Biodiversity, taxonomy and systematics of Australian microgastrine parasitoid wasps (Hymenoptera: Braconidae)

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Abstract

Microgastrine wasps are one of the most species-rich groups of Hymenoptera on the planet. There are currently over 2,700 species described in 81 genera, but the highest estimates of true species diversity reach 40,000. As endoparasitoids of lepidopteran larvae, often with high host specificity, microgastrines are successful biological control agents and have the potential to be used in many more applications. In Australia, little taxonomic work has been done on the subfamily since the 1990s, and barely any molecular studies have been undertaken that include Australian fauna. Including those described as new in this study, there are approximately 130 species in 22 genera described from Australia. In this collection of work on the Australian microgastrines, a large DNA barcoding and species delimitation study is carried out using high-throughput methods, providing a framework for rapid species descriptions and giving new insight into the diversity of the subfamily in Australia. Intragenomic variation of the internal transcribed spacer 2 region was discovered in the analysis of the DNA barcoding data, and this was explored for the genus *Diolcogaster*. A review and description of two new species in the genus *Choeras* is undertaken, and three new species from the genus *Dolichogenidea* with exceptionally long ovipositors are described. Finally, this DNA barcoding framework is used to describe several new species collected on 'Bush Blitz' surveys of regional reserves. These results and insights are discussed in the context of the broader microgastrine story, and future research directions are suggested.

Declaration

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Full citations of publications that appear in this thesis:

Fagan-Jeffries E.P., Cooper S.J.B., Bertozzi T., Bradford T.M., Austin A.D. 2018. DNA barcoding of microgastrine parasitoid wasps (Hymenoptera: Braconidae) using high-throughput methods more than doubles the number of species known for Australia. Molecular Ecology Resources. 18:1132–1143.

Fagan-Jeffries E.P., Austin A.D. 2018. Synopsis of the parasitoid wasp genus *Choeras* Mason (Hymenoptera: Braconidae: Microgastrinae) from Australasia, with the description of two new species. Austral Entomology. 57:349–358.

Fagan-Jeffries E.P., Cooper S.J.B., Austin A.D. 2018. Three new species of *Dolichogenidea* Viereck (Hymenoptera, Braconidae, Microgastrinae) from Australia with exceptionally long ovipositors. Journal of Hymenoptera Research. 64:177–190.

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Signed: _____ **Date:** 12/10/2018

Erinn Fagan-Jeffries

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Chapter 1: Introduction and a review of the literature

Like a wasp larva nestled inside a caterpillar host, this project is nestled within the broader field of insect phylogenetics and taxonomy, and in the context of the biology and life history of microgastrine wasps. An understanding of the relationships within the subfamily Microgastrinae therefore needs to be associated with an understanding of the placement of the subfamily within the wider classification of the order. This introductory chapter outlines the current situation and recent advancements in building phylogenies of the insects, hymenopterans, the braconids and the microgastrines. Background on the parasitism strategies of microgastrine wasps, their association with polydnaviruses, and their uses as biological control agents are presented. Information on DNA barcoding of the group and recently developed molecular techniques utilised in parts of this project are provided, and the project aims are presented.

Insect Taxonomy, Evolution and Phylogenetics

There is no argument that insects are the most diverse class of eukaryote organisms on the planet, with over one million species formally described (Chapman 2009), accounting for 66% of all described animal species (Zhang 2011). Recent estimates of the true number of insect species reach 5.5 million, suggesting published descriptions are just a fraction of their real diversity (Stork *et al.* 2015). The importance of taxonomy is thus not to be understated, with debate surrounding whether or not it is actually possible to name and describe insect biodiversity before it goes extinct (Mora *et al.* 2013; Costello *et al.* 2013). The impacts of an understudied earth are now beginning to be understood outside the scientific community, with popular news articles highlighting that a lack of taxonomic knowledge impinges on the ability to effectively implement conservation strategies (Wilson 2018). In Australia, the nation's Academy of Science recently published a decadal plan to attempt to address these issues and drive taxonomy and systematics into the future by establishing key goals and practices (Taxonomy Decadal Plan Working Group 2018).

Taxonomy is intrinsically linked with the understanding of systematics and evolution. The advancement of molecular technologies has led to great leaps in understanding the evolution of insects, with recent studies using genetic information to ascertain the relationships amongst insect orders with improved reliability (e.g. Wiegmann *et al.*, 2009; reviewed in Trautwein *et al.*, 2012). Even more recently, the development of Next Generation Sequencing (NGS) techniques has caused a massive shift in the amount of data available. Whilst Weigmann *et al.* (2009) used six protein-coding genes to reconstruct a phylogeny of the insects, Misof *et al.* (2014) employed transcriptome-based NGS to amass 1,478 protein coding genes. This incredible increase in the amount of information available has led to a robust and generally accepted phylogeny. The insects were recovered as a

monophyletic group within Hexapoda originating approximately 440 million years ago (mya), with Diplura (two-pronged bristletails) the closest extant relative. Zygentoma (silverfish) was the sister lineage to the winged insects (Pterygota). The Holometabola (insects that undergo complete metamorphosis) had support as a monophyletic group that originated 345 mya, with the diversification within the Hymenoptera contemporary with the radiation of flowering plants in the Early Cretaceous (Misof *et al.* 2014).

The Hymenoptera

The Hymenoptera is an incredibly diverse order of insects containing the sawflies, ants, bees and wasps, with over 153,000 species formally described (Aguiar *et al.* 2013). Despite the order Coleoptera traditionally thought to hold the title of the most diverse insect order, there is a strong argument for the Hymenoptera far exceeding this, with estimates based on parasitoid-host ratios suggesting there are likely to be over a million species of hymenopterans (Forbes *et al.* 2018). They have spread to every ice-free habitat on the planet in a huge variety of ecological niches and lifestyles; they exist as pollinators, parasitoids, predators, plant feeders, eusocial groups and solitary species.

As with all groups of organisms, the understanding of relationships within the Hymenoptera has advanced with the advent of molecular phylogenetics, and earlier attempts brought clarity to many internal relationships (Heraty *et al.* 2011; Klopfstein *et al.* 2013). Recently, however, the application of NGS techniques has resulted in an extremely well supported phylogeny of the order (Peters *et al.* 2017; Fig. 1). Using 3,256 protein-coding genes extracted from transcriptomes of 173 species, the results of Peters *et al.* (2017) suggest that the extant Hymenoptera began diversifying 281 mya, with parasitoid wasps descended from a single endophytic parasitoid ancestor at approximately 247 mya. Within a strongly supported Parasitoida clade, the Ichneumonoidea was found to be sister to the Ceraphronoidea with reasonably high support, and these two groups together formed the sister clade to the Proctotrupomorpha (Fig. 1).

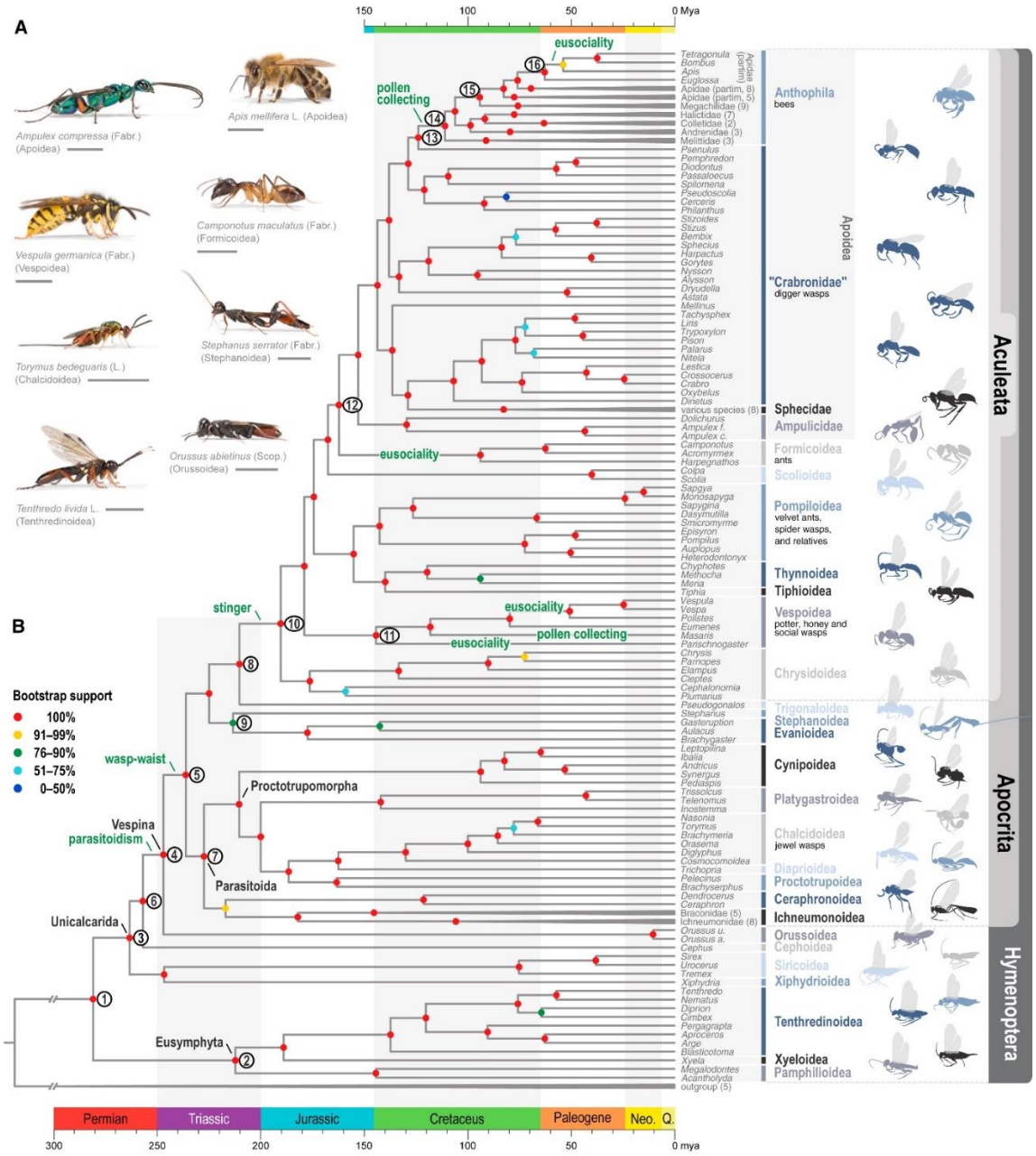

Figure 1: Evolutionary History of the Hymenoptera (A) Representatives of sawflies, wasps, ants, and bees. Scale bars represent 5 mm. (B) Phylogenetic relationships and divergence time estimates of Hymenoptera. Key evolutionary events are indicated at the respective clades (note that only the major eusocial lineages are considered). The tree was inferred under the maximum-likelihood optimality criterion, analyzing 1,505,514 amino acid sites and applying a combination of protein domain- and gene-specific substitution models. Divergence times were estimated with an independent-rates molecular clock approach and considering 14 validated fossils. Triangular branches cover multiple species (number of species in parentheses). Nodes with circled numbers are referred to in the main text. Node colours represent bootstrap support values (see figure for key to values) (from Peters *et al.* 2017; Fig. 1)

Ichneumonoidea

The two families of the Ichneumonoidea, the Ichneumonidae and Braconidae, are strongly supported as monophyletic sister lineages, and are distinguished morphologically primarily by a presence or absence of a forewing vein. The two families contain numerous ecologically and economically important species and are both incredibly diverse, with over 47,000 species described (Yu *et al.* 2016). Both families are found worldwide, mostly as parasitoids of insects or other arthropods. They are of interest not only because of their evolutionary history, but because of the diversity of their parasitic strategies, the mutualistic viruses some groups use to assist them in this endeavour, and their application as biological control agents.

Parasitoids and Parasitism

Parasitoids are parasitic organisms that must kill the host as part of the development from parasitic larva to free-living adult, as opposed to a more typical parasite, which will keep the host alive for multiple generations of the parasite. They are broadly classified into endparasitoids (attaching on the outside of the host), endoparasitoids (feeding within the host), idiobiont (prevent the host from developing after parasitism) and koinobiont (allow the host to continue developing). Species may employ a gregarious (where more than one larva develops inside a single host) or solitary (a female wasp deposits just one egg inside a host) mode of parasitism. Microgastrines are koinobiont endoparasitoids, with species covering both solitary and gregarious modes of development (Whitfield *et al.* 2018).

The challenge for all endoparasitoids is keeping their offspring alive once they are deposited in the host, as the automatic immune defence reaction of the host is to attack any foreign material. Common tactics used by parasitic wasps to combat the automatic immune response of the host are protective coatings on the eggs that resist encapsulation by the host's haemocytes, oviposition into parts of the host where haemocytes have no access, and injected venoms (reviewed in Quicke 2015). An innovative method used by two subfamilies of the Ichneumonidae (Banchinae and Campopleginae) and a monophyletic group of several subfamilies within the Braconidae (the microgastroid complex) is the transfer of a virus from the wasp to the host that causes the suppression of the immune system (Edson *et al.* 1981).

Polydnaviruses

In the late 1960s and the 1970s, particles resembling viruses were found in the reproductive tract of parasitoid wasps from the Ichneumonoidea (Rotheram 1967; Vinson and Scott 1975). These particles were later discovered to be a new family of viruses, named the Polydnaviridae because of their segmented, double stranded, circular DNA (Stoltz *et al.*

1984). A single virus genome has multiple circular molecules of DNA; depending on the species, the genome can be segmented into 15-56 different circular molecules (Dupuy *et al.* 2012). It was later discovered that there are two separate genera of viruses: those found in the ichneumonid subfamily Campopleginae (*Ichnovirus*) and those in the braconids (*Bracovirus*). There is also a virus found in the ichneumonid subfamily Banchinae that is proposed as a third type of polydnavirus (PDV) with a possible independent origin (Lapointe *et al.* 2007). These virus genera do not form a monophyletic grouping, and are suggested to have convergent lifecycles because of the similar roles they play in the parasitism of hosts by their respective wasp groups (reviewed in Strand and Burke, 2015).

Polydnaviruses are a vital component of the wasp's parasitoid strategy. The survival of the juvenile wasp relies on injection of the PDV by the female and the subsequent disabling of the immune defences (Edson *et al.*, 1981). The wasp and virus therefore have a mutualistic association, and it has been suggested that PDVs would have helped drive diversification by allowing the wasp species to adapt to using thousands of different hosts (Belle *et al.* 2002). In a study where an ichnovirus was examined in two hosts that were 'permissive' (majority of the parasitoid eggs survived) and two hosts which were 'non-permissive' (majority of the parasitoid eggs were killed by the host's immune response), it was discovered that the gene expression of the virus differed. Viral genes were less well transcribed in the non-permissive hosts, signifying the ability of the PDV to adapt to different species plays a large part in the host specification of the parasitoid (Dorémus *et al.* 2014). Very recently, PDVs have also been shown to have a potentially negative effect on the wasp progeny, allowing them to become increasingly attractive to hyperparasitoids (parasitoids which themselves parasitise parasitoids of other animals) through altered plant volatiles from the feeding of parasitised caterpillars (Zhu *et al.* 2018).

Bracoviruses are most closely related to nudiviruses, which are pathogens of a diverse range of insects. The bracoviruses are suggested to have evolved from a nudivirus-related ancestor that was incorporated into the wasp genome approximately 100 mya, at the origin of the microgastroid lineage (Murphy *et al.* 2008; Bézier *et al.* 2009). Recent visualisation of *Bracovirus* has shown that a linear form of the circular virus DNA is integrated into the wasp genome, arranged as a macro-locus on chromosome five of the microgastrines species *Cotesia congregata* (Belle *et al.* 2002). Bracoviruses have also been shown to be vectors for horizontal gene transfer between a wasp and its host. Gasmi *et al.* (2015) recently found evidence of wasp genes that had been integrated into the germ line cells of Lepidoptera, facilitated by the transferred bracovirus.

Theze *et al.* (2011) attempted to link the evolution of different arthropod virus families to the evolution of major host groups, but found a lack of co-phylogeny; the major virus families and their host orders diversified independently. On a much smaller scale, however, there appears to be a strong link between the phylogenies of species of a braconid genus and their associated bracoviruses (Whitfield, 2000; Whitfield and Asgari, 2003; Fig. 2). This work by Whitfield (2000) was novel in sequencing a PDV gene from species in the braconid genus *Cotesia* for use in constructing a virus phylogeny to compare with that of sequenced *Cotesia* species. However, no further published work has followed up on this analysis. It is now thought that because the virus genes are integrated into the genome of the wasp, they are not independent sources of genetic information, and may not be able to be used in co-evolution analyses with wasp genes (Whitfield, pers. comm.).

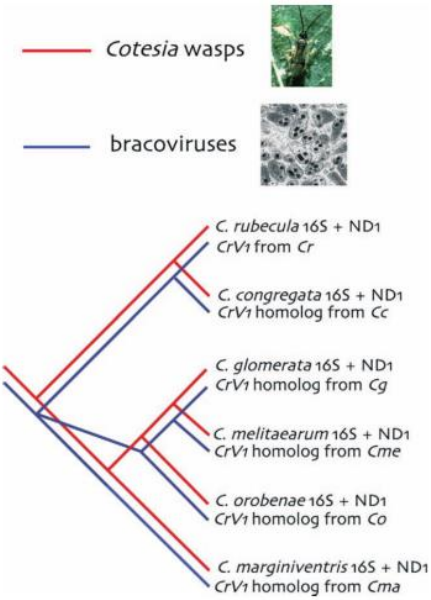

Figure 2: Co-phylogenetic pattern of *Cotesia* species and their bracoviruses (from Whitfield and Asgari 2003; Fig. 3).

Braconidae

There are over 21,000 species described of braconids (Yu *et al.* 2016), with the family traditionally being divided into the cyclostomes (depressed clypeus and concave, glabrous labrum) and the non-cyclostomes (flat or convex clypeus and flat, setose labrum). Within the non-cyclostomes is the microgastroid complex, the only group of braconid subfamilies known to possess bracoviruses. All non-cyclostomes are koinobiont endoparasitoids, whilst the cyclostomes contain ecto- and endoparasitoids, koinobionts and idiobionts, and even phytophagous species. It is suggested that ectoparasitism was the ancestral state and the switch to endoparasitism and phytophagy has occurred multiple independent times in the family (Zaldivar-Riverón *et al.* 2006).

The use of molecular data to infer the evolutionary history of the braconid subfamilies has been applied since 1998 (Dowton and Austin 1998; Dowton *et al.* 2002). The most recent attempt to analyse the relationships within the family using four nuclear genes produced a reasonably well resolved phylogeny, at least for the backbone of the tree (Sharanowski *et al.* 2011; Fig. 3), but the taxon sampling in this study was sparse for some groups. The non-cyclostomes were found to be sister to a clade containing the cyclostomes and the aphidioid complex. In the analysis of Shi *et al.* (2005), using a phylogeny built from three genes and morphological data, the cyclostomes were recovered as monophyletic, but the aphidioid complex was found within the non-cyclostomes. Both analyses found support for other informal subfamily groupings, particularly the heleconoids within the non-cyclostomes. A monophyletic microgastroid complex was recovered in both analyses; its sister group, the sigalphoid complex (also generally parasitoids of lepidopteran larvae), was weakly supported in all of the analyses of Sharanowski *et al.* (2011), but not in those of Shi *et al.* (2005). All of the above-mentioned studies lacked comprehensive taxon sampling and used only a few standard markers, and, as with the phylogeny of the Hymenoptera, the use of NGS will likely lead to stronger support for what are currently ambiguous relationships.

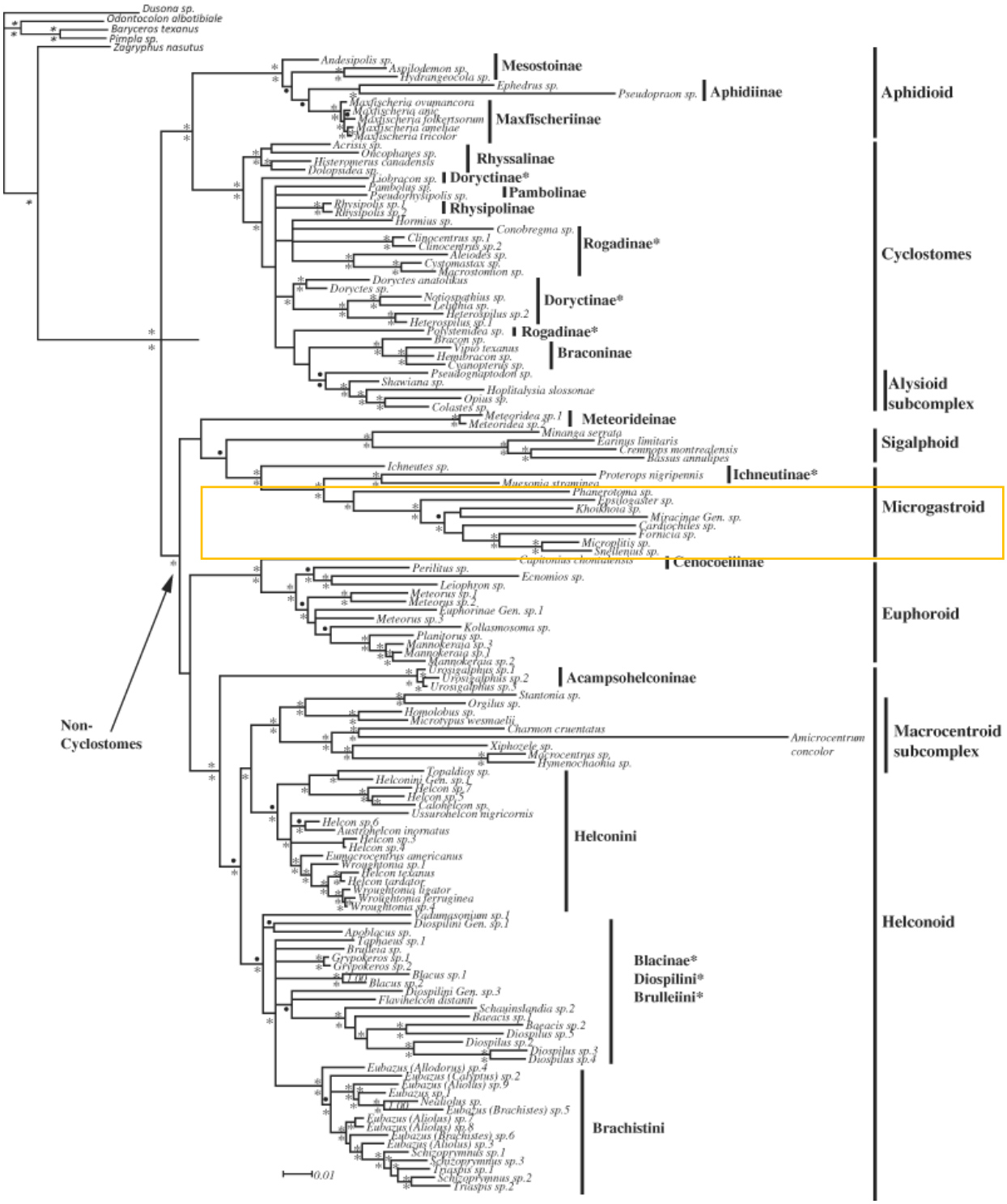

Figure 3: Inferred topology of braconid relationships, from the Bayesian analysis of four genes, posterior probabilities below the node: an asterisk if ≥0.95, a black dot if between 0.90 and 0.94. Bootstrap values above the node: an asterisk if over 70, a black dot if between 50 and 69. An orange box highlights the microgastroid complex (from Sharanowski *et al.* 2011; Fig. 2).

As stated above, the minimum age of the microgastroid lineage, and thus the association of these wasps with bracoviruses, is estimated to be approximately 100 million years (Murphy *et al.* 2008). Despite numerous studies focussing on the group (Dowton and Austin 1998; Banks and Whitfield 2006; Murphy *et al.* 2008; Sharanowski *et al.* 2011), the relationships within the complex are still contentious. Whilst it is undoubtedly a monophyletic group containing the Ichneutinae, Dirrhopinae, Cheloninae, Cardiochilinae, Khoikhoiinae, Mendesellinae, Microgastrinae and Miracinae, the relationships between these subfamilies have differed among recent analyses (Fig. 4). It is generally agreed that Ichneutinae and Cheloninae are sister clades to the rest of the microgastroids, but the relationships among other subfamilies is still in flux. The small subfamily Dirrhopinae is yet to be included in a molecular analysis (Quicke 2015). It has been suggested that the relationships within the microgastroids are particularly difficult to resolve because of the short internal branches, which are conceivably caused by a "radiation compressed in time" (Murphy *et al.*, 2008). This relates to a huge amount of diversification in a relatively rapid amount of evolutionary time, and is possibly the cause of a lack of resolution in phylogenetic trees that would otherwise appear to have sufficient data (Rokas *et al.* 2005).

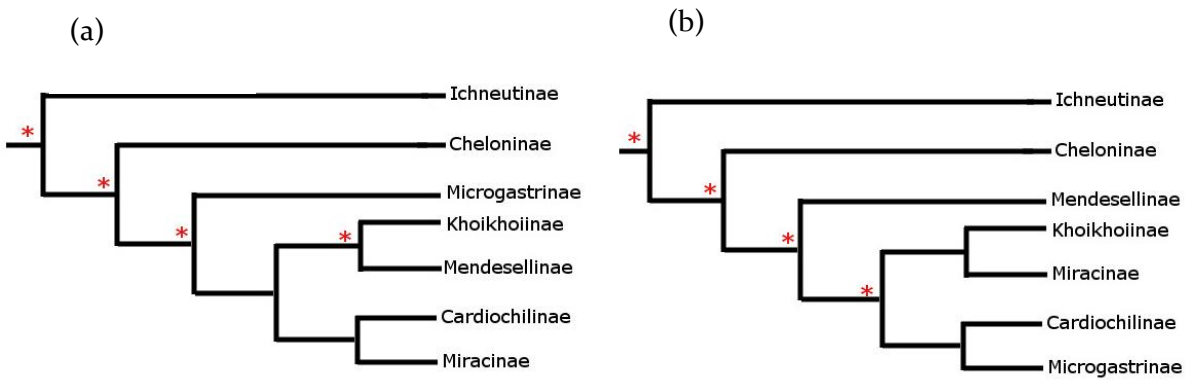

Figure 4: Conflicting relationships among microgastroid subfamilies. Simplified from (a) 7 gene dataset of Murphy *et al.* (2008) and (b) 4 gene dataset of Sharanowski *et al.* (2011). (*) indicates a node with ≥95% posterior probability in the Bayesian phylogenetic analysis. Note in (b), Ichneutinae was not recovered as monophyletic.

Microgastrinae

The Microgastrinae are a large subfamily exclusively containing koinobiont endoparasitoids of lepidopteran larvae (Whitfield *et al.* 2018), including both solitary and gregarious species that mostly oviposit into early instar caterpillars. There are approximately 2000 species described, however, recent estimates suggest the true diversity is in the range of 17,000 to 46,000 species (Rodriguez *et al.* 2013). The subfamily is hypothesised to result from a recent 'burst of radiation', with all 55 genera evolving in the

last 50 million years (Murphy *et al.* 2008). This sudden diversification is likely linked to the similarly swift radiation of their lepidopteran hosts (Mardulyn and Whitfield 1999).

The Microgastrinae subfamily is of considerable interest as biological control agents of lepidopteran pests because of the extreme host specificity of many species. In a study of 313 provisional wasp species reared from caterpillars in northwestern Costa Rica, 90% of the microgastrines were found to parasitise just one, two, or a very narrow group of caterpillar species (Smith *et al.* 2008). *Cotesia flavipes* is a commonly used parasitoid originating from the Indo-Asia region, and has been introduced to countries in Africa, and both South and North America, against sugarcane stemborer (*Diatraea saccharalis*) and other stemboring pests associated with gramineous crops. *Cotesia urabae* has been used against gum leaf skeletonisers in New Zealand (Avila *et al.* 2013), whilst *Apanteles opuntiarum* has been investigated for use against the cactus moth in Argentina (Varone *et al.* 2015). Species introduced into Australia for biological control reasons include *Apanteles subandinus*, a parasitoid of the potato tuber moth (*Phthorimaea operculella*), whilst native species used commonly in crops in Australia include *Dolichogenidea tasmanica* against light brown apple moth (*Epiphyas postvittana*). A robust phylogeny for both the subfamily and for different genera will aid the identification of other potential biocontrol agents by revealing the closest relatives to successfully developed species.

History of classification

The Microgastrinae was first erected by Foerster (1862), which he formed by splitting *Microgaster* Latreille into *Microgaster, Microplitis* and *Apanteles*, and adding the genera *Adelius*, *Mirax*, and *Dirrhope*. This classification lasted until 1965, when Nixon proposed three tribes within the family, excluding the genera *Adelius*, *Paradelius*, *Dirrhope* and *Oligoneurus*, and provided a detailed synopsis of the species-groups of *Apanteles* s.l. Mason (1981) undertook a major revision of the group, raising Nixon's tribes to subfamily level and creating five new tribes within the Microgastrinae: Apantelini, Microgastrini, Forniciini, Cotesiini, and Microplitini. He described 23 new genera, splitting the incredibly large and diverse *Apanteles* into multiple genera (many of which were recognised by Nixon (1965) as species-groups). However, to date, many species are yet to be assigned to these new genera and still remain in *Apanteles* s.l. The morphological characters used by Mason for his inferred relationships were criticised by Walker *et al.* (1990) and Austin (1990), but his generic classification system has been largely adopted. The modifications in the generic classification of the subfamily over time are neatly illustrated by Whitfield *et al.* (2018; Fig. 5). Since that review, an additional 18 new genera have been described, raising the number of recognised microgastrine genera to 81 (Xiong *et al.* 2017; Whitfield *et al.* 2018;

Fernández-Triana and Boudreault 2018) and the number of described species now exceeds 2,700 (Yu *et al.* 2016).

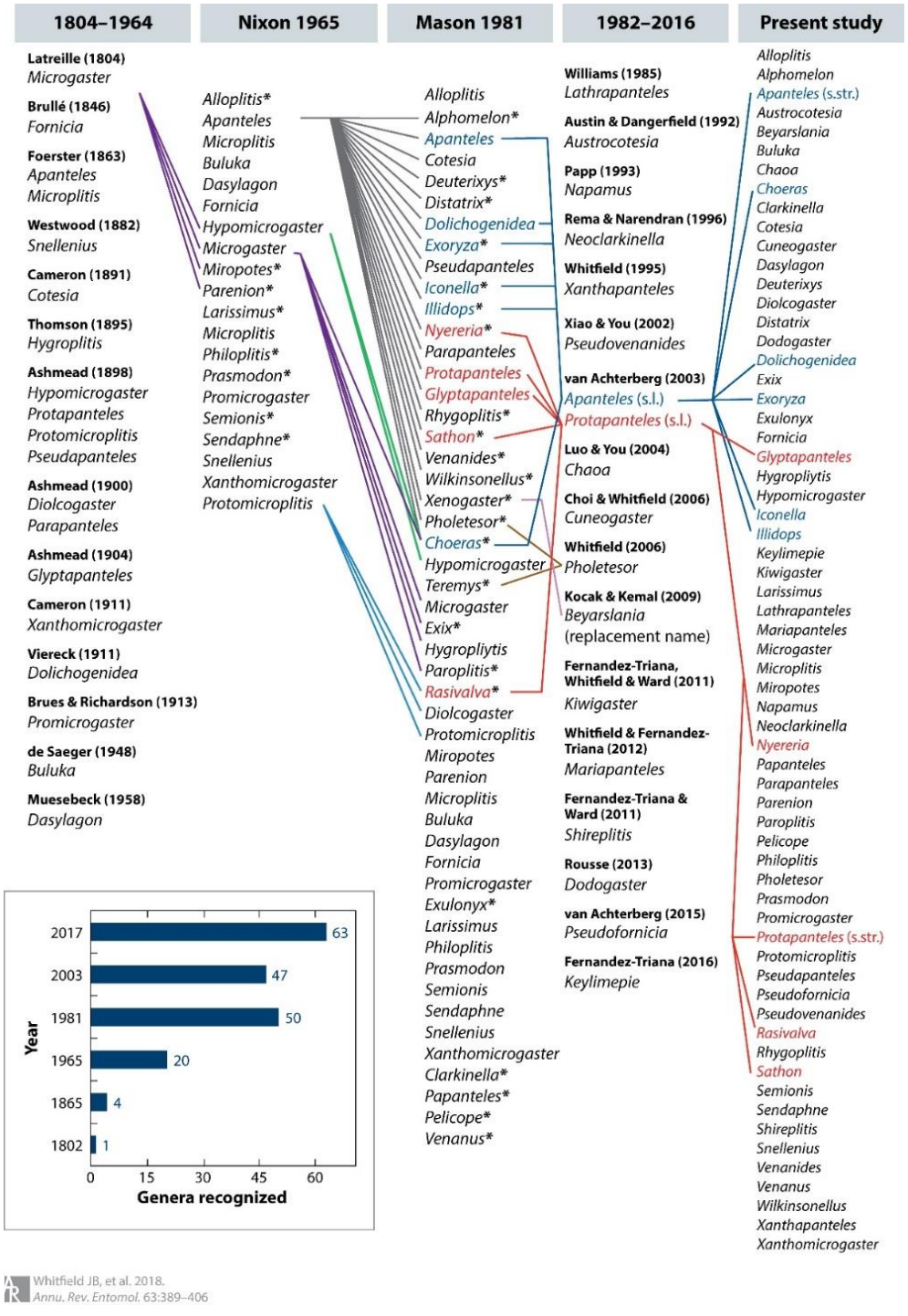

Figure 5: Historic changes in the generic classification of Microgastrinae (from Whitfield *et al.* 2018; Fig. 2).

Systematics and phylogenetics

The days of solely looking at morphology to understand the systematics and evolution of organisms have long passed. The use of molecular data to create phylogenies is now standard and with the advancement of next generation sequencing, an exponential amount of data are available for systematic studies. Using molecular data to build a phylogeny does, of course, come with issues and caveats. One such problem with using DNA sequences to create a tree is that the evolution of a gene is not necessarily the same as the evolution of the organisms involved (Nichols 2001). Most researchers attempt to combat this issue by using multiple genes and comparing the results or concatenating the data. However, it is possible for the most statistically likely gene tree of a sample to *not* be the species tree (Degnan and Rosenberg 2006). This latter point means that the addition of more genes does not necessarily resolve the issue, as the concatenated dataset will support the most frequent gene tree, regardless of whether it is truly representative of the species tree.

Another issue particularly relevant to understanding the evolution of microgastrine wasps is the difficulty of dealing with ancient rapid radiations. In these cases, the selection of appropriate genes for the timescale being analysed is incredibly important (Whitfield and Kjer 2008), but is often ignored in practice by choosing genes which are easy to amplify and sequence. The ability of NGS techniques to reveal new, phylogenetically useful markers, rather than simply adding more information, may aid the resolution of rapid radiations that currently cannot be resolved with standard, easily sequenced genes. It is also important when analysing these ancient rapid radiations to be wary of systematic bias among lineages, including differences in base composition, the sites free to vary, and rates of mutation (Whitfield and Kjer 2008). Genes that have been used with varying degrees of success in phylogenetic studies within, or including, the Microgastrinae are shown in Table 1. Even with the normalisation of next generation sequencing techniques, there are now questions around which method (e.g. Ultra-Conserved-Elements or Target-Enrichment using Exon-Capture probes) will provide the best answer for a particular question (Collins *et al.* 2018).

Table 1: Genes used in phylogenetic studies of, or including, the Microgastrinae

GENE	DESCRIPTION	TAXONOMIC LEVEL	REFERENCES
COI	Mitochondrial	Species complex (*Cotesia flavipes*)	(Muirhead *et al.* 2012)
		Genus subsection (*Cotesia*)	(Kankare and Shaw 2004; O'Connor 2011)
		Microgastrinae	(Whitfield *et al.* 2002)
		Microgastrinae	(Banks and Whitfield 2006)
		Microgastroid	(Murphy *et al.* 2008)
		Hymenoptera	(Klopfstein *et al.* 2013)
28S	Nuclear	Genus subsection (*Cotesia*)	(O'Connor 2011)
		Genus (*Cotesia*)	(Michel-Salzat and Whitfield 2004)
		Microgastrinae	(Whitfield *et al.* 2002)
		Microgastrinae	(Banks and Whitfield 2006)
		Microgastroid	(Murphy *et al.* 2008)
		Braconidae	(Sharanowski *et al.* 2011)
		Ichneumonidae	(Quicke *et al.* 2009)
		Hymenoptera	(Klopfstein *et al.* 2013)
16S	Mitochondrial	Species complex (*Cotesia flavipes*)	(Smith and Kambhampati 1999; Muirhead *et al.* 2012)
		Genus (*Cotesia*)	(Michel-Salzat and Whitfield 2004)
		Microgastrinae	(Whitfield *et al.* 2002)
		Microgastrinae	(Banks and Whitfield 2006)
		Microgastroid	(Murphy *et al.* 2008)
18S	Nuclear	Braconidae	(Sharanowski *et al.* 2011)
		Hymenoptera	(Klopfstein *et al.* 2013)
ArgK (Arginine kinase)	Nuclear	Microgastroid	(Murphy *et al.* 2008)
Long wavelength rhodopsin	Nuclear	Genus subsection (*Cotesia*)	(O'Connor 2011)
		Genus (*Cotesia*)	(Michel-Salzat and Whitfield 2004)
		Microgastroid	(Murphy *et al.* 2008)
Elongation factor 1 alpha	Nuclear	Microgastroid	(Murphy *et al.* 2008)
Wingless	Nuclear	Genus subsection (*Cotesia*)	(O'Connor 2011)
		Microgastroid	(Murphy *et al.* 2008)
NADH1	Mitochondrial	Species complex (*Cotesia flavipes*)	(Smith and Kambhampati 1999)
		Genus subsection (*Cotesia*)	(Kankare and Shaw 2004)
		Genus (*Cotesia*)	(Michel-Salzat and Whitfield 2004)
CfBN, CfCN, CfEN	Nuclear	Species complex (*Cotesia flavipes*)	(Muirhead *et al.* 2012)
CAD	Nuclear	Braconidae	(Sharanowski *et al.* 2011)
		Hymenoptera	(Klopfstein *et al.* 2013)
ACC	Nuclear	Braconidae	(Sharanowski *et al.* 2011)
RNA Polymerase II	Nuclear	Hymenoptera	(Klopfstein *et al.* 2013)
Alpha-spectrin	Nuclear	Genus subsection (*Cotesia*)	(O'Connor 2011)

The first significant attempt to use molecular information to analyse the relationships within the subfamily was by Mardulyn and Whitfield (1999). Using the genes *16S*, *28S* and *COI*, all of which theoretically had adequate phylogenetic signal, they were only able to obtain poorly resolved trees. In 2002, the same genes were combined with a morphological dataset built through collaboration with Mason, reworking much of the coding from his original 1981 research (Whitfield *et al.* 2002). Despite the large amount of data, resolution of the basal branches was still poor. It had also become clear that relying on a few significant morphological character systems was oversimplifying relationships, particularly because of convergence in ovipositor characters caused by similar parasitism strategies (Whitfield *et al.*, 2002).

Banks and Whitfield (2006) tackled the microgastrine phylogeny with a total of seven genes and morphological characters and achieved reasonable resolution in some parts of the tree in the combined dataset. Markedly, the three largest tribes erected by Mason (1981), Apantelini, Microgastrini and Cotesiini, were not monophyletic. The addition of morphological data caused the support for several branches to increase substantially compared to the molecular tree (Fig. 6). Their statistical projections imply an "enormous and likely impossible [for the time]" amount of DNA data would be needed to achieve resolution across the whole microgastrine phylogeny if only molecular data are used. However, with the advancement of sequencing technologies in the last few years, this seemingly impossible task may not be that far out of reach. Such a phylogeny will be essential for determining the validity of genera that are still controversial, such as *Iconella*, which Mason (1981) separated from *Apanteles*. *Iconella* is recognised by some authors (Fernández-Triana *et al.* 2013a), yet not by others (van Achterberg 2002). Once this phylogeny has been established, it will also provide a predictive framework for understanding the evolution of various biological traits and patterns of host utilisation. Work on building a phylogeny of the subfamily using Anchored Hybrid Enrichment techniques is currently underway and shows great promise in resolving nodes that up until now had at best limited support, but a complete published phylogeny is likely still a few years away due to the need to adequately sample the many microgastrine genera and species groups for it to be informative (Whitfield *et al.* 2018).

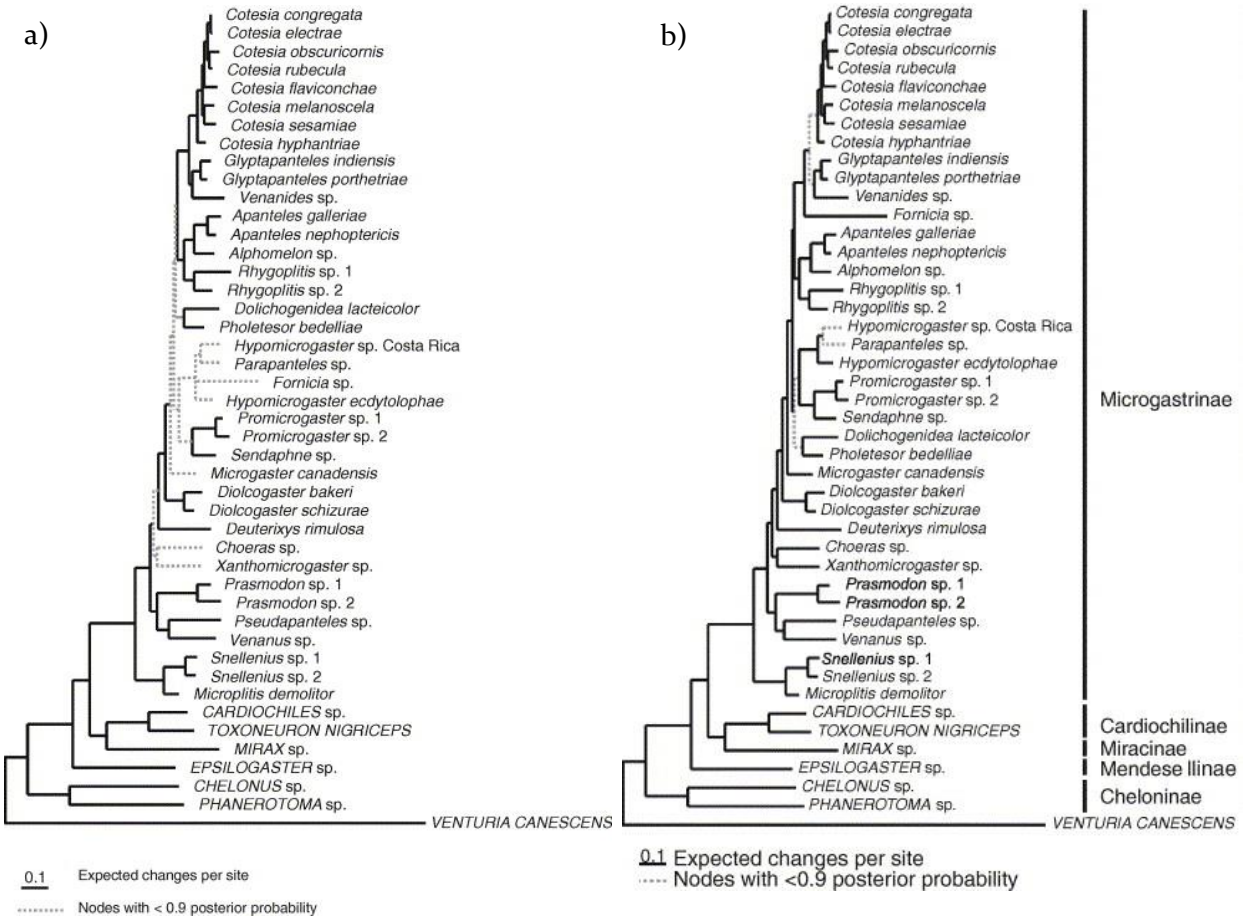

Figure 6: Bayesian analysis of microgastrine relationships of a) 7 genes, and b) 7 genes and 53 morphological characters. Solid lines indicate > 90% posterior probability support, whilst dotted lines represent less than 90% posterior probability support (from Banks and Whitfield 2006; Figs. 3 & 7).

DNA barcoding the microgastrines

An initial attempt to DNA barcode the global microgastrine fauna using the standard *COI* barcoding region (Folmer *et al.* 1994) was undertaken from 2004-2011 (Smith *et al.* 2013), with 20,000 specimens from 75 countries sequenced. A 2% distance cut-off identified 2221 species, and supported some of the findings from Banks and Whitfield (2006), albeit based on a single gene. *Snellenius* appeared to be a derived group within *Microplitis*. *Apanteles* and *Dolichogenidea* had reinforced support as different genera, although there are some undescribed intermediate species that raise doubts about the monophyly of these genera in Australia (Austin and Dangerfield, 1992). The barcoding effort did find some genera where limits were poorly defined, including those between *Glyptapanteles* and *Protapanteles* and those of *Choeras* and *Sathon*. These barcode sequences are also a useful resource for associating males of various species, which are difficult to identify (Fernández-Triana 2014), as many species and even genus descriptions rely heavily on female characters such as ovipositor shape and length. DNA barcoding appears to be a useful tool for species estimation and delimitation in the microgastrines, with established divergence thresholds

tested with morphological and ecological data (Smith *et al.* 2008; Fernández-Flores *et al.* 2013; Smith *et al.* 2013; Fernández-Triana *et al.* 2016). DNA sequences are also proposed as a tool for species description, either in conjunction with traditional morphological taxonomy, or in some cases, as the only data required for the description of a species (Cook *et al.* 2010). *COI* barcodes are now being used as part of species descriptions in the Hymenoptera (Fernández-Triana 2010; Butcher *et al.* 2012) and are a standard protocol in the processing of both hosts and parasitoids in the Area de Conservación Guanacaste (ACG) lepidopteran rearing survey in Costa Rica (Janzen *et al.* 2009).

Lepidopteran rearing surveys

Microgastrine wasps have tended to escape the interest of amateur or generalist entomologists, probably due to their small size, and generally dull colouring and taxonomic difficulty. This has meant that whilst taxonomic knowledge has been gained from specialist workers, an understanding of the biology and host relationships of most microgastrines is lacking. However, recent projects that have focussed on rearing lepidopteran caterpillars and recording, sequencing and analysing the emerging parasitoids have completely flipped this knowledge gap around. The major survey of this kind is that of the ACG in Costa Rica, where hundreds of thousands of caterpillars have been reared and had their parasitoids collected during the last 30 years (Smith *et al.* 2008). This kind of inventory provides an enormous amount of data on host relationships and biology of parasitoids, often before they have even been formally described.

The DNA barcoding of the emerging parasitoids has led to a substantial increase in their known diversity. In a study of seven microgastrine genera collected from the ACG survey, morphological analysis revealed 175 morphospecies, nearly all undescribed species. However, when *COI* barcode data were used in conjunction with host records, 142 additional provisional species were revealed. Many of these were subsequently supported as distinct species by subtle morphological characters or ecological differences (Smith *et al.*, 2008). This study is an excellent example of where using only morphology-based taxonomy can limit the delineation of species, and species detection is thus vastly improved by the addition of molecular and ecological data. A similar survey at the Yanayacu Biological Station in Ecuador yielded microgastrine parasitoids from 258 of the 50,000 caterpillar rearings. The wasps were distributed across 14 different genera, and each now are associated with host information (Whitfield *et al.* 2009). Reliable host data are not only important as an aid for species identification (Smith *et al.*, 2008), but are also vital for the further development of microgastrine wasps as biological control agents.

Australasian fauna

There are 25 recognised genera of Microgastrinae found in the Australasian region (Austin and Dangerfield 1992; Fernández-Triana *et al.* 2013b; Fernández-Triana and Boudreault 2018), of which 22 occur in continental Australia. All of the described species for Australia were transferred to Mason's (1981) generic classification by Austin and Dangerfield (1992), but there are many undescribed species yet to be placed in appropriate genera. The genera *Microplitis*, *Snellenius*, *Miropotes*, and *Diolcogaster* were revised for the Australian fauna in the 1990's (Austin 1990; Austin and Dangerfield 1993; Saeed *et al.* 1999), but little work on the subfamily has been conducted in the region since then.

Some Australasian specimens (the majority from Papua New Guinea and New Zealand) were included in the *COI* barcoding study of Smith *et al.* (2013), but there has not been a targeted molecular analysis of the Australasian fauna. Other than the Australian representative of the *Cotesia flavipes* species complex (Smith and Kambhampati 1999; Muirhead *et al.* 2008; Muirhead *et al.* 2012), very limited molecular work has been done on Australian microgastrines, while host information for Australian species is restricted mainly to those species of interest as biological control agents. No rearing projects such as those done in Costa Rica and Ecuador have been attempted in the region.

The importance of citizen science and outreach

Whether scientists have an obligation to be communicating their research findings and educating the public about their research topic is a controversial question, but it is becoming a more common expectation that they will attempt to engage stakeholders, the media and the general public in science and disseminate their findings in more than just peer reviewed journals. Outreach is a broad term and can include public lectures and talks, workshops with adults or children, traditional and social media, and citizen science. There have been many benefits to outreach shown for both scientists and the general public they are interacting with, but there are also many impediments for scientists, despite most believing it is a worthwhile endeavour (Andrews *et al.* 2005; Ecklund *et al.* 2012; Varner 2014; McClain and Neeley 2015).

Citizen science is a catch-all phrase for the involvement of the public in a scientific research project. The definition is broad, with volunteers completing tasks ranging from transcribing museum labels (e.g. http://www.notesfromnature.org) to setting up experiments, recording data and collecting specimens (e.g. http://schoolofants.net.au/). Research that involves volunteers gathering data that is initiated and guided by scientists has been coined a 'contributory' citizen science project (Bonney *et al.* 2009). These projects,

in theory, are designed to engage the public with science to provide a more scientific literate community, however, educational outcomes are difficult to measure and attitudinal change is often not as prevalent as anticipated (Brossard *et al.* 2005; Cronje *et al.* 2011; Druschke and Seltzer 2012). Whilst there are concerns about the reliability of the data collected by citizen scientists compared to scientific researchers (Galloway *et al.* 2006; Gardiner *et al.* 2012), there are several current entomological projects successfully involving citizen scientists.

The *Monarch Larva Monitoring Program*, based in the United States, has participants monitoring milkweed plants and recording data and observations of the monarch butterfly population. This program has been running since 1996 and has documented outcomes concerning the education of youth (Kountoupes and Oberhauser 2008). Pertinently, this project occasionally involves the rearing of larvae and the collection of information on parasitism patterns by volunteers (Oberhauser *et al.* 2007; Oberhauser 2011). Microgastrine wasp researchers in Canada have also conducted a pilot project using volunteers to rear caterpillars and record, photograph and submit data on the rates of parasitism (Fernández-Triana 2014). Other entomological projects that show it is possible to use volunteers to collect and send in insect specimens include *School of Ants* in the United States, which amassed ant specimens from 500 unique sites in the first 17 months of operation (Lucky *et al.* 2014), the *Australian School of Ants* (http://schoolofants.net.au/), and the *Pieris Project*, which has obtained 900 butterfly specimens from 25 American states and 10 different countries (http://www.pierisproject.org/learn.html).

Aims of the project

The overarching aim of this project was to improve the understanding and knowledge of the Australian microgastrine biodiversity, and to provide descriptions of new species, allowing for better identification of species in collections and in the environment. As an ecologically, and potentially economically, important group of insects, a clearer understanding of the species richness of the subfamily for the continent will better direct targeted taxonomy and investigations of potential agricultural applications.

The **first aim** of this project was to conduct a large DNA barcoding and species delimitation study of Australian microgastrines using high-throughput methods, to better estimate the biodiversity of the group on the continent and provide a framework for species descriptions and taxonomic revisions of targeted genera **(Chapter 2)**. As a result of Aim 1, Internal Transcribed Spacer 2 (*ITS2*) data were generated that could not be easily analysed for the work presented in Chapter 2 due to the complexity of intra-individual variation and compounding PCR errors. The **second aim** of this project was therefore to re-analyse the *ITS2* data and provide statistics and information on the intra-individual, intra-species and inter-species variation in this gene region in the Microgastrinae **(Chapter 3).**

The **third aim** of this project was to contribute to the knowledge of microgastrines in Australia by describing new taxa, prioritising species for description based on availability of specimens, availability of host data, and unique characteristics, using the framework established through the DNA barcoding results presented in Chapter 2 **(Chapters 4, 5 & 6).** Chapter 4 reviews the genus *Choeras* in Australia, and describes two new species. Chapter 5 describes three species of the genus *Dolichogenidea* from Australia, all of which have extremely long ovipositors for the group. Chapter 6 primarily uses material collected on 'Bush Blitz' surveys of regional Australia to describe 10 new species from the genera *Choeras*, *Dolichogenidea* and *Sathon*. Descriptions of these particular species have been prioritised to show the diversity of new species collected and identified on 'Bush Blitz' surveys, and thus the importance of these surveys in gathering new, DNA-grade material from remote locations. A **fourth**, non-scientific aim of the project was to disseminate research findings to the general public and perform science outreach to as many people as possible. A summary of the citizen science project and outreach activities completed as part of this project is located in Appendix 1.

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Chapter 2: DNA barcoding of microgastrine parasitoid wasps (Hymenoptera: Braconidae) using high-throughput methods more than doubles the number of species known for Australia

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Overall percentage (%)	75%
Certification:	This paper reports on original research I conducted during the period of my Higher Degree by Research candidature and is not subject to any obligations or contractual agreements with a third party that would constrain its inclusion in this thesis. I am the primary author of this paper.
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By signing the Statement of Authorship, each author certifies that:

i. the candidate's stated contribution to the publication is accurate (as detailed above);

ii. permission is granted for the candidate in include the publication in the thesis; and

iii. the sum of all co-author contributions is equal to 100% less the candidate's stated contribution.

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RESOURCE ARTICLE

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DNA barcoding of microgastrine parasitoid wasps (Hymenoptera: Braconidae) using high-throughput methods more than doubles the number of species known for Australia

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Abstract

The Microgastrinae are a hugely diverse subfamily of endoparasitoid wasps of lepidopteran caterpillars. They are important in agriculture as biological control agents and play a significant ecological role in the regulation of caterpillar populations. Whilst the group has been the focus of intensive rearing and DNA barcoding studies in the Northern Hemisphere, the Australian fauna has received little attention. In total, 99 species have been described from or have been introduced into Australia, but the real species diversity for the region is clearly much larger than this. In this study, museum ethanol samples and recent field collections were mined for hundreds of specimens of microgastrine wasps, which were then barcoded for the *COI* region, *ITS2* ribosomal spacer and the wingless nuclear genes, using a pooled sequencing approach on an Illumina Miseq system. Full *COI* sequences were obtained for 525 individuals which, when combined with 162 publicly available sequences, represented 417 haplotypes, and a total of 236 species were delimited using a consensus approach. By more than doubling the number of known microgastrine wasp species in Australia, our study highlights the value of DNA barcoding in the context of employing high-throughput sequencing methods of bulk ethanol museum collections for biodiversity assessment.

KEYWORDS
biodiversity, DNA barcoding, Hymenoptera

1 | INTRODUCTION

The Microgastrinae are a hugely diverse subfamily of braconid wasps which spend their larval phase as koinobiont endoparasitoids of lepidopteran larvae. Female wasps oviposit either single or multiple eggs, most often into early instar caterpillars (although some species oviposit into later instars and rarely into eggs), and the wasp larvae spend several instars of the host feeding on internal tissues before emerging and spinning cocoons. A symbiotic polydnavirus is normally injected into the host along with the eggs, negating the immune system and affecting behaviour of the host to aid the survival of the wasp larvae (Strand & Burke, 2015; Whitfield, Austin, & Fernandez-Triana, 2018). Most species of microgastrines seem to be extremely host specific (Smith et al., 2008), parasitizing a single or a few closely related species of host, a trait which allows them to be highly effective biological control agents for lepidopteran pests in agricultural settings (Austin & Dangerfield, 1992; Whitfield, 1997).

The global described microgastrine fauna comprises approximately 2700 species placed in 63 genera (Whitfield et al., 2018), although the robustness of generic boundaries is in doubt and likely to change as current anchored-enrichment phylogenetic studies of the subfamily are completed (Whitfield et al., 2018). In Australia,

there are 99 described species recorded from the continent, currently placed in 20 genera (Austin & Dangerfield, 1992, 1993; Fagan-Jeffries, Cooper, & Austin, 2018; Fagan-Jeffries & Austin, 2017; Fernández-Triana, van Achterberg, & Whitfield, 2014). Six of these species were intentionally introduced from outside Australia to control agricultural pests (Austin & Dangerfield, 1992). The most recent estimation for the true size of the global fauna, integrating the dramatic increase in species identified through DNA barcoding, placed the minimum and maximum estimates at 17,000 and 46,000 species, respectively (Rodriguez et al., 2013). Despite the number of described species also increasing exponentially over time (Whitfield et al., 2018), it is clear that molecular approaches are by far the fastest and most convenient for assessing regional biodiversity, compared to traditional taxonomy.

It is now well established that DNA barcoding employing the cytochrome c oxidase subunit I gene (*COI*) can be a highly effective method for estimating species richness (Hebert et al., 2016; Janzen et al., 2009; Smith et al., 2008; Telfer et al., 2015). Whilst there are numerous issues and necessary caveats of using a single gene to delimit and recognize species (Carstens, Pelletier, Reid, & Satler, 2013; Klopfstein, Kropf, & Baur, 2016), it is still one of the most convenient and cost-effective ways of rapidly sampling biodiversity of a region, particularly in groups of small, morphologically conserved insects where taxonomic impediments preclude more traditional methods of species discovery. The accuracy of species delimitation using *COI* barcodes varies among different taxonomic groups, but the Microgastrines are one of only a few groups where independent substantial evidence (e.g., morphology and host data) has been employed to determine *COI* species' thresholds with reasonable confidence (Smith et al., 2008). Using data generated from the significant rearing and DNA barcoding of microgastrines occurring in Area de Conservación Guanacaste (ACG) in north-western Costa Rica, Smith et al. (2008) found that this approach identified a significant number of provisional species that were overlooked in an initial morphological analysis, but consequently were supported by ecological host information or subtle morphological characters. This study laid the groundwork for the use of DNA barcoding for the Microgastrinae and has been adopted by projects in Canada (Fernández-Triana, 2010), Mexico (Fernández-Flores, Fernández-Triana, Martínez, & Zaldívar-Riverón, 2013), and elsewhere, leading to the accumulation of over 37,000 publicly available microgastrine *COI* barcodes (http://v4.boldsystems.org/index.php/Taxbrowser_Taxonpage?taxon=Microgastrinae&searchTax=Search+Taxonomy; accessed on 8 May 2018). In an initial release of nearly 20,000 microgastrine *COI* sequences, many with associated host information and morphological data, Smith et al. (2013) confirmed that a 2% sequence divergence threshold for species delimitation was able to accurately separate 95% of microgastrine species. Whilst over 1700 species were recognized in that study, only 10 specimens from Australia were included.

Whilst the *COI* barcoding region has been used independently in many species discovery studies, multiple lines of evidence are always preferable for generating robust estimates. Smith et al. (2008) used nuclear markers (the D2 region of 28S or the internal transcribed spacer region (*ITS1*)) to assist with species delimitation in cases where *COI* barcode divergence thresholds contradicted host range information or morphology. They found situations where the evidence from the nuclear markers agreed with the provisional species based on the *COI* divergences, but also cases where the nuclear markers supported the species delimited by ecological or host data that contradicted *COI* divergence thresholds. In this study, we additionally sequence the wingless gene (*WG*), a nuclear gene that has been used in previous microgastrine phylogenetics (Banks & Whitfield, 2006; Murphy, Banks, Whitfield, & Austin, 2008) and internal transcribed spacer 2 (*ITS2*), a fast-evolving region located between the 5.8S and 28S ribosomal subunits. *ITS2* has been previously used in hymenopteran species delimitation studies (Darwell, Al-Beidh, & Cook, 2014; Klopfstein et al., 2016), but has not been widely applied to species delimitation in the Microgastrinae. This study utilizes high-throughput methods pioneered by Cruaud, Rasplus, Rodriguez, and Cruaud (2017) and Shokralla et al. (2015) to rapidly and cost-effectively sequence these amplicons for microgastrines.

This study aimed to provide the first large-scale DNA barcoding analysis of the Australian microgastrine fauna, allowing for a preliminary estimate of species richness of this diverse group for the continent. We delimit species using three single-locus methods for the *COI* barcoding region, with two additional genes providing further support for the recognition of putative species. This approach allows us to establish molecular operational taxonomic units (MOTUs) that likely represent true species under the general lineage species concept (de Queiroz, 1998) and generate a revised estimate of species for the Australian microgastrine fauna. This study will also provide the groundwork for future systematics research aimed at revising specific genera and describing new species.

2 | METHODS

2.1 | Sampling

Over 1000 specimens of microgastrine wasps were obtained from various museum ethanol collections and from recent malaise trap sampling from across Australia. Whilst detailed data for storage conditions of samples are not available, specimens from museum collections were either stored at room temperature or in fridges, in either 100% or 70% ethanol. Many specimens came from bulk storage vials sorted to order or family level, whilst some specimens came from malaise trap collections left unsorted for several years. Female wasps were identified to genus level (Austin & Dangerfield, 1992) but as the available key requires female-only characters, males were left unidentified. In total, 724 wasps were selected for DNA extractions, ensuring full representation across sampling sites. Of these, 156 specimens were initially Sanger sequenced using the *COI* barcoding region (see methods below), and these DNA extracts were also included in the Miseq run as a method of confirming the accuracy of the high-throughput methodology. An additional 22 specimens were successfully Sanger sequenced as part of a separate project and added to the final data set. In addition, 162 *COI* sequences for Australian microgastrines were

downloaded from the BOLD database and included in the analyses. Full specimen and sequence data are presented in Supporting information (Tables S1–S2). Several specimens of the closely related subfamily Miracinae were included as outgroups.

2.2 | DNA extraction

DNA was extracted from 1 to 3 legs using either the Gentra® Puregene® DNA Purification protocol for fresh tissue with some modifications, or using a modified version of the Canadian Centre for DNA Barcoding Glass Fiber Plate DNA Extraction Protocol in PALL Acroprep ADVANCE 96-Well Filter Plates (1 ml 3.0 μm glass fibre/0.2 μm Supor) (Ivanova, Dewaard, & Hebert, 2006). Vouchers were deposited in the various collections from which specimens were obtained (Supporting information Table S1).

2.3 | Sanger sequencing

PCR amplifications were carried out on an Eppendorf MasterCycler Pro using a 25 μl reaction volume consisting of nuclease-free molecular water, 1× Immolase PCR buffer (Bioline; NSW, Australia), 1.5 mM $MgCl_2$, 0.8 mM dNTP mix, 0.05 mg/ml BSA, 0.24 μM primer (LCO1490, HCO2198 see Table 1), 0.5 u Immolase DNA polymerase and 2 μl of extracted DNA (approximately 0.1–0.4 ng). Product purification and Big Dye Terminator sequencing were conducted by The Australian Genome Research Facility (AGRF). Sequence trace files were edited in GENEIOUS version 9.0.5 (Kearse et al., 2012).

2.4 | High-throughput sequencing

A two-step PCR library preparation protocol was designed following Cruaud et al. (2017) using the indexes designed in Meyer and Kircher (2010). Primers in the first PCR step consisted of gene-specific forward and reverse primers linked to Illumina paired-end sequencing primers (Figure 1). P5 and P7 flow cell adaptors and a unique combination of 8-bp indexes, allowing unequivocal identification of sequenced gene fragments, were added in the second PCR step (Figure 1). Partial segments of the genes *ITS2* (approximately 300 bp) and *WG* (433 bp), and the barcoding *COI* region (sequenced in two fragments of 325 bp and 407 bp in size, overlapping by 82 bp) were amplified using the gene-specific primers in Table 1.

The first round of PCRs was carried out on an Eppendorf MasterCycler Pro using a 12 μl reaction volume consisting of nuclease-free molecular water, 1× Immolase PCR buffer (Bioline; NSW, Australia), 1.5 mM $MgCl_2$, 0.8 mM dNTP mix, 0.05 mg/ml BSA, 0.25 μM primer (*WG* primers were 0.5 μM), 0.25 u of Immolase DNA polymerase, and 1 μl of extracted DNA (approximately 0.1–0.4 ng). PCR set-up was conducted using a Beckman Coulter Biomek3000 robot. PCR conditions were 95°C for 10 min; 34 cycles of 95°C for 45 s, 48–54°C for 45 s and 72°C for 90 s; and a final extension at 72°C for 10 min. Annealing temperatures for each gene were as follows: *COI*, 48°C; *ITS2*, 54°C; *WG*, 49.5°C. About 10% of samples were visualized on a 1.5% agarose gel to establish success rates of amplification.

The second round of PCRs dual-indexed the samples and consisted of nuclease-free molecular water, 1× Immolase PCR buffer (Bioline; NSW, Australia), 1.5 mM $MgCl_2$, 0.8 mM dNTP mix, 0.05 mg/ml BSA, 0.4 μM of each indexing primer, 0.25 u of Immolase DNA polymerase and 2 μl of PCR product. PCR conditions were 95°C for 10 min; 7 cycles of 95°C for 45 s, 65°C for 45 s and 72°C for 90 s; and a final extension at 72°C for 10 min. PCR set-up was conducted using a Beckman Coulter Biomek3000 robot, and PCR product from round one was added to the reactions using an Eppendorf epMotion 5075 robot. Each gene fragment for a single specimen received the same index combinations. In total, 768 index combinations were used, which included extraction blanks, negative PCR controls and duplicate PCRs. A selection of indexed samples was analysed alongside the corresponding round one PCR product on the Aglient 2200 TapeStation (Aglient Technologies, Santa Clara, CA, USA) to determine whether the DNA fragments had increased in length, indicating that the Illumina adapters had successfully attached. Two microlitres of each of the indexed samples was pooled by gene fragment, resulting in four libraries that were analysed on the TapeStation and cleaned either by Agencourt AMPure XP Bead Purification (Beckman Coulter, Indianapolis, IN, USA) (both *COI* fragments and *ITS2*) or, when unwanted products were visible above 100 bp on the TapeStation for the *WG*

TABLE 1 Locus-specific primer sequences

Gene Fragment	Fragment size	Direction	Published name	Sequence 5′-3′	References
COI (first segment)	325 bp	Forward	LCO1490	GGTCAACAAATCATAAAGATATTGG	Folmer, Black, Hoeh, Lutz, & Vrijenhoek (1994)
		Reverse	Ill_C_R	GGIGGRTAIACIGTTCAICC	Shokralla et al. (2015)
COI (second segment)	407 bp	Forward	Ill_B_F	CCIGAYATRGCITTYCCICG	Shokralla et al. (2015)
		Reverse	HCO2198	TAAACTTCAGGGTGACCAAAAAATCA	Folmer et al. (1994)
ITS2	Approximately 330 bp (varied depending on indels)	Forward		TGTGAACTGCAGGACACATG	Quicke, Mori, Zaldivar-Riverón, Laurenne, & Shaw (2006)
		Reverse		ATGCTTAAATTTAGGGGGT	Quicke et al. (2006)
WG	433 bp	Forward	LepWG1	GARTGYAARTGYCAYGGYATGTCTGG	Brower & Desalle (1998)
		Reverse	LepWG2	ACTICGCRCACCARTGGAATGTRCA	Brower & Desalle (1998)

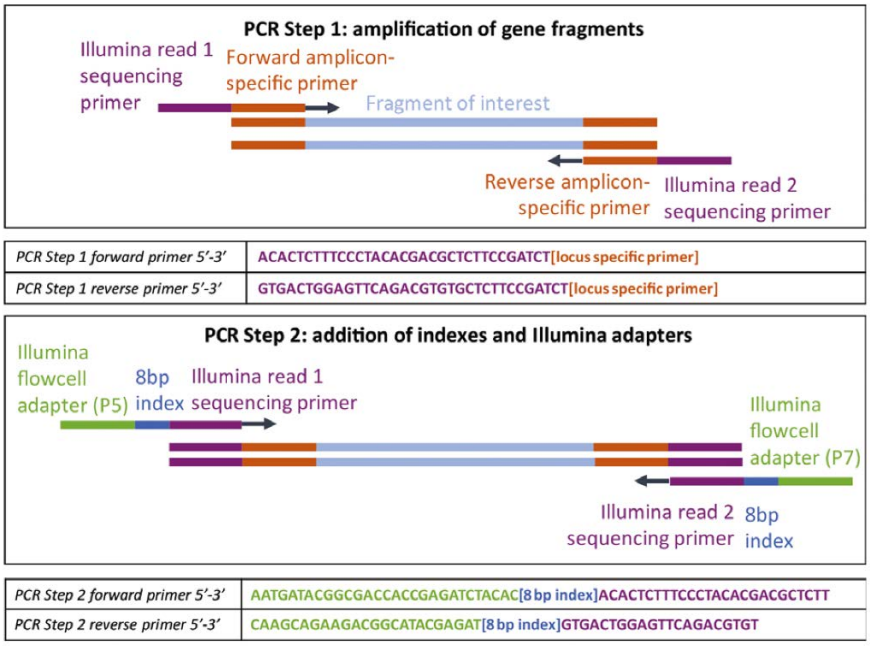

FIGURE 1 PCR protocol for the amplification and library preparation of amplicon fragments [Colour figure can be viewed at wileyonlinelibrary.com]

library, by excision from a 1.5% agarose gel after electrophoresis, and purification using the QIAquick Gel Extraction Kit (QIAGEN, Chatsworth, CA, USA). The final cleaned libraries were quantified using the TapeStation and pooled in equimolar amounts to give a final 25 μl, 17.9 nM library that was 300-bp paired-end sequenced on an Illumina MiSeq flowcell by AGRF.

2.5 | Analysis of the MiSeq data set

Quality control checks were performed on the raw reads using FASTQC version 0.11.5 (Andrews, 2010). Adapter contamination was identified and removed using BBDUK version 35.92 (https://sourceforge.net/projects/bbmap/). Forward and reverse reads were assembled using PEAR version 0.9.10 (Zhang, Kobert, Flouri, & Stamatakis, 2014). For each specimen, the four amplicons were sorted and separated by the forward primer sequence, both forward and reverse primers were removed, and reads were quality trimmed to Q20 using BBDUK version 35.92. Sequences were dereplicated, putative chimeric sequences removed, and the remaining reads were clustered at 100% similarity using VSEARCH version 2.4.3 (Rognes, Flouri, Nichols, Quince, & Mahé, 2016). For both *COI* amplicons, the cluster with the highest number of reads was outputted as a consensus sequence and used in the downstream analysis. The top two clusters were outputted for *WG* to check for the presence of heterozygote individuals, and the top three clusters were outputted for *ITS2* for the reasons outlined below. Full details of analysis parameters and scripts can be found as supplementary information (S5).

2.6 | COI

For each specimen, the consensus sequences for the two *COI* amplicons were imported into GENEIOUS version 9.0.5 (Kearse et al., 2012) and were aligned using Muscle (Edgar, 2004). Any sequences where one or both of the amplicons were missing or had less than three reads, or where the first and second *COI* amplicon did not overlap with 100% similarity, were removed. The full *COI* barcode consensus sequences were aligned with the Sanger data set to check for any discrepancies. Specimens were identified to genus level using morphology and compared to specimens with closely related sequences. Any sequences with morphology that did not agree with the genus in which the sequences clustered and had low numbers of reads were removed and assumed to be contaminants.

2.7 | WG

The consensus sequences of the two clusters with the highest number of reads were imported into Geneious and aligned using MAFFT (Katoh & Standley, 2013). All sequences with less than three reads were removed. In cases where the two sequences had approximately equal number of reads, these individuals were assumed to be heterozygotes for an allele and an ambiguity was included in the final consensus sequence for that specimen. In most cases, one sequence had less than 20% of the reads of the second sequence. These were assumed to represent sequencing errors or contamination, and the individual was considered to be a homozygote, and only the sequence with the highest number of reads was retained.

2.8 | ITS2

As *ITS2* is a ribosomal region with multiple copies present in the wasp genome, it was expected that multiple, different clusters of reads could represent true *ITS2* sequences. However, when there are low numbers of reads, determining whether a cluster was a real sequence present in the genome, or whether it was caused by errors

introduced during PCR or sequencing became difficult. Clusters of identical reads for an individual were ranked by the number of reads present in that cluster. Clusters were removed wherever the number of reads was less than 5% of the highest ranked cluster for that individual. Any clusters with less than seven reads were removed automatically. Whilst there is a possibility that these removed clusters were real *ITS2* copies, the possibility of them being errors introduced during the PCR or sequencing process could not be ruled out, and a conservative approach was taken to optimize data quality. The number of different *ITS2* sequences for an individual after this screening process ranged from one to three.

2.9 | Species delimitation

Three methods of species delimitation were compared for the *COI* barcoding data: the 2% K2P corrected pairwise distance criterion implemented through the program Species Identifier (Meier, Shiyang, Vaidya, & Ng, 2006), the general mixed Yule coalescent (GMYC) model (Fujisawa & Barraclough, 2013; Pons et al., 2006) and the bPTP online server (Zhang, Kapli, Pavlidis, & Stamatakis, 2013). The 2% divergence threshold and GMYC model were used for species delimitation of microgastrines from a Mexican forest (Fernández-Flores et al., 2013), and therefore, the use of these models here allowed for a direct comparison with the Australian fauna. Species delimitation also included determining *WG* haplotypes to establish whether differences in this gene would correspond to the species delimited using *COI*.

2.10 | Model selection

Partition Finder 2 (Lanfear, Frandsen, Wright, Senfeld, & Calcott, 2016) on the CIPRES Science Gateway (Miller, Pfeiffer, & Schwartz, 2010) was used to select the best partitioning scheme and substitution model for all methods of tree building.

2.11 | Tree building

Bayesian trees were constructed for *COI* and wingless independently and for an alignment of the two genes concatenated, both including and excluding those specimens with missing data for comparison. These were run using the program MrBayes (Ronquist et al., 2012) with a GTR+I+G model of substitution for 20,000,000 generations with no partitioning (*COI*), 15,000,000 generations with the two genes partitioned (*COI* + *WG* concatenated) or 10,000,000 generations with no partitioning (*WG*), and convergence was established using the program Tracer (Rambaut, Drummond, Xie, Baele, & Suchard, 2018). The *COI* and *WG* Bayesian trees were independently inputted into the bPTP online server and the analyses run for 500,000 generations. Determination of convergence was established by visual inspection of the likelihood plot.

An ultrametric tree for the *COI* alignment was created in BEAST (Bouckaert et al., 2014) using the CIPRES Science Gateway (Miller et al., 2010) with a relaxed lognormal clock and the GTR + I + G substitution model. Two tree priors were used and the final species delimitation results compared: a Yule model and a birth–death model. Three species of the closely related subfamily Miracinae were included as outgroups, with the Microgastrinae made monophyletic as a prior, and all other priors left as defaults. The analysis was run for 200,000,000 generations. The ultrametric *COI* trees were inputted into the GMYC model using the SPLITS package in R (http://splits.r-forge.r-project.org/).

ITS2 could not be unambiguously aligned between genera, so trees were constructed in MrBayes for select genera. Species delimitation analyses for *ITS2* were complicated by large divergences in copies from the same individual, and thus, *ITS2* was determined to be uninformative for species delimitation and ambiguous for phylogenetics. Copies from different individuals or even *COI* species were often more closely related to each other than to copies from the same individual, and this compounded the tree structure so that no real conclusions could be drawn from comparing the *ITS2* trees to the other gene trees.

Species delimitation results, including a consensus hypothesis, were mapped onto a concatenated *COI* and *WG* Bayesian tree. The following was taken into account when determining the consensus species delimitation hypothesis: Consistency between genes, consistency between *COI* methods, Bayesian posterior probability support for putative species on the concatenated gene tree and whether the species was monophyletic.

3 | RESULTS

3.1 | Sequencing success rates

COI barcodes were successfully generated for 525 microgastrine specimens representing 348 haplotypes using either the high-throughput method (501 specimens) or Sanger sequencing (45 specimens). Success rates of the Illumina pooled sequencing approach were high even for older material, with full barcodes being sequenced for specimens over 25 years old (Figure 2). *WG* was successfully sequenced for 476 specimens, and at least one *ITS2* copy was sequenced for 580 specimens. In total, 402 microgastrine specimens and two outgroup specimens were successfully sequenced for both *COI* and *WG*.

3.2 | High-throughput sequencing

A total of 16,852,940 Illumina paired-end reads were obtained with an average number of raw reads per specimen of 21,972 (range = 16–138,577). The 13 negative controls returned between 22 and 306 reads, suggesting some aerosol contamination occurred during DNA extraction or PCR. Several blank controls had reads remaining after the quality filtering steps (*COI*: 2 blank controls each with 1–2 reads; *WG*: 2 blank controls each with one read; *ITS2*: 11 blank controls ranging from 1 to 6 reads); however, these were removed from the database when the minimum read threshold was implemented for each gene (<3 reads for *COI* and *WG*, <7 reads for *ITS2*). After all quality filtering steps and construction of the final consensus sequences, there was a significant difference found between the numbers of reads for different amplicons. On average,

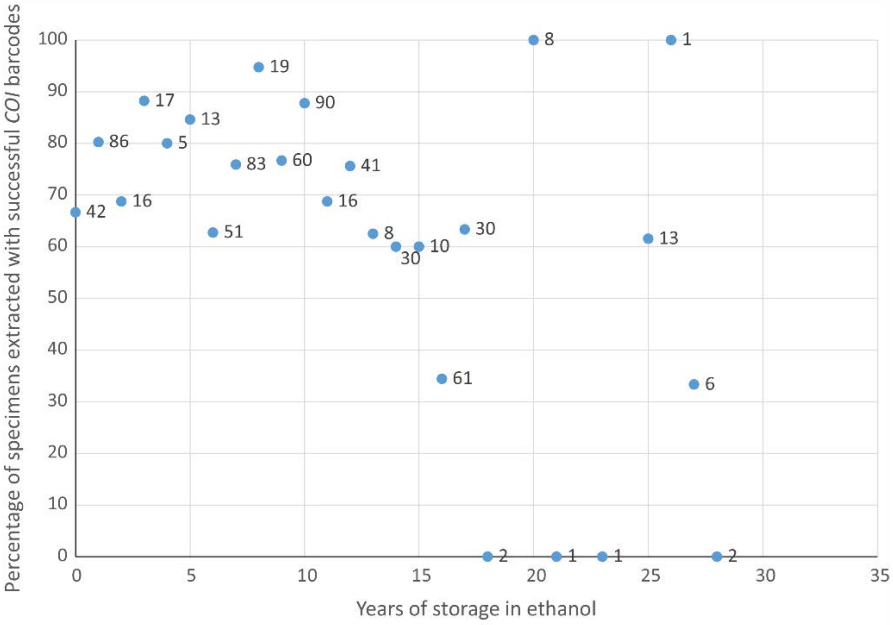

FIGURE 2 Percentage of specimens with both COI amplicons successfully sequenced in the pooled Miseq run, at increasing time since collection. Data point labels reflect the number of specimens that underwent DNA extraction and attempted sequencing [Colour figure can be viewed at wileyonlinelibrary.com]

3785 and 2147 reads were obtained per specimen for the first and second *COI* fragment, respectively (ranges of 3–16,128 and 3–12,790), whilst only 377 reads were obtained on average per specimen for *WG* (range = 3–2887). Duplicate PCR amplifications produced identical consensus sequences, indicating that there were no issues with the indexes or methodology, and no errors were found (i.e., sequences were identical) when the high-throughput sequences were aligned with the Sanger sequence of the same specimen.

3.3 | Distribution and geographical coverage

Whilst the successfully barcoded specimens included a reasonably broad coverage of the continent (Figure 3), many sampling sites represent single or few specimens, and very few sites yielded a large range of genera. All genera were found over a wide area of the continent, with no clear patterns of genera being confined to certain areas other than the small number of included specimens of *Sathon*, which were restricted to the southern half of Australia.

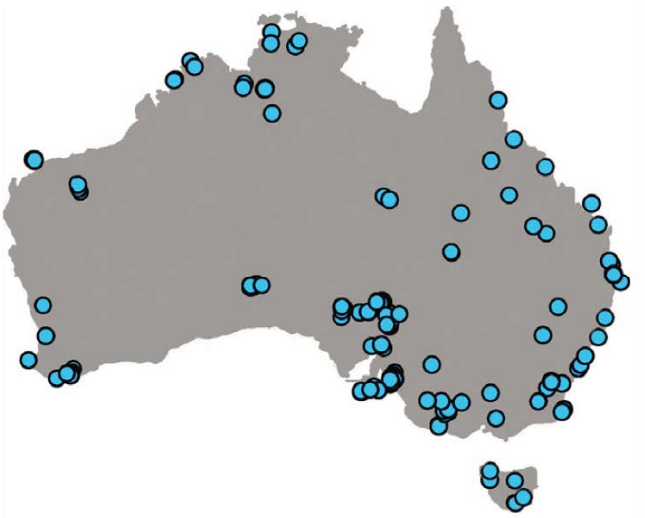

FIGURE 3 Collection location of specimens with successfully generated COI barcodes, including those downloaded from BOLD [Colour figure can be viewed at wileyonlinelibrary.com]

3.4 | Species delimitation

In general, the *COI* species delimitation methods produced similar results (Figure 4). In total, 236 putative species were found using the 2% divergence threshold, whilst 245 were indicated by GMYC model using the birth–death model tree and 250 by the bPTP server. There were no differences found between the bPTP highest supported Bayesian partition and the bPTP maximum-likelihood partition. There were three instances where the species delimited using the GMYC analysis of the birth–death model tree differed from those using the yule model tree. Of the species with full *WG* sequences, the species delimitated using the 2% *COI* divergence threshold were almost always supported by different *WG* haplotypes (136 instances). However, there were sometimes small differences (~1–3 bp) found between the *WG* sequences of a single *COI* 2% threshold species (14 instances), and sometimes *WG* haplotypes were shared between multiple *COI* 2% threshold species (8 instances). The consensus hypothesis using all lines of evidence suggests 236 species (Table 2). Of the 236 species delimited by the consensus hypothesis, 162 (69%) were represented by single *COI* haplotypes, and 132 (56%) were represented by single specimens. Full species delimitation results can be found in Supporting information (Table S3).

3.5 | Relationships among genera

Ten genera were identified through morphology and were confirmed through the clade structure of the combined *WG* + *COI* tree. Seven lineages comprising 12 delimited species could not be

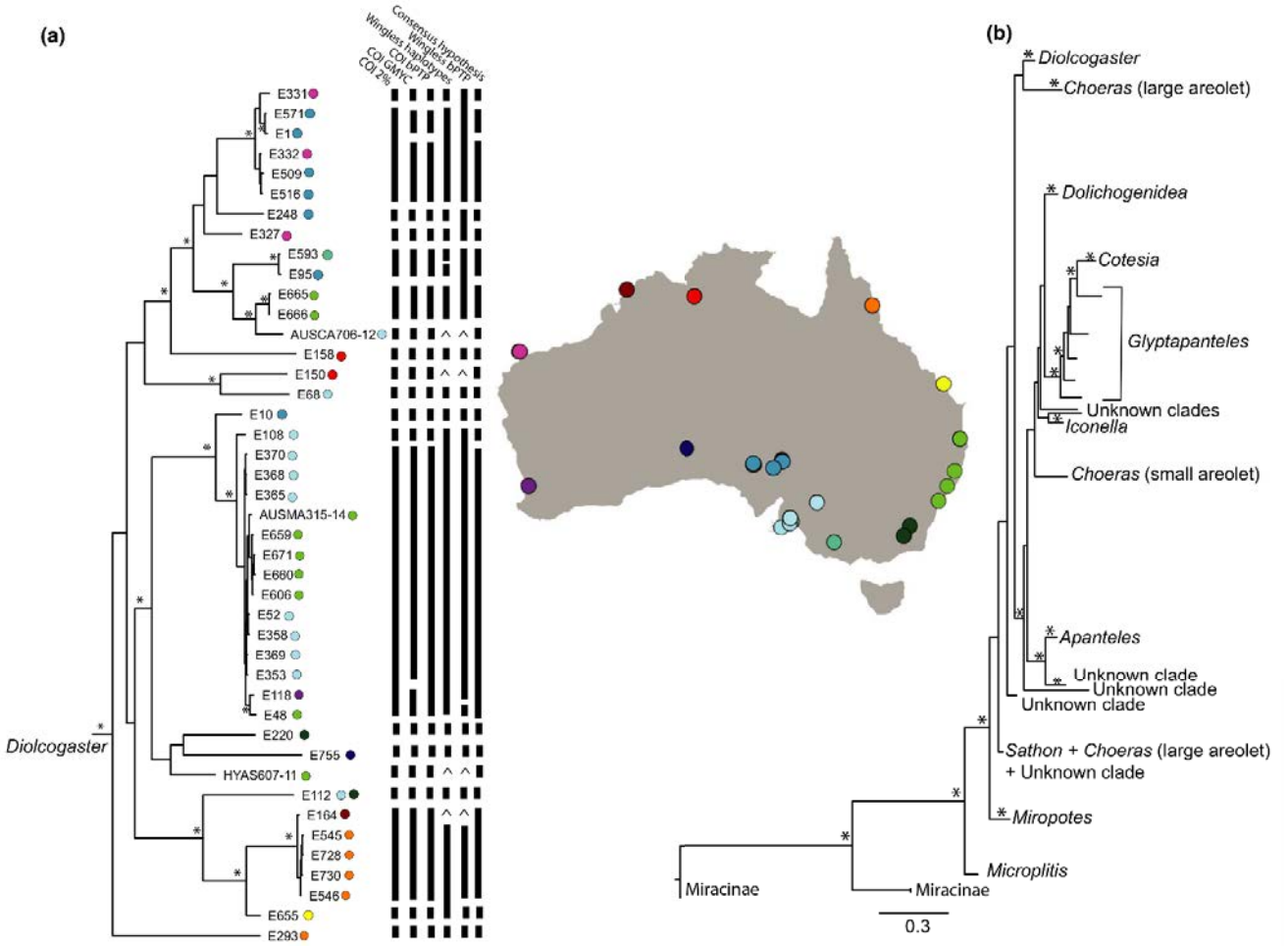

FIGURE 4 (a) *COI* + *WG* concatenated Bayesian tree showing species delimitation results compared across five methods for *Diolcogaster* as an example genus, with the consensus hypothesis also represented. ^ = missing data. Coloured circles represent sampling location, as shown on the map of Australia. (b) *COI*+*WG* concatenated Bayesian tree showing the generic relationships of the included specimens. * = >95% posterior probability [Colour figure can be viewed at wileyonlinelibrary.com]

unambiguously assigned to known genera. Whilst the expected low support across the backbone of the tree (Whitfield et al., 2018) precludes any definitive statements about relationships among genera, a clear result is the separation of specimens identified morphologically as *Choeras* into three clades: a clade containing individuals with a small forewing areolet and two clades with a large forewing areolet. This agrees with previous research implying the genus is not monophyletic (Austin & Dangerfield, 1992; Fagan-Jeffries & Austin, 2017; Mason, 1981; Smith et al., 2013). The genera *Apanteles*, *Dolichogenidea*, *Miropotes* and *Diolcogaster* are well supported as monophyletic.

