linked to a COI DNA barcode.

**Queensland:** Larva; Mareeba; −17.00, 145.43; 31 May 2021; C. MacDonald; reared from *S. frugiperda* larva on maize; BOLD: FAW-CR67.

## Diagnosis

*Chelonus trojanus* can be easily separated from any of the introduced or native species of *Chelonus* currently described from Australia by the presence of the two white oval areas in the lateral anterior of the dorsal metasoma (Figure 10b,c). This is present (in varying degrees) in all of the specimens examined, but is significantly reduced in some female specimens. For the sake of these specimens, we also diagnose

*Chelonus trojanus* against the species found in Australia that have a completely black dorsal metasoma.
*Chelonus trojanus* can be diagnosed from:

- *Chelonus rufipes* Szépligeti, 1900 and *Chelonus victoriensis* Shenefelt, 1973 by the absence of a posterior metasomal pit (referred to by some authors as an apical foramen) in the male.
- *Chelonus scrobiculatus* Szépligeti, 1900 and *Chelonus phthorimaeae* Gahan, 1917 by the female having >20 flagellomeres (these two species have the female with 16 antennal segments).

*Chelonus trojanus* can be diagnosed from the following species of *Chelonus* reared from *S. frugiperda* outside of Australia:

- From *C. cautus* Cresson, 1872 (reared from *S. frugiperda* in Mexico (Gutiérrez-Ramírez et al. 2015), *C. curvimaculatus* Cameron, 1906 (reared from *S. frugiperda* in Kenya and Zambia (several records, collated in Li et al. 2023), and from *C.* nr *blackburni* (sensu rearing record from India and figure in Sagar et al., (2022), by not having a solid white band in the anterior quarter of the metasoma.
- From *C. antillarum* Marshall 1885 (reared from *S. frugiperda* in Barbados and Nicaragua (Molina-Ochoa et al. 2004) by fore wing vein 2-SR being approximately 1.3 × longer than vein 3-SR; in *C. antellarum*, 2-SR is almost 2 × longer than 3-SR (based on specimens in the Waite Insect and Nematode Collection, reared from *Spodoptera* sp. in peanut crops in St Kitts, identified as *C. antillarum* by A. Austin in 1983).
- From *C. obscuratus* Herrich-Schaeffer, 1838 (reported by Youssef, (2021) as being reared from *S. frugiperda* in Egypt as *C. intermedius* Thomson, despite synonomy by Papp (1997)) by the female having 26 flagellomeres; *C. obscuratus*, as stated in Papp (1997), has 23 antennomeres (presumably therefore only 21 flagellomeres).
- From *C. munakatae* Munakata, 1912 (reported from *S. frugiperda* in China by (Fen et al., (2019) by the antennae of the female having only 26 flagellomeres; whilst we have not been able to examine the type series, nor the specimens identified using morphology as *C. munakatae* by Fen et al. (2019), we use the summary provided in Watanabe (1932), which states that the antennae of the female are 33–34 jointed.

It appears that there is a group of *Chelonus* species reared from *S. frugiperda* across the world, that all have the metasoma black with pale sections anterolaterally. This species group will require a dedicated project to determine the morphological differences amongst the species, and provide accurate identification materials, including COI DNA barcodes, for applied entomologists. We therefore prefer to use DNA diagnoses when available, and we do not diagnose *C. trojanus* against all of these species (listed below) using morphology. *Chelonus trojanus* can be separated from the following species through COI DNA barcoding, by examining the clade to which the sequence belongs in a phylogeny (Figure 9). Rearing records listed below are as collated in Li et al. (2023).

- *Chelonus bifoveolatus* Szepligeti, 1914 (reared from *S. frugiperda* in Benin, Burkina, China, Faso, Ghana, Senegal, Uganda, and Zambia)
- *Chelonus formosanus* Sonan, 1932 (reared from *S. frugiperda* in China and India)
- *Chelonus insularis* Cresson, 1865 (reared from *S. frugiperda* in Colombia and Mexico)
- *Chelonus sonorensis* Cameron, 1887 (recorded from *S. frugiperda* in Mexico)

## Description

### *Female*

***Colour.*** Fore, mid and hind femur brown; fore and mid tibia slightly paler than femur, hind tibia pale proximally, darkening to dark brown at mid-point to distal margin; tarsi on all legs brown, darkening distally (Figure 10a). Fore wing veins yellow to dark brown, darkening distally (Figure 10b). Dorsal metasoma black with pale, often semicircle shaped areas at the lateral margin in the anterior half of the carapace (Figure 10a,b). Rest of body black.

***Body length (including head; measured in dorsal view).*** 5.8 mm.

***Head length in lateral view (longest measurement).*** 0.87 mm; head length in dorsal view: 0.76 mm; head width in anterior view: 1.7 mm; minimum distance between eyes in anterior view: 1.0 mm; eye height in anterior view: 0.67 mm; malar distance: 0.34 mm; POL: 0.23 mm; OOL: 0.32 mm; OD: 0.10 mm; area around ocelli slightly raised; number of flagellomeres: 25; F1 length/width ratio (l/w): 3.7; penultimate flagellomere length/width ratio (l/w): 1.2; apical flagellomere length: 0.9 mm; face strongly sculptured and densely setose, with a vertical carina running between the antennal sockets that reaches half way to the clypeus (Figure 11b).

***Mesosoma length (measured in dorsal view).*** 2.2 mm. Fore wing length: 4.3 mm. Hind tibia length: 1.3 mm; longest hind tibial spur length: 0.26 mm; hind basitarsus length: 0.5 mm. Mesoscutum, scutellar disk and propodeum strongly reticulate rugose.

***Metasoma length (measured in dorsal view).*** 2.8 mm; metasoma width at widest point 1.8 mm. Ovipositor sheaths extruding 0.26 mm from margin of hypopygium, slightly bulbous at distal end before narrowing to a point, with several short setae clustered at apex.

***Variation.*** Flagellomere number varies from 23 to 26 in the eight available female paratype specimens with unbroken

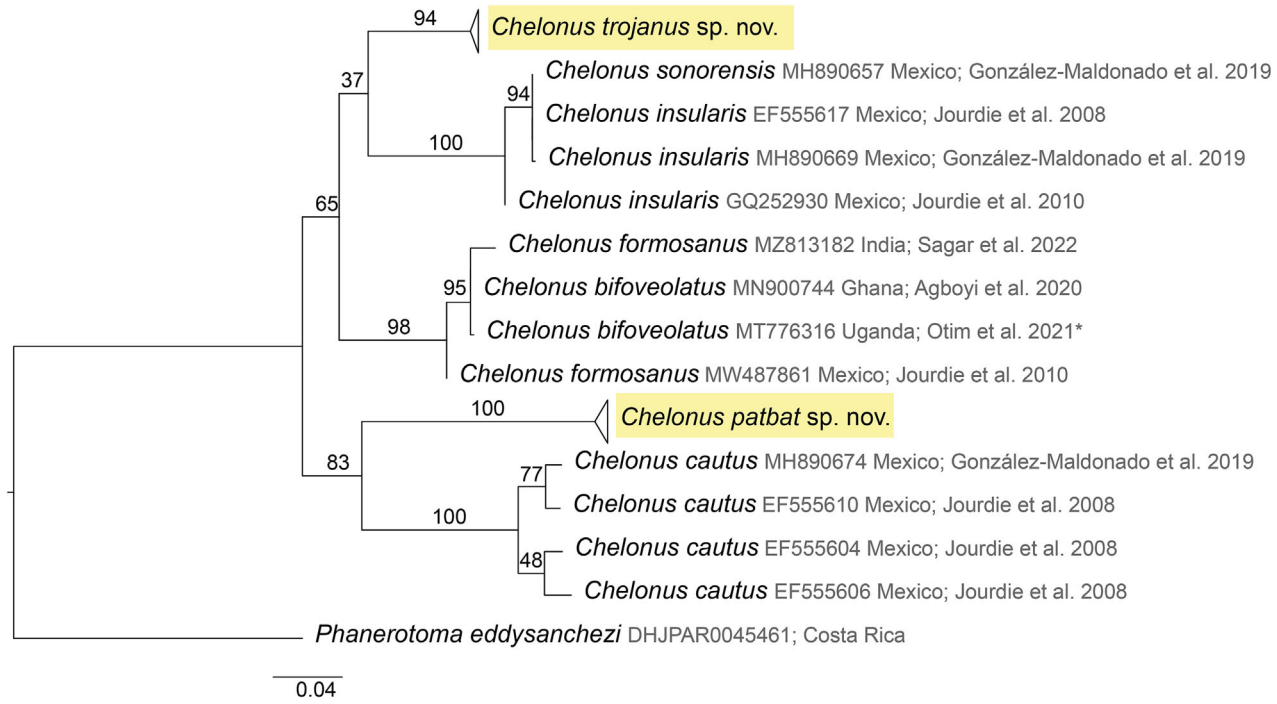


**FIGURE 9** Maximum likelihood phylogeny (COI barcoding fragment) of *Chelonus* species reared from *Spodoptera frugiperda*, where specimens have been independently identified and published. Genbank numbers, country of collection and reference are listed after the published species identification of the sequence. The new species described in this paper are highlighted in yellow. Numbers on branches are ultrafast bootstrap values. *This identification was made using a BLAST sequence match, so is not independent.

antennae. Size and extent of white semi-circle lateral patches on metasoma varies slightly amongst individuals but is never as large or misshapen as in male specimens.

### *Male*

As female, but with much larger pale areas on the dorsal metasoma (Figure 10c), not a single semicircle as in the female. In one specimen (BO-24-2022 QM: T260009) white patches extend more strongly towards centre of metasoma than in most individuals, but do not meet. Distal flagellomeres longer relative to width than in female. Of the five male paratypes with unbroken antennae, four have 26 flagellomeres and one has 24.

## Remarks

The COI DNA barcodes of the type series form BIN BOLD:AAG8391, along with five specimens from Townsville, QLD, collected in a Malaise trap by Graham Cocks in 2011 (HYQTB332-12, HYQT819-10, HYQT450-10, HYQT449-10 and HYQT448-10), indicating this species has been present in Australia for much longer than *S. frugiperda*, and is likely native. Whilst we have not examined these specimens, the images available on BOLD agree in coarse morphology.

This species has been reared from and observed on *S. frugiperda* and *S. litura* egg masses by the authors [and pers. comm. John Stanley] and emerges from the larval stage of the host.

We recognise that the *Chelonus* species known from *S. frugiperda* across the world with similar morphology are in need of a revision and are possibly often misidentified. For example, several of the COI DNA barcodes available on public databases appear to be identical despite being identified as different species (Figure 9). However, as the Australian specimens have extremely divergent COI data from any of these barcodes, and the species has likely been present in Australia since at least 2011, before the appearance of *S. frugiperda* in the country, we believe it is likely that it is a different species than those recorded from *S. frugiperda* in other countries and is likely native to Australia. We consider it important to describe and assign a scientific name to the Australian species because of potential biological control research; however, we acknowledge that future revisions should consider this species in context with those reared from *Spodoptera* in other countries.

## Etymology

This species is named by students at Columba Catholic College, Charters Towers, QLD, who were the only school to collect two female specimens of this species in their Malaise trap during the *Insect Investigators* citizen science project. Students were inspired by the wasp's life cycle and the legend of the wooden Trojan horse used by Greek warriors during the Trojan War, as described in Virgil's Aeneid.