3.6 | Comparison to the worldwide fauna

Two of the BOLD sequences from Australian specimens were identified as *Dolichogenidea stantoni* and *Dolichogenidea tasmanica*, both of which are also recorded from other countries and possibly introduced into Australia. Seven additional described species were identified in the data set through a BLAST search returning matches with pairwise identity greater than 98%: *Apanteles carpatus*, *Apanteles ippeus*, *Cotesia glomerata*, *Cotesia rubecula*, *Cotesia ruficrus*, *Choeras morialta*, *Diolcogaster perniciosus*, and *Microplitis demolitor*, of which *A. carpatus*, all three *Cotesia* species and possibly *A. ippeus* are introduced species. It is likely that more described species not previously sequenced are present in the data set; however, comparing the specimens here to available holotypes was beyond the scope of the study. Thirteen of the species delimited here were at least 98% identical to 15 sequences on GenBank from other countries. Assuming that greater than 98% similarity in the *COI* sequence indicates the same species, five of the species delimited here are also found in Papua New Guinea, two are found in New Zealand, two in French Polynesia, one in Thailand, one is found in both Thailand and Pakistan, one in Costa Rica, and one in Sweden. Including the seven described species listed above, only 20 of the 236 Australian species are known to be found elsewhere in the world. This suggests more than 90% of the species delimited here are, at least to the extent of

TABLE 2 Number of species in each genus delimited using the following methods: 2% threshold, GMYC (birth–death model), bPTP (Bayesian), *WG* haplotypes

Genus	2% threshold	GMYC (birth–death)	bPTP (Bayesian)	*WG* haplotypes[a]	Consensus hypothesis
Apanteles	36	37	37	32 (7)	37
Cotesia	22	25	26	15 (10)	22
Choeras (small areolet)	13	13	13	13 (2)	13
Choeras (large areolet – here paraphyletic)	9	8	10	4 (5)	7
Diolcogaster	20	22	21	18 (3)	21
Dolichogenidea	42	45	47	35 (15)	42
Glyptapanteles	34	35	35	27 (8)	34
Iconella	2	2	2	2 (0)	2
Microplitis	18	19	19	4 (14)	18
Miropotes	16	15	16	13 (3)	16
Sathon	12	12	12	7 (5)	12
Unknown	12	12	12	8 (4)	12
Total	236	245	250	178 (76)	236

Note. [a]Number in brackets indicates how many *COI* species had no data and therefore could not be validated.

the current barcoding data, endemic to Australia. However, as a large proportion of publically available microgastrine barcodes are from Northern Hemisphere locations, primarily Costa Rica and Canada, this remarkably high level of endemism will possibly reduce as further work is conducted in the Southern Hemisphere. Full BLAST results of specimens with GenBank matches equal or greater than 98% can be found as Supporting information (Table S4).

4 | DISCUSSION

4.1 | Size of the Australian fauna

This study presents the first large-scale DNA barcoding library for Australian Microgastrinae. We provide a solid framework for more comprehensive biodiversity estimates of the subfamily and a starting point for detailed taxonomic studies of select genera. Although we more than double the number of species for the continent, the true diversity of the Australian fauna is highly likely to be much larger than that estimated from this study. This conclusion can be drawn from the following points:

1. The number of available specimens was limited. There has been significantly lower intensity of collection in Australia compared to other parts of the world, particularly the Northern Hemisphere.
2. The breadth of environmental gradients and variability of rainfall in arid and semi-arid regions means that many habitats within Australia have been poorly collected.
3. A high proportion of species were represented by single specimens.

Even given these limitations, the current work parallels similar studies elsewhere. From a single dry tropical forest in Mexico, Fernández-Flores et al. (2013) recognized 103 species of microgastrines from 551 *COI* barcodes representing 238 different haplotypes. About 50% of the Mexican species were represented by single specimens and 60% by single haplotypes. From a slightly lower number of barcodes, we found double the number of species for Australia (207), with a greater proportion of singletons (56% of species with single specimens, 69% with single haplotypes). This greater diversity is possibly not surprising considering the much greater habitat and geographical range of the Australian continent.

In 2010, there were over 3,500 *COI* barcodes of microgastrines available from Canada and Alaska, which represented over 240 species (Fernández-Triana, 2010). As of 2018, this number has nearly tripled, with over 10,000 barcodes available on BOLD from the same region, representing over 500 Barcode Clusters (BINs: an approximate measure for MOTUs available through the BOLD database). Fernández-Triana (2010) used the average proportion of Lepidoptera to Microgastrinae available from well-studied areas such as Costa Rica to estimate that the total microgastrine fauna of the Canadian and Alaskan region as 550 species, a number remarkably close to the current *COI* barcode evidence. If we apply this reasoning to the Australian fauna, using Fernández-Triana's calculated average of 12 lepidopteran species for each Microgastrinae species and the estimate of 20,000 Lepidoptera species for Australia (Trautwein, Wiegmann, Beutel, Kjer, & Yeates, 2012), the Australian microgastrine fauna may exceed 1,500 species. If this estimate is at all close to the true diversity of the group, the current study has only DNA barcoded 10–15% of the fauna. By comparing the diversity accumulation curve of Australia to countries both with a similar number of barcoded specimens (Thailand) and with a much higher intensity of collecting (Canada and Costa Rica), it is clear that Australia is likely to be extremely rich in microgastrine diversity (Figure 5). Even with the intense collection that has occurred in Costa Rica, the species accumulation curve is yet to approach an asymptote. The slope of the accumulation curve for Australia is extremely steep, and much

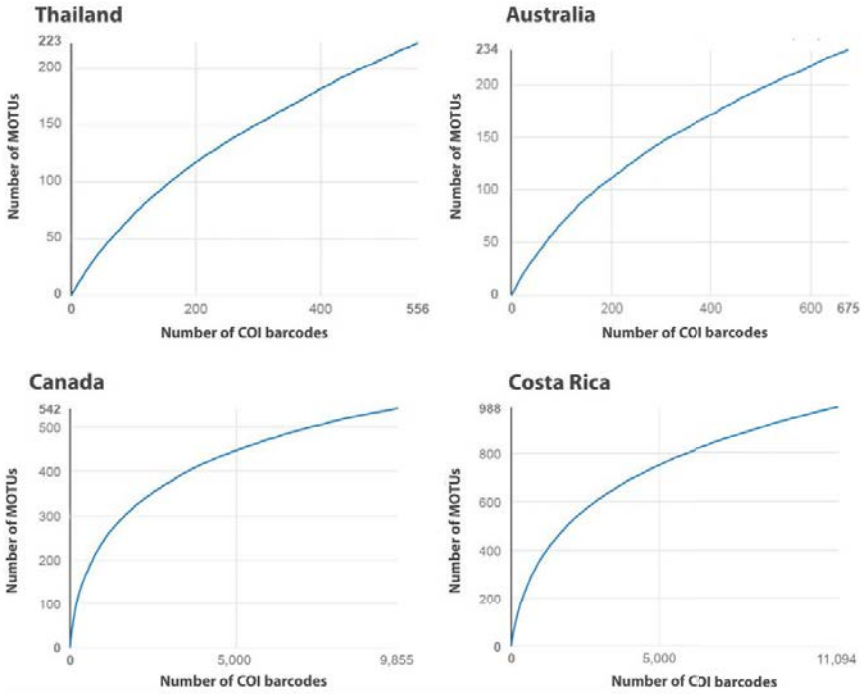

FIGURE 5 Diversity accumulation curves using BOLD BINs (approximately corresponding to MOTUs or species) for Thailand, Australia, Canada and Costa Rica. All data retrieved from BOLD, and curves built using the BOLD workbench in February 2018 [Colour figure can be viewed at wileyonlinelibrary.com]

more extensive collecting which takes into account the breadth and seasonal nature of habitats in Australia will be required before a better estimate of species numbers can be established.

4.2 | Performance of species delimitation methods

The three methods of species delimitation using the *COI* barcoding gene produced similar patterns of species delimitation. In general, the 2% threshold was the most conservative method, with GMYC and bPTP often splitting a single 2% threshold species into two or more taxa. This result is congruent with Fernández-Flores et al. (2013) who found GMYC delimited approximately 10% more microgastrine species than the 2% divergence method. GMYC and bPTP are indeed often shown to "oversplit" and recognize what would normally be considered as simply a large population or haplotype divergences as species (Carstens et al., 2013; Luo, Ling, Ho, & Zhu, 2018). Statistical species delimitation in such an unknown and undersampled fauna such as the Australian microgastrines also has the limitation of a large number of singletons, as discussed above, and poorly sampled populations. Large numbers of singletons can affect the ability of methods such as GMYC to find the correct transition point between inter- and intraspecific processes (Lim, Balke, & Meier, 2012), but perhaps not as often or directly as once thought (Ahrens et al., 2016). Regardless of the size or directness of the effect on the method, the extremely large number of singleton species in the current study no doubt limits the application of heuristic and tree-based delimitation methods.

The gene *WG* has been used broadly in microgastrine phylogenetics (Banks & Whitfield, 2006; Murphy et al., 2008), but has not been previously used as a barcoding gene for species delimitation. We show high congruence between clades with unique *WG* sequences, and species delimited using *COI*, suggesting that *WG* may act as a useful nuclear gene to support *COI* and help alleviate some of the issues inherent in single-gene mitochondrial barcoding (Galtier, Nabholz, Glémin, & Hurst, 2009; Rubinoff, Cameron, & Will, 2006). Whether the congruence of *WG* with *COI* will hold up under denser phylogenetic sampling remains to be seen, and using a haplotype approach for *WG* (i.e., any difference between sequences lending support to a species delimitation) clearly does not take into account variation due to alleles. Allelic variation is likely the cause for the instances where a single *COI* species had multiple unique *WG* sequences.

The *ITS2* gene has also been previously used in phylogenetics of the Microgastrinae (Kankare & Shaw, 2004) and in species delimitation analyses within the sister family, Ichneumonidae (Klopfstein et al., 2016). Whilst the initial objective of our study was to compare species delimitation results between *COI* and *ITS2* for the Microgastrinae, the multiplex-sequencing approached used here urges caution; multiple, closely related copies can be sequenced in similar abundances from an individual specimen. This intragenomic variation has been previously recorded in butterflies (Shapoval & Lukhtanov, 2015) and mosquitoes (Batovska, Cogan, Lynch, & Blacket, 2017). Commonly used *ITS2* primers appear to sequence different, evolutionarily distinct copies of the spacer region in different microgastrine individuals, leading to incorrect relationships being inferred if this is ignored in a Sanger sequencing approach.

How well these nuclear markers assist *COI* divergence threshold delimitation compared to the *28S* and *ITS1* markers used by Smith et al. (2008) is unclear. As Smith et al. (2008) observed with *28S*, we also found some cases where several base pair differences in *WG* between specimens did not correspond to the suggested species level divergence in the *COI* barcode, and occurrences of large (>2%)

divergences in *COI* that were not reflected by any variation in the WG gene. As we were not able to include ecological or host information into the analysis, whether these few contradictions between *COI* and *WG* could be explained with these additional data is unknown.

Despite the limitations associated with molecular species delimitation, it is likely to be the only way in which understanding of the biodiversity of such large and unexplored groups such as the Microgastrinae can be developed in a reasonable timeframe to be useful for conservation, agriculture or ecological applications. With very limited taxonomic expertise available worldwide, large-scale DNA barcoding studies utilizing pre-existing specimen collections can be used to assess the size and diversity of the fauna of poorly studied regions such as Australia and will assist with the implementation of focussed, integrative taxonomic processes. This study demonstrates that existing ethanol museum collections several decades in age, including those from less ideal bulk storage samples, can be utilized with high-throughput methods to achieve reasonable amplification success without the necessity of individualized or modified DNA extraction or PCR protocols. Recently designed metabarcoding approaches are able to amplify and sequence hundreds of specimens simultaneously from bulk samples such as malaise traps, providing rapid and cost-efficient surveys of biodiversity (Chuo Beng et al., 2016; Deagle, Clarke, Kitchener, Polanowski, & Davidson, 2017; Ji et al., 2013; Morinière et al., 2016). Metabarcoding approaches remove the time-consuming and costly PCR steps necessary for individually indexed specimens, and often use shorter amplicon fragments than those used in our study, which may increase the amplification success of older material. However, the disadvantage of metabarcoding is the inability to match a DNA barcode back to the original specimen. With the ability of the method used in our study to leave nearly all of the specimen undamaged, morphological assessment can follow the initial DNA barcoding diversity survey, identifying the previously described species and describing newly delimited lineages. Despite the best efforts of taxonomists, however, with such a vast fauna it is likely that much of the known diversity will remain as MOTUs for many years to come.

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DATA ACCESSIBILITY

DNA sequences: Genbank Accession nos: *COI*: MH138480-MH139003 *WG:* MH139004-MH139401. BOLD Accession nos: AUMIC001-18-AUMIC524-18.

AUTHOR CONTRIBUTIONS

The initial project idea was conceived by E.P.F-J, A.D.A., S.J.B.; the wet laboratory approach to be used was designed and conducted by E.P.F-J, T.M.B.; bioinformatics were conducted by E.P.F-J, T.B.; specimens were identified, data were interpreted and figures, and tables were generated by E.P.F-J with guidance from A.D.A. and S.J.B.; the manuscript was written by E.P.F-J. All authors provided comment on the manuscript prior to submission.

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SUPPORTING INFORMATION

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

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Due to its size, Supporting Information S1-5 can be found at the very end of this thesis, in Appendix 4, or for easier reading, the excel spreadsheet is available at https://onlinelibrary.wiley.com/action/downloadSupplement?doi=10.1111%2F1755-0998.12904&file=men12904-sup-0001-TableS1-S4.xlsx

Chapter 3: Intragenomic *ITS2* variation in the microgastrine genus *Diolcogaster* (Hymenoptera: Braconidae)

Statement of Authorship

Title of Paper	Intragenomic ITS2 variation discovered in the microgastrine genus *Diolcogaster* (Hymenoptera: Braconidae)
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Principal Author

Name of Principal Author (Candidate)	Erinn Fagan-Jeffries
Contribution to the Paper	Contribution to paper conception, planning, data analysis, figure generation, paper writing, morphological identifications.
Overall percentage (%)	75%
Certification:	This paper reports on original research I conducted during the period of my Higher Degree by Research candidature and is not subject to any obligations or contractual agreements with a third party that would constrain its inclusion in this thesis. I am the primary author of this paper.
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Co-Author Contributions

By signing the Statement of Authorship, each author certifies that:

i. the candidate's stated contribution to the publication is accurate (as detailed above);

ii. permission is granted for the candidate in include the publication in the thesis; and

iii. the sum of all co-author contributions is equal to 100% less the candidate's stated contribution.

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Intragenomic *ITS2* variation in the microgastrine genus *Diolcogaster* (Hymenoptera: Braconidae)

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Keywords. rRNA, rDNA, Microgastrinae, Illumina, next-generation sequencing, DNA barcoding

Abstract.

A recent DNA barcoding study of Australian microgastrines (Hymenoptera: Braconidae) sought to use next generation sequencing of the cytochrome c oxidase subunit 1 (*COI*) barcoding gene region, the wingless (*WG*) gene and the internal transcribed spacer 2 (*ITS2*) to delimit molecular species in a highly diverse group of Hymenoptera. Large intragenomic distances between *ITS2* variants, often larger than the average interspecific variation, caused difficulties in using *ITS2* for species delimitation in both threshold and tree-based approaches, and the gene was not included in the reported results of the study. We here report on the intragenomic, and the intra- and interspecies, variation in *ITS2* in the microgastrine genus *Diolcogaster* to further investigate the value of *ITS2* as a marker for species delimitation and phylogenetics of the Microgastrinae. Distinctive intragenomic variant patterns were found in different species of *Diolcogaster*, with some species possessing a single major variant, and others possessing many divergent variants. We also provide evidence of *COI* pseudogenes and possible mitochondrial heteroplasmy discovered during the reanalysis of the data from the original barcoding study. Characterising intragenomic variation of *ITS2* is critical as it is a widely used marker in hymenopteran phylogenetics and species delimitation, and large intragenomic distances such as those found in this study may obscure phylogenetic signal.

Introduction.

In this study we analyse internal transcribed spacer 2 (*ITS2*) data from Illumina sequencing of PCR generated amplicons produced during a recent DNA barcoding study of Australian microgastrine parasitoid wasps (Fagan-Jeffries *et al.* 2018). The Microgastrinae are

endoparasitoids of lepidopteran larvae, and play critical roles in the environment as well as being important tools in the biological control of lepidopteran pests in agricultural systems. The subfamily is incredibly diverse, with over 2,700 species described worldwide (Yu *et al.* 2016) and upper estimates of true diversity reaching 40,000 species (Rodriguez *et al.* 2013). With such a large undescribed fauna, molecular approaches to species discovery, such as DNA barcoding, are playing significant roles in increasing understanding of the biodiversity of the group (Smith *et al.* 2008; Smith *et al.* 2013; Fernández-Flores *et al.* 2013). Identifying other markers that can support the widely used cytochrome oxidase I gene (*COI*) allows for greater confidence in molecular species delimitation, removing the bias inherent in using a single mitochondrial gene for decisions on species boundaries.

In eukaryotes, *ITS2* is situated between the 5.8S ribosomal ribonucleic acid (rRNA) gene and the 28S rRNA gene (26S in plants). *ITS2* is transcribed along with the functional genes and internal transcribed spacer 1 (*ITS1*) as a single rRNA precursor molecule, but is subsequently excised during rRNA maturation. The function of both spacer regions is not completely understood, but they are thought to be involved in rRNA processing (Lalev and Nazar 1999). The entire ribosomal DNA (rDNA) unit occurs in hundreds or thousands of tandem repeats separated by non-transcribed intergenic spacers, with the number of repeated units in a species positively correlated with genome size (Prokopowich *et al.* 2003). These numerous copies of rDNA are generally thought to evolve by a process termed 'concerted evolution' in which copies are homogenised through mechanisms such as unequal crossing over and biased gene conversion (Brown *et al.* 1972; Szostak and Wu 1980; Dover 1982; David 1991). However, in many eukaryotic organisms, rDNA copies are not completely homogenised; significant intragenomic variation exists in some species of plants (Buckler *et al.* 1997), fungi (Li *et al.* 2013; Li *et al.* 2017), dinoflagellates (Fairley *et al.* 2005; Thornhill *et al.* 2007), tapeworms (Králová-Hromadová *et al.* 2010), spiders (Toju and Baba 2018), and insects (Keller *et al.* 2006; Shapoval and Lukhtanov 2015; Ruiz-Estévez *et al.* 2015), including in the Hymenoptera (Alvarez and Hoy 2002).

Understanding and characterising the intragenomic variation in *ITS2* is critical for validating the use of *ITS2* in phylogenetics and as a possible DNA barcoding marker for the Microgastrinae. *ITS2* has long been used in hymenopteran phylogenetics (Campbell *et al.* 1993) including in microgastrines (Kankare and Shaw 2004). It has also been used for species delimitation in the hymenopteran families Charipidae (Van Veen *et al.* 2003), Braconidae (Quicke *et al.* 2006; Kitthawee 2013) and Ichneumonoidae (Klopfstein *et al.* 2016). In all of these studies, *ITS2* was sequenced using Sanger methods, and no intragenomic variation was reported. Where divergent *ITS2* variants exist in small copy

numbers compared to the major or most common variant, intragenomic variation would appear in Sanger sequencing results as mere 'noise' in the DNA chromatogram, and the most abundant *ITS2* variant would be easily elucidated. However, where multiple variants exist in similar copy numbers in the genome, the DNA chromatogram would be disrupted and the sequences rendered undeterminable. Issues arise where paralogous copies of the rDNA are unknowingly sequenced, causing incorrect phylogenetic inferences. Such a case occurred in the plant genus *Quercus* (Fagaceae), where two very different yet highly supported phylogenies were produced using *ITS* regions of the same taxa, caused by divergent rDNA variants being employed in the two independent analyses (Mayol and Rosselló 2001).

Before the advent of next-generation sequencing (NGS) techniques, studies characterising intragenomic variants of rDNA used methods such as cloning PCR products to create monotypic products for sequencing (e.g. Králová-Hromadová *et al.* 2010), but with the ability to now sequence every product from a PCR-amplification using NGS, intragenomic variants can be characterised in much greater detail (Ruiz-Estévez *et al.* 2015; Batovska *et al.* 2017; Cunning *et al.* 2017). With this unprecedented amount of data comes new challenges, however, including quality control of raw data and recognising platform-specific sequencing errors and errors created during PCR among true variants. Whilst Illumina sequencing errors can be managed with quality filtering, sequencing overlapping paired-end reads, and discarding variants with low read numbers, PCR errors are an often ignored, but potentially compounding factor in NGS, with the majority of errors in cleaned data originating during the PCR stage (Brodin *et al.* 2013). Whilst PCR errors generally become very common only in later cycles, and thus only appear in low copy numbers (Kebschull and Zador 2015), when analysing intragenomic variation even these sequences with low numbers of reads will be detected and are difficult to exclude as potential variants. A sequence identity threshold therefore needs to be implemented that will cluster *ITS2* sequences so that variants with divergence levels indistinguishable from PCR errors are absorbed. What this sequence identity threshold should be, however, appears to often be arbitrarily chosen. Batovska *et al.* (2017) clustered Illumina-generated *ITS2* reads of mosquitos at 95% sequence identity, but acknowledged that this may have been too high, in one case masking variants that were of high enough abundance to cause issues in the corresponding Sanger sequencing of the specimen, and that subsequent clustering of the reads at 98% identity produced multiple variants. In microalgae, a clustering identity of 97% within samples was shown to collapse variation more likely to be intragenomic, whilst preserving interspecies diversity (Cunning *et al.* 2017).

We reanalysed the *COI* and wingless (*WG*) data collected at the same time as the *ITS2* data (Fagan-Jeffries *et al.* 2018) to establish a baseline of PCR error that could be used to set an appropriate clustering threshold for *ITS2*. We here report on the intragenomic, intraspecies and interspecies levels of *ITS2* variation found in the microgastrine genus *Diolcogaster*, and comment on the feasibility of using *ITS2* as a DNA barcoding gene in this subfamily of wasps.

Methods.

Initial processing

Raw sequence data, consisting of the barcoding region of *COI* (amplified in two partially overlapping fragments), *WG* and *ITS2* amplicons, for several hundred microgastrine specimens were generated using an Illumina MiSeq flowcell by the Australian Genome Research Facility. Library preparation and PCR methods are detailed in Fagan-Jeffries *et al.* (2018; see Chapter 2). *ITS2* variants were amplified using primers that anchor to part of the neighbouring conserved *5.8S* and *28S* genes. It should be noted that when *ITS2* is referred to in this study, sequences also include part of both the neighbouring genes.

Slight adjustments and improvements were made to the bioinformatics pipeline and scripts used in the original processing of these data, and they are redescribed here (scripts available as Supplementary Information S1). Quality control checks were performed on the raw reads using FASTQC version 0.11.5 (Andrews 2010). Adapter contamination was identified and removed using BBDUK version 35.92 (https://sourceforge.net/projects/bbmap/). Forward and reverse reads were assembled using PEAR version 0.9.10 (Zhang *et al.* 2014). For each specimen, the four amplicons were sorted and separated by the forward primer sequence, both forward and reverse primers were removed, and reads were quality trimmed to Q20 using BBDUK version 35.92. Sequences were dereplicated, putative chimeric sequences removed, and the remaining reads were clustered using VSEARCH version 2.4.3 (Rognes *et al.* 2016).

Setting a clustering threshold

To establish the level of PCR error, both fragments of *COI* and the *WG* reads were clustered at 100% identity using VSEARCH version 2.4.3 (Rognes *et al.* 2016) and the consensus sequences of clusters with ≥ 10 reads were imported into GENEIOUS version 9.1.8 (Kearse *et al.* 2012). Consensus sequences of clusters with < 10 reads were ignored to simplify downstream analysis. On average, 2497 sequences with a single read (range: 33-5481) and 409 sequences with 2-9 reads (range: 0-802) were discarded for the first *COI* fragment per

specimen, an average of 1963 singleton sequences (range: 1-8050) and 247 sequences with 2-9 reads (range: 0-918) were discarded for the second *COI* fragment, and an average of 983 singleton reads (range: 2-4196) and 107 sequences with 2-9 reads (range: 0-489) were discarded for *WG* per specimen. The remaining sequences were aligned using MUSCLE (Edgar 2004). For all specimens the first and second fragment of *COI*, and the *WG* amplicon, were analysed. The number of reads attributed to each different sequence, relative abundance of the sequence (number of reads of sequence / total number of *ITS2* reads for that specimen, excluding reads assigned to clusters with <10 reads), number of base pairs different from the most abundant sequence, and uncorrected percentage divergence (including indels) from the most abundant sequence were recorded (Supplementary Information S2). Contamination was detected by NCIB BLAST searches within GENEIOUS, which included the previously uploaded *COI* and *WG* sequences of the microgastrine specimens from the original barcoding project, therefore testing for contamination from sources both external and internal to the study.

Sequences that were contamination, more likely to be attributed to pseudogenes or mitochondrial heteroplasmy (see Figs. 1-2 for examples), or recognisable chimeras of the pseudogene and the true sequence that were not filtered by VSEARCH, were excluded. The highest divergence of a remaining sequence from the 'true' or most abundant sequence due to random PCR error was 3 bp (0.7%) in the *WG* amplicon and 5 bp (1.5%) in the COI amplicon. A sequence identity of 98% was therefore used to cluster the *ITS2* reads into purported 'true' intragenomic variants and remove noise associated with PCR error. Whilst it is likely that there are true *ITS2* variants less than 2% divergent from one another, it is difficult to separate them from PCR error, and therefore the results reported here are possibly an underestimate of intragenomic variability.

Analysis of ITS2 *variants*

The centroids (sequences with the largest number of reads which seeded the cluster) of 98% identity to *ITS2* clusters with ≥ 10 reads (clusters with < 10 reads were ignored to simplify analysis) were imported into GENEIOUS version 9.1.8 and aligned using MUSCLE. As with the *COI* and *WG* data, the number of reads attributed to each different sequence, relative abundance of the sequence (number of reads of sequence / total number of *ITS2* reads for that specimen, excluding reads assigned to clusters with <10 reads), number of base pairs different from the most abundant sequence and uncorrected percentage divergence (including indels) from the most abundant sequence were recorded (Supplementary Information S2). We define major variants as those with a relative abundance of greater than 20%, minor variants as those with a relative abundance greater

than 1% but less than 20%, and marginal variants as those with less than 1% relative abundance.

Visualisation of variants

To visualise the relationships among variants within a specimen or species, sequences were 'rereplicated' using VSEARCH version 2.8.2 to allow the inclusion of read frequency data in the visualisation. Either the raw number of reads (*COI*) or the relative abundance (*ITS2*) was used to rereplicate the sequences. Haplotype networks were constructed using TCS 1.21 (Clement *et al.* 2000) and visualised in tcsBU version updated 13/09/2018 (Santos *et al.* 2016) with gaps coded as a 5th state. Either 90% probability networks were created, or where a visualisation of all connections were sought, the connection limit was set as the known maximum distance between any two variants in that network (a forced connection).

Tree-building

COI and *WG* haplotypes of specimens from Fagan-Jeffries *et al.* (2018), excluding sequences downloaded from BOLD, were aligned and concatenated, and PartitionFinder2 (Lanfear *et al.* 2016) on the CIPRES Science Gateway (Miller *et al.* 2010) was used to select the best partitioning scheme and substitution model using the corrected Akaike Information Criterion (AICc). A Bayesian analysis was run using the program MrBayes version 3.2.6 (Ronquist *et al.* 2012) with no partitioning and a General Time Reversible model of substitution incorporating invariant sites and a gamma distribution (GTR+I+G) (Tavarè 1986; Yang 1994) for 15,000,000 generations. Convergence was established using the program Tracer version 1.6 (Rambaut *et al.* 2018) ensuring ESS values were >200.

ITS2 variants with > 1% relative abundance in a specimen were aligned using MUSCLE, and PartitionFinder2 on the CIPRES Science Gateway was used to select the best partitioning scheme and substitution model using AICc. A Bayesian analysis was run using the program MrBayes version 3.2.6 with no partitioning and a GTR+I+G model of substitution for 15,000,000 generations. Convergence was established using the program Tracer ensuring ESS values were >200. In addition, a Maximum Likelihood tree was built using the RAxML BlackBox (Stamatakis *et al.* 2008) using a transversion model of substitution incorporating invariant sites and a gamma distribution (TVM+I+G) (Yang 1994; Posada 2003) and default parameters. The resulting trees from all analyses were viewed in FigTree v1.3.1 (http://tree.bio.ed.ac.uk/software/figtree/). As no outgroup was included in the analysis of the *ITS2* region, the trees were rooted according to the previously run *COI+WG* concatenated Bayesian tree.

Morphological identification

Selected specimens from each of the species delimited using molecular data were identified where possible using the key in Saeed *et al.* (1999). In addition, the *COI* sequence of *D.* sp. 3 was identical to a specimen of *D. perniciosus* from New Zealand available on Genbank (Table S6).

Results.

Random PCR error, pseudogenes and possible heteroplasmy in COI *and* WG

No specimens had *WG* sequences more than 3 bp (0.7%) divergent from the most abundant sequence, indicating a small rate of PCR error. Specimens identified as heterozygotes for *WG* (two non-identical sequences of nearly equal abundance) were heterozygotes in only one or two positions. However, the *COI* amplicons were more ambiguous to analyse. Sequences 1-3 bp (0.3 – 0.9%) divergent from the most abundant sequence were considered random PCR errors, whilst sequences with much greater levels of divergence were assumed to be pseudogenes or cases of mitochondrial heteroplasmy. Both non-functional (identified through the presence of stop-codons on translation to amino acid in GENEIOUS) and potentially functional sequences, possibly representing mitochondrial heteroplasmy, were identified in numerous specimens and were sometimes shared across specimens of the same species.

Generally, these sequences were easily distinguished from those more likely to be from PCR errors, as they were sequenced in high abundance and had large (>2%) divergences from the most abundant, assumed to be the 'true' *COI* sequence (Fig. 1). In some cases, the distinction was less clear and complicated by several distinct sequences, but there was often a clear break between the divergence levels of sequences attributed to PCR error and those assumed to be pseudogenes. For example, in one specimen of species 7, there were several sequences 1-2 bp different from the most abundant sequence (0-1% divergence) which were assumed to be PCR error, and also several sequences 12-25 bp (4-8% divergence) different, which were assumed to be pseudogenes or heteroplasmy (Fig. 2). There were only a few cases of specimens with sequences of intermediate divergence (1-1.8%) from the most abundant sequence and it was unclear whether these cases should be attributed to random PCR error or the presence of a pseudogene. Therefore, the clustering threshold for *ITS2* was set at 98% identity as a conservative measure.

Three specimens (5%) had a sequence present in the first *COI* amplicon data that was attributed to contamination from another specimen within the study, possibly during DNA

extraction or PCR, all at low abundance compared to the true haplotype. Nineteen specimens (33%) across eight species (42%) had at least one sequence that did not BLAST as contamination and was thus assumed to be a pseudogene or heteroplasmy.

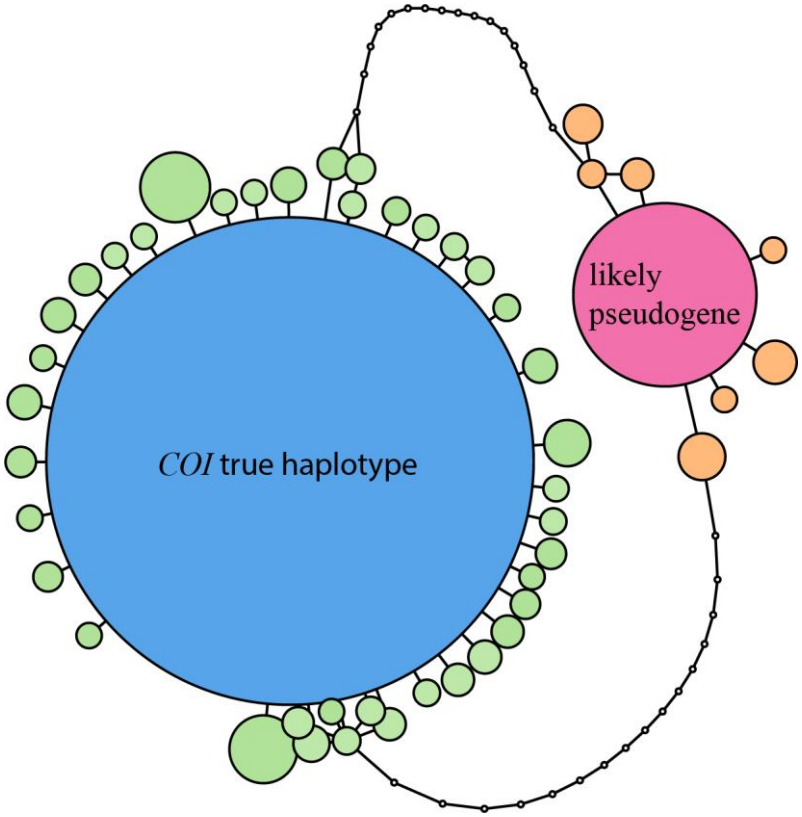

Figure 1. Haplotype visualisation of a typical result from reads assigned to *COI* in next-generation sequencing of PCR amplicons. A forced connection network of sequences with ≥ 10 reads for the first 325 bp of the *COI* barcoding region of the specimen assigned to *Diolcogaster* sp. 4 (DNA extraction code E220). The true *COI* sequence has 4594 reads (coloured blue) and is surrounded by sequences with single bp differences and many less reads, assumed to be PCR errors (coloured green). A likely pseudogene (a single bp deletion and 3 bp insertion causing multiple stop codons, plus multiple SNPs) is coloured pink, with 637 reads. This sequence is also surrounded by variants with 1-3 bp differences and smaller numbers of reads (coloured orange), assumed to be PCR errors originating from the pseudogene sequence.

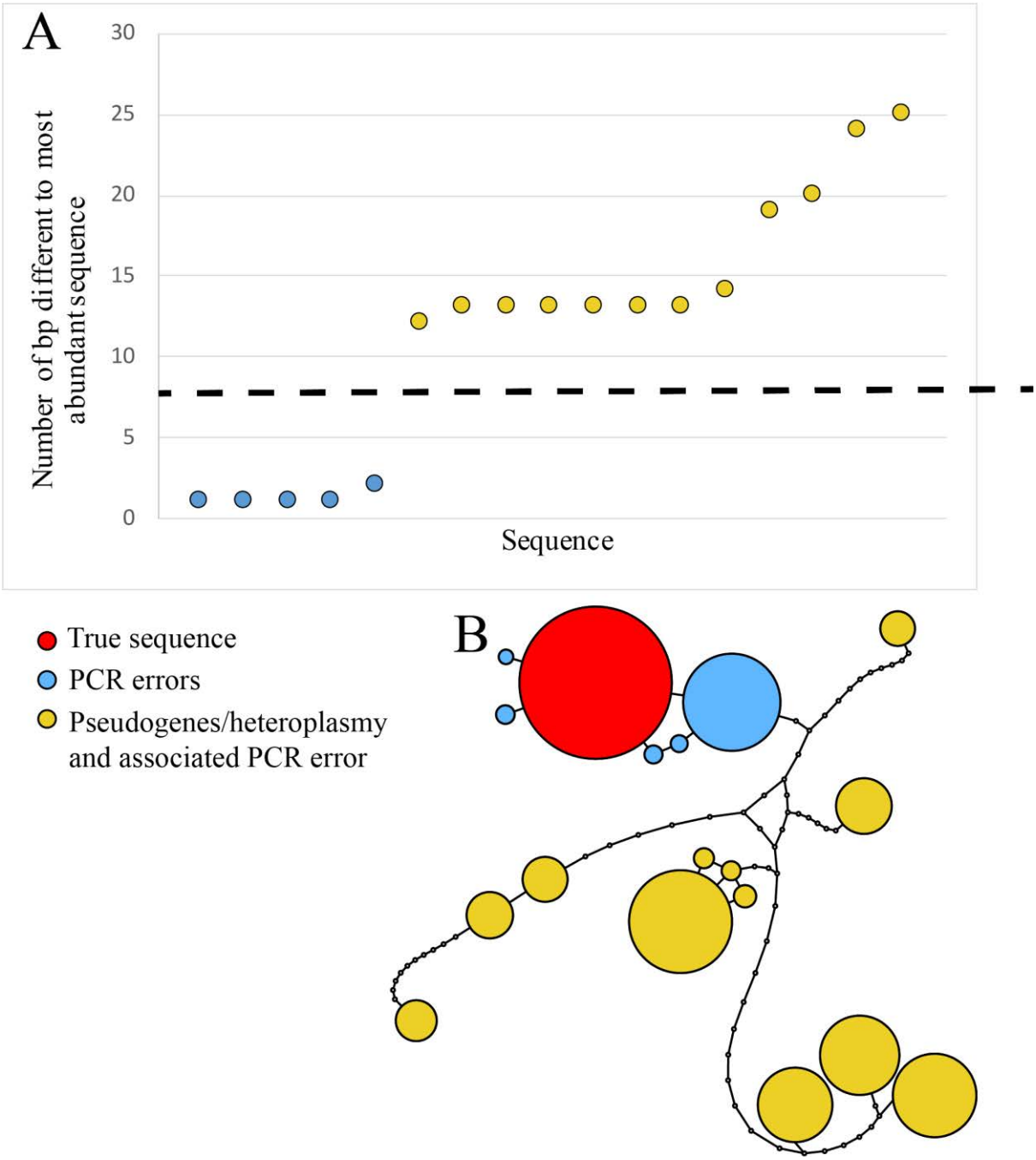

Figure 2. A) Unique sequences found within the first 325 bp of the *COI* barcoding region of a specimen assigned to *Diolcogaster* sp. 7 (DNA extraction code E332), with the numbers of bp different from the most abundant (assumed to be 'true') *COI* sequence on the y axis. A clear break in divergence levels (shown with a dashed line) separates those sequences plausibly created by random PCR error (in blue) and those assumed to be either pseudogenes or cases of heteroplasmy and their associated PCR error offspring (in yellow). B) A forced connection haplotype visualisation of the same sequences, with the size of the circles proportional to the number of reads, and the colours matching those on the graph in part A, with the 'true' *COI* sequence in red.

Levels of intragenomic ITS2 *variation and the correlation with number of reads*

After quality filtering and discarding clusters with < 10 reads, specimens had an average of 9702 *ITS2* reads (range: 24 – 31154). Of the discarded clusters, specimens had an average of 1101 (range: 1-3917) sequences discarded with a single read, and an average of 43 (range: 0-181) sequences discarded with 2-9 reads. Whilst some of these sequences are likely true variants, they would appear at very low relative abundance, and reducing the dataset was required to simplify haplotype analyses. Two specimens had contamination from outside the study (a single Diptera sequence and a single plant sequence).

There was a wide range of intragenomic and intraspecies *ITS2* variation found within *Diolcogaster*. Some species had only a single *ITS2* haplotype, or a single major variant with several marginal variants (<1% relative abundance), whilst other species had multiple major and minor variants (Fig. 3, Table S3). The pattern of *ITS2* variation within specimens was likely to be biological (i.e. reflecting actual diversity in the gene sequence) and not a random sequencing artefact, as similar patterns were found within specimens of the same species. Linear regressions of the numbers of reads per specimen compared to the number of variants suggested that whilst there was a moderate correlation between the numbers of reads and the total number of *ITS2* variants found in a specimen (R^2 = 0.5, Fig. 4A), there was nearly no correlation between the number of reads and the number of major + minor variants (R^2 = 0.04, Fig. 4B) or the number of reads and the number of major variants (R^2 = 0.01, Fig. 4C). All specimens (except one) had one or two major (>20% relative abundance) *ITS2* variants. Of those species with multiple variants, several different patterns of divergence were found, of which examples are outlined below.

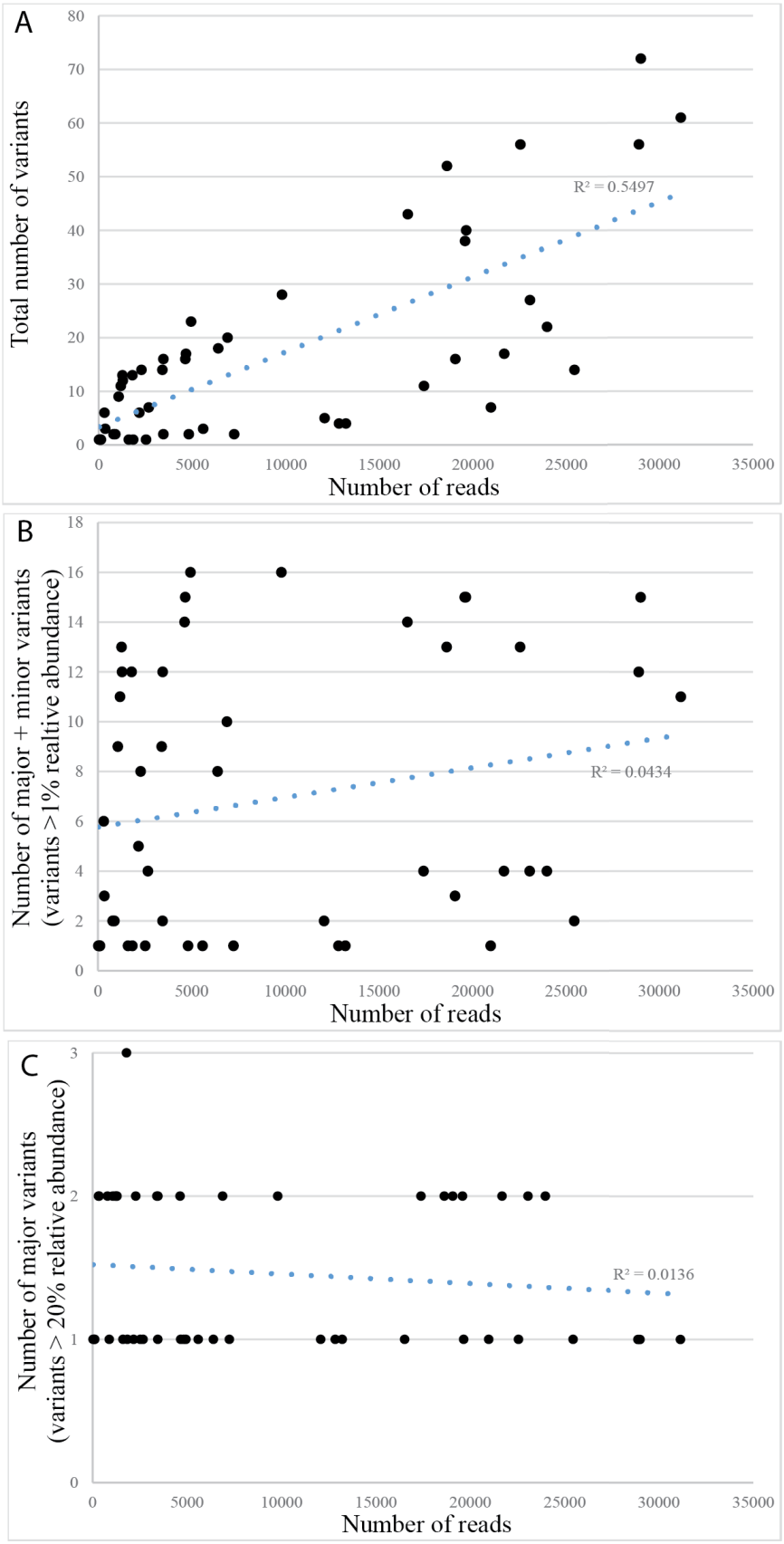

Figure 4: A) Comparison of the total number of variants and the number of reads for a specimen. B) Comparison of the number of major and minor variants (i.e. variants >1% relative abundance) and the number of reads for a specimen. C) Comparison of the number of major reads (reads >20% relative abundance) and number of reads for a specimen. Linear regressions are fitted to the data, and R^2 values displayed on the chart.

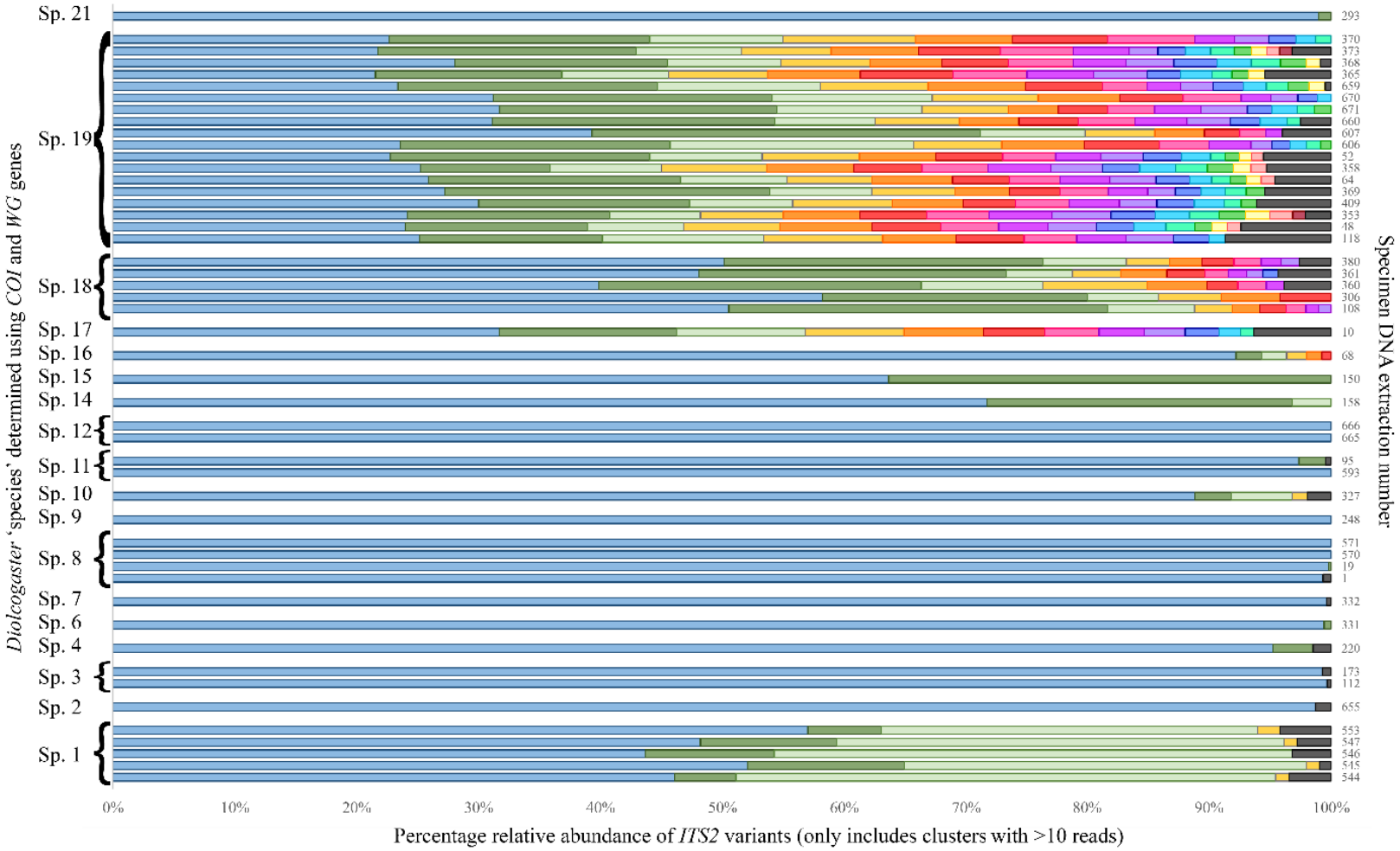

Figure 3: Presence of *ITS2* variants with ≥ 10 reads (clustered at 98% sequence identity) in the different specimens and species of *Diolcogaster*. Colours represent the different major and minor variants within each specimen, however the same coloured bar shared among specimens and species does not necessarily indicate the same sequence. The black bars are a total of all variants with < 1% relative abundance.

Example 1: A non-functional variant of equal abundance

In the five specimens belonging to *Diolcogaster* sp. 1, two variants were sequenced at similar abundances in each of the specimens (Figs. 5A and B). One of these sequences had a large deleted region in the *ITS2* region, causing it to be almost 100 bp shorter than the other variant, but the 5' and 3'ends, where the 5.8S and 28S gene regions are located, are highly conserved. This variant was found in all five specimens and thus highly unlikely to be sequencing or PCR error or contamination. It is unclear what the biological significance of this sequence is, and no similar patterns were found in any of the other species. A minor variant of approximately 10% relative abundance in each of the specimens (Fig. 5C) was identical in four specimens and 1 bp divergent in the fifth, and whilst nearly equal length to the longer of the two major variants, it is >5% divergent.

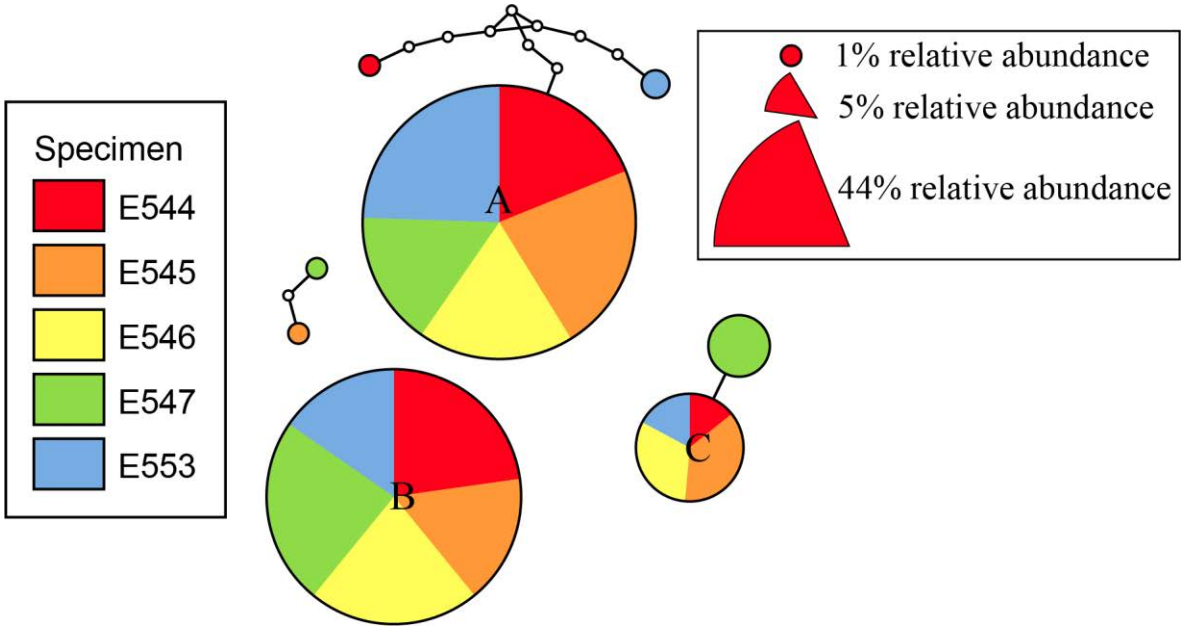

Figure 5. A 90% probability parsimony connection haplotype visualisation of the *ITS2* variants with > 1% relative abundance in *Diolcogaster* sp. 1. Colours represent different specimens (see key for colours relating to different DNA extraction codes of specimens) and the sizes of wedges and circles are proportional to the relative abundance of a variant in a specimen. Haplotype A and C are 341 bp and 336 bp long respectively, while haplotype B contains either a single large deleted section and smaller insertion, or two large deleted sections separated by an ambiguously aligned region relative to the sequence in haplotype A and C, and is 253 bp long.

Example 2: Two closely related major variants

In *Diolcogaster* sp. 15, only two variants were sequenced at an abundance ratio of approximately 2:1. These two variants were identical other than for a single 9 bp deletion in the less abundant variant relative to the most abundant (Fig. 6).

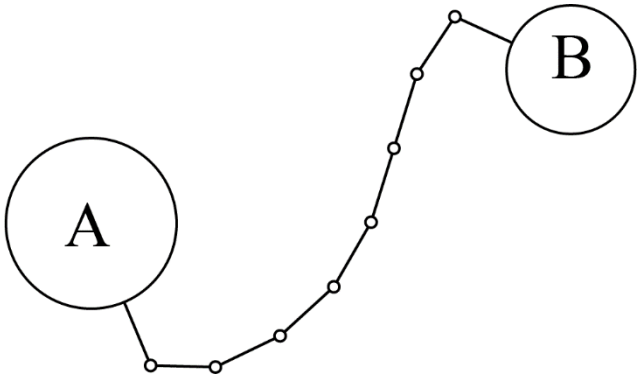

Figure 6. Forced connection network of the two major *ITS2* variants in *Diolcogaster* sp. 15 (single specimen). The less abundant sequence (B, 36% relative abundance) has a 9 bp deletion relative to sequence A, approximately one third of the way through the sequence.

Example 3: multiple major and minor variants of varying divergences and relatedness

In *Diolcogaster* sp. 17, a major (32% relative abundance) and several minor and marginal variants were sequenced, many with at least one indel (1-5 bp in length) compared to the major variant (Fig. 7). No clear pattern of relatedness between the variants was evident, and this represents a species that would be difficult to sequence using Sanger methods without a cloning step, at least with the primers and PCR conditions used in this study.

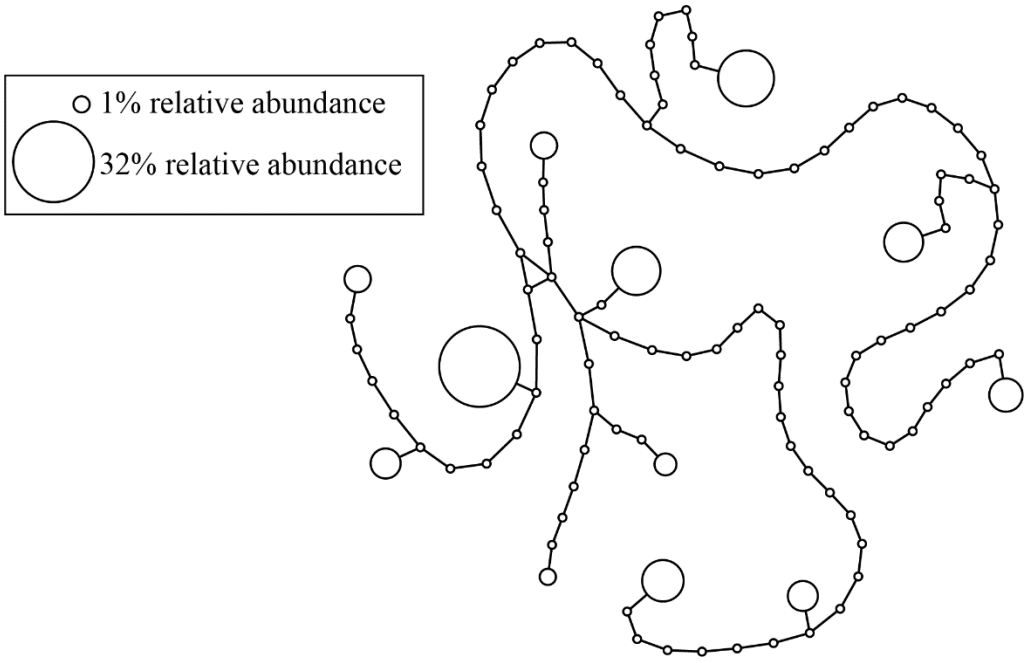

Figure 7. Forced connection haplotype visualisation of the major and minor *ITS2* variants with > 1% relative abundance in *Diolcogaster* sp. 17 (single specimen). The size of the circles is proportional to relative abundance of a variant.

Example 4: Multiple specimens in a species with both shared and unique variants

Species that had multiple specimens assigned using *COI* and *WG* allowed the opportunity to examine the levels of inter-individual variation. In *Diolcogaster* sp. 18, five specimens shared an identical *COI* haplotype, but had notable differences in the sequenced *ITS2* variants (Fig. 8). Some haplotype variants were shared among several, or all of the specimens, whilst some variants were unique to an individual. The haplotype variant with the highest abundance for each of the specimens was only identical in two individuals, with this sequence 2-4 bp (0.6-1.2%) divergent to the most abundant variant of the other three specimens.

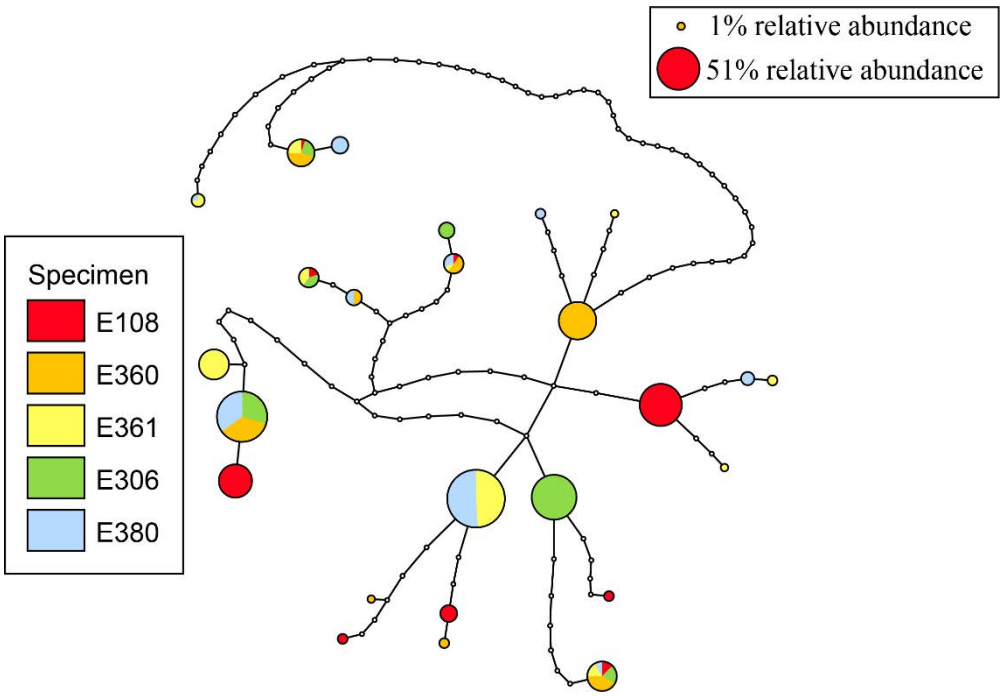

Figure 8. Forced connection haplotype visualisation of the *ITS2* variants with > 1% relative abundance in *Diolcogaster* sp. 18. Colours represent different specimens (see key for colours relating to different DNA extraction codes of specimens) and the size of the circles and wedges are proportional to the relative abundance of a variant.

Example 5: A complex pattern of variants in a species with multiple specimens

Diolcogaster sp. 19 had the largest number of specimens, and also the highest number of major and minor haplotype variants sequenced within individuals. Like in example 4 (sp. 18), many of these variants are shared amongst different specimens, with other variants appearing in only a single individual (Fig. 9).

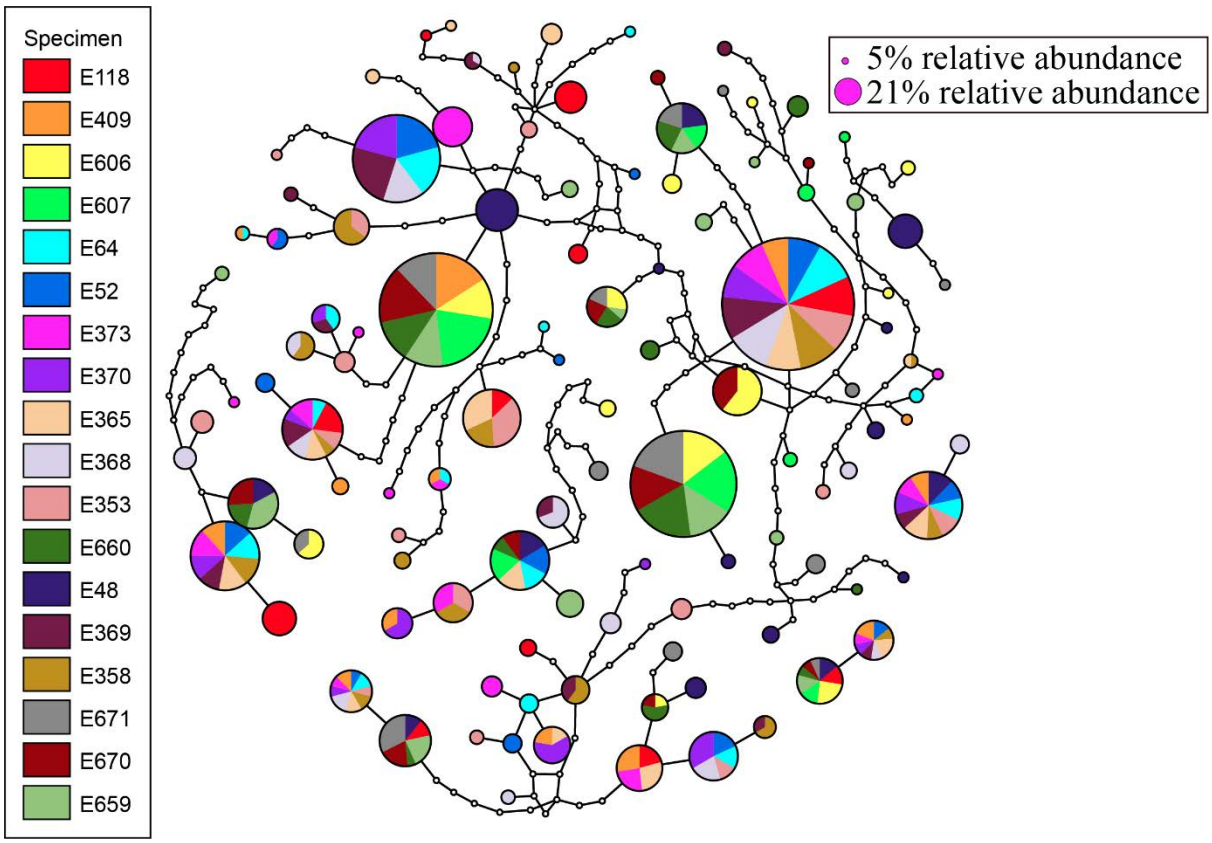

Figure 9. 90% probability parsimony connection haplotype visualisation of the *ITS2* variants with > 1% relative abundance in *Diolcogaster* sp. 19. Colours represent different specimens (see key for colours relating to different DNA extraction codes of specimens) and the size of wedges and circles is proportional to sequenced relative abundance of a variant in a specimen.

Divergence of ITS2 *variants between species*

Whilst the complex nature of the intragenomic variation in *ITS2* in this genus precludes it from being a simple DNA barcoding marker, comparative analyses of *ITS2* appear to distinguish species (Fig. 10). The only species which have shared or have very closely related *ITS2* variants are those where the delimitation using *COI* and *WG* was less certain (species 6, 7, 8; species 18, 19; Fig. 10i and 10ii respectively). The divergence of *COI* in species 6 from individuals in species 7 and 8 was only just over the 2% *COI* delimitation threshold commonly used for microgastrines (2-3% divergent in different individuals), but species 6 had a unique *WG* haplotype (2 SNPs) from that of species 7 and 8, which share a *WG* haplotype and are less than 2% divergent in the *COI* barcoding region. As species 7 and 8 were rendered paraphyletic by species 6, all three species were delimited separately in the consensus hypothesis of Fagan-Jeffries *et al.* (2018) (Fig. 10b). As species 6 and 7 share an *ITS2* haplotype which is only 1 bp different from that of species 8 (Fig. 10i), the incorporation of *ITS2* data into the delimitation decision would suggest that a better species hypothesis than that of Fagan-Jeffries *et al.* (2018) *may* be to group species 6, 7 and 8 as a

single species. Species 18 and 19 shared a *WG* haplotype, but specimens of the two species are 3-4% divergent in the *COI* barcoding region (Fagan-Jeffries *et al.* 2018) and were thus separated in the original consensus species delimitation hypothesis. These two species share *ITS2* haplotypes (Fig. 10ii) suggesting that they were over-split in the previous delimitation analysis and should be more conservatively grouped, or alternatively, if the original hypothesis is correct, that *ITS2* haplotypes are still shared between very recently diverged species.

Use of ITS2 *in phylogenetics*

The constructed Bayesian phylogeny of *Diolcogaster* using *ITS2* mostly supported the haplotype network results, with all the variants of species delimited by *COI* and *WG* forming monophyletic clades other than *Diolcogaster* spp. 6/7/8 (sp. 7 paraphyletic in respect to sp. 6 and 8, which are identical) and *Diolcogaster* spp. 18/19 (paraphyletic with respect to each other), again indicating that these species were probably over-split in the original species delimitation hypothesis (Supplementary Data S4). Species 17 was also rendered paraphyletic, but with low support on the connecting nodes. The relationships among species were similar to those found in the *COI* and *WG* concatenated tree, with only a few instances of differing topology. The RAxML tree had limited support on most nodes, less monophyletic species clades and less congruence to the *COI* and *WG* tree (Supplementary Data S5). The mostly congruent topologies between the genes, and the fact that variants of most species were monophyletic, suggests that *ITS2* can potentially be used for phylogenetic analysis for this group despite the large intra-individual variation.

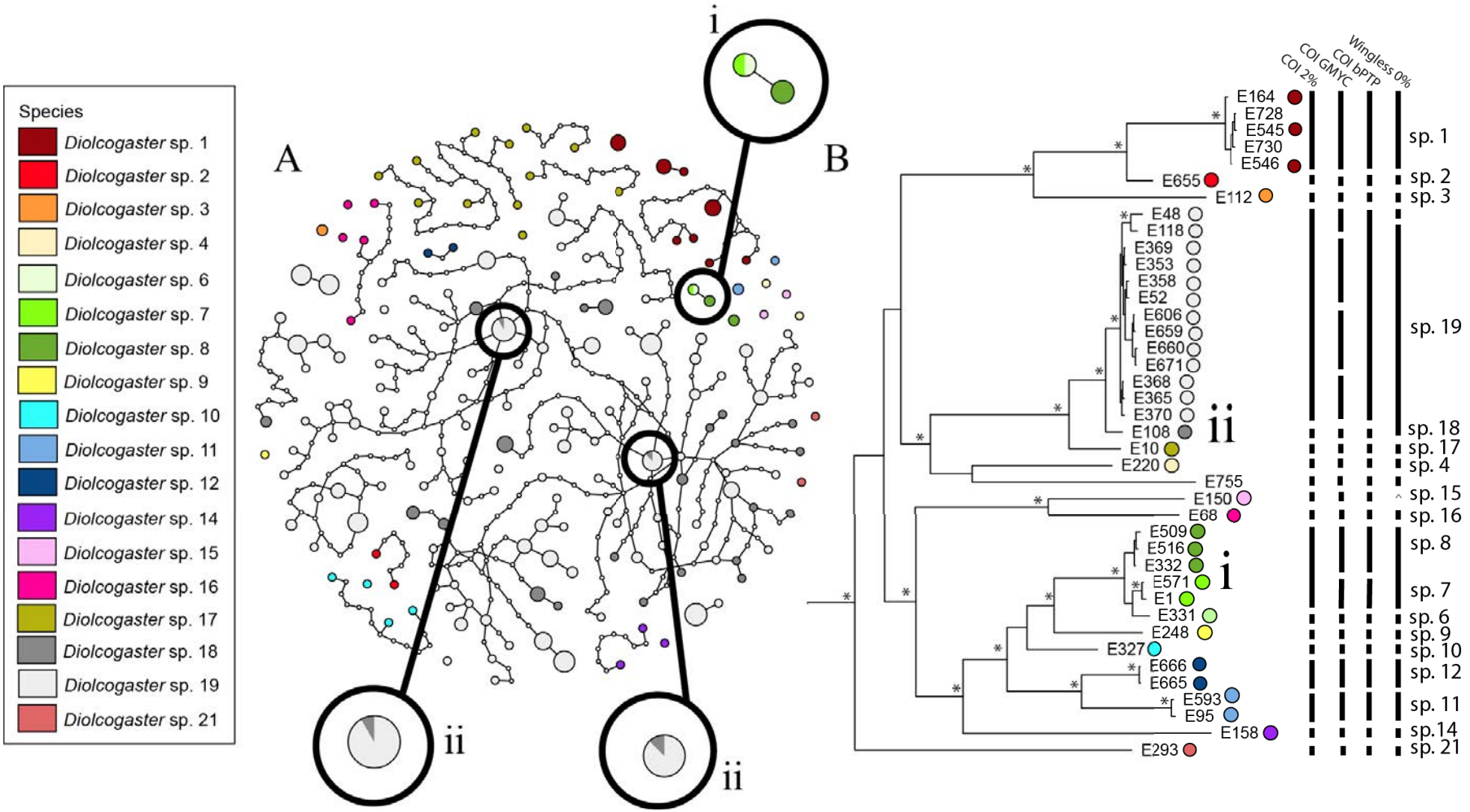

Figure 10. A) 90% probably parsimony connection haplotype visualisation of all *ITS2* variants sequenced in >1% relative abundance in all *Diolcogaster* specimens. Circles are coloured by previously hypothesised species based on *COI* and *WG* (see key to species within figure) and size is proportional to the number of specimens for which that variant was sequenced at >1% abundance. The smallest circles represent one specimen. B) *Diolcogaster* clade of a larger Bayesian *WG* + *COI* concatenated tree, nodes with posterior probabilities ≥ 95% indicated by *. Coloured circles next to specimen DNA extraction codes match those in figure part A. Previous species delimitation results and hypothesised species delimitation indicated to the right of the tree.

Discussion.

One of the major findings of this study is that levels of intragenomic *ITS2* variation are similar between individuals of the same species, but can vary widely between species of *Diolcogaster*. Some species showed limited intragenomic variation, with only a single variant with > 1% relative abundance, some species had 2-4 variants with > 1% relative abundance, and three species had more than five variants > 1% relative abundance (maximum 16 variants with > 1% relative abundance in species 19). *ITS2* divergences within a specimen between the most abundant variant and other variants with > 1% abundance ranged from just above the clustering threshold (6 bp different, 2% divergence) to maximums of either 33% divergent if indels are included in the divergence calculation (species 1), or 9% if indels are ignored (species 4).

In a similar study on *ITS2* allelic variation in several species across multiple genera of mosquitos, Batovska *et al.* (2017) found most individuals had one to three different *ITS2* variants, but two species of the genus *Dobrotworskyius* had up to 35 variants per individual. In Batovska *et al.* (2017) reads were clustered at 95% identity to determine variants, a more conservative clustering method than the 98% used in our study. Different numbers of *ITS2* variants have also been found in different species of spiders (Toju and Baba 2018) where a 97% identity clustering method was used. In both of the previously mentioned studies, the clustering threshold appears to have been chosen arbitrarily. Toju and Baba (2018) removed clusters with less than 10 reads based on the assumption that these may be potential PCR/sequencing errors, however, Batovska *et al.* (2017) did not state whether they removed clusters with low numbers of reads.

Initially, the high levels of intragenomic variation discovered in the microgastrine barcoding project (Fagan-Jeffries *et al.* 2018) were thought to exclude *ITS2* as a useful species delimitation gene, as a simple divergence threshold approach could not be undertaken. In addition, the alignment of sequences even between species of the same genus was highly ambiguous, meaning that the results of tree-based species delimitation approaches such as PTP (Zhang *et al.* 2013) and GMYC (Pons *et al.* 2006), that rely on the topology and branch lengths of the tree, are questionable. However, a haplotype visualisation approach, where the sharing of haplotypes (or haplotypes with only a single bp difference) is used as evidence for specimens belonging to the same species, appears to work well as a species delimitation method for this group of wasps. With denser sampling at both the species and population level, more work will need to be done to determine what level of variation between *ITS2* haplotypes is a suitable threshold for species delimitation; whether a single or a few bp differences between haplotypes is enough to delimit a separate

species, or whether greater variation in the major haplotypes of individuals of a species is present than was found in this study. Shared *ITS2* haplotypes were only found between species delimited using *COI* and *WG* in two cases, providing evidence that these species may have been over-split in the original species delimitation analyses. *ITS2* provides another independent piece of molecular evidence, and can add weight to species delimitation decisions in cases where *COI* divergences are near the commonly used divergence threshold or in conflict with other markers such as *WG*.

ITS2 is a widely used marker in phylogenetics and DNA barcoding of eukaryotes, with an online database solely dedicated to the collation of sequences and secondary structures of the region (Ankenbrand *et al.* 2015). However, the use of *ITS2* in phylogenetics can cause problems when divergent variants are sequenced from the same species in different studies, which cause different relationships to be inferred on the resulting phylogenies (Mayol and Rosselló 2001). In the current study, *ITS2* appears to work well as both a DNA barcoding marker and also for phylogenetic analysis at the species level. A similar result was found in crayfish, where intragenomic variation in *ITS1* and *ITS2* was enough to obscure population level relationships, but at species level the phylogenetic relationships could be determined (Harris and Crandall 2000). However, the inclusion of *ITS2* as a DNA barcoding or phylogenetic marker for microgastrines, and potentially other Hymenoptera, should be accompanied by a thorough analysis of intragenomic variation, and thus currently requires an intensive data-processing pipeline. Sanger methods are likely to cause biased results, with only those species possessing a single major variant able to be successfully sequenced. Through NGS methods, *ITS2* can be well characterised, but stringent measures accounting for PCR and sequencing error need to be applied in the data processing stage to generate the most useful and accurate results for species delimitation. In a study characterising *ITS2* variation in a genus of green algae using Illumina sequencing, Alanagreh *et al.* (2017) did not directly address PCR error, but did use multiple replicates from individuals to ensure if the intragenomic variation pattern could be reproduced; they found some variability between replicates, and also variation in the unique haplotypes recovered through Illumina sequencing compared to cloning methods. Including multiple PCR replicates of the same DNA extract in future *ITS2* NGS studies could allow differentiation between closely related variants and random PCR errors. PCR conditions, including the choice of enzyme, will affect the rate of PCR errors (McInerney *et al.* 2014; Potapov and Ong 2017) and thus using high-fidelity enzymes may reduce the number of sequences with random PCR errors and allow better representation of true *ITS2* variants. In addition to considering random PCR and sequencing errors when analysing variants, screening for PCR chimeras is an essential

filtering step in all studies, as undetected chimeras can lead to inflated numbers of variants (Thornhill *et al.* 2007).

The presence of multiple *COI* pseudogenes or heteroplasmy in many of the specimens analysed here may have implications for metabarcoding approaches for species identification and delimitation when untagged, bulk specimen libraries are prepared. Ninety-seven percent is often used as a clustering threshold for determining operational taxonomic units (OTUs) in *COI* metabarcoding data, although the choice of clustering threshold can vary the results of metabarcoding studies considerably (Alberdi *et al.* 2018). Whilst most data filtering pipelines remove sequences of the incorrect length, or with stop codons, several of the sequences found in the PCR amplicon data of *COI* in *Diolcogaster* would have been assigned as additional OTUs had these specimens been included in a metabarcoding study where individuals are not tagged, as the sequences appeared functional and were more than 3% divergent from the true *COI* sequence. The presence of these sequences highlights the importance of filtering sequences with a low number of reads from metabarcoding data, or using multiple DNA barcodes to allow comparison across markers.

Despite an initial assumption that the high levels of *ITS2* variation within individuals prevented the use of this region for species delimitation, the application of intensive data filtering has shown that *ITS2* can provide useful evidence to support commonly used markers such as *COI* through haplotype visualisation, and can be used to analyse relationships among species using phylogenetic methods, at least in the small subset of microgastrine specimens analysed in this study.

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Supplementary Data S1

```
#!/bin/bash
# usage: program.sh
# Amplicon processing pipeline (Diolcogaster ITS2)
# Erinn
# August 2018
for file in *_R1.fastq.gz
do
        FILESTEM=${file%_*}
        SAMPLE=${file%%_*}
# run all paired data through bbmap
bbduk.sh in1=$file in2=$FILESTEM"_R2.fastq.gz" out1=../no_adapters/$FILESTEM"_R1_clean.fq.gz"
out2=../no_adapters/$FILESTEM"_R2_clean.fq.gz" outs=../no_adapters/$FILESTEM"_singletons.fq.gz"
literal=AGATCGGAAGAGCAC,AGATCGGAAGAGCGT ktrim=r k=15 mink=15 hdist=0 tbo minlength=30 usejni=t
# In the original pipeline, a quality trimming step occurred using bbduk, which may have meant usable
sequences had their primers trimmed and therefore would not have been picked up later when sequences are
sorted by the forward primer
# This does not invalidate or change any results from the original barcoding paper, but may have reduced the
available data and is correct here to obtain the maximum number of ITS2 sequences

#collapse reads using PEAR
pear -f ../no_adapters/$FILESTEM"_R1_clean.fq.gz" -r ../no_adapters/$FILESTEM"_R2_clean.fq.gz" -o
../no_adapters/$SAMPLE"_peared"

#sort by primer
bbduk.sh in=../no_adapters/$SAMPLE"_peared.assembled.fastq" outm=../COIA/$SAMPLE"_COIA.fq"
outu=../COIA/$SAMPLE"_unmatchedCOIA.fq" restrictleft=25 k=25 hdist=0
literal=GGTCAACAAATCATAAAGATATTGG usejni=t;
bbduk.sh in=../COIA/$SAMPLE"_unmatchedCOIA.fq" outm=../COIB/$SAMPLE"_COIB.fq"
outu=../COIB/$SAMPLE"_unmatchedCOIB.fq" restrictleft=22 k=22 hdist=0
literal=KCWTTYCCWCGWATAAATAATA copyundefined usejni=t;
bbduk.sh in=../COIB/$SAMPLE"_unmatchedCOIB.fq" outm=../WING/$SAMPLE"_WING.fq"
outu=../WING/$SAMPLE"_unmatchedWING.fq" restrictleft=26 k=26 hdist=0
literal=GARTGYAARTGYCAYGGYATGTCTGG copyundefined usejni=t;
bbduk.sh in=../WING/$SAMPLE"_unmatchedWING.fq" outm=../ITS2/$SAMPLE"_ITS2.fq"
outu=../ITS2/$SAMPLE"_unmatchedITS2.fq" restrictleft=20 k=20 hdist=0 literal=TGTGAACTGCAGGACACATG
usejni=t;

#remove primers and quality trim
bbduk.sh in=../COIA/$SAMPLE"_COIA.fq" out=../COIA/$SAMPLE"_COIA_clean1.fq"
outs=../COIA/$SAMPLE"_COIA_singletons.fq" literal=GGTCAACAAATCATAAAGATATTGG ktrim=l k=25
hdist=0 tbo qtrim=l trimq=20 minlength=200 usejni=t;
bbduk.sh in=../COIA/$SAMPLE"_COIA_clean1.fq" out=../COIA/$SAMPLE"_COIA_clean2.fq"
outs=../COIA/$SAMPLE"_COIA_singletons2.fq" literal=GGNTGAACNGTNTATCCNCC ktrim=r k=20 tbo
hdist=0 qtrim=r trimq=20 minlength=200 copyundefined usejni=t;
bbduk.sh in=../COIB/$SAMPLE"_COIB.fq" out=../COIB/$SAMPLE"_COIB_clean1.fq"
outs=../COIB/$SAMPLE"_COIB_singletons.fq" literal=KCWTTYCCWCGWATAAATAATA ktrim=l k=22 hdist=0
tbo qtrim=l trimq=20 minlength=200 copyundefined usejni=t;
bbduk.sh in=../COIB/$SAMPLE"_COIB_clean1.fq" out=../COIB/$SAMPLE"_COIB_clean2.fq"
outs=../COIB/$SAMPLE"_COIB_singletons2.fq" literal=TGATTTTTTGGTCACCCTGAAGTTTA ktrim=r k=26
hdist=0 tbo qtrim=r trimq=20 minlength=200 usejni=t;
bbduk.sh in=../ITS2/$SAMPLE"_ITS2.fq" out=../ITS2/$SAMPLE"_ITS2_clean1.fq"
outs=../ITS2/$SAMPLE"_ITS2_singletons.fq" literal=TGTGAACTGCAGGACACATG ktrim=l k=20 hdist=0 tbo
qtrim=l trimq=20 minlength=200 usejni=t;
bbduk.sh in=../ITS2/$SAMPLE"_ITS2_clean1.fq" out=../ITS2/$SAMPLE"_ITS2_clean2.fq"
outs=../ITS2/$SAMPLE"_ITS2_singletons2.fq" literal=ACCCCCTAAATTTAAGCAT ktrim=r k=19 hdist=0 tbo
qtrim=r trimq=20 minlength=200 copyundefined usejni=t;
bbduk.sh in=../WING/$SAMPLE"_WING.fq" out=../WING/$SAMPLE"_WING_clean1.fq"
outs=../WING/$SAMPLE"_WING_singletons.fq" literal=GARTGYAARTGYCAYGGYATGTCTGG ktrim=l k=26
hdist=0 tbo qtrim=l trimq=20 minlength=200 copyundefined usejni=t;
bbduk.sh in=../WING/$SAMPLE"_WING_clean1.fq" out=../WING/$SAMPLE"_WING_clean2.fq"
outs=../WING/$SAMPLE"_WING_singletons2.fq" literal=TGYACATTCCAYTGGTGYGCGHAGT ktrim=r k=25
hdist=0 tbo qtrim=r trimq=20 minlength=200 copyundefined usejni=t;
```

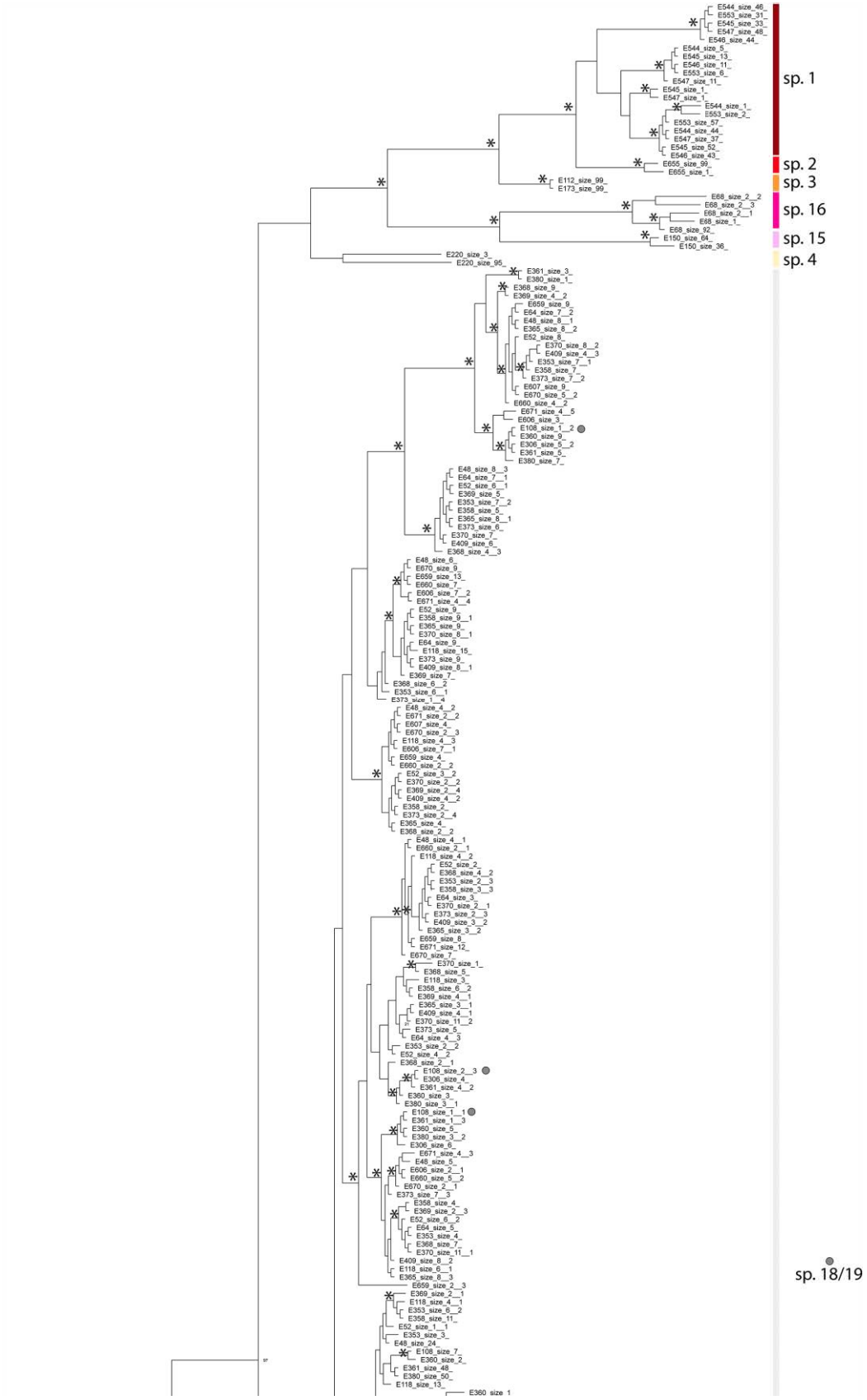
```
# dereplicate using vsearch
vsearch --derep_fulllength ../COIA/$SAMPLE"_COIA_clean2.fq" --output
../COIA/$SAMPLE"_COIA_clean2_derep.fa" --sizeout;
vsearch --derep_fulllength ../COIB/$SAMPLE"_COIB_clean2.fq" --output
../COIB/$SAMPLE"_COIB_clean2_derep.fa" --sizeout;
vsearch --derep_fulllength ../ITS2/$SAMPLE"_ITS2_clean2.fq" --output
../ITS2/$SAMPLE"_ITS2_clean2_derep.fa" --sizeout;
vsearch --derep_fulllength ../WING/$SAMPLE"_WING_clean2.fq" --output
../WING/$SAMPLE"_WING_clean2_derep.fa" --sizeout;

# remove chimeras
vsearch --uchime_denovo ../COIA/$SAMPLE"_COIA_clean2_derep.fa" --uchimeout
../COIA/$SAMPLE"_COIA_chimera_results" --nonchimeras ../COIA/$SAMPLE"_COIA_nonchimeras.fa";
vsearch --uchime_denovo ../COIB/$SAMPLE"_COIB_clean2_derep.fa" --uchimeout
../COIB/$SAMPLE"_COIB_chimera_results" --nonchimeras ../COIB/$SAMPLE"_COIB_nonchimeras.fa";
vsearch --uchime_denovo ../ITS2/$SAMPLE"_ITS2_clean2_derep.fa" --uchimeout
../ITS2/$SAMPLE"_ITS2_chimera_results" --nonchimeras ../ITS2/$SAMPLE"_ITS2_nonchimeras.fa";
vsearch --uchime_denovo ../WING/$SAMPLE"_WING_clean2_derep.fa" --uchimeout
../WING/$SAMPLE"_WING_chimera_results" --nonchimeras ../WING/$SAMPLE"_WING_nonchimeras.fa";

# cluster
vsearch  --cluster_size ../COIA/$SAMPLE"_COIA_nonchimeras.fa" --consout
../COIA/$SAMPLE"_COIA_cluster_consensus.fa" --sizein --sizeout --id 1;
vsearch  --cluster_size ../COIB/$SAMPLE"_COIB_nonchimeras.fa" --consout
../COIB/$SAMPLE"_COIB_cluster_consensus.fa" --sizein --sizeout --id 1;
vsearch  --cluster_size ../ITS2/$SAMPLE"_ITS2_nonchimeras.fa" --centroids
../ITS2/$SAMPLE"_ITS2_cluster_consensus.fa" --sizein --sizeout --id 0.98;
vsearch  --cluster_size ../WING/$SAMPLE"_WING_nonchimeras.fa" --consout
../WING/$SAMPLE"_WING_cluster_consensus.fa" --sizein --sizeout --id 1;
# In the original processing, consout was also used for ITS2. As it is possible that the consensus sequence is not
the same as the most abundant sequence we feel that using the centroid that seeded the cluser is more relaible
than the consensus. This should not impact the other amplicons, which are clustered at 100% identity and thus
should have consensus sequences which are the same as the centroid.
        done
```

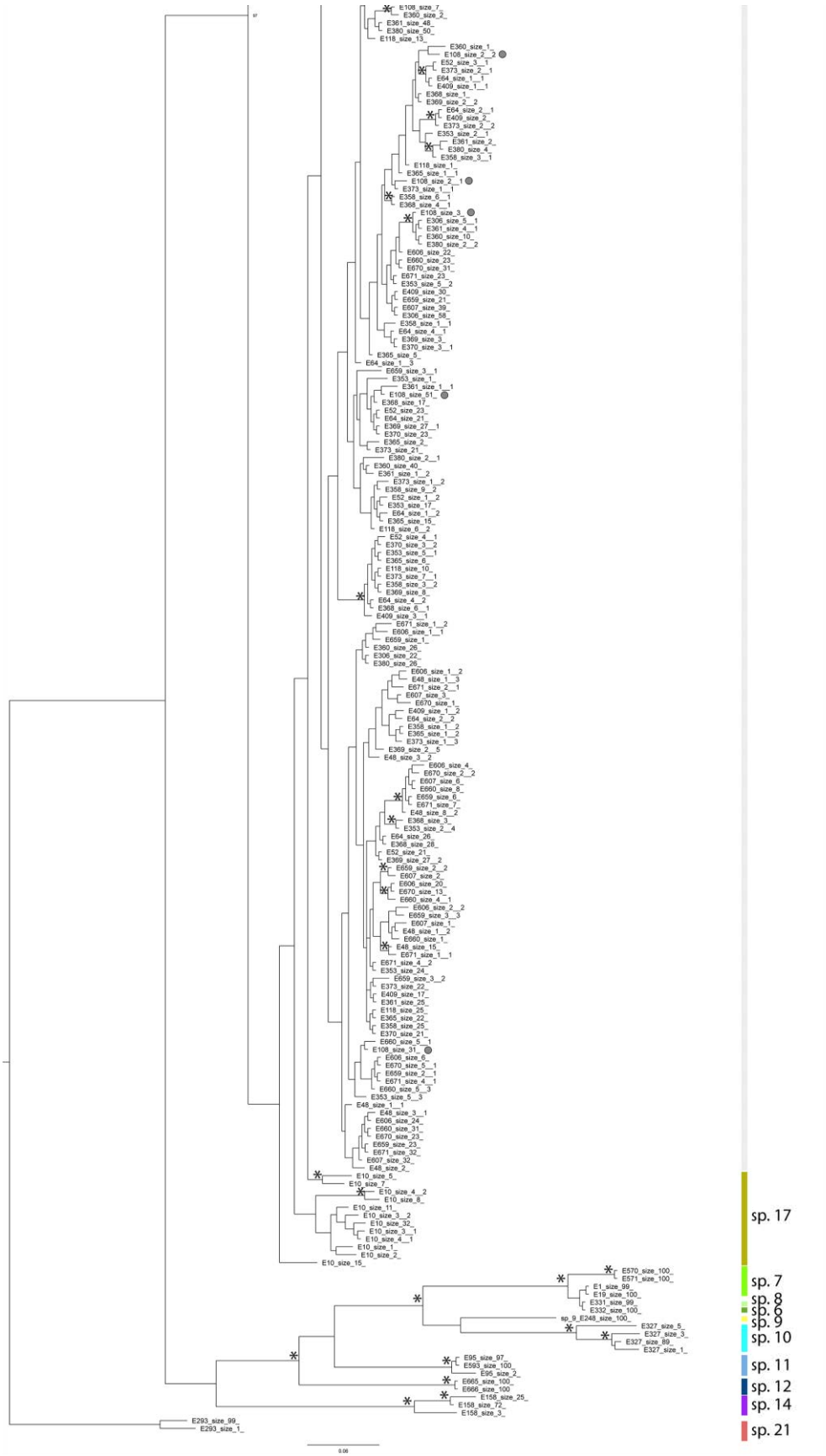
Supplementary Data S2: Tables of specimen sequence information – publically available on FigShare, DOI: 10.25909/5bb5669bab0d8

Supplementary Data: Table S3: Number of reads assigned to *ITS2* after removal of clusters with < 10 reads and variants clustered at 98% per specimen, also after removal of clusters with < 10 reads.

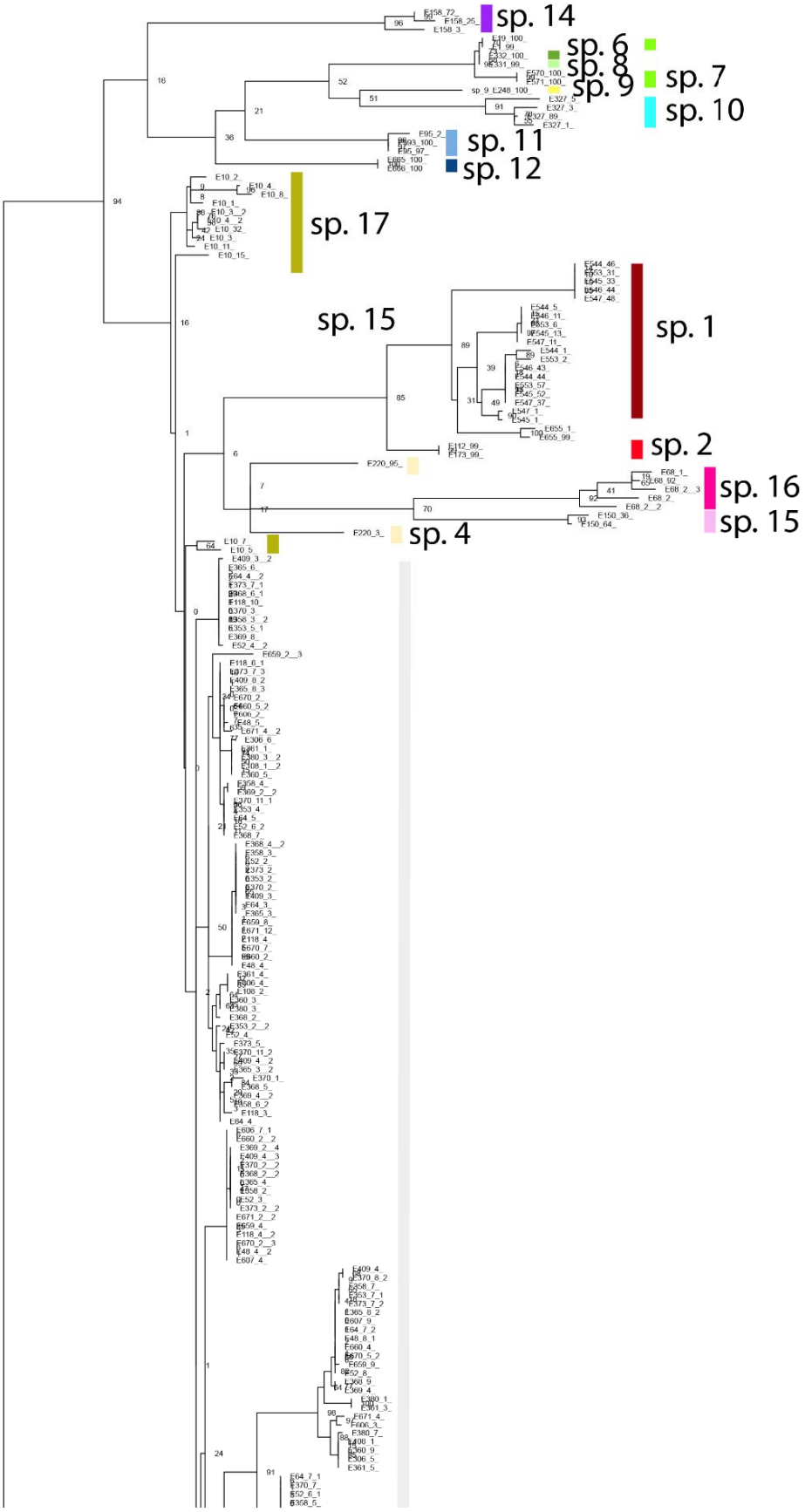
Extraction	Species	Number of reads	Number of major variants	Number of major+minor variants	Total Number of variants
E544	1	23979	2	4	22
E545	1	17394	2	4	11
E546	1	19075	2	3	16
E547	1	21684	2	4	17
E553	1	23063	2	4	27
E655	2	885	1	2	2
E112	3	5590	1	1	3
E173	3	20978	1	1	7
E220	4	25445	1	2	14
E331	6	4819	1	1	2
E332	7	12852	1	1	4
E1	8	13219	1	1	4
E19	8	7245	1	1	2
E570	8	115	1	1	1
E571	8	1842	1	1	1
E248	9	2528	1	1	1
E327	10	2676	1	4	7
E593	11	1609	1	1	1
E95	11	12082	1	2	5
E665	12	24	1	1	1
E666	12	90	1	1	1
E158	14	348	2	3	3
E150	15	789	2	2	2
E68	16	2171	1	5	6
E10	17	28912	1	12	56
E108	18	1065	2	9	9
E306	18	311	2	6	6
E360	18	6395	1	8	18
E361	18	6888	2	10	20
E380	18	3405	2	9	14
E118	19	31154	1	11	61
E48	19	29015	1	15	72
E353	19	4942	1	16	23
E409	19	22554	1	13	56
E64	19	19591	2	15	38
E358	19	19650	1	15	40
E52	19	18624	2	13	52
E606	19	1799	3	12	13
E607	19	2288	2	8	14
E660	19	3459	2	12	16
E671	19	1267	2	13	13
E670	19	1180	2	11	11
E659	19	4632	2	14	16
E365	19	16527	1	14	43
E368	19	4666	1	15	17
E373	19	9805	2	16	28
E370	19	1290	2	12	12
E293	21	3456	1	2	2

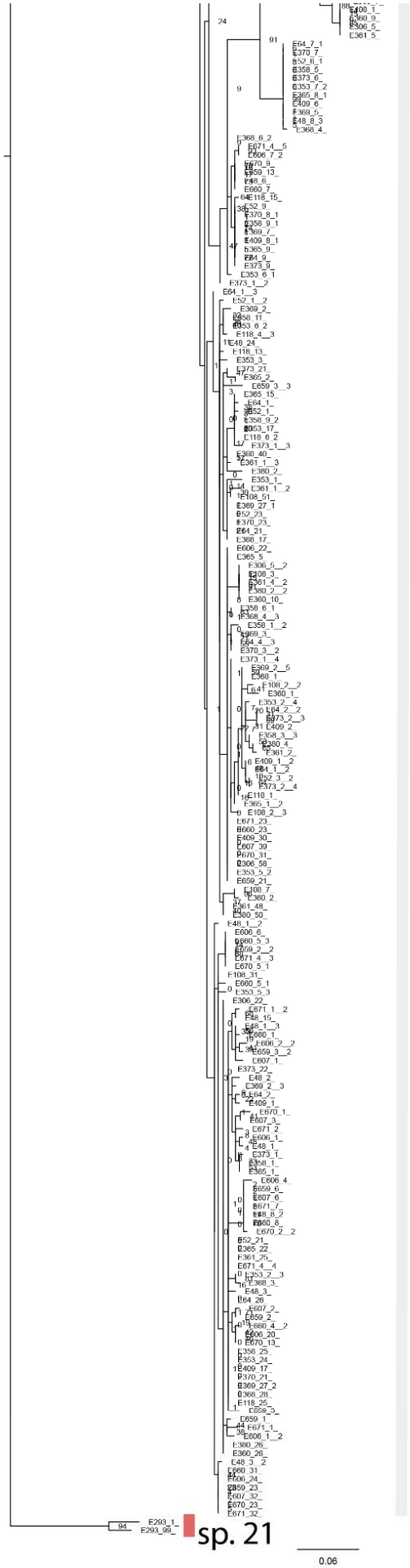
Supplementary Data S4: Bayesian phylogeny of *ITS2* variants > 1% relative abundance in all specimens, with species as delimited by *COI* and *WG* illustrated to the right of the tree. The tree is rooted as per the *COI+WG* concatenated tree (at species 21). * = posterior probability ≥ 95%. Figure extends across two pages.




sp. 17
sp. 7
sp. 8
sp. 6
sp. 9
sp. 10
sp. 11
sp. 12
sp. 14
sp. 21

Supplementary Data S5: RAxML phylogeny of *ITS2* variants > 1% relative abundance in all specimens, with species as delimited by *COI* and *WG* illustrated to the right of the tree. The tree is rooted as per the *COI+WG* concatenated tree (at species 21). Figure extends across two pages.




sp. 18/19
sp. 21
0.06

Supplementary Data: Table S6: Identification of molecular species delimited using COI + WG in Fagan-Jeffries *et al.* (2018)

Molecular species	**Identification**
1	*D. robertsi*
2	Unknown. Keys to *D. robertsi* but significant colour variation.
3	*D. perniciosus*
4	Unknown (male specimen)
5	No specimen (BOLD sequence)
6	Unknown (similar to *D. iqbali* but dramatic colour difference on mesosoma)
7	*D.* cf. *iqbali*
8	*D.* cf. *iqbali*
9	Unknown
10	*D.* cf. *hadrommatus*
11	*D.* cf. *tearae*
12	Unknown. Most closely matches *D. masoni*, but defining hind wing character difficult to determine.
13	No specimen (BOLD sequence)
14	Unknown (does not appear to be a described species)
15	Unknown
16	*D.* cf. *adiastola*
17	Unknown (single male specimen)
18	*D.* cf. *yousufi*
19	*D.* cf. *yousufi*
20	Unknown
21	Unknown (single male specimen, does not appear to be a described species)

Chapter 4: Synopsis of the parasitoid wasp genus *Choeras* Mason (Hymenoptera: Braconidae: Microgastrinae) from Australasia, with the description of two new species

Statement of Authorship

Title of Paper	Synopsis of the parasitoid wasp genus *Choeras* Mason (Hymenoptera: Braconidae: Microgastrinae) from Australasia, with the description of two new species
Publication Status	☑ Published ☐ Accepted for Publication ☐ Submitted for Publication ☐ Unpublished and Unsubmitted work written in manuscript style
Publication Details	Fagan-Jeffries E.P., Austin A.D. 2018. Synopsis of the parasitoid wasp genus *Choeras* Mason (Hymenoptera: Braconidae: Microgastrinae) from Australasia, with the description of two new species. Austral Entomology. 57:349–358.

Principal Author

Name of Principal Author (Candidate)	Erinn Fagan-Jeffries
Contribution to the Paper	Morphological descriptions, paper writing and figure creation (with advice and feedback from co-author)
Overall percentage (%)	80%
Certification:	This paper reports on original research I conducted during the period of my Higher Degree by Research candidature and is not subject to any obligations or contractual agreements with a third party that would constrain its inclusion in this thesis. I am the primary author of this paper.
Signature	Date 5/10/2018

Co-Author Contributions

By signing the Statement of Authorship, each author certifies that:

i. the candidate's stated contribution to the publication is accurate (as detailed above);

ii. permission is granted for the candidate in include the publication in the thesis; and

iii. the sum of all co-author contributions is equal to 100% less the candidate's stated contribution.

Name of Co-Author	Andrew Austin
Contribution to the Paper	Project conception, supervision, advice, discussion of morphological analysis, paper edits and review
Signature	Date 11/10/18

Austral Entomology

Austral Entomology (2018) **57**, 349–358

Synopsis of the parasitoid wasp genus *Choeras* Mason (Hymenoptera: Braconidae: Microgastrinae) from Australasia, with the description of two new species

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http://zoobank.org/urn:lsid:zoobank.org:pub:18A2ED15-DE50-4BED-AD4A-0F49895C35C3

Abstract The Microgastrinae are a highly diverse, cosmopolitan subfamily of Braconidae that parasitise Lepidoptera. In this study, we provide a synopsis of *Choeras* for Australasia; the seven described species are diagnosed on the basis of their holotypes and newly collected material, and two new species are described, *Choeras koalascatocola* sp. nov. and *Choeras morialta* sp. nov. A key to species is provided along with information on their distribution and biology; one of the new species, *C. koalascatocola* sp. nov., was reared from an unknown species of Lepidoptera feeding on koala scats. The substantial morphological variation among *Choeras* species for a number of key characters is discussed and supports the possibility that the genus is polyphyletic.

Key words biological control, koala, Lepidoptera, parasitoid.

INTRODUCTION

The Microgastrinae are a large and diverse subfamily comprising, almost entirely, koinobiont endoparasitoids of lepidopteran larvae. The group is of considerable interest as natural enemies of lepidopteran pests because of the extreme host specificity of many species. Several species have been introduced into Australia and New Zealand to combat pests such as light-brown apple moth (*Epiphyas postvittana* Walker), potato moth (*Phthorimaea operculella* Zeller) and cabbage moth (*Plutella xylostella* Linnaeus) (Austin & Dangerfield 1992). Approximately 2000 species have been described worldwide; however, recent estimates suggest the true diversity is in the range of 17 000 to 46 000 species (Rodriguez *et al.* 2013). Approximately 75 species have been described from or have been introduced into Australasia (defined as Australia, New Zealand, New Caledonia, New Guinea, Solomon Islands, Fiji Islands, Samoan Islands, Cook Islands, but not French Polynesia), but the vast numbers of undescribed species in museum collections indicate that the real species diversity for the region is much larger than this, likely by a factor of 10–20. Although monophyly of the subfamily is strongly supported, relationships among genera are still largely unresolved; some genera appear not to be natural groups. The most recent attempt to develop a robust phylogeny was by Banks and Whitfield (2006), based on seven genes and a morphological matrix. Despite the large dataset, sections of the phylogeny were not well supported, and many relationships remain contentious.

In this study, the Australasian representatives of the microgastrine genus *Choeras* Mason are re-examined following the earlier work of Austin and Dangerfield (1992) for the region. The seven existing species are diagnosed, and summaries of their distributions and biology (where available) are given. Two new species are described: *Choeras koalascatocola* sp. nov., reared from an unknown lepidopteran associated with faecal pellets of koalas (*Phascolarctos cinereus* Goldfuss) near Springsure, Queensland (Melzer *et al.* 1994); and *Choeras morialta* sp. nov. collected recently at multiple locations around Adelaide, South Australia. A key to species for the region is presented, along with a brief discussion of the substantial morphological variation among species for a number of critical characters, possibly indicating the non-monophyly of the genus. The current study aims to provide a new basis for identification of species worldwide and thus enable more accurate resolution of the phylogeny of the Microgastrinae on a global basis.

MATERIALS AND METHODS

Morphology

Terms for general morphology follow Fernández-Triana *et al.* (2014) who attempted to combine traditional microgastrine morphological terms such as those used by Mason (1981) with the standards introduced in the Hymenoptera Anatomy Ontology (HAO) project (Yoder *et al.* 2010). Terms for sculpturing follow Eady (1968). The following acronyms are used throughout the paper: T1, T2 and T3 for the first, second and third mediotergites, respectively. We define colour as either pale (white, cream or

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pale yellow), orange (light to dark orange), light brown or dark (dark brown or black). Descriptions, including morphological measurements, are based on both female and male specimens, except for female-specific characters such as ovipositor length. Distribution and host data are taken from Austin and Dangerfield (1992).

The following abbreviations are used for collections: ANIC, Australian National Insect Collection, Canberra; BMNH, The Natural History Museum, London; HNHM, Hungarian Natural History Museum, Budapest; LUIC, Lincoln University Insect Collection, Lincoln; NZAC, New Zealand Arthropod Collection, Auckland; QPIIC, Queensland Primary Industries Insect Collection, Brisbane; QM, Queensland Museum Insect Collection, Brisbane; SAM, South Australian Museum, Adelaide; WINC, Waite Insect and Nematode Collection, Adelaide. The following abbreviations are used for states and territories in Australia: Qld, Queensland; NSW, New South Wales; ACT, Australian Capital Territory; Vic, Victoria; Tas, Tasmania; S Aust, South Australia; NT, Northern Territory; WA, Western Australia.

DNA sequencing

DNA extractions were performed on ethanol-preserved specimens using the Gentra Systems PUREGENE DNA Purification Kit following the manufacturer's instructions for 'DNA purification from 5–10 mg fresh or frozen solid tissue' with minor modifications. PCRs were carried out on an Eppendorf MasterCycler Pro using a 25 μL reaction volume consisting of 15.5 μL of nuclease-free molecular water, 5 μL of 5× Immolase PCR buffer (Bioline; NSW, Australia), 1.2 μL of each 5 μM primer (forward primer: LCO1490, reverse primer HCO2198 from Folmer *et al.* 1994), 0.1 μL of Immolase DNA polymerase (5 U/μL) and 2 μL of extracted DNA. The following protocol was followed: initial enzyme activation at 95°C for 10 min, 35 cycles of 95°C for 45 s, 48°C for 45 s and 72°C for 90 s, and finally a single elongation step at 72°C for 7 min. Product purification and sequencing were conducted by The Australian Genome Research Facility (AGRF).

TAXONOMY

Choeras Mason 1981

Choeras Mason 1981: 76; Austin & Dangerfield 1992: 18; van Achterberg 2002 (treated as a subgenus of *Apanteles* Foerster); Song *et al.* 2014: 502 (treated as a subgenus of *Apanteles*).

Type species: *Apanteles* (*Pseudapanteles*) *consimilis* Viereck, 1911, by original designation.

Diagnosis

Fore wing areolet absent, small or large; propodeum either with median longitudinal carina or carina absent, but never with any indication of an areola, surface smooth to coarsely rugose; T1 parallel sided or apically tapered; T2 either transverse rectangular, subtriangular, broadly pentagonal or almost linear; hypopygium medio-longitudinally folded with several striae (as in *Apanteles*), degree of striations variable to the point where hypopygium has only faint lateral creases; ovipositor sheaths from about half as long as hind tibia to longer.

Distribution

Choeras is a cosmopolitan genus, with 65 species described worldwide (Yu *et al.* 2012; Song *et al.* 2014). The majority of species are described from the Palaearctic (including all of China) (76% spp.), with 4% from the Nearctic, 12% from Australasia and 8% from the Indo-Oriental region. However, the latter two regions are relatively poorly collected, and undescribed species are known from Mexico, Costa Rica, Yemen, New Caledonia, South Africa and Nepal (Smith *et al.* 2013).

Phylogenetic status

Choeras is morphologically diverse, with characters such as the fore wing areolet size and shape, form of the hypopygium and shape of T1 and T2 varying substantially among species. Williams (1988) noted that there is a possibility *Choeras* is paraphyletic in relation to *Sathon* Mason and discussed difficulties in separating the two genera based solely on the metanotum and hypopygium. He mentioned that there are specimens of *Choeras* that closely resemble the *Sathon lateralis* species group. Mason (1981) had originally pointed out that *S. lateralis* may 'fit amongst the diverse elements of *Choeras*'. One species group of *Sathon* has been recognised as a new genus (*Lathrapanteles* Williams) since Mason's original description, despite Williams (1985) noting that this new genus may be paraphyletic.

Austin and Dangerfield (1992), in recognising the substantial variation for these two genera, stated that *Choeras* is probably the most difficult microgastrine genus to identify in the Australasian fauna. In the 25 years since their study, little additional work has been undertaken on the genus other than descriptions of new species, and the above statement still holds true.

Some *Choeras* are clearly similar to *Sathon*, particularly those species that have only a few creases along the ventral longitudinal hypopygium, and such species can be difficult to place in one or other of these genera. In a *COI* barcoding project involving nearly 20 000 sequences and morphological data, Smith *et al.* (2013) commented that the limits between *Sathon* and *Choeras* were ill-defined when using both morphology and barcoding, and that further study would be needed to determine their status. Fernández-Triana *et al.* (2014) further noted that several species groups of *Choeras*, particularly those of the Australasian and Oriental regions, are likely to constitute new genera.

The new species described here exemplify this situation, possessing character states that make them difficult to place in either genus incontrovertibly. The form of the hypopygium in *Choeras koalascatocola* and *Choeras morialta* lacks the obvious medial folds with clear striations present in other Australian species, and as stated in the original description of the genus (Mason 1981). However, they do possess indistinct lateral creases implying more flexibility than is found in the completely solid hypopygium of *Sathon*. For the present, we have chosen to

place these new species in *Choeras* based on the partially flexible hypopygium and the absence of an exposed phragma of the scutellum, character states that exclude them from the current definition of *Sathon*. Unfortunately, host data for most Australasian species of both genera are lacking, and on a global basis, there does not appear to be a clear pattern of host preference that would help differentiate the genera or make it easier to place new species. The hosts that we suggest as likely possibilities for *C. koalascatocola* do not eliminate the placement of the species in either *Choeras* or *Sathon* based on the current knowledge of host ranges.

The phylogenetic placement and questionable monophyly of *Choeras* will remain unresolved until a comprehensive combined molecular and morphological analysis is undertaken that includes a detailed sampling of *Choeras* and morphologically similar genera such as *Sathon, Lathropanteles*, *Promicrogaster* Brues and Richardson, and *Hypomicrogaster* Ashmead.

TAXONOMY

Key to the described Australasian species of *Choeras* (females)

1 Fore wing with large areolet (Fig. 1a,b).....2
– Fore wing with small areolet (Fig. 2a–c).....7
2 Propodeum without median longitudinal carina, smooth or with some rugose sculpturing (Fig. 3c,d).....3
– Propodeum with median longitudinal carina and with rugose sculpturing covering majority of propodeum (Figs 3a,b, 5b, 6b).....4
3 T1 narrowing posteriorly to approximately half medial width, T2 median field narrow and subtriangular (Fig. 3c) .....*Choeras tegularis*
– T1 narrowing posteriorly only slightly, T2 median field broad, rectangular, with lateral sides sloping downwards (Fig. 3d) .....*Choeras cetus*
4 T1 parallel sided or widening posteriorly, T2 broad (Figs 3a, 5b).....5
– T1 narrowing posteriorly, T2 median field subtriangular or rectangular, with lateral sides sloping (Figs 3b, 6a,b) 6
5 Metasoma orange, wings with distal infuscate shading, T1 smooth, with no or only weak sculpturing (Figs 2b, 3a) .....*Choeras epaphus*
– Metasoma dark, wings hyaline, T1 reticulate rugose, particularly in posterior half (Fig. 5a–c) .....*Choeras koalascatocola* sp. nov.
6 T1 rugose for most of length, body light brown, head dark (Fig. 3b).....*Choeras helespas*
– T1 with sculpturing only in posterior half, mainly punctate rather than rugose, body black, legs orange to light brown, hypopygium with pale markings (Fig. 6) .....*Choeras morialta* sp. nov.
7 T1 clearly narrowing posteriorly, body orange (Fig. 4a) .....*Choeras papua*
– T1 parallel sided or at most narrowing posteriorly only slightly, mesosoma dark, metasoma dark, light brown or pale (Fig. 4b,c).....8
8 Fore wing vein r sharply angled (Fig. 2a), mesoscutellar disc densely covered with setae (Fig. 4c) .....*Choeras dissors*
– Fore wing vein r smoothly curved (Fig. 2b), mesoscutellar disc smooth with setae around margin only or with sparse, short setae on disc (Fig. 4b).....*Choeras calacte*

Choeras calacte (Nixon, 1965)

(Figs 2b, 4b)

Promicrogaster calacte Nixon, 1965: 230.
Choeras calacte (Nixon). – Mason 1981: 47; Austin & Dangerfield 1992: 21.

Material examined

Holotype

♀ 'Victoria, Melbourne' (BMNH 3c.1458).

Paratype

♀ 'ACT, Brindabella, 24.xi.1931, L.F. Graham' (BMNH).

Other material

9♀ 'Qld, Mareeba, 16km up Davis Crk Rd, M/T 6.xi-2.xii.84, Story/Halfpapp' (QPIIC, WINC); ♀ 'Qld, Mt. Glorious ii-vi.1977 A. Hiller' (BMNH); 2♀ 'Qld, Beerwah, 26.15S,

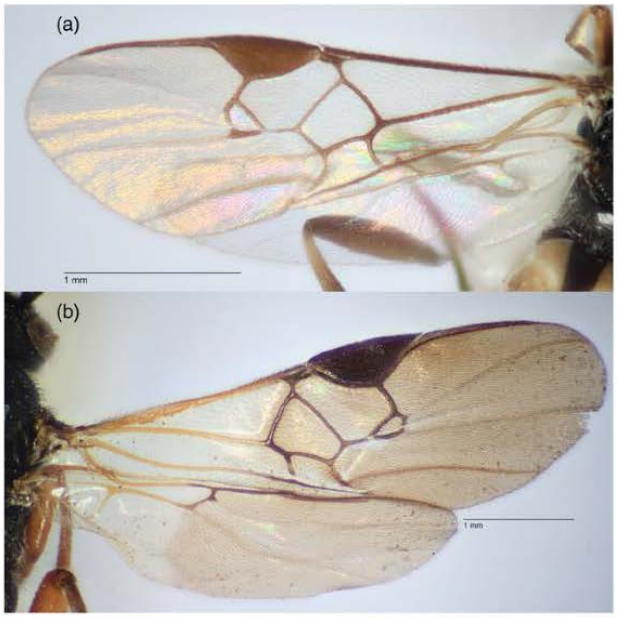

Fig. 1. Wing morphology of *Choeras* spp. (a) Fore wing of *C. tegularis* (WA Stirling Ranges), ♀; (b) fore wing and hind wing of *C. epaphus*, (Vic. Wilkur), ♀. [Color figure can be viewed at wileyonlinelibrary.com]

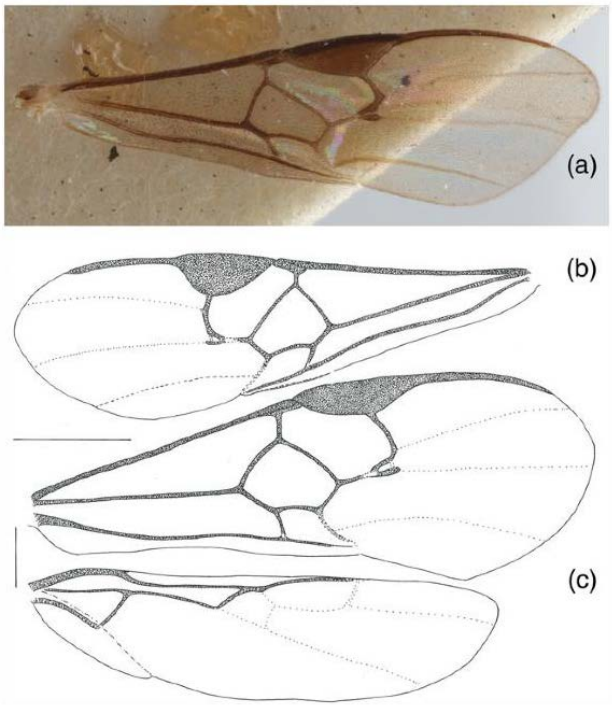

Fig. 2. Wing morphology of *Choeras* spp. (a) Fore wing of *C. dissors*, holotype, ♀; (b) fore wing of *C. calacte*, holotype, ♀; (c) fore wing and hind wing of *C. papua*, holotype ♀. (b and c reproduced from Austin and Dangerfield (1992), with permission from CSIRO Publishing). [Color figure can be viewed at wileyonlinelibrary.com]

152.57E, 28.ix-29.x.1986, B.K. Cantrell, M/T' (QPIIC); ♀ 'Qld, 7.5km NNW Kuranda, M/T, 20.ii-20.iii.1985, Story/Halfpapp' (QPIIC); ♀ 'Qld, Mt. Glorious, iii.1982, Hiller, M/T'; ♀ 'Australia, Qld, MHKS, 22–29.iii.1985, M/T' (WINC).

Diagnosis

A small fore wing areolet (Fig. 2b) distinguishes *Choeras calacte* from all other described species other than *Choeras dissors* and *Choeras papua*. Easily distinguished from *C. papua* by much darker colouration of the meso- and metasoma and absence of a distinct, percurrent median longitudinal carina on the propodeum (Fig. 4b). Can be distinguished from *C. dissors* by the sparser covering of setae on the mesoscutellar disc (Fig. 4b). Scutellum, propodeum and T1–2 dark, remaining dorsal tergites light brown; non-sclerotised areas of T1 pale; fore legs pale, mid and hind legs mostly light brown with pale areas on the anterior tibia and coxa; propodeum with rugose and punctate sculpturing; T1 almost parallel sided, narrowing slightly at boundary with T2, with punctate and rugose sculpturing in posterior half; T2 short, rectangular with sides sloping, ratio of width at posterior margin to length approximately 3.7.

Distribution

Widespread in eastern Australia.

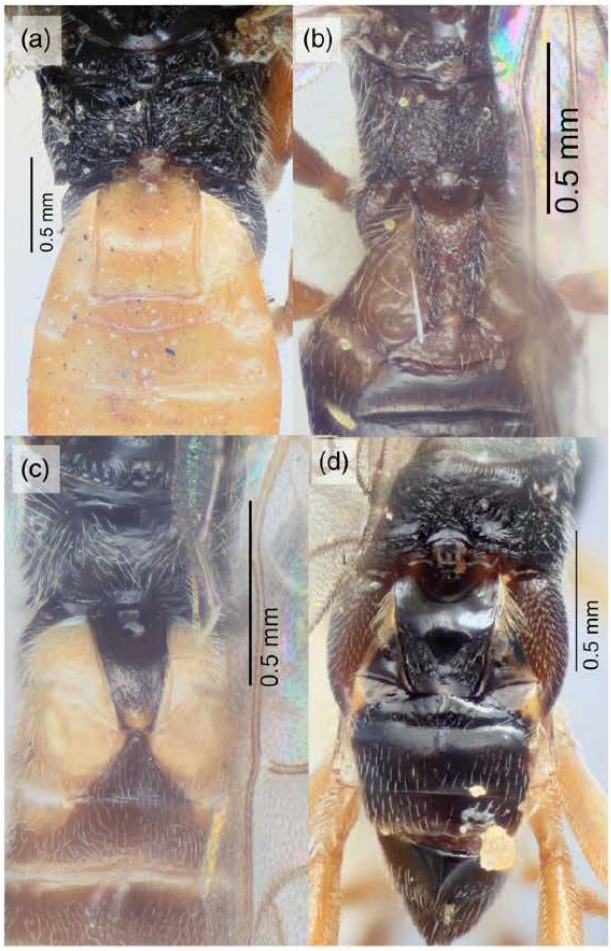

Fig. 3. Dorsal propodeum and T1–3 of *Choeras* spp. with a large fore wing areolet (a) *C. epaphus* (Vic. Wilkur), ♀; (b) *C. helespas* (N.Z., St. Arnaud), ♂; (c) *C. tegularis* (Stirling Range), ♀; (d) *C. cetus* (ACT Pine Island Reserve), ♀. [Color figure can be viewed at wileyonlinelibrary.com]

Host

Unknown.

Choeras cetus (Nixon, 1965)

(Fig. 3d)

Hypomicrogaster ceto Nixon, 1965: 217.
Choeras cetus (Nixon). – Austin & Dangerfield 1992: 21.

Material examined

Holotype

♀ 'ACT, Blundell's, Jan 1931, bred from *Eriococcus* complex on *Eucalyptus*, A.L. Tonnoir' (BMNH 3c.1439).

Paratypes

♀, 3♂ same data as holotype (BMNH).

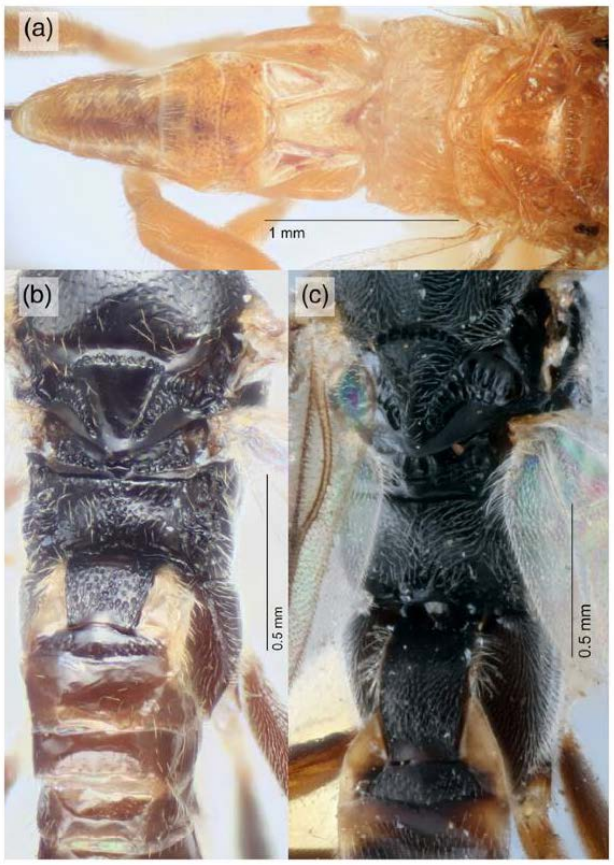

Fig. 4. Dorsal scutellum, propodeum and T1–3 of *Choeras* spp. with a small fore wing areolet (a) *C. papua* (Indonesia), ♀; (b) *C. calacte* (S.E. Qld., Beerwah), ♀; (c) *C. dissors*, holotype, ♀. [Color figure can be viewed at wileyonlinelibrary.com]

Other material

♀ 'ACT, Pine Island Reserve, 10 mi. S. Canberra, 12.i.1970' (WINC).

Diagnosis

A large fore wing areolet easily distinguishes *Choeras cetus* from *Choeras calacte, Choeras dissors* and *Choeras papua*, all of which have a small areolet. The absence of a median longitudinal carina (Fig. 3d) separates *C. cetus* from all other described species with a large areolet other than *Choeras tegularis*, from which it differs in having a broader T1 and T2. Scutellum, propodeum and all tergites dark; non-sclerotised area of T1 pale in paratype, mostly dark with lateral pale patches in specimen from Pine Island Reserve; all legs pale other than hind coxae which are light brown; propodeum mostly smooth, with rugose sculpturing medially and at lateral edges; T1 almost parallel sided, narrowing slightly posteriorly, mostly smooth and shiny but with rugose and punctate sculpturing posteriorly; T2 mostly smooth and shiny, short, rectangular with sides sloping.

Distribution

Australia (ACT).

Host

Incorrectly associated with *Eriococcus* (Coccoidea: Eriococcidae); true host unknown. Associated with *Eucalyptus*.

Choeras dissors (Nixon, 1965)

(Figs 2a, 4b)

Promicrogaster dissors Nixon, 1965: 230.
Choeras dissors (Nixon). – Mason 1981: 47; Austin & Dangerfield 1992: 21.

Material examined

Holotype

♀ 'ACT, Black Mt, 28.v.1930, W. Rafferty' (BMNH 3c.1457).

Diagnosis

A small fore wing areolet (Fig. 2a) distinguishes *Choeras dissors* from the other described species other than *Choeras calacte* and *Choeras papua*. Easily distinguishable from *C. papua* by having much darker colouration of both the meso- and metasoma and the absence of a distinct, percurrent median longitudinal carina on the propodeum (Fig. 4b). Scutellum, propodeum and T1–2 dark, remaining tergites dark with lateral pale patches. Very similar to *Choeras calacte* but can be separated by subtle differences in the shape of T1–T2, and the setal density on the mesoscutellum (see key to species).

Distribution

Australia (ACT). The species has not been recorded since its description.

Host

Unknown.

Choeras epaphus (Nixon, 1965)

(Figs 1b, 3a)

Hypomicrogaster epaphus Nixon, 1965: 215.
Choeras epaphus (Nixon). – Mason 1981: 77; Austin & Dangerfield 1992: 21.

Material examined

Holotype

♀ 'Qld, Tambourine Mts, 1–19.v.1935, R.E. Turner' (BMNH 3c.1438).

Paratype

♀ 'ACT, Blundell's, 23.iii.1930, I.M. Mackerras' (BMNH).

Other material

♀ 'ACT, 24.ii.1959, E.F. Riek' (WINC); ♀ 'NSW, Penrose State Forest, 14.x.1966. em 9 Dec 1966. M. Upton' 'ex *Garrha euselma* Meyrick (Oecophoridae) feeding on *Eucalyptus globoidea*' (ANIC); ♀ 'NSW, Kiandra, Alpine Creek, 21. iii.1962, E.F. Riek' (ANIC); ♂ 'NSW, Barrington Tops, 10. iv.1949, T.G. Campbell' (ANIC); ♀ 'Vic, Wilkur, iv.1955, Spurrell' (WINC).

Diagnosis

A large fore wing areolet distinguishes *Choeras epaphus* from *Choeras calacte*, *Choeras dissors* and *Choeras papua*, all with small fore wing areolets. Infuscation on the distal half of the wings (Fig. 1b) and orange colouration of the metasoma (Fig. 3a) are the defining characters which easily separate *C. calacte* from the other described species with a large fore wing areolet. Scutellum and propodeum dark, legs dark with a pale hind femur.

Distribution

Widespread in eastern Australia and Tasmania (Austin & Dangerfield 1992) although no specimens from Tasmania were examined in this study.

Host

Euchaetis parthenopa (Meyrick) (Oecophoridae). Syn. *Heliocausta euselma* Meyrick. Presumed correction from *Garrha euselma* on label data.

Choeras helespas Walker, 1996

(Fig. 3b)

Choeras helespas Walker, 1996: 44.

Material examined

Holotype

♀ 'New Zealand: South Island, Kohuamarua Bluff, M7D, 13 Jan 1982, J.W. Early, sweeping scrub and ferns' (LUIC).

Paratypes

289♀, 170♂ (mostly in NZAC and BMNH; some in ANIC and LUIC).

Other material

4♀, 4♂ 'New Zealand: BR 2000, St. Arnaud, 1.i.1988, sweeping in swampy open grass' 'Identified A. Walker' (WINC).

Diagnosis

A large fore wing areolet distinguishes *Choeras helespas* from *Choeras calacte*, *Choeras dissors* and *Choeras papua*, all with a small fore wing areolets. The consistent light-brown colouration of the propodeum and metasoma is the easiest character to separate *C. helespas* from the other described *Choeras* species. Propodeum with median longitudinal carina and rugose sculpturing; T1 rugose for nearly entire length, clearly narrowing posteriorly (Fig. 3b). Legs light brown to pale.

Distribution

New Zealand (North and South Islands).

Host

Unknown. Two genera were suggested in the original description as potential hosts: *Glyphipterix* sp. (Glyphipterigidae) and *Protosynaema* sp. (Plutellidae).

Choeras koalascatocola sp. nov.

(Fig. 5a-d)

http://zoobank.org/urn:lsid:zoobank.org:act:5C524956-C831-4DF5-B051-08FCB812C43F

Material examined

Holotype

♀ 'QLD: Springsure, 24°07′S 148°05′E, Aug 1989, A. Melzer, ex. koala dung' (QM T207496).

Paratypes

2♂, same data as holotype (QM T207497-8).

Diagnosis

Choeras koalascatocola differs from the described Australasian *Choeras* in the following ways. A relatively large fore wing areolet (Fig. 5c) separates it from *Choeras calacte*, *Choeras dissors* and *Choeras papua*, all of which have small areolets. The presence of a percurrent, median longitudinal carina on the propodeum of *C. koalascatocola* (Fig. 5b) differs significantly from the propodeum of *Choeras tegularis* and *Choeras cetus*. Whilst the areolet size and sculpturing of the propodeum are similar to *Choeras epaphus*, *Choeras helespas* and *Choeras morialta*, *C. koalascatocola* can be easily distinguished from *C. epaphus* by the dark tergites, and from *C. helespas* by both the darker tergites and much broader T1 and T2. *C. koalascatocola* can be distinguished from *C. morialta* by the widespread orange colouration of the hind legs and the broader T1 and T2.

Description

Colour: Dark except for pale to orange pleurites, nonsclerotised areas around mediotergites and hypopygium; antenna dark; coxae (fore, mid, hind coxa): orange, orange, dark; femora (fore, mid, hind femur): orange, orange, orange; tibiae (fore, mid, hind tibia): orange, orange, dark orange; tegula and humeral complex orange; pterostigma dark; fore wing veins dark. *Head*: Antennae slightly longer than body length; body length (head to apex of metasoma): 2.6–3 mm; ocular–ocellar line/posterior ocellus diameter: 1.6–1.7; interocellar distance/posterior ocellus

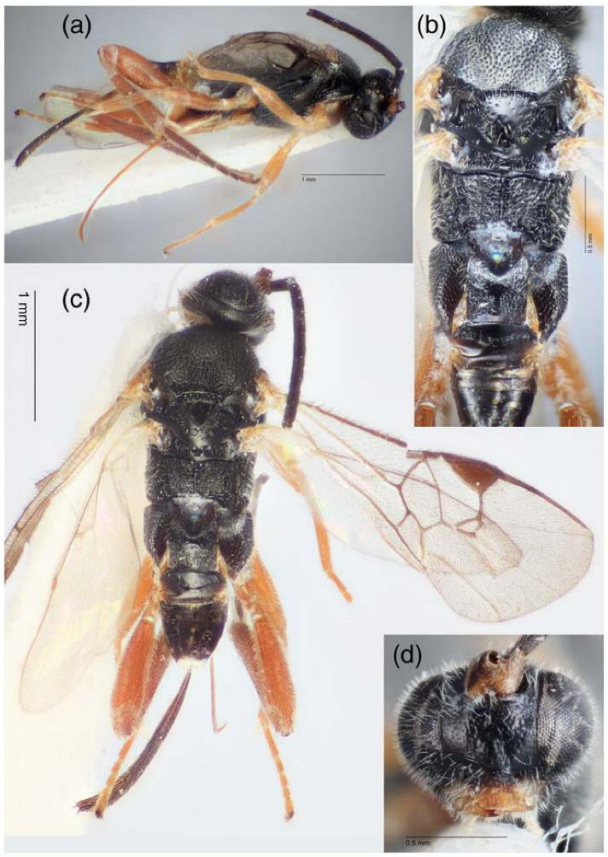

Fig. 5. *Choeras koalascatocola* sp. nov. (a) lateral habitus; (b) scutum, propodeum and metasomal tergites; (c) dorsal habitus; (d) head. [Color figure can be viewed at wileyonlinelibrary.com]

diameter: 1–1.3. *Mesosoma*: Anteromesoscutum: evenly and densely punctate; mesoscutellar disc mostly with few widely separate punctures, covered in fine setae; number of pits in scutoscutellar sulcus 8 or 9; maximum height of mesoscutellum lunules/maximum height of lateral face of mesoscutellum 0.4–0.5. *Wings*: fore wing length 2.8–2.9 mm; length of veins r/2RS 0.9–1; length of veins 2RS/2 M 1–1.1; length of veins 2 M/(RS + M)b 1.1–1.7; pterostigma length/width 2.1–2.3. *Legs*: Hind tibia inner spur length/hind basitarsus length 0.5–0.6; propodeum with percurrent median longitudinal carina and longitudinal lateral carinae creating border around spiracles; area between lateral carinae and spiracle relatively smooth. *Metasoma*: T1 length/width at posterior margin 1.6–1.8; T1 shape broad, rectangular, almost parallel-sided; T1 sculpture reticulate rugose; T2 width at posterior margin/length 3–4.9; T2 sculpture smooth and shiny; T3 sculpture smooth and shiny; hypopygium large with some lateral creases, no completely membranous area; ovipositor sheaths length/hind tibial length 1.7; areolet large, enclosed.

Etymology

The species name *koalascatocola* is from 'koala': the common name of the animal responsible for the dung from which the specimens emerged; 'scato-': dung; and '-cola': dweller, inhabitant.

Distribution

Only known from the type locality, most likely due to poor sampling rather than a restricted distribution.

Host

Whilst the host of *Choeras koalascatocola* is not confirmed, there are several likely possibilities. Specimens of *Argyrotoxa pompica* (Lepidoptera: Tortricidae) and *Blastobasis* sp. (Lepidoptera: Blastobasidae) also emerged from the koala scats that *C. koalascatocola* was collected from (Melzer *et al.* 1994) and are therefore potential host species. Three species of *Telanepsia* (Lepidoptera: Oecophoridae) have also been described feeding on koala dung, including one from Queensland (Common & Horak 1994).

Choeras morialta sp. nov.

(Fig. 6a-d)
http://zoobank.org/urn:lsid:zoobank.org:act:99691AE9-2C25-40C3-BA1C-3825BA14B03A

Material examined

Holotype

♀ 'S Aust Morialta Cons. Pk. Off Hogan's Track near cluster of olive trees. 34.90413°S, 138.69839°E, 26.iii-10.iv.2016, E. Fagan-Jeffries, M/T' (SAM 32-035442).

Paratypes

2♂ same data as holotype (SAM, WINC 32-035443); ♀ 'S Aust Belair N.P., Gate 11, 08-30.iii.2008, J.T. Jennings, M/T' (WINC); 1♀ 'S. Aust, Morialta Cons. Pk. 34.90413°S, 138.69839°E, 10-24.iv.2016, E. Fagan-Jeffries, M/T' (WINC); 1♀ 'S Aust Kangaroo Is. Flinders Chase. 35°57.08′S, 137° 44.27′E, 22.iii.2011, G.S. Taylor, E. Kinnaird, Light trap & window, Flinders Baudin Research Centre' (WINC); 1♀ 'S Aust Kangaroo Is. 35°58.423′S, 136°44.940′E, 17.iii-24.iii.2011, G.S. Taylor, E. Kinnaird & R. Kittel, MT4' (WINC).

Diagnosis

Choeras morialta is distinguishable from the other Australasian species with a large fore wing areolet and median propodeal longitudinal carina (*Choeras epaphus*, *Choeras koalascatocola* and *Choeras helespas*) by the darker colouration of T1–T2 (for *C. epaphus and C. helespas*). *C. morialta* has a broader, more nearly parallel T1 than *C. helespas*, but a more narrowly tapered T1 than *C. koalascatocola*. It can also be distinguished from *C. koalascatocola* by the reduced orange colouration on the hind legs.

Description

Colour: Dark with pale pleurites and a pale stripe along ventral edge of hypopygium; sclerotised regions of T1–T3 dark, often with an orange region on T1 where it attaches to propodeum, non-sclerotised areas pale; ovipositor sheaths dark; antenna scape dark, pedicel orange at base, flagellum dark; coxae (fore, mid, hind coxa) orange, orange, dark; femora (fore, mid, hind femur): orange, orange, orange changing to dark distally in most specimens (all dark in specimens from Kangaroo Island); tibiae (fore, mid, hind tibia): orange, light brown, dark; tegula and humeral complex pale; pterostigma dark; fore wing veins dark. *Head*: antenna length/body length about as long as or longer than body; body length (head to apex of metasoma) 3.2–3.6 mm; ocular–ocellar line/posterior ocellus diameter 1.5–1.8; interocellar distance/posterior ocellus diameter 1–1.4. *Mesosoma*: antero-mesoscutum evenly and densely punctate, sparsely setose; mesoscutellar disc punctate, but much less densely so than antero-mesoscutum; number of pits in scutoscutellar sulcus 10 or 11; maximum height of mesoscutellum lunules/maximum height of lateral face of mesoscutellum; 0.3–0.4; propodeum with percurrent median longitudinal carina, punctate with rugose sculpturing laterally. *Wings*: fore wing length 3.2–3.9 mm; areolet large, enclosed; length of veins r/2RS 0.8–0.9; length of veins 2RS/2 M 1–1.3; length of veins 2 M/(RS + M)b 1–1.6; pterostigma length/width 2.1–2.3. *Legs*: mid tibia inner spur length/mid basitarsus length 0.4–0.5. *Mesosoma*: T1 length/width at posterior margin: 2.3–3.1; T1 shape narrowing towards posterior margin; sculpture smooth on anterior half with shallow punctate sculpturing on posterior half; T2 width at posterior margin/length 2.6–3.5, sculpture mostly smooth and shiny; T3 sculpture smooth and shiny (Fig. 6a,b); hypopygium appears mostly solid, some lateral creases implying flexibility (folded inwards in dried specimens); ovipositor sheaths covered in fine hairs, length/mid tibial length 1.5–1.8.

Remarks

At present, there are no DNA (*COI*) barcode sequences available for any Australasian *Choeras* species, largely due to the age of currently available museum specimens. However, to provide additional diagnostics for *Choeras morialta*, we have lodged a *COI* sequence from a male specimen with the same data as the holotype (destructively sampled) in Genbank (accession number: KY359139).

Etymology

The species is named for Morialta Conservation Park, the collecting location of the majority of specimens. The species name is a noun in apposition.

Distribution

South Australia: collected from the Adelaide and Mount Lofty Ranges and Kangaroo Island regions. Distribution likely to expand with further collecting efforts.

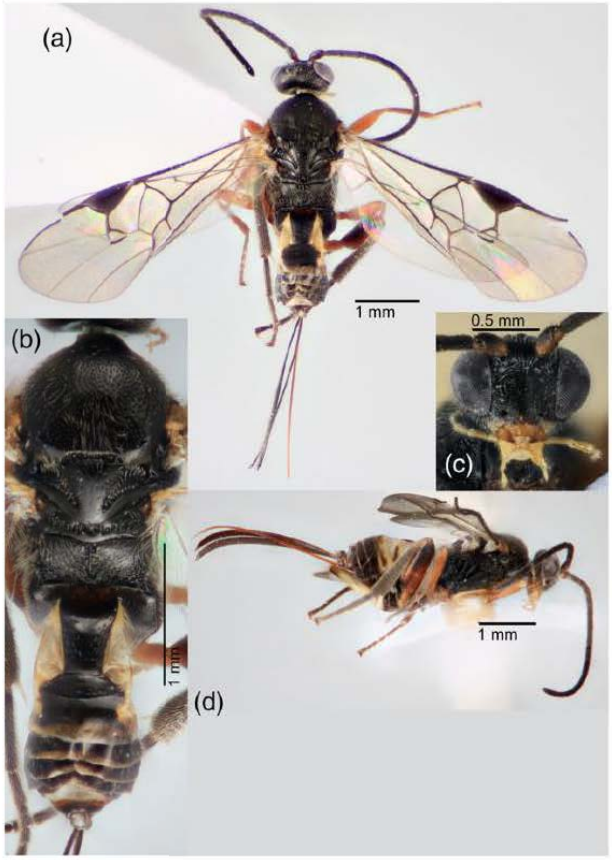

Fig. 6. *Choeras morialta* sp. nov. (a) dorsal habitus; (b) scutum, propodeum and metasomal tergites; (c) head; (d) dorsal habitus. [Color figure can be viewed at wileyonlinelibrary.com]

Host

Unknown.

Choeras papua (Wilkinson, 1936)

(Figs 2c, 4a)

Microgaster papua Wilkinson 1936: 86.
Hypomicrogaster papua (Wilkinson). – Nixon 1965: 218.
Choeras papua (Wilkinson). – Mason 1981: 77; Austin & Dangerfield 1992: 21.

Material examined

Holotype

♀ 'Papua: Kokoda, 1200 ft, iv.1933 L.E. Cheesman' (BMNH 3c.1148).

Paratypes

♀, ♂, same locality as holotype, iv.1933 (BMNH); ♀ same locality as holotype, vi.1933 (WINC); ♀, ♂ same locality as holotype, ix.1933, L.E. Cheesman (BMNH); ♂ 'Mafulu, 4000

ft, x.1933, L.E. Cheesman' (BMNH); ♂ 'Mafulu, 4000 ft, i.1933, L.E. Cheesman' (BMNH).

Other material

♀ 'Papua New Guinea: Okapa, vi.1964 R. Hornabrook, ex. ethanol' (WINC); ♀ 'Indonesia: Irian J. 20km W Sentani, 300m, 2°40 S, 140°30 E, 2.iv.1988, R. Hensen' (WINC).

Diagnosis

Entire body orange in colour, which combined with a small fore wing areolet (Fig. 2c) and an obvious percurrent median longitudinal carina on the propodeum (Fig. 4a) separates *Choeras papua* from all other described species in the Australasian region.

Distribution

New Guinea and Indonesia.

Host

Unknown.

Choeras tegularis (Szépligeti, 1905)

(Fig. 1a, 3c)

Microgaster tegularis Szépligeti 1905: 49; Wilkinson 1929: 105.
Protomicroplitis tegularis (Szépligeti). – Nixon 1965: 235.
Choeras tegularis (Szépligeti). – Austin & Dangerfield 1992: 21.

Material examined

Holotype

♂ 'NSW, Mt. Victoria' (HNHM) (apparently lost).

Other material

♂ 'WA, Stirling Range Drive, Stirling Range Nat Pk, 23.iv.1981 I.D. Naumann & J.C. Cardale, ex. ethanol' (ANIC).

Diagnosis

A large fore wing areolet (Fig. 1a) distinguishes *Choeras tegularis* from the species with a small fore wing areolet (*Choeras calacte*, *Choeras dissors* and *Choeras papua*). The absence of a percurrent median longitudinal carina on the propodeum (Fig. 3c) separates the species from *Choeras epaphus*, *Choeras helespas*, *Choeras koalascatocola* and *Choeras morialta*. A narrower T1 and more triangular-shaped T2 in *C. tegularis* distinguishes the species from *Choeras cetus*. Scutellum, propodeum and T1–2 dark, remaining tergites light brown; non-sclerotised areas of T1–2 pale; legs light brown to dark, with pale areas on the anterior of the tibia.

Remarks

This species was described from a single male specimen. A second male from Stirling Range National Park in Western Australia (Fig. 3c) appears to be conspecific but compared with the holotype has more punctation on the scutum and head, and a slightly narrower T1/T2 boundary. No female has yet been identified, and so, without being able to study the form of the hypopygium, the placement of this species within *Choeras* is uncertain.

Distribution

Australia (NSW, WA).

Host

Unknown.

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We thank Gavin Broad for assistance and access to type material and imaging equipment at the Natural History Museum, London. We thank Jim Whitfield and José Fernández-Triana for useful discussions on the status of *Choeras* and *Sathon*. The authors were granted permit number U26467-1 by the Government of South Australia Department of Environment, Water and Natural Resources for the collection of specimens in Morialta Conservation Park. We wish to thank CSIRO Publishing for allowing us to reproduce Fig. 2b,c. This work was funded by an Australian Biological Resources Study (ABRS) PhD top-up grant (CT215-08) to EFJ and an ABRS Capacity Building grant (RF214-16) to ADA. EFJ acknowledges the support of an Australian Government Research Training Program Scholarship. The authors declare no conflict of interest.

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Chapter 5: Three new species of *Dolichogenidea* Viereck (Hymenoptera, Braconidae, Microgastrinae) from Australia with exceptionally long ovipositors

Statement of Authorship

Title of Paper	Three new species of *Dolichogenidea* Viereck (Hymenoptera, Braconidae, Microgastrinae) from Australia with exceptionally long ovipositors.
Publication Status	☑ Published ☐ Accepted for Publication ☐ Submitted for Publication ☐ Unpublished and Unsubmitted w ork w ritten in manuscript style
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Principal Author

Name of Principal Author (Candidate)	Erinn Fagan-Jeffries
Contribution to the Paper	Morphological analysis, writing of species descriptions, writing of paper, creation of figures.
Overall percentage (%)	80%
Certification:	This paper reports on original research I conducted during the period of my Higher Degree by Research candidature and is not subject to any obligations or contractual agreements with a third party that would constrain its inclusion in this thesis. I am the primary author of this paper.
Signature	Date 5/10/18

Co-Author Contributions

By signing the Statement of Authorship, each author certifies that:

i. the candidate's stated contribution to the publication is accurate (as detailed above);

ii. permission is granted for the candidate in include the publication in the thesis; and

iii. the sum of all co-author contributions is equal to 100% less the candidate's stated contribution.

Name of Co-Author	Andrew Austin
Contribution to the Paper	Paper concept, sourcing of specimens, discussion and advice regarding species delimitation and discussion, review and edits of paper.
Signature	Date 11/10/18

Name of Co-Author	Steve Cooper
Contribution to the Paper	Advice and discussion on species concepts, molecular species delimitation and inclusion of molecular information in species descriptions, paper review and edits.
Signature	Date 8/10/18

Please cut and paste additional co-author panels here as required.

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RESEARCH ARTICLE

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Three new species of *Dolichogenidea* Viereck (Hymenoptera, Braconidae, Microgastrinae) from Australia with exceptionally long ovipositors

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Abstract

The subfamily Microgastrinae contains an extraordinarily rich diversity of parasitoid wasps which parasitise larval lepidopterans. The Australian fauna has generally been poorly studied, particularly for the very speciose genera. One such genus is *Dolichogenidea* Vierek, which in Australia is known from only six described species. Here we describe three new species of *Dolichogenidea* from Australia, which are distinguished by possessing extremely long ovipositors compared with the typical form for the genus. These are *D. finchi* Fagan-Jeffries & Austin, **sp. n.**, *D. mediocaudata* Fagan-Jeffries & Austin, **sp. n.**, and *D. xenomorph* Fagan-Jeffries & Austin, **sp. n.** In describing these new species we also discuss relationships within the genus, and the diversity and biology of the Australian fauna.

Keywords

Microgastrinae, *Dolichogenidea*, parasitoid, ovipositor

Introduction

The subfamily Microgastrinae are agriculturally and environmentally important as endoparasitoid wasps of larval lepidopterans. There are currently over 2700 species described worldwide (Yu et al. 2016), with estimates from cytochrome c oxidase subunit I (*COI*) DNA barcoding suggesting this could be as little as 6% of the true global diversity (Whitfield et al. 2018, Rodriguez et al. 2013). The subfamily comprises 81 genera (Fernandez-Triana and Boudreault in review), several of which are very large, including *Dolichogenidea* Viereck, with over 180 described species (Yu et al. 2016). This genus was initially described as a subgenus of *Apanteles* Foerster (Viereck 1911) for the placement of his new species *D. banksi* because of its elongated genae. Subsequently, it was treated as one or more species-groups of *Apanteles* sensu lato (Wilkinson 1928, Nixon 1965), but was then raised to genus level by Mason (1981) in his reclassification of the large and polyphyletic *Apanteles* sensu lato, which previously contained the majority of described microgastrine species. Mason's (1981) concept of *Dolichogenidea* included three of Nixon's (1965) species-groups; the *ultor*-group, the *laevigata*-group, and the *longipalpis*-group. Whilst Mason (1981) proposed several characters to distinguish *Dolichogenidea* from *Apanteles* sensu stricto, including *Dolichogenidea* having 'punctures of the mesonotum typically distinctly separated and never breaking into aciculations posterolaterally', many species have strongly reduced cuticular sculpturing, making the punctation characters unusable for placement in the correct genus. Analysis of thousands of specimens by Fernández-Triana et al. (2014) suggests that "the only reliable character is the number and density of setae fringing on the median portion of the vannal lobe" of the hind wing. *Dolichogenidea* has a convex to almost straight vannal lobe, which is uniformly fringed by setae, while in *Apanteles* sensu stricto the vannal lobe is strongly concave to almost straight and is lacking setae at the midlength. This lack of setae may be partial (i.e. there may be some small and sparse setae on the lobe) or total (i.e. no setae at all). The two genera are also generally resolved as separate monophyletic clades using molecular data and thus are distinguishable in DNA barcoding studies (Fagan-Jeffries et al. in press, Smith et al. 2013).

The Australasian members of *Dolichogenidea* were reviewed by Austin and Dangerfield (1992) and currently the genus contains six species from Australia: *D. biroi* (Szépligeti, 1905), *D. eucalypti* (Austin and Allen, 1989), *D. hyposidrae* (Wilkinson, 1928), *D. lipsis* (Nixon, 1967), *D. miris* (Nixon, 1967), and *D. tasmanica* (Cameron, 1912). Long-term sorting of microgastrines in Australian collections and a recent large barcoding study (Fagan-Jeffries et al. in press) have revealed several remarkable specimens belonging to three species of *Dolichogenidea* that possess extremely long ovipositors. We here describe these species as a contribution to on-going studies on Australian members of the genus.

Materials and methods

Terms for general morphology follow Fernández-Triana et al. (2014) who combined traditional microgastrine morphological terms, such as those used by Mason (1981), with the standards introduced in the Hymenoptera Anatomy Ontology (HAO) pro-

ject (Yoder et al. 2010). Terms for sculpturing follow Eady (1968). The following acronyms and abbreviations are used throughout the paper: T1, T2, T3 for the first, second and third mediotergites, respectively; S1–3 for the first, second and third sternites; ACT, Australian Capital Territory; NSW, New South Wales; Qld, Queensland; Vic, Victoria; WA, Western Australia. The following abbreviations are used for collections: **ANIC**, Australian National Insect Collection, Canberra; **WAM**, Western Australian Museum, Perth. We define colour as either pale (white, cream or pale yellow), orange, or dark (brown or black).

Taxonomy

Dolichogenidea Viereck

Dolichogenidea Viereck, 191 1: 173 (as a subgenus of *Apanteles* Foerster s.1.). Type species, by original designation, *Apanteles* (*Dolichogenidea*) *banksi* Viereck. Generic status by Mason 1981: 34. See Shenefelt (1972) for bibliographic history and Mason (1981) for discussion of relationships.

Diagnosis. Fore wing areolet (second submarginal cell) absent (i.e. vein r-m absent); hind wing vannal lobe convex to almost straight and uniformly fringed by setae; propodeum often with a complete areola, sometimes areola reduced with at least posterior diverging carinae present, rarely with these carinae completely absent; metasoma with T2 variable in shape, but usually rectangular or subrectangular; hypopygium membranous mid-ventrally and expandable (sometimes folded inwards and hidden by laterotergites in dead specimens); ovipositor protruding from posterior metasoma, usually as long as or longer than length of metatibia.

Remarks. In resurrecting *Dolichogenidea,* Mason (1981) allocated three of Nixon's (1965) species-groups to the genus: the *ultor*-, *laevigatus*-, and *longipalpis*-groups. The *longipalpis*-group was erected by Nixon for a single European species, *D. longipalpis* (Reinhard, 1880), which has unusually long mouthpart palps. The *ultor*-group was defined by Nixon (1965) for those species with a complete or partially complete propodeal areola, and the *laevigatus*-group for species with the areola represented only by two basal diverging carinae, or the propodeum virtually completely devoid of carinae. However, there are numerous species that represent intermediates between these conditions, and Mason (1981) was instrumental in recognising that there were likely to be independent pathways for reduction and eventual loss of the areola (Whitfield et al. 2018). Hence, it is very likely that neither the presence of a propodeal areola or its loss define monophyletic groups. This said, the three species described here most closely resemble the condition found in classic '*laevigatus*-group species', having a smooth and shiny propodeum, a transverse T2 (rather than triangular) and an ovipositor much longer than the metatibia.

Identification of the species described here. *Dolichogenidea* is highly speciose and there are large numbers of undescribed species in Australia. Austin and Dangerfield (1992) estimated that fauna to be 50–70 species. However, it may be much larger

than this given that a recent DNA barcoding study of Australian microgastrines recognised 236 species from 525 individuals, 42 of which belonged to *Dolichogenidea* (Fagan-Jeffries et al. in press). Given this considerable number of additional species in *Dolichogenidea*, it is pointless to present a key to the described fauna; rather we provide the characters that distinguish the three species treated here from the six described species, as follows: the absence of a conspicuous white blotch on the gena separates the three species from *D. lipsis*, *D. biroi*, and *D. tasmanica*; *D. hyposidrae* and *D. eucalypti* both have ovipositors significantly shorter than the metatibia and a clearly defined propodeal areola, whilst the species described here all have ovipositors significantly longer than the metatibia and a propodeal areola only indicated at most by short posterior diverging carinae; *D. miris* is separated by the presence of a partially defined areola with lateral costula, and a shorter T2 with strong rugose sculpturing, differing from the smooth or almost smooth T2 of the three new species here. In addition, the lengths of the ovipositor and sheaths of all undescribed *Dolichogenidea* we have seen in Australian collections do not exceed approximately 1.5 × that of the metatibia, compared with 1.8–4.2 × for the three new species.

The newly described species appear to be quite rare, although two are widespread (Fig. 1). After considerable collecting effort and searching of both pinned and ethanol museum material from all major Australian collections, only 14 specimens have been located.

Dolichogenidea finchi Fagan-Jeffries & Austin, sp. n.

http://zoobank.org/CDDB476E-FE7F-4404-AE6D-5764C44ACE9F

Figure 2

Material examined. Holotype ♀: AUSTRALIA, WA, Kariijini NP, Kariijini Dr, 22.5716°S, 118.3072°E; 19-25/iv/2003, C Lambkin & T Weir, malaise in open *Eucalyptus* grassland, 814 m (WAM: E94085). Paratypes: ♀ WA, Kariijini NP, Weano Gorge Rd, 22°21'19"S, 118°15'00"E; 25/iv/2003 - 15/v/2003, C Lambkin & T Weir, malaise in grassy dry creek *Eucalyptus-Acacia* scrub, 695 m (WAM: E94086); ♀ NSW, Wilcannia, 23/xi/1949, E.F. Riek (ANIC: #32 130282); ♀ QLD, Binna Burra, Lamington National Park, 29/v/1966, Z. Liepa, at light (ANIC: #32 130284); ♀ QLD, Brisbane, vi/1904, RCL Perkins (NHM: #NHMUK010880682); ♀ QLD, 3.5 km SW by S of Mt Baird, 15.10°S, 145.07°E; 3-5/v/1981, I.D. Nauman, ex. ethanol, collected at light (ANIC: #32 130286); ♀ Vic, 18 km NW by N Omeo, 28/ii/1980, J.C. Cardale, ex alcohol (ANIC: #32 130283); ♀ WA, Millstream, 26/x/1970, J.C. Cardale (ANIC: #32 130285); ♀ WA, 21 km E by N Yellowdine, 10/x/1981, I.D. Naumann, J.C. Cardale, ex ethanol, on *Eucalyptus* flowers (WAM: E94087); ♀ WA, 1 km NNW of Eucla Pass, 31.40°S 128.52°E, 20/v/1984, E.S. Nielson, E.D. Edwards (WAM: E94088).

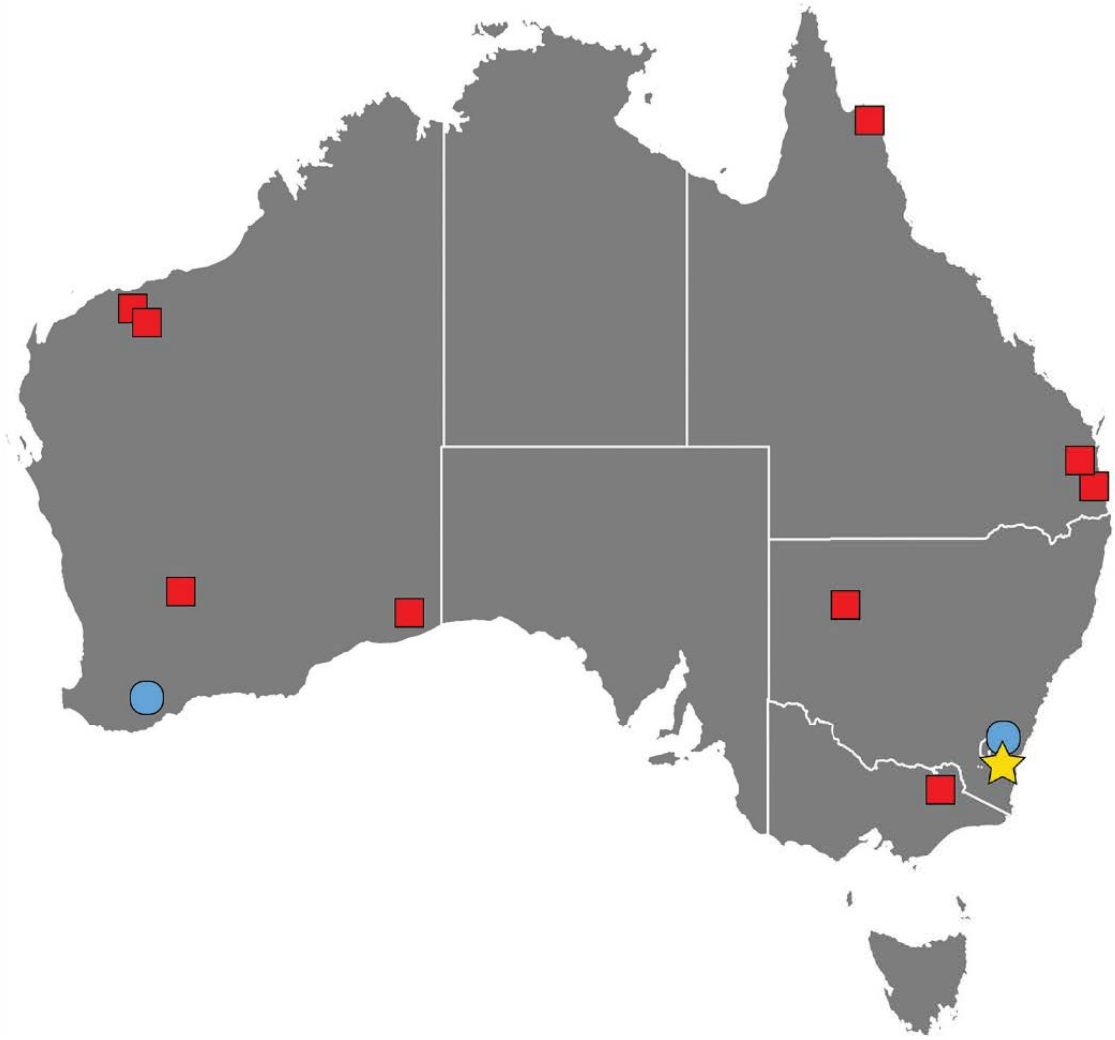

Figure 1. Known distributions of *D. xenomorph* (blue circles) *D. finchi* (red squares) and *D. mediocaudata* (yellow star).

Diagnosis. *Dolichogenidea finchi* can be separated from *D. mediocaudata* by having a longer ovipositor, smoother T1, and more consistent pale orange colouration of the legs; and from *D. xenomorph* by absence of a strong sculpturing pattern on the propodeum (Fig. 2d) and lighter colouration of the lateral metasoma (Fig. 2b).

Description. (Female). Colour. Head and body dark; tergites dark, T3 sometimes orange on lateral thirds (Fig. 2a); S1-3 paler than posterior sternites; antenna dark; coxae (pro-, meso-, metacoxa): dark, dark, dark; femora (pro-, meso-, metafemur): pale/orange, pale/orange, pale/orange; tibiae (pro-, meso-, metatibia): pale/orange, pale/orange, pale/orange anteriorly and subtly darker at basitarsus boundary; tegula and humeral complex pale; pterostigma dark, often with subtle to distinct pale patch at proximal end; fore wing veins pale proximally transitioning to dark distal to pterostigma.

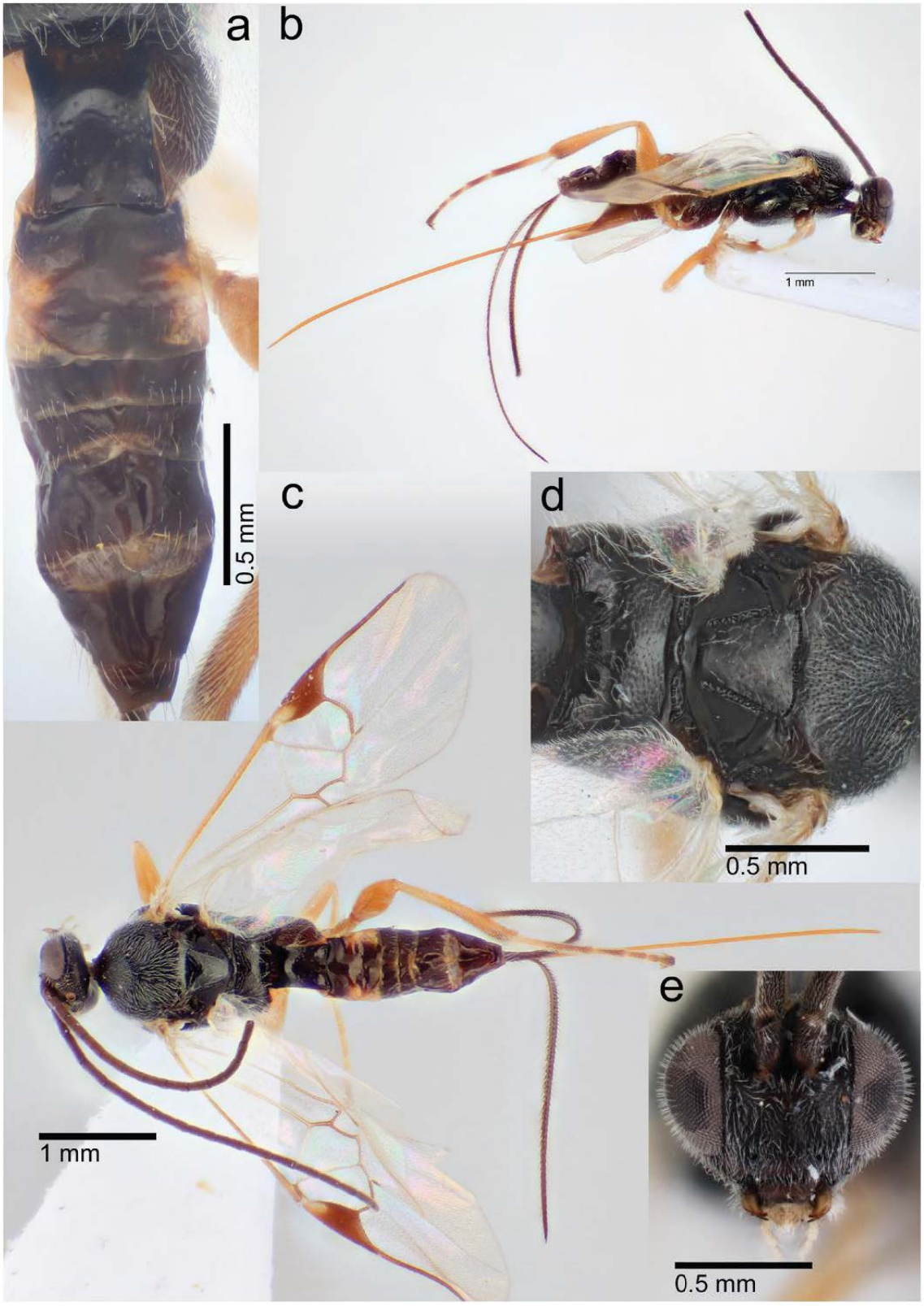

Figure 2. *Dolichogenidea finchi* (holotype): **a** metasoma **b** lateral habitus **c** dorsal habitus **d** mesosoma **e** head.

Head. Antennae slightly shorter than body length; body length (head to apex of metasoma): 3.4–4.4 mm; ocular–ocellar line/posterior ocellus diameter: 1.4–1.9; interocellar distance/posterior ocellus diameter: 1.3–2.3.

Mesosoma. Anteromesoscutum densely and evenly punctate; mesoscutellar disc mostly smooth and shining with sparse punctures mostly associated with setae, lateral faces of the mesoscutellum normally smooth and shining to lunules but sometimes with a distinct line of pits or with subtle area of sculpturing posterior to lunules; number of pits in scutoscutellar sulcus: varies from 12 to 22; maximum height of mesoscutellum lunules/maximum height of lateral face of mesoscutellum 0.7–0.8. Propodeum with sparse punctures associated with setae, areola only indicated by smoother area in centre of propodeum and short carinae diverging from centre posterior margin of propodeum.

Fore wing length 3.2–4 mm; length of veins r/2RS 1.5-2.2; length of veins 2RS/2M 1.0–1.7; length of veins 2M/(RS+M)b 0.5-0.8; pterostigma length/width 2.6–3.1.

Legs. Metatibia inner spur length/metabasitarsus length 0.2–0.4.

Metasoma. T1 length/width at posterior margin 1.2–1.8; T1 shape broad, rectangular, almost parallel-sided; T1 mostly smooth with sparse punctures associated with short setae on lateral sides of posterior half; T2 width at posterior margin/length 2.1–3.1; T2 sculpture smooth and shiny, few shallow punctures associated with setae; T2/T3 boundary indistinct and sinuate. T3 smooth and shiny, at least twice as long as T2; hypopygium large with lateral creases, ovipositor sheath length/metatibial length 2.9–3.9.

Male. Unknown.

COI Genbank accession numbers. MH138733 (Holotype) MH138940 (Paratype WAM: E94086)

Remarks. It is possible that if more specimens become available and are amenable to DNA sequencing, *D. finchi*, as described here, will turn out to be a species complex of several closely related species. There is variation in several morphological characters such as subtle differences in the length and shape of the metanotum, the colour of T3, and length of the ovipositor in relation to the metatibia. However, with so few specimens and a lack of molecular data we feel it is more practical at this stage to treat them as one variable species. Further, the *COI* sequences of the two specimens, sequenced as part of a parallel study (Fagan-Jeffries et al. in press), are 2.5% divergent, which is above the 2% divergence of the *COI* barcoding region threshold considered to delimit species of microgastrines in 95% of cases (Smith et al. 2013).

Etymology. This species is named for the late grandfather of one of us (EFJ), Alexander Finch, who was a sheep pastoralist near the town of Wilcannia, the locality for one of the paratypes.

Distribution. This species occurs widely across the continent (Fig. 1) and is recorded from WA, Qld, Vic and NSW.

Host. Whilst the host for this species has not been recorded, two specimens were collected in association with *Eucalyptus*. As *D. xenomorph* is the parasitoid of a larva feeding on *Eucalyptus*, it is a strong possibility that *D. finchi* also parasitises a *Eucalyptus*-associated lepidopteran.

Dolichogenidea mediocaudata **Fagan-Jeffries & Austin, sp. n.**
http://zoobank.org/8AD0F877-7CBD-4B6C-82EE-C77F58B6EE4E
Figure 3

Material examined. Holotype ♀: AUSTRALIA, NSW, 8 miles ESE of Nimmitable 3600ft, emerged 03/xii/1969, I.F.B. Common & J. Cusbert, L19. Larva tying leaves on fallen dead branch of *Eucalyptus pauciflora* (ANIC: #32 130288).

Diagnosis. This species can be separated from *D. finchi* and *D. xenomorph* by having a shorter ovipositor (Fig. 3a) and deeper sculpturing on both the propodeum and T1 (Fig. 3e), and presence of distinct dark colouration on the distal half of the metatibia.

Description. (Female). Colour. Head and body dark other than S1-3 which are distinctly paler than posterior sternites; antenna dark; coxae (pro-, meso-, metacoxa): dark, dark, dark; femora (pro-, meso-, metafemur): pale, dark, dark; tibiae (pro-, meso-, metatibia): pale, pale, pale anteriorly, posterior half distinctly darker; tegula and humeral complex pale; pterostigma dark; fore wing veins pale proximally transitioning to dark distally.

Head. Antennae slightly shorter than body length; body length (head to apex of metasoma): 3 mm; ocular–ocellar line/posterior ocellus diameter: 2.2; interocellar distance/posterior ocellus diameter: 1.9.

Mesosoma. Anteromesoscutum densely and evenly punctate, no punctures at posterior margin; mesoscutellar disc mostly smooth and shining with sparse punctures mostly associated with setae, lateral faces of the mesoscutellum smooth and shining but with a distinct line of pits posterior to lunules; number of pits in scutoscutellar sulcus: varies from 12–13; maximum height of mesoscutellum lunules/maximum height of lateral face of mesoscutellum 0.7. Propodeum with deep non-uniform punctures, posterior half with rugose sculpturing, areola only indicated by a central depression and short carinae diverging from centre posterior margin of propodeum.

Fore wing length 2.7 mm; length of veins r/2RS 1.3; length of veins 2RS/2M 1.8; length of veins 2M/(RS+M)b 0.6; pterostigma length/width 2.8.

Legs. Metatibia inner spur length/metabasitarsus length 0.4.

Metasoma. T1 length/width at posterior margin 1.6; T1 shape broad, rectangular, almost parallel-sided; T1 with rugose sculpturing and sparse punctures over most of length; T2 width at posterior margin/length 2.0; T2 sculpture smooth and shiny, few shallow punctures associated with setae; T2/T3 boundary indistinct and sinuate. T3 smooth and shiny, at least twice as long as T2; hypopygium large with lateral creases, ovipositor sheath length/metatibial length 1.8.

Male. Unknown.

Etymology. This species is named for the length of the ovipositor, which appears to be intermediate between most *Dolichogenidea* and the extremely long ovipositors of *D. xenomorph* and *D. finchi*.

Distribution. This species is only known from the holotype collected near Nimmitable in south-eastern NSW.

Host. This specimen was reared from a lepidopteran larva tying leaves together on a dead branch of *Eucalyptus pauciflora*.

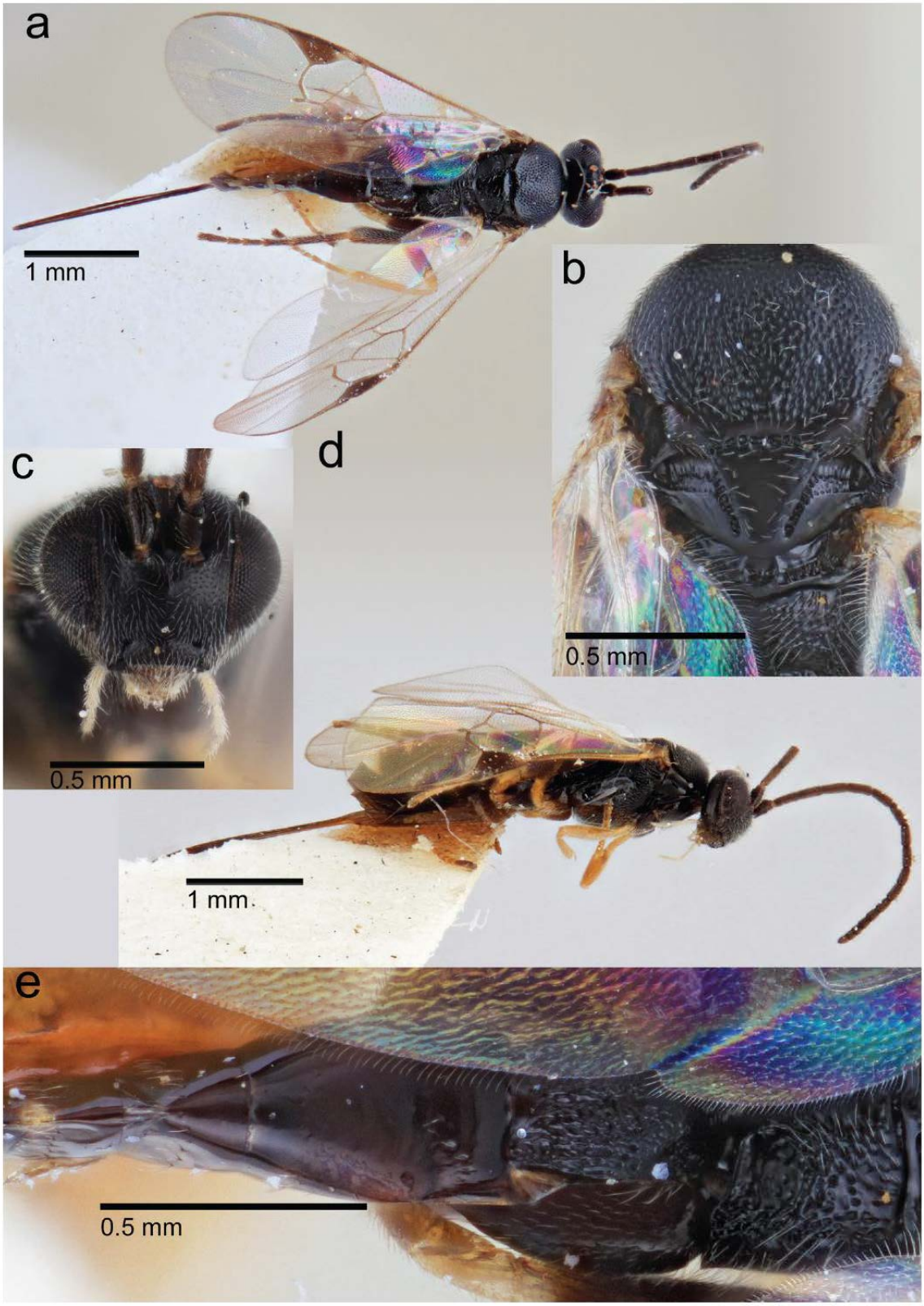

Figure 3. *Dolichogenidea mediocaudata* (holotype): **a** dorsal habitus **b** anteromesoscutum, mesoscutellum and metanotum **c** head **d** lateral habitus **e** propodeum and tergites.