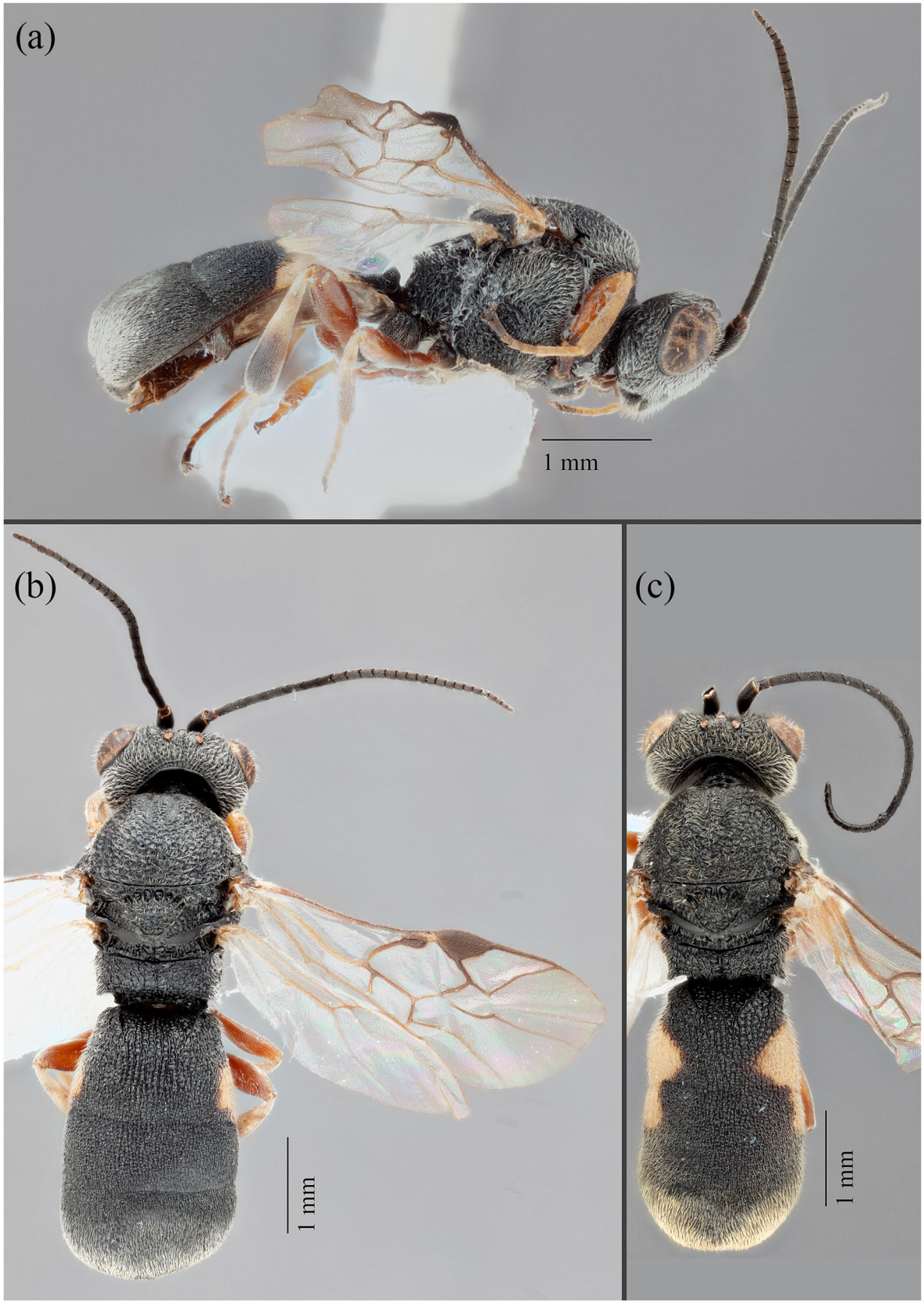


**FIGURE 10** *Chelonus trojanus* sp. nov. (a) Holotype, lateral habitus. (b) Holotype, dorsal habitus. (c) Male (QM: T260023), dorsal habitus.

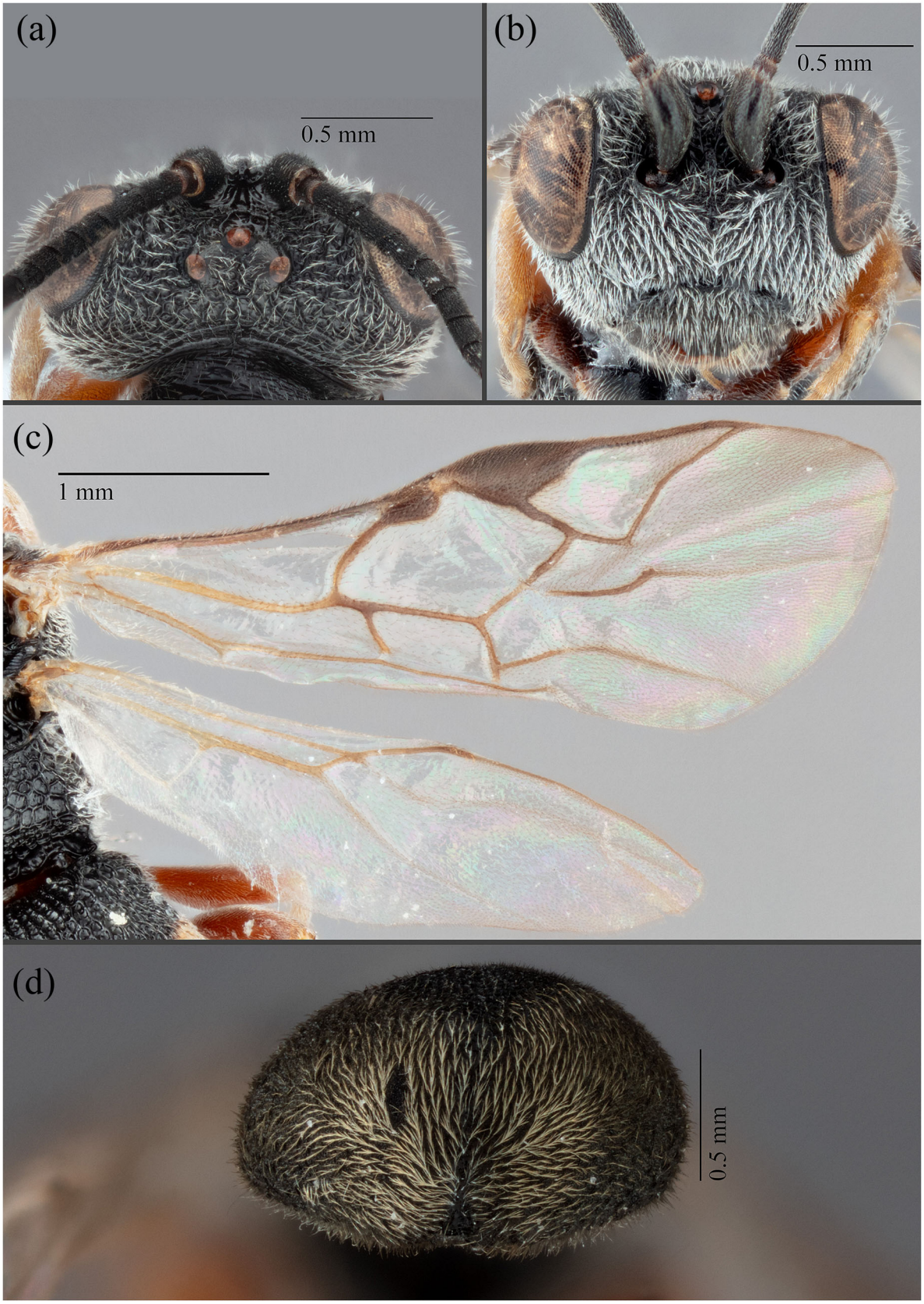


**FIGURE 11** *Chelonus trojanus* sp. nov. (a-d) Holotype male (WAM: T260023). (a) Dorsal head. (b) Anterior head. (c) Fore and hind wing. (d) Posterior metasoma, showing absence of posterior metasoma pit.

## Distribution

Currently known from the northern coast of the Northern Territory and throughout the east coast of Queensland.

## *Chelonus patbat* Fagan-Jeffries, sp. nov

(Figures 12 and 13)

https://zoobank.org/urn:lsid:zoobank.org:act: D38BED87-3C89-4FCC-AA38-58435EF21058.

## Material examined

### *Holotype*

♀; South Australia; Roxby Downs; −30.55932, 136.89679; 15–22 March 2022; Roxby Downs Area School students; Malaise trap; BOLD: ASMII3788-22; QM: T260005.

### *Paratypes*

**Queensland:** ♂; Winton; −22.38460, 143.04069; 17–23 March 2022; St Patrick's Catholic School Winton students; Malaise trap; BOLD: ASMII12532-22; QM: T260006. ♂; Bowen; −20.007, 148.194; 13 January 2021; V. Sivasubramaniam; reared from *S. frugiperda* larva on sweet corn; field code: BO-14-2022; QM T260007. ♀; Bowen; −19.985; 148.227; 13 January 2022; V. Sivasubrmaniam; reared from *S. frugiperda* larva on sorghum; volunteer crop; field code: BO-25-2022; BOLD: FAW-CR125-BO-25-2022; QM: T260000. ♀; Gatton; − 27.54, 152.33; 15 January 2023; J. Duff; reared from *S. frugiperda* larva on sweet corn; field code: LV-01-2022; BOLD: FAW-CR91-LV-01-2022; QM: T260001. ♂; Gatton; −27.54, 152.33; 6 December 2022; M. Miles; reared from *S. frugiperda* larva on maize; spray trial plot; field code: FAW2228; BOLD: FAW-CRM10-FAW2228; QM: T260002. ♂; collection data as previous except: field code: FAW2229; BOLD: FAW-CRM11-FAW2229; QM: T260003. ♀; collection data as previous except: 1 March 2023; NPV trial plot; field code: FAW2234; BOLD: FAW-CRM13-FAW2234; QM: T260004. ♀; collection data as previous except: 3 March 2023; trial plot; field code: FAW2243; BOLD: FAW-CRM18-FAW2243; QDPC: 0-178 473. **South Australia:** ♀; Brownlow, Kangaroo Island; −35.67, 137.616; 15–22 March 2022; Kangaroo Island Community Education students; Malaise trap; BOLD: ASMII1992-22; SAMA: 32-036068.

## Diagnosis

*Chelonus patbat* can be separated from all of the species of *Chelonus* known from Australia, other than those noted specifically below, by the metasoma being black with a large semi-triangular pale patch dorsally, in the anterior half of the metasoma (Figure 12b).

*Chelonus patbat* can be separated from *C. megaspilus* Cameron, 1911, which is described as having a large white mark on the basal third of the abdomen, by having the entire wing hyaline (*C. megaspilus* described as having the wing tinged with fuscious to the stigma) and by the antennae of the female always having 14 flagellomeres (*C. megaspilus* female described as having antennae at least 33-jointed).

*Chelonus patbat* can be separated from *C. curvimaculatus* Cameron, 1906 (introduced to Australia (Kittle & Austin, 2014) and reared from *S. frugiperda* in Kenya and Zambia (several records, collated in Li et al. 2023)) by the hind femur and tibia being mostly brown and reddish in colouration (*C. curvimaculatus*, based on images of a Madagascan specimen in Braet et al. (2012) and the redescription in van Achterberg & Polaszek (1996), has the hind femur black and the hind tibia with an ivory band in the centre. The posterior metasomal pit of the male of *C. patbat* is also dorso-ventrally thinner than that of *C. curvimaculatus*, and the pale section on the dorsal metasoma much more triangular (i.e., the length of the posterior margin of the white patch is much longer relative to the anterior margin length in *C. patbat* than in *C. curvimaculatus*).

*Chelonus patbat* can be separated from all other species of *Chelonus* reared from *S. frugiperda* in other parts of the world by having the dorsal metasoma black with a triangular white section that does not reach the edges of the carapace (*C. blackburni* and *C. cautus*, which also have white areas on the anterior metasoma, have a white band reaching the lateral margins of the metasoma).

## Description

### *Female*

***Colour.*** Antennae dark brown; legs other than coxae mostly orange-brown, tarsi darkening posteriorly; tegula yellowish-brown; wings hyaline with veins brown, very pale in hind wing and proximal to pterostigma in forewing (Figure 13c); metasoma with pale area anteriorly (Figure 12b); rest of body black.