***Dolichogenidea xenomorph* Fagan-Jeffries & Austin, sp. n.**
http://zoobank.org/F7E2A57E-8F65-45F3-9752-C3165DD513DC
Figure 4

Material examined. Holotype ♀: AUSTRALIA, NSW, 2.7 km NE of Queanbeyan, emerged 28/x/1979, I.F.B. Common, ex *Ocystola euanthes* Meyr (ANIC: #32 130289). Paratype ♀: same data as holotype (ANIC: #32 130290). Other material ♀: AUSTRALIA, WA, Stirling National Park, 22/ix/1965, E. Britton, U. Baker (ANIC: #32 130287).

Diagnosis. *Diolichogenidea xenomorph* can be separated from *D. mediocaudata* by having a longer ovipositor, smoother T1, and lighter, more consistent colouration of the femora and tibiae. The species is very similar to *D. finchi*, but can be separated by the stronger sculpturing pattern on the propodeum (Fig. 4d) and darker colouration of the lateral metasoma (Fig. 4b).

Description. (Female). Colour. Head and body dark, including tergites and sternites; antenna dark; coxae (pro-, meso-, metacoxa): dark, dark, dark; femora (pro-, meso-, metafemur): orange, orange, dark to orange; tibiae (pro-, meso-, metatibia): orange, orange, orange; tegula and humeral complex orange; pterostigma dark; fore wing veins pale proximally transitioning to dark distally.

Head. Antennae slightly longer than body length; body length (head to apex of metasoma): 4 mm; ocular–ocellar line/posterior ocellus diameter: 1.8–2.1; interocellar distance/posterior ocellus diameter: 1.7–2.5.

Mesosoma. Anteromesoscutum densely and evenly punctate; mesoscutellar disc mostly smooth and shining with sparse punctures mostly associated with setae, lateral faces of mesoscutellum with anterior shallow sculpturing posterior to lunules (Fig. 4c); number of pits in scutoscutellar sulcus: 16; maximum height of mesoscutellum lunules/maximum height of lateral face of mesoscutellum 0.7–0.8. Propodeum with sparse punctures associated with setae, areola only indicated by smoother area in centre of propodeum and short carinae diverging from centre posterior margin of propodeum. Propodeum with rugose sculpturing in posterior half.

Fore wing length 4.3–4.4 mm; length of veins r/2RS 1.3–1.9; length of veins 2RS/2M 1.1–1.2; length of veins 2M/(RS+M)b 0.8–1; pterostigma length/width 2.6–3.

Legs. Metatibia inner spur length/metabasitarsus length 0.3–0.4.

Metasoma. T1 length/width at posterior margin 1.1–1.4; T1 shape broad, rectangular, almost parallel-sided; T1 mostly smooth with sparse punctures associated with short setae on lateral sides of posterior half; T2 width at posterior margin/length 4; T2 sculpture smooth and shiny, few shallow punctures associated with setae; T2/T3 boundary indistinct and sinuate. T3 smooth and shiny, at least twice as long as T2; hypopygium large with lateral creases, ovipositor sheath length/metatibial length 3.7–4.2.

Male. Unknown.

Remarks. The specimen from WA is here assigned to this species, but excluded from the type series due to its disjunct distribution which is also outside the known

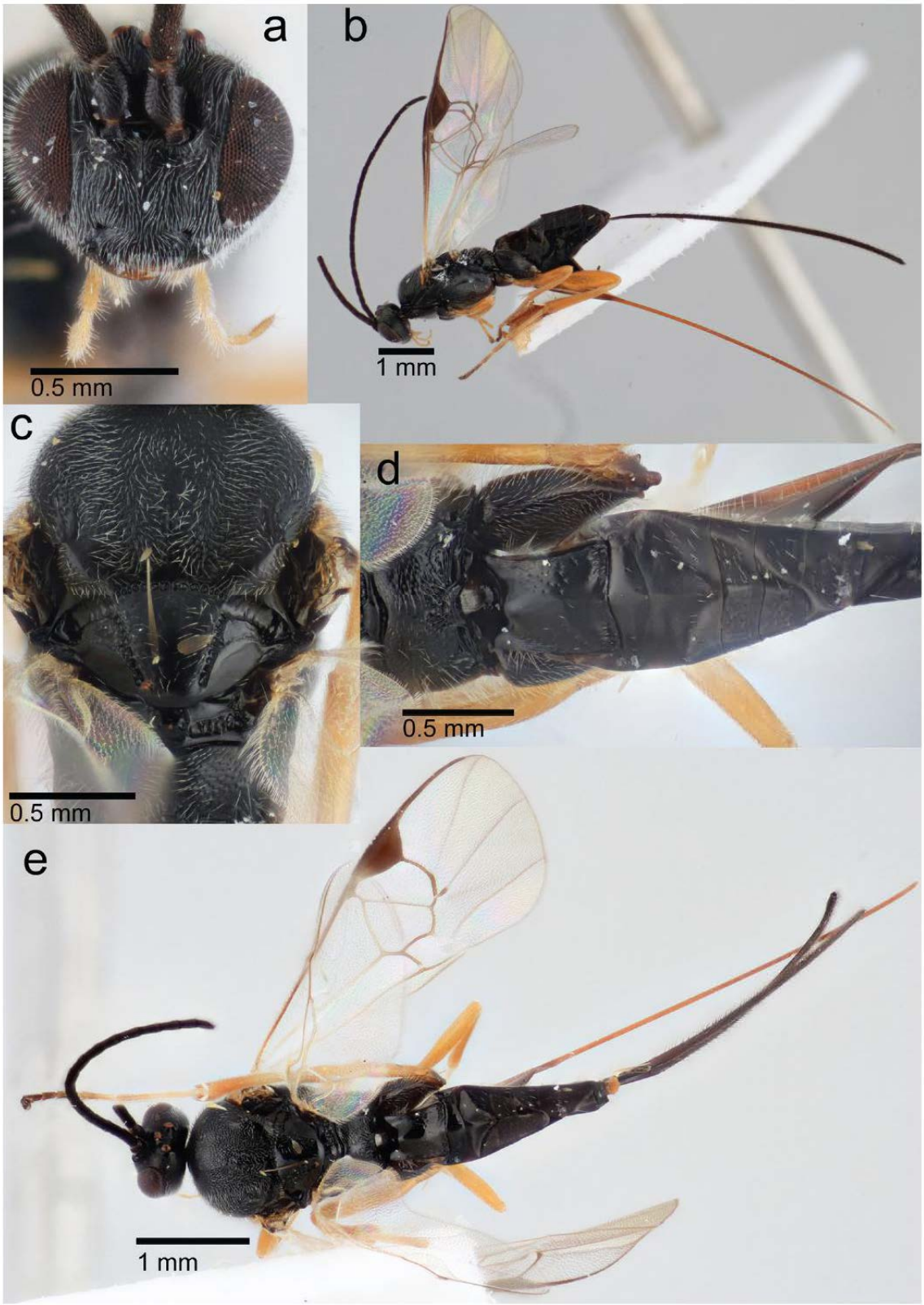

Figure 4. *Dolichogenidea xenomorph*: **a** head (paratype) **b** lateral habitus (paratype) **c** anteromesoscutum, mesoscutellum and metanotum (holotype) **d** propodeum and tergites (holotype) **e** dorsal habitus (holotype).

range of the host species. However, other species of the host genus are known from WA, but we take a more conservative approach until further specimens and host data become available.

Etymology. This species is named for the fictional creature from the movie franchise 'Alien', which reportedly was inspired by the lifecycle of parasitic wasps. The name of the fictional creature comes from the Greek 'xeno' (strange) and 'morphe' (form) which is also appropriate, considering the remarkably long ovipositor of this species compared to other members of the genus. The species name is a noun in apposition.

Distribution. Recorded from NSW and south-western WA.

Host. Reared from *Antipterna euanthes* (Meyrick, 1885) (Oecophoridae), a species in which the larvae fold over the tip of a *Eucalyptus* leaf and continue developing even after the leaf is shed from the tree (Common 1994). This lepidopteran species is recorded from ACT, NSW and Vic, however the genus extends into eastern Qld, Tasmania, and south-western WA (Common 1994). The holotype and paratype of *D. xenomorph* have the same locality and host information. Whether they emerged singularly from two host larvae collected on the same date, or were gregarious in the one host is unknown.

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Chapter 6: New species of Australian microgastrine parasitoid wasps (Hymenoptera: Braconidae: Microgastrinae) documented through the ‘Bush Blitz’ surveys of national reserves

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Overall percentage (%)	75%
Certification:	This paper reports on original research I conducted during the period of my Higher Degree by Research candidature and is not subject to any obligations or contractual agreements with a third party that would constrain its inclusion in this thesis. I am the primary author of this paper.
Signature	Date 5/10/18

Co-Author Contributions

By signing the Statement of Authorship, each author certifies that:

i. the candidate's stated contribution to the publication is accurate (as detailed above);

ii. permission is granted for the candidate in include the publication in the thesis; and

iii. the sum of all co-author contributions is equal to 100% less the candidate's stated contribution.

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Signature	Date 11/10/18

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Contribution to the Paper	Advice on molecular species delimitation and species concepts, paper review and edits.
Signature	Date 8/10/18

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New species of Australian microgastrine parasitoid wasps (Hymenoptera: Braconidae: Microgastrinae) documented through the 'Bush Blitz' surveys of national reserves

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Abstract

The braconid subfamily Microgastrinae are ecologically important parasitoids of larval lepidopterans, but are poorly studied in many regions of the world. In this study, we focus on describing new species of microgastrine wasps, in part from specimens collected on six different 'Bush Blitz' surveys of regional reserves in South Australia and Tasmania. Ten species of Microgastrinae are described as new and DNA barcodes of the genes *cytochrome oxidase subunit I* and *wingless* are provided: three species in the genus *Choeras* Mason: *C. bushblitz* Fagan-Jeffries & Austin sp. nov., *C. parvoculus* Fagan-Jeffries & Austin sp. nov., and *C. zygon* Fagan-Jeffries & Austin sp. nov.; six species in the genus *Dolichogenidea* Viereck*: D. bonbonensis* Fagan-Jeffries & Austin sp. nov., *D. brabyi* Fagan-Jeffries & Austin sp. nov., *D. forrestae* Fagan-Jeffries & Austin sp. nov., *D. garytaylori* Fagan-Jeffries & Austin sp. nov., *D. kelleri* Fagan-Jeffries & Austin sp. nov., and *D. lobesiae* Fagan-Jeffries & Austin sp. nov.; and one species from the genus *Sathon* Mason: *S. oreo* Fagan-Jeffries & Austin sp. nov. These new species represent just a small fraction of the potential of 'Bush Blitz' surveys in regional Australia, which provide DNA-quality material allowing an integrative taxonomic approach and offer a window into the biodiversity of some of the least studied areas of the continent.

Introduction

Species discovery and documentation is the foundation of all environmental biology and directly underpins studies in fields as disparate as ecology, conservation, biological control, and biosecurity. In Australia, there is an estimated 205,000 species of insects (Yeates *et al.* 2003), a figure that is likely to be a substantial underestimate, but only 69,000 are formally described (ABRS 2017). Major collections contain a huge number of undescribed species but

large areas of the continent have, to date, been poorly surveyed and many species are yet to be discovered. To improve this situation, a large nature discovery program was initiated in 2010 to document the biodiversity of the national reserve system. The 'Bush Blitz' program, coordinated by the Federal Government's Australian Biological Resources Study, is a multi-institutional partnership that aims to bring together taxonomists, traditional land owners, property owners and park rangers to intensely survey the flora and fauna of reserves across the continent and describe the new species discovered during the process (ABRS 2018).

One insect assemblage virtually absent in outputs from the 'Bush Blitz' program are the parasitic Hymenoptera (but see Kittel & Austin 2016). An important component of this assemblage is the Microgastrinae, a subfamily of wasps that are endoparasitoids of lepidopteran larvae (Whitfield *et al.* 2018), which are often collected by a range of methods including Malaise traps and sweep netting. Whilst new species of microgastrines can be discovered simply by sorting material in museum collections, surveys such as 'Bush Blitz' have been instrumental in collecting fresh specimens from remote locations that are viable for DNA sequencing. DNA data allow for faster, directed taxonomy, enabling species delimitation and descriptions that combine both molecular and morphological evidence into a comprehensive approach. An integrative species discovery approach is particularly important for megadiverse, yet morphologically conservative groups such as the Microgastrinae.

Microgastrine wasps are an extraordinarily diverse group of insects with over 2,700 species described worldwide (Yu *et al.* 2016) and a true fauna estimated to be as high as 40,000 species (Rodriguez *et al.* 2013). For Australia, approximately 120 species have been described in 22 genera (Austin & Dangerfield 1992, 1993; Saeed *et al.* 1999; Fernández-Triana *et al.* 2014a; Fagan-Jeffries & Austin 2018; Fagan-Jeffries *et al.* 2018a; Fernandez-Triana & Boudreault 2018). However, estimates based on DNA barcoding suggest that this number of species may represent only about 10% of the true size of the Australian fauna (Fagan-Jeffries *et al.* 2018b). Microgastrines play important roles in regulating caterpillar populations, both in native ecosystems and in agricultural systems, against both native and introduced lepidopteran pests (Whitfield *et al.* 2018). With the incredible size of the undescribed fauna, and the cosmopolitan nature of many of the larger genera, complete generic revisions are untenable at the present time. The lack of clarity surrounding the limits of large genera and the relationships among them further hampers thorough taxonomic work on the subfamily, but there have been several major revisions of regional

faunas in recent years, particularly in Costa Rica (Fernández-Triana *et al.* 2014b; Fernández-Triana *et al.* 2014c) and Canada (Fernández-Triana 2010; Fernández-Triana 2018).

In this study, we describe 10 new species of microgastrine wasps, eight of which are based on material collected during Bush Blitz surveys. We describe three species in the genus *Choeras* Mason, six species in the genus *Dolichogenidea* Viereck and one species in the genus *Sathon* Mason. All species have been DNA barcoded for the cytochrome oxidase subunit I gene (*COI*) and some also for the nuclear gene wingless (*WG*) (Fagan-Jeffries *et al.* 2018b), to provide an integrative approach to species delimitation using a general lineage concept (de Queiroz 1998). Descriptions of these particular species have been prioritised because of available host records, unique morphological characteristics, or to show the diversity of new species collected and identified on 'Bush Blitz' surveys, and thus the importance of these surveys in gathering new, DNA-grade material from remote locations.

Materials and methods

Terms for general morphology follow Fernández-Triana *et al.* (2014c) who combined traditional microgastrine morphological terms, such as those used by Mason (1981), with the standards introduced in the Hymenoptera Anatomy Ontology (HAO) project (Yoder *et al.* 2010). Measurements are given as ranges, when differences were observed between paratypes or when multiple measurements of the same specimen produced different results, to account for imprecision (see Fernández-Triana *et al.* (2014c) for measurement terminology and appendix 1 in the same paper for discussion on characters prone to variable results when measuring).

Terms for sculpturing follow Eady (1968). The following acronyms and abbreviations are used throughout the paper: T1, T2, T3 for the first, second and third mediotergites, respectively; S1, S2, S3 for the first, second and third sternites; ACT, Australian Capital Territory; NSW, New South Wales; Qld, Queensland; S Aust, South Australia; Tas, Tasmania; Vic, Victoria; WA, Western Australia. The following collection acronyms are used: ANIC, Australian National Insect Collection, Canberra; BMNH, British Museum of Natural History, London; MV, Museum Victoria, Melbourne; QM, Queensland Museum, Brisbane; SAMA, South Australian Museum, Adelaide; TMAG, Tasmanian Museum and Art Gallery, Hobart. We define colour as either pale (white, cream or pale yellow), orange, light brown or dark (dark brown or black).

Nearly all specimens included in this study have had legs removed for DNA extraction, and thus nearly all type specimens are missing 1–3 legs. DNA extraction and sequencing methods follow Fagan-Jeffries *et al.* (2018b). A Bayesian tree of the specimens sequenced in Fagan-Jeffries *et al.* (2018b) and 44 additional specimens sequenced for *COI* using the Sanger methods outlined in the previously mentioned study was constructed using the program MrBayes version 3.2.6 (Ronquist *et al.* 2012). The genes *COI* and *WG* were concatenated and partitioned, and both genes were modelled with a GTR+I+G model of evolution. The tree was run for 15,000,000 generations and convergence was established using the program Tracer version 1.6 (Rambaut *et al.* 2018) ensuring Estimated Sampel Size (ESS) values were >200.

As the previously mentioned DNA barcoding study has shown that there are many more additional undescribed species of *Choeras*, *Sathon* and *Dolichogenidea* in Australia to those treated here (Fagan-Jeffries *et al.* 2018b), we feel that it is premature to update the key to Australasian *Choeras* in Fagan-Jeffries and Austin (2018) or provide keys to Australian *Dolichogenidea* and *Sathon*, and instead provide clear comparative diagnoses for the following new species. To facilitate clear diagnostic differences for the new species, all holotypes from the Australasian region, including the South-West Pacific, have been examined, with the exception of *Dolichogenidea upoluensis* (Fullaway 1941) and *D. agonoxenae* (Fullaway 1941), where the original description was used, and *D. stantoni* (Ashmead 1904), where the original description and a series of specimens (BMNH) identified by G. E. J. Nixon were examined. A summary of the diagnostic characters for the Australasian *Dolichogenidea* species is provided (Table 1).

Taxonomy

***Choeras* Mason, 1981**

Choeras Mason, 1981: 76; Austin & Dangerfield 1992: 18; van Achterberg 2002 (treated as a subgenus of *Apanteles* Foerster); Song *et al.* 2014: 502 (treated as a subgenus of *Apanteles*); Ghafouri Moghaddam *et al.* 2018: 457. See Shenefelt (1973) for earlier bibliographic history of species, and Fagan-Jeffries and Austin (2018) for a review and comments on the Australasian fauna.

Type species: *Apanteles* (*Pseudapanteles*) *consimilis* Viereck 1911, by original designation.

Diagnosis. Fore wing areolet absent, small or large; propodeum either with median longitudinal carina or carina absent, but never with any indication of an areola, surface smooth to coarsely rugose; T1 parallel-sided or apically tapered; T2 either transverse rectangular, subtriangular, broadly pentagonal or almost linear; hypopygium medio-longitudinally folded with several striae (as in *Apanteles*), degree of striations variable to the point where hypopygium has only faint lateral creases; ovipositor sheaths from about half as long as metatibia to longer.

Remarks. *Choeras* is a cosmopolitan genus, with nearly 60 species described worldwide (Yu *et al.* 2016; Fagan-Jeffries and Austin 2018; Ghafouri Moghaddam *et al.* 2018). There are currently nine species described from Australasia: *C. calacte* (Nixon 1965), *C. ceto* (Nixon 1965), *C. dissors* (Nixon 1965), *C. epaphus* (Nixon 1965), *C. helespas* Walker (1996), *C. koalascatocola* Fagan-Jeffries & Austin (2017), *C. morialta* Fagan-Jeffries & Austin (2017), *C. papua* (Wilkinson 1936), and *C. tegularis* (Szepligeti 1905). The genus is likely to be paraphyletic (Williams D.J.M. 1988; Austin and Dangerfield 1992), with the Australian fauna forming two main clades in a recent molecular study (Fagan-Jeffries *et al.* 2018b); one clade including species possessing a small, slit-like fore wing areolet, and a second clade of species with a large fore wing areolet that includes species appearing to be morphologically intermediate between *Choeras* and *Sathon* (Fig. 1). It is clear that the genus needs to be revised, however, a world-wide sampling effort and inclusion of several morphologically-related genera such as *Sathon* and *Lathrapanteles* Williams would be required for a detailed treatment that does not cause further confusion to generic boundaries in the Microgastrinae. As such, we here place species from both of the Australian molecular clades (with fore wing areolets both large and small) into *Choeras*, but present detailed descriptions, images and molecular data, so that they can be more easily assessed in future studies. The distribution of two of the new species is restricted to a single collection locality in Tasmania, whilst the third species has a broad distribution across south-western Australia (Fig. 2).

We here formally recognise the corrected species name *Choeras ceto* (Nixon), which was mistakenly changed to *Choeras cetus* by Austin and Dangerfield (1992).

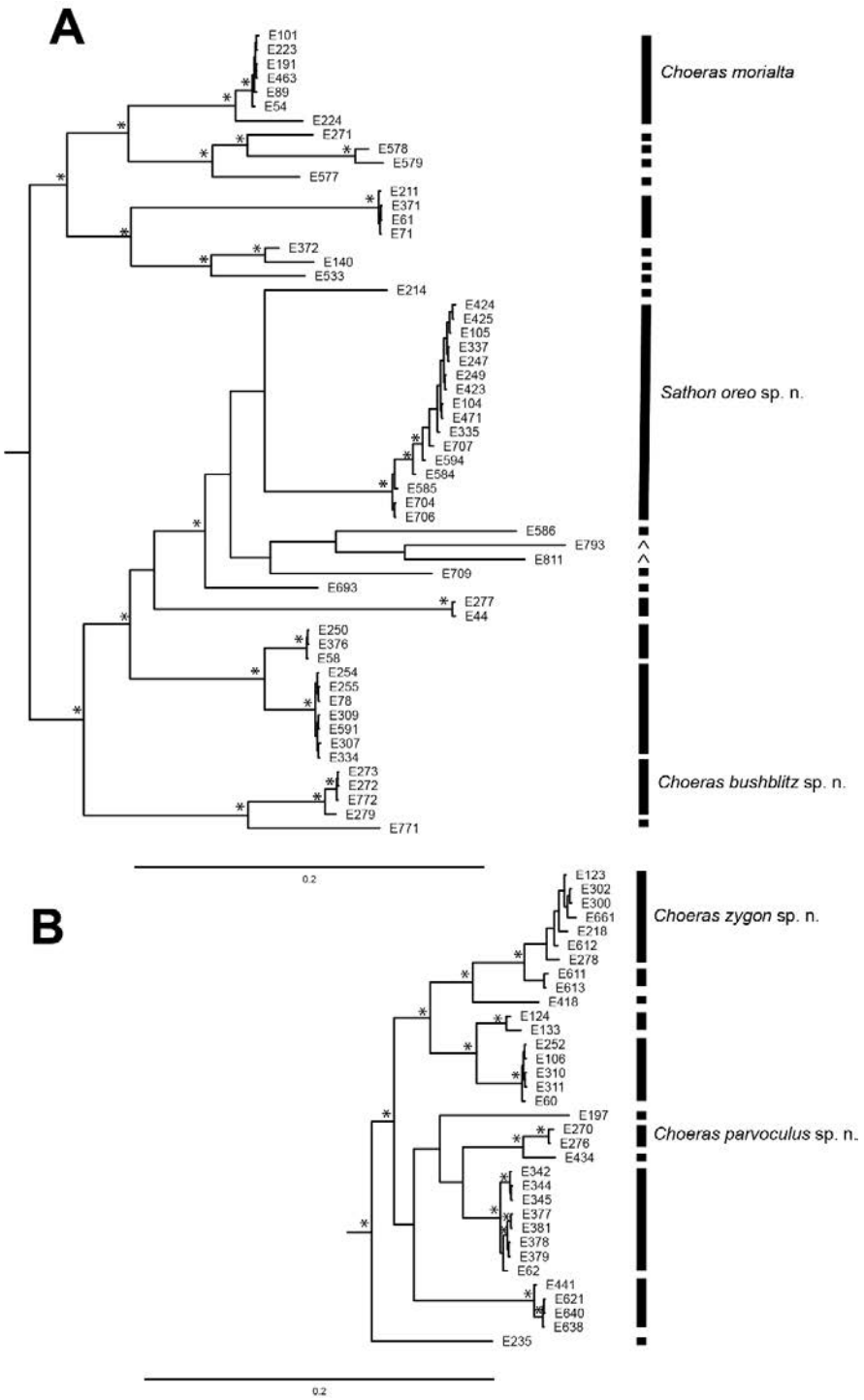

Figure 1: A) The clade of specimens morphologically identified as either *Choeras* or *Sathon* (i.e. possessing either a solid hypopygium or a flexible hypopygium, respectively) with a large fore wing areolet, and B) the clade of *Choeras* specimens with a small fore wing areolet. Clades are isolated from a larger concatenated *COI* and *WG* Bayesian tree of Microgastrinae. * indicates nodes with ≥ 95% posterior probability support. The consensus species delimitation hypothesis as determined in Fagan-Jeffries *et al.* (2018b) is indicated with bars to the right of the tree. ^ indicates the specimen was newly sequenced since Fagan-Jeffries *et al.* (2018b). These clades (A and B) are not closely related in the larger phylogeny, but there is limited support in the connecting nodes. Refer to Fagan-Jeffries *et al.* (2018b, figure 4b) for a simplified version of the complete phylogeny depicting the relationships among genera, including between these two *Choeras* clades.

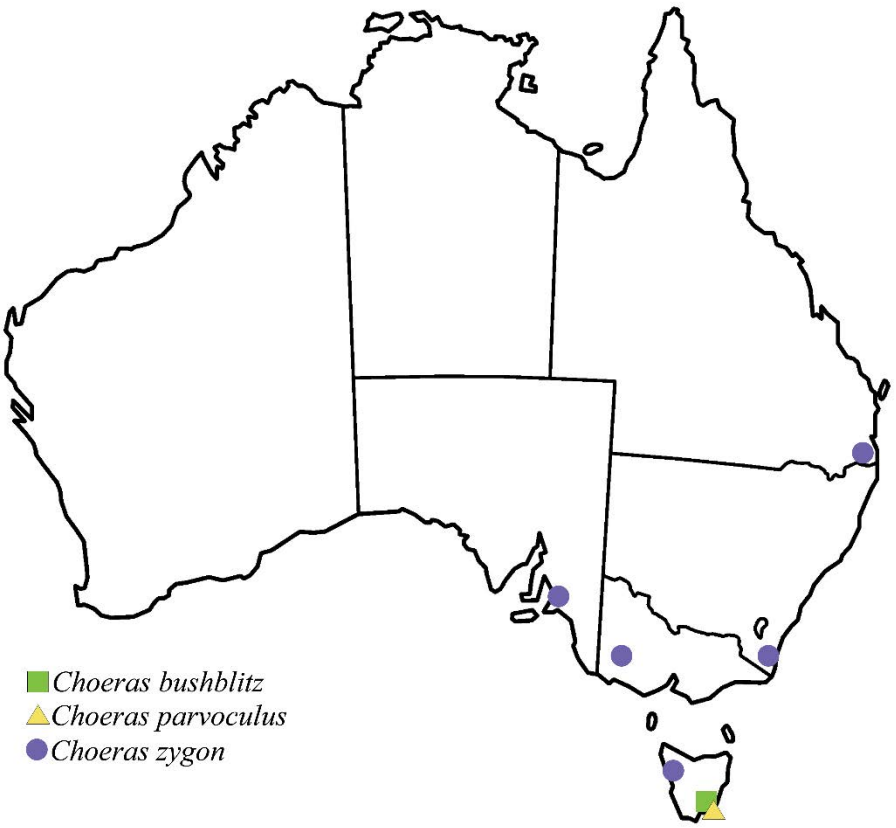

Figure 2: Known distribution of the three new *Choeras* species described in this study.

***Choeras bushblitz* Fagan-Jeffries & Austin sp. nov.**

(Fig. 3)

Material examined (including Genbank numbers of DNA barcodes). *Holotype.* f#, Australia, Tas, Southwest National Park Bush Blitz, SSS1, -43.199° 146.78481°, 01–09/ii/2016, K. Moore, pitfall trap (TMAG: F59023; Genbank *COI*: MH138610 *WG*: MH139104). *Paratypes.* f#, Australia, Tas, Southwest National Park Bush Blitz, SSS1, -43.199° 146.78481°, 01–09/ii/2016, K. Moore, malaise trap (TMAG: F59022; Genbank *COI*: MH138609). f#, Australia, Tas, Southwest National Park Bush Blitz, SSS1, -43.199° 146.78481°, 01–09/ii/2016, K. Moore, yellow pan traps (TMAG: F59029; Genbank *COI*: MH138613; stored in ethanol). m#, Australia, Tas, Southwest National Park Bush Blitz, SSS1, -43.199° 146.78481°, 01–09/ii/2016, K. Moore, pitfall trap (TMAG: F94025).

Diagnosis. This species can be separated from the other Australian species of *Choeras* with large fore wing areolets by the following combination of characters: presence of a medial longitudinal carina on the propodeum (opposed to *C. tegularis* and *C. ceto* which do not possess a medial longitudinal carina), T1 narrowing posteriorly (opposed to *C. epaphus* and *C. koalascatocola*, which have T1 parallel sided or broadening posteriorly) and by the

distinctive colouration of the anteromesoscutum and the strong rugose carinae of the propodeum, which differs from the colouration and sculpturing of all described Australian species.

Description. Female. *Colour*: Head dark, antennae light brown with scape and pedicle paler in colouration, anteromesoscutum dark with light brown to orange area in centre covering approximately half the dorsal width, scutellum and mesoscutum light brown to orange, propodeum light brown or orange at centre with darker outer edges, tergites dark, T1 with pale posterior section at boundary to T2, non-scleratised area around T1 pale, non-sclerotised area around T2 light brown, sternites and hypopygium dark; coxae (pro-, meso-, metacoxa) pale, pale, pale; femora (pro-, meso-, metafemur) pale, pale, pale with darker blotch posteriorly; tibiae (pro-, meso-, metatibia) pale, pale, pale transitioning to light brown posteriorly; tegula and humeral complex pale; pterostigma dark; fore wing veins dark. *Head*: Antennae similar length to body length; body length (head to apex of metasoma) 2.5–3 mm; ocular–ocellar line/posterior ocellus diameter 2.5–2.8; interocellar distance/posterior ocellus diameter 1.5–1.6. *Mesosoma*: Anteromesoscutum mostly smooth, with shallow punctures associated with setae, more visible in anterior and lateral thirds; mesoscutellar disc completely smooth; number of pits in scutoscutellar sulcus 10; maximum height of mesoscutellum lunules/maximum height of lateral face of mesoscutellum 0.3–0.4. *Wings*: fore wing length 2.7 mm; length of veins r/2RS 0.6–0.8; length of veins 2RS/2M 0.8–0.9; length of veins 2M/(RS+M)b 1.7–2.0; pterostigma length/width 2.8–3.0; fore wing areolet large, enclosed. *Legs*: Metatibia inner spur length/metabasitarsus length 0.4. *Propodeum:* percurrent median longitudinal carina and strong rugose sculpturing, carinae often appearing to form pentagonal areola bisected by the longitudinal carina. *Metasoma*: T1 length/width at posterior margin 3; T1 shape clearing narrowing posteriorly with rugulose sculpturing on lateral edges, smoother in centre; T2 width at posterior margin/length 3.6; T2 trapezoid shaped, broadening posteriorly, sculpture smooth and shiny; T3 sculpture smooth and shiny; hypopygium large with some lateral creases and membranous area along ventral margin; ovipositor sheaths length/metatibial length 1.1–1.2.

Male. Very similar to female, however antennae are longer than body length.

Etymology. This species is named for the Bush Blitz expeditions on which it was collected. These expeditions are a significant contribution to documenting Australia's biodiversity. The species name is a noun in apposition.

Distribution. This species has currently only been collected from the south-west of Tasmania.

Remarks. The molecular data for *C. bushblitz* places it in the clade of Australian species that possess a large fore wing areolet, along with taxa that morphologically can be identified

as *Choeras* and *Sathon* (i.e. a clade of species with both membranous and solid hypopygia) (Fig. 1). This species clearly has a membranous area on the hypopygium, and we therefore place it in *Choeras*. It represents the first member of *Choeras* in at least the Australian fauna to possess a propodeum where the rugose surface give the false impression of an areola bisected by a longitudinal carina. There is no information known about possible host species. The *COI* divergence within this species is slightly higher than the commonly used 2% delimitation threshold (2.3%) and there are no species with available sequence data within 10% divergence.

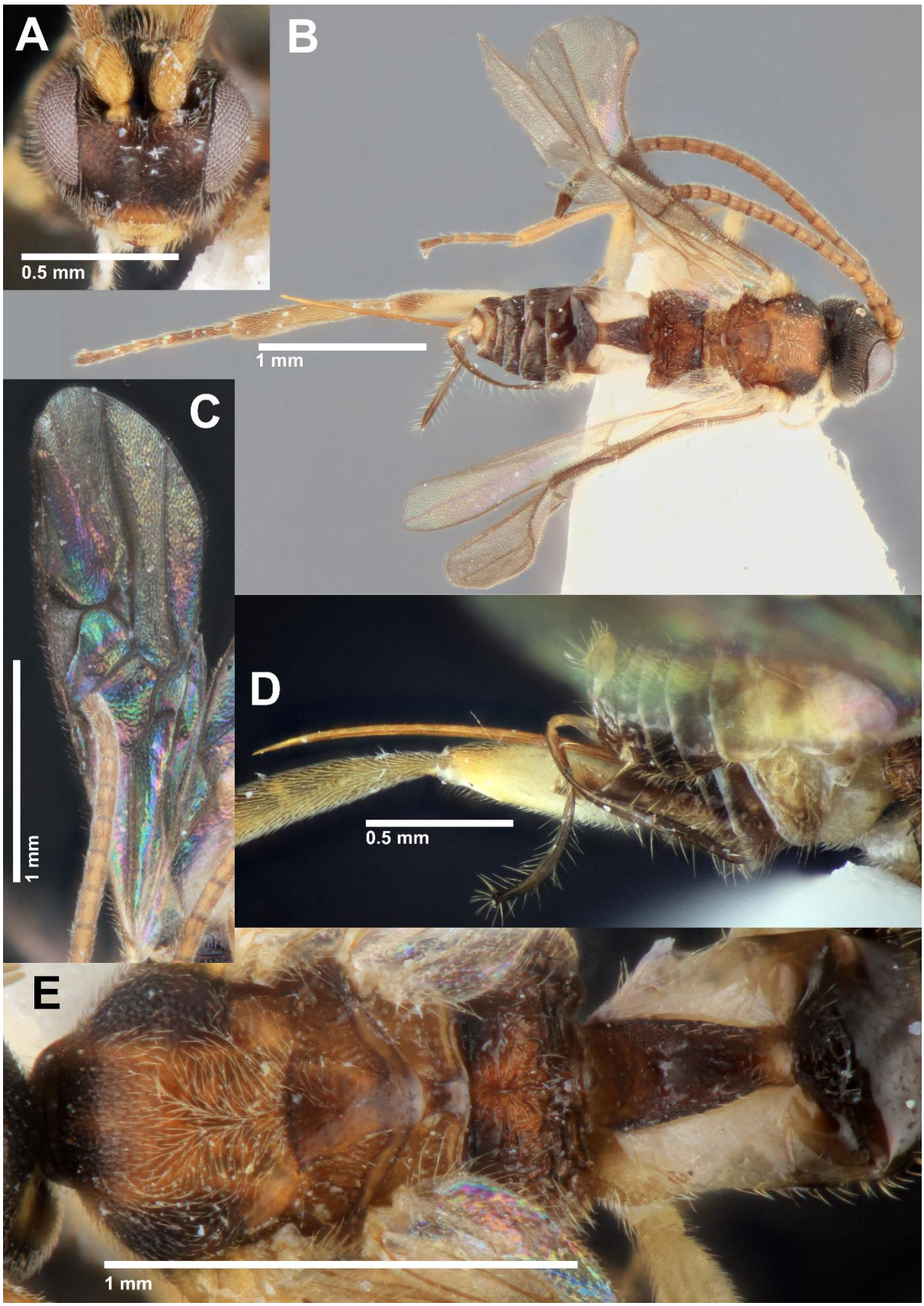

Figure 3: *C. bushblitz* holotype A. anterior view of head; B. dorsal habitus; C. fore wing; D. lateral view of metasoma; E. dorsal mesosoma and T1–2.

***Choeras parvoculus* Fagan-Jeffries & Austin sp. nov.**

(Fig. 4)

Material examined (including Genbank numbers of DNA barcodes). *Holotype.* f#, Australia, Tas, Southwest National Park Bush Blitz, SSS2, -43.1413° 146.76241°, 03–09/ii/2016, K. Moore, malaise trap (TMAG: F59020; Genbank *COI*: MH138608 *WG*: MH139103). *Paratype*. f#, Australia, Tas, Southwest National Park Bush Blitz, SSS2, -43.1413° 146.76241°, 03–09/ii/2016, K. Moore, malaise trap (TMAG: F59026; Genbank *COI*: MH138611 *WG*: MH139105).

Diagnosis. Differs from *C. bushblitz*, C. *tegularis*, *C. ceto*, *C. epaphus*, *C. koalascatocola*, *C. helespas* and *C. morialta* by the presence of a small areolet in the fore wing; previously mentioned species all have a large fore wing areolet. Differs from *C. dissors* by having less slender antennae, the fore wing vein r curved rather than sharply angled, and the mesoscutellar disc not densely covered with setae. Differs from *C. calacte* by having smaller eyes (ocular–ocellar line/posterior ocellus diameter 2.7–3.0 compared to 2.0–2.2 in *C. calacte*) and shorter flagellomeres (*C. calacte* has flagellomere 14 1.3 x as long as wide, whilst in *C. parvoculus* flagellomere 14 is as long as wide. Differs from *C. zygon* by smaller eyes and an almost parallel-sided T1 compared to T1 of *C. zygon*, which narrows posteriorly.

Description. Female. *Colour*: all dark other than pale non-scleratised area of T1–2, antennae dark; coxae (pro-, meso-, metacoxa) dark, dark, dark; femora (pro-, meso-, metafemur) dark lightening at distal end, dark lightening at distal end, dark; (pro-, meso-, metatibia) dark, dark with white band at proximal end, proximal third white distal two thirds dark; tegula and humeral complex light brown; pterostigma dark; fore wing veins dark, paler at proximal end of wings. *Head*: Antennae approximately equal to body length; body length (head to apex of metasoma) 1.9–2.0 mm; ocular–ocellar line/posterior ocellus diameter 2.7–3.0; interocellar distance/posterior ocellus diameter 2.0–2.5. *Mesosoma*: Anteromesoscutum smooth other than small punctures associated with setae; mesoscutellar disc completely smooth and shining; number of pits in scutoscutellar sulcus 10–12; maximum height of mesoscutellum lunules/maximum height of lateral face of mesoscutellum 0.3–0.4. *Wings*: fore wing length 2.0–2.1 mm; fore wing areolet small, enclosed; length of veins r/2RS 1.8–2; length of veins 2RS/2M 0.6–0.7; length of veins 2M/(RS+M)b 1.3–1.4; pterostigma length/width 2.2–2.4. *Legs*: Metatibia inner spur length/metabasitarsus length 0.9–1.0. *Propodeum:* multiple short carinae diverging from posterior centre, medial longitudinal carina in posterior half, rugose appearance in the posterior centre margin, otherwise smooth and shining. *Metasoma*: T1 length/width at posterior margin 1.4–1.8; T1 shape broad, rectangular, almost parallel-sided; T1 sculpture

smooth in anterior half, posterior half with shallow striations; T2 width at posterior margin/length 4.1–4.4; T2 sculpture smooth and shiny with a few scattered punctures; T3 sculpture smooth and shiny; hypopygium large with membranous area ventrally; ovipositor sheaths length/metatibial length 0.9–1.1. **Male.** Unknown.

Etymology. The species epithet *parvoculus* combines the Latin 'parvus' meaning little, and 'oculus' meaning eyes, referring to the smaller eyes of this species compared to the morphologically similar *Choeras calacte*. It is a noun in apposition.

Distribution. This species has currently only been collected from Southwest National Park, Tasmania.

Remarks. In this species, we also tentatively place the following specimens, which have been sequenced for the *COI* barcoding region by the Biodiversity Institute of Ontario, and are stored in the Centre for Biodiversity Genomics, and are publically available on the Barcode of Life Database (BOLD). These specimens are all collected from Tasmania, and whilst they were not available to be compared to the type series, the *COI* sequences fall within the 2% divergence threshold that generally discriminates species in the Microgastrinae. BOLD numbers: GMATR1295-16, GMATT3228-16, GMATT3510-16, GMATT3519-16, GMATT3806-16, GMATV2548-16, GMATS2612-16, GMATV2575-16, GMATU3015-16. The nearest neighbour to this group with available sequence information are specimens from Canberra, Australia, at 2.1% *COI* divergence. Based on images of these specimens available on BOLD, they appear to be a distinct species with a larger fore wing areolet and T1 narrowing more strongly posteriorly. The *WG* sequences for the type specimens of *C. parvoculus* are identical. No information about the host is known.

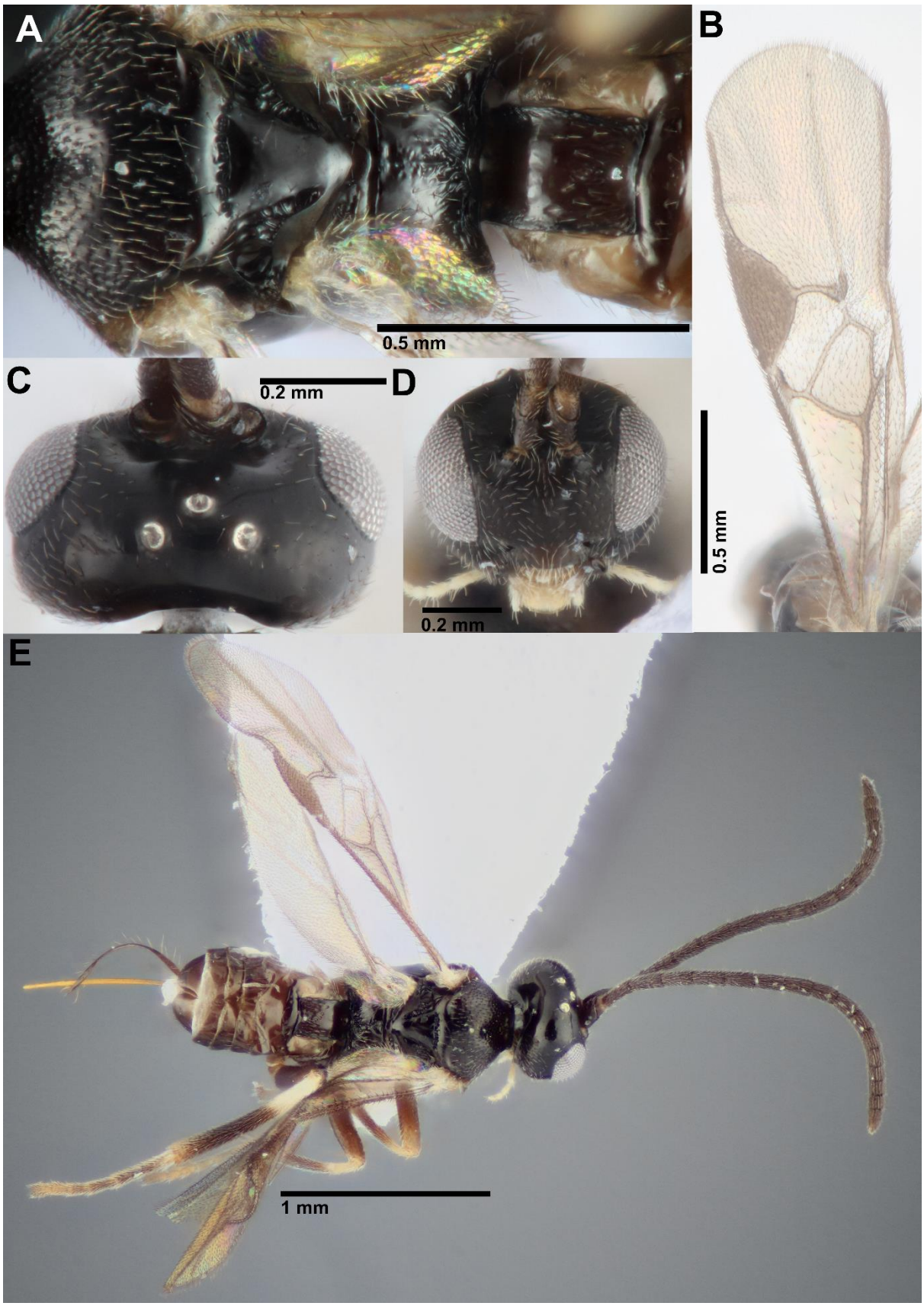

Figure 4: *C. parvoculus* holotype: A. mesosoma and partial metasoma; B. fore wing; C. dorsal view of the head; D. anterior view of the head; E. dorsal habitus.

***Choeras zygon* Fagan-Jeffries & Austin sp. nov.**

(Figs 5–6)

Material examined (including Genbank numbers of DNA barcodes). *Holotype.* f# Australia, Qld, Lamington NP -28.21° 153.139°, 15–25/i/2007, C. Lambkin, N. Starick, 474m, IBISCA Plot # IQ-500-C, rainforest malaise trap (QM: T208374; Genbank *COI*: MH138822 *WG*: MH139278). *Paratypes.* f# Australia, S Aust, Cox Scrub Conservation Park, 35°19'52"S 138°44'51"E, 25/i/2016–13/ii/2016, A. Austin, malaise trap (WINC; Genbank *COI*: MH138601 *WG*: MH139098). f# Australia, NSW, East Boyd State Forest, Goanna Rd, 37°12'05"S 149°46'30"E, 06/xii/2004–12/i/2005, C. Lambkin & N. Starick, malaise across disused snig-track in forest 56 km SE Bombala, 219 m (ANIC: 32 130201; Genbank *COI*: MH138605). f# Australia, Vic, Grampians National Park Bioscan, 37°19'51"S 142°11'36" E, 26–28/xi/2012, B. Patullo, P. Lillywhite, malaise trap, Ming Ming Swamp GB442 (MV: HYM-61350; Genbank *COI*: MH138614). f# Australia, Vic, Grampians National Park Bioscan, 37°19'53"S 142°11'17" E, 26–28/xi/2012, B. Patullo, P. Lillywhite, malaise trap, Ming Ming Swamp GB442 (MV: HYM-61351; Genbank *COI*: MH138615 *WG*: MH139107; stored in ethanol). f# Australia, Qld, Lamington NP, -28.262 153.17, 11–21/iii/2008, C. Lambkin & N. Starick, 1140m, IBISCA Plot # IQ-1100-D, rainforest malaise trap (QM: T208375; Genbank *COI*: MH138872). f# Australia, Tas, Pieman River State Reserve Bush Blitz: E of Corinna campground, SSS2, -41.6556 145.0819, 27/i/2015, S. Grove, malaise trap (TMAG: F59027; Genbank *COI*: MH138612 *WG*: MH139106).

Diagnosis. *C. zygon* can be separated from the other Australasian species of *Choeras* with a small fore wing areolet by having T2 narrowing posteriorly (opposed to the almost parallel sided T1 of *C. calacte* and *C. parvoculus*) and differs from *C. papua* by a lack of pale orange colouration over the entire body.

Description. Female. *Colour*: body dark, ranging from 'black' in Tas, S Aust and Vic specimens to 'reddish-brown' in specimens from Qld and NSW, pale non-scleratised areas of T1-2, sternites, and hypopygium; antennae dark, sometimes with paler scape and pedicle; coxae (pro-, meso-, metacoxa) pale, pale, dark fading to pale in distal half; femora (pro-, meso-, metafemur) dark, dark, dark, although colour much paler in Qld and NSW specimens; tibiae (pro-, meso-, metatibia) dark with pale area in proximal third, colour much paler in Qld and NSW specimens; tegula and humeral complex pale in Qld and NSW specimens, dark in others; pterostigma dark; fore wing veins dark. *Head*: antennae approximately equal to body length; body length (head to apex of metasoma) 2.3–2.9 mm; ocular–ocellar line/posterior ocellus diameter 2.0–2.6; interocellar distance/posterior ocellus diameter 1.5–2.0. *Mesosoma*: Anteromesoscutum smooth with shallow punctures

associated with setae; mesoscutellar disc completely smooth with sparse setae; number of pits in scutoscutellar sulcus 8–10, maximum height of mesoscutellum lunules/maximum height of lateral face of mesoscutellum 0.3–0.6. *Wings*: fore wing length 2.2–2.6 mm; length of veins r/2RS 1.5–2.0; vein r slightly curved; length of veins 2RS/2M 0.7–0.9; length of veins 2M/(RS+M)b 0.9–1.4; pterostigma length/width 2.5–2.8; fore wing areolet small and closed. *Legs*: Metatibia inner spur length/metabasitarsus length 0.3–0.4. *Propodeum:* often with short carinae or rugosity radiating from centre of posterior boundary, sometimes with a medial longitudinal carina in posterior half, or a complete medial longitudinal carina, posterior lateral corners of propodeum rugose, sometimes area either side of medial longitudinal carina rugose, remainder of propodeum smooth. *Metasoma*: T1 length/width at posterior margin 2.1–2.7; T1 narrowing slightly posteriorly, anterior half often with rugosity on lateral edges, often smooth in centre, posterior half shallowly punctate with surrounding rugosity, sometimes with smooth semi-circle at border with T2; T2 width at posterior margin/length 2.6–4.0; T2 sculpture mostly smooth, sometimes with longitudinal striations right at border with T1, sometimes with very shallow pits near border with T3; hypopygium large with membranous area mid-ventrally; ovipositor sheaths length/metatibial length 1.1–1.2.

Etymology. The name 'zygon' references the shape-shifting race of aliens on the BBC television show *Doctor Who*. The shape-shifting nature of this fictional race mirrors the large morphological variability within *C. zygon*, which appears to 'shape shift' (i.e. variation in colour and sculpturing patterns) between different populations whilst retaining extremely small molecular divergences. The Zygon in *Doctor Who* also consume their 'host', a trait particularly relevant to endoparasitoid wasps. The species name is a noun in apposition.

Distribution. This species is widespread and currently known from South Australia, southern Queensland, New South Wales, Victoria and Tasmania.

Remarks. This species shows variation in characters often used to separate species of Microgastrinae, namely the sculpturing of the propodeum and T1, and also shows geographical variation in colour. However, there is less than 1.4% divergence among the *COI* sequences of these specimens, well below the threshold often used to delimit species in this subfamily. As such, we describe this species as one with substantial morphological variation associated with different populations, which nonetheless has distinct characters that separate it from other described species of *Choeras* from Australasia. However, the variation in the propodeal and T1 sculpturing will need to be taken into account when more species are described, particularly those which are shown from molecular analyses to be closely related. Specimens from South Australia, Victoria and Queensland shared a *WG*

haplotype, however the *WG* sequence of the specimen from Tasmania is 4 bp (of a total 443 bp sequence length) different. The nearest neighbour with available *COI* DNA barcodes is an unidentified species of *Choeras* from Queensland, at a distance of 2.9%.

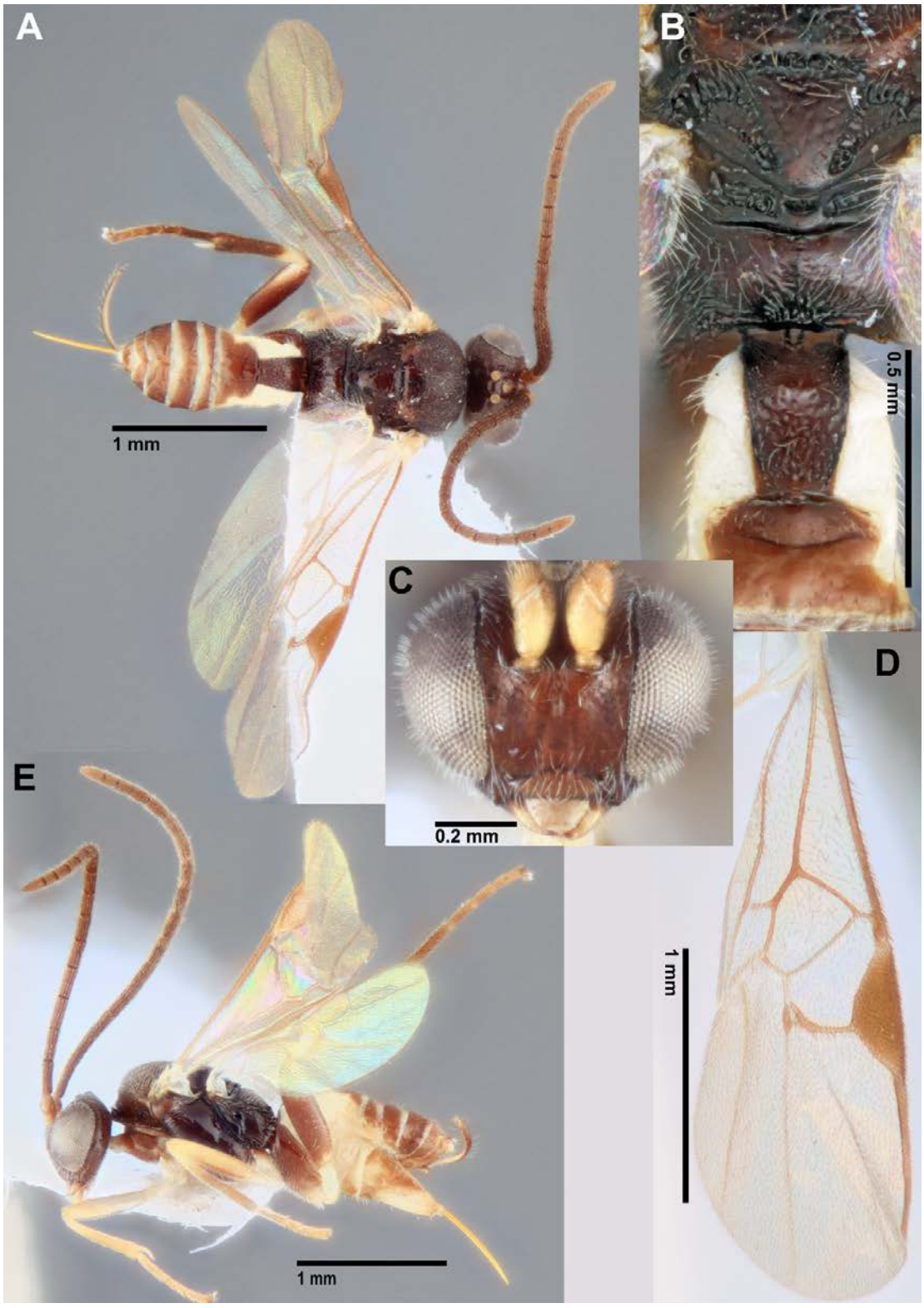

Figure 5: *C. zygon* holotype. A. dorsal habitus; B. mesosoma and T1–2; C. anterior head; D. fore wing; E. lateral habitus.

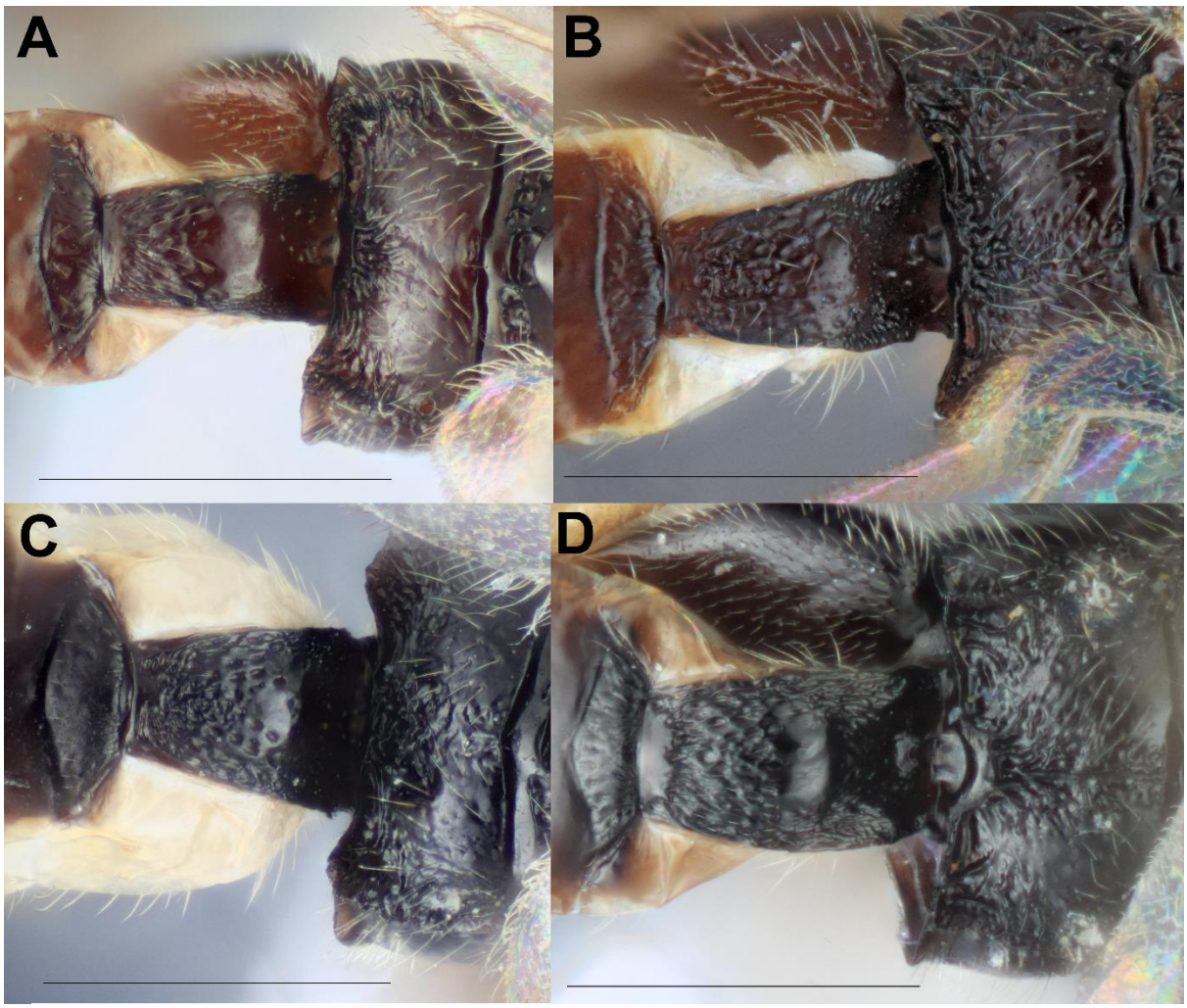

Figure 6: *C. zygon* range of propodeal and T1 sculpturing. A. specimen from NSW, propodeum with radiating short carinae and no clear longitudinal medial carina with much reduced rugosity in medial area; B. paratype from Qld, indistinct medial carina, rugosity around centre longitudinal area; C. specimen from Tas, as in B; D. specimen from Vic, strong medial longitudinal carina, rugosity surrounding medial area, T1 with smooth area at border with T2. Scale bars = 0.5 mm.

***Dolichogenidea* Viereck**

Dolichogenidea Viereck 1911: 173 (as a subgenus of *Apanteles* Foerster s.l.); Generic status by Mason 1981: 34. Austin and Dangerfield 1992: 27. See Shenefelt (1972) for earlier bibliographic history, Mason (1981) for discussion of relationships, and Fagan-Jeffries and Austin (2018a) for comments on the Australian fauna.

Type species, by original designation, *Apanteles* (*Dolichogenidea*) *banksi* Viereck.

Diagnosis. Fore wing areolet (second submarginal cell) absent (i.e. vein r-m absent); hind wing vannal lobe convex to almost straight and uniformly fringed by setae; propodeum often with a complete areola, sometimes areola reduced with at least posterior diverging carinae present, rarely with these carinae completely absent; metasoma with T2 variable in shape, but usually rectangular or subrectangular; hypopygium membranous mid-ventrally

and expandable (sometimes folded inwards and hidden by laterotergites in dead specimens); ovipositor protruding from posterior metasoma, often as long as or longer than length of metatibia, but also commonly shorter than the metatibia.

Remarks. *Dolichogenidea* is a cosmopolitan genus with approximately 200 described species (Yu *et al.* 2016; Fagan-Jeffries *et al.* 2018a; Liu *et al.* 2018). There are currently nine species described from Australia: *D. biroi* (Szepligeti 1905), *D. eucalypti* Austin and Allen 1989, *D. finchi* Fagan-Jeffries and Austin 2018, *D. hyposidrae* (Wilkinson 1928), *D. lipsis* (Nixon 1967), *D. mediocaudata* Fagan-Jeffries and Austin 2018, *D. miris* (Nixon 1967), *D. tasmanica* (Cameron 1912), and *D. xenomorph* Fagan-Jeffries and Austin 2018. There are an additional 17 species recorded from the Australasian region, mostly from Papua New Guinea and Fiji. The genus is generally monophyletic in molecular studies, and is clearly distinct from the morphologically similar genus *Apanteles* Foerster (Smith *et al.* 2013; Fagan-Jeffries *et al.* 2018b). Most of the species described in this study have restricted known distributions (Fig. 7), however, this is likely to relate to inadequate sampling rather than representing true distributions. The six species described here are just a fraction of the diversity suggested by molecular data (Fig. 8)

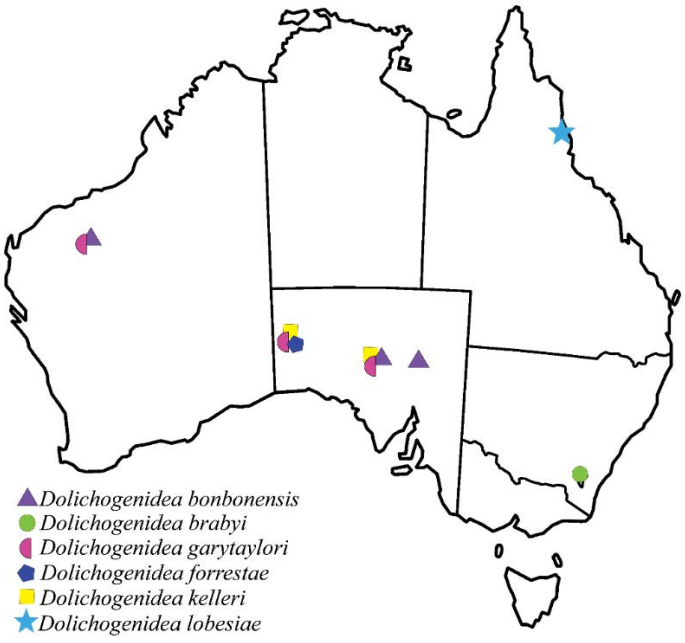

Figure 7. Known distributions of the six *Dolichogenidea* species described in this study.

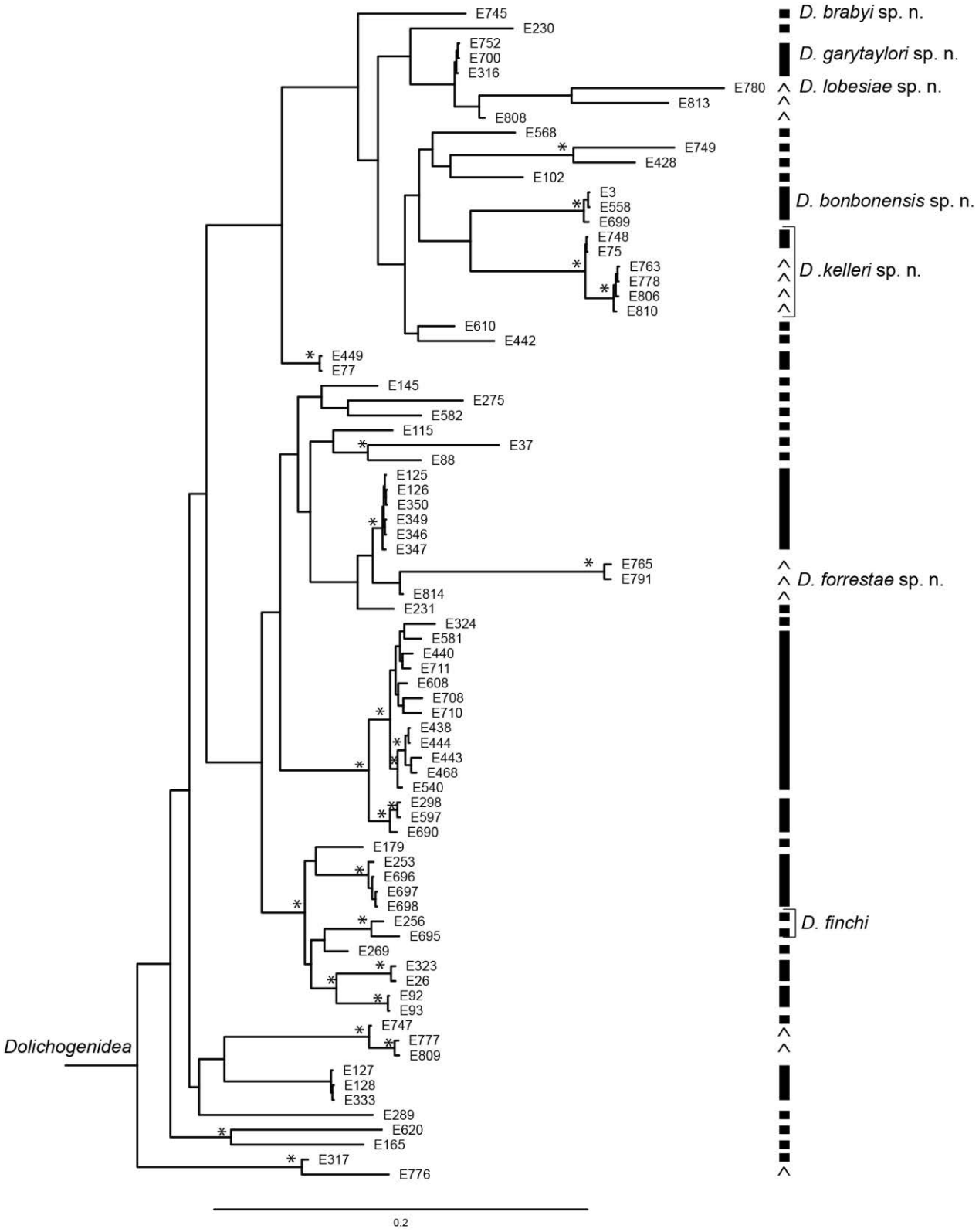

Figure 8: The *Dolichogenidea* clade isolated from a larger concatenated *COI* and *WG* Bayesian tree of Microgastrinae. * indicates nodes with ≥ 95% posterior probability support. The consensus species delimitation hypothesis as determined in Fagan-Jeffries *et al.* (2018b) is indicated with bars to the right of the tree. ^ indicates the specimen was newly sequenced since Fagan-Jeffries *et al.* (2018b).

***Dolichogenidea bonbonensis* Fagan-Jeffries & Austin sp. nov.**
(Fig. 9)

Material examined (including Genbank numbers of DNA barcodes). *Holotype.* f# Australia, S Aust, Bon Bon Stn, 30°18'50"S 135°32'50"E, 28/x/2010, R. Kittel, Bush Blitz Svy RK129 on *Acacia victoriae* sweep netting (SAMA: 32-036126; Genbank *COI*: MH138727 *WG*: MH139204). *Paratypes.* f# Australia, S Aust, Witchelina Stn, 30°01'07"S 137°54'04"E, 23/x/2010, R. Kittel, Bush Blitz Svy RK091 sweeping *Acacia victoriae* (SAMA: 32-036127; Genbank *COI*: MH138708 *WG*: MH139188). f# Australia, WA, Kariijini NP, Weano Gorge Rd, 22°21'19"S 118°15'00"E, 25/iv/2003–15/v/2003, C. Lambkin & T. Weir, malaise grassy dry creek *Eucalyptus* & *Acacia* scrub, 695 m (ANIC: 32 130220; Genbank *COI*: MH138946 *WG*: MH139367).

Diagnosis. *Dolichogenidea bonbonensis* can be separated from *D. biroi*, *D. ilione* (Nixon 1967), *D. lipsis* and *D. tasmanica* by the absence of a white cheek blotch. *Dolichogenidea bonbonensis* has ovipositor sheaths slightly shorter than the metatibia (ovipositor sheaths length/metatibial length 0.7–0.9) whilst *D. acratos* (Nixon 1967), *D. brabyi*, *D. eucalypti, D. expulsa* (Turner 1918), *D. garytaylori, D. hyposidrae* and *D. orelia* (Nixon 1967) all have ovipositors much shorter, half the length of the metatibia or less, whilst *D. carposinae* (Wilkinson 1938), *D. coequata* (Nixon 1967), *D. cyamon* (Nixon 1967), *D. finchi, D. hyblaeae* (Wilkinson 1928), *D. ilione, D. inquisitor* (Wilkinson 1928), *D. iulis* (Nixon 1967), *D. labaris* (Nixon 1967), *D. lobesiae*, *D. mediocaudata, D. miris*, *D. platyedrae* (Wilkinson 1928), *D. stantoni,* and *D. xenomorph* all have ovipositor sheaths longer than the metatibia. *Dolichogenidea kelleri* has slightly longer ovipositor sheaths than *D. bonbonensis* (equal to metatibia) and a less well-defined areola. *Dolichogenidea gentilis* (Nixon 1967) has a similar ovipositor sheath length/metatibia ratio to *D. bonbonensis,* but *D. gentilis* has the propodeal areola poorly defined, whilst *D. bonbonensis* has a clearly defined areola. *Dolichogenidea heterusiae* (Wilkinson 1928) has ovipositor sheaths approximately equal to the metatibia, but can also be separated from *D. bonbonensis* by having a more rugulose propodeum (*D. bonbonensis* has a mostly smooth propodeum). *Dolichogenidea heterusiae* can also be separated by the prominent carinae on the lateral margins of T1, which are not present in *D. bonbonensis*. *Dolichogenidea upoluensis* (described from a single male) and *D. agonoxenae* are described as having a rugose propodeum, whilst *D. bonbonensis* has a mostly smooth propodeum (Table 1).

Description. Female. *Colour*: All dark, antennae dark; coxae (pro-, meso-, metacoxa) dark, dark, dark; femora (pro-, meso-, metafemur) pale/light brown, dark, dark; tibiae (pro-,

meso-, metatibia) light brown, dark, dark; tegula and humeral complex dark; pterostigma dark; fore wing veins dark. *Head*: Antennae slightly shorter than body length; body length (head to apex of metasoma) 1.9–2.1 mm; ocular–ocellar line/posterior ocellus diameter 1.6–1.8; interocellar distance/posterior ocellus diameter 2.6–2.8. *Mesosoma*: Anteromesoscutum evenly and densely punctate; mesoscutellar disc with a few fine punctures associated with setae; number of pits in scutoscutellar sulcus 13–15; maximum height of mesoscutellum lunules/maximum height of lateral face of mesoscutellum 0.5. *Wings*: fore wing length 2.1–2.3 mm; length of veins r/2RS 1.1–1.6; length of veins 2RS/2M 1.0–1.3; length of veins 2M/(RS+M)b 1.2–1.3; pterostigma length/width 2.5–2.8. *Legs*: Metatibia inner spur length/metabasitarsus length 0.5. *Propodeum:* clearly defined areola, open at anterior end, lateral carinae present and reasonably straight, otherwise mostly smooth with some reticulate rugose sculpturing at anterior centre. *Metasoma*: T1 length/width at posterior margin 1.1–1.2; T1 shape broad, rectangular, almost parallel-sided; T1 sculpture rugose with irregularly shaped punctures, longitudinal strigosity or rugosity in posterior half; T2 width at posterior margin/length 3.8–4.3; T2 sculpture almost smooth, some sparse punctures associated with setae; T3 sculpture smooth and shiny; hypopygium with central membranous area mid-ventrally; ovipositor sheaths length/metatibial length 0.7–0.9. **Male.** Unknown.

Etymology. The species name *bonbonensis* is from the collecting locality of the holotype, Bon Bon Station. It is a Latin 2nd declension adjective.

Distribution. This species has been collected from central South Australia and northern WA.

Remarks. The specimen from WA shows slight variation in colour of the metasoma, and in the curvature of the carinae at the base of the propodeal areola. However, there is less than 0.5% difference in the *COI* sequences of this specimen and those from South Australia, and all specimens share a *WG* haplotype. As such, we include the WA specimen in the type series despite the small morphological differences.

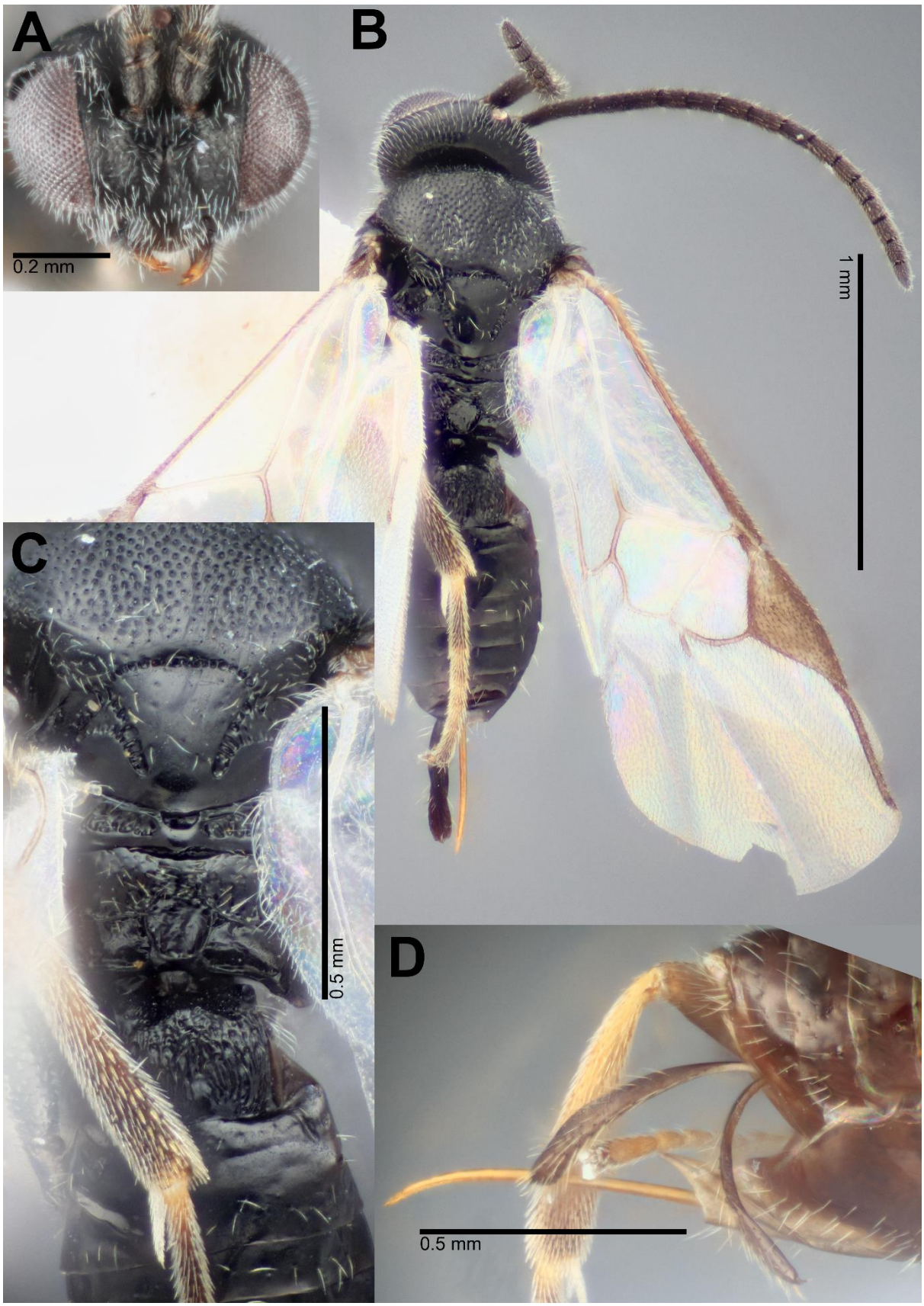

Figure 9: *D. bonbonensis* A. holotype, anterior head; B. holotype, dorsal habitus; C. holotype, meso- and metasoma (in part); D. paratype, hypopygium and ovipositor sheaths.

***Dolichogenidea brabyi* Fagan-Jeffries & Austin sp. nov.**

(Fig. 10)

Material examined (including Genbank numbers of DNA barcodes). *Holotype:* f# Australia, ACT, Black Mountain, emerged 6/iii/2017, M.F. Braby, reared from larva of *Pollanisus apicalis* (Lep: Zyg) (ANIC: 32 130291; Genbank *COI*: MH138906). *Paratypes*: 2m#, same data as holotype (ANIC: 32 130292, 32 130293).

Diagnosis. *Dolichogenidea brabyi* can be separated from *D. biroi*, *D. ilione, D. lipsis,* and *D. tasmanica* by the absence of a white cheek blotch. It can be separated from *D. bonbonensis*, *D. carposinae, D. coequata, D. cyamon, D. finchi, D. gentilis, D. heterusiae, D. hyblaeae, D. ilione, D. inquisitor, D. iulis, D. kelleri*, *D. labaris, D. lobesiae*, *D. mediocaudata, D. miris*, *D. platyedrae, D. stantoni,* and *D. xenomorph*, by having ovipositor sheaths shorter, approximately 0.4 x the length of the metatibia, whilst the species listed above all have ovipositors all at least 0.7 x as long as the metatibia and generally much longer. *Dolichogenidea brabyi* has a similar ovipositor sheath length to *D. acratos*, *D. expulsa* and *D. orelia,* but can be distinguished from *D. acratos* by the slightly broadening T1 (*D. acratos* has T1 parallel-sided), from *D. expulsa* by a smoother anterior half of T2 and different T1 sculpturing (*D. expulsa* has densely rugulose T2) and from *D. orelia* by a smoother propodeum (*D. orelia* has the propodeal surface coarsely rugose). Of the species described here, *D. brabyi* is most similar to *D. eucalypti* (particularly in the form of the propodeum), but has a different host and T2 sculptured (smooth in *D. eucalypti*) with distinctive anterior curved corners. *D. brabyi* also closely resembles *D. garytaylori* and *D. hyposidrae*, but the distinctive T2 sculpturing and shape clearly differentiates *D. brabyi* from these two species. The punctate sculpturing on the anteromesoscutum also differs among *D. brabyi* and *D. garytaylori* and *D. hyposidrae*; they are sparser and more irregular in *D. hyposidrae* than *D. brabyi*, and finer and shallower in *D. garytaylori* than *D. brabyi*. Both *D. agonexenae* and *D. upoluensis* are described as possessing a rugose propodeum whilst *D. brabyi* has a mostly smooth propodeum (Table 1).

Description. Female. *Colour:* All dark but with slightly lighter non-scleratised area around T1–2, antennae dark; coxae (pro-, meso-, metacoxa) dark, dark, dark; femora (pro-, meso-, metafemur) dark to pale at posterior end, dark to paler at posterior end, dark; tibiae (pro-, meso-, metatibia) pale though darkening towards posterior end, pale though darkening towards posterior end, dark with lighter area at anterior third; tegula and humeral complex dark; pterostigma dark; fore wing veins pale proximally, dark distal to pterostigma. *Head*: Antennae slightly longer than body length; body length (head to apex of metasoma) 2.1 mm; ocular–ocellar line/posterior ocellus diameter 2.0; interocellar distance/posterior

ocellus diameter 2.2. *Mesosoma*: Anteromesoscutum punctate with punctures irregularly spaced and sized, mesoscutellar disc smooth with scattered tiny shallow punctures associated with setae; number of pits in scutoscutellar sulcus 6; maximum height of mesoscutellum lunules/maximum height of lateral face of mesoscutellum 0.4. *Wings*: fore wing length 2.5 mm; length of veins r/2RS 1.5; length of veins 2RS/2M 1.3; length of veins 2M/(RS+M)b 0.8; pterostigma length/width 3.1. *Legs*: Metatibia inner spur length/metabasitarsus length 0.5. *Propodeum:* areola clearly defined in posterior half and most of anterior half, but open at anterior end, lateral carinae clear and mostly straight, anterior half of propodeum with shallow punctate sculpturing which is more pronounced in anterior centre where areola is open, posterior half of propodeum and centre of areola mostly smooth. *Metasoma*: T1 length/width at posterior margin 1.2; T1 shape broad, slightly broadening posteriorly; T1 sculpture reticulate rugose with occasional irregularly shaped punctures; T2 width at posterior margin/length 3.5; T2 with indistinct shallow sculpture and visibly not smooth, line of ridges/pits at border with T3; T3 sculpture smooth and shiny; hypopygium with central membranous area mid-ventrally; ovipositor sheaths length/metatibial length 0.4. **Male.** As female but with 8 pits in scutoscutellar sulcus, slight variations in measurements.

Etymology. This species is named for the collector and prominent lepidopterist Dr Michael Braby, who has generously provided EPF-J with many reared specimens throughout her PhD. The authors would like to note that many host records for small parasitoids such as microgastrines exist because of the diligence of lepidopterists in keeping and preserving parasitoid specimens that often appear 'undesirably' when they are attempting to rear adult butterflies and moths, and we would like to extend thanks to those who preserve them in collections. The species name is an invariable genitive.

Distribution. This species is known from the Australian Capital Territory, however the host is widely distributed in the eastern states, including in Tasmania, South Australia, and southern Queensland, thus it is highly possible that *D. brabyi* also occurs in these regions.

Remarks. This species is gregarious and has been reared from *Pollanisus apicalis* Walker (1854) (Lepidoptera: Zygaenidae), a small metallic green day-flying moth. The caterpillars are known to feed on the plant *Hibbertia obtusifolia*.

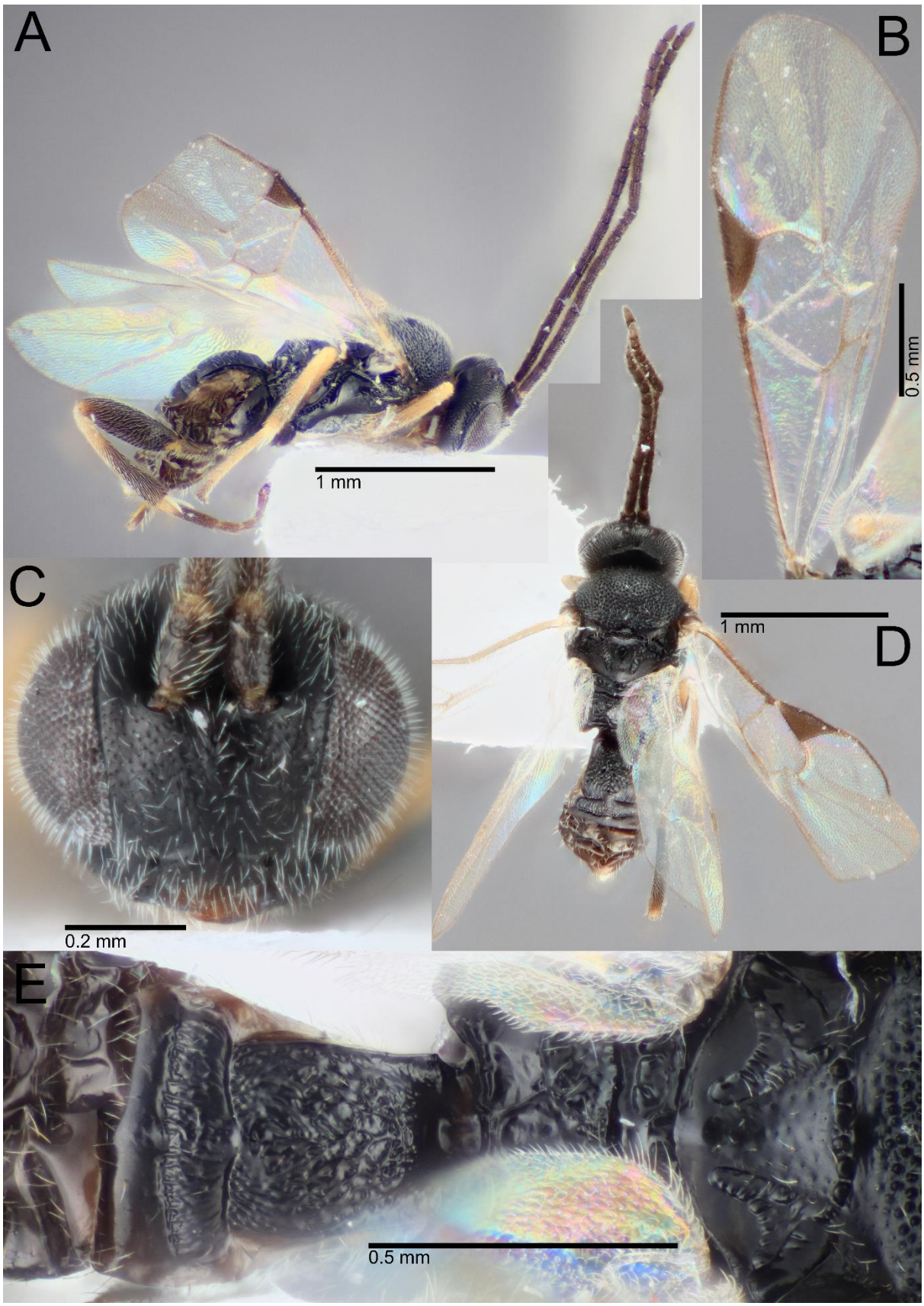

Figure 10: *D. brabyi* holotype A. lateral habitus; B. fore wing; C. anterior head; D. dorsal habitus; E. dorsal mesoscutellum, propodeum and T1–3.

***Dolichogenidea forrestae* Fagan-Jeffries & Austin sp. nov.**

(Fig. 1l)

Material examined (including Genbank numbers of DNA barcodes).

Holotype. #f Australia, S Aust, Great Victoria Desert between Oak Valley and 64km NW, 29°00'24.23"S, 130°15'37.37"E to 29°24'57.70"S, 130°43'51.83"E, 3/ix/2015, J.A. Forrest, R. Leijs, vehicle net, *Euc*. woodland (SAMA: 32-036145). *Other material*. #m Australia, S Aust, Great Victoria Desert, Cook Road, 28.9684°S, 130.0772°E to 29.0449°S, 129.9475°E, 29/viii/2015, J.A. Forrest, R. Leijs, vehicle net (SAMA 32-036146).