***Body length (including head; measured in dorsal view).*** 3.9 mm.

***Head length in lateral view (longest measurement).*** 0.59 mm; head length in dorsal view: 0.56 mm; head width in anterior view: 1.2 mm; minimum distance between eyes in anterior view: 0.78 mm; eye height in anterior view: 0.55 mm; malar distance: 0.36 mm; POL: 0.2 mm; OOL: 0.24 mm; OD: 0.06 mm; are around ocelli only very slightly raised; number of flagellomeres: 14; F1 length/width ratio (l/w): 3.4; penultimate flagellomere l/w ratio: 1.3; apical flagellomere length: 0.13 mm; face finely

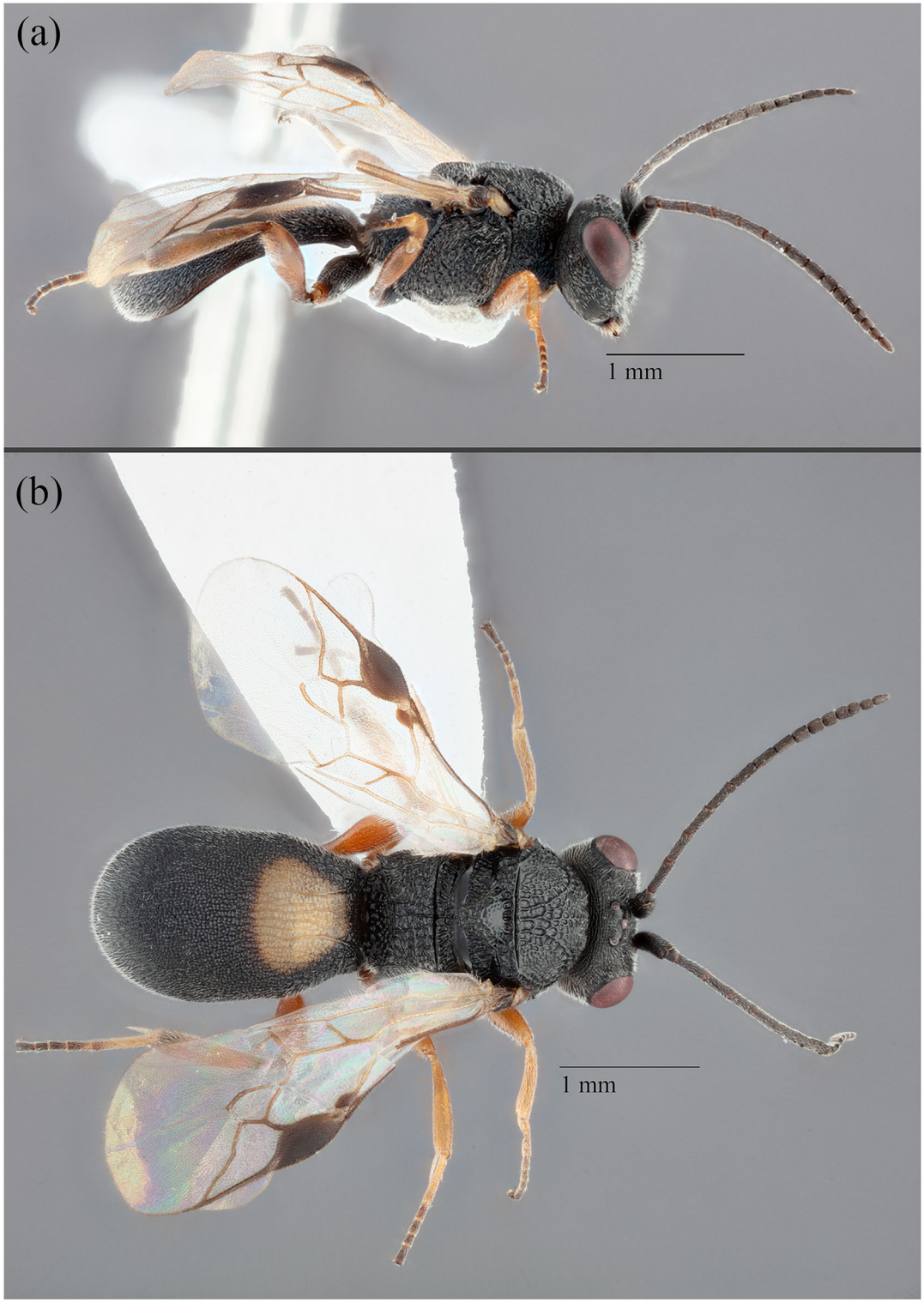


**FIGURE 12** *Chelonus patbat*. sp. nov. holotype. (a) Lateral habitus. (b) Dorsal habitus.

sculptured and densely setose; clypeus smoother than surrounding face and shallowly punctured.

***Mesosoma length (measured in dorsal view).*** 1.7 mm. Fore wing length: 3.1 mm. Hind tibia length: 1.0 mm; longest hind tibial spur length: 0.24 mm; hind basitarsus length: 0.41 mm; Mesoscutum and propodeum strongly reticular rugose, scutellar disk with smother patch in centre. Propodeum strongly angled with a projecting spine at each lateral corner.

***Metasoma length (measured in dorsal view).*** 1.9 mm; metasoma width at widest point: 1.2 mm. Ovipositor sheaths extruding 0.22 mm from margin of hypopygium

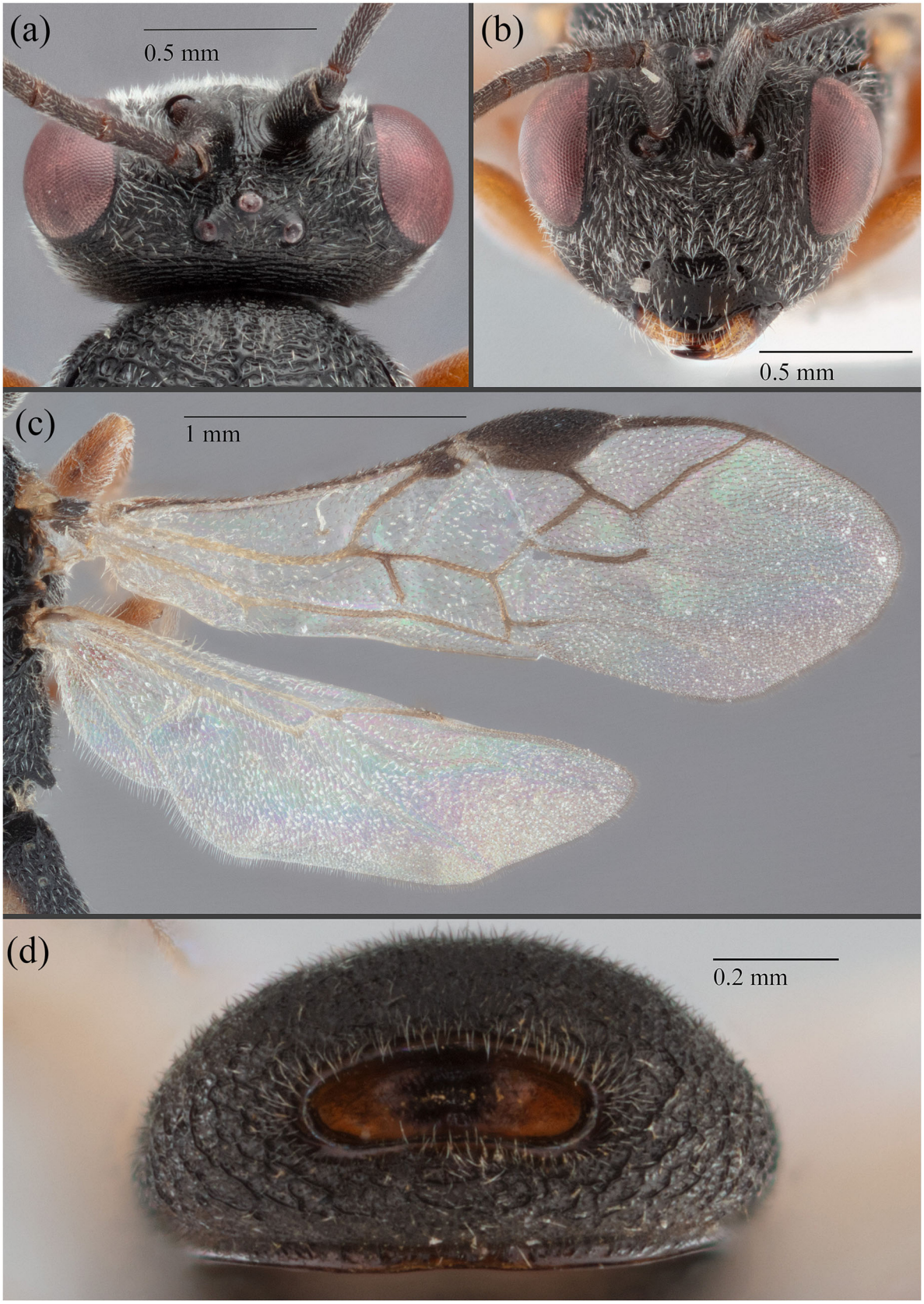


**FIGURE 13** *Chelonus patbat* sp. nov. (a-d) Holotype male (QM: T260006). (a) Dorsal head. (b) Anterior head. (c) Fore and hind wing. (d) Posterior metasomal pit.

(measured on paratype BIOUG84495 as ventral metasoma compressed into carapace in holotype); posterior tip of sheaths narrowing to point, with one or two spines at posterior end.

***Variation.*** Measurements not taken on paratypes, but from visual observation all paratypes appear consistent with holotype, with only slight variation in the shape of the pale patch on the dorsal metasoma.

### *Male*

As female, abdomen with posterior metasoma pit (Figure 13d) and antennae much longer than in females. Shape of pale patch on dorsal metasoma varying slightly.

## Remarks

The COI DNA barcodes of specimens reared from fall armyworm are more than 99% similar to sequences collected by school students (Queensland: St Patrick's Catholic School Winton; South Australia: Kangaroo Island Community Education and Roxby Downs Area School) as part of the *Insect Investigators* citizen science project (https://insectinvestigators.com.au). The presence of this species in South Australia, including Kangaroo Island, strengthens the argument this is a native species that has broadened its host preference to *S. frugiperda* after fall armyworm arrived in Australia.

The species is known to emerge from the larval stage of *S. frugiperda*, but it is yet unknown if oviposition occurs in the larval stage, or into eggs. However, as all *Chelonus* species known from *S. frugiperda* are egg-larval parasitoids, it is highly likely that *C. patbat* also attacks the egg life stage of the host.

## Etymology

This species is named by the students at St Patrick's Winton School, QLD, who were one of the three schools who collected specimens of this species in their Malaise trap during the *Insect Investigators* citizen science project. The word is formed through combining 'pat' short for '[Saint] Patrick's' and 'bat', short for battalion (and also short for the Latin battalia, 'to battle'.) The students envision this species as forming a St Patrick's battalion to fight fall armyworm. The name should be treated as an indeclinable noun.

## Distribution

Currently known from the Far North region of South Australia and south to Kangaroo Island, and from Central West Queensland.

## Braconidae: Microgastrinae

## *Cotesia icipe* Fernández-Triana & Fiaboe, 2017

(Figure 14)

## Material examined

**Queensland:** ♂; Kairi Research Station; −17.21, 145.57; 28 September 2021; C. MacDonald; reared from *S. frugiperda* larva on maize; field code: T3B1; QDPC: 0-178 485. ♂; field code: T1C3; QDPC: 0-178 486. ♂; Gatton; −27.54, 152.33; 6 December 2022; A. Quade; reared from *S. frugiperda* larva on maize; spray trial plot; field code: FAW2205; BOLD: FAW-CRM1-FAW2205; QDPC: 0-178 487 (in ethanol). ♀; collection data as previous except: field code: FAW2206; BOLD: FAW-CRM2-FAW2206; QDPC: 0-178 488 (in ethanol). ♀; collection data as previous except: field code: FAW2219; BOLD: FAW-CRM7-FAW2219; QDPC: 0-178 489 (in ethanol). ♀; collection data as previous except: field code: FAW2218; BOLD: FAW-CRM6-FAW2218; QM: T260066. ♀; collection data as previous except: field code: FAW2221; BOLD: FAW-CRM8-FAW2221; QM: T260067. ♂; Ayr Research Station; −19.61, 147.37; 26 March 2021; M. Miles; cocoons attached to leaves in maize field; seed treatment trial plots; field code: FAW-55; BOLD: FAW-CR33-FAW-55; QM: T260065 (vial also contained hyperparasitoid specimen deposited in WINC (Figure 16b)).

## Identification

The specimens listed above match the description and photographs of *C. icipe* in Fiaboe et al. (2017), and are less than 2% divergent than the available COI barcodes of the specimens from which *C. icipe* were described (e.g., BIN BOLD AAHYM369-16).

## Remarks

*Cotesia icipe* has been reared from *S. frugiperda* larva as a solitary parasitoid in QLD. *Cotesia icipe* was described from the Afrotropical region (Kenya, Madagascar, Saudi Arabia, South Africa, and Yemen), and was reared from *Spodoptera exigua* (Hübner) and *S. littoralis* (Boisduval). It has since been shown to parasitise *S. frugiperda* under laboratory conditions in Africa (Abuelgasim Mohamed et al. 2021). Fagan-Jeffries & Austin (2020) identified specimens that appeared to be *C. icipe* during a review of *Cotesia* in Australia, but because *COI* divergence levels were between 1 and 1.5%, the presence of *C. icipe* in Australia was not confirmed as no host data was available. As the specimens in the current study have been reared from *S. frugiperda*, a known host of *C. icipe*, we hypothesise *C. icipe* is a broadly

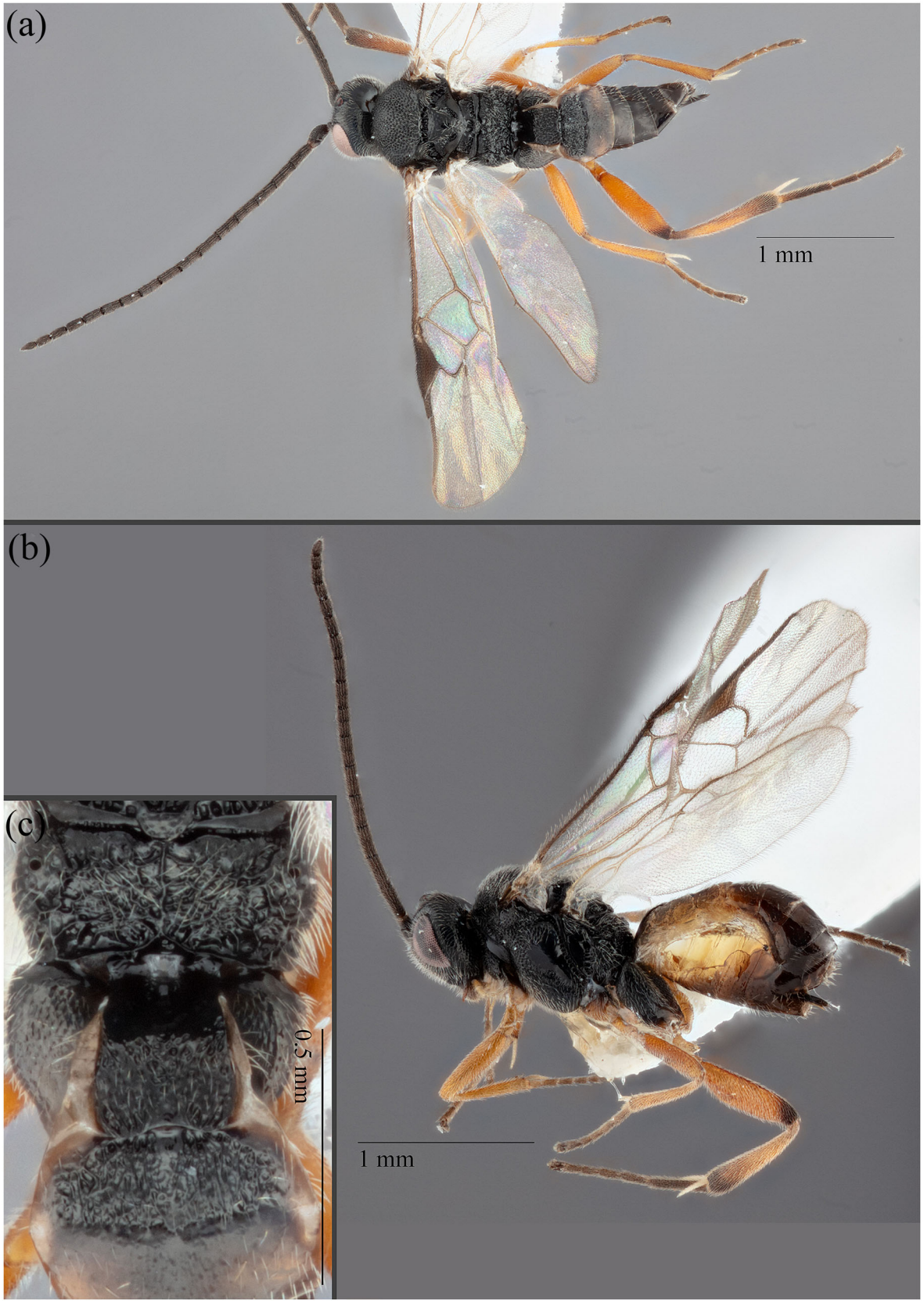


**FIGURE 14** *Cotesia icipe* female. (a) (QM: T260067) dorsal habitus. (b) (QM: T260066) lateral habitus. (c) (QM: T260067) propodeum and T1–2.

distributed species with multiple *COI* lineages, that has been present in Australia since at least 2010 (the date of the oldest available COI DNA barcode from Australia: HYQT433-10). We note that the COI DNA barcodes of the Australian specimens listed above are not identical to those of the type series of *C. icipe*, but are well within the often used 2% divergence threshold amongst species of Microgastrinae. Future taxonomic work to confirm the species limits and distribution would be valuable.

## *Cotesia ruficrus* (Haliday, 1834)

(Figure 15)

### Material examined

**Queensland:** ♂; Home Hill; −19.80, 147.33; 3 January 2020; H. Brier; reared from *S. frugiperda* larva on sorghum; field survey; field code: FAW-4; BOLD: FAW-CR40-FAW-4; QDPC: 0-178 498 (ethanol). ♀; Mackay; −21.30, 148.99; 7 January 2020; D. Gonzalez; reared from *S. frugiperda* larva on maize; field survey; field code: FAW-8; BOLD: FAW-CR44-FAW-8; QDPC: 0-178 499 (ethanol). ♀; Norwin; −27.54, 151.37; 16 February 2021; A. Quade; reared from *S. frugiperda* larva on maize; field code: FAW-33; BOLD: FAW-CR13-FAW-33; QDPC: 0-178 491 (ethanol). ♀; Dalby; −27.22, 151.34; 2 November 2021; A. Quade; reared from *S. frugiperda* larva on maize; field code: FAW-34; BOLD FAW-CR14-FAW-34; QDPC: 0-178 493. ♂; collection data as previous except: −28.16, 151.86; 17 February 2021; field code: FAW-35; BOLD: FAW-CR15-FAW-35; QDPC: 0-178 494 (ethanol). ♂; Wheatvale; −28.16, 151.86; 17 February 2021; A. Quade; reared from *S. frugiperda* larva on maize; field survey; field code: FAW-36; BOLD: FAW-CR16-FAW-36; QDPC: 0-178 495. ♀; Gatton; −27.54, 152.33; 6 December 2022; M. Miles; reared from *S. frugiperda* larva on maize; spray trial plot; field code: FAW2224; BOLD: FAW-CRM9-FAW2224; QM: T260071. ♀; same data as previous except field: field code: FAW2216; BOLD: FAW-CRM4-FAW2216; cocoons in field, no host present (WINC) (vial also contained hyperparasitoid deposited in WINC (Fig. 16a). ♀; Gumlu; −19.85, 147.61; 3 June 2021; S. Subramaniam; reared from *S. frugiperda* larva on capsicum; sprayed crops; field code: GU-01-2022; BOLD: FAW-CR141-GU-01-2022; QDPC: 0-178 492 (ethanol). ♀; Home Hill; −19.75, 147.27; 19 July 2021; S. Subramaniam; reared from *S. frugiperda* larva on sweet corn; sprayed crops; field code: BU-03-2022; BOLD: FAW-CR137-BU-03-2022; QDPC: 0-178 490 (ethanol). ♀; Bowen; −20.007, 148.194; 29 May 2021; S. Subramaniam; reared from *S. frugiperda* larva on sweet corn; field code: BO-29-2022; BOLD: FAW-CR124-BO-29-2022; QM: T260069 (ethanol). ♀; collection data as previous except: 25 May 2021; field code: BO-02-2021; BOLD: FAW-CR62-BO-02-2021; QM: T260070. ♂; collection data as previous except: 10 May 2021; V. Sivasubramaniam; field code: BO-28-2022; BOLD: FAW-CR103_22-BO-28-2022; QM: T260068 (ethanol). ♀; Bowen; −20.007, 148.194; 15 May 2021; V. Sivasubramaniam; collected as adult on sweet corn; field code: BO-37-2022; BOLD: FAW-CR133-BO-27-2022; QDPC: T260072 (ethanol). ♀; Bowen; −20.007, 148.194; 9 August 2021; S. Subramaniam; collected as pupae on tomato; field code: BO-30-2022; QDPC: 0-178 502 (ethanol). ♀; Fassifern Valley; −27.86, 152.64; 25 January 2022; A Godage and V Sivasubramaniam; reared from *S. frugiperda* larva on sweet corn; field code: FV-02-2022; BOLD: FAW-CR90-FV-02-2022; QDPC: 0-178 500. **New South Wales:** ♀; Wee Waa; −30.14, 149.46; 15 November 2020; A. Madden; reared from *S. frugiperda* larva on maize; commercial field; field code: FAW-46; BOLD: FAW-CR25-FAW-46; QDPC: 0-178 496 (ethanol). ♂; collection data as previous except: 20 December 2020; field code: FAW-47; BOLD: FAW-CR26-FAW-47; QDPC: 0-178 497 (ethanol). **Western Australia:** ♂; Kununurra; −15.5748, 128.7730; 28 August 2021; S. Adnan; reared from *S. frugiperda* larva on maize; field survey; field code: 103; BOLD: FAW-CR103-103; WAM: 116178 (ethanol). ♂; Kununarra; −15.4669, 128.8503; 9 August 2021; S. Adnan; reared from *S. frugiperda* larva on maize; field survey; field code: 105; BOLD: FAW-CR105-105; WAM: 116179 (ethanol). ♀; Kununurra; −15.6517, 128.7131; 28 September 2021; S. Adnan; reared from *S. frugiperda* larva on maize; field survey; field code: 108; BOLD: FAW-CR108-108; WAM: 116180 (ethanol). ♀; Kununurra; −15.8806, 128.7297; 30 September 2021; S. Adnan; reared from *S. frugiperda* larva on maize; field survey; field code: 111; BOLD: FAW-CR111-111; WAM: 116181 (ethanol). ♀; Carnarvon; −24.8259, 113.7621; 29 August 2021; S. Adnan; reared from *S. frugiperda*, larva on sweet corn; field survey; field code: 113; BOLD: FAW-CR113-113; WAM: 116182 (ethanol). ♀; Carnarvon; −24.8383, 113.7386; 10 February 2021; S. Adnan; reared from *S. frugiperda* larva on sweet corn; field survey; field code: 119; BOLD: FAW-CR119-119; WAM: 116183 (ethanol). ♀; Carnarvon; −24.8251, 113.7663; 21 August 2021; S. Adnan; reared from *S. frugiperda* larva on sweet corn; field survey; field code: 121; BOLD: FAW-CR121-121; WAM: 116184 (ethanol). ♀; Carnarvon; −24.8588, 113.7104; 23 September 2021; S. Adnan; reared from *S. frugiperda* larva on sweet corn; field survey; field code: 122; BOLD: FAW-CR122-122; WAM: 116185 (ethanol).