Diagnosis. *Dolichogenidea forrestae* can be separated from *D. biroi*, *D. ilione, D. lipsis,* and *D. tasmanica* by the absence of a white cheek blotch. *Dolichogenidea bonbonensis*, *D. carposinae, D. coequata, D. cyamon, D. finchi, D. gentilis, D. heterusiae, D. hyblaeae, D. ilione, D. inquisitor, D. iulis, D. kelleri*, *D. labaris, D. lobesiae*, *D. mediocaudata, D. miris*, *D. platyedrae, D. stantoni, D. xenomorph* all have ovipositor sheaths at least 0.7 x as long as the metatibia, generally much longer, whilst *D. forrestae* has ovipositor sheaths only 0.6 x the length of the metatibia. *Dolichogenidea bonbonensis,* which has ovipositor 0.7 x the metatibia, is also differentiated by a more clearly differentiated areola. *Dolichogenidea brabyi, D. eucalypti, D. garytaylori,* and *D. hyposidrae* all have the propodeal areola at least partially defined, whilst *D. forrestae* only has several fine diverging carinae at the posterior centre of the propodeum. *Dolichogenidea orelia* has a complete areola and shorter ovipositor sheaths compared to *D. forrestae*. *Dolichogenidea acratos* has a similar ovipositor sheath to metatibia ratio (0.5) to *D. forrestae* (0.6) but has a strongly carinate, complete propodeal areola easily separated from the indistinct areola of *D. forrestae. Dolichogenidea agonoxenae* is described as having a strongly formed propodeal areola and costulae, which distinguishes the species from the indistinct areola of *D. forrestae*. *Dolichogenidea expulsa* can be differentiated from *D. forrestae* by a complete areola, T1 broadening posteriorly (*D. forrestae* has T1 with parallel margins) and T2 densely rugose (*D. forrestae* has T2 almost smooth). *Dolichogenidea upoluensis* is described as have an indistinct areola and costulae with very weak carinae, implying that the costulae carinae are still able to be distinguished, which separates this species from *D. forrestae* which has a propodeum with no trace of lateral carinae (Table 1).

Description. Female. *Colour*: All dark, antennae dark; coxae (pro-, meso-, metacoxa) dark, dark, dark; femora (pro-, meso-, metafemur) dark, dark to paler at posterior end, dark; tibiae (pro-, meso-, metatibia) dark, dark with lighter area anteriorly, dark with lighter area anteriorly; tegula and humeral complex pale; pterostigma dark; fore wing veins mostly dark, M+CU1, 1-M and 1-SR+M pale. *Head*: Antennae approximately equal to body length; body

length (head to apex of metasoma) 2.5 mm; ocular–ocellar line/posterior ocellus diameter 1.6; interocellar distance/posterior ocellus diameter 2.3. *Mesosoma*: Anteromesoscutum punctate, punctures mostly evenly sized and spaced, but generally smaller and more distinct over notouli; mesoscutellar disc with numerous tiny shallow scattered punctures associated with setae; number of pits in scutoscutellar sulcus 21–22; maximum height of mesoscutellum lunules/maximum height of lateral face of mesoscutellum 0.5–0.6. *Wings*: fore wing length 2.5 mm; length of veins r/2RS 1.5; length of veins 2RS/2M 1.3; length of veins 2M/(RS+M)b 2; pterostigma length/width 2.6. *Legs*: Metatibia inner spur length/metabasitarsus length 0.6. *Propodeum:* generally smooth, scattered shallow punctures, areola only indicated by slight depression and area of rugosity in posterior centre of propodeum and multiple short diverging carinae posteriorly. *Metasoma*: T1 length/width at posterior margin 1.2; T1 shape broad, rectangular, almost parallel-sided, T1 sculpture punctate; T2 width at posterior margin/length 3.5; T2 sculpture almost smooth; T3 sculpture smooth and shiny; hypopygium with central membranous area mid-ventrally; ovipositor sheaths length/metatibial length 0.6.

Etymology. This species is named for Jan Forrest (OAM) who collected the specimens, and who once supervised a young high school student (author EPF-J) volunteering in the South Australian Museum entomology collection and exposed her to the world of professional insect collections for the first time. The species name is an invariable genitive.

Distribution. Currently only collected from the Great Victoria Desert, in western S Aust.

Remarks. We include in the examined material a male specimen from the same location that resembles the female in the form of the propodeum, but with T1 narrower and longer (T1 length/width at posterior margin ratio larger) and much smoother, and T2 more triangular. The differences in the tergites between the male and female specimens were quite pronounced and larger than what we would generally consider species-level variation. However, the sequenced *COI* barcode has a divergence of only 5 SNPs (0.08% divergent), well within the normal genetic threshold of a microgastrine species. As such, we include it here, but with the substantial morphological variation we question the validity of the DNA barcode, and do not place this specimen in the type series.

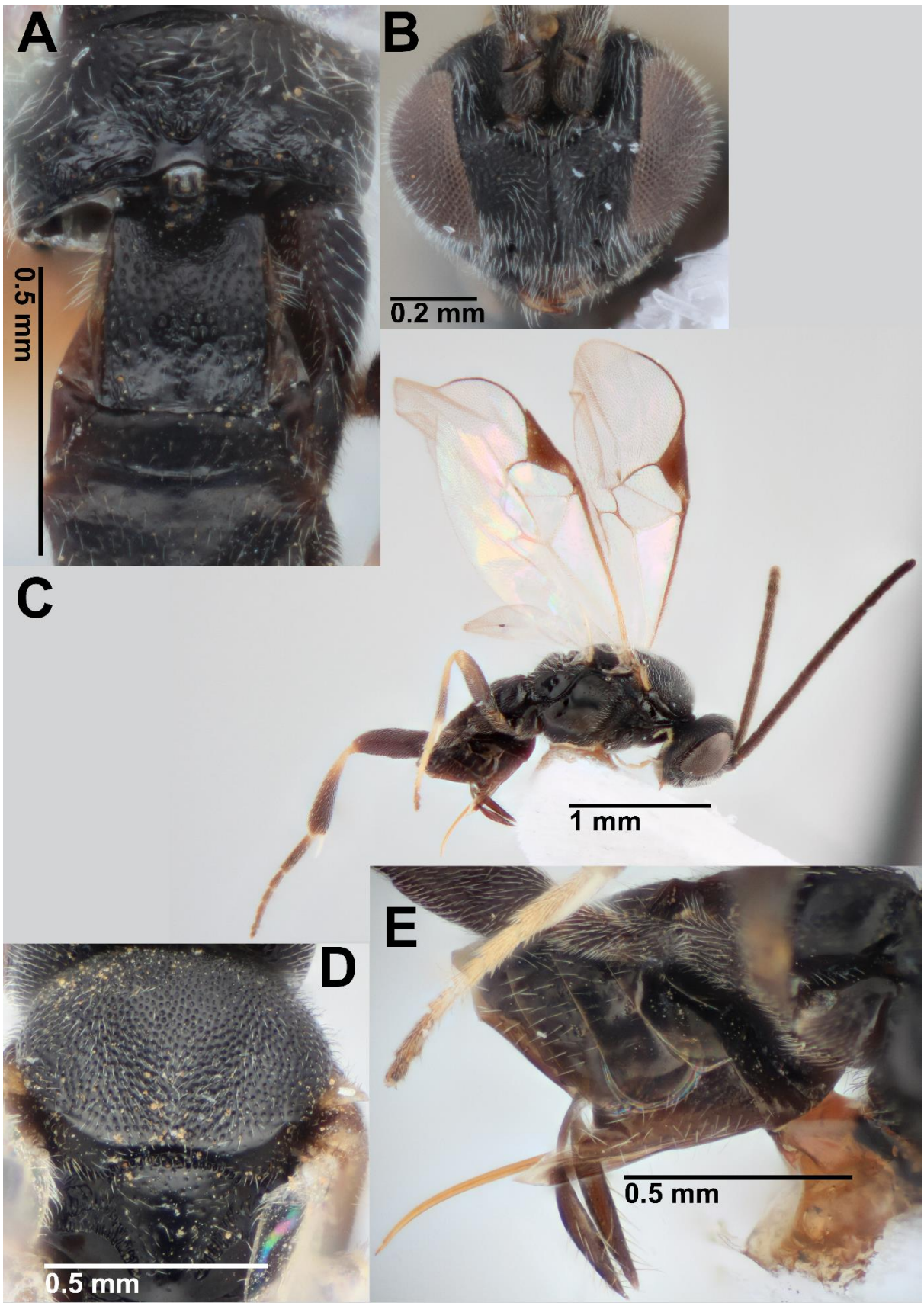

Figure 11: *D. forrestae*: holotype. A. propodeum, T1–2; B. anterior head; C. lateral habitus; D. anteromesoscutum, mesoscutellar disk; E. hypopygium and ovipositor sheaths.

***Dolichogenidea garytaylori* Fagan-Jeffries & Austin sp. nov.**

(Fig. 12)

Material examined (including Genbank numbers of DNA barcodes). *Holotype.* f# Australia, S Aust, Great Victoria Desert Bush Blitz, -28.9258159° 129.5377178°, 22/ix/2017, B. Parslow (SAMA: 32-035467; Genbank *COI*: MH138913 *WG*: MH139348). *Paratypes*. f# Australia, S Aust, Bon Bon Stn, 30°18.828'S 135°32.848'E, 28/x/2010, G.S. Taylor, swept *Acacia victoriae*, 2010 069 (B30) Bush Blitz svy (SAMA: 32-036128; Genbank *COI*: MH138726 *WG*: MH139203). f# Australia, WA, Kariijini NP, Weano Gorge Rd, 22°21'19"S 118°15'00"E, 25/iv/2003–15/v/2003, C. Lambkin & T. Weir, malaise grassy dry creek *Eucalyptus* & *Acacia* scrub, 695 m (ANIC: 32 130221; Genbank *COI*: MH138949 *WG*: MH139370). m# Australia, S. Aust. Great Victoria Desert Bush Blitz, vehicle net Rodinia Road SSS2 to airstrip, -28.8161 129.5358 to -29.11530 129.54124, 18/ix/2017, R. Leijs (SAMA: 32-036129)

Diagnosis. *Dolichogenidea garytaylori* closely resembles *D. hyposidrae*, but the latter has a smooth propodeum other than the carinae of the areola and lateral carinae, and the areola is also only open at the anterior end, whereas *D. garytaylori* has the propodeal areola poorly defined in whole anterior half. The fore wing r vein is also less continuously curved with 2RS (more differentiated) in *D. garytaylori* compared to *D. hyposidrae*. *Dolichogenidea garytaylori* also closely resembles *D. brabyi*, but *D. brabyi* has a distinctive T2 shape (curved at anterior corners) and sculpturing (strongly sculptured in posterior half). *Dolichogenidea eucalypti* has a more defined anterior areola and a smoother propodeum, particularly within the areola, than *D. garytaylori*. *D. garytaylori* can be separated from *D. biroi*, *D. lipsis, D. ilione,* and *D. tasmanica* by the absence of a white cheek blotch. *Dolichogenidea bonbonensis*, *D. carposinae, D. coequata, D. cyamon, D. finchi, D. gentilis, D. heterusiae, D. hyblaeae D. ilione, D. inquisitor, D. iulis, D. kelleri*, *D. labaris, D. lobesiae*, *D. mediocaudata, D. miris*, *D. platyedrae, D. stantoni,* and *D. xenomorph* all have ovipositors at least 0.7 x as long as the metatibia, generally much longer, whilst *D. brabyi* has an ovipositor only 0.4 x the length of the metatibia. *D. expulsa* can be differentiated by a smoother propodeum and more coarsely sculptured T2 than *D. garytaylori*. *Dolichogenidea orelia* can be separated by having rugulose and strigate sculpturing on T2, opposed to the very shallow sculpturing of *D. garytaylori*. *Dolichogenidea acratos* has slightly longer ovipositor sheaths than *D. garytaylori* (ovipositor sheath to metatibia ratio 0.5), and also has T1 parallel-sided, without the slightly broadening area posteriorly of *D. garytaylori*. *Dolichogenidea agonexenae* and *D. upoluensis* are described as having a rugose propodeum, which differentiates these species

from *D. garytaylori*, which has a mostly smooth propodeum other than the centre of the areola and directly anterior to the areola, which is strongly sculptured (Table 1).

Description. Female. *Colour*: All dark, antennae dark; coxae (pro-, meso-, metacoxa) dark, dark, dark; femora (pro-, meso-, metafemur) pale, dark to paler at posterior end, dark; tibiae (pro-, meso-, metatibia) dark, dark, dark with lighter area anteriorly; tegula and humeral complex dark; pterostigma dark; fore wing veins pale proximally, dark distal to pterostigma. *Head*: Antennae approximately equal to body length; body length (head to apex of metasoma) 2.4–2.7 mm; ocular–ocellar line/posterior ocellus diameter 1.6–1.8; interocellar distance/posterior ocellus diameter 2.1–2.2. *Mesosoma*: Anteromesoscutum punctate, punctures not regularly sized and spaced over whole of anteromesocutum; mesoscutellar disc with several shallow punctures down lateral edges associated with setae; number of pits in scutoscutellar sulcus 10–12; maximum height of mesoscutellum lunules/maximum height of lateral face of mesoscutellum 0.4*. *Wings*: fore wing length 2.5–2.8 mm; length of veins r/2RS 1.4–1.7; length of veins 2RS/2M 1.3–1.6; length of veins 2M/(RS+M)b 0.8–0.9; pterostigma length/width 2.8–3.5. *Legs*: Metatibia inner spur length/metabasitarsus length 0.4–0.5. *Propodeum:* areola clearly defined in posterior half and lateral carinae clear and mostly straight, anterior part of areola and centre area with less well defined carinae but with irregular reticulate rugose and punctate sculpturing, rest of propodeum mostly smooth. *Metasoma*: T1 length/width at posterior margin 1.3*; T1 shape broad, rectangular, almost parallel–sided, very slightly broadening posteriorly; T1 sculpture irregularly reticulate rugose and punctate, sometimes with smoother area at posterior border with T2; T2 width at posterior margin/length 3.2*; T2 sculpture almost smooth, some very shallow sculpturing in anterior half and scattered shallow punctures associated with setae; T3 sculpture smooth and shiny; hypopygium with central membranous area mid-ventrally; ovipositor sheaths length/metatibial length 0.2–0.4. **Male.** As female, but with antennae longer than body length, propodeum smoother in centre of areola, anterior carinae of areola much more defined than in female, but with anterior end of areola still open with reticulate rugose sculpturing.

Etymology. This species is named for Dr Gary Taylor, who collected a paratype of this species plus many other microgastrine specimens on Bush Blitz expeditions, and who has provided author EPF-J with many hours of valuable advice both at the microscope and in the field. The species name is an invariable genitive.

Distribution. Currently only collected from central and western S Aust and northern WA.

Remarks. Measurements or ratios (indicated with an asterisk) were only able to be taken accurately on the holotype due to wing placement in the two paratypes, thus, there is likely more variation in these measurements than listed here. There is no *COI* or *WG* variation in

the specimens of this species listed and sequenced here, and the *COI* sequences are approximately 5% divergent from the nearest relative, and 4% divergent from the closest sequence on Genbank.

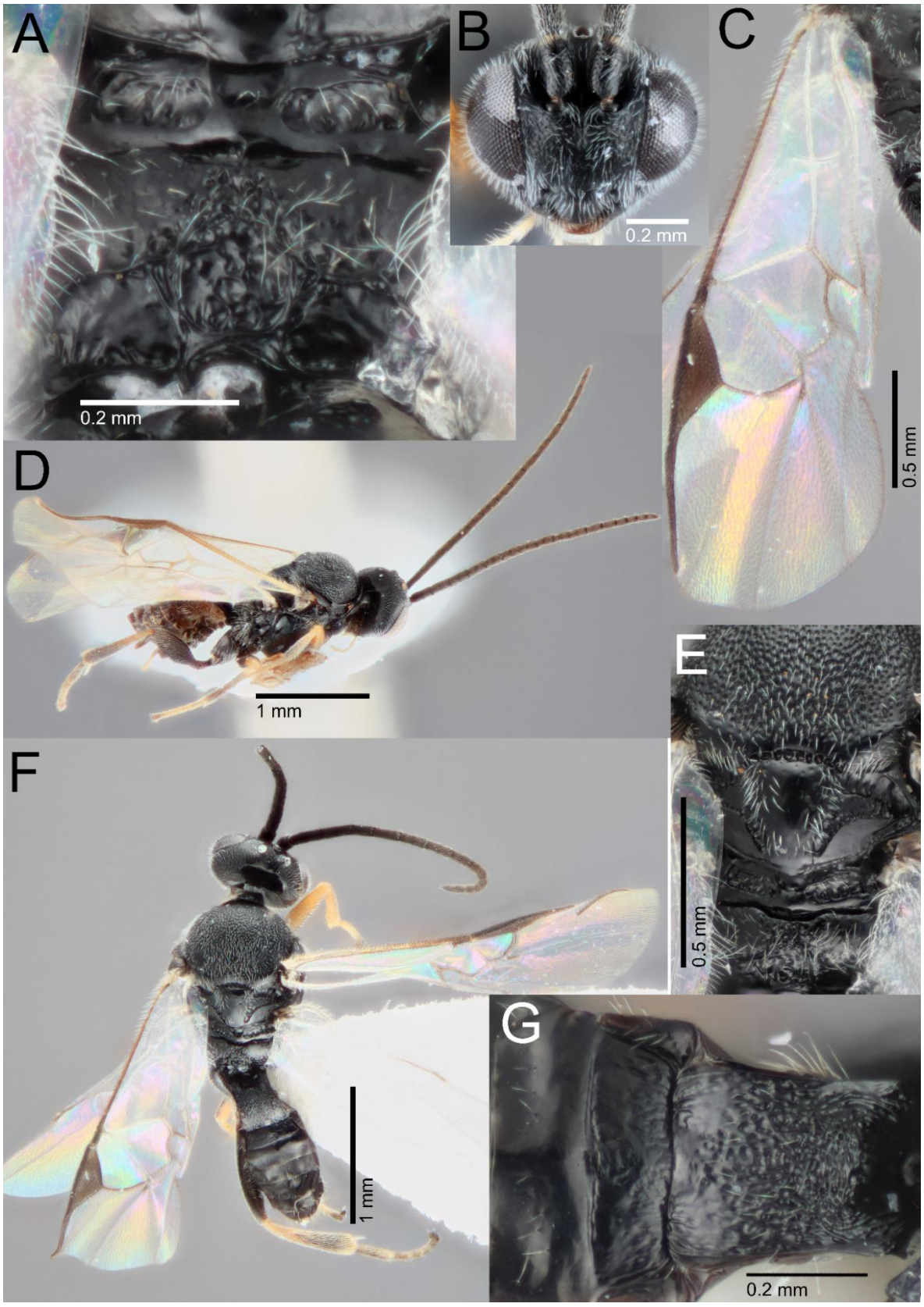

Figure 12: *D. garytaylori* holotype (A–C, E–G) paratype (D). A. propodeum; B. anterior head; C. fore wing; D. lateral habitus; E. mesosoma (part); F. dorsal habitus; G. T1–3.

***Dolichogenidea kelleri* Fagan-Jeffries & Austin sp. nov.**

(Fig. 13)

Material examined (including Genbank numbers of DNA barcodes). *Holotype.* f# Australia, S Aust, Bon Bon Stn, 30°37'34"S 135°24'11"E, 25–28/x/2010, S. Mantel, F.C., R. Kittel, G. Taylor, Bush Blitz Svy malaise 9 amongst *Senna artemisioides*, *Acacia tetragonophila*, *A. aneura*, & *A. victoriae* (SAMA 32-036130; Genbank *COI*: MH138911 *WG*: MH139346).*Paratypes.* f# Australia, S Aust, Great Victoria Desert Bush Blitz, 29°6'49"S 129°32'29"E, 23/ix/2017, E. Fagan-Jeffries, sweeping general vegetation, 250 m (SAMA: 32-035459; Genbank *COI*: MH138909 *WG*: MH139344). m# Australia, S Aust, Great Victoria Desert, Cook Road, -28.9684°S 130.0772°E to -29.0449°S 129.9475°E, 29/viii/2015, J.A. Forrest, R. Leijs, vehicle net (SAMA: 32-036131). 2m# Australia, S Aust, Great Victoria Desert, 29.453611°S 129.534722°E, 24/ix/2017, E. Fagan-Jeffries, sweeping *Senna artemisioides* (one in ethanol) (SAMA: 32-036132 pinned, SAMA: 32-036133 in ethanol). m#, Australia, S Aust, Great Victoria Desert, 29.176111°S 129.949722°E, 26/ix/2017, E. Fagan-Jeffries, sweeping *Dodonaea* sp. (SAMA: 32-036134).

Diagnosis. *Dolichogenidea kelleri* can be separated from *D. bonbonensis* by having a longer ovipositor (ovipositor sheaths equal in length to metatibia rather than shorter than metatibia), a narrower T1, and a less clearly defined propodeal areola. *Dolichogenidea kelleri* can be separated from *D. biroi*, *D. lipsis, D. ilione* and *D. tasmanica* by the absence of a white cheek blotch. *Dolichogenidea acratos, D. brabyi*, *D. hyposidrae*, *D. eucalypti*, *D. expulsa*, *D. garytaylori* and *D. orelia* all have ovipositor sheaths shorter than *D. kelleri*, less than half the length of the metatibia. *Dolichogenidea carposinae, D. coequata, D. cyamon, D. finchi, D. ilione, D. iulis, D. labaris, D. lobesiae*, *D. mediocaudata, D. miris*, *D. platyedrae, D. stantoni,* and *D. xenomorph* all have ovipositor sheaths longer than the metatibia, and clearly longer than that of *D. kelleri*. *Dolichogenidea hyblaeae* has ovipositor slightly longer than the metatibia, and a completely smooth propodeum with only a slight depression indicating the areola, whilst *D. kelleri* has the areola clearly defined in the posterior half. *D. inquisitor* also has ovipositor sheaths only slightly longer than the metatibia (ratio measured as 1.25 on holotype, description states 1.5), but can be separated by having a complete propodeal areola, which is strongly carinate anteriorly, opposed to the more indistinct anterior half of the areola in *D. kelleri*. *D. gentilis* and *D. heterusiae* both have strong carinae along the lateral margins of T1 which are absent in *D. kelleri*. *Dolichogenidea agonoxenae* is described as having a strongly formed propodeal areola and costulae, distinguishing this species from *D. kelleri*, which has a more indistinct areola with formed by small diverging carinae rather than a single strong carina. The description of *D.*

upoluensis was not clear enough to confirm any diagnostic differences, but we consider it almost certainly a distinct species based on the geographic location; *D. upoluensis* was bred from a leaf-roller on *Ficus* sp. in Samoa, whilst *D. kelleri* is from arid South Australia (Table 1).

Description. Female. *Colour*: All dark, antennae dark; coxae (pro-, meso-, metacoxa) dark, dark, dark; femora (pro-, meso-, metafemur) dark to paler at posterior end, dark to paler at posterior end, dark; tibiae (pro-, meso-, metatibia) pale, pale, pale in anterior half, dark in posterior half; tegula and humeral complex dark; pterostigma dark; fore wing veins pale proximally, dark distally. *Head*: antennae slightly shorter than body length; body length (head to apex of metasoma) 2.2–2.6 mm; ocular–ocellar line/posterior ocellus diameter 1.7–2.0; interocellar distance/posterior ocellus diameter 1.8–2.1. *Mesosoma*: Anteromesoscutum evenly and densely punctate; mesoscutellar disc with a few fine punctures associated with setae; number of pits in scutoscutellar sulcus 12–14; maximum height of mesoscutellum lunules/maximum height of lateral face of mesoscutellum 0.5–0.6. *Wings*: fore wing length 2.3–2.5 mm; length of veins r/2RS 1.3–1.7; length of veins 2RS/2M 1.0–1.3; length of veins 2M/(RS+M)b 0.8–1.1; pterostigma length/width 2.5–2.8. *Legs*: Metatibia inner spur length/metabasitarsus length 0.5. *Propodeum:* areola clearly defined in posterior half, anterior half less well defined, carinae forming anterior half of areola and lateral carinae formed of small diverging carinae rather than a single clear carina, areola open at anterior end, propodeum otherwise mostly smooth. *Metasoma*: T1 length/width at posterior margin 1.2–1.3; T1 shape broad, rectangular, almost parallel-sided; T1 sculpture rugose with irregularly shaped punctures, longitudinal strigosity or rugosity in posterior half, smoother area centrally; T2 width at posterior margin/length 3.5–4.0; T2 sculpture almost smooth, some sparse punctures associated with setae; T3 sculpture smooth and shiny; hypopygium with central membranous area mid-ventrally; ovipositor sheaths length/metatibial length 1.0. **Male.** As female, but with antennae longer than body, T1 and T2 slightly longer relative to width.

Etymology. This species is named for Professor Mike Keller, who hosted author EPF-J as part of the 'CSIRO Student Research Project' many years ago, and helped inspire a high school student to a career in entomology. The species name is an invariable genitive.

Distribution. This species is currently only known from the arid zone of central South Australia.

Remarks. The measurement of the ovipositor sheaths length was made difficult by the highly curved sheaths of the holotype, and the missing sheaths in the paratype. This species is closely related to *D. bonbonensis* based on both morphological and molecular evidence. The *WG* sequences of these two species differ by only 1–3 bp, however, the *COI* sequences

are at least 10% different, far above the 2% divergence often used for species delimitation in the microgastrines. Morphologically there are also clear differences that can be used to separate the two species (see diagnosis). No information is known about possible host species.

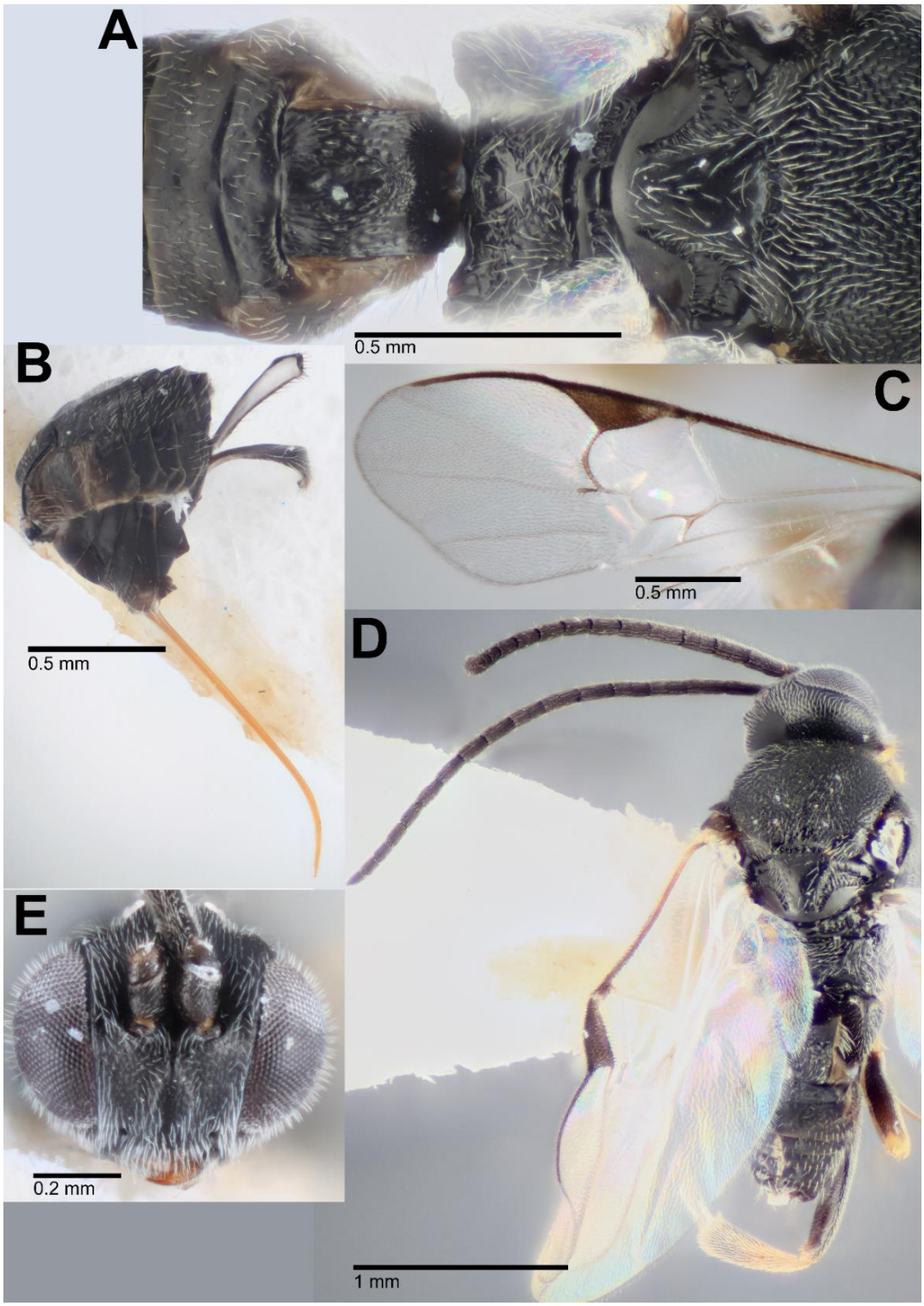

Figure 13: *Dolichogenidea kelleri* A. holotype, dorsal mesosoma and metasoma (part); B. holotype, lateral metasoma; C. paratype, fore wing; D. paratype, dorsal habitus; E. holotype, anterior head.

***Dolichogenidea lobesiae* Fagan-Jeffries & Austin sp. nov.**

(Fig. 14)

Material examined (including Genbank numbers of DNA barcodes). *Holotype.* f# Australia, Qld, Tolga, Costa Berries Rangeview, 243 Marnane Road (Rocky Creek locality), 30.ix.2017, -17.193 145.438, J. Cheesman, ex. *Lobesia physophora* on blueberries. *Paratypes.* 2f#, same data as holotype. 2m#, same data as holotype.

Diagnosis. Of the currently described species from Australia, *D. lobesiae* most closely resembles *D. miris*, but can be separated by having a broadening T1 whilst *D. miris* has T1 almost parallel-sided, and by having a clearly curved vein r in the fore wing, whilst in *D. miris* it is much straighter. *Dolichogenidea lobesiae* can be separated from *D. biroi*, *D. lipsis, D. ilione* and *D. tasmanica* by the absence of a white cheek blotch. *Dolichogenidea brabyi, D. hyposidrae*, *D. eucalypti, D. expulsa*, *D. garytaylori* and *D. orelia* all have ovipositor sheaths much shorter than the metatibia, *D. bonbonensis* and *D. acratos* have ovipositor sheaths slightly shorter than the metatibia and *D. kelleri, D. gentilis* and *D. heterusiae* have sheaths approximately equal to the metatibia. All these species can be easily distinguished from *D. lobesiae*, which has an ovipositor approximately 1.3 x longer than the metatibia. *Dolichogenidea coequata, D. cyamon, D. finchi*, *D. ilione*, *D. labaris*, *D. mediocaudata, D. platyedrae* and *D. xenomorph* all have ovipositor sheaths longer than 1.5 x the metatibia, and thus can be differentiated from *D. lobesiae* which has ovipositor sheaths 1.2–1.4 x the metatibia. In addition, *D. gentilis, D. mediocaudata, D. finchi and D. xenomorph* have the propodeal areola poorly defined, whilst *D. lobesiae* has a clearly carinate areola. *Dolichogenidea iulis* can be separated by T1 sculpturing (T1 in *D. iulis* is punctate, becoming strigate in the posterior one-third opposed to reticulate rugose sculpturing in *D. lobesiae*) and general body colouration; *D. iulis* has the metasoma all black, and the hind legs dark. *Dolichogenidea carposinae* and *D. inquisitor* also possess an all dark metasoma, opposed to the lighter orange colouration of *D. lobesiae*, and, in addition, *D. carposinae* has punctate propodeal sculpturing opposed to the nearly smooth propodeum of *D. lobesiae*, while *D. inquisitor* has punctate sculpturing on T1 opposed to the reticulate rugose sculpturing of *D. lobesiae*. *Dolichogenidea agonoxenae* and *D. upoluensis* are both described as having a rugose propodeum, which separates these species from *D. lobesiae*, which has a mostly smooth propodeum (other than the areola and lateral carinae). *Dolichogenidea hyblaeae* can be separated by the presence of rugosity on the propodeum near the lateral carinae, opposed to the smooth propodeum of *D. lobesiae*. It should be noted that the co-types of *D. hyblaeae* from Java differ in the form of the propodeum compared to the holotype from Samoa; the propodeum of the co-types is smooth with the areola indicated by a depression,

and weak posterior carinae, and are, therefore, also easily distinguished from the propodeum of *D. lobesiae.* Based on what we currently know about the expected level of morphological variation in *Dolichogenidea*, we suspect that the paratypes of *D. hyblaeae* from Java are a different species to the holotype. *Dolichogenidea lobesia* resembles *D. stantoni* in ovipositor length, propodeum and general body form and colouration, but it can be distinguished by the fore wing r vein, which is curved in *D. lobesiae* and straight, meeting vein 2RS at an approximately 145° angle in *D. stantoni* (Table 1).

Description. Female. *Colour*: Dark except for orange to light brown sclerites and areas of posterior tergites; antennae dark; coxae (pro-, meso-, metacoxa) orange, orange, orange; femora (pro-, meso-, metafemur) orange, orange, orange with darker area posteriorly; tibiae (pro-, meso-, metatibia) orange, orange, orange with darker area posterioirly; tegula and humeral complex dark; pterostigma dark; fore wing veins dark. *Head*: Antennae similar length to body length; body length (head to apex of metasoma) 1.9–2.2 mm; ocular–ocellar line/posterior ocellus diameter 1.7–2.0; interocellar distance/posterior ocellus diameter 1.8–2.1; no white cheek/gena spot. *Mesosoma*: Anteromesoscutum evenly and densely punctate; mesoscutellar disc mostly smooth, sparsely covered in fine setae; number of pits in scutoscutellar sulcus 12–13; maximum height of mesoscutellum lunules/maximum height of lateral face of mesoscutellum 0.5. *Wings*: fore wing length 2.3–2.7 mm; length of veins r/2RS 1.7–2.3; length of veins 2RS/2M 0.8–0.9; length of veins 2M/(RS+M)b 1.2–1.5; pterostigma length/width 2.6–2.8. *Legs*: Metatibia inner spur length/metabasitarsus length 0.4–0.5. *Propodeum*: almost complete hexagonal areolet, carina forming anterior side of hexagonal missing so that areola is open anteriorly, strong straight lateral carinae present, rest of propodeum mostly smooth with some reticulate rugose sculpturing in anterior half and small carinae emerging from posterior boundary approximately a third of the distance from lateral edge to centre. *Metasoma*: T1 length/width at posterior margin 1.0–1.2; T1 shape broad, broadening slightly posteriorly, T1 sculpture irregularly reticulate rugose; T2 width at posterior margin/length 4.5–5.2; T2 sculpture rugose with crenulate margin at border with T3; T3 sculpture smooth and shiny; hypopygium with membranous area mid-ventrally; ovipositor sheaths length/metatibial length 1.2–1.4. **Male.** As female, although antennae longer than body and T2 sculpturing much less defined.

Etymology. This species is named for the host, *Lobesia physophora* (Lower, 1901) (Tortricidae), a significant pest of blueberries in Australia, and could be a key parasitoid for its control (Ian Newton, pers. com.). The species name is an invariable genitive.

Distribution. Currently this species is only known from the type locality, Tolga, north Queensland.

Remarks. The host, *L. physophora*, is also recorded from the Solomon Islands (Bradley, 1955) and possibly from Papua New Guinea (BOLD, data not publically released). A single *COI* barcode of *D. lobesiae* was sequenced, which is at least 7% divergent from the nearest relative, and from any sequences on Genbank.

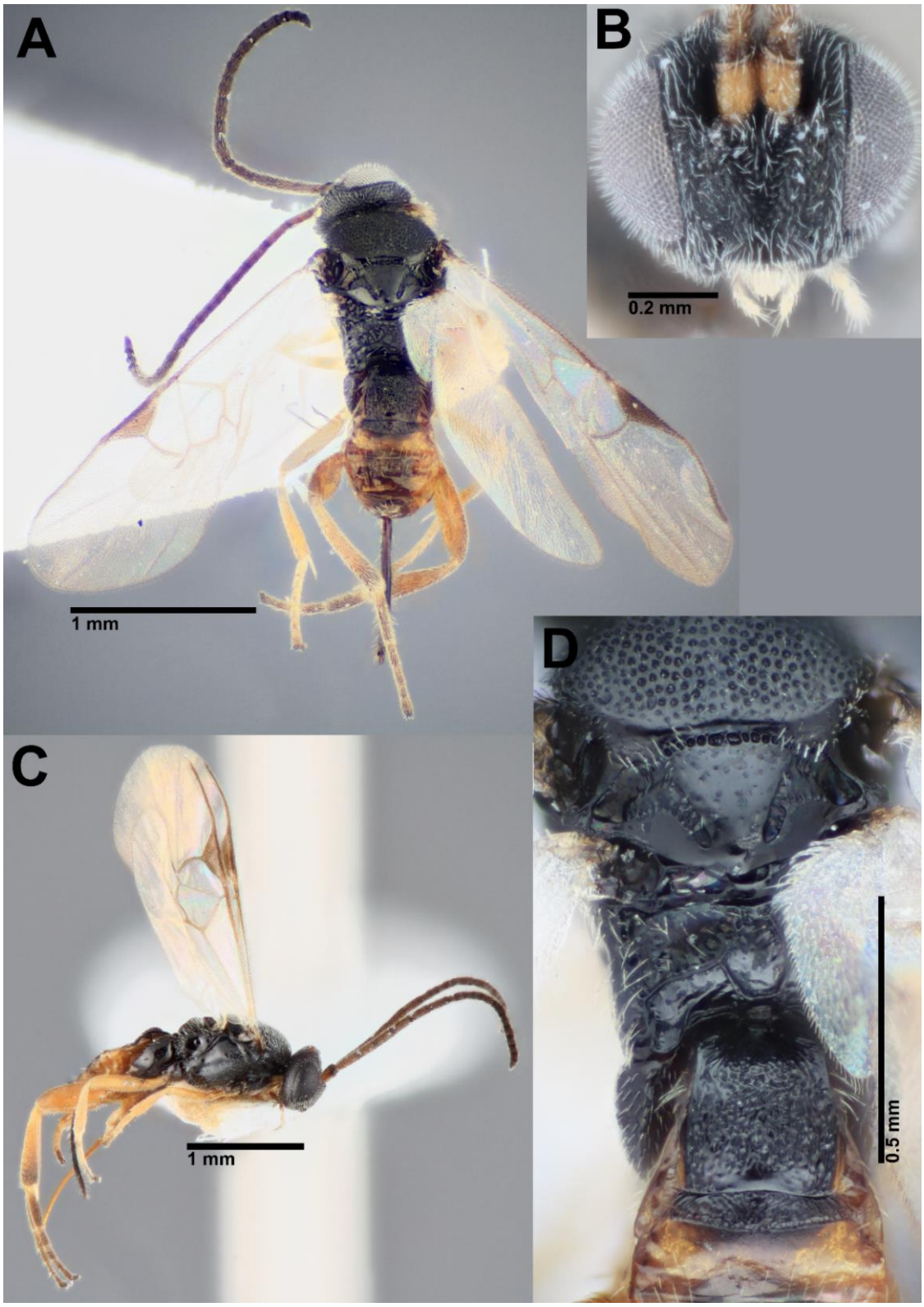

Figure 14: *D. lobesiae* A. holotype, dorsal habitus; B. holotype, anterior head; C. paratype, lateral habitus; D. holotype, dorsal meso- and metasoma (in part).

***Sathon* Mason, 1981**

Sathon Mason 1981: 78; Williams 1988: 540. Austin & Dangerfield 1992: 52. Type species: *Apanteles neornexicanus* Muesebeck, 1920, by original designation.

Diagnosis. *Sathon* is characterised by a large, inflexible hypopygium without striae midventrally, ovipositor sheaths at least half as long as metatibia, propodeum lacking an areola and either with a complete longitudinal carina or carina reduced or absent, anterior margin of the metanotum with reduced lateral lobes, and the postero-lateral phragma of the scutellum exposed. Species have been described in the genus with fore wing areolet both present and absent, but currently all described species from Australia have a fore wing areolet present.

Remarks. There are only four species described in this genus from Australia: *S. albicoxus* Austin and Dangerfield (1992), *S. moratus* (Wilkinson 1929), *S. naryciae* Austin and Dangerfield (1992), and *S. resplendens* (Wilkinson 1929), and one species (*S. belippae*) recorded from Fiji, although this may be a misidentification (Austin and Dangerfield 1992). The genus in Australia appears to be solely represented by species with a large fore wing areolet, and appears to be polyphyletic in regard to the lineage of *Choeras* that also has a large fore wing areolet (Fig. 1). See Fagan-Jeffries and Austin (2017) for further discussion on the relationship between these genera. There are only 14 species described worldwide (Yu *et al.* 2016), and limits of the genus are not well resolved.

***Sathon oreo* Fagan-Jeffries & Austin sp. nov.**

(Fig. 15)

Material examined (including Genbank numbers of DNA barcodes). *Holotype:* f# Australia, S Aust, Mt Billy Con. Pk. Fleurieu Peninsula, 25/x/2000, C. Stephens, malaise trap in bridal creeper invaded eucalypt woodland (SAMA: 32-036135; Genbank *COI*: MH138935). *Paratypes:* f# Australia, S Aust, Mt Billy Con. Pk. Fleurieu Peninsula, 25/x/2000, C. Stephens, malaise trap in bridal creeper invaded eucalypt woodland (SAMA: 32-036136; Genbank *COI*: MH138944; in ethanol). f# Australia, S Aust, Mt Billy Con. Pk. Fleurieu Peninsula, 12/x/2000, C. Stephens, malaise trap in bridal creeper invaded eucalypt woodland (SAMA: 32-036137; Genbank *COI*: MH138932). f# Australia, S Aust, Mt Billy Con. Pk. Fleurieu Peninsula, 25/x/2000, C. Stephens, malaise trap in bridal creeper invaded eucalypt woodland (SAMA 32-036138; Genbank *COI*: MH138937). f# Australia, S Aust, Mt Billy Con. Pk. Fleurieu Peninsula, 35°27'13"S 138°36'22"E, 20/x/2016–05/xi/2016, E. Fagan-

Jeffries, malaise trap (SAMA: 32-036139; Genbank *COI*: MH138799). f# Australia, S Aust, Mt Billy Con. Pk. Fleurieu Peninsula, 35°27'13"S 138°36'22"E, 05/xi/2016–20/xi/2016, E. Fagan-Jeffries, malaise trap (SAMA: 32-036140; Genbank *COI*: MH138798; in ethanol). f# Australia, S Aust, Mt Billy Con. Pk. Fleurieu Peninsula, 25/x/2000, C. Stephens, malaise trap in native plot within bridal creeper invaded eucalypt woodland (SAMA: 32-036141; Genbank *COI*: MH138843). f# Australia, S Aust, Mt Billy Con. Pk. Fleurieu Peninsula, 25/x/2000, C. Stephens, malaise trap in native plot within bridal creeper invaded eucalypt woodland (SAMA: 32-036142; Genbank *COI*: MH138842). f# Australia, S Aust, Mt Billy Con. Pk. Fleurieu Peninsula, 25/x/2000, C. Stephens, malaise trap in native plot within bridal creeper invaded eucalypt woodland (SAMA: 32-036143; Genbank *COI*: MH138915; in ethanol). f# Australia, S Aust, Mt Billy Con. Pk. Fleurieu Peninsula, 25/x/2000, C. Stephens, malaise trap in native plot within bridal creeper invaded eucalypt woodland (SAMA: 32-036144; Genbank *COI*: MH138914 in ethanol). f# Australia, Vic, Grampians Bioscan site 426, Strachans Camp Ground near interesction Sawmill Track, Glenelg River Road, and Jensens Road, 37°22'32"S, 142°16'57"E, 24/xi/2012, P. Lillywhite & B. Patullo malaise trap GRB426 (MV: HYM-61363; Genbank *COI*: MH138844). f# Australia, Vic, Grampians Bioscan site 407, Mount Difficult Road, between two intersections with Longpoint Track, 37°02'02"S, 142°28'02"E, 19–23/xi/2012, M.Mackenzie, P. Lillywhite, J. Grubb, K. Pawley, malaise trap GRB407 (MV: HYM-61361; Genbank *COI*: MH138845 *WG*: MH139294). f# Australia, Vic, Grampians Bioscan site 406, 37°03'41"S 142°22'50"E, 19/xi/2012, J. Grubb, M. Mackenzie, P. Lillywhite, K. Pawley, malaise trap, Cooinda Burrong Scout Camp, basecamp and surrounds (MV: HYM-61362; Genbank *COI*: MH138852; in ethanol). f# Australia, ACT, Canberra, Black Mtn, Behind CSIRO, 35°16'S 149°06'E, 23/ix/2002–31/x/2002, C. Lambkin (ANIC: 32 130223; Genbank *COI*: MH138874). f# Australia, ACT, Canberra, Black Mtn, Behind CSIRO, 35°16'S 149°06'E, 23/ix/2002–31/x/2002, C. Lambkin (ANIC: 32 130224; Genbank *COI*: MH138875). f# Australia, ACT, Canberra, Black Mtn, Behind CSIRO, 35°16'S 149°06'E, 23/ix/2002–31/x/2002, C. Lambkin (ANIC: 32 130225; Genbank *COI*: MH138877 in ethanol). f#, Australia, Vic, Otway Ranges, Melba Gully, 4/ii/90, R. Wharton. f#, Australia, S Aust, Fleurieu Peninsula, Deep Creek Cons. Pk., 7–21/ii/90, malaise trap, J. Bracken & R. Wharton (WINC). f#, Australia, ACT, Black Mountain CSIRO land, malaise trap, 9–14/xi/91, Austin & Dangerfield (WINC). f#, Australia, S Aust, Ferries Macdonald Cons. Pk., 1–14/i/96, malaise trap. J. Jennings (WINC).

Diagnosis. The thick white stripe on the antennae of the female easily separates this species from the other species of *Sathon* described from Australasia.

Description. Female. *Colour:* Dark except for nonsclerotised areas around T–3 and sternites which are often a striking white; antennae dark other than flagellomeres 6–7

which are white; coxae (pro-, meso-, metacoxa) pale, pale, dark; femora (pro-, meso-, metafemur) dark with paler area posteriorly, dark, dark; tibiae (pro-, meso-, metatibia) dark, dark, dark; tegula and humeral complex light brown; pterostigma dark; fore wing veins dark. *Head*: Antennae slightly longer than body length; body length (head to apex of metasoma) 2.4–2.9 mm; ocular–ocellar line/posterior ocellus diameter 2.3–2.5; interocellar distance/posterior ocellus diameter 1–1.4. *Mesosoma*: Anteromesoscutum evenly and densely punctate; mesoscutellar disc with numerous shallow punctures associated with setae; number of pits in scutoscutellar sulcus 8–14; maximum height of mesoscutellum lunules/maximum height of lateral face of mesoscutellum 0.2–0.3. *Wings*: fore wing length 2.5–3.0 mm; length of veins r/2RS 0.5–0.7; length of veins 2RS/2M 1.0; length of veins 2M/(RS+M)b 0.9–1.2; pterostigma length/width 2.5–2.8, areolet large, enclosed, vein r-m unpigmented. *Legs*: Metatibia inner spur length/metabasitarsus length 0.3–0.4. *Propodeum:* reticulate rugose, with very short medial longitudinal carina at anterior end, often diverging carinae from this medial carina that appear to form the anterior half of an areola, and diverging carinae from posterior centre also give the impression of an areola, but these carinae often indistinguishable from other sculpturing, often smooth sections at anterior corners. *Metasoma*: T1 length/width at posterior margin 2.7–3.3; T1 clearly narrowing posteriorly, mostly smooth but often with faint longitudinal branching carinae; T2 width at posterior margin/length 2–2.6, T2 with no clear sculpturing, but not completely smooth; T3 sculpture smooth and shiny; hypopygium with completely membranous area midventrally; ovipositor sheaths length/metatibial length 0.5–0.6. **Male:** known only from photograph on BOLD, antennal segments all dark.

Etymology. This species is named for the brown antennae with a thick white stripe caused by the white flagellomeres 6–7 resembling the brown-white-brown colouration pattern of the Oreo cream-centred chocolate biscuits. The species name is a noun in apposition.

Distribution. This species appears to occur in large numbers in specific areas of the country, including in South Australia, Victoria, and at Black Mountain, Canberra. There is also an associated BOLD sequence (see below) that extends the distribution to Tasmania (Fig. 16)

Remarks. In this species we also tentatively place the following seven specimens, which have been sequenced for the *COI* barcoding region by the Biodiversity Institute of Ontario, are stored in the Centre for Biodiversity Genomics, and are publically available on the BOLD. The *COI* barcoding region is less than 1.2% divergent between these specimens and the others detailed above, and available images of these specimens agree in general morphology and possess the distinctive white band on the antennae. BOLD numbers:

ASQAS157-11 (Australia), MCCAA2641-12 (ACT), HYAT465-11 (Tas), MCCAA1444-12 (ACT), ASQAS156-11 (Australia), CNBAN190-13 (ACT), MCCAA1052-12 (ACT).

White bands on the antennae of females are not common in the Microgastrinae, but have been reported for *Apanteles taeniaticornis* Wilkinson (1928) from Java with the 9th–12th flagellomeres reported as cream-white, *Diolcogaster duocolor* Gupta and Fernández-Triana (2015) from India with flagellomeres 5–7 white, *Diolcogaster laetimedia* Zeng and Chen (2011) from China, with 3–4 white flagellomeres medially in the antennae, *Diolcogaster robertsi* Saeed *et al.* (1999) from Australia with flagellomeres 5–8 white, the South African *Exulonyx camma* (Nixon, 1965) with flagellomeres 5–6 with a white band, and in *Pseudapanteles alfiopivai* Fernández-Triana and Whitfield (2014) from Costa Rica, which has flagellomeres 4–8 white-yellow. White bands also occur in many species of Ichneumonidae, and in a few other groups of braconids (Quicke 2015). The function of these white bands is not known, although suggestions include possible involvement in providing visual feedback of antennal separation (Quicke 2015).

Figure 16: Known distribution of *Sathon oreo*

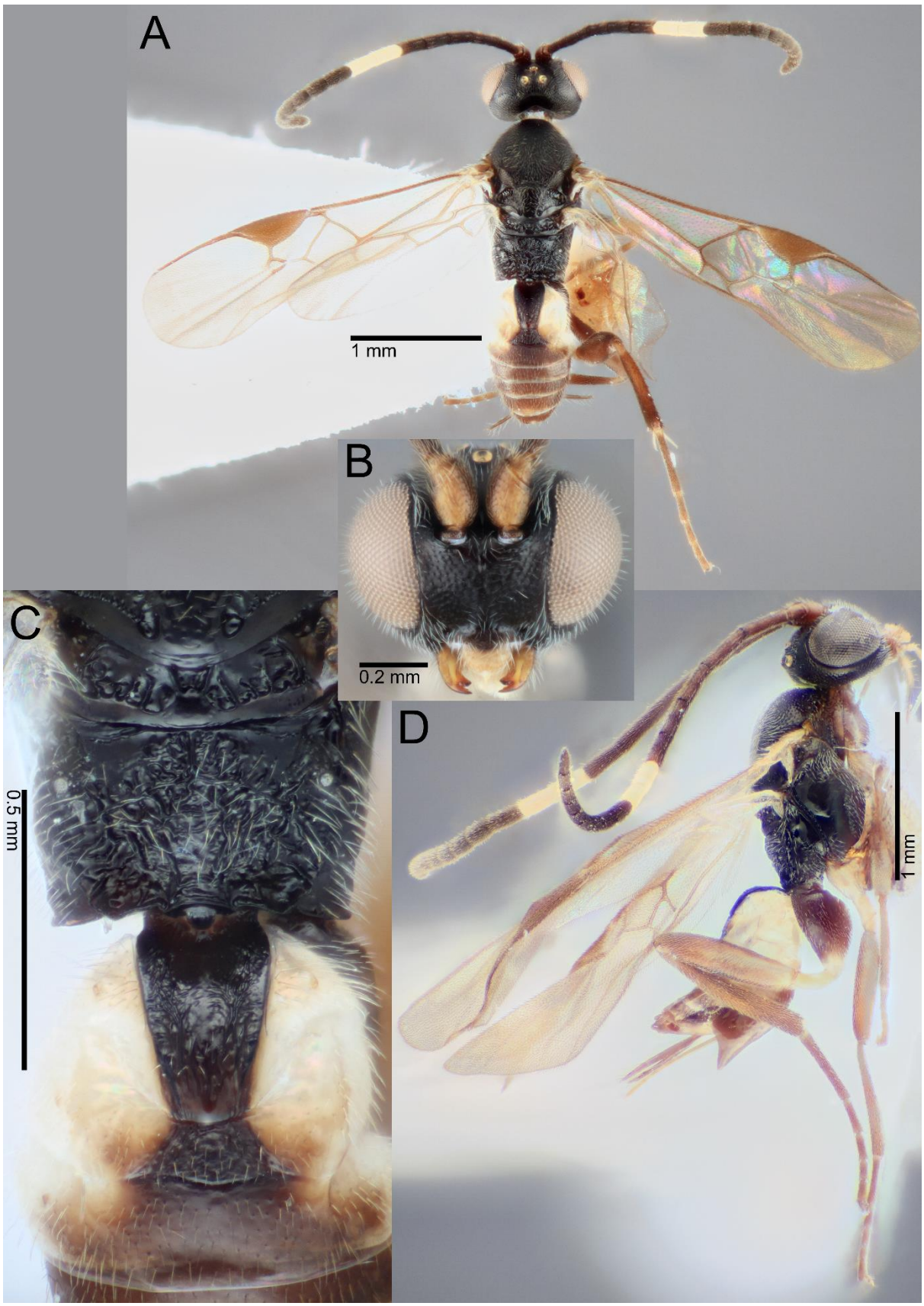

Figure 15: *S. oreo* A–C: holotype; D: paratype. A. dorsal habitus; B. anterior head. C. metanotum, propodeum and T1–3; D. lateral habitus.

Table 1. Summary of distinguishing characters for Australasian species of *Dolichogenidea*. * = type locality.

Dolichogenidea sp.	Distribution	White cheek blotch	Propodeal areola	Propodeal sculpturing	T1 length/width at posterior margin	T1 sculpture	T1 shape	T2 sculpture	Ovipositor sheath length/metatibia length	Comments
Australian spp.										
biroi (Szepligeti 1905)	Australia (NSW)	present					parallel-sided			Type not seen, description used, "ovipositor as long as abdomen"
bonbonensis sp. nov.	Australia (SA, WA)	absent	clearly defined, lateral carinae present	mostly smooth, some reticulate rugose sculpturing antero-medially	1.1-1.2	rugose with irregularly shaped punctures	almost parallel-sided	almost smooth, sparse punctures	0.7-0.9	
brabyi sp. nov.	Australia (ACT)	absent	clearly defined in posterior half, partially defined in anterior half, lateral carinae present	anterior half with shallow punctate sculpturing which is more pronounced antero-medially, posterior half and centre of areola mostly smooth	1.2	reticulate rugose with occasional irregularly shaped punctures	slightly broadening posteriorly	shallow sculpture, line of pits and ridges at border with T3	0.4	
eucalypti Austin & Allen 1989	Australia (SA)	absent	clearly defined, lateral carinae present	anterior half mostly smooth, posterior half with faint rugose-punctate sculpturing	1.1	mostly punctate, striate-punctate along lateral margins	slightly broadening posteriorly	mostly smooth, faint scattered punctures	0.2	
finchi Fagan-Jeffries & Austin 2018	Australia (NSW, Qld, WA, Vic)	absent	only indicated by smoother area medially and short	rugose sculpturing in posterior half	1.2–1.8	mostly smooth with sparse punctures associated with short	almost parallel-sided	smooth and shiny, few shallow punctures	2.9 – 3.9	

			carinae diverging from postero-medial margin, lateral carinae absent			setae on lateral sides of posterior half		associated with setae	
forrestae sp. nov.	Australia (SA)	absent	only indicated by slight depression and area of rugosity postero-medially and multiple short diverging carinae posteriorly, lateral carinae absent	generally smooth, scattered shallow punctures	1.2	punctate	broad, almost parallel-sided	almost smooth	0.6
garytaylori sp. nov.	Australia (SA, WA)	absent	clearly defined in posterior half, anterior half with less well-defined carinae, lateral carinae present	irregular reticulate rugose and punctate sculpturing antero-medially and within areola, otherwise smooth	1.3	irregularly reticulate rugose and punctate	broad, almost parallel-sided	almost smooth, some shallow sculpturing in anterior half and scattered shallow punctures	0.2-0.4
hyposidrae (Wilkinson 1928)	Australia (Qld), New Guinea, New Britain (also Java*, India, Burma, Malay peninsula)	absent	clearly defined, lateral carinae present	mostly smooth, some rugose sculpturing antero-medially	1.5	longitudinally strigose in posterior half	slightly broadening posteriorly	almost smooth	0.1
kelleri sp. nov.	Australia (SA)	absent	clearly defined in posterior half, anterior half less well-defined with carinae, or areola and lateral carinae formed by small diverging carinae	mostly smooth	1.2-1.3	rugose with irregularly shaped punctures	broad, almost parallel-sided	almost smooth, sparse punctures	1

lobesiae sp. nov.	Australia (Qld)	absent	clearly defined, lateral carinae present	mostly smooth with some reticulate rugose sculpturing in anterior half	1-1.2	irregularly reticulate rugose	broad, slightly broadening posteriorly	rugose with crenulate margin at border with T3	1.2-1.4	
lipsis (Nixon 1967)	Australia (WA)	present	not well-defined, lateral carinae absent	mostly smooth, punctate sculpturing		mostly smooth, some punctures	almost parallel-sided	mostly smooth	1.5	
mediocaudata Fagan-Jeffries & Austin 2018	Australia (NSW)	absent	only indicated by central depression, lateral carinae absent	deep non-uniform punctures, posterior half with rugose sculpturing	1.6	rugose sculpturing	broad, almost parallel-sided	smooth	1.8	
miris (Nixon 1967)	Australia (ACT)	absent	clearly defined, lateral carinae present	some rugose sculpturing in posterior half, anteriorly		longitudinally strigose in posterior half, some general rugosity medially	almost parallel-sided	faintly sculptured	1.5	propodeum partly hidden by wings
tasmanica (Cameron 1912)	Australia (Tas*, Vic, ACT, Qld), New Zealand	present	Indicated by strong depression in centre	Strongly rugose in posterior half, punctate in anterior half.	1.6	ruogse, reticulate rugose	parallel-sided	mostly smooth, shallow punctures	1.6 but damaged	Some characters described from non-type specimens
xenomorph Fagan-Jeffries & Austin 2018	Australia (NSW, WA)	absent	only indicated by smoother area in centre of propodeum and short carinae diverging from centre posterior margin, lateral carinae absent	sparse punctures associated with setae	1.1-1.4	mostly smooth with sparse punctures associated with short setae on lateral sides of posterior half	broad, almost parallel-sided	smooth	3.7-4.2	
Non-Australian spp.										
acratos (Nixon 1967)	New Guinea	absent	complete, lateral carinae present	rugose		rugose with some longitudinal elements	parallel-sided	longitudinally strigose	0.5	wings obscuring T1
agonoxenae (Fullaway 1941)	Samoa*, Tonga, introduced into Fiji, Hawaii	absent	complete, lateral carinae present	rugose		rugose	"little wider at apex than base"	rugose		type not seen, description used. "ovipositor sheaths longer than basitarsus, almost as long as femora"

carposinae (Wilkinson 1938)	New Zealand	absent	complete but carinae small and indistinct due to surface sculpture	rugose-punctate, becoming smoother posteriorly	1.3	rugose-punctate	parallel-sided	rugose-punctate	1.4	
coequata (Nixon 1967)	Niue	absent	complete, lateral carinae indistinct due to surface sculpturing	moderately densely rugose-punctate	1.6	with dense fine granulate sculpture becoming longitudinally strigose laterally	margins slightly convex	mostly smooth	2	
cyamon (Nixon 1967)	Vanuatu	absent		at least partly rugulose		rugulose	margins slightly convex	mostly smooth with faint striae	1.9	4 specimens on one card; holotype ovipositor hidden so measured on paratype, wings obscuring propodeum and T1
expulsa (Turner 1918)	Fiji*, Samoa (also Marquesas Is., Ceylon).	absent	complete, lateral carinae present	mostly smooth	1	densely rugulose	margins evenly diverging so much broader posteriorly	densely rugulose	0.5	
gentilis (Nixon 1967)	New Guinea*, New Britain, Solomon Is (Banika Is)	absent	complete, lateral carinae difficult to discern due to surface sculpturing	coarsely carinate-rugulose	1	rugulose with some longitudinal elements	slightly convex, margins with prominent flange-like carina	strigose	0.9	"Fullaway (1957) is the only record of this species occurring in Fiji...this may be based on a misidentification and the species may not occur in the Australasian region." (Austin and Dangerfield 1992)
heterusiae (Wilkinson 1928)	Fiji (also Ceylon*, India, Taiwan and China)	absent	complete, lateral carinae present	mostly rugulose, smoother inside areola		rugulose -punctate	broadening posteriorly, margins with prominent flange like carina	strigose	1	holotype damaged, metasoma missing
hyblaeae (Wilkinson 1928)	Samoa, Opolu Is.*, Fiji (also Java, Malay peninsula).	absent	Complete, lateral carinae difficult to discern due to surface sculpturing	rugulose						metasoma missing from holotype, “ovipositor sheaths about as long as the hind tarsus”

ilione (Nixon 1967)	Fiji	present	complete, partially indistinct due to surface sculpture	coarsely rugulose	1.1	rugose -punctate	T1 broadening posteriorly	rugose strigate laterally, smoother medially	1.5	
inquisitor (Wilkinson 1928)	Fiji (also peninsula Malaysia* and China)	absent	complete, lateral carinae present	mostly smooth	1.3	punctate, becoming strigate in posterior 1/3	virtually parallel-sided	smooth in medial 2/3, partly rugose laterally	1.2	
iulis (Nixon 1967)	New Guinea	absent	complete, lateral carinae present	sparsely punctate in anterior part, becoming smoother posteriorly, smooth inside areola	1.4	punctate, becoming strigate in posterior 1/3			1.4	
labaris (Nixon 1967)	Fiji	absent	complete, lateral carinae present			punctate	virtually parallel-sided	rugose punctate, smooth medially	2.6	areola and T1 partly hidden by wings
orelia (Nixon 1967)	Fiji	absent	complete, lateral carinae present	surface coarsely rugose	0.7	rugulose	strongly broadened posteriorly	rugulose, more strigate laterally	0.4	
platyedrae (Wilkinson 1928)	Fiji	absent				Punctate but smoother in posterior 1/3?	parallel-sided	moderately smooth, faint sculpturing	1.8	propodeum and T1 obscured by wings
stantoni (Ashmead 1904)	New Britain, Fiji, Philippines*, India *synonym, China, peninsula Malaysia	absent	complete, lateral carinae present	smooth	1.5	irregularly reticulate rugose in anterior half, becoming longitudinally strigose in posterior half	parallel-sided	mostly smooth, very faint striate sculpturing	1.3	
upoluensis (Fullaway 1941)	Samoa	absent	"indistinctly formed areola and costulae, of which the carinae are very weak"	rugose				smooth		Holotype male not seen

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Chapter 7: General discussion

The overarching aim of this project was to improve the understanding and knowledge of Australian microgastrine biodiversity, and to provide descriptions of new species for an economically and environmentally important group of specious, yet morphologically conservative parasitoid wasps. With many large genera having cosmopolitan distributions, and a clear understanding of the relationships between genera eluding researchers even after decades of work (Whitfield *et al.* 2018), it can be challenging for short-term projects to make a significant contribution to this colossal group. Despite the complexity and diversity of the subfamily, this study has provided a wealth of new information about the microgastrine fauna of the continent; high-throughput DNA barcoding has been conducted for the first time for this group in Australia, providing species delimitation hypotheses and revised biodiversity estimates; integrative taxonomy has been used to describe 15 new species in three genera, and novel information on the use of *ITS2* as a species delimitation marker has been documented.

Biodiversity estimates, locality sampling and the importance of museum ethanol collections

Over 1,000 microgastrine specimens were used in this study, with nearly 800 undergoing DNA extraction and nearly 600 successfully sequenced for the *COI* barcoding region. All of these specimens came from ethanol storage, but only a small proportion were collected during field work as part of this project. Most of the specimens came from museum ethanol collections, often from bulk Hymenoptera vials or unsorted Malaise traps. The importance of these bulk, unpinned collections are often undervalued, but are a vital resource for projects like this that seek to achieve the most complete sampling across as large a geographic region as possible. As different species of microgastrines are likely to be abundant at different times of the year, and with the diversity of habitats that exist across Australia, accessing years and sometimes decades of sampling by different researchers was critical to the success of the DNA barcoding component of this study.

Whilst a surprisingly broad expanse of the continent was represented in the specimen localities, dense sampling was highly skewed towards a few locations surrounding the capital cities, particularly Adelaide, South Australia. In addition to the limited sampling, over 60% of the species delimited in this study using molecular data were represented by single specimens, indicating that a large amount of biodiversity is yet to be recorded. The presence of singletons is not an uncommon occurrence in arthropod surveys, however, the 60% of singletons found in this study is double the average number found in tropical arthropod surveys (Coddington *et al.* 2009), indicating that there was significant under-sampling present. Rare species are likely to be a real phenomenon, with various

mechanisms underlying the differences in abundance (Kunin and Gaston 1993), and some of the singletons in the dataset are likely to be true rare species, rather than an artefact of limited sampling.

Species abundances in a habitat are expected to follow a log normal distribution. However, in large assemblages there are often more rare species than would be expected, possibly either because of the presence of both persistent species biologically associated with the habitat and occasional species which have different habitat requirements (Magurran and Henderson 2003) or because of sampling artefacts associated with accumulating repeated small samples (McGill 2003). Rare species often have small distributions, and therefore are of high conservation priority, but are often under-sampled (Blackburn and Gaston 2009; Beck *et al.* 2018). Large numbers of rare species in a biodiversity survey can cause significant issues in statistically estimating species richness (Mao and Colwell 2005) and in delimitating species (Lim *et al.* 2012). A statistical study on tropical arthropod inventories suggests drastically greater sampling intensity is required for realistic species richness evaluations (Coddington *et al.* 2009), and that combining multiple collection methods will be needed to achieve species accumulation curves that approach a plateau (Longino *et al.* 2002).

The need to increase sampling intensity and breadth for accurate biodiversity estimates is particularly relevant in a continent the size and scope of Australia. In a recent study of pinned material of the microgastroid subfamily Cheloninae in which over 5000 specimens were separated into morphospecies, many were represented by a single specimen (Kittel 2014), indicating the issue of under-sampling of arthropod diversity in Australia is confined neither to the microgastrines nor to ethanol material. In addition, singleton species are not uncommon in many studies, with Lim *et al.* (2012) finding that nearly 20% of invertebrate species are described from single specimens, although this was a small case study examining the literature spanning 10 years from a single institution. Due to time constraints, no attempt was made during the DNA barcoding and species delimitation component of this study (Chapter 2) to match specimens used in the molecular analyses to pinned material in museum collections, an avenue that would likely expand the species richness estimates and possibly identify any described species in the dataset.

Next-generation sequencing for rapid species discovery methods

With possibly 80% of the eukaryotic species on earth still to be described (Mora *et al.* 2011), increasing the rate at which species are discovered and documented is an essential component of implementing conservation outcomes in a rapidly changing world.

Accelerating the discovery, naming and documenting of new species is considered such a priority that it is the first strategic action listed in the inaugural decadal plan for taxonomy and biosystematics in Australia and New Zealand (Taxonomy Decadal Plan Working Group 2018). In this study, Next-Generation Sequencing (NGS) methods were applied to quickly and cost-effectively DNA barcode hundreds of microgastrine specimens, using methods developed in the last few years (Shokralla *et al.* 2015; Cruaud *et al.* 2017). There are several new methods for rapid DNA barcoding being developed, using different combinations of sequencing technologies and bioinformatics pipelines (Liu *et al.* 2017; Hebert *et al.* 2018). Methods for further reducing the cost per barcode include removing the expensive DNA extraction step; direct PCR has been used to sequence *COI* barcodes of hundreds of midge specimens using Illumina sequencing technology for less than $1 per barcode (Meier *et al.* 2016), although this method does not allow the retention of a DNA voucher that could be utilised in the future. Whichever method is applied, reducing the cost of large-scale biodiversity surveys will open new avenues to species discovery, for both the Microgastrinae and across the entire tree of life. DNA barcoding has been an integral part of documenting microgastrine diversity across the globe (Smith *et al.* 2008; Janzen *et al.* 2009; Smith *et al.* 2013; Fernández-Flores *et al.* 2013; Fernández-Triana *et al.* 2017) and will likely continue to be so, with this study making a significant number of Australian specimens available publically for the first time.

In the DNA barcoding component of this study, species delimitation applying the widely used 2% *COI* threshold was compared to two other commonly used methods, namely GMYC (Pons *et al.* 2006) and bPTP (Zhang *et al.* 2013). As with a previous species delimitation study of microgastrines (Fernández-Flores *et al.* 2013), concordance was generally found between the 2% threshold and GMYC, and when discordance occurred the 2% threshold was most often the more conservative (i.e. delimiting fewer species) of the three methods. It has been argued that methods such as GMYC are not able to distinguish between phylogeographic structure at the intra-specific level from true speciation, especially in datasets with large numbers of singleton species (Lim *et al.* 2012; Carstens *et al.* 2013; Luo *et al.* 2018). With the general agreement among the 2% *COI* threshold, wingless and *ITS2* haplotypes, and morphology in the current study, this simple threshold appears to work well as a method for the general estimate of diversity. However, all available evidence should be used before the formal description of species, as there were several cases where the 2% threshold over-split species compared to morphology (*Dolichogenidea finchi*, Chapter 5) and *ITS2* (*Diolcogaster* sp. 6,7,8 and *D.* sp. 18,19, Chapter 3).

Species descriptions and targeted taxonomy

As for numerous hyperdiverse taxa, but particularly for parasitoid wasps (Forbes *et al.* 2018), there are most likely hundreds of microgastrine species awaiting description in Australia, but there are several challenges to smoothly tackling this dearth of knowledge. Many of the descriptions made prior to the 1970s are quite brief, and holotypes are scattered across museums in the Northern Hemisphere. Very few genera are endemic to Australia, and therefore thorough revisions of the Australian fauna need to consider species described from other regions. With this in mind, a decision was made in this study to focus on describing species that were either clearly unique morphologically and therefore had potential relevance to refining the limits of specific genera, or had molecular and/or host data available. *Choeras koalascatocola* (Chapter 4) was the first species described due to its unique life history and clear distinction from other *Choeras* species, with *C. morialta* being discovered through field work early in the project and therefore being described alongside the morphologically similar *C. koalascatocola*. The three *Dolichogenidea* species described in Chapter 5 were prioritised due to their extremely long ovipositors, easily identifiable from all other *Dolichogenidea* described from the region, and relevant to redefining the genus in future through recognising a trait which is obviously host related. The focus of the 10 new species treated in Chapter 6 was to formally describe species identified from the DNA barcoding and species delimitation results of Chapter 2, focusing primarily on those collected from 'Bush Blitz' surveys of regional Australia with multiple specimens, and those species with host data or particularly unique morphological characters. Using the information from DNA barcoding, I was able to clarify species boundary decisions using both morphological and molecular data, which facilitated making the most informed species hypotheses possible as a researcher previously unfamiliar with the group.

Whilst *COI* has been used extensively for the Microgastrinae as a tool of estimating species richness, it can be useful (if not essential) to have additional markers that can be used to support species boundary decisions, particularly in cases where *COI* divergence is close to the commonly used 2% threshold, or is in conflict with ecological or morphological data. There are also inherent concerns in relying on only *COI* for species delimitation, with issues such as mitochondrial heteroplasmy (Magnacca and Brown 2010) and DNA introgression facilitated by *Wolbachia* (Klopfstein *et al.* 2016) distorting species delimitation. The rRNA gene *28S* and spacer region *ITS1* have been used to support *COI* species delimitation of microgastrines in the past (Smith *et al.* 2008), and in this study we showed that wingless and *ITS2* can also be employed to support species delimitation, with the caveat that

sequencing of rRNA genes should be conducted with some caution due to a departure from concerted evolution in this gene family in various species.

Host records

The most significant issue with microgastrine collections is that specimens are primarily collected in Malaise traps and sweep netting surveys, which, whilst collecting a large number of species for morphological and molecular studies, provides no information about their biology or potential host species. Documenting host data is integral to understanding the relationships of microgastrine species to lepidopteran populations and subsequently to caterpillar host plants, knowledge which is particularly relevant as these interactions are likely to change as the climate and habitats shift in the future (Jeffs and Lewis 2013; Wetherington *et al.* 2017). Host taxon and specificity information is also critical for identifying microgastrine species that may be potential biological control agents for current or future agricultural pests. Species complexes of microgastrines, which are difficult to separate morphologically, can have different hosts, causing confusion in biological control programs if host data are not matched to correctly delimited species, or if correct molecular identifications are not made prior to introductions (e.g. Muirhead *et al.* 2008, 2012).

Unsuccessful attempts were made in this study to Sanger sequence host DNA from the metasoma of adult wasps, following the partial success of this method in microgastrines previously (Rougerie *et al.* 2011; Hrcek *et al.* 2011). If this technique could be developed further, it could lead to a significant increase in the numbers of species with known hosts, particularly as over 10,000 species of Australian Lepidoptera have already been DNA barcoded for the *COI* region (Hebert *et al.* 2013), providing a ready-made database within which to match gut-extracted host sequences. NGS may assist with improving the success rate of this technique, considering the ability of Illumina technologies to sequence even small amounts of DNA from a PCR amplification. Only a couple of DNA extractions from wasp metasomas (rather than legs) were included in the Miseq run of the DNA barcoding component of the current study, and no lepidopteran *COI* sequences were obtained. However, the PCR products included from those extractions were amplified with internal *COI* primers that were designed for Hymenoptera, not the targeted lepidopteran primers used in the studies of Hrcek *et al.* (2011) and Rougerie *et al.* (2011).

The primary source of host data in this study was through the rearing of lepidopteran larvae by both professional and amateur lepidopterists. Reared material can sometimes be found in museum collections, particularly in agricultural department collections, but it is often in poor condition and unusable for DNA studies. Fostering collaborations and networks

between the Lepidoptera community (both the professional community and the passionate amateur societies and individuals) is likely to be the way forward for increasing host data for this group of parasitoids in Australia. Rearing projects on the incredible scale of those conducted in Costa Rica (Janzen *et al.* 2009; Fernández-Triana *et al.* 2014a; Fernández-Triana *et al.* 2014b) are unlikely to be financially or practically feasible for most countries, including Australia, but they provide a best-practice model for information that is possible to gather with a focussed, long-term project rearing lepidopteran larvae. The citizen science project attempted in this study had the best intentions of harnessing the 'power of the public' to rear Lepidoptera, but was not hugely successful for reasons discussed in Appendix 1. However, with a number of adjustments, improvements and financial support, citizen science may be a possible way to increase the numbers of microgastrine species with host data.

Future research directions

The most significant challenge in studying microgastrines at the present time is the lack of a robust phylogeny for the subfamily, through which genera limits and relationships could be tested. There is consensus that many of the current genera are inadequately defined (Whitfield *et al.* 2018), and sometimes clearly incorrect with several taxa likely to be para- or polyphyletic (e.g. *Choeras* and *Sathon*, discussed in Chapters 4 and 6). However, with thousands of species and nearly 100 genera, a phylogeny of the subfamily with adequate taxon sampling will be a huge undertaking. There is ongoing work using hybrid enrichment kits, with 370+ genes for 90 species currently included in a preliminary phylogeny (Whitfield *et al.* 2018) and a complimentary study investigating the use of Ultra Conserved Elements as an alternative tool for tackling this massive task is beginning (Fernández-Triana, pers. com.). Alongside, and possibly dependent on this better understanding of generic limits and relationships, is the need for a key to the world genera of microgastrines, and updated keys to the genera for specific regions including Australasia. Revised, expanded, and accessible keys would allow easier identification of described taxa by workers attempting to put names to microgastrines in museum collections, for agriculture, and during biodiversity surveys.

This study provided a significant increase in the number of Australian microgastrines sequenced for several DNA barcoding markers, with much of these data now publically available online. This study is also a proof-of-concept that high-throughput methods can be used to DNA barcode hundreds of hymenopteran specimens at once, whilst retaining most of the specimen (minus legs used for DNA extraction) for subsequent morphological

analyses and descriptions of new species. Future work could look to scale this up, both in the number of specimens DNA barcoded from museum ethanol collections and field work, but also in potentially testing the use of pinned specimens from museum accessions and identified material in this pipeline. Using pinned material for DNA extractions is now relatively common, but often requires modified protocols. However, there are numerous studies researching the best approaches of using pinned material, and all suggest that much more is now possible using NGS than was previously the case with Sanger methods (Andersen and Mills 2012; Sproul and Maddison 2017; Chen *et al.* 2018; Santos *et al.* 2018). As the NGS method used in this study was able to obtain *COI* barcodes from ethanol specimens many years old without modified extraction or PCR protocols, it is possible that it may also be successful on recently pinned material, particularly for material initially preserved in ethanol (Austin and Dillon 1997).

There is considerable work yet to do to develop a more complete understanding of microgastrine species richness, distribution and biogeography, not to mention in discerning the nature of their evolution with their hosts and the evolution of various morphological characters. In Australia alone, we have barely scratched the surface in describing the known biodiversity exposed through previous morphological examinations of collections (Austin and Dangerfield 1992) and through the DNA barcoding of the current study. Currently, there is significant work being conducted on the subfamily world-wide, in particular in Canada (Fernández-Triana 2010; Fernández-Triana *et al.* 2016), China (Liu *et al.* 2014; Song *et al.* 2014; Liu *et al.* 2018), Costa Rica (Fernández-Triana *et al.* 2014b; Fernández-Triana *et al.* 2014a), India (Gupta and Kalesh 2012; Gupta *et al.* 2014; Gupta and Fernández-Triana 2015), and Iran (Ghafouri Moghaddam *et al.* 2018). With collaboration, communication, and the sharing of specimens and knowledge across country and continental boundaries, easier now than ever before, the future of microgastrine taxonomy and systematics looks bright; an exponential increase in the number of new species, and strengthened confidence in the systematics of the subfamily, are both likely to occur within the next decade.

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Appendix 1: A summary of the citizen science and other outreach activities undertaken during this project

Citizen Science Project

At the beginning of this research, a citizen science project was designed and launched to engage the general public's involvement in rearing native caterpillars to increase the number of available microgastrine specimens with host data. The project was titled 'The Caterpillar Conundrum' and the portal can be found at www.thecaterpillarconundrum.org.

The website provided background information on parasitoids and the microgastrine project, and instructions on how to take part in the project and submit data. Participants were asked to collect caterpillars from host plants they had easy access to, photograph the caterpillar, and rear the caterpillar through to an adult, photographing and uploading information to a *BowerBird* project (http://www.bowerbird.org.au/projects/8033) at each life stage. If parasitoids emerged from the caterpillar, participants were asked to contact the project and send in the specimens. Resources for teachers, including a pdf download of the project instructions, worksheets and certificates for students, and curriculum links were available on the website. Effort was expended in advertising the project through social media and already established citizen science networks such as the *Discovery Circle* in South Australia. The project was featured on the Australian Chanel 10 children's science TV show, SCOPE: https://youtu.be/kpk4TcvUM2E and in the local Adelaide newspaper, The Advertiser.

The project had some small successes. Due to the website and associated social media, several people contacted me when they found wasp cocoons in their garden, or when they were already rearing caterpillars and had parasitoids emerge, or who were amateur entomologists with pinned parasitoids from past rearings that they wished to donate. Whilst the number of specimens that resulted from these contacts was small, due to the relative scarcity of host information, each specimen with host data was a significant contribution, and not to be undervalued. From hearing about the project in the public news media, a collaboration was set up with a butterfly garden, which provided many useful specimens from known hosts. A few people completed the project and uploaded data to the publically accessible *BowerBird* platform, which feeds into the *Atlas of Living Australia*. Thus, although the project did not achieve the reach and volume of host data hoped for, it

did allow a platform for targeted outreach and a story for the media to pick up on and advertise that was greater than the specific aims of the research.

On reflection, the project had limited success for the numerous reasons outlined below, and if the project was to be relaunched, improvements could be made that would likely increase its reach and ultimate success.

1. A citizen science project must balance the time-commitment required by the volunteers with the number of participants likely to complete the project – i.e. a project that requires minimal time commitment and which can be conducted at any time, from anywhere, will be accessible to many more people than a project which asks volunteers to invest weeks, if not months, into rearing caterpillars which they first have to physically find. This was a fault in the design of the project, but is difficult to mitigate simply because of the necessity of the data required.

2. A catchy name goes a long way. There are hundreds of citizen science projects available to volunteers who wish to contribute to science, and thus any project is competing for participants' time and dedication. A rebrand of the project as something simpler and more family/school friendly, such as 'Catch a Caterpillar!' or 'Wasp Warriors' may help in the initial attraction of people to the project amidst the many other projects being advertised through citizen science portals. It is difficult for a project on insects to compete with a project on cute and cuddly animals such as echidnas, but a more enticing name may help.

3. Projects such as this that require large time inputs from volunteers are much more successful when personal contact and collaboration is made. Whilst I talked about the project in person to numerous schools and community groups, I believe that spending more targeted time with fewer, carefully chosen groups of people would be more effective. For example, forming a formal partnership with some 'Friends of Parks' groups, who are already frequently in bushland and likely to come across native caterpillars, may be the best approach. However, the energy and time required to set up and maintain relationships such as this are not to be underestimated.

4. Many people, likely because of the name of the project, assumed I was a caterpillar expert. With little to no knowledge of caterpillar identification, I was often unable to help the numerous people who contacted me with identification requests. A significant improvement to the project would be to involve a lepidopterist who could both assist the public with identification requests and provide some training in caterpillar identification.

Outreach

As discussed in chapter 1, outreach by scientists has numerous benefits to both the scientist and the wider community. A non-scientific aim during this PhD was to communicate the research topic and specific research findings to the public, and spread an awareness of the importance of taxonomy and biodiversity science. Over 1500 people heard about or interacted with the research in person through lectures, workshops and science communication competitions (Table 1). In addition, hundreds of people were more casually exposed to the research through interactive displays at University Open Days and *Science Alive*, a public exhibition hall at National Science Week.

Table 1: Outreach conducted during the project

Date	Style	Audience name	Audience demographic	Approx. audience size
2018	Workshop	Morialta Conservation Park MiniBlitz	General Public (families)	40
2018	Artistic Performance	Perform Your Science – A National Science Week event	General Public	200
2017	Lecture (1 hr)	Butterfly Conservation Society South Australia	Adults	60
2017	Lecture (1 hr)	Friends of the Australian Arid Lands Botanic Gardens	Adults	40
2017	Lecture (1 hr)	Junior Field Naturalists South Australia	Children 5-15 years of age and their parents	60
2017	Lecture (1 hr)	Bright Sparks Science Club South Australia	Children 5-15 years of age and their parents	50
2017	Lecture (30 mins)	South Australian Museum Indian Pacific train passenger visit	General public (adults and families travelling on the Indian Pacific train)	50
2017	Workshop	'Bush Buddies' Friends of Belair National Park children's group	Children 5-15 years	25
2017	Workshop	National Youth Science Forum STEM Explorer Program	Year 9 high school students from regional areas	30
2017	Lecture (30 mins)	Children's University Regional Lecture Series	Year 7 & 8 high school students from regional areas (9 sessions, 6 different schools)	250

2017	3 Minute Thesis Presentation	Adelaide University Research Tuesdays	University community, general public	100
2016 & 2017	Workshop	Discovery Circle BioBlitz	General Public (across multiple sessions at 3 different bioblitzs)	150
2016	Presentation	Famelab research presentation competition (semi-final, Australian final, international semi-final, international final)	General Public	400
2015 & 2016	Workshop	Adelaide Compass, 'A Bug's Life'	Year 2 primary school students from disadvantaged Adelaide schools (6 classes from 5 different schools)	150
Total people reached (in person)				**1555**

Additionally, a number of people interacted with the research through media exposure, but accurate numbers or the level of impact is difficult to measure. The research was featured on two episodes of SCOPE (a children's television show) and on a *Children's University* produced video uploaded to YouTube and part of a package sent to regional schools.

A media strategy was developed for one of the published papers (Chapter 5, the description of three new species of *Dolichogenidea*) as an opportunity to choose a new species name that would allow for public engagement with taxonomy. Whilst the naming of species is a serious endeavour, there is room for occasionally selecting a name which can provide a gateway to public outreach, and thus communicate the importance of taxonomy and species discovery. The name *Dolichogenidea xenomorph* was chosen for a species that in appearance is shiny, black and possesses an extremely long ovipositor. This, plus the biology of parasitoid wasps, was used to link the species to the fictional creature called a Xenomorph in the *Alien* movie franchise, thus appealing to pop-culture references and a 'gross-out' factor that could hook the media into telling a story of species discovery and the importance of parasitoid wasps in the environment. The media strategy was very successful, and the story was picked up by online news outlets, blogs, radio and social media. The Altmetrics show that the paper performed highly, ranking in the top 5% of research outputs scored by the platform, and is in the 98th percentile of media attention of research outputs of the same age (Fig. 1). In total, the research was mentioned in two print newspapers, nine ABC radio news reports across Australia, and on 83 online articles from 17 different countries (Table 1).