### Remarks

The examined material keys to *C. ruficrus* in Fagan-Jeffries & Austin (2020). The COI DNA barcode data indicates two different lineages are present in Australia, approximately 2% divergent. These two lineages are most closely related to two different BINs in BOLD, both of which include specimens identified as *C. ruficrus* from several countries. The COI barcodes of the first lineage (informally 'strain A';

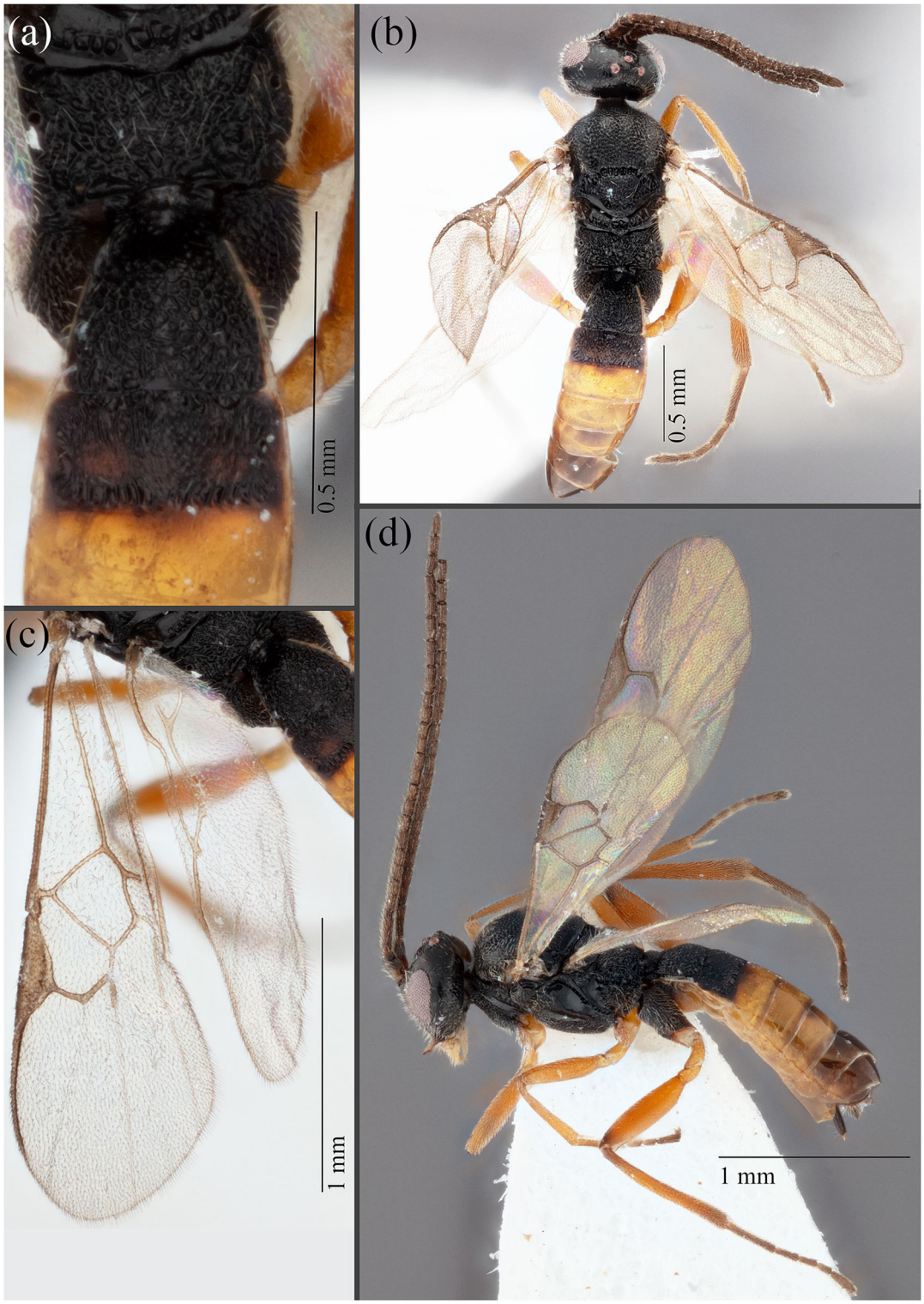


**FIGURE 15** *Cotesia ruficrus* (QM: T260071). (a) Propodeum and T1–2. (b) Dorsal habitus. (c) Fore and hind wings. (d) Lateral habitus.

specimens collected from QLD and NSW) are identical to members of the BIN BOLD:ABZ1947, which includes specimens from Australia (ACT & NSW), China, Pakistan, India, Nepal, New Caledonia, New Zealand, Philippines, and Thailand. The COI barcodes of the second lineage (informally 'strain B'; specimens from QLD and WA) are less than 1% divergent from members of the BIN BOLD:AAH1084, which includes specimens from Australia (QLD), Bangladesh, Egypt, French Polynesia, India, Pakistan, Papua New Guinea, United Arab Emirates, and West Papua.

## Biology and distribution

*Cotesia ruficrus* is a gregarious parasitoid and has been reared from *S. frugiperda* larvae in QLD, NSW and WA. The species has had a convoluted taxonomic history; as it is currently recognised is found in every region of the globe except the Nearctic (Fernández-Triana et al. 2020). In Australia, *C. ruficrus* is also known to parasitise a broad range of noctuid genera (Fagan-Jeffries & Austin 2020) and the species has been previously documented parasitising *S. frugiperda* in both India (Gupta, Ramesh Babu, & Kumar 2019) and Egypt (Youssef 2021). We have also reared an unidentified hyperparasitoid (Hymenoptera: Pteromalidae) from a *C. ruficrus* cocoon masses collected in Gatton, QLD (Figure 16a).

## *Microplitis abrs* Austin & Dangerfield, 1993

(Figure 4d)

## Material examined

**Queensland:** ♀; Georgetown; −18.25, 143.08; 3 January 2020; M. Miles; reared from *S. litura* larva on sorghum; field survey; field code: FAW-3; BOLD: FAW-CR39-FAW-3; QDPC: 0-178 508. ♀; collection data as previous except: field code: FAW-1; BOLD: FAW-CR37-FAW-1; QDPC: 0-178 506. ♀; collection data as previous except: field code: FAW-2; BOLD: FAW-CR38-FAW-2; QDPC: 0-178 507. ♂; Bowen; −20.007, 148.184; 7 August 2021; S. Subramaniam; reared from *S. frugiperda* larva on

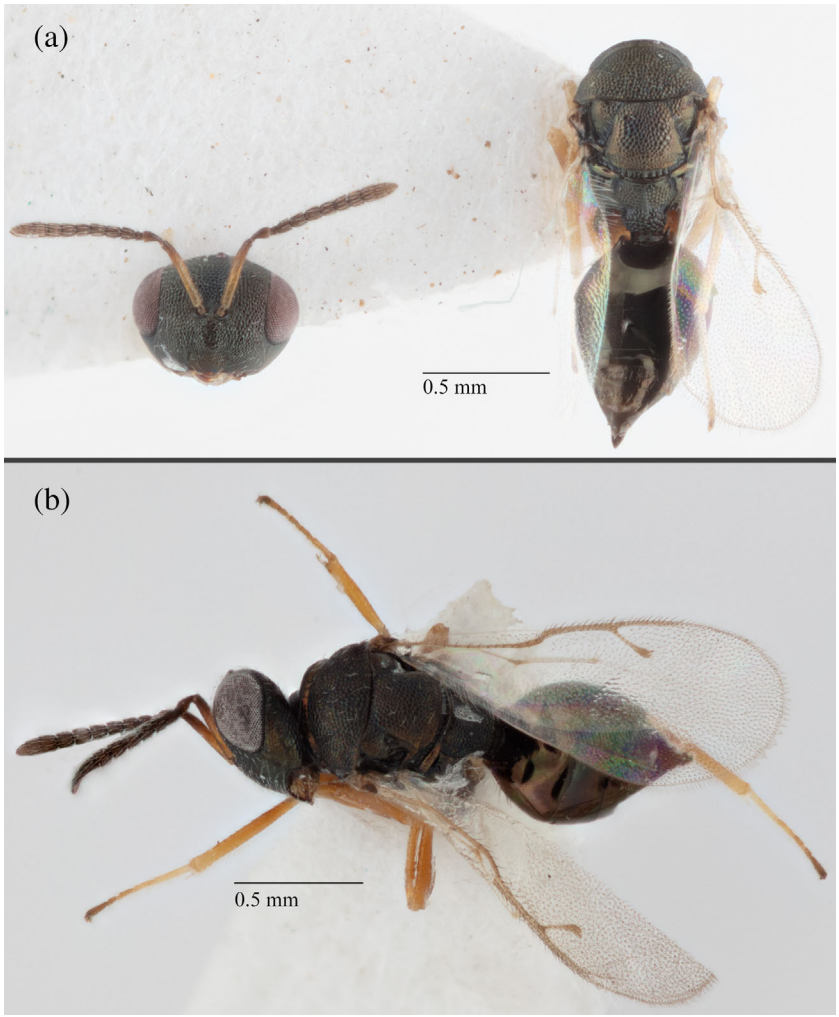


**FIGURE 16** (a) Hyperparasitoid (hymenoptera: Pteromalidae) reared from *Cotesia ruficrus* cocoons. (b) Hyperparasitoid (hymenoptera: Pteromalidae) reared from *Cotesia icipe* cocoons.

sweet corn; field code: BO-43-2022; BOLD: FAW-CR106_22-BO-43-2022; QDPC: 0-178 504 (ethanol). ♂; Bowen; −19.985, 148.227; 29 May 2021; S. Subramaniam; reared from *S. frugiperda* larva on sweet corn; field code: BO-45-2022; BOLD: FAW-CR105_22-BO-45-2022; QDPC: 0-178 503. ♀; Burdekin; −19.55, 147.43; 3 May 2021; S. Subramaniam; reared from *S. frugiperda* larva on sweet corn; field code: BU-02-2022; BOLD: FAW-CR138-BU-02-2022; QDPC: 0-178 505. ♂; Gatton; −27.54, 152.33; 25 January 2022; J. Duff; reared from *S. frugiperda* larva on sweet corn; field code: LV-02-2022; BOLD: FAW-CR92-LV-02-2022; QDPC: 0-178 509. DNA only (pupa used for DNA extraction); Mt Tarampa; −27.46, 152.51; 2 December 2021; M. Miles; emerged from *S. litura* in sweet corn; commercial crop; field code: FAW-51; BOLD: FAW-CR29-FAW-51 (DNA only).

## Remarks

The specimens above key to *M. abrs* in Austin & Dangerfield (1993), which is known from *Spodoptera* spp., and the specimens compare well to the paratype series in the Waite Insect and Nematode Collection, which were examined. Several attempts were made to extract and sequence DNA from paratypes without success, and therefore only morphology was used to determine the identification. There is a possibility it is an undescribed species, as morphology in microgastrine wasps can be very conserved, but we tentatively identify this species as *M. abrs* until DNA data is available to dispute the identification.

## Biology and distribution

*Microplitis abrs* was reared as a solitary parasitoid from *S. frugiperda* larva in QLD. The species is currently known only from QLD, and the paratype series includes material reared from *S. littura* (Fabricius). Another *Microplitis* species found in northern Australia, *M. manilae* Ashmead, is known to parasitise *Spodoptera* in other regions, including *S. exigua* (Hübner) in China (Qiu, Zhou, & Xu 2013). *Microplitis manilae* has also been shown to parasitise *S. frugiperda* under laboratory conditions (Rajapakse, Ashley, & Waddill 1985) and has been reared from *S. frugiperda* in China (Gulinuer, Xing, & Yang 2023).

# Ichneumonidae

## *Eriborus* Förster, 1869

### *Eriborus* sp. cf. *iavialai* (Cheesman, 1936)
(Figure 17)

## Material examined

**Queensland:** ♀; Gatton; −27.54, 152.33; 3 March 2023; A. Quade; reared from *S. frugiperda* larva on maize; field code: FAW2242; BOLD: FAW-CRM17-FAW2242; QM: T260074. ♀; Walkamin Research Station; −17.13, 145.27; 26 August 2021; C. MacDonald; reared from *S. frugiperda* larva on maize; field code: T2C4; BOLD: FAW-CR77-T2C4; QM: T260073. ♂; Bowen; −20.007, 148.194; 15 July 2022; S. Subramaniam; reared from *S. frugiperda* larva on sweet corn; field code: BO-27-2022; QDPC: 0-178501.

## Remarks

COI DNA barcode data most closely matches to several species of *Eriborus* (genetic similarly >93%). The specimens key to the genus *Eriborus* in Gauld (1984) and keys to *Eriborus iavialai* in the key to Australasian species of *Eriborus* (Vas 2019). Whilst the specimens we have available closely resemble the images of the holotype available online (Natural History Museum 2014), we are yet to examine the holotype in person and therefore leave this identification with the qualifier.

## Biology

*Eriborus* sp. cf. *iavialai* has been reared from *S. frugiperda* in maize crops in QLD. A species of *Eriborus* has been reared from *S. frugiperda* in southern India (Sharanabasappa et al. 2019), but no diagnostic characters or images are provided with the record, and therefore we were unable to compare our species to that reared from the same host in India.

## *Temelucha* Förster, 1869

### *Temelucha* sp.
(Figure 18)

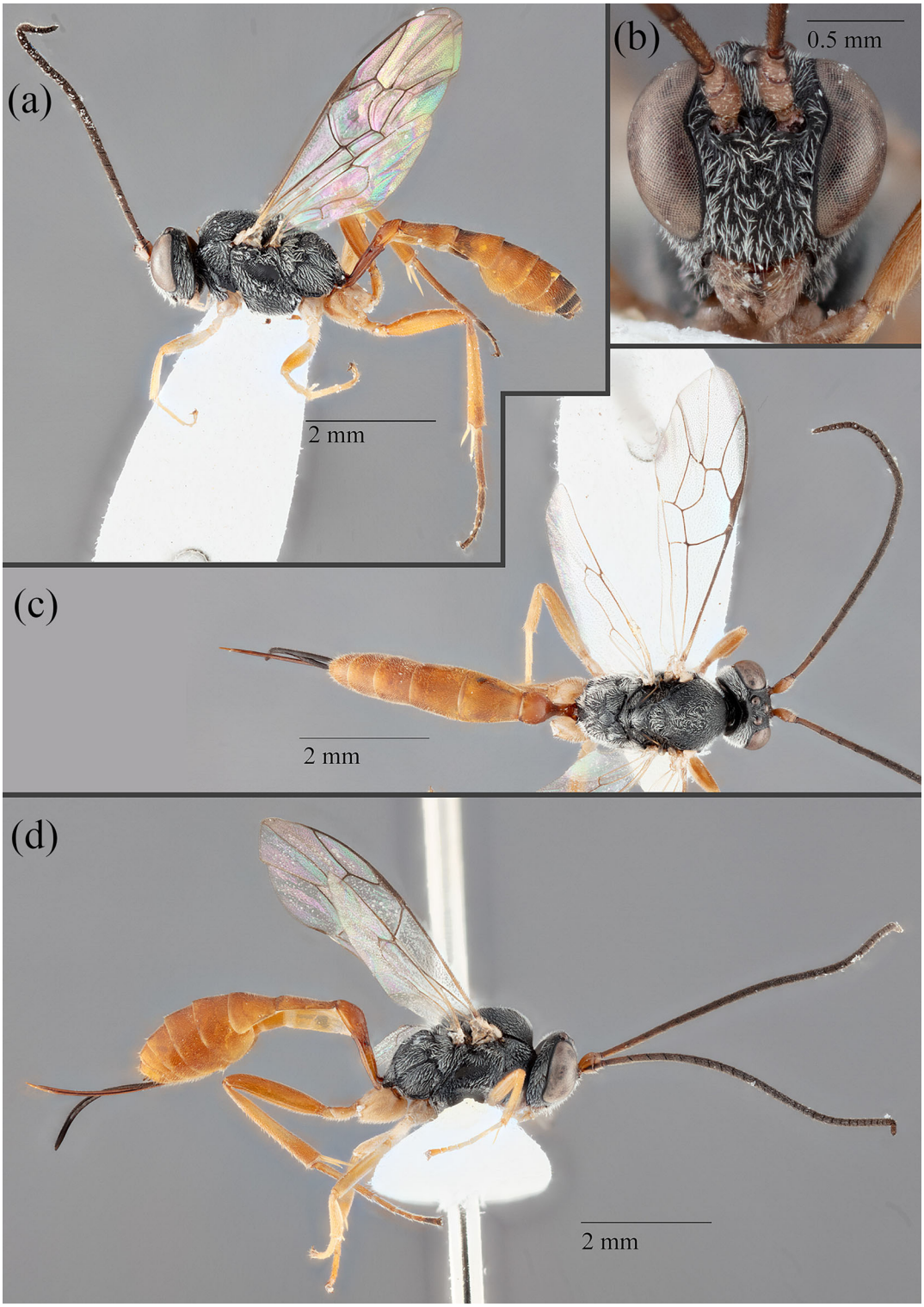


**FIGURE 17** *Eriborus* sp. (a) Male (QM: T260072) lateral habitus. (b) Female (QM: T260074) dorsal habitus. (c) Female (QM: T260074) lateral habitus.

## Material examined

**Queensland:** ♀; Bowen; −20.007, 148.194; 3 January 2022; S. Subramaniam; reared from *S. frugiperda* larva on sorghum; field code: BO-12-2022; BOLD: FAW-CR101-BO-12-2022; QM: T260075. ♀; collection data as previous except: 10 January 2022; J. Stanley; collected as adult; field code: BO-46-2022; BOLD: FAW-CR134-BO-46-2022; QM: T260076. ♀; Bowen; −20.03, 148.37; 8 June 2022; V. Sivasubramaniam; reared from *S. frugiperda* larva on

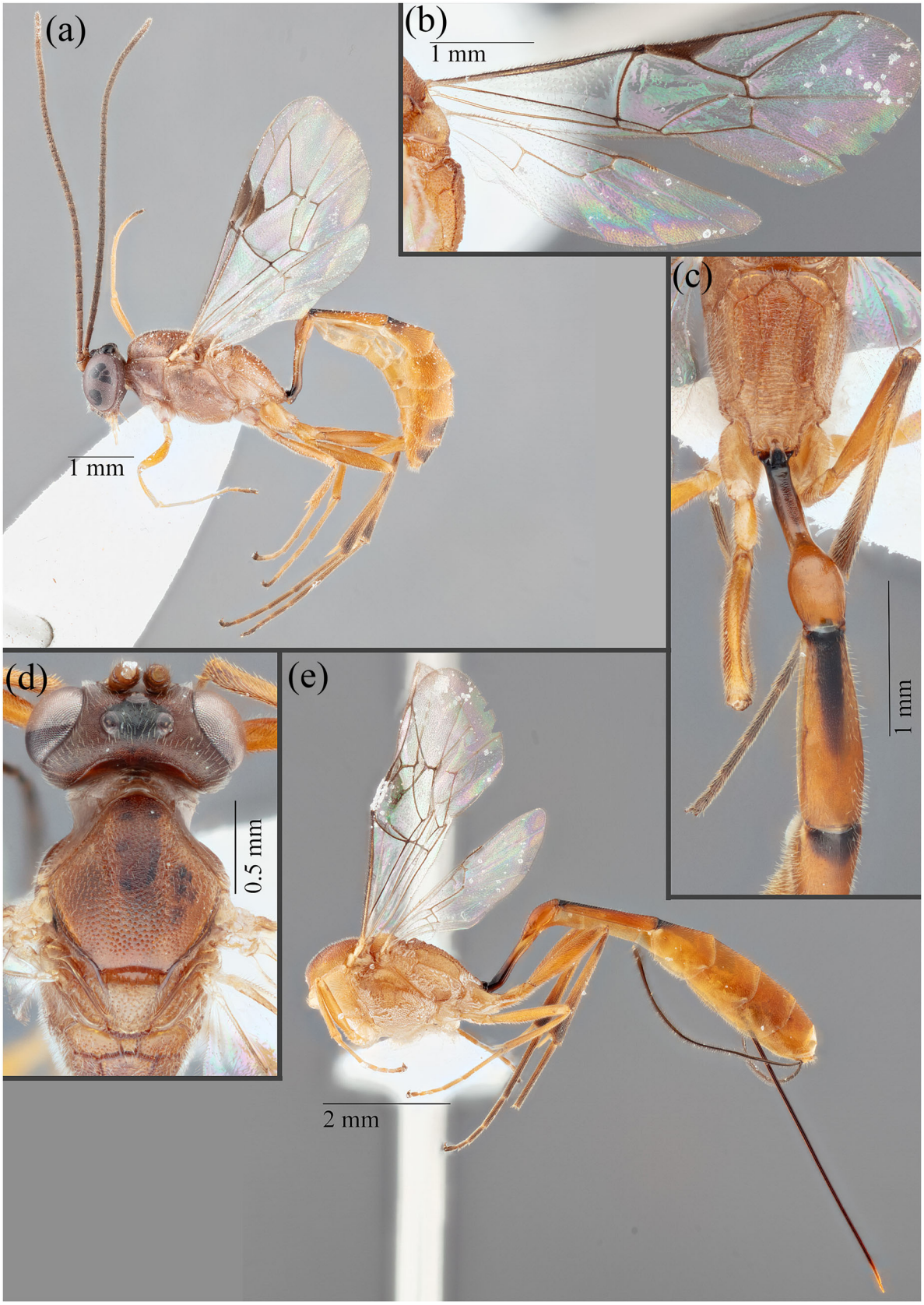


**FIGURE 18** *Temelucha* sp. (a) Male (QM: T260077) lateral habitus. (b) Female (QM: T260075) fore and hind wings. (c) Female (QM: T260075) dorsal propodeum and first two metasomal tergites. (d) Female (QM: T260075) dorsal head and mesoscutum. (e) Female (QM: T260076) lateral habitus.

sweet corn; field code: BO-57-2022; QDPC: 0-178 512 (ethanol). ♂; Fassifern Valley; −27.86, 152.64; 9 March 2022; A Godage & V. Sivasubramaniam; reared from *S. frugiperda* larva on sweet corn; field code: FV-01-2022; QDPC: 0-178 513. ♂; Gatton; −27.54, 152.33; 3 March 2023; M. Miles; reared from *S. frugiperda* larva on maize; field code: FAW2244; BOLD: FAW-CRM19-FAW2244; QM: T260077. ♂; Mareeba, Lockwood Rd.; −17.06, 145.46; 24 August 2021; C. MacDonald; reared from *S. frugiperda* larva on maize; field code: T3A3; QDPC: 0-178514.

### Remarks

COI DNA barcode data places these specimens with a clade of sequences identified as belonging to *Temelucha*, and the specimens key to *Temelucha* in Gauld (1984). This species keys to *Temelucha* 'species 4' in Gauld (1980) but we have not compared the specimens to those identified by Gauld as such. The male specimen listed in the material examined has not been confirmed to be conspecific to the females with DNA, but appears to be very similar morphologically, but with much larger ocelli than the female.

An unidentified species of *Temelucha* has been recorded as a native parasitoid of *S. frugiperda* in South Florida, USA (Ashley et al. 1982). The genus has also been reared from fall armyworm in North India (Sagar et al. 2022). We do not attempt to describe this species here, but note that a review or revision of the genus in Australia is warranted to be able to properly diagnose this potentially economically important parasitoid.

## DISCUSSION

*Spodoptera frugiperda* is an economically significant crop pest that continues to spread across the world, and applied research would benefit extraordinarily from collaborative efforts to accurately diagnose and identify the parasitoids being reared in different countries. Several of the genera identified above (e.g., *Chelonus*, *Eriborus* and *Temelucha*) should be priorities for taxonomic revisions within Australia to be able to place the parasitoids of *S. frugiperda* in context of the undescribed native fauna.

Many publications reporting the parasitoids reared from economic pests such as *Spodoptera frugiperda* fail to include methods of identification (e.g., the keys used or material compared with the specimens), high resolution images of the specimens, DNA barcoding data, or even often museum accession numbers of the specimens so that they could be re-examined. This means that it is often impossible to determine how accurate the identifications may actually be, and how much overlap is occurring in the parasitoid communities of particular pests in different countries. We urge entomologists to cite the keys used for identifications, accession the identified material in public collections, and where funding allows, include images of the reared species and DNA barcoding data.

We hope this initial documentation of the hymenopteran parasitoids of *S. frugiperda* assists entomologists with identification of reared material, and that the description of five new species facilitates the investigation of their potential as biological control agents of fall armyworm.