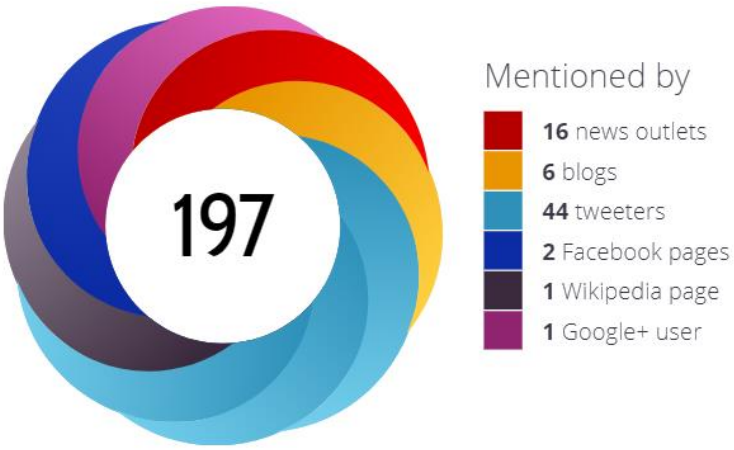


Figure 1: Altmetrics summary and score, full data available here: https://www.altmetric.com/details/44162939

Table 1: University Media Report on the reach of the paper describing *Dolichogenidea xenomorph* (Chapter 5)

Country	Source	Format	Headline
Australia	Shepparton News	Newspaper, pg. 2	Gruesome 'Alien' wasp species discovered
Australia	Adelaide Advertiser	Newspaper, pg. 24	'Alien' wasp a horror hit
Australia	Alor Blog	Online article	The Metaphor of the WASP By Brian Simpson
Australia	NewsMaker	Online article	Newly discovered Xenomorph wasp has Alien-like lifecycle
Australia	COSMOS Magazine	Online article	You know Alien, the movie. Now meet Alien, the wasp
Australia	The Daily Telegraph	Online article	Newly discovered parasitic Australian wasp named Xenomorph in homage to movie Alien
Australia	The Advertiser	Online article	Newly discovered parasitic Australian wasp named Xenomorph in homage to movie Alien
Australia	Science Media Exchange - Scimex	Online article	Newly discovered Xenomorph wasp has Alien-like lifecycle
Australia	FIVEaa | Adelaide	Online article	Local Scientists Have Discovered A New Species That Acts Just Like The Alien Monster
Australia	InDaily	Online article	Alien detection: SA researcher discovers new parasitic wasp - InDaily
Australia	Cryptozoology news	Online article	Newly discovered Xenomorph wasp has alien-like lifecycle
Australia	Science Daily	Online article	Newly discovered Xenomorph wasp has Alien-like lifecycle
Australia	Herald Sun	Online article	Newly discovered parasitic Australian wasp named Xenomorph in homage to movie Alien
Belgium	De Standaard	Online article	'We zijn helemaal alleen in het heelal'
Bosnia and Herzegovina	Radio Sarajevo	Online article	Australija / Nazvane prema čudovištu iz filma Alien: Otkrivena čudnovata vrsta osa
British Indian Ocean Territory	Tech Site	Online article	'Alien' wasps lay eggs inside caterpillars that burst through them
Canada	IFL Science	Online article	Student Named New Wasp After This Fictional Alien For An Obvious Reason
France	The Science Page	Online article	Student Named New Wasp After This Fictional Alien For An Obvious Reason
Ireland	The Irish Sun	Online article	Terrifying 'alien' invades victims' bodies, eats their insides and then lays eggs that burst out
Italy	ANSA.it	Online article	La vespa Alien, imita la fantascienza - Scienza & Tecnica
Italy	Giornale Di Sicilia	Online article	La vespa Alien, imita la fantascienza
Italy	Leggo	Online article	Scoperta la vespa Alien: le sue larve divorano i bruchi dall'interno

Italy	IL Mattino	Online article	Scoperta la vespa Alien: le sue larve divorano i bruchi dall'interno
Italy	Il Messaggero.it	Online article	Scoperta la vespa Alien: le sue larve divorano i bruchi dall'interno
Italy	Il Gazzettino.it	Online article	Scoperta la vespa Alien: le sue larve divorano i bruchi dall'interno
Italy	Il Mattino	Online article	Scoperta la vespa Alien: le sue larve divorano i bruchi dall'interno
Italy	Alto Adige	Online article	La vespa Alien, imita la fantascienza
Italy	Trentino	Online article	La vespa Alien, imita la fantascienza
Latin America	Infosurhoy	Online article	'Alien' wasp injects eggs into caterpillars so larvae EAT way out
Mexico	Tiempo.com.mx	Online article	Descubren científicos nueva especie de avispa
Mexico	Puente Libre	Online article	Descubren científicos nueva especie de avispa
Mexico	Plano Informativo	Online article	La avispa que se parece al 'Alien' de las películas
Russia	News -w	Online article	Terrifying wasp invades victims bodies, feasts on their insides and bursts out like a monster from the Alien films
Singapore	Micetimes.asia	Online article	Scientists found the OS similar to the monsters from the movie "Aliens"
Spain	Código Espagueti	Online article	Nombran nueva especie de avispa en honor de "Alien" por su horrible forma de madurar - Código Espagueti
Sweden	Natursidan	Online article	Nyupptäckt stekel döps efter varelse i Alien-filmerna
Sweden	Natursidan	Online article	Nyupptäckt geting döps efter varelse i Alien-filmerna
United Kingdom	Daily Star	Online article	Nightmare wasps lay EGGS inside victims that then EAT their way out like in Alien
United Kingdom	Metro.co.uk	Online article	Terrifying wasp invades victims' bodies, feasts on their insides and bursts out like a monster from the Alien films
United Kingdom	Daily Star	Online article	Nightmare wasps lay EGGS inside victims that then EAT their way out like in Alien
United Kingdom	Mail On Sunday	Online article	The terrifying 'alien' wasp that injects its eggs into live caterpillars so its offspring can EAT their way out
United Kingdom	Daily Mail Online	Online article	'Alien' wasp injects eggs into caterpillars so larvae EAT way out | Daily Mail Online
United Kingdom	Daily Mail	Online article	The terrifying 'alien' wasp that injects its eggs into live caterpillars so its offspring can EAT their way out
United Kingdom	Scienmag	Online article	Newly discovered Xenomorph wasp has alien-like lifecycle
United Kingdom	Bright Surf	Online article	Newly discovered Xenomorph wasp has alien-like lifecycle
United Kingdom	Alpha Galileo	Online article	Newly discovered Xenomorph wasp has Alien-like lifecycle
United Kingdom	Bright Surf	Online article	Journal of Hymenoptera Research links Crocodile Dundee, Toblerone, Game of Thrones & Alien
United States	HowStuffWorks	Online article	Parasitic Wasp Larvae Eat Host From Inside Out
United States	SYFY WIRE	Online article	This new species of wasp has been appropriately named after a Xenomorph from Alien
United States	Fox News	Online article	'Alien' wasps lay eggs inside caterpillars that burst through them
United States	LiveScience	Online article	Game Over, Man: This Australian Wasp Lays Chest-Bursting 'Alien' Eggs Inside Caterpillars
United States	New York Post	Online article	Terrifying bug injects victims with eggs and eats them from the inside out
United States	Midland Reporter Telegram	Online article	New Predatory Wasp Echoes Behavior Of Alien Movie Monster
United States	Firenews	Online article	Terrifying 'alien' invades victims' bodies, eats their insides and then lays eggs that burst out
United States	Vaaju.com	Online article	Scary foreign wasps invade victims to fasten on their insides
United States	SpaceDaily.Com	Online article	Newly discovered Xenomorph wasp has alien-like lifecycle
United States	ScienceDaily	Online article	Newly discovered Xenomorph wasp has Alien-like lifecycle
United States	One News Page United States	Online article	New Predatory Wasp Echoes Behavior Of Alien Movie Monster
United States	Usa Science News	Online article	Newly discovered Xenomorph wasp has alien-like lifecycle
United States	Georgia Newsday	Online article	'Alien' wasp injects eggs into caterpillars so larvae EAT way out
United States	Tekcrispy	Online article	Nueva especie de avispa xenomórfica tiene un espeluznante ciclo de vida
United States	Sci-News.com	Online article	New Species of Parasitic Wasp Has Alien-Like Lifecycle

United States	EnvironmentGuru	Online article	Newly discovered Xenomorph wasp has alien-like lifecycle
United States	SpaceRef	Online article	Newly discovered Xenomorph wasp has alien-like lifecycle
United States	EurekAlert!	Online article	Newly discovered Xenomorph wasp has alien-like lifecycle
United States	Long Room	Online article	The 'Alien' wasp that injects eggs into live caterpillars so its offspring can EAT their way out
United States	Phys.org	Online article	Journal of Hymenoptera Research links Crocodile Dundee, Toblerone, Game of Thrones and Alien
United States	Stories Flow	Online article	Newly discovered Xenomorph wasp has alien-like lifecycle
Viet Nam	Viet Bao Viet Nam	Online article	Sinh vật trên Trái đất có hành vi như sinh vật ngoài hành tinh
Viet Nam	Công Nghệ	Online article	Sinh vật trên Trái đất có hành vi như sinh vật ngoài hành tinh
Viet Nam	Báo Mới	Online article	Sinh vật trên Trái đất có hành vi như sinh vật ngoài hành tinh
Viet Nam	XãLuận.com	Online article	Kì thi THPT Quốc gia năm 2018 đã kết thúc, song giám khảo môn Ngữ văn tại TP.HCM vẫn còn d
Viet Nam	Kienthuc.net.vn	Online article	Sinh vật trên Trái đất có hành vi như sinh vật ngoài hành tinh
Viet Nam	Khoahoc	Online article	Loài vật trên Trái đất có hành vi như sinh vật ngoài hành tinh
Viet Nam	Công Nghệ	Online article	Loài vật trên Trái đất có hành vi như sinh vật ngoài hành tinh
Viet Nam	VN.City	Online article	Loài côn trùng đáng sợ được đặt tên theo sinh vật hư cấu ngoài hành tinh.
Viet Nam	Báo Mới	Online article	Loài côn trùng đáng sợ được đặt tên theo sinh vật hư cấu ngoài hành tinh
Viet Nam	VTC News	Online article	Loài côn trùng đáng sợ được đặt tên theo sinh vật hư cấu ngoài hành tinh
Viet Nam	Báo Mới	Online article	Loài vật trên Trái đất có hành vi như sinh vật ngoài hành tinh
Viet Nam	Tin247.com	Online article	Loài vật biết kiểm soát hành động con mồi như sinh vật ngoài hành tinh
Viet Nam	Báo Mới	Online article	Loài vật biết kiểm soát hành động con mồi như sinh vật ngoài hành tinh
Viet Nam	24h	Online article	Loài vật biết kiểm soát hành động con mồi như sinh vật ngoài hành tinh
Viet Nam	Viet Bao Viet Nam	Online article	Loài vật trên Trái đất có hành vi như sinh vật ngoài hành tinh
Viet Nam	Báo Dân Việt	Online article	Loài vật biết kiểm soát hành động con mồi như sinh vật ngoài hành tinh
Viet Nam	Báo Dân Việt	Online article	Loài vật trên Trái đất có hành vi như sinh vật ngoài hành tinh
Viet Nam	Thời Báo	Online article	Loài vật trên Trái đất có hành vi như sinh vật ngoài hành tinh
Australia	ABC Radio Brisbane	Radio, 10:00 news	A new native species of wasp, which injects its eggs into live caterpillars, enabling the ...
Australia	ABC South East SA	Radio, 6:30 news	University of Adelaide researchers have named a new species of alien-like wasp
Australia	ABC Alice Springs	Radio, 6:30 news	University of Adelaide researchers have discovered a new native species of wasp
Australia	ABC Radio Adelaide	Radio, 7:00 news	University of Adelaide researchers have discovered an alien-like wasp named
Australia	ABC Radio Darwin	Radio, 7:00 news	University of Adelaide researchers have discovered a new native species of wasp
Australia	ABC Radio Canberra	Radio, 7:45 news	University of Adelaide researchers have named a new species of alien-like wasp
Australia	ABC Radio Adelaide	Radio, 7:45 news	University of Adelaide researchers have discovered an alien-like wasp named
Australia	ABC Radio Darwin	Radio, 7:45 news	A newly-discovered native species of wasp, named Xenomorph by University of Adelaide ...
Australia	ABC Radio Hobart	Radio, 9:00 news	A new native species of wasp, which injects its eggs into live caterpillars, enabling the ...

Appendix 2: Conference Presentations relating to this project

Fagan-Jeffries, E.P. Cooper, S. J. B., Bertozzi, T., Bradford, T. M., and Austin, A. D. Australian Entomological Society Conference, Alice Springs Australia, September 2018. Oral Presentation: *Using high-throughput amplicon sequencing to explore the biodiversity of Australian microgastrine parasitoid wasps*.

Fagan-Jeffries, E.P. Cooper, S. J. B., Bertozzi, T., Bradford, T. M., and Austin, A. D. International Society of Hymenopterists Congress, Matsuyama Japan, July 2018. Oral Presentation: *Using high-throughput amplicon sequencing to explore the biodiversity of Australian microgastrine parasitoid wasps*.

Fagan-Jeffries, E.P. Cooper, S. J. B., Bertozzi, T., Bradford, T. M., and Austin, A. D. Society of Systematic Biologists Conference, Adelaide Australia, November 2017. Oral Presentation: *Using high-throughput amplicon sequencing to explore the biodiversity of Australian microgastrine parasitoid wasps*.

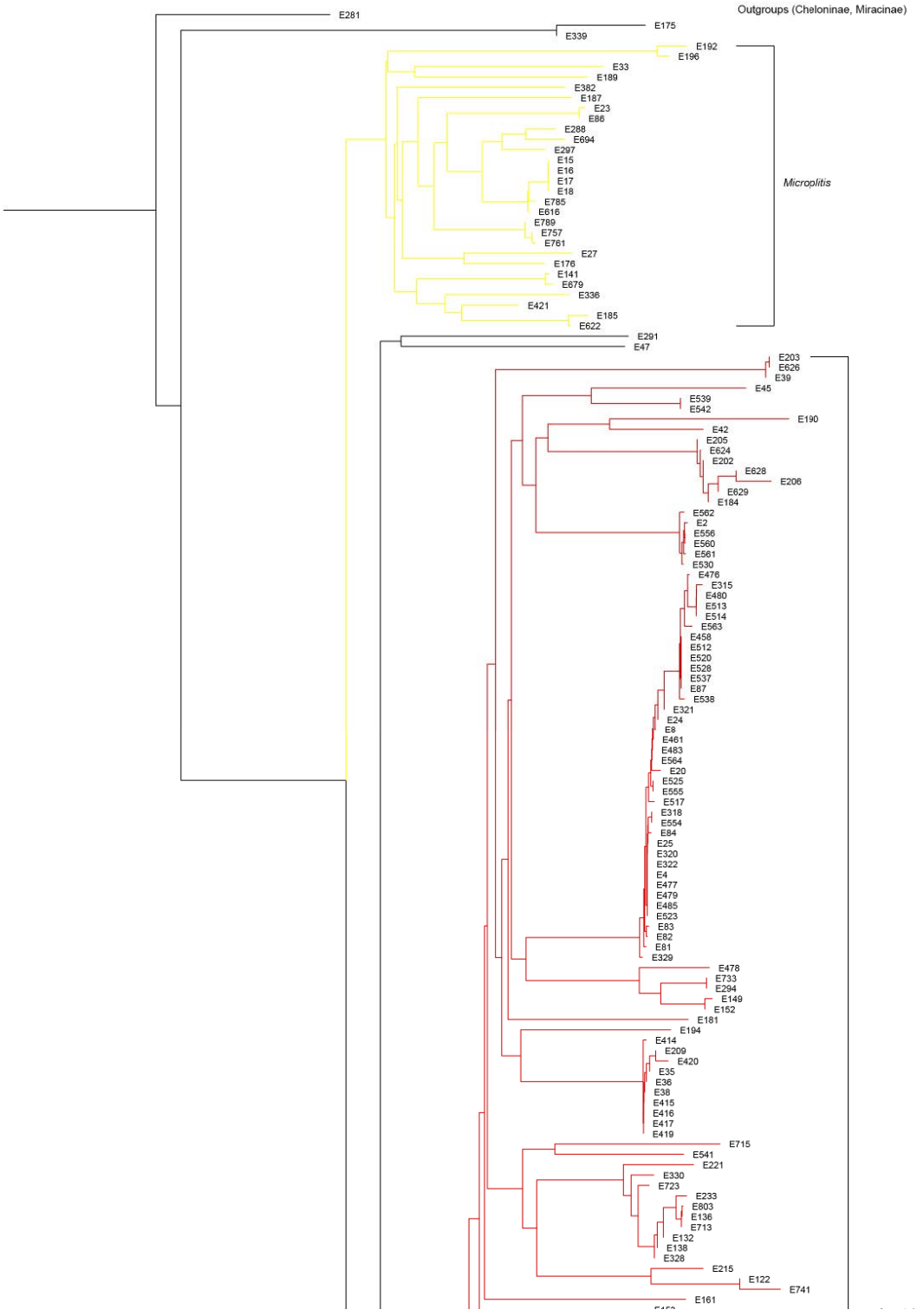
Fagan-Jeffries, E.P. Cooper, S. J. B., Bertozzi, T., Bradford, T. M., and Austin, A. D. Centre for Biodiversity Analysis Conference, Canberra Australia, September 2017. Oral Presentation: *Using high-throughput amplicon sequencing of museum ethanol collections to explore the biodiversity of Australian microgastrine parasitoid wasps*.

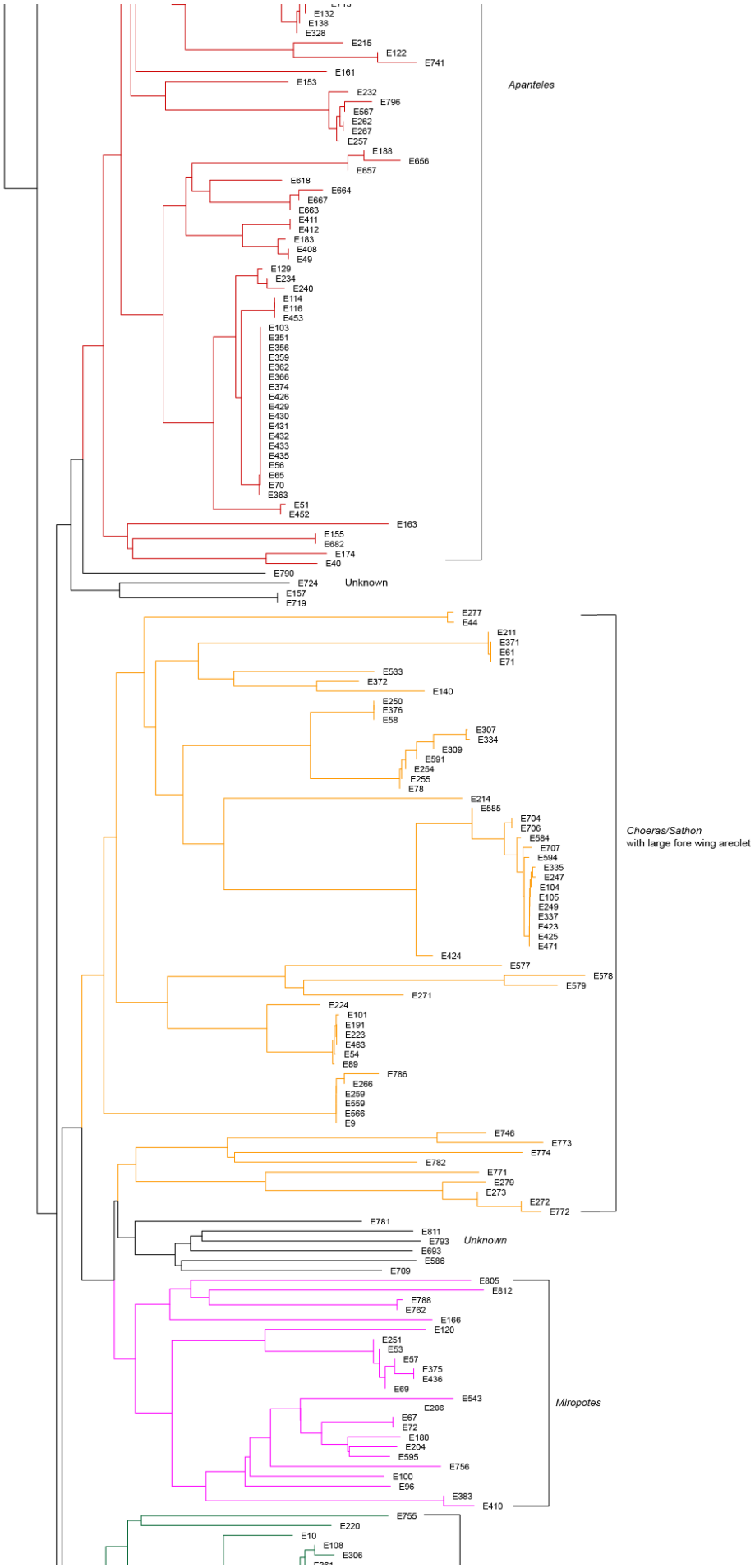
Fagan-Jeffries, E.P. Cooper, S. J. B., and Austin, A. D. International Congress of Entomology, Orlando USA, September 2016. Oral Presentation: *Australian microgastrine parasitoid wasps: Systematics meets citizen science*.

Fagan-Jeffries, E.P. Cooper, S. J. B., and Austin, A. D. School of Biological Sciences Symposium, Adelaide Australia, June 2016. Poster Presentation: *Systematics and Taxonomy of microgastrine parasitoid wasps*.

Fagan-Jeffries, E.P. Cooper, S. J. B., and Austin, A. D. Society of Systematic Biologists Conference, Perth Australia, December 2015. Oral Presentation: *Systematics and evolution of Australian microgastrine parasitoid wasps: A PhD project with a twist*.

Appendix 3: NJ tree of microgastrines sequenced in Chapters 2 & 6

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E122
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E161
E153
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E267
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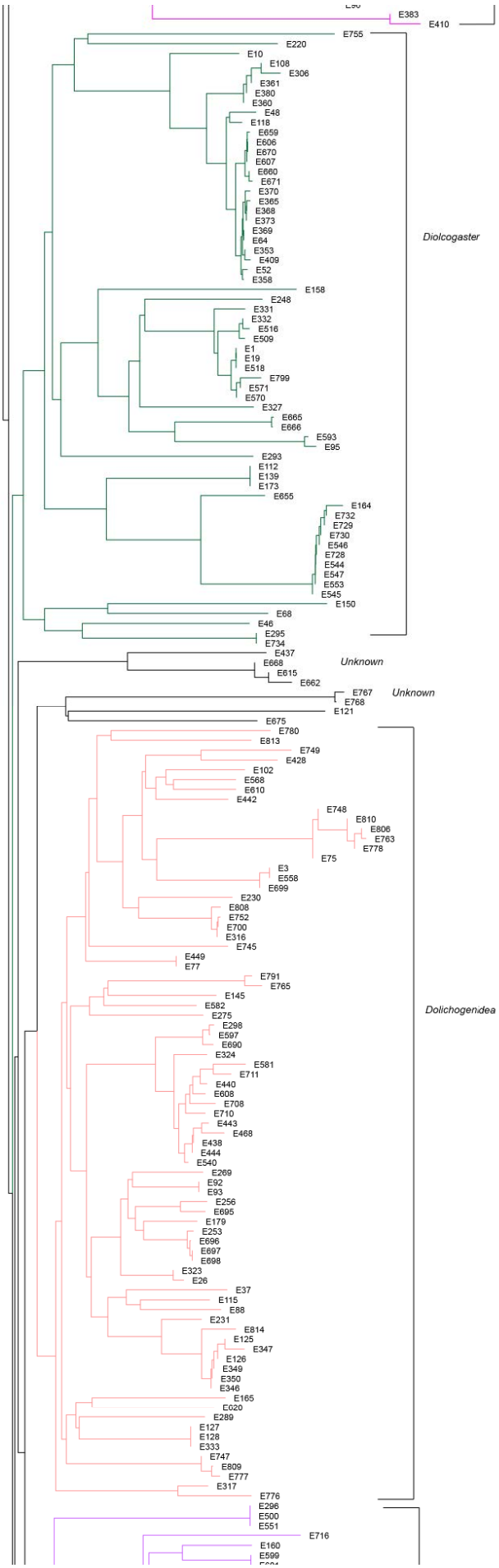
E657
E618
E664
E667
E663
E411
E412
E183
E408
E49
E129
E234
E240
E114
E116
E453
E103
E351
E356
E359
E362
E366
E374
E426
E429
E430
E431
E432
E433
E435
E56
E65
E70
E363
E51
E452
E163
E155
E682
E174
E40
E790
E724
E157
E719
Unknown
Apanteles
E277
E44
E211
E371
E61
E71
E533
E372
E140
E250
E376
E58
E307
E334
E309
E591
E254
E255
E78
E214
E585
E704
E706
E584
E707
E594
E335
E247
E104
E105
E249
E337
E423
E425
E471
E424
E577
E578
E579
E271
E224
E101
E191
E223
E463
E54
E89
E786
E266
E259
E559
E566
E9
E746
E773
E774
E782
E771
E279
E273
E272
E772
Choeras/Sathon
with large fore wing areolet
E781
E811
E793
E693
E586
E709
Unknown
E805
E812
E788
E762
E166
E120
E251
E53
E57
E375
E436
E69
E543
C206
E67
E72
E180
E204
E595
E756
E100
E96
E383
E410
Miropotes
E755
E220
E10
E108
E306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E220
E10
E108
E306
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E360
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E659
E606
E670
E607
E660
E671
E370
E365
E368
E373
E369
E64
E353
E409
E52
E358
Diolcogaster
E158
E248
E331
E332
E516
E509
E1
E19
E518
E799
E571
E570
E327
E665
E666
E593
E95
E293
E112
E139
E173
E655
E164
E732
E729
E730
E546
E728
E544
E547
E553
E545
E150
E68
E46
E295
E734
E437
E668
E615
E662
Unknown
E767
E768
E121
Unknown
E675
E780
E813
E749
E428
E102
E568
E610
E442
E748
E810
E806
E763
E778
E75
E3
E558
E699
E230
E808
E752
E700
E316
E745
E449
E77
E791
E765
E145
E582
E275
E298
E597
E690
E324
E581
E711
E440
E608
E708
E710
E443
E468
E438
E444
E540
E269
E92
E93
E256
E695
E179
E253
E696
E697
E698
E323
E26
E37
E115
E88
E231
E814
E125
E347
E126
E349
E350
E346
E165
E020
E289
E127
E128
E333
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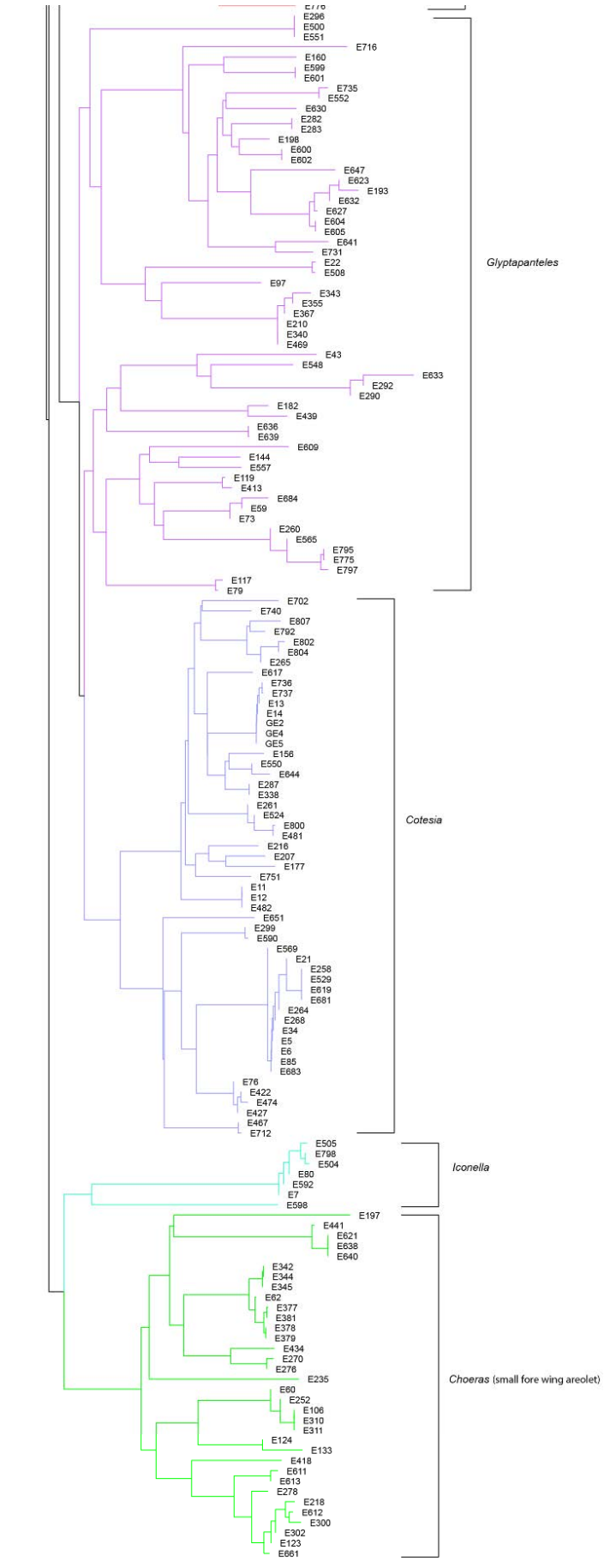
E809
E777
E317
Dolichogenidea
E776
E296
E500
E551
E716
E160
E599


E296
E500
E551
E716
E160
E599
E601
E735
E552
E630
E282
E283
E198
E600
E602
E647
E623
E193
E632
E627
E604
E605
E641
E731
E22
E508
E97
E343
E355
E367
E210
E340
E469
E43
E548
E633
E292
E290
E182
E439
E636
E639
E609
E144
E557
E119
E413
E684
E59
E73
E260
E565
E795
E775
E797
E117
E79
Glyptapanteles
E702
E740
E807
E792
E802
E804
E265
E617
E736
E737
E13
E14
GE2
GE4
GE5
E156
E550
E644
E287
E338
E261
E524
E800
E481
E216
E207
E177
E751
E11
E12
E482
E651
E299
E590
E569
E21
E258
E529
E619
E681
E264
E268
E34
E5
E6
E85
E683
E76
E422
E474
E427
E467
E712
Cotesia
E505
E798
E504
E80
E592
E7
E598
Iconella
E197
E441
E621
E638
E640
E342
E344
E345
E62
E377
E381
E378
E379
E434
E270
E276
E235
E60
E252
E106
E310
E311
E124
E133
E418
E611
E613
E278
E218
E612
E300
E302
E123
E661
Choeras (small fore wing areolet)
0.04

Appendix 4:

Chapter 2: Supplementary Table S1

Specimen information for all specimens successfully and unsuccessfully DNA barcoded with Genbank and BOLD numbers

Extraction code	BOLD process ID	Genbank accession COI	Genbank accession WG	Institution	Institution voucher/accession number	State	Locality	Latitude (as on label)	Longitude (as on label	Latitude (for mapping)	Longitude (for mapping)	Date	Collector	Elevation	Label notes	Sex	Genus ID	Species ID
E1	AUMIC004-18	MH138684	MH139168	WINC	FreezerPro_1480380	S. Aust	Bon Bon Stn	30°23'41"S	135°26'52"E	-30.39472	135.44778	25/10/2010	S. Mantel		Bush Blitz Svy SM134 at light in swale with Rutidosis helichrysoides	F	Diolcogaster sp_8	
E10	AUMIC005-18	MH138693	MH139177	WINC	FreezerPro_1480389	S. Aust	Bon Bon Stn	30°19'94"S	135°28'42"E	-30.33233	135.49306	25-28/10/2010	S. Mantel, F. Colombo, R.K., G. Taylor		Malaise trap 6	M	Diolcogaster sp_17	
E100	AUMIC006-18	MH138984	MH139388	WINC	FreezerPro_1480459	S. Aust	Kangaroo Is. Flinders Chase	35°56.085'S	136°43.655'E	-35.93475	136.72757	19/03/2011	GS Taylor, E Kinnaird		Platypus Waterhole carpark, swept heath & groundcover	M	Miropotes sp_6	
E101	AUMIC007-18	MH138599	MH139097	WINC	FreezerPro_1480460	S. Aust	Kangaroo Is. Flinders Chase	35°57.08'S	136°44.27'E	-35.95134	136.73784	22/03/2011	GS Taylor, E Kinnaird		Light trap & window, Flinders Baudin Research Centre	F	Choeras morialta	
E102	AUMIC008-18	MH138745	MH139217	WINC	FreezerPro_1480461	S. Aust	Middleback Research Centre, 20 km NW Whyalla	32°56.790'S	137°23.676'E	-32.9465	137.39459	3/07/2011	G.S. Taylor		swept Acacia papyrocarpa	F	Dolichogenidea sp_11	
E103	AUMIC009-18	MH138551	MH139058	WINC	FreezerPro_1480462	S. Aust	Mt Barker, 8km S Bugle Ranges	35°06'47"S	138°52'15"E	-35.11305	138.87083	31/03-07/04/2008	R. Lavigne		Mallee Scrub	F	Apanteles sp_6	
E104	AUMIC010-18	MH138944		WINC	FreezerPro_1480463	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula			-35.45361	138.60611	25/10/2000	C. Stephens		Malaise trap in bridal creeper invaded eucalypt woodland	F	unknown sp_3	
E105	AUMIC011-18	MH138932		WINC	FreezerPro_1480464	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula			-35.45361	138.60611	12/10/2000	C. Stephens		Malaise trap in bridal creeper invaded eucalypt woodland	F	unknown sp_3	
E106	AUMIC012-18	MH138600		WINC	FreezerPro_1480465	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula			-35.45361	138.60611	23/11/2000	C. Stephens		Malaise trap in bridal creeper invaded eucalypt woodland	F	Choeras sp_1	
E108	AUMIC013-18	MH138670	MH139155	WINC	FreezerPro_1480466	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula			-35.45361	138.60611	23/11/2000	C. Stephens		Malaise trap in bridal creeper invaded eucalypt woodland	F	Diolcogaster sp_18	perniciosa
E11	AUMIC014-18	MH138649	MH139135	WINC	FreezerPro_1480390	VIC	Australian Bible Museum Butterfly Garden, St. Arnaud			-36.61281	143.25478	2013	E. Reid		Reared Cabbage white butterfly	?	Cotesia sp_12	
E112	AUMIC015-18	MH138663	MH139148	WINC	FreezerPro_1480467	S. Aust	Wild Dogs Glen, Waite Campus Adelaide University			-34.9679	138.6302	16/11/2000			MT Uphill	F	Diolcogaster sp_3	
E114	AUMIC016-18	MH138568	MH139074	WINC	FreezerPro_1480468	WA	Albany Highway. Gleneagle State Forest.			-32.27111	116.16334	03/04-07/05/2005	M.S. Harvey		Malaise trap	F	Apanteles sp_7	
E115	AUMIC017-18	MH138744	MH139216	WINC	FreezerPro_1480469	WA	Cowaramup Bay Rd.			-33.8587	115.0426	6/02/2009	S. Thompson		Sweeping cliff top coastal heathland	F	Dolichogenidea sp_19	
E116	AUMIC018-18	MH138569	MH139075	WINC	FreezerPro_1480470	WA	Gleneagle State Forest			-32.27111	116.16334	29/11/2005	M.S. Harvey		Malaise Trap	F	Apanteles sp_7	
E117	AUMIC019-18	MH138764	MH139234	WINC	FreezerPro_1480471	WA	Gleneagle State Forest			-32.27111	116.16334	29/11/2005	M.S. Harvey		Malaise Trap	F	Glyptapanteles sp_3	
E118	AUMIC020-18	MH138703	MH139185	WINC	FreezerPro_1480472	WA	Gleneagle State Forest			-32.27111	116.16334	29/11/2005	M.S. Harvey		Malaise Trap	F	Diolcogaster sp_19	
E119	AUMIC021-18	MH138753	MH139224	WINC	FreezerPro_1480473	WA	Gleneagle State Forest			-32.27111	116.16334	09-08/10/2005	M.S. Harvey		M/T	F	Glyptapanteles sp_17	
E12	AUMIC022-18	MH138646	MH139132	WINC	FreezerPro_1480390	VIC	Australian Bible Museum Butterfly Garden, St. Arnaud			-36.61281	143.25478	2013	E. Reid		Cabbage white butterfly	?	Cotesia sp_12	
E120	AUMIC023-18	MH138975	MH139382	WINC	FreezerPro_1480474	WA	Talyuberlup Peak Picnic Site Warndoo open forest	34.24.53S,	117.57.27E.347	-34.41472	117.9575	7-10/02/2009	S. Thompson/A. Austin		Warndoo open forest	F	Miropotes sp_2	
E121	AUMIC024-18	MH138792	MH139255	WINC	FreezerPro_1480475	WA	Walpole-Nomalup NP Valley of the Gaints Road	34°58'57"S	116°55'16"E	-34.9825	116.92111	11/02/2009	S. Thompson		sweep net	F	unknown sp_9	
E122	AUMIC025-18	MH138576	MH139079	WINC	FreezerPro_1480476	ACT	Lyneham Ridge			-35.2507	149.1108	emg. Late 2016	M.F. Braby		Reared from Jalmenus spp.	F	Apanteles sp_30	
E123	AUMIC026-18	MH138601	MH139098	WINC	FreezerPro_1480477	S. Aust	Cox Scrub Con. Pk.	35°19'52"S	138°44'51"E	-35.33111	138.7475	25/01/2016-13/02/2016	A. Austin		M/T	F	Choeras sp_3	
E124	AUMIC027-18	MH138602	MH139099	WINC	FreezerPro_1480478	S. Aust	Cox Scrub Con. Pk.	35°19'55"S	138°44'45"E	-35.33194	138.74583	9-25/01/2016	A. Austin		M/T	F	Choeras sp_2	
E125	AUMIC028-18	MH138743	MH139215	WAD PIRD	N5561-1	WA	Barrow Island	WGS84: 337659	WGS84: -7697280	-20.81724	115.43975	25/09/2006	S. Callan & R. Graham		CC2 SUC2	F	Dolichogenidea sp_25	
E126	AUMIC029-18	MH138742	MH139214	WAD PIRD	N5561-2	WA	Barrow Island	WGS84: 337659	WGS84: -7697280	-20.81724	115.43975	25/09/2006	S. Callan & R. Graham		CC2 SUC2	M	Dolichogenidea sp_25	
E127	AUMIC030-18	MH138741	MH139213	WAD PIRD	N5562-1	WA	Barrow Island	WGS84: 334264	WGS84: -7691974	-20.86475	115.40669	6/05/2006	S. Callan & R. Graham		N05 SUC	F	Dolichogenidea sp_5	
E128	AUMIC031-18	MH138740	MH139212	WAD PIRD	N5562-2	WA	Barrow Island	WGS84: 334264	WGS84: -7691974	-20.86475	115.40669	6/05/2006	S. Callan & R. Graham		N05 SUC	F	Dolichogenidea sp_5	
E129	AUMIC032-18	MH138592	MH139094	WAD PIRD	N5562-3	WA	Barrow Island	WGS84: 334264	WGS84: -7691974	-20.86475	115.40669	6/05/2006	S. Callan & R. Graham		N05 SUC	F	Apanteles sp_8	
E13	AUMIC033-18	MH138645	MH139131	WINC	FreezerPro_1480391	VIC	Australian Bible Museum Butterfly Garden, St. Arnaud			-36.61281	143.25478	2013	E. Reid		Reared Delias aganippe	?	Cotesia sp_9	
E132	AUMIC034-18	MH138496	MH139019	ANIC	32 130182	QLD	Nardoo Patch, 11km NNE 12 Mile Bore	23°4'0"S	138°11'32"E	-23.06667	138.19223	18-21/04/2007	0		malaise trap	F	Apanteles sp_32	
E133	AUMIC035-18	MH138603		ANIC	32 130183	WA	Watheroo NP, Jingemia Caves	30°15'15"S	115°59'56"E	-30.25417	115.99889	17/09/2003 - 07/11/2003	C Lambkin N starick J Recsei		malaise closed heath 273 m	F	Choeras sp_2	

E136	AUMIC036-18	MH138498		ANIC	32 130184	WA	Karijini NP, Juna Downs Rd	22°44'22"S	118°24'46"E	-22.73944	118.41278	25/04/2003 - 14/05/2003	C Lambkin T weir		malaise dry Turee creek grassy open Eucalypt scrub	F	Apanteles sp_32
E138	AUMIC037-18	MH138501	MH139022	ANIC	32 130185	NT	Keep River National Park; Bail-Me-Up Cr. 23.7 km SSW Jarrnarm Camp Ground	15°57'55"S	129°01'52"E	-15.96528	129.03111	13-20/06/2001	ME Irwin, FD Parker, C Lambkin		malaise in dry creekbed	F	Apanteles sp_32
E139	AUMIC038-18	MH138701	MH139183	ANIC	32 130186	ACT	Taouk Trail just South of Cotter Hut	35°39'19.2"S	148°49'44.4"E	-35.65528	148.8289	10-12/12/2013	D Yeates, C Manchester, K Meusemann		small malaise trap, grassy gully over watercourse in open Eucalyptus forest, 1074m	F	Diolcogaster sp_3
E14	AUMIC039-18	MH138641	MH139128	WINC	FreezerPro_1480391	VIC	Australian Bible Museum Butterfly Garden, St. Arnaud			-36.61281	143.25478	2013	E. Reid		Reared from Delias aganippe	?	Cotesia sp_9
E140	AUMIC040-18	MH138990		ANIC	32 130187	WA	Porongerup NP over small running creek in Jarrah woodland 351m	34°40.384'S	117°53.551'E	-34.67307	117.89252	03-15/11/2003	C Lambkin, J Recsei		malaise	F	Sathon sp_4
E141	AUMIC041-18	MH138958		ANIC	32 130188	WA	Watheroo NP, Jingemia Caves	30°15'15"S	115°59'56"E	-30.25417	115.99889	17/09/2003 - 07/11/2003	C Lambkin N starick J Recsei		malaise closed heath 273 m	F	Microplitis sp_8
E144	AUMIC042-18	MH138771	MH139241	ANIC	32 130189	WA	23 km NNW Albany	34°51.191S	117°48.565E	-34.85318	117.80942	16/11/2000	T Simmul S Cunningham		malaise remnant vegetation	F	Glyptapanteles sp_18
E145	AUMIC043-18	MH138739		ANIC	32 130190	WA	21 km nth of Albany	34°50.266S	117°45.669E	-34.83776	117.76115	16/11/2000	M Court S Cunningham		malaise cleared between native renmant Euc globulus plantation	F	Dolichogenidea sp_27
E149	AUMIC044-18	MH138510	MH139029	ANIC	32 130191	NT	Keep River National Park; Nigli Gap, 1.5 km E Jarrnarm Camp Ground	15°45'42"S	129°06'45"E	-15.76167	129.1125	11-20/06/2001	ME Irwin, FD Parker, C Lambkin		malaise over running stream	F	Apanteles sp_4
E15	AUMIC045-18	MH138952	MH139371	WINC	FreezerPro_1480392	VIC	Australian Bible Museum Butterfly Garden, St. Arnaud			-36.61281	143.25478	2013	E. Reid		Reared from Vanessa itea	?	Microplitis sp_2
E150	AUMIC046-18	MH138698		ANIC	32 130192	NT	Gregory NP; 5.7 km N Humbert Junction	16°03'44"S	130°27'04"E	-16.06222	130.45111	12-16/06/2001	ME Irwin, FD Parker, C Lambkin		malaise trap in dry creek bed	F	Diolcogaster sp_15
E152	AUMIC047-18	MH138512	MH139031	ANIC	32 130193	NT	Gregory NP: Limestone Gorge	16°03'01"S	130°24'07"E	-16.05028	130.40193	06-13/06/2001	ME Irwin, FD Parker, C Lambkin		malaise in dry gully	F	Apanteles sp_4
E153	AUMIC048-18	MH138513	MH139032	ANIC	32 130194	NT	Gregory NP: Limestone Gorge	16°03'01"S	130°24'07"E	-16.05028	130.40193	06-13/06/2001	ME Irwin, FD Parker, C Lambkin		malaise in dry gully	F	Apanteles sp_27
E155	AUMIC049-18	MH138514		ANIC	32 130195	QLD	3.6 km NW Homestead on Plum Pudding Track, Cravens Peak Station	23°18'46"S	138°33'45"E	-23.31278	138.5625	21-24/04/2007	C Lemann		malaise trap, spinifex	F	Apanteles sp_35
E156	AUMIC050-18	MH138638		ANIC	32 130196	NT	76.9 km NNE Lajamanu	17°40'30"S	130°54'14"E	-17.675	130.90388	11-17/06/2001	M.E. Irwin, F.D. Parker, C. Lambkin		malaise in deep dry gully below water hold	F	Cotesia sp_11
E157	AUMIC051-18	MH138903	MH139340	ANIC	32 130197	NT	Gregory Nat Park 8.3 km N Humbert Junction	16°02'26"S	130°27'18"E	-16.04056	130.455	06-12/06/2001	ME Irwin, FD Parker, C Lambkin		malaise in dry bed nr flowing ck	F	unknown sp_11
E158	AUMIC052-18	MH138697	MH139180	ANIC	32 130198	NT	Gregory Nat Park 8.3 km N Humbert Junction	16°02'26"S	130°27'18"E	-16.04056	130.455	06-12/06/2001	ME Irwin, FD Parker, C Lambkin		malaise in dry bed nr flowing ck	F	Diolcogaster sp_14
E16	AUMIC053-18	MH138957	MH139373	WINC	FreezerPro_1480392	VIC	Australian Bible Museum Butterfly Garden, St. Arnaud			-36.61281	143.25478	2013	E. Reid		Reared from Vanessa itea	?	Microplitis sp_2
E160	AUMIC054-18	MH138772	MH139242	ANIC	32 130199	NT	Gregory National Park, Station Creek, 0.2 km NNW Bullita Cmp Grnd	16°06'42"S	130°25'23"E	-16.11167	130.42307	12/01/2001	ME Irwin, FD Parker, C Lambkin		malaise trap	F	Glyptapanteles sp_10
E161	AUMIC055-18	MH138517	MH139034	ANIC	32 130200	NT	Gregory National Park; Bullita Camp Ground	16°06'47"S	130°25'24"E	-16.11306	130.42334	05-14/06/2001	FD Parker ME Irwin C Lambkin		malaise in dry creekbed	F	Apanteles sp_14
E163	AUMIC056-18	MH138518		CSIRO WA	FreezerPro_1480376	WA	Northwest Kimberly	-15.4011 S	124.6495 E	-15.4011	124.6495	28/01/2013	OR Edwards & RK Didham CSIRO		Dambimangari Spatial block 2 26/1 Malaise trap sample (7days) M26/1R3se	F	Apanteles sp_15
E164	AUMIC057-18	MH138696		CSIRO WA	FreezerPro_1480377	WA	Northwest Kimberly	-15.5039 S	124.5628 E	-15.5039	124.5628	28/01/2013	OR Edwards & RK Didham CSIRO		Dambimangari Spatial block 2 26/3 Malaise trap sample (7days) M26/3R4se	F	Diolcogaster sp_1
E165	AUMIC058-18	MH138738	MH139211	CSIRO WA	FreezerPro_1480378	WA	Northwest Kimberly	-14.2462 S	125.6165 E	-14.2462	125.6165	12/01/2013	OR Edwards & RK Didham CSIRO		Wunambal Gaambera spatial block 4 9/2 Malaise trap sample (7days) M09/2R3se	M	Dolichogenidea sp_38
E166	AUMIC059-18	MH138977		CSIRO WA	FreezerPro_1480379	WA	Northwest Kimberly	-14.6222 S	125.87 E	-14.6222	125.87	13/01/2013	OR Edwards & RK Didham CSIRO		Wunambal Gaambera spatial block 4 11/2 Malaise trap sample (7days) M11/2S1nw	F	Miropotes sp_7
E17	AUMIC060-18	MH138953	MH139372	WINC	FreezerPro_1480393	VIC	Australian Bible Museum Butterfly Garden, St. Arnaud			-36.61281	143.25478	2013	E. Reid		Reared Vanessa itea	?	Microplitis sp_2
E173	AUMIC061-18	MH138695	MH139179	WINC	FreezerPro_1480479	S. Aust	Cox Scrub Con. Pk.	35°19'52"S	138°44'51"E	-35.33111	138.7475	20/03-03/04/2016	E. Fagan-Jeffries		M/T	F	Diolcogaster sp_3
E174	AUMIC062-18	MH138521		WINC	FreezerPro_1480480	S. Aust	Cox Scrub Con. Pk.	35°19'55"S	138°44'45"E	-35.33194	138.74583	03-17/04/2016	E. Fagan-Jeffries		M/T	F	Apanteles sp_17
E176	AUMIC063-18	MH138970	MH139378	WINC	FreezerPro_1480481	S. Aust	Cox Scrub Con. Pk.	35°19'52"S	138°44'51"E	-35.33111	138.7475	17/04/2016 - 01/05/2016	E. Fagan-Jeffries		M/T	F	Microplitis sp_15
E177	AUMIC064-18	MH138634	MH139124	WINC	FreezerPro_1480482	S. Aust	Cox Scrub Con. Pk.	35°19'55"S	138°44'45"E	-35.33194	138.74583	17/04/2016 - 01/05/2016	E. Fagan-Jeffries		M/T		Cotesia sp_7
E179	AUMIC065-18	MH138737	MH139210	QM	T208384	QLD	Lamington NP	28.21	153.127	-28.21	153.127	06-22/01/2009	G. Monteith	0	IBISCA 900 OF malaise trap	F	Dolichogenidea sp_30
E18	AUMIC066-18	MH138967	MH139375	WINC	FreezerPro_1480393	VIC	Australian Bible Museum Butterfly Garden, St. Arnaud			-36.61281	143.25478	2013	E. Reid		Reared Vanessa itea	?	Microplitis sp_2

E180	AUMIC067-18	MH138974	MH139381	QM	T208410	QLD	Lamington NP	28.21	153.127	-28.21	153.127	06-22/01/2009	G. Monteith	0	IBISCA 900 OF malaise trap	F	Miropotes sp_10
E181	AUMIC068-18	MH138523	MH139037	QM	T208356	QLD	Cainbable Quarry, OF	28.145	153.113	-28.145	153.113	03-19/02/2009	F. Turco	0	malaise trap	F	Apanteles sp_20
E182	AUMIC069-18	MH138751	MH139222	QM	T208408	QLD	Cainbable Quarry, OF	28.145	153.113	-28.145	153.113	03-19/02/2009	F. Turco	0	malaise trap	F	Glyptapanteles sp_29
E183	AUMIC070-18	MH138524	MH139038	QM	T208347	QLD	Cainbable Quarry, OF	28.145	153.113	-28.145	153.113	06-22/01/2009	G. Monteith	0	malaise trap	F	Apanteles sp_9
E184	AUMIC071-18	MH138525	MH139039	QM	T208357	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	23/09/2014-5/10/2014	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Apanteles sp_21
E185	AUMIC072-18	MH138959		QM	T208369	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	23/09/2014-5/10/2014	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Microplitis sp_9
E187	AUMIC073-18	MH138951		QM	T208368	QLD	Cudmore NP	-22.969	146.379	-22.969	146.379	28/10/ 2010 - 02/08/2011	Lambkin, Starick & Bailey	351m	CM3M Melaleuca heath nr drying creek malaise trap	M	Microplitis sp_6
E188	AUMIC074-18	MH138526	MH139040	QM	T208348	QLD	Masthead Island	23.537	151.721	-23.537	151.721	05-07/10/2008	QM/QPWS party	0-5m	site 7 Casuarina forest malaise trap	F	Apanteles sp_11
E189	AUMIC075-18	MH138966		QM	T208373	QLD	Lamington NP	28.216	153.142	-28.216	153.142	15-25/01/2007	C Lambkin, N. Starick	560m	IBISCA Plot # IQ-500-A rainforest malaise trap	F	Microplitis sp_13
E19	AUMIC076-18	MH138694	MH139178	WINC	FreezerPro_1480394	S. Aust	Witchelina Stn	30°11'07"S	137°58'38"E	-30.18528	137.97722	18-22/10/2010	S. Mantel, F.C., R.K.		Bush Blitz Svy Malaise 2 in dry creek bed Eremophila freelingi and Acacia tetragonophila	F	Diolcogaster sp_8
E190	AUMIC077-18	MH138528	MH139041	QM	T208364	QLD	Lamington NP	28.148	153.137	-28.148	153.137	13-23/01/2007	C Lambkin, N. Starick	267m	IBISCA Plot # IQ-300-A rainforest malaise trap	F	Apanteles sp_25
E191	AUMIC078-18	MH138631	MH139121	WINC	FreezerPro_1480483	S. Aust	Morialta Conservation park			-34.90413	138.69839	26/03-10/04/2016	E. Fagan-Jeffries		M/T	M	Choeras morialta
E192	AUMIC079-18	MH138965		QM	T208371	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	08/02/2015-28/03/2015	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Microplitis sp_12
E193	AUMIC080-18	MH138754		QM	T208393	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	08/02/2015-28/03/2015	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Glyptapanteles sp_7
E194	AUMIC081-18	MH138530	MH139042	QM	T208355	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	08/02/2015-28/03/2015	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Apanteles sp_16
E196	AUMIC082-18	MH138954		QM	T208372	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	08/02/2015-28/03/2015	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Microplitis sp_12
E197	AUMIC083-18	MH138604	MH139100	QM	T208378	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	06/01/2015-8/02/2015	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Choeras sp_11
E198	AUMIC084-18	MH138756	MH139226	QM	T208400	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	06/01/2015-8/02/2015	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Glyptapanteles sp_9
E2	AUMIC085-18	MH138532	MH139044	WINC	FreezerPro_1480381	S. Aust	Bon Bon Stn	30°18'50"S	135°32'50"E	-30.31389	135.44778	08/02/2015-28/03/2015	R. Kittle		Bush Blitz Svy RK129 on Acacia victoriae sweep netting	F	Apanteles sp_22
E20	AUMIC086-18	MH138533	MH139045	WINC	FreezerPro_1480395	S. Aust	Witchelina Stn	30°11'07"S	137°58'38"E	-30.18528	137.97722	18-22/10/2010	S. Mantel, F.C., R.K.		Bush Blitz Svy Malaise 2 in dry creek bed Eremophila freelingi and Acacia tetragonophila	F	Apanteles sp_5
E202	AUMIC087-18	MH138534	MH139046	QM	T208361	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	05-22/10/2014	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap		Apanteles sp_21
E203	AUMIC088-18	MH138535	MH139047	QM	T208365	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	22/10/2014-14/11/2014	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Apanteles sp_28
E204	AUMIC089-18	MH138982	MH139387	QM	T208411	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	22/10/2014-14/11/2014	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Miropotes sp_13
E205	AUMIC090-18	MH138536	MH139048	QM	T208362	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	14/11/2014-16/12/2014	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Apanteles sp_21
E206	AUMIC091-18	MH138537		QM	T208358	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	14/11/2014-16/12/2014	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Apanteles sp_21
E207	AUMIC092-18	MH138661	MH139146	WINC	FreezerPro_1480484	S. Aust	Cox Scrub Con. Pk.	35°19'55"S	138°44'45"E	-35.33194	138.74583	03-17/04/2016	E. Fagan-Jeffries		M/T	F	Cotesia sp_3
E209	AUMIC093-18	MH138539	MH139050	WINC	FreezerPro_1480485	S. Aust	Cox Scrub Con. Pk.	35°19'52"S	138°44'51"E	-35.33111	138.7475	01-14/05/2016	E. Fagan-Jeffries		M/T	M	Apanteles sp_19
E21	AUMIC094-18	MH138659	MH139144	WINC	FreezerPro_1480396	S. Aust	Witchelina Stn	30°11'07"S	137°58'38"E	-30.18528	137.97722	18-22/10/2010	S. Mantel, F.C., R.K.		Bush Blitz Svy Malaise 2 in dry creek bed Eremophila freelingi and Acacia tetragonophila	F	Cotesia sp_13
E210	AUMIC095-18	MH138761	MH139231	WINC	FreezerPro_1480486	S. Aust	Mt Barker Summit			-35.066103	138.922692	07-20/03/2016	A. Austin		M/T	F	Glyptapanteles sp_25
E211	AUMIC096-18	MH138985	MH139389	WINC	FreezerPro_1480487	S. Aust	Belair N.P. (lower site)			-35.009	138.65401	27/10/2007/-10/11/2007	J.T. Jennings		M/T	F	Sathon sp_7
E214	AUMIC097-18	MH138876	MH139318	WINC	FreezerPro_1480488	S. Aust	Kangraoo Is. Emu Bay Sect 193 Hd Menzies			-35.592	137.541	24/10/2005	F. Vickery		Sample 2 Malaise Trap	F	unknown sp_4
E215	AUMIC098-18	MH138541	MH139052	WINC	#N/A	NSW	Broken Head	S 28.698408	E 153.599038	-28.698408	153.599038	1/03/2015	T. Moore		Pseudodipsas cephenes 1st instar	F	Apanteles sp_31
E216	AUMIC099-18	MH138658	MH139143	WINC	#N/A	NSW	Mine Rd Dubbo	S 32.254261	E 148.534345	-32.254261	148.534345	12/10/2014	T. Moore		Ogyris genoveva gela	M	Cotesia sp_5
E218	AUMIC100-18	MH138605		ANIC	32 130201	NSW	East Boyd State Forest, Goanna Rd,	37°12'05"S	149°46'30"E	-37.20139	149.77499	06/12/2004 - 12/01/2005	C Lambkin N Starick		malaise across disused snig track in forest 56 km SE Bombala 219 m	F	Choeras sp_3
E22	AUMIC101-18	MH138768	MH139238	WINC	FreezerPro_1480397	S. Aust	Witchelina Stn	30°11'07"S	137°58'38"E	-30.18528	137.97722	18-22/10/2010	S. Mantel, F.C., R.K.		Bush Blitz Svy Malaise 2 in dry creek bed Eremophila freelingi and Acacia tetragonophila	F	Glyptapanteles sp_27
E220	AUMIC102-18	MH138692	MH139176	ANIC	32 130202	NSW	Kosciuszko NP, 1.8 km NE of Thredbo	36°29'49"S	148°18'51"E	-36.49694	148.31416	15-17/03/2003	C Lambkin N starick J Recsei		malaise over narrow stream in grassland 1480m	M	Diolcogaster sp_4

E221	AUMIC103-18	MH138545		ANIC	32 130203	NT	Gregory NP, 17.4 km N Humbert Junction	15°58'17"S	130°29'17"E	-15.97139	130.48805	24/05-04/06/2001	T Weir, K pullen, P Bouchard		malaise in damp meadow	F	Apanteles sp_34
E223	AUMIC104-18	MH138630	MH139120	WINC	#N/A	S. Aust	Morialta Conservation park	34.90413°S,	138.69839°E	-34.90413	138.69839	24/04/2016 - 08/05/16/2016	E. Fagan-Jeffries		M/T	M	Choeras morialta
E224	AUMIC105-18	MH138633	MH139123	WINC	#N/A	S. Aust	Morialta Conservation park	34.90413°S,	138.69839°E	-34.90413	138.69839	24/04/2016 - 08/05/16/2016	E. Fagan-Jeffries		M/T	M	Choeras morialta
E23	AUMIC106-18	MH138955		WINC	FreezerPro_1480398	S. Aust	Witchelina Stn	30°00'01"S	137°46'58"E	-30.00028	137.78278	20/10/2010	R. Kittel		Bush Blitz Svy RK066 sweeping	F	Microplitis sp_7
E230	AUMIC107-18	MH138736	MH139209	WINC	FreezerPro_1480489	Qld	Kuranda			-16.81538	145.6425	18-31/10/2016	M.S. Moulds		M/T	M	Dolichogenidea sp_15
E231	AUMIC108-18	MH138735	MH139208	WINC	FreezerPro_1480490	NT	Baramundie Falls Kakadu NP			-13.32184	132.437039	19/11/1992	Austin/PCD		Sweep net	M	Dolichogenidea sp_26
E232	AUMIC109-18	MH138548	MH139056	WINC	FreezerPro_1480491	NT	Kakadu NP Mirray Lookout			-12.8768	132.7038	17/11/1992	Austin/PCD		Sweep net open acacia	M	Apanteles sp_29
E233	AUMIC110-18	MH138549		WINC	FreezerPro_1480492	NT	Kakadu NP Mirray Lookout			-12.8768	132.7038	17/11/1992	Austin/PCD		Sweep net open acacia	M	Apanteles sp_32
E234	AUMIC111-18	MH138550	MH139057	WINC	FreezerPro_1480493	NT	Casurina coastal Reserve Darwin			-12.36172	130.867971	1992	Austin/PCD		sweeping	F	Apanteles sp_8
E235	AUMIC112-18	MH138606	MH139101	WINC	FreezerPro_1480494	NT	Litchfield NP Termite mounds			-13.10330	130.84482	14/11/1992	Dangerfield		sweeping	F	Choeras sp_13
E24	AUMIC113-18	MH138552	MH139059	WINC	FreezerPro_1480399	S. Aust	Witchelina Stn	30°01'22"S	137°54'10"E	-30.02278	137.90277	13/10/2010	S. Mantel		Bush Blitz Svy SM034 sweeping Acacia salicina	F	Apanteles sp_5
E240	AUMIC114-18	MH138553		QM	T208346	QLD	Plevna Downs, Tompilly Hill base (PD6 M)	26.728S	142.651E	-26.728	142.651	16/09/2008 - 2/10/2008	Lambkin Mackenzie Starick	187m	Gidgee malaise	F	Apanteles sp_8
E247	AUMIC115-18	MH138937		WINC	FreezerPro_1480495	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula			-35.45361	138.60611	25/10/2000	C. Stephens		M/T in native plot within bridal creeper invaded eucalypt woodland	F	unknown sp_3
E248	AUMIC116-18	MH138685	MH139169	WINC	FreezerPro_1480496	S. Aust	Bon Bon Stn	30°25'29"S	135°28'41"E	-30.42472	135.53778	26/10/2010	S. Mantel		Bush Blitz Svy SM164 Under Acacia aneura at light.	F	Diolcogaster sp_9
E249	AUMIC117-18	MH138935		WINC	FreezerPro_1480497	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula			-35.45361	138.60611	25/10/2000	C. Stephens		Malaise trap in bridal creeper invaded eucalypt woodland	F	unknown sp_3
E25	AUMIC118-18	MH138555	MH139061	WINC	FreezerPro_1480400	S. Aust	Witchelina Stn	30°01'10"S	137°52'34"E	-30.01944	137.87611	13/10/2010	F. Colombo, R. Kittle, S. Mantel		Bush Blitz Svy SM031 yellow pan trap in Swainsona stipularis	F	Apanteles sp_5
E250	AUMIC119-18	MH138998	MH139397	WINC	FreezerPro_1480498	S. Aust	Belair N.P. Gate 9			-35.009	138.65401	25/11-01/12/2007	J.T. Jennings		Malaise Trap	F	Sathon sp_2
E251	AUMIC120-18	MH138972	MH139380	WINC	FreezerPro_1480499	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	01-08/03/2008	J.T. Jennings		Malaise Trap	F	Miropotes sp_3
E252	AUMIC121-18	MH138607	MH139102	WINC	FreezerPro_1480500	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	25/11/2016-14/12/2016	M.S. Moulds		M/T	F	Choeras sp_1
E253	AUMIC122-18	MH138734	MH139207	WAD PIRD	N5563-1	WA	Barrow Island	WGS84 (50) 336732	7698579	-20.80554	115.43121	1/05/2007	S. Callan K. Edwards		N15 SUC	F	Dolichogenidea sp_31
E254	AUMIC123-18	MH139003	MH139401	WINC	FreezerPro_1480501	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula	35°27'13"S	138°36'22"E	-35.45361	138.60611	19/12/2016-30/12/2016	E. Fagan-Jeffries		M/T	F	Sathon sp_1
E255	AUMIC124-18	MH138988	MH139392	WINC	FreezerPro_1480502	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula	35°27'13"S	138°36'22"E	-35.45361	138.60611	03/11/2016-19/12/2016	E. Fagan-Jeffries		M/T	F	Sathon sp_1
E256	AUMIC125-18	MH138733	MH139206	WAM	E94085	WA	Karijini NP, Karijini Dr	22°34'18"S	118°18'26"E	-22.57167	118.30723	19-25/04/2003	C Lambkin T Weir		malaise open Eucalyptus grassland 814m	F	Dolichogenidea sp_32
E257	AUMIC126-18	MH138557	MH139063	SAM	SAMA 32-035446	SA	Andamooka Station	from -30.8198802 to -30.6998403	137.1783585 t0 - 137.1574435	-30.72701	137.2036	31/08/2016	R. Leijs		Vehicle net, Bush Blitz Lake Torrens	F	Apanteles sp_29
E258	AUMIC127-18	MH138640		SAM	SAMA 32-035449	SA	Andamooka Station	from -30.8198802 to -30.6998403	137.1783585 t0 - 137.1574435	-30.72701	137.2036	31/08/2016	R. Leijs		Vehicle net, Bush Blitz Lake Torrens	F	Cotesia sp_13
E259	AUMIC128-18	MH138928	MH139360	SAM	SAMA 32-035453	SA	Andamooka Station	from -30.8198802 to -30.6998403	137.1783585 t0 - 137.1574435	-30.72701	137.2036	31/08/2016	R. Leijs		Vehicle net, Bush Blitz Lake Torrens	F	unknown sp_6
E26	AUMIC129-18	MH138732		WINC	FreezerPro_1480401	S. Aust	Witchelina Stn	29°59'46"S	138°04'02"E	-29.99611	138.06721	11/10/2010	S. Mantel		Bush Blitz Svy SM001sweeping Senecio lanibractus and bluebush	F	Dolichogenidea sp_35
E260	AUMIC130-18	MH138770	MH139240	SAM	SAMA 32-035451	SA	Andamooka Station	from -30.8198802 to -30.6998403	137.1783585 t0 - 137.1574435	-30.72701	137.2036	31/08/2016	R. Leijs		Vehicle net, Bush Blitz Lake Torrens	F	Glyptapanteles sp_23
E261	AUMIC131-18	MH138637	MH139126	SAM	SAMA 32-035455	SA	Andamooka	-30.72701	137.2036	-30.72701	137.2036	30/08/2016	B.A. Parslow		sweeping, Bush Blitz Lake Torrens	F	Cotesia sp_6
E262	AUMIC132-18	MH138560	MH139066	SAM	SAMA 32-035790	SA	Andamooka Station, 3.1 km ESE Andamooka HS	30.73944S	137.22946E	-30.73944	137.22946	31/08/2003-03/09/2016	B.A. Parslow & G. Taylor		Malaise, chenopods on gibber BS 1097 AND002, Bushblitz Lake Torrens	F	Apanteles sp_29
E264	AUMIC133-18	MH138662	MH139147	SAM	SAMA 32-935852	SA	Roxby Downs Station, 14.2 km WSW Roxby Downs HS	30.769	136.62545	-30.769	136.62545	1/09/2016	B.A. Parslow		LT1 Bushblitz Lake Torrens	F	Cotesia sp_13
E265	AUMIC134-18	MH138660	MH139145	SAM	SAMA 32-035867	SA	Andamooka Station, Andamooka HS to Wirrda Well	30.72627-30.67943	137.20149-137.07232	-30.72627	137.20149	31/08/2016	R. Leijs		Vehicle net VN2, Bushblitz Lake Torrens	F	Cotesia sp_2
E266	AUMIC135-18	MH138836	MH139290	SAM	SAMA 32-035458	SA	Andamooka Station, Andamooka HS to Wirrda Well	30.72627-30.67943	137.20149-137.07232	-30.72627	137.20149	31/08/2016	R. Leijs		Vehicle net VN2, Bushblitz Lake Torrens	F	unknown sp_6
E267	AUMIC136-18	MH138563	MH139069	SAM	SAMA 32-035456	SA	Andamooka Station, Andamooka HS to Wirrda Well	30.72627-30.67943	137.20149-137.07232	-30.72627	137.20149	31/08/2016	R. Leijs		Vehicle net VN2, Bushblitz Lake Torrens	F	Apanteles sp_29
E268	AUMIC137-18	MH138656	MH139141	SAM	SAMA 32-035457	SA	Andamooka Station, Andamooka HS to Wirrda Well	30.72627-30.67943	137.20149-137.07232	-30.72627	137.20149	31/08/2016	R. Leijs		Vehicle net VN2, Bushblitz Lake Torrens	F	Cotesia sp_13

E269	AUMIC138-18	MH138731		SAM	SAMA 32-035850	SA	Bosworth Station, 12.4 km WSW Bosworth HS	30.99847	137.41405	-30.99847	135.44778	5/09/2016	B. A. Parslow	LT26, Bushblitz Lake Torrens	F	Dolichogenidea sp_34
E27	AUMIC139-18	MH138962	MH139374	WINC	FreezerPro_1480402	S. Aust	Witchelina Stn	30°11'07"S	137°58'38"E	-30.18528	137.97722	18-22/10/2010	S. Mantel, F.C., R.K.	Bush Blitz Svy Malaise2A	F	Microplitis sp_16
E270	AUMIC140-18	MH138608	MH139103	TMAG	F59020	TAS	SW SSS2	-43.1413	146.76241	-43.1413	146.76241	03-09/02/2016	Kirrily Moore	Bush Blitz malaise trap (old)	F	Choeras sp_8
E271	AUMIC141-18	MH138999	MH139398	TMAG	F59021	TAS	SW SSS2	-43.1413	146.76241	-43.1413	146.76241	03-09/02/2016	Kirrily Moore	Bush Blitz malaise trap (old)	M	Sathon sp_11
E272	AUMIC142-18	MH138609		TMAG	F59022	TAS	SW SSS1	-43.199	146.78481	-43.199	146.78481	01-09/02/2016	Kirrily Moore	Bush Blitz malaise trap (new)	F	Choeras sp_4
E273	AUMIC143-18	MH138610	MH139104	TMAG	F59023	TAS	SW SSS1	-43.199	146.78481	-43.199	146.78481	01-09/02/2017	Kirrily Moore	Bush Blitz Pitfall trap 1	F	Choeras sp_4
E275	AUMIC144-18	MH138730		TMAG	F59024	TAS	Arve Forest: Conways Rd Incorrect SSS2	-43.14459	146.8421	-43.14459	146.8421	01-03/02/2016	Kirrily Moore	Bush Blitz Malaise trap	F	Dolichogenidea sp_28
E276	AUMIC145-18	MH138611	MH139105	TMAG	F59026	TAS	SW SSS2	-43.1413	146.76241	-43.1413	146.76241	03-09/02/2016	Kirrily Moore	Bush Blitz Malaise (new)	F	Choeras sp_8
E277	AUMIC146-18	MH138986	MH139390	TMAG	F59028	TAS	Tarkine SSS2	-41.6556	145.0819	-41.6556	145.0819	27/01/2015	Simon Grove	Malaise trap Bush Blitz Pieman River: E of Corinna campground	M	Sathon sp_3
E278	AUMIC147-18	MH138612	MH139106	TMAG	F59027	TAS	Tarkine SSS2	-41.6556	145.0819	-41.6556	145.0819	27/01/2015	Simon Grove	Malaise trap Bush Blitz Pieman River: E of Corinna campground	F	Choeras sp_3
E279	AUMIC148-18	MH138613		TMAG	F59029	TAS	SW SSS1	-43.199	146.78481	-43.199	146.78481	01-09/02/2016	Kirrily Moore	Yellow Pans	F	Choeras sp_4
E282	AUMIC149-18	MH138758	MH139228	WINC	FreezerPro_1480503	QLD	Toohey State Forest	27°32'15"E	153°03'25"S	-27.5375	153.05695	11/12/2016-02/01/2017	M.Rix	M/T	F	Glyptapanteles sp_13
E283	AUMIC150-18	MH138757	MH139227	WINC	FreezerPro_1480504	QLD	Toohey State Forest	27°32'15"E	153°03'25"S	-27.5375	153.05695	29.xi-11.xii.2016	M.Rix	M/T	F	Glyptapanteles sp_13
E286	AUMIC151-18	MH138971	MH139379	WINC	FreezerPro_1480505	QLD	Toohey State Forest	27°32'15"E	153°03'25"S	-27.5375	153.05695	15-28.i.2017	M.Rix	M/T	M	Miropotes sp_8
E287	AUMIC152-18	MH138657	MH139142	WINC	FreezerPro_1480506	S. Aust	Mt Remarkable National Park	32°50'18"S	138°2'12"E	-32.83833	138.03667	22/01/2017-18/2/2017	E. Fagan-Jeffries	M/T	F	Cotesia sp_11
E288	AUMIC153-18	MH138969	MH139377	WINC	FreezerPro_1480507	S. Aust	Wirrabara State Forest	33°5'26"S	138°10'54"E	-33.09055	138.18167	22/01/2017-18/2/2017	E. Fagan-Jeffries	M/T	M	Microplitis sp_4
E289	AUMIC154-18	MH138729	MH139205	WINC	FreezerPro_1480508	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	01/01/2017 - 21/01/2017	M.S. Moulds	M/T	F	Dolichogenidea sp_18
E290	AUMIC155-18	MH138752	MH139223	WINC	FreezerPro_1480509	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	01/01/2017 - 21/01/2017	M.S. Moulds	M/T	F	Glyptapanteles sp_33
E291	AUMIC156-18	MH138964		WINC	FreezerPro_1480510	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	01/01/2017 - 21/01/2017	M.S. Moulds	M/T	M	Microplitis sp_18
E292	AUMIC157-18	MH138750	MH139221	WINC	FreezerPro_1480511	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	01/01/2017 - 21/01/2017	M.S. Moulds	M/T	M	Glyptapanteles sp_33
E293	AUMIC158-18	MH138683	MH139167	WINC	FreezerPro_1480512	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	15/12/2016-31/12/2016	M.S. Moulds	M/T	M	Diolcogaster sp_21
E294	AUMIC159-18	MH138573	MH139077	WINC	FreezerPro_1480513	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	22/1/2017-8/2/2017	M.S. Moulds	M/T	F	Apanteles sp_3
E295	AUMIC160-18	MH138821	MH139277	WINC	#N/A	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	22/1/2017-8/2/2017	M.S. Moulds	M/T	F	unknown sp_7
E296	AUMIC161-18	MH138746	MH139218	WINC	FreezerPro_1480514	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	25/11/2016-14/12/2016	M.S. Moulds	M/T	F	Glyptapanteles sp_16
E297	AUMIC162-18	MH138968	MH139376	MV	HYM-61349	VIC	Homestead, Ned's Corner Bush Blitz, Patrick's light station	34°08'27"S	141°19'35"S	-34.14083	141.32639	23/11/2011	P. Lillywhite, P. Honan	BBNC 423 Light Trap	F	Microplitis sp_3
E298	AUMIC163-18	MH138728		MV	HYM-61353	VIC	Lake Coondah Mission Base Camp, on track to Betty Boo's Camp	38°04'47"S	141°47'10"S	-38.07972	141.78612	24-21/03/2011	R Marchant, S Hinkley	Malaise trap BBLC 414, Hym60916	F	Dolichogenidea sp_24
E299	AUMIC164-18	MH138654	MH139139	MV	HYM-61357	VIC	Tyrendarra	38°11'33"S	141°45'51"S	-38.1925	141.76416	22-31/03/2011	P. Lillywhite, S. Hinkley	malaise trap BBLC 411, HYM-60906	F	Cotesia sp_17
E3	AUMIC165-18	MH138727	MH139204	WINC	FreezerPro_1480382	S. Aust	Bon Bon Stn	30°18'50"S	135°32'50"E	-30.31389	135.44778	28/10/2010	R. Kittle	Bush Blitz Svy RK129 on Acacia victoriae sweep netting	F	Dolichogenidea sp_7
E300	AUMIC166-18	MH138614		MV	HYM-61350	VIC	Grampians National Park Bioscan	37°19'51"S	142°11'36" E	-37.33083	142.193333	26-28/11/2012	B. Patullo, P. Lillywhite	Malaise trap, Ming Ming Swamp GB442	F	Choeras sp_3
E302	AUMIC167-18	MH138615	MH139107	MV	HYM-61351	VIC	Grampians National Park Bioscan	37°19'53"S	142°11'17" E	-37.331389	142.188056	26-28/11/2012	B. Patullo, P. Lillywhite	Malaise trap, Ming Ming Swamp GB444	F	Choeras sp_3
E306	AUMIC168-18	MH138682		WINC	FreezerPro_1480515	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula	35°27'13"S	138°36'22"E	-35.45361	138.60611	19/12/2016-30/12/2016	E. Fagan-Jeffries	M/T	F	Diolcogaster sp_18
E307	AUMIC169-18	MH139000		WINC	FreezerPro_1480516	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula	35°27'13"S	138°36'22"E	-35.45361	138.60611	03/11/2016-19/12/2016	E. Fagan-Jeffries	M/T	F	Sathon sp_1
E309	AUMIC170-18	MH138996	MH139395	WINC	FreezerPro_1480517	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula	35°27'13"S	138°36'22"E	-35.45361	138.60611	03/11/2016-19/12/2016	E. Fagan-Jeffries	M/T	F	Sathon sp_1
E310	AUMIC171-18	MH138616		WINC	FreezerPro_1480518	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula	35°27'13"S	138°36'22"E	-35.45361	138.60611	03/11/2016-19/12/2016	E. Fagan-Jeffries	M/T	F	Choeras sp_1
E311	AUMIC172-18	MH138617		WINC	FreezerPro_1480519	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula	35°27'13"S	138°36'22"E	-35.45361	138.60611	03/11/2016-19/12/2016	E. Fagan-Jeffries	M/T	F	Choeras sp_1

E315	AUMIC173-18	MH138580		WINC FreezerPro_1480520	S. Aust	Witchelina Stn	30°04'22"S	138°07'52"E	-30.07278	138.13112	14/10/2010	D. A. Young	sweeping Bush Blitz Svy SM049 on Acacia salicina	F	Apanteles sp_5
E316	AUMIC174-18	MH138726	MH139203	WINC FreezerPro_1480521	S. Aust	Bon Bon Stn	30°18.828'S	135°32.848'E	-30.3138	135.53889	28/10/2010	G.S. Taylor	Swept Acacia victoriae 2010 069 (B30) Bush Blitz svy	F	Dolichogenidea sp_14
E317	AUMIC175-18	MH138725	MH139202	WINC FreezerPro_1480522	S. Aust	Bon Bon Stn	30°29'05"S	135°32'16'E	-30.48472	135.59361	26/10/2010	R. Kittel	Bush Blitz Svy RK106 on Melaleuca interioris on sand dunes	F	Dolichogenidea sp_42
E318	AUMIC176-18	MH138581	MH139083	WINC FreezerPro_1480523	S. Aust	Witchelina Stn	30°08'19"S	137°57'38'E	-30.13861	137.96056	22/10/2010	F. Colombo, R Kittel, S. Mantel	Yello pan Bush Blitz survey Rk077 in Acacia and grasses alongside dam	F	Apanteles sp_5
E320	AUMIC177-18	MH138582	MH139084	WINC FreezerPro_1480524	S. Aust	Witchelina Stn	30°04'22"S	138°07'52"E	-30.07278	138.13112	14/10/2010	S. Mantel	Bushblitz survey SM048 flowering Cullen australasicum	F	Apanteles sp_5
E321	AUMIC178-18	MH138583	MH139085	WINC FreezerPro_1480525	S. Aust	Witchelina Stn	30°04'22"S	138°07'52"E	-30.07278	138.13112	14/10/2010	S. Mantel	Bushblitz survey SM048 flowering Cullen australasicum	F	Apanteles sp_5
E322	AUMIC179-18	MH138584	MH139086	WINC FreezerPro_1480526	S. Aust	Witchelina Stn	30°04'22"S	138°07'52"E	-30.07278	138.13112	14/10/2010	S. Mantel	Bushblitz survey SM048 flowering Cullen australasicum	F	Apanteles sp_5
E323	AUMIC180-18	MH138724	MH139201	WINC FreezerPro_1480527	S. Aust	Witchelina Stn	29°58'38"S	138°05'08"E	-29.97722	138.08556	11/10/2010	D. A. Young	sweeping Bush Blitz Svy SM011 on Ermophilla freelingi	F	Dolichogenidea sp_35
E324	AUMIC181-18	MH138723	MH139200	WINC FreezerPro_1480528	S. Aust	Witchelina Stn	29°58'38"S	138°05'08"E	-29.97722	138.08556	11/10/2010	D. A. Young	sweeping Bush Blitz Svy SM011 on Ermophilla freelingi	F	Dolichogenidea sp_22
E327	AUMIC182-18	MH138681	MH139166	WAD PIRD N5564-1	WA	Barrow Island	WGS84 (50) 337148	7697310	-20.81704	115.43509	1/05/2007	S. Callan K. Edwards	N26 SUC	F	Diolcogaster sp_10
E328	AUMIC183-18	MH138586	MH139088	WAD PIRD N5565-1	WA	Barrow Island	WGS84 (50) 332830	7700852	-20.78467	115.39395	1/05/2007	S. Callan K. Edwards	N28 DHC	F	Apanteles sp_32
E329	AUMIC184-18	MH138587	MH139089	WAD PIRD N5565-2	WA	Barrow Island	WGS84 (50) 332830	7700852	-20.78467	115.39395	1/05/2007	S. Callan K. Edwards	N28 DHC	F	Apanteles sp_5
E33	AUMIC185-18	MH138960		WINC FreezerPro_1480403	NSW	Braidwood, Glenmore Rd			-35.42317	149.7715	17-29/12/2005	C. Stephens	M/T Exotic/Native garden blend in pasture setting	F	Microplitis sp_14
E330	AUMIC186-18	MH138588	MH139090	WAD PIRD N5565-3	WA	Barrow Island	WGS84 (50) 332830	7700852	-20.78467	115.39395	1/05/2007	S. Callan K. Edwards	N28 DHC	F	Apanteles sp_33
E331	AUMIC187-18	MH138680	MH139165	WAD PIRD N5566-1	WA	Barrow Island	WGS84 (50) 328389	7699655	-20.79507	115.35118	1/05/2007	S. Callan K. Edwards		F	Diolcogaster sp_6
E332	AUMIC188-18	MH138679	MH139164	WAD PIRD N5566-2	WA	Barrow Island	WGS84 (50) 328389	7699655	-20.79507	115.35118	1/05/2007	S. Callan K. Edwards		F	Diolcogaster sp_7
E333	AUMIC189-18	MH138722	MH139199	WAD PIRD N5567-1	WA	Barrow Island	WGS84 (50) 335990	7699985	-20.79278	115.42422	1/05/2007	S. Callan K. Edwards	N06a SUC	F	Dolichogenidea sp_5
E334	AUMIC190-18	MH138993		WINC FreezerPro_1480529	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula	35°27'13"S	138°36'22"E	-35.45361	138.60611	20/11/2016-03/12/2016	E. Fagan-Jeffries	M/T	F	Sathon sp_1
E335	AUMIC191-18	MH138799		WINC FreezerPro_1480530	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula	35°27'13"S	138°36'22"E	-35.45361	138.60611	20/10/2016 - 05/11/2016	E. Fagan-Jeffries	M/T	F	unknown sp_3
E336	AUMIC192-18	MH138956		ANIC 32 130205	VIC	2.1 km NNW Rose Gap, Grampian NP	36°59'59"S	142°25'29"E	-36.99972	142.42473	26/09-02/10/2001	CNM, ID&JS Lambkin, NT Starick	malaise in wide grassy creek bed, Eucalyptus	M	Microplitis sp_11
E337	AUMIC193-18	MH138798		WINC FreezerPro_1480531	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula	35°27'13"S	138°36'22"E	-35.45361	138.60611	05/11/2016-20/11/2016	E. Fagan-Jeffries	M/T	F	unknown sp_3
E338	AUMIC194-18	MH138655	MH139140	WINC FreezerPro_1480532	S. Aust	Cox Scrub Con. Pk.	35°19'55"S	138°44'45"E	-35.33194	138.74583	17/04/2016 - 01/05/2016	E. Fagan-Jeffries	M/T	F	Cotesia sp_11
E34	AUMIC195-18	MH138643	MH139129	WINC FreezerPro_1480404	NSW	Braidwood, Glenmore Rd			-35.42317	149.7715	17-29/12/2005	C. Stephens	M/T Exotic/Native garden blend in pasture setting	F	Cotesia sp_13
E340	AUMIC196-18	MH138759	MH139229	WINC FreezerPro_1480533	S. Aust	Mt Barker Summit			-35.066103	138.922692	03-22/04/2016	A. Austin	M/T	F	Glyptapanteles sp_25
E342	AUMIC197-18	MH138618	MH139108	WINC FreezerPro_1480534	S. Aust	Cox scrub	35°19'55"S	138°44'45"E	-35.33194	138.74583	20/03-03/04/2016	E. Fagan-Jeffries	M/T	F	Choeras sp_10
E343	AUMIC198-18	MH138749		WINC FreezerPro_1480535	S. Aust	Mt Barker Summit			-35.066103	138.922692	20/03-03/04/2016	A. Austin, E Fagan-Jeffries	M/T	F	Glyptapanteles sp_25
E344	AUMIC199-18	MH138598	MH139096	WINC FreezerPro_1480536	S. Aust	Cox Scrub Con. Pk.	35°19'55"S	138°44'45"E	-35.33194	138.74583	5-20/03/2016	E. Fagan-Jeffries	M/T	F	Choeras sp_10
E345	AUMIC200-18	MH138619	MH139109	WINC FreezerPro_1480537	S. Aust	Cox Scrub Con. Pk.	35°19'55"S	138°44'45"E	-35.33194	138.74583	5-20/03/2016	E. Fagan-Jeffries	M/T	F	Choeras sp_10
E346	AUMIC201-18	MH138721	MH139198	WAD PIRD N5568-1	WA	Barrow Island	WGS84: 337670	WGS84: -7699230	-20.79972	115.44028	25/09/2006	S. Callan & R. Graham	GP8 SUC	F	Dolichogenidea sp_25
E347	AUMIC202-18	MH138720		WAD PIRD N5569-1	WA	Barrow Island	WGS84: 337659	WGS84: -7697280	-20.81724	115.43975	25/09/2006	S. Callan & R. Graham	CC2 DHC	F	Dolichogenidea sp_25
E349	AUMIC203-18	MH138719	MH139197	WAD PIRD N5570-1	WA	Barrow Island	WGS84: 337659	WGS84: -7697280	-20.81724	115.43975	25/09/2006	S. Callan & R. Graham	CC2 SUC2	F	Dolichogenidea sp_25
E35	AUMIC204-18	MH138483	MH139007	WINC FreezerPro_1480405	NSW	Braidwood, Glenmore Rd			-35.42317	149.7715	17-29/12/2005	C. Stephens	M/T Exotic/Native garden blend in pasture setting	F	Apanteles sp_19
E350	AUMIC205-18	MH138718	MH139196	WAD PIRD N5570-2	WA	Barrow Island	WGS84: 337659	WGS84: -7697280	-20.81724	115.43975	25/09/2006	S. Callan & R. Graham	CC2 SUC2	F	Dolichogenidea sp_25
E351	AUMIC206-18	MH138484	MH139008	WINC FreezerPro_1480538	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	11-24/11/2007	J.T. Jennings	M/T	F	Apanteles sp_6
E353	AUMIC207-18	MH138676	MH139161	WINC FreezerPro_1480539	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	11-24/11/2007	J.T. Jennings	M/T	F	Diolcogaster sp_19
E355	AUMIC208-18	MH138760	MH139230	WINC FreezerPro_1480540	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	11-24/11/2007	J.T. Jennings	M/T	F	Glyptapanteles sp_25
E356	AUMIC209-18	MH138480	MH139004	WINC FreezerPro_1480541	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	08-30/03/2008	J.T. Jennings	M/T		Apanteles sp_6
E358	AUMIC210-18	MH138675	MH139160	WINC FreezerPro_1480542	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	08-30/03/2008	J.T. Jennings	M/T	F	Diolcogaster sp_19
E359	AUMIC211-18	MH138481	MH139005	WINC FreezerPro_1480543	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	08-30/03/2008	J.T. Jennings	M/T	F	Apanteles sp_6
E36	AUMIC212-18	MH138482	MH139006	WINC FreezerPro_1480406	NSW	Braidwood, Glenmore Rd.			-35.42317	149.7715	17-29/12/2005	C. Stephens	malaise trap in exotic/native garden blend pasture setting	F	Apanteles sp_19
E360	AUMIC213-18	MH138674	MH139159	WINC FreezerPro_1480544	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	08-30/03/2008	J.T. Jennings	M/T	F	Diolcogaster sp_18
E361	AUMIC214-18	MH138673	MH139158	WINC FreezerPro_1480545	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	08-30/03/2008	J.T. Jennings	M/T	F	Diolcogaster sp_18