## ACKNOWLEDGMENTS

The authors thank Dr Zoltán Vas of the Hungarian Natural History Museum for photographing and generously sharing images of the Australasian *Chelonus* types held in the collection; and Jason Weintraub for providing images and information of the Cresson lectotype of *C. cautus* held in the ANSP (Academy of Natural Sciences, Philadelphia). We thank Susan Wright (Queensland Museum) for facilitating the visit to examine specimens of *Euplectrus* type material. EFJ thanks Dr Rebecca Kittel for discussions about Australian *Chelonus* species, and Dr Seraina Klopfstein for information on the genus *Eriborus*. We thank Justin Bartlett (QDPC), Nikolai Tatarnic (WAM), Karin Koch (QM) and Ben Parslow (SAM) for accessioning the material. *Coccygidium necatrix* includes specimens collected on the Wilinggin-West Kimberley Bush Blitz. EFJ acknowledges and thanks the Custodians of Wilinggin Country, the Ngarinyin People, the Traditional Rangers, the managers of the properties surveyed on the expedition, and the Bush Blitz Expedition Team who facilitated the collection of these specimens. EFJ is supported by an Australian Biological Resources Study Research Grant (NTRGI000021). *Insect Investigators* received funding from the Australian Government Inspiring Australia Citizen Science Grants. We thank the following teachers and students who collected material of species described in this paper through the *Insect Investigators* citizen science project: Madeleine Carter and students at Columba Catholic College, Charters Towers; Kylie Judd and students at Kogan State School; Sallyann Neve and students at Prospect Creek State School; Peter Spencer and students at Springsure State School; Anne Fleming and students at Yeppoon State School; Clare Triggell, Katie McDermott, Ryan Henry, Josh Newby, Wendy Wooton, Kathy Lyons and students at Yeronga State School; Bridget Tully and students at St Patrick's Catholic School Winton; Rachel Pillar and the students at Kangaroo Island Community Education in Kingscote; and Dave Roe-Simons and the students at Roxby Downs Area School. Project MT19015, 'Identifying potential parasitoids of the fall armyworm, *Spodoptera frugiperda*, and the risk to Australian horticulture', was funded by Hort Innovation using the melon, nursery, sweet potato and vegetable research and development levies and contributions from the Australian Government. We thank following agronomists, who supported field surveys, project planning and rearing insects: Andrew Sippel and Dr Surachat Vuthapanich - Mulgowie Farming Company; Tuo Deng and Achinda Godage Muditha – VeeJay Kalfresh Pty Ltd; Callum Hutcheson – E. E Muirs. We thank project staff for guidance, technical advice, sample collections and rearing

of fall armyworm and curation of specimens: Technical officers Arzoo Arzoo, Charlee Macdonald, Holly Cattermole, Kim Saligari, Leon Lenzo and Asitha Wijayasiriwardhana; Entomologists: Dr Helen Spafford, Dr Brian Thistleton, Dr Ian Newton and Dr John Stanley. Additional collection of material from across Queensland by staff from the Queensland Department of Agriculture and Fisheries was made possible by investment from the Queensland Treasury through the 'Fall Armyworm Response' Project (2020-2024). The authors thank the two reviewers, Ankita Gupta and José Fernández-Triana, for their corrections and suggestions which greatly improved the manuscript. Open access publishing facilitated by The University of Adelaide, as part of the Wiley - The University of Adelaide agreement via the Council of Australian University Librarians.

## CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

## ORCID

*Erinn P. Fagan-Jeffries* https://orcid.org/0000-0002-3322-6255
*Tareva-Chine C. Atkin-Zaldivar* https://orcid.org/0009-0009-6718-6405
*Andy G. Howe* https://orcid.org/0000-0002-7460-5227
*Saleh M. Adnan* https://orcid.org/0000-0003-4448-7626

## REFERENCES

Abuelgasim Mohamed, S., Wamalwa, M., Obala, F., Tonnang, H.E.Z., Tefera, T., Calatayud, P.-A., et al. (2021) A deadly encounter: alien invasive *Spodoptera frugiperda* in Africa and indigenous natural enemy, *Cotesia icipe* (Hymenoptera, Braconidae). *PLoS ONE*, 16(7), e0253122. Available from: https://doi.org/10.1371/journal.pone.0253122

Agboyi, L.K., Goergen, G., Beseh, P., Mensah, S.A., Clottey, V.A., Glikpo, R., et al. (2020) Parasitoid complex of fall armyworm, Spodoptera frugiperda, in Ghana and Benin. *Insects 2020*, 11, 68. Available from: https://doi.org/10.3390/INSECTS11020068

Ashley, T.R. (1986) Geographical distributions and parasitization levels for parasitoids of the fall armyworm, Spodoptera frugiperda. *Source: the Florida Entomologist*, 69(3), 516–524. Available from: https://doi.org/10.2307/3495384

Ashley, T.R., Waddill, V.H., Mitchell, E.R. & Rye, J. (1982) Impact of native parasites on the fall armyworm, *Spodoptera frugiperda* (Lepidoptera: Noctuidae), in South Florida and release of the exotic parasite, *Eiphosoma vitticole* (Hymenoptera: Ichnuemonidae). *Environmental Entomology*, 11(4), 833–837. Available from: https://academic.oup.com/ee/article/11/4/833/2392774, https://doi.org/10.1093/ee/11.4.833

Austin, A.D. & Dangerfield, P. (1993) Systematics of Australian and New Guinean *Microplitis* Foerster and *Snellenius* Westwood (Hymenoptera: Braconidae: Microgastrinae), with a review of their biology and host relationships. *Invertebrate Systematics*, 7(5), 1097–1166. Available from: https://doi.org/10.1071/IT9931097

Bouček, Z. (1998) *Australasian Chalcidoidea (Hymenoptera): a biosystematic revision of genera of fourteen families, with a reclassification of species*. C.A.B. International.

Coromoto Colmenarez, Y., Babendreier, D., Ramón, F., Wurst, F., Luis Vásquez-Freytez, C. & de Freitas Bueno, A. (2022) The use of *Telenomus remus* (Nixon, 1937) (Hymenoptera: Scelionidae) in the management of *Spodoptera* spp.: potential, challenges and major benefits. *CABI Agriculture and Bioscience*, 3(1), 5. Available from: https://doi.org/10.1186/S43170-021-00071-6

Davies, A.P. & Zalucki, M.P. (2008) Collection of *Trichogramma* Westwood (Hymenoptera: Trichogrammatidae) from tropical northern Australia: a survey of egg parasitoids for potential pest insect biological control in regions of proposed agricultural expansion. *Australian Journal of Entomology*, 47(2), 160–167. Available from: https://doi.org/10.1111/j.1440-6055.2008.00644.x

de Lourdes Corrêa Figueiredo, M., Cruz, I., da Silva, R.B. & Foster, J.E. (2015) Biological control with *Trichogramma pretiosum* increases organic maize productivity by 19.4%. *Agronomy for Sustainable Development*, 35(3), 1175–1183. Available from: https://doi.org/10.1007/s13593-015-0312-3

Eady, R.D. (1968) Some illustrations of microsculpture in the hymenoptera. *Proceedings of the Royal Entomological Society of London Series a, General Entomology*, 43(4–6), 66–72. Available from: https://doi.org/10.1111/j.1365-3032.1968.tb01029.x

Edgar, R.C. (2004) MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Research*, 32(5), 1792–1797. Available from: https://doi.org/10.1093/nar/gkh340

Fagan-Jeffries, E.P. & Austin, A.D. (2020) Synopsis of the parasitoid wasp genus *Cotesia* Cameron, 1891 (Hymenoptera: Braconidae: Microgastrinae) in Australia, with the description of seven new species. *European Journal of Taxonomy*, 667(667), 1–70. Available from: https://doi.org/10.5852/ejt.2020.667

Fen, L.I., Likui, W., Baoqian, L.Ü., Fengqin, C., Linlin, Y. & Wu, S. (2019) The report of *Chelonus munakatae* parasitizing fall armyworm *Spodoptera Frugiperda* (Lepidoptera: Noctuidae) in Hainan, China. *中国生物防治学报 Chinese Journal of Biological Control*, 12. Available from: https://doi.org/10.16409/j.cnki.2095-039x.2019.06.003

Fernández-Triana, J., Shaw, M.R., Boudreault, C., Beaudin, M. & Broad, G.R. (2020) Annotated and illustrated world checklist of Microgastrinae parasitoid wasps (hymenoptera, Braconidae). *ZooKeys*, 920, 1–1089. Available from: https://doi.org/10.3897/zookeys.920.39128

Fiaboe, K.K.M., Fernández-Triana, J., Nyamu, F.W. & Agbodzavu, K.M. (2017) *Cotesia icipe* sp. n., a new Microgastrinae wasp (Hymenoptera, Braconidae) of importance in the biological control of lepidopteran pests in Africa. *Journal of Hymenoptera Research*, 61, 49–64. Available from: https://doi.org/10.3897/jhr.61.21015

Folmer, O., Black, M.B., Hoeh, W., Lutz, R. & Vrijenhoek, R.C. (1994) DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates. *Molecular Marine Biology and Biotechnology*, 3(5), 294–299.

García-González, F., Rios-Velasco, C. & Iglesias-Pérez, D. (2020) *Chelonus* and *Campoletis* species as main parasitoids of *Spodoptera frugiperda* (J.E. Smith) in forage maize of Lagunera region, Mexico. *Southwestern Entomologist*, 45(3), 639–642. Available from: https://doi.org/10.3958/059.045.0306

Gauld, I.D. (1980) Notes on an economically important species of *Temelucha* Foerster (Hymenoptera: Ichneumonidae) and a preliminary key to Australian species. *Bulletin of Entomological Research*, 70(1), 43–47. Available from: https://doi.org/10.1017/S0007485300009755

Gauld, I.D. (1984) *An introduction to the Ichneumonidae of Australia*. British Museum (Natural History).

Goergen, G., Kumar, P.L., Sankung, S.B., Togola, A. & Tamò, M. (2016) First report of outbreaks of the fall armyworm *Spodoptera frugiperda* (J E Smith) (Lepidoptera, Noctuidae), a new alien invasive pest in West and Central Africa. *PLoS ONE*, 11(10), e0165632. Available from: https://doi.org/10.1371/journal.pone.0165632

Gulinuer, A., Xing, B. & Yang, L. (2023) Host transcriptome analysis of *Spodoptera frugiperda* larvae parasitized by *Microplitis manilae*. *Insects*, 14(2), 100. Available from: https://doi.org/10.3390/insects14020100

Gupta, A., Ramesh Babu, S. & Kumar, M.S. (2019) *Cotesia ruficrus* (Haliday, 1834) (hymenoptera: Braconidae) emerging as a common natural parasitoid of *Spodoptera frugiperda* (J. E. Smith) (Lepidoptera: Noctuidae) in Indian maize fields. *Journal of Biological Control*, 33(3), 193–196. Available from: https://doi.org/10.18311/JBC/2019/24118

Gupta, A., Soujanya, P.L., van Achterberg, C. & Sekhar, J.C. (2020) *Coccygidium transcaspicum* (Kokujev) (Hymenoptera: Braconidae) parasitizing larvae of invasive pest *Spodoptera frugiperda* (J. E. Smith) (Lepidoptera: Noctuidae) in India. *Zootaxa*, 4750(2), zootaxa.4750.2.13. Available from: https://doi.org/10.11646/ZOOTAXA.4750.2.13

Gutiérrez-Ramírez, A., Robles-Bermúdez, A., Cambero-Campos, J., Santillán-Ortega, C., Ortíz-Catón, M., Coronado-Blanco, J.M., et al. (2015) Parasitoids of *Spodoptera frugiperda* (Lepidoptera: Noctuidae) found in Nayarit, Mexico. *Southwestern Entomologist*, 40(3), 555–564. Available from: https://doi.org/10.3958/059.040.0314

Hansson, C., Alex Smith, M., Janzen, D.H. & Hallwachs, W. (2015) Integrative taxonomy of New World *Euplectrus* Westwood (Hymenoptera, Eulophidae), with focus on 55 new species from Area de Conservación Guanacaste, northwestern Costa Rica. *ZooKeys*, 485(485), 1–236. Available from: https://doi.org/10.3897/ZOOKEYS.485.9124

Jaraleño-Teniente, J., Lomeli-Flores, J.R., Rodríguez-Leyva, E., Bujanos-Muñiz, R. & Rodríguez-Rodríguez, S.E. (2020) Egg parasitoids survey of *Spodoptera frugiperda* (Smith) (Lepidoptera: Noctuidae) in maize and sorghum in Central Mexico. *Insects*, 11(3), 157. Available from: https://doi.org/10.3390/INSECTS11030157

Kenis, M., du Plessis, H., Van den Berg, J., Ba, M.N., Goergen, G., Kwadjo, K.E., et al. (2019) *Telenomus remus*, a candidate parasitoid for the biological control of *Spodoptera frugiperda* in Africa, is already present on the continent. *Insects*, 10(4), 92. Available from: https://doi.org/10.3390/INSECTS10040092

Kittel, R.N. & Austin, A.D. (2014) Synopsis of Australian chelonine wasps (Hymenoptera: Braconidae: Cheloninae) with description of two new genera. *Austral Entomology*, 53(2), 183–202. Available from: https://doi.org/10.1111/aen.12070

Li, T.H., de Freitas Bueno, A., Desneux, N., Zhang, L., Wang, Z., Dong, H., et al. (2023) Current status of the biological control of the fall armyworm *Spodoptera frugiperda* by egg parasitoids. *Journal of Pesticide Science*, 96(4), 1345–1363. Available from: https://doi.org/10.1007/s10340-023-01639-z

Liao, Y.L., Yang, B., Xu, M.F., Lin, W., Sen, W.D., Chen, K.W., et al. (2019) First report of *Telenomus remus* parasitizing *Spodoptera frugiperda* and its field parasitism in southern China. *Journal of Hymenoptera Research*, 73, 95–102. Available from: https://doi.org/10.3897/JHR.73.39136

Meagher, R.L., Nuessly, G.S., Nagoshi, R.N. & Hay-Roe, M.M. (2016) Parasitoids attacking fall armyworm (Lepidoptera: Noctuidae) in sweet corn habitats. *Biological Control*, 95, 66–72. Available from: https://doi.org/10.1016/j.biocontrol.2016.01.006

Michael, P.J., Woods, W., Lawrence, P.J. & Fisher, W. (1984) Introduced parasites for the control of Australian noctuid pests. Proceedings of the Fourth Australian Applied Entomological Research Conference, Adelaide 24-28 September 1984. Pest Control: Recent Advances and Future Prospects 294–303.