E362	AUMIC215-18	MH138487	MH139010	WINC FreezerPro_1480546	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	08-30/03/2008	J.T. Jennings	M/T	F	Apanteles sp_6
E363	AUMIC216-18	MH138488	MH139011	WINC FreezerPro_1480547	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	08-30/03/2008	J.T. Jennings	M/T	F	Apanteles sp_6
E365	AUMIC217-18	MH138672	MH139157	WINC FreezerPro_1480548	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	08-30/03/2008	J.T. Jennings	M/T		Diolcogaster sp_19
E366	AUMIC218-18	MH138490	MH139013	WINC FreezerPro_1480549	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	08-30/03/2008	J.T. Jennings	M/T	F	Apanteles sp_6
E367	AUMIC219-18	MH138755	MH139225	WINC FreezerPro_1480550	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	25/11/2007-01/12/2007	J.T. Jennings	M/T	F	Glyptapanteles sp_25
E368	AUMIC220-18	MH138671	MH139156	WINC FreezerPro_1480551	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	25/11/2007-01/12/2007	J.T. Jennings	M/T	F	Diolcogaster sp_19
E369	AUMIC221-18	MH138668	MH139153	WINC FreezerPro_1480552	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	25/11/2007-01/12/2007	J.T. Jennings	M/T	F	Diolcogaster sp_19
E37	AUMIC222-18	MH138717	MH139195	WINC FreezerPro_1480407	NSW	Braidwood, Glenmore Rd.			-35.42317	149.7715	17-29/12/2005	C. Stephens	malaise trap in exotic/native garden blend pasture setting	F	Dolichogenidea sp_21
E370	AUMIC223-18	MH138669	MH139154	WINC FreezerPro_1480553	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	25/11/2007-01/12/2007	J.T. Jennings	M/T	F	Diolcogaster sp_19
E371	AUMIC224-18	MH139001	MH139399	WINC FreezerPro_1480554	S. Aust	Belair N.P. (lower site)			-35.009	138.65401	27/10/2007/-10/11/2007	J.T. Jennings	M/T	F	Sathon sp_7
E372	AUMIC225-18	MH138987	MH139391	WINC FreezerPro_1480555	S. Aust	Belair N.P. (lower site)			-35.009	138.65401	20-27/10/2007	J.T. Jennings	M/T	F	Sathon sp_5
E373	AUMIC226-18	MH138667	MH139152	WINC FreezerPro_1480556	S. Aust	Belair N.P. (lower site)			-35.009	138.65401	20-27/10/2007	J.T. Jennings	M/T	F	Diolcogaster sp_19
E374	AUMIC227-18	MH138495	MH139018	WINC FreezerPro_1480557	S .Aust	Belair N.P. Gate 9			-35.009	138.65401	01-08/03/2008	J.T. Jennings	M/T	F	Apanteles sp_6
E375	AUMIC228-18	MH138983		WINC FreezerPro_1480558	S .Aust	Belair N.P. Gate 9			-35.009	138.65401	01-08/03/2008	J.T. Jennings	M/T	F	Miropotes sp_3
E376	AUMIC229-18	MH138994	MH139393	WINC FreezerPro_1480559	S. Aust	Belair N.P. Gate 9			-35.009	138.65401	11-24/11/2007	J.T. Jennings	M/T	F	Sathon sp_2
E377	AUMIC230-18	MH138620	MH139110	WINC FreezerPro_1480560	S. Aust	Belair N.P. Gate 9			-35.009	138.65401	11-24/11/2007	J.T. Jennings	M/T	F	Choeras sp_10
E378	AUMIC231-18	MH138621	MH139111	WINC FreezerPro_1480561	S. Aust	Belair N.P. Gate 9			-35.009	138.65401	11-24/11/2007	J.T. Jennings	M/T	F	Choeras sp_10
E379	AUMIC232-18	MH138622	MH139112	WINC FreezerPro_1480562	S. Aust	Belair N.P. Gate 9			-35.009	138.65401	11-24/11/2007	J.T. Jennings	M/T	F	Choeras sp_10
E38	AUMIC233-18	MH138499	MH139020	WINC FreezerPro_1480408	NSW	Braidwood, Glenmore Rd.			-35.42317	149.7715	17-29/12/2005	C. Stephens	malaise trap in exotic/native garden blend pasture setting	F	Apanteles sp_19
E380	AUMIC234-18	MH138666	MH139151	WINC FreezerPro_1480563	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	27/10/2007-10/11/2007	J.T. Jennings	M/T	F	Diolcogaster sp_18
E381	AUMIC235-18	MH138623	MH139113	WINC FreezerPro_1480564	S. Aust	Belair N.P. Gate 9			-35.009	138.65401	11-24/11/2007	J.T. Jennings	M/T	F	Choeras sp_10
E382	AUMIC236-18	MH138963		WINC FreezerPro_1480565	S. Aust	Cox scrub site 1			-35.33111	138.7475	29/10/2007-25/11/2007	A.D. Austin	malaise trap	F	Micropiltis sp_17
E383	AUMIC237-18	MH138976	MH139383	WINC FreezerPro_1480566	S. Aust	Cox scrub site 1			-35.33111	138.7475	29/10/2007-25/11/2007	A.D. Austin	malaise trap	F	Miropotes sp_15
E39	AUMIC238-18	MH138502	MH139023	WINC FreezerPro_1480409	NSW	Eden, Bungo Street			-37.06112	149.90268	21-27/12/2005	C. Stephens	malaise trap in exotic natic garden blend nr Eucalypt Forest	F	Apanteles sp_28
E4	AUMIC239-18	MH138503	MH139024	WINC FreezerPro_1480383	S. Aust	Witchelina Stn	30°01'21"S	137°54'10"E	-30.0225	137.90277	13/10/2010	R. Kittle	Bush Blitz Svy RK027 on vegetation around dam	F	Apanteles sp_5
E40	AUMIC240-18	MH138504		WINC FreezerPro_1480410	NSW	Eden, Bungo Street			-37.06112	149.90268	21-27/12/2005	C. Stephens	malaise trap in exotic natic garden blend nr Eucalypt Forest	F	Apanteles sp_18
E408	AUMIC241-18	MH138505	MH139025	WINC FreezerPro_1480567	NSW	Pearl Beach, Cormellin Biological Field Station	33.5511°S	151.2978°E	-33.5511	151.29781	November 2009	A.D. Austin		F	Apanteles sp_9
E409	AUMIC242-18	MH138665	MH139150	WINC FreezerPro_1480568	S. Aust	Belair N.P. (lower site)			-35.009	138.65401	14-20/10/2007	J.T. Jennings	M/T	F	Diolcogaster sp_19
E410	AUMIC243-18	MH138980		WINC FreezerPro_1480569	S. Aust	South Para Reservoir 35km NE Adl.	UTM Zone 54H 0305878	UTM Zone 54H 6158568	-34.6963	138.8805	17/10/2006	L. Farrington	M/T collection 6/7	F	Miropotes sp_15
E411	AUMIC244-18	MH138507	MH139027	WINC FreezerPro_1480570	NSW	Pearl Beach, Cormellin Biological Field Station	33.5511°S	151.2978°E	-33.5511	151.29781	December 2009	A.D. Austin		F	Apanteles sp_10
E412	AUMIC245-18	MH138506	MH139026	WINC FreezerPro_1480571	NSW	Pearl Beach, Cormellin Biological Field Station	33.5511°S	151.2978°E	-33.5511	151.29781	December 2009	A.D. Austin		F	Apanteles sp_10
E413	AUMIC246-18	MH138769	MH139239	WINC FreezerPro_1480572	WA	Gleneagle State Forest			-32.27111	116.16334	09-08/10/2005	M.S. Harvey	M/T	F	Glyptapanteles sp_17
E414	AUMIC247-18	MH138500	MH139021	WINC FreezerPro_1480573	NSW	Braidwood, Glenmore Rd			-35.42317	149.7715	17-29/12/2005	C. Stephens	M/T Exotic/Native garden blend in pasture setting	F	Apanteles sp_19
E415	AUMIC248-18	MH138494	MH139017	WINC FreezerPro_1480574	NSW	Braidwood, Glenmore Rd			-35.42317	149.7715	17-29/12/2005	C. Stephens	M/T Exotic/Native garden blend in pasture setting	F	Apanteles sp_19
E416	AUMIC249-18	MH138493	MH139016	WINC FreezerPro_1480575	NSW	Braidwood, Glenmore Rd			-35.42317	149.7715	17-29/12/2005	C. Stephens	M/T Exotic/Native garden blend in pasture setting	F	Apanteles sp_19
E417	AUMIC250-18	MH138492	MH139015	WINC FreezerPro_1480576	NSW	Braidwood, Glenmore Rd			-35.42317	149.7715	17-29/12/2005	C. Stephens	M/T Exotic/Native garden blend in pasture setting	F	Apanteles sp_19
E418	AUMIC251-18	MH138624	MH139114	WINC FreezerPro_1480577	NSW	Braidwood, Glenmore Rd			-35.42317	149.7715	17-29/12/2005	C. Stephens	M/T Exotic/Native garden blend in pasture setting	F	Choeras sp_5
E419	AUMIC252-18	MH138491	MH139014	WINC FreezerPro_1480578	NSW	Braidwood, Glenmore Rd			-35.42317	149.7715	17-29/12/2005	C. Stephens	M/T Exotic/Native garden blend in pasture setting	F	Apanteles sp_19
E42	AUMIC253-18	MH138489	MH139012	WINC FreezerPro_1480411	NSW	Eden, Bungo Street			-37.06112	149.90268	21-27/12/2005	C. Stephens	malaise trap in exotic natic garden blend nr Eucalypt Forest	F	Apanteles sp_26
E420	AUMIC254-18	MH138486		WINC FreezerPro_1480579	NSW	Braidwood, Glenmore Rd			-35.42317	149.7715	17-29/12/2005	C. Stephens	M/T Exotic/Native garden blend in pasture setting	F	Apanteles sp_19
E421	AUMIC255-18	MH138961		WINC FreezerPro_1480580	NSW	Braidwood, Glenmore Rd			-35.42317	149.7715	17-29/12/2005	C. Stephens	M/T Exotic/Native garden blend in pasture setting	M	Microplitis sp_10
E422	AUMIC256-18	MH138644	MH139130	WINC FreezerPro_1480581	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula			-35.45361	138.60611	25/10/2000	C. Stephens	M/T in native plot within bridal creeper invaded eucalypt woodland	F	Cotesia sp_15
E423	AUMIC257-18	MH138843		WINC FreezerPro_1480582	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula			-35.45361	138.60611	25/10/2000	C. Stephens	M/T in native plot within bridal creeper invaded eucalypt woodland	F	unknown sp_3
E424	AUMIC258-18	MH138842	MH139293	WINC FreezerPro_1480583	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula			-35.45361	138.60611	25/10/2000	C. Stephens	M/T in native plot within bridal creeper invaded eucalypt woodland	F	unknown sp_3
E425	AUMIC259-18	MH138915		WINC FreezerPro_1480584	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula			-35.45361	138.60611	25/10/2000	C. Stephens	M/T in native plot within bridal creeper invaded eucalypt woodland	F	unknown sp_3

E426	AUMIC260-18	MH138485	MH139009	WINC FreezerPro_1480585	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	08-30/03/2008	J.T. Jennings	Malaise Trap	F	Apanteles sp_6
E427	AUMIC261-18	MH138653	MH139138	WINC FreezerPro_1480586	S. Aust	Cox Scrub Site 1			-35.33111	138.7475	20/01-10/02/2008	A.D Austin	Malaise Trap	F	Cotesia sp_15
E428	AUMIC262-18	MH138704	MH139186	WINC FreezerPro_1480587	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	08-30/03/2008	J.T. Jennings	Malaise Trap	F	Dolichogenidea sp_9
E429	AUMIC263-18	MH138593	MH139095	WINC FreezerPro_1480588	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	08-30/03/2008	J.T. Jennings	Malaise Trap	F	Apanteles sp_6
E43	AUMIC264-18	MH138763	MH139233	WINC FreezerPro_1480412	NSW	Mt Keira via Wollongong			-34.40351	150.85738	Feb-April 2004	A.D. Austin, M. Dowton	Malaise trap	F	Glyptapanteles sp_32
E430	AUMIC265-18	MH138591	MH139093	WINC FreezerPro_1480589	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	08-30/03/2008	J.T. Jennings	Malaise Trap	F	Apanteles sp_6
E431	AUMIC266-18	MH138590	MH139092	WINC FreezerPro_1480590	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	01-08/03/2008	J.T. Jennings	Malaise Trap	F	Apanteles sp_6
E432	AUMIC267-18	MH138585	MH139087	WINC FreezerPro_1480591	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	01-08/03/2008	J.T. Jennings	Malaise Trap	F	Apanteles sp_6
E433	AUMIC268-18	MH138577	MH139080	WINC FreezerPro_1480592	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	01-08/03/2008	J.T. Jennings	Malaise Trap	F	Apanteles sp_6
E434	AUMIC269-18	MH138625	MH139115	WINC FreezerPro_1480593	S. Aust	Nr Wistow			-35.115	138.912	spring 2001		Malaise trap	F	Choeras sp_9
E435	AUMIC270-18	MH138559	MH139065	WINC FreezerPro_1480594	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	01-08/03/2008	J.T. Jennings	Malaise Trap	F	Apanteles sp_6
E436	AUMIC271-18	MH138973		WINC FreezerPro_1480595	S. Aust	Nr Wistow			-35.115	138.912	spring 2001		Malaise trap	F	Miropotes sp_3
E437	AUMIC272-18	MH138626	MH139116	WINC FreezerPro_1480596	NSW	Royal National Park South end Lady Carrington Drive Rainforest			-34.1482	151.0312	24/11/1996-10/01/1997	A.D. Austin	Malaise trap	F	Choeras sp_2
E438	AUMIC273-18	MH138716	MH139194	WINC FreezerPro_1480597	NSW	Royal National Park South end Lady Carrington Drive Rainforest			-34.1482	151.0312	24/11/1996-10/01/1997	A.D. Austin	Malaise trap	F	Dolichogenidea sp_23
E439	AUMIC274-18	MH138748	MH139220	WINC FreezerPro_1480598	NSW	Royal National Park South end Lady Carrington Drive Rainforest			-34.1482	151.0312	24/11/1996-10/01/1997	A.D. Austin	Malaise trap	F	Glyptapanteles sp_30
E44	AUMIC275-18	MH138995	MH139394	WINC FreezerPro_1480413	NSW	Crommelin Biological Field Station	33.55030-4961S	151.29793-682E	-33.5503	151.29793	18/24/2008	A.D Austin		F	Sathon sp_3
E440	AUMIC276-18	MH138715	MH139193	WINC FreezerPro_1480599	NSW	Royal National Park South end Lady Carrington Drive Rainforest			-34.1482	151.0312	24/11/1996-10/01/1997	A.D. Austin	Malaise trap	F	Dolichogenidea sp_23
E441	AUMIC277-18	MH138627	MH139117	WINC FreezerPro_1480600	NSW	Royal National Park South end Lady Carrington Drive Rainforest			-34.1482	151.0312	24/11/1996-10/01/1997	A.D. Austin	Malaise trap	F	Choeras sp_12
E442	AUMIC278-18	MH138714	MH139192	WINC FreezerPro_1480601	NSW	Royal National Park South end Lady Carrington Drive Rainforest			-34.1482	151.0312	24/11/1996-10/01/1997	A.D. Austin	Malaise trap	F	Dolichogenidea sp_13
E443	AUMIC279-18	MH138713	MH139191	WINC FreezerPro_1480602	NSW	Royal National Park South end Lady Carrington Drive Rainforest			-34.1482	151.0312	24/11/1996-10/01/1997	A.D. Austin	Malaise trap	F	Dolichogenidea sp_23
E444	AUMIC280-18	MH138712	MH139190	WINC FreezerPro_1480603	NSW	Royal National Park South end Lady Carrington Drive Rainforest			-34.1482	151.0312	24/11/1996-10/01/1997	A.D. Austin	Malaise trap	F	Dolichogenidea sp_23
E449	AUMIC281-18	MH138711		WINC FreezerPro_1480604	NSW	Eden, Bungo Street			-37.06112	149.90268	21-27/12/2005	C. Stephens	malaise trap in exotic natic garden blend nr Eucalypt Forest	F	Dolichogenidea sp_17
E45	AUMIC282-18	MH138546	MH139054	WINC FreezerPro_1480414	NSW	Near Crommellin Biological Field Stn.	33.55180-196S,	151.29851-23E	-33.5518	151.29851	18-24/02/2008	A.D. Austin	sweeping	F	Apanteles sp_23
E452	AUMIC283-18	MH138544		WINC FreezerPro_1480605	S. Aust	Cox Scrub Con. Pk.			-35.33111	138.7475	27/12/2003-17/01/2004	A. Austin	Malaise trap	F	Apanteles sp_6
E453	AUMIC284-18	MH138522	MH139036	WINC FreezerPro_1480606	WA	Gleneagle State Forest			-32.27111	116.16334	29/11/2005	M.S. Harvey	Malaise Trap	F	Apanteles sp_7
E458	AUMIC285-18	MH138519		WINC FreezerPro_1480607	S. Aust	Flinders Ranges, Akaba Creek	31°41.305'S	138°34.000'E	-31.68842	138.56667	4/04/2011	R. Kittel	Sweeping creek vegetation	F	Apanteles sp_5
E46	AUMIC286-18	MH138917	MH139350	WINC FreezerPro_1480415	NSW	Near Crommellin Biological Field Stn.	33.55180-196S,	151.29851-23E	-33.5518	151.29851	18-24/02/2008	A.D. Austin	sweeping	F	unknown sp_8
E461	AUMIC287-18	MH138566	MH139072	WINC FreezerPro_1480608	S. Aust	Flinders Ranges, Akaba Creek	31°41.305'S	138°34.000'E	-31.68842	138.56667	4/04/2011	R. Kittel	Sweeping creek vegetation	F	Apanteles sp_5
E463	AUMIC288-18	MH138632	MH139122	WINC FreezerPro_1480609	S. Aust	Kangaroo Is.	35°45.198'S	137°19.285'E	-35.7533	137.32141	17-24/03/2011	G. Taylor, E. Kinnaird, R. Kittel	Malaise trap MT3	F	Choeras morialta
E467	AUMIC289-18	MH138650	MH139136	WINC FreezerPro_1480610	NSW	Eden, Bungo Street			-37.06112	149.90268	21-27/12/2005	C. Stephens	malaise trap in exotic natic garden blend nr Eucalypt Forest	F	Cotesia sp_16
E468	AUMIC290-18	MH138710		WINC FreezerPro_1480611	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula			-35.45361	138.60611	20/12/2000	C. stephens	Malaise trap in bridal creeper invaded eucalypt woodland	F	Dolichogenidea sp_23
E469	AUMIC291-18	MH138773	MH139243	WINC FreezerPro_1480612	S. Aust	Millbrook Reservoir Gate 28, 25km NE Adelaide	UTM Zone 54 H0301233	UTM Zone 54 6146102	-34.8078	138.82695	12/09/2007	L. Farrington	Malaise trap (pooled)	F	Glyptapanteles sp_25
E47	AUMIC292-18	MH138841	MH139292	WINC FreezerPro_1480416	NSW	Pearl Beach, Cormellin Biological Field Station	33.5511°S	151.2978°E	-33.5511	151.29781	1/05/2009	A.D. Austin		F	unknown sp_10
E471	AUMIC293-18	MH138914		WINC FreezerPro_1480613	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula			-35.45361	138.60611	25/10/2000	C. Stephens	Malaise trap in bridal creeper invaded eucalypt woodland	F	unknown sp_3
E474	AUMIC294-18	MH138651		WINC FreezerPro_1480614	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula			-35.45361	138.60611	25/10/2000	C. Stephens	Malaise trap in bridal creeper invaded eucalypt woodland	F	Cotesia sp_15
E476	AUMIC295-18	MH138497		WINC FreezerPro_1480615	S. Aust	Flinders Ranges, Moralana Scenic drive	31°33.671'S	138°27.103'E	-31.56118	138.45172	04/04//2011	R. Kittel	Sweeping shrubs and native pine	F	Apanteles sp_5
E477	AUMIC296-18	MH138579	MH139082	WINC FreezerPro_1480616	S. Aust	Flinders Ranges, Moralana Scenic drive	31°33.671'S	138°27.103'E	-31.56118	138.45172	04/04//2011	R. Kittel	Sweeping shrubs and native pine	F	Apanteles sp_5
E478	#N/A	#N/A	#N/A	WINC FreezerPro_1480617	S. Aust	Flinders Ranges, Parachilna Road	31°07.500'S	138°30.500'E	-31.125	138.50833	6/04/2011	R. Kittel	Sweeping creek vegetation	F	Apanteles sp_3
E479	AUMIC297-18	MH138578	MH139081	WINC FreezerPro_1480618	S. Aust	Flinders Ranges, Brachina Gorge	31°20.475'S	138°34.007'E	-31.34125	138.56679	5/04/2011	R. Kittel	sweeping creek vegetation	F	Apanteles sp_5
E48	AUMIC298-18	MH138687	MH139171	WINC FreezerPro_1480417	NSW	Pearl Beach, Cormellin Biological Field Station	33.5511°S	151.2978°E	-33.5511	151.29781	December 2009	A.D. Austin		F	Diolcogaster sp_19
E480	AUMIC299-18	MH138543		WINC FreezerPro_1480619	S. Aust	Flinders Ranges, Brachina Gorge	31°20.475'S	138°34.007'E	-31.34125	138.56679	5/04/2011	R. Kittel	sweeping creek vegetation	F	Apanteles sp_5
E481	AUMIC300-18	MH138642		WINC FreezerPro_1480620	S. Aust	Flinders Ranges, Brachina Gorge	31°20.475'S	138°34.007'E	-31.34125	138.56679	5/04/2011	R. Kittel	sweeping creek vegetation	F	Cotesia sp_6
E482	AUMIC301-18	MH138647	MH139133	WINC FreezerPro_1480621	S. Aust	Wild Dogs Glen, Waite Campus Adelaide University			-34.9679	138.6302	16/11/2000		MT Uphill	F	Cotesia sp_12

E483	AUMIC302-18	MH138556	MH139062	WINC FreezerPro_1480622	S. Aust	Flinders Ranges	30°46.335'S	138°29.040'E	-30.77225	138.48401	7/04/2011	R. Kittel	Road to Warraweena, sweeping E. camaldulensis & S. molle	F	Apanteles sp_5
E485	AUMIC303-18	MH138531	MH139043	WINC FreezerPro_1480623	S. Aust	Flinders Ranges	31°19.960'S	138°35.850'E	-31.33267	138.59749	5/04/2011	R. Kittel	ABC lockout, sweeping Myoporum platycarpum	F	Apanteles sp_5
E49	AUMIC304-18	MH138565	MH139071	WINC FreezerPro_1480418	NSW	Pearl Beach, Cormellin Biological Field Station	33.5511°S	151.2978°E	-33.5511	151.29781	December 2009	A.D. Austin		F	Apanteles sp_9
E5	AUMIC305-18	MH138652	MH139137	WINC FreezerPro_1480384	S. Aust	Witchelina Stn	30°01'21"S	137°54'10"E	-30.0225	137.90277	13/10/2010	R. Kittle	Bush Blitz Svy RK027 on vegetation around dam	F	Cotesia sp_13
E500	AUMIC306-18	MH138765	MH139235	WINC FreezerPro_1480624	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	10/02/2015-15/03/2017	M.S. Moulds	M/T	F	Glyptapanteles sp_16
E504	AUMIC307-18	MH138777		WINC FreezerPro_1480625	S. Aust	Mt Remarkable National Park	32°50'18"S	138°2'12"E	-32.83833	138.03667	18/2/2017-01/04/2017	E. Fagan-Jeffries	M/T	F	Iconella sp_2
E505	AUMIC308-18	MH138776		WINC FreezerPro_1480626	S. Aust	Mt Remarkable National Park	32°50'18"S	138°2'12"E	-32.83833	138.03667	18/2/2017-01/04/2017	E. Fagan-Jeffries	M/T	F	Iconella sp_2
E508	AUMIC309-18	MH138775	MH139245	WINC FreezerPro_1480627	S. Aust	Witchelina Stn	30°07'16"S	137°55'24"E	-30.12111	137.92334	19/10/2010	F. Colombo	Bush Blitz Svy FC055 sweeping	F	Glyptapanteles sp_27
E509	AUMIC310-18	MH138664	MH139149	WINC FreezerPro_1480628	S. Aust	Witchelina Stn	30°01'20"S	138°02'46"E	-30.02222	137.92195	13/10/2010	R. Kittel	Bush Blitz Svy RK028 at light	F	Diolcogaster sp_7
E51	AUMIC311-18	MH138567	MH139073	WINC FreezerPro_1480419	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	01-08/03/2008	J.T. Jennings	Malaise Trap	F	Apanteles sp_6
E512	AUMIC312-18	MH138570		WINC FreezerPro_1480629	S. Aust	Witchelina Stn	30°09'07"S	137°53'54"E	-30.15194	137.89833	19/10/2010	S. Mantel	Bush Blitz Svy SM097 sweeping on Crotalaria eremaea in sand dunes	F	Apanteles sp_5
E513	AUMIC313-18	MH138575		WINC FreezerPro_1480630	S. Aust	Witchelina Stn	30°01'30"S	138°02'41"E	-30.025	138.04472	17/10/2010	S. Mantel	Bush Blitz Svy SM072 sweeping Swainsona sp.	F	Apanteles sp_5
E514	AUMIC314-18	MH138594		WINC FreezerPro_1480631	S. Aust	Witchelina Stn	30°01'30"S	138°02'41"E	-30.025	138.04472	17/10/2010	S. Mantel	Bush Blitz Svy SM072 sweeping Swainsona sp.	F	Apanteles sp_5
E516	AUMIC315-18	MH138702	MH139184	WINC FreezerPro_1480632	S. Aust	Bon Bon Stn	30°25'28"S	135°28'39"E	-30.42444	135.47137	28/10/2010	R. Kittel	Bush Blitz Svy RK133 at light	F	Diolcogaster sp_7
E517	AUMIC316-18	MH138508	MH139028	WINC FreezerPro_1480633	S. Aust	Witchelina Stn	30°01'19"S	138°02'19"E	-30.02194	138.03862	18/10/2010	D.A. Young	Bush Blitz Svy SM111 at light	F	Apanteles sp_5
E518	AUMIC317-18	MH138700	MH139182	WINC FreezerPro_1480634	S. Aust	Witchelina Stn	30°09'07"S	137°53'52"E	-30.15194	137.89778	18/10/2010	D.A. Young	Bush Blitz Svy FC066 sweeping Acacia sp.	F	Diolcogaster sp_8
E52	AUMIC318-18	MH138699	MH139181	WINC FreezerPro_1480420	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	01-08/03/2008	J.T. Jennings	Malaise Trap	F	Diolcogaster sp_19
E520	AUMIC319-18	MH138509		WINC FreezerPro_1480635	S. Aust	Witchelina Stn	30°00'37"S	137°46'35"E	-30.01028	137.77638	20/10/2010	F. Colombo	Bush Blitz Svy FC060A sweeping	F	Apanteles sp_5
E523	AUMIC320-18	MH138511	MH139030	WINC FreezerPro_1480636	S. Aust	Witchelina Stn	30°05'44"S	138°08'09"E	-30.09556	138.13583	14/10/2010	S. Mantel	Bush Blitz Svy SM051 on grasses and flowering Swainsona campylantha	F	Apanteles sp_5
E524	AUMIC321-18	MH138639	MH139127	WINC FreezerPro_1480637	S. Aust	Witchelina Stn	30°05'44"S	138°08'09"E	-30.09556	138.13583	14/10/2010	S. Mantel	Bush Blitz Svy SM051 on grasses and flowering Swainsona campylantha	F	Cotesia sp_6
E525	AUMIC322-18	MH138515	MH139033	WINC FreezerPro_1480638	S. Aust	Witchelina Stn	30°05'44"S	138°08'09"E	-30.09556	138.13583	14/10/2010	S. Mantel	Bush Blitz Svy SM051 on grasses and flowering Swainsona campylantha	F	Apanteles sp_5
E528	AUMIC323-18	MH138516		WINC FreezerPro_1480639	S. Aust	Witchelina Stn	30°11'07"S	137°58'38"E	-30.18528	137.97722	18-22/10/2010	S. Mantel, F.C., R.K.	Bush Blitz Svy Malaise2A	F	Apanteles sp_5
E529	AUMIC324-18	MH138636		WINC FreezerPro_1480640	S. Aust	Witchelina Stn	30°00'36"S	137°46'35"E	-30.01	137.77638	20/10/2010	F. Colombo, R. Kittle, S. Mantel	Bush Blitz Svy SM109 Yellow Pan trap in saltbush & Eucalyptus near creek	F	Cotesia sp_13
E53	AUMIC325-18	MH138978	MH139384	WINC FreezerPro_1480421	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	01-08/03/2008	J.T. Jennings	Malaise Trap	F	Miropotes sp_3
E530	AUMIC326-18	MH138520	MH139035	WINC FreezerPro_1480641	S. Aust	Witchelina Stn	30°06'20"S	137°44'15"E	-30.10556	137.7375	20/10/2010	R. Kittle	Bush Blitz Svy RK069 sweeping Acacia sp. in sand dune	F	Apanteles sp_22
E533	AUMIC327-18	MH139002	MH139400	ANIC 32 130206	NSW	Ridge west of Lake George, 822m	35°00'31.4S	149°22'24.8E	-31.33267	138.59749	10-17/09/2014	J. Lumbers	0	F	Sathon sp_6
E537	AUMIC328-18	MH138527		WINC FreezerPro_1480642	S. Aust	Witchelina Stn	30°00'60"S	137°46'57"E	-30.01667	137.7825	20/10/2010	G.S. Taylor	Swept Atriplex nummularia 021 (W12)	F	Apanteles sp_5
E538	AUMIC329-18	MH138529		WINC FreezerPro_1480643	S. Aust	Witchelina Stn	30°00'38"S	137°46'35"E	-30.01056	137.77638	13/10/2010	R. Kittle	Bush Blitz Svy RK025 sweeping on dense eucalyptus and saltbush	F	Apanteles sp_5
E539	AUMIC330-18	MH138538	MH139049	WINC FreezerPro_1480644	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	16/03/2017-12/04/2017	M.S. Moulds	M/T	F	Apanteles sp_24
E54	AUMIC331-18	MH138629	MH139119	WINC FreezerPro_1480422	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	08-30/03/2008	J.T. Jennings	Malaise Trap	F	Choeras morialta
E540	AUMIC332-18	MH138709	MH139189	WINC FreezerPro_1480645	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	16/03/2017-12/04/2017	M.S. Moulds	M/T	F	Dolichogenidea sp_23
E541	AUMIC333-18	MH138540	MH139051	WINC FreezerPro_1480646	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	16/03/2017-12/04/2017	M.S. Moulds	M/T	F	Apanteles sp_36
E542	AUMIC334-18	MH138542	MH139053	WINC FreezerPro_1480647	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	16/03/2017-12/04/2017	M.S. Moulds	M/T	F	Apanteles sp_24
E543	AUMIC335-18	MH138979	MH139385	WINC FreezerPro_1480648	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	16/03/2017-12/04/2017	M.S. Moulds	M/T	F	Miropotes sp_12
E544	AUMIC336-18	MH138691	MH139175	WINC FreezerPro_1480649	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	16/03/2017-12/04/2017	M.S. Moulds	M/T	F	Diolcogaster sp_1
E545	AUMIC337-18	MH138690	MH139174	WINC FreezerPro_1480650	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	16/03/2017-12/04/2017	M.S. Moulds	M/T	F	Diolcogaster sp_1
E546	AUMIC338-18	MH138689	MH139173	WINC FreezerPro_1480651	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	16/03/2017-12/04/2017	M.S. Moulds	M/T	F	Diolcogaster sp_1
E547	AUMIC339-18	MH138688	MH139172	WINC FreezerPro_1480652	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	16/03/2017-12/04/2017	M.S. Moulds	M/T	F	Diolcogaster sp_1
E548	AUMIC340-18	MH138774	MH139244	WINC FreezerPro_1480653	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	16/03/2017-12/04/2017	M.S. Moulds	M/T	F	Glyptapanteles sp_31

E550	AUMIC341-18	MH138648	MH139134	WINC	FreezerPro_1480654	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	16/03/2017-12/04/2017	M.S. Moulds	M/T	F	Cotesia sp_11
E551	AUMIC342-18	MH138762	MH139232	WINC	FreezerPro_1480655	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	16/03/2017-12/04/2017	M.S. Moulds	M/T	F	Glyptapanteles sp_16
E552	AUMIC343-18	MH138767	MH139237	WINC	FreezerPro_1480656	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	16/03/2017-12/04/2017	M.S. Moulds	M/T	F	Glyptapanteles sp_14
E553	AUMIC344-18	MH138686	MH139170	WINC	FreezerPro_1480657	QLD	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	16/03/2017-12/04/2017	M.S. Moulds	M/T	M	Diolcogaster sp_1
E554	AUMIC345-18	MH138547	MH139055	WINC	FreezerPro_1480658	S. Aust	Witchelina Stn	30°00'38"S	137°46'35"E	-30.01056	137.77638	13/10/2010	R. Kittle	Bush Blitz Svy RK025 sweeping on dense eucalyptus and saltbush	F	Apanteles sp_5
E555	AUMIC346-18	MH138554	MH139060	WINC	FreezerPro_1480659	S. Aust	Witchelina Stn	30°00'38"S	137°46'35"E	-30.01056	137.77638	13/10/2010	R. Kittle	Bush Blitz Svy RK025 sweeping on dense eucalyptus and saltbush	F	Apanteles sp_5
E556	AUMIC347-18	MH138558	MH139064	WINC	FreezerPro_1480660	S. Aust	Bon Bon Stn	30°21'610"S	135°28'247"E	-30.36017	149.53584	28/10/2010	G.S. Taylor	Swept Acacia aneura 063 (B24)	F	Apanteles sp_22
E557	AUMIC348-18	MH138766	MH139236	WINC	FreezerPro_1480661	S. Aust	Witchelina Stn	30°01'07"S	137°54'04"E	-30.01861	137.90111	23/10/2010	R. Kittel	Bush Blitz Svy RK091 sweeping Acacia victoriae	F	Glyptapanteles sp_19
E558	AUMIC349-18	MH138708	MH139188	WINC	FreezerPro_1480662	S. Aust	Witchelina Stn	30°01'07"S	137°54'04"E	-30.01861	137.90111	23/10/2010	R. Kittel	Bush Blitz Svy RK091 sweeping Acacia victoriae	F	Dolichogenidea sp_7
E559	AUMIC350-18	MH138924	MH139356	WINC	FreezerPro_1480663	S. Aust	Witchelina Stn	30°01'07"S	137°54'04"E	-30.01861	137.90111	23/10/2010	R. Kittel	Bush Blitz Svy RK091 sweeping Acacia victoriae	F	unknown sp_6
E56	AUMIC351-18	MH138561	MH139067	WINC	FreezerPro_1480423	S. Aust	Belair N.P. Gate 9			-35.009	138.65401	02-05/12/2006	J.T. Jennings	Malaise Trap	F	Apanteles sp_6
E560	AUMIC352-18	MH138562	MH139068	WINC	FreezerPro_1480664	S. Aust	Witchelina Stn	30°01'07"S	137°54'04"E	-30.01861	137.90111	23/10/2010	R. Kittel	Bush Blitz Svy RK091 sweeping Acacia victoriae	F	Apanteles sp_22
E561	AUMIC353-18	MH138564	MH139070	WINC	FreezerPro_1480665	S. Aust	Witchelina Stn	30°01'07"S	137°54'04"E	-30.01861	137.90111	23/10/2010	R. Kittel	Bush Blitz Svy RK091 sweeping Acacia victoriae	F	Apanteles sp_22
E562	AUMIC354-18	MH138571	MH139076	WINC	FreezerPro_1480666	S. Aust	Witchelina Stn	30°01'07"S	137°54'04"E	-30.01861	137.90111	23/10/2010	R. Kittel	Bush Blitz Svy RK091 sweeping Acacia victoriae	F	Apanteles sp_22
E563	AUMIC355-18	MH138572		WINC	FreezerPro_1480667	S. Aust	Witchelina Stn	30°01'30"S	138°02'41"E	-30.025	138.04472	17/10/2010	S. Mantel	Bush Blitz Svy SM073 sweeping on Acacia papyrocarpa	F	Apanteles sp_5
E564	AUMIC356-18	MH138574	MH139078	WINC	FreezerPro_1480668	S. Aust	Witchelina Stn	30°01'30"S	138°02'41"E	-30.025	138.04472	17/10/2010	S. Mantel	Bush Blitz Svy SM073 sweeping on Acacia papyrocarpa	F	Apanteles sp_5
E565	AUMIC357-18	MH138747	MH139219	SAM	SAMA 32-035452	SA	Andamooka Station	from -30.8198802 to -30.6998403	137.1783585 to 137.1574435	-30.72701	137.2036	31/08/2016	R. Leijs	Vehicle net, Bush Blitz Lake Torrens	F	Glyptapanteles sp_23
E566	AUMIC358-18	MH138925	MH139357	SAM	SAMA 32-035454	SA	Andamooka Station	from -30.8198802 to -30.6998403	137.1783585 to 137.1574435	-30.72701	137.2036	31/08/2016	R. Leijs	Vehicle net, Bush Blitz Lake Torrens	F	unknown sp_6
E567	AUMIC359-18	MH138589	MH139091	SAM	SAMA 32-035447	SA	Andamooka Station	from -30.8198802 to -30.6998403	137.1783585 to 137.1574435	-30.72701	137.2036	31/08/2016	R. Leijs	Vehicle net, Bush Blitz Lake Torrens	F	Apanteles sp_29
E568	AUMIC360-18	MH138707	MH139187	SAM	SAMA 32-035448	SA	Andamooka Station	from -30.8198802 to -30.6998403	137.1783585 to 137.1574435	-30.72701	137.2036	31/08/2016	R. Leijs	Vehicle net, Bush Blitz Lake Torrens	F	Dolichogenidea sp_12
E569	AUMIC361-18	MH138635	MH139125	SAM	SAMA 32-035450	SA	Andamooka Station	from -30.8198802 to -30.6998403	137.1783585 to 137.1574435	-30.72701	137.2036	31/08/2016	R. Leijs	Vehicle net, Bush Blitz Lake Torrens	F	Cotesia sp_13
E57	AUMIC362-18	MH138981	MH139386	WINC	FreezerPro_1480424	S. Aust	Belair N.P. Gate 9			-35.009	138.65401	16/02-01/03/2008	J.T. Jennings	Malaise Trap	F	Miropotes sp_3
E570	AUMIC363-18	MH138678	MH139163	SAM	SAMA 32-035444	SA	Andamooka Station, 2.5 km WNW Andamooka HS	30.71416	137.17928	-30.71416	137.17928	1/09/2016	P. Hudson	at light, BS1097, AND001	F	Diolcogaster sp_8
E571	AUMIC364-18	MH138677	MH139162	SAM	SAMA 32-035445	SA	Andamooka Station, 2.5 km WNW Andamooka HS	30.71416	137.17928	-30.71416	137.17928	1/09/2016	P. Hudson	at light, BS1097, AND001	F	Diolcogaster sp_8
E577	AUMIC365-18	MH138991		MV	HYM-61365	VIC	Coranderrk, 1.9km Sth Healesville, site 5	37°411'S	145°316'E	-37.68361	145.51833	27/10/1991-03/11/1991	C. Meehan, D. Hooper	Eucalyptus aromoghloia Pitfall trap	F	Sathon sp_8
E578	AUMIC366-18	MH138992		MV	HYM-61367	VIC	Coranderrk, 2km Sth Healesville, site6	37°412'S	145°317'E	-37.68389	145.5186	17-24/05/1992	C. Meehan, D. Hooper	Eucalyptus macrohyncha Pitfall trap	F	Sathon sp_10
E579	AUMIC367-18	MH138989		MV	HYM-61366	VIC	Coranderrk, 2.5km Sth Healesville, site 9	37°415'S	145°317'E	-37.68472	145.5186	15-22/03/1992	C. Meehan, D. Hooper	Eucalyptus viminalis Pitfall trap	F	Sathon sp_9
E58	AUMIC368-18	MH138997	MH139396	WINC	FreezerPro_1480425	S. Aust	Belair N.P. Gate 9			-35.009	138.65401	25/11-01/12/2007	J.T. Jennings	Malaise Trap	F	Sathon sp_2
E581	AUMIC369-18	MH138706		MV	HYM-61352	TAS	Projection Bluff, 5km NNE of Breona, 22.5 km SSE of Deloraine on the Lake Hwy	41°43'S	146°44'E	-41.71667	146.73334	26/02/1990	P. Lillywhite, R. Coy & AL Yen	Canopy fogging of Nothofagus cunningamii Species 14	F	Dolichogenidea sp_23
E582	AUMIC370-18	MH138705		MV	HYM-61355	TAS	Projection Bluff, 5km NNE of Breona, 22.5 km SSE of Deloraine on the Lake Hwy	41°43'S	146°44'E	-41.71667	146.73334	26/02/1990	P. Lillywhite, R. Coy & AL Yen	Canopy fogging of Nothofagus cunningamii Species 14	F	Dolichogenidea sp_29
E584	AUMIC371-18	MH138844		MV	HYM-61363	VIC	Grampians Bioscan site 426			-37.212	142.39799	14/11/2012		Malaise trap GRB426	F	unknown sp_3
E585	AUMIC372-18	MH138845	MH139294	MV	HYM-61361	VIC	Grampians Bioscan site 407			-37.212	142.39799	?/11/2012		Malaise trap GRB407	F	unknown sp_3
E586	AUMIC373-18	MH138846		MV	HYM-61360	VIC	Grampians Bioscan site 407			-37.212	142.39799	?/11/2012		Malaise trap GRB407	F	unknown sp_2
E59	AUMIC374-18	MH138847	MH139295	WINC	FreezerPro_1480426	S. Aust	Belair N.P. Gate 9			-35.009	138.65401	25/11-01/12/2007	J.T. Jennings	Malaise Trap	F	Glyptapanteles sp_24
E590	AUMIC375-18	MH138848	MH139296	MV	HYM-61358	VIC	Grampians National Park Bioscan	37°19'51"S	142°11'36" E	-37.33083	142.193333	26-28/11/2012	B. Patullo, P. Lillywhite	Malaise trap, Ming Ming Swamp GB442	F	Cotesia sp_17

E591	AUMIC376-18	MH138849	MH139297	MV	HYM-61364	VIC	Grampians Bioscan site 411	37°09'02"S	142°06'34"E	-37.150556	142.109444	?/11/2012	M. Mackenzie, P. Lillywhite. J. Grubb, R. Zugaro, H. Stewart		Malaise trap. Black Range State Forest, Rocklands Cherrypool Road, east side of road 450-600m by road N of intersection with Hogans Road	F	Sathon sp_1		
E592	AUMIC377-18	MH138850	MH139298	MV	HYM-61356	VIC	Grampians Bioscan site 411	37°09'02"S	142°06'34"E	-37.150556	142.109444	?/11/2012	M. Mackenzie, P. Lillywhite. J. Grubb, R. Zugaro, H. Stewart		Malaise trap. Black Range State Forest, Rocklands Cherrypool Road, east side of road 450-600m by road N of intersection with Hogans Road	F	Iconella sp_2		
E593	AUMIC378-18	MH138851	MH139299	MV	HYM-61348	VIC	Grampians Bioscan site 406	37°03'41"S	142°22'50"E	-37.061389	142.380556	19/11/2012	J. Grubb, M. Mackenzie, P. Lillywhite, K. Pawley		Malaise trap, Cooinda Burrong Scout Camp, basecamp and surrounds	F	Diolcogaster sp_11		
E594	AUMIC379-18	MH138852		MV	HYM-61362	VIC	Grampians Bioscan site 406	37°03'41"S	142°22'50"E	-37.061389	142.380556	19/11/2012	J. Grubb, M. Mackenzie, P. Lillywhite, K. Pawley		Malaise trap, Cooinda Burrong Scout Camp, basecamp and surrounds	F	unknown sp_3		
E595	AUMIC380-18	MH138853	MH139300	MV	HYM-61359	VIC	Grampians Bioscan site 406	37°03'41"S	142°22'50"E	-37.061389	142.380556	19/11/2012	J. Grubb, M. Mackenzie, P. Lillywhite, K. Pawley		Malaise trap, Cooinda Burrong Scout Camp, basecamp and surrounds	F	Miropotes sp_11		
E597	AUMIC381-18	MH138854		MV	HYM-61354	VIC	Picola			-36.01115	145.13281	16/11/2004			ESAI Shelterbelt NE-FN/23/0118 6 P1 2-1 Water trap sample	F	Dolichogenidea sp_24		
E598	AUMIC382-18	MH138855	MH139301	QM	T208386	QLD	Lamington NP	28.155°S	153.139°E	-28.155	153.13901	13-23/01/2007	C Lambkin, N. Starick	282m	IBISCA Plot # IQ-300-B rainforest malaise trap	F	Iconella sp_1		
E599	AUMIC383-18	MH138856	MH139302	QM	T208401	QLD	Lamington NP	28.155°S	153.139°E	-28.155	153.13901	13-23/01/2007	C Lambkin, N. Starick	282m	IBISCA Plot # IQ-300-B rainforest malaise trap	F	Glyptapanteles sp_11		
E6	AUMIC384-18	MH138857	MH139303	WINC	FreezerPro_1480385	S. Aust	Witchelina Stn	30°08'14"S	137°57'19"E	-30.13722	137.95528	19/10/2010	F. Colombo, R.K., S.M.		Bush Blitz Svy SM095 dam flood out with Acacia victoriae	F	Cotesia sp_13		
E60	AUMIC385-18	MH138858	MH139304	WINC	FreezerPro_1480427	S. Aust	Belair N.P. Gate 9			-35.009	138.65401	25/11-01/12/2007	J.T. Jennings		Malaise Trap	F	Choeras sp_1		
E600	AUMIC386-18	MH138859	MH139305	QM	T208403	QLD	Lamington NP	28.155°S	153.139°E	-28.155	153.13901	13-23/01/2007	C Lambkin, N. Starick	282m	IBISCA Plot # IQ-300-B rainforest malaise trap	F	Glyptapanteles sp_12		
E601	AUMIC387-18	MH138860	MH139306	QM	T208402	QLD	Lamington NP	28.155°S	153.139°E	-28.155	153.13901	13-23/01/2007	C Lambkin, N. Starick	282m	IBISCA Plot # IQ-300-B rainforest malaise trap	F	Glyptapanteles sp_11		
E602	AUMIC388-18	MH138861	MH139307	QM	T208404	QLD	Lamington NP	28.155°S	153.139°E	-28.155	153.13901	13-23/01/2007	C Lambkin, N. Starick	282m	IBISCA Plot # IQ-300-B rainforest malaise trap	F	Glyptapanteles sp_12		
E604	AUMIC389-18	MH138862	MH139308	QM	T208397	QLD	Lamington NP	28.142°S	153.133°E	-28.142	153.133	08-18/04/2007	C Lambkin, N. Starick	248m	IBISCA Plot # IQ-300-D rainforest malaise trap	F	Glyptapanteles sp_7		
E605	AUMIC390-18	MH138863	MH139309	QM	T208398	QLD	Lamington NP	28.142°S	153.133°E	-28.142	153.133	08-18/04/2007	C Lambkin, N. Starick	248m	IBISCA Plot # IQ-300-D rainforest malaise trap	F	Glyptapanteles sp_7		
E606	AUMIC391-18	MH138864	MH139310	QM	T208340	QLD	Lamington NP	28.227	153.131	-28.227	153.131	12-22/04/2007	C Lambkin, N. Starick	920m	IBISCA Plot # IQ-900-D rainforest malaise trap	F	Diolcogaster sp_19		
E607	AUMIC392-18	MH138865	MH139311	QM	T208341	QLD	Lamington NP	28.227	153.131	-28.227	153.131	12-22/04/2007	C Lambkin, N. Starick	920m	IBISCA Plot # IQ-900-D rainforest malaise trap	F	Diolcogaster sp_19		
E608	AUMIC393-18	MH138866	MH139312	QM	T208383	QLD	Lamington NP	28.258	153.159	-28.258	153.159	11-21/04/2007	C Lambkin, N. Starick	1141m	IBISCA Plot # IQ-1100-A rainforest malaise trap	F	Dolichogenidea sp_23		
E609	AUMIC394-18	MH138867		QM	T208405	QLD	Lamington NP	28.259	153.162	-28.259	153.162	11-21/03/2007	C Lambkin, N. Starick	1142m	IBISCA Plot # IQ-1100-B rainforest malaise trap	F	Glyptapanteles sp_20		
E61	AUMIC395-18	MH138868	MH139313	WINC	FreezerPro_1480428	S. Aust	Belair N.P. Gate 9			-35.009	138.65401	25/11-01/12/2007	J.T. Jennings		Malaise Trap	F	Sathon sp_7		
E610	AUMIC396-18	MH138870	MH139315	QM	T208382	QLD	Lamington NP	28.26	153.167	-28.26	153.167	11-21/03/2007	C Lambkin, N. Starick	1106m	IBISCA Plot # IQ-1100-C rainforest malaise trap	F	Dolichogenidea sp_10		
E611	AUMIC397-18	MH138871	MH139316	QM	T208376	QLD	Lamington NP	28.262	153.17	-28.262	153.17	11-21/03/2008	C Lambkin, N. Starick	1140m	IBISCA Plot # IQ-1100-D rainforest malaise trap	F	Choeras sp_4		
E612	AUMIC398-18	MH138872		QM	T208375	QLD	Lamington NP	28.262	153.17	-28.262	153.17	11-21/03/2008	C Lambkin, N. Starick	1140m	IBISCA Plot # IQ-1100-D rainforest malaise trap	F	Choeras sp_3		
E613	AUMIC399-18	MH138873	MH139317	QM	T208377	QLD	Lamington NP	28.234	153.141	-28.234	153.141	14-24/01/2007	C Lambkin, N. Starick	904m	IBISCA Plot # IQ-900-A rainforest malaise trap	F	Choeras sp_4		
E615	AUMIC400-18	MH138778	MH139246	QM	T208412	QLD	Lamington NP	28.234	153.141	-28.234	153.141	14-24/01/2007	C Lambkin, N. Starick	904m	IBISCA Plot # IQ-900-A rainforest malaise trap	F	Choeras sp_3		
E616	AUMIC401-18	MH138779		QM	T208367	QLD	4km SSE HS Noonbah Station (NB3 M)	24.142S	143.196E	-24.142	143.196	19/01/2009 - 7/02/2009	A. Emmott	188m	Sandy Plain, Ghost gums malaise	F	Microplitis sp_2		
E617	AUMIC402-18	MH138780		QM	T208387	QLD	4km SSE HS Noonbah Station (NB3 M)	24.142S	143.196E	-24.142	143.196	19/01/2009 - 7/02/2009	A. Emmott	188m	Sandy Plain, Ghost gums malaise	F	Cotesia sp_10	morialta	

E618	AUMIC403-18	MH138781	MH139247	QM	T208351	QLD	4km SSE HS Noonbah Station (NB3 M)	24.142S	143.196E	-24.142	143.196	19/01/2009 - 7/02/2009	A. Emmott	188m	Sandy Plain, Ghost gums malaise	F	Apanteles sp_12	
E619	AUMIC404-18	MH138782		QM	T208389	QLD	Plevna Downs, 2.5km WNW HS (PD3)	26.67S	142.577E	-26.67	142.577	16/10/2008 - 20/10/2008	Lambkin Mackenzie Starick	133m	Gidgee malaise	F	Cotesia sp_13	
E62	AUMIC405-18	MH138783	MH139248	WINC	FreezerPro_1480429	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	26/01-02/02/2008	J.T. Jennings		M/T	F	Choeras sp_10	
E620	AUMIC406-18	MH138784	MH139249	QM	T208385	QLD	Plevna Downs, 2.5km WNW HS (PD3)	26.67S	142.577E	-26.67	142.577	16/10/2008 - 20/10/2008	Lambkin Mackenzie Starick	133m	Gidgee malaise	F	Dolichogenidea sp_37	
E621	AUMIC407-18	MH138785	MH139250	QM	T208379	QLD	Cainbable Quarry, OF	28.145	153.113	-28.145	153.113	03-19/02/2009	F. Turco	0	malaise trap	F	Choeras sp_12	
E622	AUMIC408-18	MH138786		QM	T208370	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	23/09/2014-5/10/2014	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Microplitis sp_9	
E623	AUMIC409-18	MH138787	MH139251	QM	T208394	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	23/09/2014-5/10/2014	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Glyptapanteles sp_7	
E624	AUMIC410-18	MH138789	MH139252	QM	T208363	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	22/10/2014-14/11/2014	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Apanteles sp_21	
E626	AUMIC411-18	MH138793	MH139256	QM	T208366	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	22/10/2014-14/11/2014	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Apanteles sp_28	
E627	AUMIC412-18	MH138794	MH139257	QM	T208396	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	05-22/10/2014	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Glyptapanteles sp_7	
E628	AUMIC413-18	MH138795	MH139258	QM	T208359	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	05-22/10/2014	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Apanteles sp_21	perniciosa
E629	AUMIC414-18	MH138796	MH139259	QM	T208360	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	06/01/2015-8/02/2015	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Apanteles sp_21	
E630	AUMIC415-18	MH138797	MH139260	QM	T208392	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	08/02/2015-28/03/2015	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Glyptapanteles sp_6	
E632	AUMIC416-18	MH138800	MH139261	QM	T208395	QLD	Samsonvale Cemetery	27°16'13"S	152°51'20"E	-27.27028	152.85556	08/02/2015-28/03/2015	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap	F	Glyptapanteles sp_7	
E633	AUMIC417-18	MH138801		QM	T208409	QLD	Lamington NP	28.216	153.142	-28.216	153.142	9-19/03/2007	C Lambkin, N. Starick	560m	IBISCA Plot # IQ-500-A rainforest malaise trap	F	Glyptapanteles sp_33	
E636	AUMIC418-18	MH138802	MH139262	QM	T208406	QLD	Lamington NP	28.21	153.139	-28.21	153.13901	09-19/04/2007	C Lambkin, N. Starick	474m	IBISCA Plot # IQ-500-C rainforest malaise trap	F	Glyptapanteles sp_28	
E638	AUMIC419-18	MH138803	MH139263	QM	T208381	QLD	Lamington NP	28.207	153.137	-28.207	153.13699	09-19/04/2007	C Lambkin, N. Starick	471m	IBISCA Plot # IQ-500-D rainforest malaise trap	F	Choeras sp_12	
E639	AUMIC420-18	MH138804	MH139264	QM	T208407	QLD	Lamington NP	28.148	153.137	-28.148	153.13699	08-18/07/2007	C Lambkin, N. Starick	267m	IBISCA Plot # IQ-300-A rainforest malaise trap	F	Glyptapanteles sp_28	
E64	AUMIC421-18	MH138805	MH139265	WINC	FreezerPro_1480430	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	08-30/03/2008	J.T. Jennings		M/T	F	Diolcogaster sp_19	
E640	AUMIC422-18	MH138807	MH139267	QM	T208380	QLD	Lamington NP	28.193	153.128	-28.193	153.12801	13-23/01/2007	C Lambkin, N. Starick	748m	IBISCA Plot # IQ-700-C rainforest malaise trap	F	Choeras sp_12	
E641	AUMIC423-18	MH138808	MH139268	QM	T208391	QLD	Lamington NP	28.193	153.128	-28.193	153.12801	13-23/01/2007	C Lambkin, N. Starick	748m	IBISCA Plot # IQ-700-C rainforest malaise trap	F	Glyptapanteles sp_5	
E644	AUMIC424-18	MH138809		QM	T208388	QLD	Cudmore NP	-22.969	146.379	-22.969	146.379	28/10/ 2010 - 02/08/2011	Lambkin, Starick & Bailey	351m	CM3M Melaleuca heath nr drying creek malaise trap	F	Cotesia sp_11	
E647	AUMIC425-18	MH138810		QM	T208399	QLD	Lonesome NP	25.495	148.812	-25.495	148.812	03-26/11/2010	Lambkin et al.	585m	nr lookout (LNP4M) closed euc. Woodland on rocky ridge malaise trap	F	Glyptapanteles sp_8	
E65	AUMIC426-18	MH138812	MH139270	WINC	FreezerPro_1480431	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	08-30/03/2008	J.T. Jennings		M/T	F	Apanteles sp_6	
E651	AUMIC427-18	MH138813		QM	T208390	QLD	Carnarvon NP	25.02	147.93	-25.02	147.93	13/11/2010 - 13/12/ 2010	Reeves, Sternberg & Spinaze	765m	Mt Moffatt sect. nr. HQ (MM3M) Callitris in flowering heath malaise trap	F	Cotesia sp_14	
E655	AUMIC428-18	MH138814	MH139271	QM	T208337	QLD	Masthead Island	23.537	151.726	-23.537	151.726	05-07/10/2008	QM/QPWS party	0-5m	site 4 Pisonia forest malaise trap	F	Diolcogaster sp_2	
E656	AUMIC429-18	MH138815		QM	T208350	QLD	Masthead Island	23.537	151.723	-23.537	151.723	05-07/10/2008	QM/QPWS party	0-5m	site 6 Casuarina camp site malaise trap	F	Apanteles sp_11	
E657	AUMIC430-18	MH138816	MH139272	QM	T208349	QLD	Masthead Island	23.537	151.723	-23.537	151.723	05-07/10/2008	QM/QPWS party	0-5m	site 6 Casuarina camp site malaise trap	F	Apanteles sp_11	
E659	AUMIC431-18	MH138817	MH139273	QM	T208345	QLD	Lamington NP	28.216	153.142	-28.216	153.142	15-25/01/2007	C Lambkin, N. Starick	560m	IBISCA Plot # IQ-500-A rainforest malaise trap	F	Diolcogaster sp_19	
E660	AUMIC432-18	MH138819	MH139275	QM	T208342	QLD	Lamington NP	28.212	153.141	-28.212	153.141	15-25/01/2007	C Lambkin, N. Starick	514m	IBISCA Plot # IQ-500-B rainforest malaise trap	F	Diolcogaster sp_19	perniciosa
E661	AUMIC433-18	MH138822	MH139278	QM	T208374	QLD	Lamington NP	28.21	153.139	-28.21	153.139	15-25/01/2007	C Lambkin, N. Starick	474m	IBISCA Plot # IQ-500-C rainforest malaise trap	F	Choeras sp_3	
E662	AUMIC434-18	MH138823		QM	T208413	QLD	Lamington NP	28.21	153.139	-28.21	153.139	15-25/01/2007	C Lambkin, N. Starick	474m	IBISCA Plot # IQ-500-C rainforest malaise trap	F	Choeras sp_3	
E663	AUMIC435-18	MH138825	MH139280	QM	T208352	QLD	Lamington NP	28.21	153.139	-28.21	153.139	15-25/01/2007	C Lambkin, N. Starick	474m	IBISCA Plot # IQ-500-C rainforest malaise trap	F	Apanteles sp_13	
E664	AUMIC436-18	MH138826		QM	T208354	QLD	Lamington NP	28.21	153.139	-28.21	153.139	15-25/01/2007	C Lambkin, N. Starick	474m	IBISCA Plot # IQ-500-C rainforest malaise trap	F	Apanteles sp_13	
E665	AUMIC437-18	MH138827	MH139281	QM	T208338	QLD	Lamington NP	28.227	153.131	-28.227	153.131	14-24/01/2007	C Lambkin, N. Starick	920m	IBISCA Plot # IQ-900-D rainforest malaise trap	F	Diolcogaster sp_12	

E666	AUMIC438-18	MH138828	MH139282	QM	T208339	QLD	Lamington NP	28.188	153.121	-28.188	153.121	10-20/04/2007	Lambkin, Marcora, Starick	746m	IBISCA Plot # IQ-700-A rainforest malaise trap	F	Diolcogaster sp_12	morialta
E667	AUMIC439-18	MH138830	MH139284	QM	T208353	QLD	Lamington NP	28.188	153.121	-28.188	153.121	10-20/04/2007	Lambkin, Marcora, Starick	746m	IBISCA Plot # IQ-700-A rainforest malaise trap	F	Apanteles sp_13	
E668	AUMIC440-18	MH138831	MH139285	QM	T208414	QLD	Lamington NP	28.234	153.141	-28.234	153.14101	12-22/04/2007	C Lambkin, N. Starick	904m	IBISCA Plot # IQ-900-A rainforest malaise trap	F	Choeras sp_3	
E67	AUMIC441-18	MH138832	MH139286	WINC	FreezerPro_1480432	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	11-24/11/2007	J.T. Jennings		M/T	F	Miropotes sp_14	
E670	AUMIC442-18	MH138834	MH139288	QM	T208344	QLD	Lamington NP	28.234	153.141	-28.234	153.14101	12-22/04/2007	C Lambkin, N. Starick	904m	IBISCA Plot # IQ-900-A rainforest malaise trap	F	Diolcogaster sp_19	
E671	AUMIC443-18	MH138835	MH139289	QM	T208343	QLD	Lamington NP	28.234	153.141	-28.234	153.14101	12-22/04/2007	C Lambkin, N. Starick	904m	IBISCA Plot # IQ-900-A rainforest malaise trap	F	Diolcogaster sp_19	
E675	AUMIC444-18	MH138837		ANIC	32 130207	WA	Watheroo NP, Jingemia Caves	30°15'15"S	115°59'56"E	-30.25417	115.99889	17/09/2003 - 07/11/2003	C Lambkin N starick J Recsei		malaise closed heath 273 m		Dolichogenidea sp_39	
E679	AUMIC445-18	MH138838		ANIC	32 130208	WA	Watheroo NP, Jingemia Caves	30°15'15"S	115°59'56"E	-30.25417	115.99889	17/09/2003 - 07/11/2003	C Lambkin N starick J Recsei		malaise closed heath 273 m	F	Micropiltis sp_8	
E68	AUMIC446-18	MH138839	MH139291	WINC	FreezerPro_1480433	S. Aust	Belair N.P. Gate 9			-35.009	138.65401	11-24/11/2007	J.T. Jennings		M/T	F	Diolcogaster sp_16	
E681	AUMIC447-18	MH138840		ANIC	32 130209	WA	Watheroo NP, Jingemia Caves	30°15'15"S	115°59'56"E	-30.25417	115.99889	17/09/2003 - 07/11/2003	C Lambkin N starick J Recsei		malaise closed heath 273 m	F	Cotesia sp_13	morialta
E682	AUMIC448-18	MH138929		ANIC	32 130210	WA	Watheroo NP, Jingemia Caves	30°15'15"S	115°59'56"E	-30.25417	115.99889	17/09/2003 - 07/11/2003	C Lambkin N starick J Recsei		malaise closed heath 273 m	F	Apanteles sp_35	morialta
E683	AUMIC449-18	MH138930	MH139361	ANIC	32 130211	WA	Watheroo NP, Jingemia Caves	30°15'15"S	115°59'56"E	-30.25417	115.99889	17/09/2003 - 07/11/2003	C Lambkin N starick J Recsei		malaise closed heath 273 m	F	Cotesia sp_13	
E684	AUMIC450-18	MH138933		ANIC	32 130212	WA	Watheroo NP, Jingemia Caves	30°15'15"S	115°59'56"E	-30.25417	115.99889	17/09/2003 - 07/11/2003	C Lambkin N starick J Recsei		malaise closed heath 273 m	F	Glyptapanteles sp_24	
E69	AUMIC451-18	MH138934	MH139362	WINC	FreezerPro_1480434	S .Aust	Belair N.P. Gate 9			-35.009	138.65401	01-08/03/2008	J.T. Jennings		M/T	F	Miropotes sp_3	
E690	AUMIC452-18	MH138936		ANIC	32 130213	WA	21 km nth of Albany	34°50.266S	117°45.669E	-34.83776	117.76115	16/11/2000	M Court S Cunningham		malaise cleared between native renmant Euc globulus plantation	F	Dolichogenidea sp_24	
E693	AUMIC453-18	MH138938		ANIC	32 130214	WA	10km W of Mt Barker	34°42.647S	117°34.213E	-34.71078	117.57021	9/11/2000	T Simmul S Cunningham		malaise edge Euc. Globulus plantation	F	unknown sp_5	
E694	AUMIC454-18	MH138939		ANIC	32 130215	WA	Kariijini NP, Kariijini Dr	22°34'18"S	118°18'26"E	-22.57167	118.30723	19-25/04/2003	C Lambkin T Weir		malaise open Eucalyptus grassland 814m	F	Microplitis sp_5	
E695	AUMIC455-18	MH138940	MH139363	WAM	E94086	WA	Kariijini NP, Weano Gorge Rd	22°21'19"S	118°15'00"E	-22.35528	118.25	25/04/2003 - 15/05/2003	C Lambkin T Weir		malaise grassy dry creek Eucalyptus Acacia scrub 695 m	F	Dolichogenidea sp_33	
E696	AUMIC456-18	MH138941	MH139364	ANIC	32 130217	WA	Kariijini NP, Weano Gorge Rd	22°21'19"S	118°15'00"E	-22.35528	118.25	25/04/2003 - 15/05/2003	C Lambkin T Weir		malaise grassy dry creek Eucalyptus Acacia scrub 695 m	F	Dolichogenidea sp_31	
E697	AUMIC457-18	MH138942	MH139365	ANIC	32 130218	WA	Kariijini NP, Weano Gorge Rd	22°21'19"S	118°15'00"E	-22.35528	118.25	25/04/2003 - 15/05/2003	C Lambkin T Weir		malaise grassy dry creek Eucalyptus Acacia scrub 695 m	F	Dolichogenidea sp_31	
E698	AUMIC458-18	MH138943	MH139366	ANIC	32 130219	WA	Kariijini NP, Weano Gorge Rd	22°21'19"S	118°15'00"E	-22.35528	118.25	25/04/2003 - 15/05/2003	C Lambkin T Weir		malaise grassy dry creek Eucalyptus Acacia scrub 695 m	F	Dolichogenidea sp_31	
E699	AUMIC459-18	MH138946	MH139367	ANIC	32 130220	WA	Kariijini NP, Weano Gorge Rd	22°21'19"S	118°15'00"E	-22.35528	118.25	25/04/2003 - 15/05/2003	C Lambkin T Weir		malaise grassy dry creek Eucalyptus Acacia scrub 695 m	F	Dolichogenidea sp_7	
E7	AUMIC460-18	MH138947	MH139368	WINC	FreezerPro_1480386	S. Aust	Bon Bon Stn	30°23'41"S	135°26'52"E	-30.39472	135.47137	25/10/2010	R. Kittle		Bush Blitz Svy SM134 at light in swale with Rutidosis helichrysoides	F	Iconella sp_2	
E70	AUMIC461-18	MH138948	MH139369	WINC	FreezerPro_1480435	S. Aust	Belair N.P. Gate 11			-35.009	138.65401	25/11/2007-01/12/2007	J.T. Jennings		M/T	F	Apanteles sp_6	
E700	AUMIC462-18	MH138949	MH139370	ANIC	32 130221	WA	Kariijini NP, Weano Gorge Rd	22°21'19"S	118°15'00"E	-22.35528	118.25	25/04/2003 - 15/05/2003	C Lambkin T Weir		malaise grassy dry creek Eucalyptus Acacia scrub 695 m	F	Dolichogenidea sp_14	
E702	AUMIC463-18	MH138950		ANIC	32 130222	VIC	Little Desert NP Eastern Block, McCabes Hut Track	36°31'39"S	141°55'01"E	-36.5275	141.91695	16-22/11/2002	C Lambkin, D Yeates N Starick J Rescsei		malaise 12.6 km SW Dimbool	F	Cotesia sp_8	
E704	AUMIC464-18	MH138874		ANIC	32 130223	ACT	Canberra, Black Mtn, Behind CSIRO	35°16'S	149°06'E	-35.26667	149.10001	23/09/2002 - 31/10/2002	C Lambkin		0	F	unknown sp_3	
E706	AUMIC465-18	MH138875		ANIC	32 130224	ACT	Canberra, Black Mtn, Behind CSIRO	35°16'S	149°06'E	-35.26667	149.10001	23/09/2002 - 31/10/2002	C Lambkin		0	F	unknown sp_3	
E707	AUMIC466-18	MH138877		ANIC	32 130225	ACT	Canberra, Black Mtn, Behind CSIRO	35°16'S	149°06'E	-35.26667	149.10001	23/09/2002 - 31/10/2002	C Lambkin		0	F	unknown sp_3	
E708	AUMIC467-18	MH138878	MH139319	ANIC	32 130226	NSW	East Boyd State Forest, Goanna Rd,	37°12'05"S	149°46'30"E	-37.20139	149.77499	06/12/2004 - 12/01/2005	C Lambkin N Starick		malaise across disused snig track in forest 56 km SE Bombala 219 m	F	Dolichogenidea sp_23	
E709	AUMIC468-18	MH138879		ANIC	32 130227	VIC	Little Desert NP Western Block, Mount Moffat Track 60km WSW Nhill	36°29'32"S	141°01'10"E	-36.49222	141.01944	19-22/11/2002	C Lambkin D Yeates N Starick J Recsei		malaise	F	unknown sp_1	
E71	AUMIC469-18	MH138880	MH139320	WINC	FreezerPro_1480436	S. Aust	Belair N.P. (lower site)			-35.009	138.65401	14-20/10/2007	J.T. Jennings		M/T	F	Sathon sp_7	

E710	AUMIC470-18	MH138881	MH139321	ANIC	32 130228	VIC	Little Desert NP Western Block, Mount Moffat Track 60km WSW Nhill	36°29'32"S	141°01'10"E	-36.49222	141.01944	19-22/11/2002	C Lambkin D Yeates N Starick J Recsei	malaise		F	Dolichogenidea sp_23
E711	AUMIC471-18	MH138882		ANIC	32 130229	NSW	Kosciuszko NP, 3.6 km SW of Thredbo, nr Dead Horse Gap, over Thredbo R.	36°32'26"S	148°15'52"E	-36.54055	148.26445	11-13/01/2004	C&M&N Lambkin NT Starick	malaise 1500 m		F	Dolichogenidea sp_23
E712	AUMIC472-18	MH138883		ANIC	32 130230	NSW	Kosciuszko NP, 3.6 km SW of Thredbo, nr Dead Horse Gap, over Thredbo R.	36°32'26"S	148°15'52"E	-36.54055	148.26445	11-13/01/2004	C&M&N Lambkin NT Starick	malaise 1500 m		F	Cotesia sp_16
E713	AUMIC473-18	MH138884		ANIC	32 130231	NT	Keep River National Park; Bail-Me-Up Cr. 23.7 km SSW Jarrnarm Camp Ground	15°57'55"S	129°01'52"E	-15.96528	129.03111	13-20/06/2001	ME Irwin, FD Parker, C Lambkin	malaise in dry creekbed		F	Apanteles sp_32
E715	AUMIC474-18	MH138885	MH139322	ANIC	32 130232	NT	Keep River National Park; Bail-Me-Up Cr. 23.7 km SSW Jarrnarm Camp Ground	15°57'55"S	129°01'52"E	-15.96528	129.03111	13-20/06/2001	ME Irwin, FD Parker, C Lambkin	malaise in dry creekbed		F	Apanteles sp_37
E716	AUMIC475-18	MH138886	MH139323	ANIC	32 130233	NT	Keep River National Park; Bail-Me-Up Cr. 23.7 km SSW Jarrnarm Camp Ground	15°57'55"S	129°01'52"E	-15.96528	129.03111	13-20/06/2001	ME Irwin, FD Parker, C Lambkin	malaise in dry creekbed		F	Glyptapanteles sp_15
E719	AUMIC476-18	MH138887	MH139324	ANIC	32 130234	NT	Gregory Nat Park 8.3 km N Humbert Junction	16°02'26"S	130°27'18"E	-16.04056	130.455	06-12/06/2001	ME Irwin, FD Parker, C Lambkin	malaise in dry bed nr flowing ck		F	unknown sp_11
E72	AUMIC477-18	MH138888	MH139325	WINC	FreezerPro_1480437	S. Aust	Belair NP			-35.009	138.65401	27/10/2008 - 10/11/2008	J.T. Jennings	Gate 11 M/T		F	Miropotes sp_14
E723	AUMIC478-18	MH138889	MH139326	ANIC	32 130235	NT	Gregory NP, 5.7 km N Humbert Junction	16°03'44"S	130°27'04"E	-16.06222	130.45111	06-12/06/2001	ME Irwin, FD Parker, C Lambkin	malaise in dry creekbed		F	Apanteles sp_32
E724	AUMIC479-18	MH138890	MH139327	ANIC	32 130236	NT	Gregory NP, 5.7 km N Humbert Junction	16°03'44"S	130°27'04"E	-16.06222	130.45111	06-12/06/2001	ME Irwin, FD Parker, C Lambkin	malaise in dry creekbed		F	unknown sp_12
E728	AUMIC480-18	MH138891	MH139328	WINC	FreezerPro_1480669	Qld	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	19/05/2017-08/07/2017	M.S. Moulds	M/T		F	Diolcogaster sp_1
E729	AUMIC481-18	MH138892	MH139329	WINC	FreezerPro_1480670	Qld	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	19/05/2017-08/07/2017	M.S. Moulds	M/T		F	Diolcogaster sp_1
E73	AUMIC482-18	MH138893	MH139330	WINC	FreezerPro_1480438	S. Aust	Bibaringa, Wistow			-35.112	138.887	Jan-Feb 2008	A. Austin			F	Glyptapanteles sp_24
E730	AUMIC483-18	MH138894	MH139331	WINC	FreezerPro_1480671	Qld	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	19/05/2017-08/07/2017	M.S. Moulds	M/T		F	Diolcogaster sp_1
E731	AUMIC484-18	MH138895	MH139332	WINC	FreezerPro_1480672	Qld	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	19/05/2017-08/07/2017	M.S. Moulds	M/T		F	Glyptapanteles sp_4
E732	AUMIC485-18	MH138896	MH139333	WINC	FreezerPro_1480673	Qld	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	19/05/2017-08/07/2017	M.S. Moulds	M/T		M	Diolcogaster sp_1
E733	AUMIC486-18	MH138897	MH139334	WINC	FreezerPro_1480674	Qld	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	18/04/2017-08/07/17	M.S. Moulds	M/T		F	Apanteles sp_3
E734	AUMIC487-18	MH138899	MH139336	WINC	FreezerPro_1480675	Qld	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	18/04/2017-08/07/17	M.S. Moulds	M/T		F	unknown sp_7
E735	AUMIC488-18	MH138900	MH139337	WINC	FreezerPro_1480676	Qld	Kuranda	16°48.923S	145°38.550E	-16.81538	145.6425	18/04/2017-08/07/17	M.S. Moulds	M/T		F	Glyptapanteles sp_14
E736	AUMIC489-18	MH138901	MH139338	WINC	FreezerPro_1480677	Vic	Bible Museum			-36.61281	143.25478	Sept 2017	Ellen Reid	Reared from ?		F	Cotesia sp_9
E737	AUMIC490-18	MH138902	MH139339	WINC	FreezerPro_1480678	Vic	Bible Museum			-36.61281	143.25478	Sept 2017	Ellen Reid	Reared from ?		M	Cotesia sp_9
E740	AUMIC491-18	MH138904	MH139341	WINC	FreezerPro_1480679	QLD	Burra Range, White Mountains NP	20.72461°S	145.17805°E	-20.724610	145.17805	Collected 4 April, emerged 22 April 2017	M. F. Braby	Reared from larva of Candalides delospila (Lep: Lyc)		F	Cotesia sp_1
E741	AUMIC492-18	MH138905		WINC	FreezerPro_1480680	ACT	Lyneham Ridge			-35.2386	149.116	emerged 11 Feb 2017	M. F. Braby	Reared from larva of Jalmenus ictinus (Lep: Lyc)		F	Apanteles sp_30
E745	AUMIC493-18	MH138906		WINC	FreezerPro_1480681	ACT	Black Mountain			-35.27389	149.11034	emerged 6 March 2017	M. F. Braby	Reared from larva of Pollanisus apicalis (Lep: Zyg)		F	Dolichogenidea sp_16
E746	AUMIC494-18	MH138907	MH139342	SAM	SAMA 32-035460	SA	In or nr. Mamungari Conservation Park	28°48'57"S	129°53'41"E	-28.815833	129.894722	21/09/2017	E. Fagan-Jeffries	330 m		F	Miropotes sp_1
E747	AUMIC495-18	MH138908	MH139343	SAM	SAMA 32-035461	SA	In or nr. Mamungari Conservation Park	from -28.816037°to -28.86196	129.85944° to 129.53459°	-28.816037	129.85944	20/09/2017	R. Leijs, B. Parslow	2nd Vehicle Net		F	Dolichogenidea sp_1
E748	AUMIC496-18	MH138909	MH139344	SAM	SAMA 32-035459	SA	In or nr. Mamungari Conservation Park	29°6'49"S	129°32'29"E	-29.113611	129.541389	23/09/2017	E. Fagan-Jeffries	250 m	sweeping general vegetation	F	Dolichogenidea sp_6
E749	AUMIC497-18	MH138910	MH139345	SAM	SAMA 32-035463	SA	In or nr. Mamungari Conservation Park	-28.91	130.28	-28.91	130.28	23/09/2017	R. Leijs, B. Parslow	Vehicle net, Bush Blitz GVD		F	Dolichogenidea sp_8
E75	AUMIC498-18	MH138911	MH139346	WINC	FreezerPro_1480439	S. Aust	Bon Bon Stn	30°37'34"S	135°24'11"E	-30.62611	135.47749	25-28/10/2010	S. Mantel, F.C., R.K., G.T.	Bush Blitz Svy Malaise9 amongst Senna artemisiodes, Acacia tetragonophila, A. aneura, A. victoriae		F	Dolichogenidea sp_6

E751	AUMIC499-18	MH138912	MH139347	SAM	SAMA 32-035462	SA	In or nr. Mamungari Conservation Park	-28.97	129.543	-28.97	129.543	22/09/2017	R. Leijs, B. Parslow	Vehicle net, Bush Blitz GVD	F	Cotesia sp_4
E752	AUMIC500-18	MH138913	MH139348	SAM	SAMA 32-035467	SA	In or nr. Mamungari Conservation Park	-28.9258159	129.5377178	-28.9258159	129.5377178	22/09/2017	B. Parslow		F	Dolichogenidea sp_14
E755	AUMIC501-18	MH138916	MH139349	SAM	SAMA 32-035465	SA	In or nr. Mamungari Conservation Park	-29.06	129.74	-29.06	129.74	22/09/2017	R. Leijs, B. Parslow	Vehicle net, Bush Blitz GVD	F	Diolcogaster sp_20
E756	AUMIC502-18	MH138918	MH139351	SAM	SAMA 32-035466	SA	In or nr. Mamungari Conservation Park	-28.97	129.543	-28.97	129.543	26/09/2017	R. Leijs, B. Parslow	Vehicle net, Bush Blitz GVD	F	Miropotes sp_4
E757	AUMIC503-18	MH138919		SAM	SAMA 32-035464	SA	In or nr. Mamungari Conservation Park	-28.91	130.28	-28.91	130.28	23/09/2017	R. Leijs, B. Parslow	Vehicle net, Bush Blitz GVD	M	Microplitis sp_1
E76	AUMIC504-18	MH138920	MH139352	WINC	FreezerPro_1480440	S. Aust	Cox Scrub Site 1			-35.33111	138.7475	07-28/10/2007	A.D. Austin	M/T	F	Cotesia sp_15
E77	AUMIC505-18	MH138788		WINC	FreezerPro_1480441	S. Aust	Cox Scrub Site 2			-35.33111	138.7475	20/01-10/02/2008	A.D. Austin	M/T	F	Dolichogenidea sp_17
E78	AUMIC506-18	MH138790	MH139253	WINC	FreezerPro_1480442	S. Aust	Cox scrub site 2			-35.33111	138.7475	29/10/2007-25/11/2007	A.D. Austin	malaise trap	F	Sathon sp_1
E79	AUMIC507-18	MH138791	MH139254	WINC	FreezerPro_1480443	S. Aust	Douglas Scrub	35°11.063'S	138°35.971'E	-35.18438	138.59952	27-28/09/2010	GS Taylor, S. Mantel	Malaise Trap 2010 001	F	Glyptapanteles sp_3
E8	AUMIC508-18	MH138806	MH139266	WINC	FreezerPro_1480387	S. Aust	Witchelina Stn	30°04'22"S	137°45'08"E	-30.07278	137.75223	20/10/2010	F. Colombo	Bush Blitz Svy FC061A sweeping	F	Apanteles sp_5
E80	AUMIC509-18	MH138811	MH139269	WINC	FreezerPro_1480444	S. Aust	Flinders Ranges	30°51.510'S	139°14.030'E	-30.8585	139.23384	8/04/2011	R. Kittel	Wearing Gorge, Sweeping Acacia sp.	F	Iconella sp_2
E81	AUMIC510-18	MH138818	MH139274	WINC	FreezerPro_1480445	S. Aust	Flinders Ranges	30°51.510'S	139°14.030'E	-30.8585	139.23384	8/04/2011	R. Kittel	Wearing Gorge, Sweeping Acacia sp.	F	Apanteles sp_5
E82	AUMIC511-18	MH138824	MH139279	WINC	FreezerPro_1480446	S. Aust	Flinders Ranges	30°51.510'S	139°14.030'E	-30.8585	139.23384	8/04/2011	R. Kittel	Wearing Gorge, Sweeping Acacia sp.	F	Apanteles sp_5
E83	AUMIC512-18	MH138829	MH139283	WINC	FreezerPro_1480447	S. Aust	Flinders Ranges	30°56.058'S	138°20.850'E	-30.9343	138.34749	7/04/2011	G.S. Taylor	breakfasttime creek, sweeping Eucalyptus camaldulensis 2011 098 FR31	F	Apanteles sp_5
E84	AUMIC513-18	MH138833	MH139287	WINC	FreezerPro_1480448	S. Aust	Flinders Ranges, Mora Mora station	31.546799'S	138.392226'E	-31.5468	138.39223	5/04/2011	R. Kittel	light trap	F	Apanteles sp_5
E85	AUMIC514-18	MH138927	MH139359	WINC	FreezerPro_1480449	S. Aust	Flinders Ranges, Mora Mora station	31.546799'S	138.392226'E	-31.5468	138.39223	5/04/2011	R. Kittel	light trap	F	Cotesia sp_13
E86	AUMIC515-18	MH138931		WINC	FreezerPro_1480450	S. Aust	Flinders Ranges, Wearing Gorge	30°51.510'S	139°14.030'E	-30.8585	139.23384	8/04/2011	GS Taylor	Swept flowering Acacia 2011 106 FR39	F	Miicropiltis sp_7
E87	AUMIC516-18	MH138945		WINC	FreezerPro_1480451	S. Aust	K.I. Emu Bay			-35.592	137.541	30/07/2005	F. Vickery	M/T Sect 193 Hd Menzies	F	Apanteles sp_5
E88	AUMIC517-18	MH138898	MH139335	WINC	FreezerPro_1480452	S. Aust	K.I. Emu Bay			-35.592	137.541	30/07/2005	F. Vickery	M/T Sect 193 Hd Menzies	F	Dolichogenidea sp_20
E89	AUMIC518-18	MH138628	MH139118	WINC	FreezerPro_1480453	S. Aust	Kangaroo Is.	35°57.080'S	138°44.292'E	-35.95134	136.7382	20/03/2011	R. Kittel	Light Trap Station with Melaleuca	F	Choeras morialta
E9	AUMIC519-18	MH138921	MH139353	WINC	FreezerPro_1480388	S. Aust	Bon Bon Stn	30°19'94"S	135°28'42"E	-30.33233	135.49306	25-28/10/2010	S. Mantel, F. Colombo, R.K., G. Taylor	Malaise trap 6	F	unknown sp_6
E92	AUMIC520-18	MH138922	MH139354	WINC	FreezerPro_1480454	S. Aust	Kangaroo Is.	35°53.983'S	136°43.078E	-35.89972	136.71796	19/03/2011	R. Kittel	sweeping ground vegetation	F	Dolichogenidea sp_36
E93	AUMIC521-18	MH138923	MH139355	WINC	FreezerPro_1480455	S. Aust	Kangaroo Is.	35°53.983'S	136°43.078E	-35.89972	136.71796	19/03/2011	R. Kittel	sweeping ground vegetation	F	Dolichogenidea sp_36
E95	AUMIC522-18	MH138869	MH139314	WINC	FreezerPro_1480456	S. Aust	Kangaroo Is.	35°47.872'S	137°52.041'E	-35.79787	137.86736	17-24/03/2011	G. Taylor, E. Kinnaird, R. Kittel	Malaise trap MT1	F	Diolcogaster sp_11
E96	AUMIC523-18	MH138820	MH139276	WINC	FreezerPro_1480457	S. Aust	Kangaroo Is.	35°47.872'S	137°52.041'E	-35.79787	137.86736	17-24/03/2011	G. Taylor, E. Kinnaird, R. Kittel	Malaise trap MT1	F	Miropotes sp_5
E97	AUMIC524-18	MH138926	MH139358	WINC	FreezerPro_1480458	S. Aust	Kangaroo Is.	35°45.198'S	137°19.285'E	-35.7533	137.32141	17-24/03/2011	G. Taylor, E. Kinnaird, R. Kittel	Malaise trap MT3	F	Glyptapanteles sp_26