Minh, B.Q., Schmidt, H.A., Chernomor, O., Schrempf, D., Woodhams, M.D., von Haeseler, A., et al. (2020) IQ-TREE 2: new models and efficient methods for phylogenetic inference in the genomic era. *Molecular Biology and Evolution*, 37(5), 1530–1534. Available from: https://doi.org/10.1093/MOLBEV/MSAA015

Molina-Ochoa, J., Carpenter, J.E., Heinrichs, E.A. & Foster, J.E. (2003) Parasitoids and parasites of *Spodoptera frugiperda* (Lepidoptera: Noctuidae) in the Americas and the Caribbean Basin: an inventory. *Florida Entomologist*, 86(3), 254–289. Available from: https://doi.org/10.1653/0015

Molina-Ochoa, J., Carpenter, J.E., Lezama-Gutiérrez, R., Foster, J.E., González-Ramírez, M., Andres Angel-Sahagún, C., et al. (2004) Natural distribution of hymenopteran parasitoids of *Spodoptera frugiperda* (Lepidoptera: Noctuidae) larvae in Mexico. *The Florida Entomologist*, 87(4), 461–472. Available from: https://doi.org/10.1653/0015-4040(2004)087[0461:NDOHPO]2.0.CO;2

Murúa, M.G., Molina-Ochoa, J. & Fidalgo, P. (2009) Natural distribution of parasitoids of larvae of the fall armyworm, *Spodoptera frugiperda in Argentintina*. *Journal of Insect Science*, 9(20), 20. Available from: https://doi.org/10.1673/031.009.2001

Natural History Museum. (2014) Specimens (from Collection specimens). Available from: https://data.nhm.ac.uk/dataset/collection-specimens/resource/05ff2255-c38a-40c9-b657-13944ccb55ab2feb

Nguyen, L.T., Schmidt, H.A., Von Haeseler, A. & Minh, B.Q. (2015) IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Molecular Biology and Evolution*, 32(1), 268–274. Available from: https://doi.org/10.1093/molbev/msu300

Nixon, G.E.J. (1937) Some Asiatic Telenominae (Hym., Proctrupoidea). *Annals and Magazine of Natural History*, 20(118), 444–475. Available from: https://doi.org/10.1080/00222933708655367

Ogunfunmilayo, A.O., Kazeem, S.A., Idoko, J.E., Adebayo, R.A., Fayemi, E.Y., Adedibu, O.B., et al. (2021) Occurrence of natural enemies of fall armyworm, *Spodoptera frugiperda* (Lepidoptera: Noctuidae) in Nigeria. *PLoS ONE*, 16(7), e0254328. Available from: https://doi.org/10.1371/journal.pone.0254328

Otim, M.H., Aropet, S.A., Opio, M., Kanyesigye, D., Opolot, H.N. & Tay, W.T. (2021) Parasitoid distribution and parasitism of the fall armyworm *Spodoptera frugiperda* (Lepidoptera: Noctuidae) in different maize producing regions of Uganda. *Insects*, 12(2), 1–20. Available from: https://doi.org/10.3390/INSECTS12020121

Papp, J. (1997) Revision of the *Chelonus* s. str. Species described by C. G. Thomson (Hymenoptera: Braconidae, Cheloninae). *Stobaeana: Occasional Papers Published by the Museum of Zoology, Lund University, Sweden*, 10(10), 1–21. Available from: https://doi.org/10.5962/p.345490

Plant Health Australia. (2023) Genomic insights of FAW movement in Australia.

Pomari, A.F., Bueno de, F.A. & Bueno RCO de F, Junior ADOM & Fonseca ACPF. (2013) Releasing number of *Telenomus remus* (Nixon) (Hymenoptera: Platygastridae) against *Spodoptera frugiperda* Smith (Lepidoptera: Noctuidae) in corn, cotton and soybean. *Ciência Rural*, 43(3), 377–382. Available from: https://doi.org/10.1590/S0103-84782013005000013

Qi, G.J., Ma, J., Wan, J., Ren, Y.L., McKirdy, S., Hu, G., et al. (2021) Source regions of the first immigration of fall armyworm, *Spodoptera frugiperda* (Lepidoptera: Noctuidae) invading Australia. *Insects*, 12(12), 1104. Available from: https://doi.org/10.3390/insects12121104

Qiu, B., Zhou, Z. & Xu, Z. (2013) Age preference and fitness of *Microplitis manilae* (Hymenoptera: Braconidae) reared on *Spodoptera exigua* (Lepidoptera: Noctuidae). *Florida Entomologist*, 96(2), 602–609. Available from: https://doi.org/10.1653/024.096.0227

Rajapakse, R.H.S., Ashley, T.R. & Waddill, V.H. (1985) Biology and host acceptance of *Microplitis manilae* (Hymenoptera: Braconidae) raised on fall armyworm larvae *Spodoptera frugiperda* (Lepidoptera: Noctuidae). *The Florida Entomologist*, 68(4), 653–657. Available from: https://doi.org/10.2307/3494869

Ratnasingham, S. & Hebert, P.D.N. (2013) A DNA-based registry for all animal species: the barcode index number (BIN) system. *PLoS ONE*, 8(8), e66213. Available from: https://doi.org/10.1371/journal.pone.0066213

Sagar, D., Suroshe, S.S., Keerthi, M.C., Poorani, J., Gupta, A. & Chandel, R.K. (2022) Native parasitoid complex of the invasive fall armyworm, *Spodoptera frugiperda* (J. E. Smith) from Northern India. *International Journal of Tropical Insect Science*, 42(3), 2773–2778. Available from: https://doi.org/10.1007/s42690-022-00743-4

Sartiami, D., Dadang, H.I.S., Kusumah, Y.M. & Anwar, R. (2020) First record of fall armyworm (*Spodoptera frugiperda*) in Indonesia and its occurrence in three provinces. *IOP Conference Series: Earth and Environmental Science*, 468(1), 012021. Available from: https://doi.org/10.1088/1755-1315/468/1/012021

Serrano-Domínguez, A.K., Coronado-Blanco, J.M., Ruíz-Cancino, E., López-Santillán, J.A., Estrada-Drouaillet, B. & Salas-Araiza, M.D. (2021) Parasitoids of fall armyworm, *Spodoptera frugiperda* (J.E. Smith), at three localities of the state of Tamaulipas, Mexico. *South West Entomology*, 45(4), 907–916. Available from: https://doi.org/10.3958/059.045.0407

Sharanabasappa, D., Kalleshwaraswamy, C.M., Poorani, J., Maruthi, M.S., Pavithra, H.B. & Diraviam, J. (2019) Natural enemies of *Spodoptera*

*frugiperda* (J. E. Smith) (Lepidoptera: Noctuidae), a recent invasive pest on maize in South India. *Florida Entomologist*, 102(3), 619–623. Available from: https://doi.org/10.1653/024.102.0335

Shauff, M.E. & Janzen, D.H. (2001) Taxonomy and ecology of Costa Rican *Euplectrus* (Hymenoptera: Eulophidae), parasitoids of caterpillars (Lepidoptera). *Journal of Hymenoptera Research*, 10(2), 181–230.

Sparks, A.N. (1979) A review of the biology of the fall armyworm. *The Florida Entomologist*, 62(2), 82–87. Available from: https://doi.org/10.2307/3494083

Stevens, N.B., Austin, A.D. & Jennings, J.T. (2010) Synopsis of Australian agathidine wasps (Hymenoptera: Braconidae: Agathidinae). *Zootaxa*, 26(2480), 1–26. Available from: https://doi.org/10.11646/zootaxa.2480.1.1

Sturza, V.S., Bastos Dequech, S.T., Tavares, M.T., Guths, C., Walker, M.P. & Bolzan, A. (2013) *Euplectrus furnius* parasitizing *Spodoptera frugiperda* in maize in Brazil. *Ciência Rural*, 43(11), 1958–1960. Available from: https://doi.org/10.1590/S0103-84782013001100006

Sun, X.X., Hu, C.X., Jia, H.R., Wu, Q.L., Shen, X.J., Zhao, S.Y., et al. (2021) Case study on the first immigration of fall armyworm, *Spodoptera frugiperda* invading into China. *Journal of Integrative Agriculture*, 20(3), 664–672. Available from: https://doi.org/10.1016/S2095-3119(19)62839-X

Trifinopoulos, J., Nguyen, L.T., von Haeseler, A. & Minh, B.Q. (2016) W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. *Nucleic Acids Research*, 44(W1), W232–W235. Available from: https://doi.org/10.1093/NAR/GKW256

Vas, Z. (2019) Contributions to the taxonomy, identification, and biogeography of *Eriborus* Förster, 1869 and Nepiesta Förster, 1869 (Hymenoptera: Ichneumonidae: Campopleginae). *Opuscula Zoologica*, 50(1), 87–98. Available from: https://doi.org/10.18348/opzool.2019.1.87

Watanabe, C. (1932) A revision of braconid-species parasitic in the injurious insects of rice-plant and sugar-cane in Japan and Formosa. *Transactions of the Sapporo Natural History Society*, 12(2), 63–71.

Wengrat, A.P.G.S., Coelho Junior, A., Parra, J.R.P., Takahashi, T.A., Foerster, L.A., Corrêa, A.S., et al. (2021) Integrative taxonomy and phylogeography of *Telenomus remus* (Scelionidae), with the first record of natural parasitism of *Spodoptera* spp. in Brazil. *Scientific Reports*, 11(1), 14110. Available from: https://doi.org/10.1038/s41598-021-93510-3

Yoder, M.J., Mikó, I., Seltmann, K.C., Bertone, M.A. & Deans, A.R. (2010) A gross anatomy ontology for hymenoptera. *PLoS ONE*, 5(12), e15991. Available from: https://doi.org/10.1371/journal.pone.0015991

Youssef, M.A.M. (2021) The first report to record the parasitoids of the fall armyworm, *Spodoptera frugiperda* in Egypt. *SVU-International Journal of Agricultural Sciences*, 3(2), 52–57. Available from: https://doi.org/10.21608/svuijas.2021.65535.1086

Zhu, C.-D. & Huang, D.-W. (2003) A study of the genus *Euplectrus* Westwood (Hymenoptera: Eulophidae) in China. *Zoological Studies*, 42(1), 140–164.

## SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

**How to cite this article:** Fagan-Jeffries, E.P., Miles, M.M., Atkin-Zaldivar, T.-C.C., Howe, A.G., Subramaniam, S., Chambers, D.M. et al. (2024) Hymenopteran parasitoids of fall armyworm (*Spodoptera frugiperda* (J.E. Smith) (Lepidoptera: Noctuidae)) in Australia, with the description of five new species in the families Braconidae and Eulophidae. *Austral Entomology*, 63(2), 136–174. Available from: https://doi.org/10.1111/aen.12682