Unsuccessfully barcoded

Extraction code	collection	collection code	State	Location	Latitude	Longitude	Date	Collectors	Elevation	Notes
E130	ANIC		NSW	Black Ra. Tallaganda Natl Pk, 14.3 km fr. Hoskinstown	35°24'52"S	149°32'09"E	03-21/02/2004	C Lambkin, N Starick		malaise flowering heath
E131	ANIC		WA	Porongerup NP over small running creek in Jarrah woodland 351m	34°40.384'S	117°53.551'E	03-15/11/2003	C Lambkin, J Recsei		malaise
E134	ANIC		WA	12 km E Mt Barker	34°41.540S	117°48.305E	15-22/10/1999	M Court S cunningham		malaise edge Euc. Globulus plantation/ pasture interface
E135	ANIC		WA	23 km NNW Albany	34°51.191S	117°48.565E	16/11/2000	T Simmul S Cunningham		malaise remnant vegetation
E137	ANIC		VIC	Little Desert NP Eastern Block, McCabes Hut Track	36°31'39"S	141°55'01"E	16-22/11/2002	C Lambkin, D Yeates N Starick J Rescsei		malaise 12.6 km SW Dimbool
E142	ANIC		WA	Watheroo NP, Marchagee Rd: hilltop	30°06'50"S	115°56'15"E	17/09/2003 - 07/ 11/2003	C Lambkin N starick J Recsei		closed heath malaise 247m
E143	ANIC		WA	12 km E Mt Barker	34°41.540S	117°48.305E	15-22/10/1999	M Court S cunningham		malaise edge Euc. Globulus plantation/ pasture interface
E146	ANIC		WA	10km W of Mt Barker	34°42.647S	117°34.213E	09/11/2000	T Simmul S Cunningham		malaise edge Euc. Globulus plantation
E147	ANIC		NT	Keep River NP; Hazard Creek, 23.7 km SSW Jarrnarm Camp Ground	15°57'33"S	129°01'44"E	03-8/06/2001	ME Irwin, FD Parker, C Lambkin		malaise
E148	ANIC		NT	Keep River NP; Hazard Creek, 23.7 km SSW Jarrnarm Camp Ground	15°57'33"S	129°01'44"E	03-8/06/2001	ME Irwin, FD Parker, C Lambkin		malaise
E151	ANIC		NT	Gregory NP; 5.7 km N Humbert Junction	16°03'44"S	130°27'04"E	12-16/06/2001	ME Irwin, FD Parker, C Lambkin		malaise trap in dry creek bed
E154	ANIC		NT	Gregory NP, Humbert Track 5.6 km SSE Bullita Campground	16°09'45"S	130°26'31"E	12/01/2001	ME Irwin, FD Parker, C Lambkin		malaise white sand
E159	ANIC		NT	Gregory National Park, Station Creek, 0.2 km NNW Bullita Cmp Grnd	16°06'42"S	130°25'23"E	12/01/2001	ME Irwin, FD Parker, C Lambkin		malaise trap
E162	ANIC		NT	Gregory NP, 5.7 km N Humbert Junction	16°03'44"S	130°27'04"E	06-12/06/2001	ME Irwin, FD Parker, C Lambkin		malaise in dry creekbed
E217	ANIC		NSW	East Boyd State Forest, Goanna Rd,	37°12'05"S	149°46'30"E	06/12/2004 - 12/01/2005	C Lambkin N Starick		malaise across disused snig track in forest 56 km SE Bombala 219 m
E219	ANIC		NSW	East Boyd State Forest, Goanna Rd,	37°12'05"S	149°46'30"E	06/12/ 2004 - 12/01/2005	C Lambkin N Starick		malaise across disused snig track in forest 56 km SE Bombala 219 m
E222	ANIC		NT	Gregory NP, 17.4 km N Humbert Junction	15°58'17"S	130°29'17"E	24/05-04/06/2001	T Weir, K pullen, P Bouchard		malaise in damp meadow
E532	ANIC		NSW	Ridge west of Lake George, 889m	34°59'24.0S	149°22'34.0E	10-17/09/2014	J. Lumbers		
E534	ANIC		NSW	Ridge west of Lake George, 822m	35°00'31.4S	149°22'24.8E	17-24/09/2014	J. Lumbers		
E672	ANIC		WA	Watheroo NP, Jingemia Caves	30°15'15"S	115°59'56"E	17/09/2003 - 07/ 11/2003	C Lambkin N starick J Recsei		malaise closed heath 273 m
E673	ANIC		WA	Watheroo NP, Jingemia Caves	30°15'15"S	115°59'56"E	17/09/2003 - 07/ 11/2003	C Lambkin N starick J Recsei		malaise closed heath 273 m
E674	ANIC		WA	Watheroo NP, Jingemia Caves	30°15'15"S	115°59'56"E	17/09/2003 - 07/ 11/2003	C Lambkin N starick J Recsei		malaise closed heath 273 m
E676	ANIC		WA	Watheroo NP, Jingemia Caves	30°15'15"S	115°59'56"E	17/09/2003 - 07/ 11/2003	C Lambkin N starick J Recsei		malaise closed heath 273 m
E677	ANIC		WA	Watheroo NP, Jingemia Caves	30°15'15"S	115°59'56"E	17/09/2003 - 07/ 11/2003	C Lambkin N starick J Recsei		malaise closed heath 273 m
E678	ANIC		WA	Watheroo NP, Jingemia Caves	30°15'15"S	115°59'56"E	17/09/2003 - 07/ 11/2003	C Lambkin N starick J Recsei		malaise closed heath 273 m
E680	ANIC		WA	Watheroo NP, Jingemia Caves	30°15'15"S	115°59'56"E	17/09/2003 - 07/ 11/2003	C Lambkin N starick J Recsei		malaise closed heath 273 m
E685	ANIC		WA	Watheroo NP, Jingemia Caves	30°15'15"S	115°59'56"E	17/09/2003 - 07/ 11/2003	C Lambkin N starick J Recsei		malaise closed heath 273 m
E686	ANIC		WA	Watheroo NP, Marchagee Rd: hilltop	30°06'50"S	115°56'15"E	17/09/2003 - 07/ 11/2003	C Lambkin N starick J Recsei		closed heath malaise 247m
E687	ANIC		WA	23 km NNW Albany	34°51.191S	117°48.565E	16/11/2000	T Simmul S Cunningham		malaise remnant vegetation
E688	ANIC		WA	23 km NNW Albany	34°51.191S	117°48.565E	16/11/2000	T Simmul S Cunningham		malaise remnant vegetation
E689	ANIC		WA	23 km NNW Albany	34°51.191S	117°48.565E	16/11/2000	T Simmul S Cunningham		malaise remnant vegetation
E691	ANIC		WA	21 km nth of Albany	34°50.266S	117°45.669E	16/11/2000	M Court S Cunningham		malaise cleared between native renmant Euc globulus plantation
E692	ANIC		WA	10km W of Mt Barker	34°42.647S	117°34.213E	09/11/2000	T Simmul S Cunningham		malaise edge Euc. Globulus plantation
E701	ANIC		VIC	Little Desert NP Eastern Block, McCabes Hut Track	36°31'39"S	141°55'01"E	16-22/11/2002	C Lambkin, D Yeates N Starick J Rescsei		malaise 12.6 km SW Dimbool
E703	ANIC		ACT	Canberra, Black Mtn, Behind CSIRO	35°16'S	149°06'E	23/09/2002 - 31/10/2002	C Lambkin		
E705	ANIC		ACT	Canberra, Black Mtn, Behind CSIRO	35°16'S	149°06'E	23/09/2002 - 31/10/2002	C Lambkin		
E714	ANIC		NT	Keep River National Park; Bail-Me-Up Cr. 23.7 km SSW Jarrnarm Camp Ground	15°57'55"S	129°01'52"E	13-20/06/2001	ME Irwin, FD Parker, C Lambkin		malaise in dry creekbed
E717	ANIC		NT	Keep River National Park; Bail-Me-Up Cr. 23.7 km SSW Jarrnarm Camp Ground	15°57'55"S	129°01'52"E	13-20/06/2001	ME Irwin, FD Parker, C Lambkin		malaise in dry creekbed
E718	ANIC		NT	Keep River National Park; Bail-Me-Up Cr. 23.7 km SSW Jarrnarm Camp Ground	15°57'55"S	129°01'52"E	13-20/06/2001	ME Irwin, FD Parker, C Lambkin		malaise in dry creekbed
E720	ANIC		NT	Gregory National Park; Bullita Camp Ground	16°06'47"S	130°25'24"E	05-14/06/2001	FD Parker ME Irwin C Lambkin		malaise in dry creekbed
E721	ANIC		VIC	Bendoc-Bonang SF: Bonang Hwy: 74km NNE Orbost	37°05'48"S	148°45'50"E	08/03/2005 - 22/ 04/2005	C Lambkin N Starick		malaise in gully, 875 m
E722	ANIC		VIC	Bendoc-Bonang SF: Bonang Hwy: 74km NNE Orbost	37°05'48"S	148°45'50"E	08/03/2005 - 22/ 04/2005	C Lambkin N Starick		malaise in gully, 875 m
E725	ANIC		NT	Gregory NP, 5.7 km N Humbert Junction	16°03'44"S	130°27'04"E	06-12/06/2001	ME Irwin, FD Parker, C Lambkin		malaise in dry creekbed
E726	ANIC		NT	Gregory NP, 5.7 km N Humbert Junction	16°03'44"S	130°27'04"E	06-12/06/2001	ME Irwin, FD Parker, C Lambkin		malaise in dry creekbed
E727	ANIC		NT	Gregory NP, 5.7 km N Humbert Junction	16°03'44"S	130°27'04"E	06-12/06/2001	ME Irwin, FD Parker, C Lambkin		malaise in dry creekbed
E301	MV		VIC	Grampians National Park Bioscan	37°19'51"S	142°11'36" E	26-28/11/2012	B. Patullo, P. Lillywhite		Malaise trap, Ming Ming Swamp GB442
E303	MV		NT	Uluru, Kata Tjura			01/10/1994			Malaise Site 8 Swale, MoV Horn Expedition
E572	MV		VIC	Coranderrk, 1.9km Sth Healesville, site 5	37°411'S	145°316'E	17/05/1992-24/05/1992	C. Meehan, D. Hooper		Eucalyptus aromoghloia Pitfall trap
E573	MV		VIC	Coranderrk, 1.9km Sth Healesville, site 5	37°411'S	145°316'E	17/05/1992-24/05/1992	C. Meehan, D. Hooper		Eucalyptus aromoghloia Pitfall trap
E574	MV		VIC	Coranderrk, 1.9km Sth Healesville, site 5	37°411'S	145°316'E	17/05/1992-24/05/1992	C. Meehan, D. Hooper		Eucalyptus aromoghloia Pitfall trap
E575	MV		VIC	Coranderrk, 1.9km Sth Healesville, site 5	37°411'S	145°316'E	17/05/1992-24/05/1992	C. Meehan, D. Hooper		Eucalyptus aromoghloia Pitfall trap
E576	MV		VIC	Coranderrk, 1.9km Sth Healesville, site 5	37°411'S	145°316'E	15/03/1992-22/03/1992	C. Meehan, D. Hooper		Eucalyptus aromoghloia Pitfall trap

E580	MV		TAS	Mount Michael, Rainforest vetween Mt. Michael & Little Mt. Michael	41°11'S	148°00'E	21/02/1990	P. Lillywhite, R. Coy & AL Yen		Canopy fogging of Nothofagus cunningamii Species 18
E583	MV		TAS	Projection Bluff, 5km NNE of Breona, 22.5 km SSE of Deloraine on the Lake Hwy	41°43'S	146°44'E	26/02/1990	P. Lillywhite, R. Coy & AL Yen		Canopy fogging of Nothofagus cunningamii Species 14
E587	MV		TAS	Savage River Pipeline Rd. at the 22 mile marker	41°14'S	145°20'E	26/02/1990	P. Lillywhite, R. Coy & AL Yen		Canopy fogging of Nothofagus cunningamii Species 14
E588	MV		TAS	Projection Bluff, 5km NNE of Breona, 22.5 km SSE of Deloraine on the Lake Hwy	41°43'S	146°44'E	26/02/1990	P. Lillywhite, R. Coy & AL Yen		Canopy fogging of Nothofagus cunningamii Species 52
E589	MV		VIC	Grampians National Park Bioscan	37°19'51"S	142°11'36" E	26-28/11/2012	B. Patullo, P. Lillywhite		Malaise trap, Ming Ming Swamp GB442
E596	MV		VIC	Picola			16/11/2004			ESAI Shelterbelt NE-FN/23/118 6 P1 1-1 Water trap sample
E186	QM	18491	QLD	Nairana NP	-21.688	146.924	25/10/2010 - 10/11/ 2010	Lambkin, Starick, H&D Hanrahan	254m	NR1M Open Eucalypt Woodld/spinifex malaise trap
E195	QM		QLD	Samsonvale Cemetery	27°16'13'S	152°51'20'E	08/02/2015-28/03/2015	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap
E199	QM		QLD	Samsonvale Cemetery	27°16'13'S	152°51'20'E	06/01/2015-8/02/2015	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap
E200	QM		QLD	Samsonvale Cemetery	27°16'13'S	152°51'20'E	06/01/2015-8/02/2015	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap
E201	QM		QLD	Samsonvale Cemetery	27°16'13'S	152°51'20'E	06/01/2015-8/02/2015	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap
E239	QM		QLD	Plevna Downs, Tompilly Hill base (PD6 M)	26.728S	142.651E	25/11/2008 - 18/12/2008	R Mackenzie	187m	Gidgee malaise
E603	QM	22020	QLD	Lamington NP	28.142°S	153.133°E	08-18/04/2007	C Lambkin, N. Starick	248m	IBISCA Plot # IQ-3-D rainforest malaise trap
E614	QM	22153	QLD	Lamington NP	28.234	153.141	14-24/01/2007	C Lambkin, N. Starick	904m	IBISCA Plot # IQ-9-A rainforest malaise trap
E625	QM		QLD	Samsonvale Cemetery	27°16'13'S	152°51'20'E	22/10/2014-14/11/2014	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap
E631	QM		QLD	Samsonvale Cemetery	27°16'13'S	152°51'20'E	08/02/2015-28/03/2015	S. Wright	50m	8.5km SSE Dayboro Casuarina/open forest malaise trap
E634	QM	22018	QLD	Lamington NP	28.151	153.138	08-18/04/2007	C Lambkin, N. Starick	260m	IBISCA Plot # IQ-3-C rainforest malaise trap
E635	QM	22018	QLD	Lamington NP	28.151	153.138	08-18/04/2007	C Lambkin, N. Starick	260m	IBISCA Plot # IQ-3-C rainforest malaise trap
E637	QM	22026	QLD	Lamington NP	28.21	153.139	09-19/04/2007	C Lambkin, N. Starick	474m	IBISCA Plot # IQ-5-C rainforest malaise trap
E642	QM	22036	QLD	Lamington NP	28.204	153.129	10-20/04/2007	C Lambkin, N. Starick	748m	IBISCA Plot # IQ-7-D rainforest malaise trap
E643	QM	18517	QLD	Cudmore NP	-22.969	146.379	28/10/ 2010 - 02/08/2012	Lambkin, Starick & Bailey	351m	CM3M Melaleuca heath nr drying creek malaise trap
E645	QM	19421	QLD	Carnarvon stn	24.836	147.631	07-25/11/2010	Lambkin, Starick & Zwick	690m	(CN3M1) Callitrus nr damp with forbs malaise trap
E646	QM	19421	QLD	Carnarvon stn	24.836	147.631	07-25/11/2010	Lambkin, Starick & Zwick	690m	(CN3M1) Callitrus nr damp with forbs malaise trap
E648	QM	19380	QLD	Lonesome NP	25.495	148.812	03-26/11/2010	Lambkin et al.	585m	nr lookout (LNP4M) closed euc. Woodland on rocky ridge malaise trap
E649	QM	19403	QLD	Carnarvon NP	25.02	147.93	13/11/2010 - 13/12/ 2010	Reeves, Sternberg & Spinaze	765m	Mt Moffatt sect. nr. HQ (MM3M) Callitris in flowering heath malaise trap
E650	QM	19403	QLD	Carnarvon NP	25.02	147.93	13/11/2010 - 13/12/ 2010	Reeves, Sternberg & Spinaze	765m	Mt Moffatt sect. nr. HQ (MM3M) Callitris in flowering heath malaise trap
E652	QM	19403	QLD	Carnarvon NP	25.02	147.93	13/11/2010 - 13/12/ 2010	Reeves, Sternberg & Spinaze	765m	Mt Moffatt sect. nr. HQ (MM3M) Callitris in flowering heath malaise trap
E653	QM	19403	QLD	Carnarvon NP	25.02	147.93	13/11/2010 - 13/12/ 2010	Reeves, Sternberg & Spinaze	765m	Mt Moffatt sect. nr. HQ (MM3M) Callitris in flowering heath malaise trap
E654	QM	19403	QLD	Carnarvon NP	25.02	147.93	13/11/2010 - 13/12/ 2010	Reeves, Sternberg & Spinaze	765m	Mt Moffatt sect. nr. HQ (MM3M) Callitris in flowering heath malaise trap
E658	QM	22142	QLD	Lamington NP	28.216	153.142	15-25/01/2007	C Lambkin, N. Starick	560m	IBISCA Plot # IQ-5-A rainforest malaise trap
E669	QM	22038	QLD	Lamington NP	28.234	153.141	12-22/04/2007	C Lambkin, N. Starick	904m	IBISCA Plot # IQ-9-A rainforest malaise trap
E263	SAM		SA	Andamooka Station, 2.5 km WNW Andamooka HS	30.71416	137.17928	01/09/2016	P. Hudson		at light, BS197, AND1
E750	SAM		SA	In or nr. Mamungari Conservation Park	-28.97	129.543	22/09/2017	R. Leijs, B. Parslow		Vehicle net, Bush Blitz GVD
E753	SAM		SA	In or nr. Mamungari Conservation Park	-29.11531 to -28.91363	129.54124 to 130.27775	28/09/2017	R. Leijs, B. Parslow		Vehicle net, Bush Blitz GVD
E754	SAM		SA	In or nr. Mamungari Conservation Park	-29.11531 to -28.91363	129.54124 to 130.27775	28/09/2017	R. Leijs, B. Parslow		Vehicle net, Bush Blitz GVD
E274	TMAG	F29320	TAS	Arve Forest: Conways Rd Incorrect SSS2	-43.14459	146.8421	01-03/02/2016	Kirrily Moore		Bush Blitz Malaise trap
E280	TMAG	F29325	TAS	Parasitic Hymenoptera from Helena Gummoth						Apanteles sp. idet Naumann 1981 =H11
E212	WADPIRD		WA	Barrow Island	WGS84: 326266,	WGS84: -7691041	06/05/2006	S. Callan & R. Graham		N27 SUC
E213	WADPIRD		WA	Barrow Island	WGS84: 326266,	WGS84: -7691041	06/05/2006	S. Callan & R. Graham		N27 SUC
E326	WADPIRD		WA	Barrow Island	WGS84 (50) 332912	7697030	01/05/2007	S. Callan K. Edwards		N23 DHC (original vial kept)
E348	WADPIRD		WA	Barrow Island	WGS84: 337659	WGS84: -7697280	25/09/2006	S. Callan & R. Graham		CC2 SUC2
E41	WINC		NSW	Eden, Bungo Street			21-27/12/2005	C. Stephens		malaise trap in exotic natic garden blend nr Eucalypt Forest
E50	WINC		S. Aust	Belair N.P.			25/02-03/03/1996	J.T. Jennings		M.T.
E55	WINC		S. Aust	Belair N.P. Gate 11			08-30/03/2008	J.T. Jennings		Malaise Trap
E63	WINC		S. Aust	Belair N.P. Gate 9			1-14/04/2008	J.T. Jennings		M/T
E66	WINC		S. Aust	Belair N.P. Gate 11			08-30/03/2008	J.T. Jennings		M/T
E74	WINC		S. Aust	Bon Bon Stn	30°25'22"S	135°28'41"E	24/10/2010	D.A. Young		Bush Blitz Svy SM145 under Acacia aneura
E90	WINC		S. Aust	Kangaroo Is.	35°41.900'S	137°01.956'E	18/03/2011	R. Kittel		sweeping Leptospremum sp.
E91	WINC		S. Aust	Kangaroo Is.	35°49.884'S	137°16.702'E	24/03/2011	R. Kittel		sweeping Eucalyptus & Acacia sp.
E94	WINC		S. Aust	Kangaroo Is.	35°41.957'S	137°10.147'E	18/03/2011	R. Kittel		Sweeping Eucalyptus obliqua
E98	WINC		S. Aust	Kangaroo Is.	35°58.423'S	136°44.940'E	17-24/03/2011	GS Taylor, E Kinnaird, R. Kittel		Malaise Trap 4
E99	WINC		S. Aust	Kangaroo Is. Flinders Chase	35°57.136'S	136°39.468'E	22/03/2011	GS Taylor, E Kinnaird		Snake Lagoon, Swept Acacia sp. 211 53 KI53
E107	WINC		S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula			23/11/2000	C. Stephens		Malaise trap in bridal creeper invaded eucalypt woodland
E109	WINC		S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			01/12/2000-03/01/2001	N. Stevens		malaise trap in remnant sclerophyll woodland
E110	WINC		S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			01/12/2000-03/01/2001	N. Stevens		malaise trap in remnant sclerophyll woodland

E111	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			01/12/2000-03/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E113	WINC	S. Aust	Wild Dogs Glen, Waite Campus Adelaide University			16/11/2000		MT Uphill
E167	WINC	S. Aust	Mt Barker Summit			03-22/04/2016	A. Austin	M/T
E168	WINC	S. Aust	Mt Barker Summit			20/03-03/04/2016	A. Austin, E Fagan-Jeffries	M/T
E169	WINC	S. Aust	Morialta Conservation park	34.90413°S,	138.69839°E	24/04/2016 -08/05/16/2016	E. Fagan-Jeffries	M/T
E170	WINC	S. Aust	Morialta Conservation park			26/03-10/04/2016	E. Fagan-Jeffries	M/T
E171	WINC	S. Aust	Cox Scrub Con. Pk.	35°19'55"S	138°44'45"E	5-20/03/2016	E. Fagan-Jeffries	M/T
E172	WINC	S. Aust	Cox Scrub Con. Pk.	35°19'52"S	138°44'51"E	20/03-03/04/2016	E. Fagan-Jeffries	M/T
E175	WINC	S. Aust	Cox Scrub Con. Pk.	35°19'55"S	138°44'45"E	03-17/04/2016	E. Fagan-Jeffries	M/T
E178	WINC	S. Aust	Cox Scrub Con. Pk.	35°19'52"S	138°44'51"E	01-14/05/2016	E. Fagan-Jeffries	M/T
E208	WINC	S. Aust	Cox Scrub Con. Pk.	35°19'52"S	138°44'51"E	01-14/05/2016	E. Fagan-Jeffries	M/T
E241	WINC	NSW	Queanbeyan			28 Oct 1979	IFB Common	Ex. Ocystola euanthes Meyr
E246	WINC	WA	Albany Highway. Gleneagle State Forest.			03/04-07/05/2005	M.S. Harvey	Malaise trap
E281	WINC	WA	Gleneagle State Forest	32°16'16"E	116°09'48"S	02/01/2017-18/02/2017	M.S. Harvey & E.Harvey	M/T
E284	WINC	QLD	Toohey State Forest	27°32'15"E	153°03'25"S	29.xi-11.xii.2016	M.Rix	M/T
E285	WINC	QLD	Toohey State Forest	27°32'15"E	153°03'25"S	15-28.i.2017	M.Rix	M/T
E304	WINC	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula	35°27'13"S	138°36'22"E	19/12/2016-30/12/2016	E. Fagan-Jeffries	M/T
E305	WINC	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula	35°27'13"S	138°36'22"E	19/12/2016-30/12/2016	E. Fagan-Jeffries	M/T
E308	WINC	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula	35°27'13"S	138°36'22"E	03/11/2016-19/12/2016	E. Fagan-Jeffries	M/T
E319	WINC	S. Aust	Witchelina Stn	30°09'08"S	137°53'52"E	18/10/2010	D.A. Young	Bushblitz svy FC68 sweeping on blue bush
E325	WINC	WA	Millstream Chichester Nat Pk	21.03.19S	116.07.57E	23/11/2003-08/05/2004		PW5 CALM Pilbara Survey Pitfall traps ethylene glycol
E339	WINC	S. Aust	Cox Scrub Con. Pk.	35°19'52"S	138°44'51"E	17/04/2016 -01/05/2016	E. Fagan-Jeffries	M/T
E341	WINC	S. Aust	Mt Barker Summit			03-22/04/2016	A. Austin	M/T
E352	WINC	S. Aust	Belair N.P. Gate 11			11-24/11/2007	J.T. Jennings	M/T
E354	WINC	S. Aust	Belair N.P. Gate 11			11-24/11/2007	J.T. Jennings	M/T
E357	WINC	S. Aust	Belair N.P. Gate 11			08-30/03/2008	J.T. Jennings	M/T
E364	WINC	S. Aust	Belair N.P. Gate 11			08-30/03/2008	J.T. Jennings	M/T
E384	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			01/12/2000-03/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E385	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			01/12/2000-03/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E386	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			01/12/2000-03/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E387	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			01/12/2000-03/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E388	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			01/12/2000-03/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E389	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			01/12/2000-03/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E390	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			01/12/2000-03/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E391	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			01/12/2000-03/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E392	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			01/12/2000-03/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E393	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			01/12/2000-03/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E394	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			01/12/2000-03/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E395	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			01/12/2000-03/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E396	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			01/12/2000-03/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E397	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			01/12/2000-03/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E398	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			01/12/2000-03/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E399	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			01/12/2000-03/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E400	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			03/01/2001-14/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E401	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			03/01/2001-14/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E402	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			03/01/2001-14/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E403	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			03/01/2001-14/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E404	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			03/01/2001-14/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E405	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			03/01/2001-14/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E406	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			03/01/2001-14/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E407	WINC	S. Aust	Woorabinda Stirling Linear Park, Mt Lofty Ranges			03/01/2001-14/01/2001	N. Stevens	malaise trap in remnant sclerophyll woodland
E445	WINC	S. Aust	Cox Scrub Site 2			07/10/2007-20/01/2008	A.D. Austin	emergence trap
E446	WINC	S. Aust	Cox Scrub Site 2			07/10/2007-20/01/2008	A.D. Austin	emergence trap
E447	WINC	S. Aust	Cox Scrub Site 2			07/10/2007-20/01/2008	A.D. Austin	emergence trap
E448	WINC	S. Aust	South Para Reservoir 35km NE Adl.	UTM Zone 54H 0305878	UTM Zone 54H 6158568	28/09/2006	L. Farrington	Malaise trap
E450	WINC	S. Aust	South Para Reservoir 35km NE Adl.	UTM Zone 54H 0305878	UTM Zone 54H 6158568	23/10/2006	L. Farrington	Malaise trap (collection 7/7)
E451	WINC	S. Aust	South Para Reservoir 35km NE Adl.	UTM Zone 54H 0305878	UTM Zone 54H 6158568	23/10/2006	L. Farrington	Malaise trap (collection 7/7)
E454	WINC	WA	Gleneagle State Forest			29/11/2005	M.S. Harvey	Malaise Trap

E455	WINC	WA	Gleneagle State Forest			29/11/2005	M.S. Harvey	Malaise Trap
E456	WINC	WA	Porongurup N.P. Waddy's Hut.	34.40.55S	117.50.57E	06-09/02/2009	S. Thompson/A. Austin	Karri open forest, yellow pan trap
E457	WINC	S. Aust	Mt Barker, 8km S Bugle Ranges	35°06'47"S	138°52'15"E	14-21/04/2008	R. Lavigne	MT Mallee scrub
E459	WINC	S. Aust	Flinders Ranges, Akaba Creek	31°41.305'S	138°34.000'E	04/04/2011	R. Kittel	Sweeping creek vegetation
E460	WINC	S. Aust	Flinders Ranges, Akaba Creek	31°41.305'S	138°34.000'E	04/04/2011	R. Kittel	Sweeping creek vegetation
E462	WINC	S. Aust	Flinders Ranges, Akaba Creek	31°41.305'S	138°34.000'E	04/04/2011	R. Kittel	Sweeping creek vegetation
E464	WINC	S. Aust	Kangaroo Is.	35°45.198'S	137°19.285'E	17-24/03/2011	G. Taylor, E. Kinnaird, R. Kittel	Malaise trap MT3
E465	WINC	S. Aust	Kangaroo Is.	30°47.872'S	137°52.041'E	17-24/03/2011	G. Taylor, E. Kinnaird, R. Kittel	Malaise trap MT1
E466	WINC	S. Aust	KI Emu Bay sect 193 Hd Menzies			24/10/2005	F. Vickery	Malaise trap sample 1
E470	WINC	S. Aust	Cox Scrub site 1			7/10/2007-20/01/2008	A.D. Austin	Em. Trap
E472	WINC	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula			25/10/2000	C. Stephens	Malaise trap in bridal creeper invaded eucalypt woodland
E473	WINC	S. Aust	Mt Billy Con. Pk. Fleurieu Peninsula			25/10/2000	C. Stephens	Malaise trap in bridal creeper invaded eucalypt woodland
E475	WINC	S. Aust	Bibaringa, Wistow			Jan-Feb 2008	A. Austin	
E484	WINC	S. Aust	Kangaroo Is.	35°58.423'S	136°44.940'E	17-24/03/2011	GS Taylor, E Kinnaird, R. Kittel	Malaise Trap 4
E486	WINC	S. Aust	Flinders Ranges	31°19.960'S	138°35.850'E	05/04/2011	R. Kittel	ABC lockout, sweeping Myoporum platycarpum
E487	WINC	S. Aust	Flinders Ranges	30°56.058'S	138°20.850'E	07/04/2011	R. Kittel	breakfasttime creek, sweeping Eucalyptus camaldulensis
E488	WINC	S. Aust	Mt. Barker 8km Bugle Ranges	35°06'47"S	138°52'15"E	10-17/03/2008	R. Lavigne	M/T Mallee scrub
E489	WINC	S. Aust	Mt. Barker 8km Bugle Ranges	35°06'47"S	138°52'15"E	10-17/03/2008	R. Lavigne	M/T Mallee scrub
E490	WINC	S. Aust	Belair NP			27/10/2008 -10/11/2008	J.T. Jennings	Gate 11 M/T
E491	WINC	S. Aust	Belair NP			27/10/2008 -10/11/2008	J.T. Jennings	Gate 11 M/T
E493	WINC	NSW	Braidwood, Glenmore Rd.			17-29/12/2005	C. Stephens	malaise trap in exotic/native garden blend pasture setting
E494	WINC	S. Aust	Flinders Ranges	30°51.510'S	139°14.030'E	08/04/2011	R. Kittel	Wearing Gorge, Sweeping Acacia sp.
E495	WINC	S. Aust	Flinders Ranges	30°51.510'S	139°14.030'E	08/04/2011	R. Kittel	Wearing Gorge, Sweeping Acacia sp.
E496	WINC	S. Aust	Flinders Ranges	31.095369'S	138.678507'E	07/04/2011	R. Kittel, G. Taylor	light trap, Blinman, Rose Cottage
E497	WINC	S. Aust	Flinders Ranges	31.095369'S	138.678507'E	07/04/2011	R. Kittel, G. Taylor	light trap, Blinman, Rose Cottage
E498	WINC	S. Aust	Flinders Ranges	31.095369'S	138.678507'E	08/04/2011	R. Kittel	light trap, Blinman, Rose Cottage
E499	WINC	S. Aust	Witchelina Stn	30°05'44"S	138°08'09"E	14/10/2010	F. Colombo	Bush Blitz Svy FC28 sweeping various vegetation in creek bed
E501	WINC	QLD	Kuranda	16°48.923S	145°38.550E	10/02/2015- 15/03/2017	M.S. Moulds	M/T
E502	WINC	S. Aust	Mt Remarkable National Park	32°50'18"S	138°2'12"E	18.ii-1.iv.2017	E. Fagan-Jeffries	M/T
E503	WINC	S. Aust	Mt Remarkable National Park	32°50'18"S	138°2'12"E	18.ii-1.iv.2017	E. Fagan-Jeffries	M/T
E506	WINC	Vic	Sharan Avenue, Mentone			2017	T. Campbell	
E507	WINC	S. Aust	Witchelina Stn	30°07'16"S	137°55'24"E	19/10/2010	F. Colombo	Bush Blitz Svy FC55 sweeping
E510	WINC	S. Aust	Witchelina Stn	30°07'16"S	137°55'26"E	19-22/10/2010	S. Mantel, F. Colombo, R. Kittle	Bush Blitz Svy Malaise 5 dam flood out, young Eucalyptus sp. & flowering herbs
E511	WINC	S. Aust	Witchelina Stn	30°11'07"S	137°58'38"E	18-22/10/2010	S. Mantel, F.C., R.K.	Bush Blitz Svy Malaise 2 in dry creek bed Eremophila freelingi and Acacia tetragonophila
E515	WINC	S. Aust	Witchelina Stn	30°01'30"S	138°02'41"E	17/10/2010	S. Mantel	Bush Blitz Svy SM72 sweeping Swainsona sp.
E519	WINC	S. Aust	Witchelina Stn	30°00'37"S	137°46'35"E	20/10/2010	F. Colombo	Bush Blitz Svy FC6A sweeping
E521	WINC	S. Aust	Witchelina Stn	30°00'37"S	137°46'35"E	20/10/2010	F. Colombo	Bush Blitz Svy FC6A sweeping
E522	WINC	S. Aust	Witchelina Stn	30°05'44"S	138°08'09"E	14/10/2010	S. Mantel	Bush Blitz Svy SM51 on grasses and flowering Swainsona campylantha
E526	WINC	S. Aust	Bon Bon Stn	30°25'29"S	135°28'41"E	26/10/2010	S. Mantel	Bush Blitz Svy SM164 Under Acacia aneura at light.
E527	WINC	S. Aust	Witchelina Stn	30°11'07"S	137°58'38"E	18-22/10/2010	S. Mantel, F.C., R.K.	Bush Blitz Svy Malaise2A
E531	WINC	S. Aust	Witchelina Stn	30°06'20"S	137°44'15"E	20/10/2010	R. Kittle	Bush Blitz Svy RK69 sweeping Acacia sp. in sand dune
E549	WINC	QLD	Kuranda	16°48.923S	145°38.550E	16/03/2017-12/04/2017	M.S. Moulds	M/T
E738	WINC	NT	200m elev. Buntine Hwy, 31 km SW Top Springs	16.75994°S	131.61429°E	Collected 28 July, emerged 12 August 2010	M. F. Braby	Reared from larva of Ogyris zosine (Lep: Lyc)
E739	WINC	NT	200m elev. Buntine Hwy, 31 km SW Top Springs	16.75994°S	131.61429°E	Collected 28 July, emerged 12 August 2010	M. F. Braby	Reared from larva of Ogyris zosine (Lep: Lyc)
E742	WINC	NT	Limbunya Station, Victoria River District	17.30592°S	129.77728°E	collected 24 July emerged 29 July 2010	M. F. Braby	Reared from larva of Ogyris zosine (Lep: Lyc)
E743	WINC	NT	Limbunya Station, Victoria River District	17.30592°S	129.77728°E	collected 24 July emerged 29 July 2010	M. F. Braby	Reared from larva of Ogyris zosine (Lep: Lyc)
E744	WINC	ACT	Black Mountain			emerged 6 March 2017	M. F. Braby	Reared from larva of Pollanisus apicalis (Lep: Zyg)

Chapter 2 Supplementary Table S2

BOLD sequences used in the species delimitation analysis, information downloaded from BOLD

Process ID	Identification	Extra Info	Institution	Collectors	Collection Date	Country/Ocean	State/Province	Region	Sector	Exact Site	Lat	Lon	Elev	Habitat
HYAS060-10	Apanteles	Malaise Trap	Centre for Biodiversity Genomics	Paul D.N. Hebert	26-Dec-2009	Australia	NSW			Hat Head	-31.063	153.052	36.58	Dry Sclerophyll Forest
HYAS097-10	Apanteles	Malaise Trap	Centre for Biodiversity Genomics	Paul D.N. Hebert	26-Dec-2009	Australia	NSW			Hat Head	-31.063	153.052	36.58	Dry Sclerophyll Forest
GBAH1626-06	Cotesia rubecula		Mined from GenBank, NCBI			Australia								
ASQAS186-11	Glyptapanteles		Natural History Museum, London			Australia								
ASQAS187-11	Glyptapanteles		Natural History Museum, London			Australia								
ASQAS156-11	Microgastrinae		Natural History Museum, London			Australia								
ASQAS157-11	Microgastrinae		Natural History Museum, London			Australia								
ASQAS181-11	Cotesia		Natural History Museum, London			Australia								
HYAS217-11	Snellenius	Malaise Trap	Centre for Biodiversity Genomics	Paul Hebert	24-Dec-2010	Australia	NSW	Smiths Lake			-32.377	152.504		
HYAS353-11	Dolichogenidea	Malaise Trap	Centre for Biodiversity Genomics	Christy Carr, Paul Hebert, Stephanie Kirk, Jaclyn McCormick, Jayme Sones	22-Oct-2010	Australia	ACT	Canberra	Cook	8 Moss Street	-35.261	149.059	632	
HYAS375-11	Choeras	Malaise Trap	Centre for Biodiversity Genomics	Christy Carr, Paul Hebert, Stephanie Kirk, Jaclyn McCormick, Jayme Sones	22-Oct-2010	Australia	ACT	Canberra	CSIRO	behind CSIRO	-35.275	149.111	590	
HYAS454-11	Cotesia	Malaise Trap	Centre for Biodiversity Genomics	Paul D.N. Hebert	17-Dec-2010	Australia	NSW			Hat Head	-31.063	153.052	36.58	Dry Sclerophyll Forest
HYAS463-11	Apanteles	Malaise Trap	Centre for Biodiversity Genomics	Paul D.N. Hebert	17-Dec-2010	Australia	NSW			Hat Head	-31.063	153.052	36.58	Dry Sclerophyll Forest
HYAS607-11	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Paul Hebert	24-Dec-2010	Australia	NSW	Smiths Lake			-32.377	152.504		
HYAS621-11	Cotesia	Malaise Trap	Centre for Biodiversity Genomics	Paul Hebert	24-Dec-2010	Australia	NSW	Smiths Lake			-32.377	152.504		
HYAS623-11	Cotesia	Malaise Trap	Centre for Biodiversity Genomics	Paul Hebert	24-Dec-2010	Australia	NSW	Smiths Lake			-32.377	152.504		
HYAS632-11	Parapanteles	Malaise Trap	Centre for Biodiversity Genomics	Paul Hebert	24-Dec-2010	Australia	NSW	Smiths Lake			-32.377	152.504		
HYAS645-11	Cotesia	Malaise Trap	Centre for Biodiversity Genomics	Paul Hebert	24-Dec-2010	Australia	NSW	Smiths Lake			-32.377	152.504		
HYAS646-11	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Paul Hebert	24-Dec-2010	Australia	NSW	Smiths Lake			-32.377	152.504		
HYAS671-11	Dolichogenidea	Malaise Trap	Centre for Biodiversity Genomics	Paul Hebert	24-Dec-2010	Australia	NSW	Smiths Lake			-32.377	152.504		
HYAS700-11	Cotesia	Malaise Trap	Centre for Biodiversity Genomics	Paul Hebert	24-Dec-2010	Australia	NSW	Smiths Lake			-32.377	152.504		
HYAT095-11	Cotesia	Malaise Trap	Centre for Biodiversity Genomics	Christy Carr, Paul Hebert, Stephanie Kirk, Jaclyn McCormick, Jayme Sones	09-Oct-2010	Australia	ACT	Canberra	Cook	8 Moss Street	-35.261	149.059	632	
HYAT274-11	Dolichogenidea	Malaise Trap	Centre for Biodiversity Genomics	Christy Carr, Paul Hebert, Stephanie Kirk, Jaclyn McCormick, Jayme Sones	09-Oct-2010	Australia	ACT	Canberra	Cook	8 Moss Street	-35.261	149.059	632	
HYAT275-11	Cotesia	Malaise Trap	Centre for Biodiversity Genomics	Christy Carr, Paul Hebert, Stephanie Kirk, Jaclyn McCormick, Jayme Sones	09-Oct-2010	Australia	ACT	Canberra	Cook	8 Moss Street	-35.261	149.059	632	
HYAT341-11	Microplitis	Collected March 23-30	Centre for Biodiversity Genomics	Bob Ward	30-Mar-2010	Australia	Tas	Hobart	Kingston Beach		-42.986	147.317		
HYAT366-11	Microplitis	Collected March 6-14	Centre for Biodiversity Genomics	Bob Ward	14-Mar-2010	Australia	Tas	Hobart	Kingston Beach		-42.986	147.317		
HYAT371-11	Glyptapanteles	Collected April 25-30	Centre for Biodiversity Genomics	Bob Ward	30-Apr-2010	Australia	Tas	Hobart	Kingston Beach		-42.986	147.317		
HYAT386-11	Microplitis	Collected March 23-30	Centre for Biodiversity Genomics	Bob Ward	30-Mar-2010	Australia	Tas	Hobart	Kingston Beach		-42.986	147.317		
HYAT393-11	Dolichogenidea	Collected March 23-30	Centre for Biodiversity Genomics	Bob Ward	30-Mar-2010	Australia	Tas	Hobart	Kingston Beach		-42.986	147.317		
HYAT396-11	Glyptapanteles	Collected March 23-30	Centre for Biodiversity Genomics	Bob Ward	30-Mar-2010	Australia	Tas	Hobart	Kingston Beach		-42.986	147.317		
HYAT400-11	Choeras	Collected March 23-30	Centre for Biodiversity Genomics	Bob Ward	30-Mar-2010	Australia	Tas	Hobart	Kingston Beach		-42.986	147.317		
HYAT424-11	Glyptapanteles	Collected Sep 14-18	Centre for Biodiversity Genomics	Bob Ward	18-Sep-2010	Australia	Tas	Hobart	Kingston Beach		-42.986	147.317		
HYAT425-11	Glyptapanteles	Collected Sep 14-18	Centre for Biodiversity Genomics	Bob Ward	18-Sep-2010	Australia	Tas	Hobart	Kingston Beach		-42.986	147.317		
HYAT465-11	Pseudapanteles	Collected March 6-14	Centre for Biodiversity Genomics	Bob Ward	14-Mar-2010	Australia	Tas	Hobart	Kingston Beach		-42.986	147.317		
HYAT466-11	Dolichogenidea	Collected March 6-14	Centre for Biodiversity Genomics	Bob Ward	14-Mar-2010	Australia	Tas	Hobart	Kingston Beach		-42.986	147.317		
MCCAA154-12	Choeras	Malaise	Centre for Biodiversity Genomics	P. Hebert	07-Nov-2011	Australia	ACT	Canberra	CSIRO	CSIRO property	-35.275	149.111	588	
MCCAA178-12	Choeras	Malaise	Centre for Biodiversity Genomics	P. Hebert	07-Nov-2011	Australia	ACT	Canberra	CSIRO	CSIRO property	-35.275	149.111	588	
MCCAA222-12	Cotesia	Malaise	Centre for Biodiversity Genomics	P. Hebert	07-Nov-2011	Australia	ACT	Canberra	CSIRO	CSIRO property	-35.275	149.111	588	
MCCAA225-12	Microgastrinae	Malaise	Centre for Biodiversity Genomics	P. Hebert	07-Nov-2011	Australia	ACT	Canberra	CSIRO	CSIRO property	-35.275	149.111	588	
MCCAA1052-12	Microgastrinae	Malaise	Centre for Biodiversity Genomics	P. Hebert	21-Nov-2011	Australia	ACT	Canberra	CSIRO	CSIRO property	-35.275	149.111	588	
MCCAA1058-12	Microgastrinae	Malaise	Centre for Biodiversity Genomics	P. Hebert	21-Nov-2011	Australia	ACT	Canberra	CSIRO	CSIRO property	-35.275	149.111	588	
MCCAA2641-12	Microgastrinae	Malaise	Centre for Biodiversity Genomics	P. Hebert	24-Oct-2011	Australia	ACT	Canberra	CSIRO	CSIRO property	-35.275	149.111	588	
MCCAA1444-12	Microgastrinae	Malaise	Centre for Biodiversity Genomics	P. Hebert	21-Nov-2011	Australia	ACT	Canberra	CSIRO	CSIRO property	-35.275	149.111	588	

AUSBC910-12	Miropotes	Malaise	Centre for Biodiversity Genomics	P. Hebert	05-Dec-2011	Australia	SA			Border Cliffs Resort on property, near Renmark	-33.979	140.953		
AUSBC925-12	Miropotes	Malaise	Centre for Biodiversity Genomics	P. Hebert	05-Dec-2011	Australia	SA			Border Cliffs Resort on property, near Renmark	-33.979	140.953		
AUSBC1041-12	Miropotes	Malaise	Centre for Biodiversity Genomics	P. Hebert	05-Dec-2011	Australia	SA			Border Cliffs Resort on property, near Renmark	-33.979	140.953		
AUSBC1048-12	Miropotes	Malaise	Centre for Biodiversity Genomics	P. Hebert	05-Dec-2011	Australia	SA			Border Cliffs Resort on property, near Renmark	-33.979	140.953		
AUSBC290-12	Miropotes	Malaise	Centre for Biodiversity Genomics	P. Hebert	05-Dec-2011	Australia	SA			Border Cliffs Resort on property, near Renmark	-33.979	140.953		
AUSBC1173-12	Miropotes	Malaise	Centre for Biodiversity Genomics	P. Hebert	05-Dec-2011	Australia	SA			Border Cliffs Resort on property, near Renmark	-33.979	140.953		
AUSBC1273-12	Miropotes	Malaise	Centre for Biodiversity Genomics	P. Hebert	05-Dec-2011	Australia	SA			Border Cliffs Resort on property, near Renmark	-33.979	140.953		
AUSBC1467-12	Miropotes	Malaise	Centre for Biodiversity Genomics	P. Hebert	05-Dec-2011	Australia	SA			Border Cliffs Resort on property, near Renmark	-33.979	140.953		
AUSBC1500-12	Miropotes	Malaise	Centre for Biodiversity Genomics	P. Hebert	05-Dec-2011	Australia	SA			Border Cliffs Resort on property, near Renmark	-33.979	140.953		
AUSCA706-12	Diolcogaster	UV trap (by catch)	Centre for Biodiversity Genomics	P. Hebert	07-Dec-2011	Australia	SA			Calpernum Stn. Humphee Pt.	-34.042	140.712		
AUSBC1635-12	Miropotes	Malaise	Centre for Biodiversity Genomics	P. Hebert	10-Dec-2011	Australia	SA			Border Cliffs Resort on property, near Renmark	-33.979	140.953		
AUSBC1677-12	Miropotes	Malaise	Centre for Biodiversity Genomics	P. Hebert	10-Dec-2011	Australia	SA			Border Cliffs Resort on property, near Renmark	-33.979	140.953		
AUSBC1686-12	Miropotes	Malaise	Centre for Biodiversity Genomics	P. Hebert	10-Dec-2011	Australia	SA			Border Cliffs Resort on property, near Renmark	-33.979	140.953		
AUSBC1690-12	Miropotes	Malaise	Centre for Biodiversity Genomics	P. Hebert	10-Dec-2011	Australia	SA			Border Cliffs Resort on property, near Renmark	-33.979	140.953		
AUSBC1692-12	Miropotes	Malaise	Centre for Biodiversity Genomics	P. Hebert	10-Dec-2011	Australia	SA			Border Cliffs Resort on property, near Renmark	-33.979	140.953		
AUSBC2061-12	Miropotes	Malaise	Centre for Biodiversity Genomics	P. Hebert	10-Dec-2011	Australia	SA			Border Cliffs Resort on property, near Renmark	-33.979	140.953		
AUSBC2068-12	Miropotes	Malaise	Centre for Biodiversity Genomics	P. Hebert	10-Dec-2011	Australia	SA			Border Cliffs Resort on property, near Renmark	-33.979	140.953		
AUSBC2074-12	Miropotes	Malaise	Centre for Biodiversity Genomics	P. Hebert	10-Dec-2011	Australia	SA			Border Cliffs Resort on property, near Renmark	-33.979	140.953		
HYAS1265-12	Microgastrinae		Centre for Biodiversity Genomics	P. Hebert	15-Nov-2011	Australia	ACT	Canberra		CSIRO property	-35.275	149.111		
HYAS1268-12	Microgastrinae		Centre for Biodiversity Genomics	P. Hebert	15-Nov-2011	Australia	ACT	Canberra		CSIRO property	-35.275	149.111		
HYAS1270-12	Microgastrinae		Centre for Biodiversity Genomics	P. Hebert	15-Nov-2011	Australia	ACT	Canberra		CSIRO property	-35.275	149.111		
CNBAN190-13	Microgastrinae	Malaise	Centre for Biodiversity Genomics	P. Hebert	31-Oct-2011	Australia	ACT			8 Moss Street	-35.261	149.059	632	
AUSMA270-14	Apanteles	Malaise trap	Centre for Biodiversity Genomics	Paul Hebert	27-Dec-2012	Australia	NSW			Hat Head	-31.063	153.052	36.58	
AUSMA277-14	Apanteles	Malaise trap	Centre for Biodiversity Genomics	Paul Hebert	27-Dec-2012	Australia	NSW			Hat Head	-31.063	153.052	36.58	
AUSMA315-14	Microgastrinae	Malaise trap	Centre for Biodiversity Genomics	Paul Hebert	27-Dec-2012	Australia	NSW			Hat Head	-31.063	153.052	36.58	
AUSMG170-14	Microgastrinae	Malaise trap #1	Centre for Biodiversity Genomics	Paul Hebert	03-Jan-2013	Australia	NSW			Glendale Road, Berowra, Brooklyn	-33.599	151.164	205	
GMATB979-15	Cotesia	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	20-May-2014	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER		-43.095	146.654	112	Forest
GMATR1295-16	Choeras	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	30-Dec-2014	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER		-43.095	146.654	112	Forest
GMATS2567-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	13-Jan-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER		-43.095	146.654	112	Forest
GMATS2612-16	Choeras	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	13-Jan-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER		-43.095	146.654	112	Forest
GMATS2618-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	13-Jan-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER		-43.095	146.654	112	Forest
GMATS2668-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	13-Jan-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER		-43.095	146.654	112	Forest
GMATS2678-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	13-Jan-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER		-43.095	146.654	112	Forest
GMATT3210-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	28-Jan-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER		-43.095	146.654	112	Forest
GMATT3228-16	Choeras	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	28-Jan-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER		-43.095	146.654	112	Forest
GMATT3267-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	28-Jan-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER		-43.095	146.654	112	Forest
GMATT3510-16	Choeras	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	28-Jan-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER		-43.095	146.654	112	Forest
GMATT3519-16	Choeras	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	28-Jan-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER		-43.095	146.654	112	Forest
GMATT3567-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	28-Jan-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER		-43.095	146.654	112	Forest
GMATT3570-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	28-Jan-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER		-43.095	146.654	112	Forest
GMATT3602-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	28-Jan-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER		-43.095	146.654	112	Forest
GMATT3691-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	28-Jan-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER		-43.095	146.654	112	Forest

GMATT3731-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	28-Jan-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATT3806-16	Choeras	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	28-Jan-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU158-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU161-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU165-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU176-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU192-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU198-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU202-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU246-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU2659-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU2660-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU2674-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU2690-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU2743-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU2750-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU2760-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU2768-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU2915-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU2939-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU2947-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU2957-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU3004-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU3015-16	Choeras	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU3019-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU3020-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU3060-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU3069-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU3112-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU3114-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU3126-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATU3355-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	10-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATW073-16	Microplitis	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	11-Mar-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2193-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2215-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2226-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2228-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2240-16	Dolichogenidea	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2265-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2279-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2281-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2317-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2324-16	Dolichogenidea	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2337-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2379-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2402-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2403-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2434-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2435-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2465-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2489-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2548-16	Choeras	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2554-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2560-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2570-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATV2575-16	Choeras	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	24-Feb-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATW1405-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	11-Mar-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATW1621-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	11-Mar-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATX2213-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	07-Apr-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest
GMATX2218-16	Microgastrinae	Malaise Trap	Centre for Biodiversity Genomics	Tim Wardlaw	07-Apr-2015	Australia	Tas	Tasn Wilderness World Heritage Forest	Warra LTER	-43.095	146.654	112	Forest

CNCHW200-09	Dolichogenidea		Canadian National Collection of Insects, Arachnids and Nematodes	Skevington & Cumming	15-Oct-2002	Australia	Queensland		Brisbane Forest Park, Scrubb Creek	-27.4281	152.838	
HYCNE493-11	Cotesia		Canadian National Collection of Insects, Arachnids and Nematodes	V.Nealis	22-Feb-1981	Australia	ACT		Canberra	-35.28	149.130000	
HYCNE959-11	Dolichogenidea stantoni	On Hibiscus	Canadian National Collection of Insects, Arachnids and Nematodes	T.Fenner	28-Apr-1986	Australia	NT		Darwin	-12.41	130.880000	
HYCNE967-11	Dolichogenidea tasmanica		Canadian National Collection of Insects, Arachnids and Nematodes		28-Feb-1912	Australia	Tas		Togari	-40.941	144.878329	
HYCNF356-11	Sathon		Canadian National Collection of Insects, Arachnids and Nematodes	G.B.Monteith	08-Sep-1964	Australia	Queensland		Acacia Ridge, 10 miles South Brisbane	-27.587	153.014351	
GBAH3018-07	Cotesia sp. Bundaberg		Mined from GenBank, NCBI			Australia		Giru		-19.45	147.130000	
GBAH3009-07	Cotesia sp. Mackay		Mined from GenBank, NCBI			Australia		Bundaberg		-24.86	152.350000	
HYQTB014-11	Apanteles	malaise trap	Centre for Biodiversity Genomics			Australia		Mackay		-21.14	149.180000	
HYQTB084-11	Microgastrinae	malaise trap	Centre for Biodiversity Genomics	G. Cocks	18-Mar-2011	Australia	Queensland	Townsville	Hermit Park	-19.2828	146.801	10
HYQTB088-11	Apanteles	malaise trap	Centre for Biodiversity Genomics	G. V. Cocks	20-Jun-2011	Australia	Queensland	Townsville	Hermit Park	-19.283	146.801	10
HYQTB094-11	Apanteles	malaise trap	Centre for Biodiversity Genomics	G. V. Cocks	23-Jun-2011	Australia	Queensland	Townsville	Hermit Park	-19.283	146.801	10
HYQTB106-11	Microgastrinae	malaise trap	Centre for Biodiversity Genomics	G. V. Cocks	05-Jul-2011	Australia	Queensland	Townsville	Hermit Park	-19.283	146.801	
HYQTB107-11	Cotesia	malaise trap	Centre for Biodiversity Genomics	G. V. Cocks	21-Jul-2011	Australia	Queensland	Townsville	Hermit Park	-19.283	146.801	10
HYQTB145-12	Microgastrinae	malaise trap	Centre for Biodiversity Genomics	G. V. Cocks	21-Jul-2011	Australia	Queensland	Townsville	Hermit Park	-19.283	146.801	10
HYQTB326-12	Cotesia	malaise trap	Centre for Biodiversity Genomics	G. V. Cocks	11-Sep-2011	Australia	Queensland	Townsville	Hermit Park	-19.283	146.801	10
HYQTB354-12	Microgastrinae	malaise trap	Centre for Biodiversity Genomics	G. V. Cocks	22-Dec-2011	Australia	Queensland	Townsville	Hermit Park	-19.283	146.801	10
HYQT050-08	Microgastrinae	malaise trap	Centre for Biodiversity Genomics	G. V. Cocks	06-Jan-2012	Australia	Queensland	Townsville	Hermit Park	-19.283	146.801	10

Chapter 2: Supplementary Table S3:

Species delimitation results, colour coded to represent species boundaries as established by the different methods.

Genus	Extraction code	2% species	GMYC species birth death	GMYC species yule	bPTP (baysian) species	bPTP (max liklihood) species	bPTP wingless	Wingless 0%	Notes	Consensus
Diolcogaster	E728	Cluster 49	Species 53	Species 70	Species 57	Species 57	Species 29	Cluster 131		Diolcogaster sp_1
Diolcogaster	E547	Cluster 49	Species 53	Species 70	Species 57	Species 57	Species 29	Cluster 131		Diolcogaster sp_1
Diolcogaster	E544	Cluster 49	Species 53	Species 70	Species 57	Species 57	Species 29	Cluster 131		Diolcogaster sp_1
Diolcogaster	E553	Cluster 49	Species 53	Species 70	Species 57	Species 57	Species 29	Cluster 131		Diolcogaster sp_1
Diolcogaster	E732	Cluster 49	Species 53	Species 70	Species 57	Species 57	Species 29	Cluster 131		Diolcogaster sp_1
Diolcogaster	E545	Cluster 49	Species 53	Species 70	Species 57	Species 57	Species 29	Cluster 131		Diolcogaster sp_1
Diolcogaster	E729	Cluster 49	Species 53	Species 70	Species 57	Species 57	Species 29	Cluster 131		Diolcogaster sp_1
Diolcogaster	E730	Cluster 49	Species 53	Species 70	Species 57	Species 57	Species 29	Cluster 131		Diolcogaster sp_1
Diolcogaster	E546	Cluster 49	Species 53	Species 70	Species 57	Species 57	Species 29	Cluster 131		Diolcogaster sp_1
Diolcogaster	E164	Cluster 49	Species 53	Species 70	Species 57	Species 57	*	*		Diolcogaster sp_1
Diolcogaster	E655	Cluster 187	Species 188	Species 214	Species 56	Species 56	Species 29	Cluster 156	E655 wingless is 2 base pair difference to E732	Diolcogaster sp_2
Diolcogaster	E112	Cluster 19	Species 187	Species 213	Species 21	Species 21	Species 30	Cluster 7		Diolcogaster sp_3
Diolcogaster	E173	Cluster 19	Species 187	Species 213	Species 21	Species 21	Species 30	Cluster 7		Diolcogaster sp_3
Diolcogaster	E139	Cluster 19	Species 187	Species 213	Species 21	Species 21	Species 30	Cluster 7		Diolcogaster sp_3
Diolcogaster	E220	Cluster 83	Species 189	Species 215	Species 30	Species 30	Species 22	Cluster 57		Diolcogaster sp_4
Diolcogaster	HYAS607-11	Cluster 224	Species 190	Species 216	Species 29	Species 29	*	*		Diolcogaster sp_5
Diolcogaster	E331	Cluster 130	Species 180	Species 206	Species 237	Species 241	Species 115	Cluster 99	E331 wingless is 2 base pairs different to E332	Diolcogaster sp_6
Diolcogaster	E516	Cluster 131	Species 50	Species 67	Species 223	Species 227	Species 115	Cluster 46	Cluster 123 is not monophyletic (paraphyletic with E331)	Diolcogaster sp_7
Diolcogaster	E509	Cluster 131	Species 50	Species 67	Species 223	Species 227	Species 115	Cluster 46		Diolcogaster sp_7
Diolcogaster	E332	Cluster 131	Species 50	Species 67	Species 223	Species 227	Species 115	Cluster 46		Diolcogaster sp_7
Diolcogaster	E1	Cluster 131	Species 49	Species 66	Species 236	Species 240	Species 115	Cluster 46		Diolcogaster sp_8
Diolcogaster	E518	Cluster 131	Species 49	Species 66	Species 236	Species 240	Species 115	Cluster 46		Diolcogaster sp_8
Diolcogaster	E19	Cluster 131	Species 49	Species 66	Species 236	Species 240	Species 115	Cluster 46		Diolcogaster sp_8
Diolcogaster	E570	Cluster 131	Species 49	Species 66	Species 236	Species 240	Species 115	Cluster 46		Diolcogaster sp_8
Diolcogaster	E571	Cluster 131	Species 49	Species 66	Species 236	Species 240	Species 115	Cluster 46		Diolcogaster sp_8
Diolcogaster	E248	Cluster 92	Species 181	Species 207	Species 81	Species 82	Species 116	Cluster 64	E248 wingless 4 base pairs different to E327, 3 base pairs different to E332	Diolcogaster sp_9
Diolcogaster	E327	Cluster 129	Species 179	Species 205	Species 83	Species 83	Species 116	Cluster 97		Diolcogaster sp_10
Diolcogaster	E593	Cluster 169	Species 48	Species 65	Species 103	Species 103	Species 66	Cluster 140	E593 is 6 bp different to E95	Diolcogaster sp_11
Diolcogaster	E95	Cluster 169	Species 48	Species 65	Species 103	Species 103	Species 66	Cluster 184		Diolcogaster sp_11
Diolcogaster	E665	Cluster 189	Species 47	Species 64	Species 164	Species 164	Species 66	Cluster 158	E665 wingless is 4 base pairs different to E593	Diolcogaster sp_12
Diolcogaster	E666	Cluster 189	Species 47	Species 64	Species 164	Species 164	Species 66	Cluster 158		Diolcogaster sp_12
Diolcogaster	AUSCA706-12	Cluster 6	Species 178	Species 204	Species 163	Species 163	*	*		Diolcogaster sp_13
Diolcogaster	E158	Cluster 45	Species 182	Species 208	Species 4	Species 4	Species 158	Cluster 27		Diolcogaster sp_14
Diolcogaster	E150	Cluster 40	Species 185	Species 211	Species 39	Species 39	*	*		Diolcogaster sp_15
Diolcogaster	E68	Cluster 192	Species 186	Species 212	Species 40	Species 40	Species 8	Cluster 161		Diolcogaster sp_16
Diolcogaster	E10	Cluster 17	Species 184	Species 210	Species 162	Species 162	Species 94	Cluster 6		Diolcogaster sp_17
Diolcogaster	E108	Cluster 16	Species 183	Species 209	Species 222	Species 226	Species 95	Cluster 5	All species 35 wingless are identical, other than E48, 1 bp different	Diolcogaster sp_18
Diolcogaster	E306	Cluster 16	Species 183	Species 209	Species 222	Species 226	*	*		Diolcogaster sp_18
Diolcogaster	E361	Cluster 16	Species 183	Species 209	Species 222	Species 226	Species 95	Cluster 5		Diolcogaster sp_18
Diolcogaster	E360	Cluster 16	Species 183	Species 209	Species 222	Species 226	Species 95	Cluster 5		Diolcogaster sp_18
Diolcogaster	E380	Cluster 16	Species 183	Species 209	Species 222	Species 226	Species 95	Cluster 5		Diolcogaster sp_18
Diolcogaster	E118	Cluster 8	Species 52	Species 69	Species 221	Species 225	Species 95	Cluster 5		Diolcogaster sp_19
Diolcogaster	E48	Cluster 8	Species 52	Species 69	Species 221	Species 225	Species 95	Cluster 125		Diolcogaster sp_19
Diolcogaster	E353	Cluster 8	Species 51	Species 68	Species 221	Species 225	Species 95	Cluster 5		Diolcogaster sp_19
Diolcogaster	E409	Cluster 8	Species 51	Species 68	Species 221	Species 225	Species 95	Cluster 5		Diolcogaster sp_19
Diolcogaster	E369	Cluster 8	Species 51	Species 68	Species 221	Species 225	Species 95	Cluster 5		Diolcogaster sp_19
Diolcogaster	E64	Cluster 8	Species 51	Species 68	Species 221	Species 225	Species 95	Cluster 5		Diolcogaster sp_19
Diolcogaster	E358	Cluster 8	Species 51	Species 68	Species 221	Species 225	Species 95	Cluster 5		Diolcogaster sp_19
Diolcogaster	E52	Cluster 8	Species 51	Species 68	Species 221	Species 225	Species 95	Cluster 5		Diolcogaster sp_19
Diolcogaster	AUSMA315-14	Cluster 8	Species 51	Species 68	Species 221	Species 225	*	*		Diolcogaster sp_19
Diolcogaster	E606	Cluster 8	Species 51	Species 68	Species 221	Species 225	Species 95	Cluster 5		Diolcogaster sp_19
Diolcogaster	E607	Cluster 8	Species 51	Species 68	Species 221	Species 225	Species 95	Cluster 5		Diolcogaster sp_19
Diolcogaster	E660	Cluster 8	Species 51	Species 68	Species 221	Species 225	Species 95	Cluster 5		Diolcogaster sp_19
Diolcogaster	E671	Cluster 8	Species 51	Species 68	Species 221	Species 225	Species 95	Cluster 5		Diolcogaster sp_19
Diolcogaster	E670	Cluster 8	Species 51	Species 68	Species 221	Species 225	Species 95	Cluster 5		Diolcogaster sp_19
Diolcogaster	E659	Cluster 8	Species 51	Species 68	Species 221	Species 225	Species 95	Cluster 5		Diolcogaster sp_19
Diolcogaster	E365	Cluster 8	Species 51	Species 68	Species 221	Species 225	Species 95	Cluster 5		Diolcogaster sp_19
Diolcogaster	E368	Cluster 8	Species 51	Species 68	Species 221	Species 225	Species 95	Cluster 5		Diolcogaster sp_19
Diolcogaster	E373	Cluster 8	Species 51	Species 68	Species 221	Species 225	Species 95	Cluster 5		Diolcogaster sp_19
Diolcogaster	E370	Cluster 8	Species 51	Species 68	Species 221	Species 225	Species 95	Cluster 5		Diolcogaster sp_19
Diolcogaster?	E755	Cluster 211	Species 224	Species 131	Species 6	Species 6	Species 20	Cluster 178	Note: COI places with E44 (Sathon)	Diolcogaster sp_20
Diolcogaster?	E293	Cluster 118	Species 208	Species 192	Species 19	Species 19	Species 293	Cluster 87	Note: COI (1000+ reads) places E293 with strong support with Glyptapanteles. Wingless (62 reads) place 293 basal to Diolcogaster. Specimen is male, has areolet (therefore not Glyptapanteles) but could be Diolcogaster.	Diolcogaster sp_21
	62	20	22	22	21	21	12	18		
Apanteles	HYQTB014-11	Cluster 236	Species 231	Species 115	Species 118	Species 118	*	*		Apanteles sp_1
Apanteles	HYQTB354-12	Cluster 239	Species 247	Species 130	Species 24	Species 24	*	*		Apanteles sp_2
Apanteles	E733	Cluster 203	Species 230	Species 114	Species 175	Species 175	Species 104	Cluster 88		Apanteles sp_3
Apanteles	E294	Cluster 203	Species 230	Species 114	Species 175	Species 175	Species 104	Cluster 88		Apanteles sp_3
Apanteles	E478	Cluster 203	Species 230	Species 114	Species 175	Species 175	*	*		Apanteles sp_3
Apanteles	E149	Cluster 38	Species 73	Species 21	Species 174	Species 174	Species 105	Cluster 23		Apanteles sp_4
Apanteles	E152	Cluster 38	Species 73	Species 21	Species 174	Species 174	Species 105	Cluster 34		Apanteles sp_4
	HYQTB088-11	Cluster 38	Species 73	Species 21	Species 174	Species 174	*	*		Apanteles sp_4
	HYQTB094-11	Cluster 38	Species 73	Species 21	Species 174	Species 174	*	*		Apanteles sp_4
Apanteles	E20	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E315	Cluster 76	Species 74	Species 22	Species 58	Species 58	*	*		Apanteles sp_5
Apanteles	E480	Cluster 76	Species 74	Species 22	Species 58	Species 58	*	*		Apanteles sp_5
Apanteles	E513	Cluster 76	Species 74	Species 22	Species 58	Species 58	*	*		Apanteles sp_5
Apanteles	E514	Cluster 76	Species 74	Species 22	Species 58	Species 58	*	*		Apanteles sp_5
Apanteles	E517	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E476	Cluster 76	Species 74	Species 22	Species 58	Species 58	*	*		Apanteles sp_5
Apanteles	E24	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E321	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E564	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E461	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E483	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E563	Cluster 76	Species 74	Species 22	Species 58	Species 58	*	*		Apanteles sp_5
Apanteles	E81	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E8	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E525	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E555	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E83	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5

Apanteles	E82	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E537	Cluster 76	Species 74	Species 22	Species 58	Species 58	*	*		Apanteles sp_5
Apanteles	E25	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E84	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E320	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E512	Cluster 76	Species 74	Species 22	Species 58	Species 58	*	*		Apanteles sp_5
Apanteles	E4	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E322	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E87	Cluster 76	Species 74	Species 22	Species 58	Species 58	*	*		Apanteles sp_5
Apanteles	E485	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E329	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E477	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E520	Cluster 76	Species 74	Species 22	Species 58	Species 58	*	*		Apanteles sp_5
Apanteles	E479	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E538	Cluster 76	Species 74	Species 22	Species 58	Species 58	*	*		Apanteles sp_5
Apanteles	E318	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E554	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E528	Cluster 76	Species 74	Species 22	Species 58	Species 58	*	*		Apanteles sp_5
Apanteles	E458	Cluster 76	Species 74	Species 22	Species 58	Species 58	*	*		Apanteles sp_5
Apanteles	E523	Cluster 76	Species 74	Species 22	Species 58	Species 58	Species 43	Cluster 51		Apanteles sp_5
Apanteles	E103	Cluster 14	Species 226	Species 110	Species 219	Species 223	Species 32	Cluster 4		Apanteles sp_6
Apanteles	E435	Cluster 14	Species 226	Species 110	Species 219	Species 223	Species 32	Cluster 4		Apanteles sp_6
Apanteles	E363	Cluster 14	Species 226	Species 110	Species 219	Species 223	Species 32	Cluster 103		Apanteles sp_6
Apanteles	E426	Cluster 14	Species 226	Species 110	Species 219	Species 223	Species 32	Cluster 4		Apanteles sp_6
Apanteles	E431	Cluster 14	Species 226	Species 110	Species 219	Species 223	Species 32	Cluster 4		Apanteles sp_6
Apanteles	E56	Cluster 14	Species 226	Species 110	Species 219	Species 223	Species 32	Cluster 4		Apanteles sp_6
Apanteles	E366	Cluster 14	Species 226	Species 110	Species 219	Species 223	Species 32	Cluster 4		Apanteles sp_6
Apanteles	E70	Cluster 14	Species 226	Species 110	Species 219	Species 223	Species 32	Cluster 4		Apanteles sp_6
Apanteles	E374	Cluster 14	Species 226	Species 110	Species 219	Species 223	Species 32	Cluster 4		Apanteles sp_6
Apanteles	E429	Cluster 14	Species 226	Species 110	Species 219	Species 223	Species 32	Cluster 4		Apanteles sp_6
Apanteles	E356	Cluster 14	Species 226	Species 110	Species 219	Species 223	Species 32	Cluster 4		Apanteles sp_6
Apanteles	E452	Cluster 14	Species 226	Species 110	Species 219	Species 223	*	*		Apanteles sp_6
Apanteles	E51	Cluster 14	Species 226	Species 110	Species 219	Species 223	*	*		Apanteles sp_6
Apanteles	E351	Cluster 14	Species 226	Species 110	Species 219	Species 223	Species 32	Cluster 4		Apanteles sp_6
Apanteles	E359	Cluster 14	Species 226	Species 110	Species 219	Species 223	species 32	Cluster 4		Apanteles sp_6
Apanteles	E430	Cluster 14	Species 226	Species 110	Species 219	Species 223	Species 32	Cluster 4		Apanteles sp_6
Apanteles	E433	Cluster 14	Species 226	Species 110	Species 219	Species 223	Species 32	Cluster 4		Apanteles sp_6
Apanteles	E432	Cluster 14	Species 226	Species 110	Species 219	Species 223	Species 32	Cluster 4		Apanteles sp_6
Apanteles	E65	Cluster 14	Species 226	Species 110	Species 219	Species 223	Species 32	Cluster 4		Apanteles sp_6
Apanteles	E362	Cluster 14	Species 226	Species 110	Species 219	Species 223	Species 32	Cluster 4		Apanteles sp_6
Apanteles	E114	Cluster 20	Species 227	Species 111	Species 218	Species 222	Species 32	Cluster 4	E114 wingless is identical to E103, and 2 base pairs different to E234, and 3 base pairs different E129	Apanteles sp_7
Apanteles	E453	Cluster 20	Species 227	Species 111	Species 218	Species 222	Species 32	Cluster 4		Apanteles sp_7
Apanteles	E116	Cluster 20	Species 227	Species 111	Species 218	Species 222	Species 32	Cluster 4		Apanteles sp_7
Apanteles	E129	Cluster 31	Species 69	Species 17	Species 220	Species 224	Species 32	Cluster 19		Apanteles sp_8
Apanteles	E234	Cluster 31	Species 69	Species 17	Species 220	Species 224	Species 32	Cluster 62		Apanteles sp_8
Apanteles	E240	Cluster 31	Species 69	Species 17	Species 220	Species 224	*	*		Apanteles sp_8
Apanteles	E183	Cluster 60	Species 70	Species 18	Species 180	Species 180	Species 52	Cluster 39	E183 wingless is identical to E411	Apanteles sp_9
Apanteles	E408	Cluster 60	Species 70	Species 18	Species 180	Species 180	Species 52	Cluster 39		Apanteles sp_9
Apanteles	E49	Cluster 60	Species 70	Species 18	Species 180	Species 180	Species 52	Cluster 39		Apanteles sp_9
Apanteles	E411	Cluster 140	Species 228	Species 112	Species 181	Species 181	Species 52	Cluster 39		Apanteles sp_10
Apanteles	E412	Cluster 140	Species 228	Species 112	Species 181	Species 181	Species 52	Cluster 39		Apanteles sp_10
Apanteles	E188	Cluster 64	Species 71	Species 19	Species 117	Species 117	Species 63	Cluster 41		Apanteles sp_11
Apanteles	E657	Cluster 64	Species 71	Species 19	Species 117	Species 117	Species 63	Cluster 41		Apanteles sp_11
Apanteles	E656	Cluster 64	Species 71	Species 19	Species 117	Species 117	*	*		Apanteles sp_11
Apanteles	E618	Cluster 180	Species 229	Species 113	Species 143	Species 143	Species 64	Cluster 151	E618 is 2 base pairs different to E667	Apanteles sp_12
Apanteles	E663	Cluster 188	Species 72	Species 20	Species 142	Species 142	Species 64	Cluster 157		Apanteles sp_13
Apanteles	E667	Cluster 188	Species 72	Species 20	Species 142	Species 142	Species 64	Cluster 157		Apanteles sp_13
Apanteles	E664	Cluster 188	Species 72	Species 20	Species 142	Species 142	*	*		Apanteles sp_13
Apanteles	E161	Cluster 47	Species 245	Species 127	Species 22	Species 22	Species 16	Cluster 30		Apanteles sp_14
Apanteles	E163	Cluster 48	Species 232	Species 116	Species 43	Species 43	*	*		Apanteles sp_15
Apanteles	E194	Cluster 69	Species 233	Species 117	Species 44	Species 44	Species 17	Cluster 43		Apanteles sp_16
Apanteles	E174	Cluster 52	Species 234	Species 118	Species 196	species 196	*	*		Apanteles sp_17
Apanteles	E40	Cluster 139	Species 235	Species 119	Species 197	Species 197	*	*		Apanteles sp_18
Apanteles	E209	Cluster 75	Species 75	Species 23	Species 102	Species 102	Species 39	Cluster 50		Apanteles sp_19
Apanteles	E38	Cluster 75	Species 75	Species 23	Species 102	Species 102	Species 39	Cluster 50		Apanteles sp_19
Apanteles	E35	Cluster 75	Species 75	Species 23	Species 102	Species 102	Species 39	Cluster 50		Apanteles sp_19
Apanteles	E419	Cluster 75	Species 75	Species 23	Species 102	Species 102	Species 39	Cluster 50		Apanteles sp_19
Apanteles	E36	Cluster 75	Species 75	Species 23	Species 102	Species 102	Species 39	Cluster 50		Apanteles sp_19
Apanteles	E415	Cluster 75	Species 75	Species 23	Species 102	Species 102	Species 39	Cluster 50		Apanteles sp_19
Apanteles	E417	Cluster 75	Species 75	Species 23	Species 102	Species 102	Species 39	Cluster 50		Apanteles sp_19
Apanteles	E420	Cluster 75	Species 75	Species 23	Species 102	Species 102	*	*		Apanteles sp_19
Apanteles	E416	Cluster 75	Species 75	Species 23	Species 102	Species 102	Species 39	Cluster 50		Apanteles sp_19
Apanteles	E414	Cluster 75	Species 75	Species 23	Species 102	Species 102	Species 39	Cluster 50		Apanteles sp_19
Apanteles	E181	Cluster 58	Species 236	Species 109	Species 20	Species 20	Species 34	Cluster 37		Apanteles sp_20
Apanteles	E184	Cluster 61	Species 67	Species 15	Species 65	Species 65	Species 53	Cluster 40		Apanteles sp_21
Apanteles	E206	Cluster 61	Species 67	Species 15	Species 65	Species 65	*	*		Apanteles sp_21
Apanteles	E628	Cluster 61	Species 67	Species 15	Species 65	Species 65	Species 53	Cluster 40		Apanteles sp_21
Apanteles	E629	Cluster 61	Species 67	Species 15	Species 65	Species 65	Species 53	Cluster 40		Apanteles sp_21
Apanteles	E202	Cluster 61	Species 67	Species 15	Species 65	Species 65	Species 53	Cluster 40		Apanteles sp_21
Apanteles	E205	Cluster 61	Species 67	Species 15	Species 65	Species 65	Species 53	Cluster 40		Apanteles sp_21
Apanteles	E624	Cluster 61	Species 67	Species 15	Species 65	Species 65	Species 53	Cluster 40		Apanteles sp_21
	HYAS060-10	Cluster 61	Species 67	Species 15	Species 65	Species 65	*	*		Apanteles sp_21
Apanteles	E2	Cluster 124	Species 68	Species 16	Species 66	Species 66	Species 33	Cluster 92		Apanteles sp_22
Apanteles	E561	Cluster 124	Species 68	Species 16	Species 66	Species 66	Species 33	Cluster 92		Apanteles sp_22
Apanteles	E556	Cluster 124	Species 68	Species 16	Species 66	Species 66	Species 33	Cluster 92		Apanteles sp_22
Apanteles	E560	Cluster 124	Species 68	Species 16	Species 66	Species 66	Species 33	Cluster 92		Apanteles sp_22
Apanteles	E530	Cluster 124	Species 68	Species 16	Species 66	Species 66	Species 33	Cluster 92		Apanteles sp_22
Apanteles	E562	Cluster 124	Species 68	Species 16	Species 66	Species 66	Species 33	Cluster 92		Apanteles sp_22
Apanteles	E45	Cluster 151	Species 237	Species 120	Species 104	Species 104	Species 106	Cluster 120		Apanteles sp_23
Apanteles	E539	Cluster 156	Species 238	Species 121	Species 105	Species 105	Species 107	Cluster 128		Apanteles sp_24
Apanteles	E542	Cluster 156	Species 238	Species 121	Species 105	Species 105	Species 107	Cluster 128		Apanteles sp_24
Apanteles	E190	Cluster 66	Species 225	Species 108	Species 99	Species 99	Species 113	Cluster 42		Apanteles sp_25
Apanteles	E42	Cluster 7	Species 66	Species 14	Species 98	Species 98	Species 114	Cluster 112		Apanteles sp_26
	AUSMA277-14	Cluster 7	Species 66	Species 14	Species 98	Species 98	*	*		Apanteles sp_26
	HYAS463-11	Cluster 7	Species 66	Species 14	Species 98	Species 98	*	*		Apanteles sp_26
	AUSMA270-14	Cluster 7	Species 66	Species 14	Species 98	Species 98	*	*		Apanteles sp_26
	HYAS097-10	Cluster 7	Species 66	Species 14	Species 98	Species 98	*	*		Apanteles sp_26
Apanteles	E153	Cluster 41	Species 246	Species 129	Species 25	Species 25	Species 27	Cluster 25		Apanteles sp_27
Apanteles	E203	Cluster 72	Species 79	Species 27	Species 23	Species 23	Species 25	Cluster 47		Apanteles sp_28
Apanteles	E626	Cluster 72	Species 79	Species 27	Species 23	Species 23	Species 25	Cluster 47		Apanteles sp_28
Apanteles	E39	Cluster 72	Species 79	Species 27	Species 23	Species 23	Species 25	Cluster 47		Apanteles sp_28

	HYQTB106-11	Cluster 72	Species 79	Species 27	Species 23	Species 23	*	*		Apanteles sp_28
	HYQTB145-12	Cluster 72	Species 79	Species 27	Species 23	Species 23	*	*		Apanteles sp_28
Apanteles	E232	Cluster 89	Species 78	Species 26	Species 26	Species 26	Species 28	Cluster 61		Apanteles sp_29
Apanteles	E257	Cluster 89	Species 78	Species 26	Species 26	Species 26	Species 28	Cluster 61		Apanteles sp_29
Apanteles	E567	Cluster 89	Species 78	Species 26	Species 26	Species 26	Species 28	Cluster 61		Apanteles sp_29
Apanteles	E262	Cluster 89	Species 78	Species 26	Species 26	Species 26	Species 28	Cluster 61		Apanteles sp_29
Apanteles	E267	Cluster 89	Species 78	Species 26	Species 26	Species 26	Species 28	Cluster 61		Apanteles sp_29
Apanteles	E741	Cluster 26	Species 76	Species 24	Species 190	Species 190	*	*		Apanteles sp_30
Apanteles	E122	Cluster 26	Species 76	Species 24	Species 190	Species 190	Species 117	Cluster 14		Apanteles sp_30
Apanteles	E215	Cluster 81	Species 239	Species 122	Species 191	Species 191	Species 118	Cluster 54		Apanteles sp_31
Apanteles	E723	Cluster 33	Species 77	Species 25	Species 249	Species 249	Species 123	Cluster 168	E723 is 5 bp different to E132	Apanteles sp_32
Apanteles	E132	Cluster 33	Species 77	Species 25	Species 249	Species 249	Species 122	Cluster 20		Apanteles sp_32
Apanteles	E136	Cluster 33	Species 77	Species 25	Species 249	Species 249	*	*		Apanteles sp_32
Apanteles	E713	Cluster 33	Species 77	Species 25	Species 249	Species 249	*	*		Apanteles sp_32
Apanteles	E138	Cluster 33	Species 77	Species 25	Species 249	Species 249	Species 122	Cluster 20		Apanteles sp_32
Apanteles	E328	Cluster 33	Species 77	Species 25	Species 249	Species 249	Species 122	Cluster 20		Apanteles sp_32
Apanteles	E233	Cluster 33	Species 77	Species 25	Species 249	Species 249	*	*		Apanteles sp_32
Apanteles	E330	Cluster 33	Species 241	Species 124	Species 248	Species 248	Species 122	Cluster 98	E330 is 2 bp different to E328	Apanteles sp_33
Apanteles	E221	Cluster 84	Species 242	Species 125	Species 215	Species 215	*	*		Apanteles sp_34
Apanteles	E155	Cluster 42	Species 240	Species 123	Species 31	Species 31	*	*		Apanteles sp_35
Apanteles	E682	Cluster 42	Species 240	Species 123	Species 31	Species 31	*	*		Apanteles sp_35
Apanteles	E541	Cluster 157	Species 243	Species 126	Species 68	Species 68	Species 60	Cluster 130		Apanteles sp_36
Apanteles	E715	Cluster 199	Species 244	Species 128	Species 67	Species 67	Species 61	Cluster 166		Apanteles sp_37
	151	36	37	37	37	37	27	33		37
Microplitis	E757	Cluster 213	Species 196	Species 219	Species 97	Species 97	*	*		Microplitis sp_1
Microplitis	E15	Cluster 39	Species 55	Species 73	Species 188	Species 188	Species 119	Cluster 28		Microplitis sp_2
Microplitis	E18	Cluster 39	Species 55	Species 73	Species 188	Species 188	Species 119	Cluster 28		Microplitis sp_2
Microplitis	E17	Cluster 39	Species 55	Species 73	Species 188	Species 188	Species 119	Cluster 28		Microplitis sp_2
Microplitis	E16	Cluster 39	Species 55	Species 73	Species 188	Species 188	Species 119	Cluster 28		Microplitis sp_2
Microplitis	E616	Cluster 39	Species 55	Species 73	Species 188	Species 188	*	*		Microplitis sp_2
Microplitis	E297	Cluster 121	Species 194	Species 217	Species 189	Species 189	Species 119	Cluster 28	1 bp diffrernce with 288, 0 with E15	Microplitis sp_3
Microplitis	E288	Cluster 114	Species 192	Species 74	Species 240	Species 238	Species 119	Cluster 84		Microplitis sp_4
Microplitis	E694	Cluster 194	Species 193	Species 74	Species 241	Species 239	*	*		Microplitis sp_5
Microplitis	E187	Cluster 63	Species 195	Species 218	Species 95	Species 95	*	*		Microplitis sp_6
Microplitis	E23	Cluster 91	Species 56	Species 75	Species 96	Species 96	*	*		Micropiltis sp_7
Microplitis	E86	Cluster 91	Species 56	Species 75	Species 96	Species 96	*	*		Micropiltis sp_7
Microplitis	E141	Cluster 35	Species 54	Species 71	Species 125	Species 125	*	*		Micropiltis sp_8
Microplitis	E679	Cluster 35	Species 54	Species 71	Species 125	Species 125	*	*		Micropiltis sp_8
Microplitis	E185	Cluster 62	Species 58	Species 76	Species 166	Species 166	*	*		Microplitis sp_9
Microplitis	E622	Cluster 62	Species 58	Species 76	Species 166	Species 166	*	*		Microplitis sp_9
Microplitis	HYAS217-11	Cluster 62	Species 58	Species 76	Species 166	Species 166	*	*		Microplitis sp_9
Microplitis	E421	Cluster 142	Species 60	Species 77	Species 242	Species 246	*	*		Microplitis sp_10
Microplitis	GMATW073-16	Cluster 142	Species 60	Species 77	Species 242	Species 246	*	*		Microplitis sp_10
Microplitis	HYAT341-11	Cluster 142	Species 201	Species 225	Species 243	Species 247	*	*		Microplitis sp_10
Microplitis	E336	Cluster 132	Species 59	Species 78	Species 114	Species 114	*	*		Microplitis sp_11
Microplitis	HYAT366-11	Cluster 132	Species 59	Species 78	Species 114	Species 114	*	*		Microplitis sp_11
Microplitis	HYAT386-11	Cluster 132	Species 59	Species 78	Species 114	Species 114	*	*		Microplitis sp_11
Microplitis	E192	Cluster 67	Species 57	Species 72	Species 10	Species 10	*	*		Microplitis sp_12
Microplitis	E196	Cluster 67	Species 57	Species 72	Species 10	Species 10	*	*		Microplitis sp_12
Microplitis	E189	Cluster 65	Species 199	Species 223	Species 75	Species 75	*	*		Microplitis sp_13
Microplitis	E33	Cluster 133	Species 200	Species 224	Species 74	Species 74	*	*		Microplitis sp_14
Microplitis	E176	Cluster 54	Species 191	Species 220	Species 88	Species 88	Species 120	Cluster 33		Microplitis sp_15
Microplitis	E27	Cluster 110	Species 197	Species 221	Species 89	Species 89	Species 121	Cluster 80		Microplitis sp_16
Microplitis	E382	Cluster 137	Species 198	Species 222	Species 11	Species 11	*	*		Micropiltis sp_17
Microplitis	E291	Cluster 117	Species 202	Species 226	Species 12	Species 12	*	*		Microplitis sp_18
	31	18	19	18	19	19	4	5		
Choeras	E106	Cluster 15	Species 36	Species 53	Species 170	Species 170	*	*		Choeras sp_1
Choeras	E310	Cluster 15	Species 36	Species 53	Species 170	Species 170	*	*		Choeras sp_1
Choeras	E252	Cluster 15	Species 36	Species 53	Species 170	Species 170	Species 54	Cluster 67		Choeras sp_1
Choeras	E311	Cluster 15	Species 36	Species 53	Species 170	Species 170	*	*		Choeras sp_1
Choeras	E60	Cluster 15	Species 36	Species 53	Species 170	Species 170	Species 54	Cluster 67	One base pair difference between E60 and E124	Choeras sp_1
Choeras	E124	Cluster 28	Species 37	Species 54	Species 171	Species 171	Species 54	Cluster 16	1 bp difference with E252	Choeras sp_2
Choeras	E133	Cluster 28	Species 37	Species 54	Species 171	Species 171	*	*		Choeras sp_2
Choeras	E123	Cluster 27	Species 34	Species 55	Species 216	Species 216	Species 102	Cluster 15		Choeras sp_3
Choeras	E300	Cluster 27	Species 34	Species 55	Species 216	Species 216	*	*		Choeras sp_3
Choeras	E302	Cluster 27	Species 34	Species 55	Species 216	Species 216	Species 102	Cluster 15		Choeras sp_3
Choeras	E218	Cluster 27	Species 34	Species 55	Species 216	Species 216	*	*		Choeras sp_3
Choeras	E661	Cluster 27	Species 34	Species 55	Species 216	Species 216	Species 102	Cluster 15		Choeras sp_3
Choeras	E612	Cluster 27	Species 34	Species 55	Species 216	Species 216	*	*		Choeras sp_3
Choeras	E278	Cluster 27	Species 34	Species 55	Species 216	Species 216	Species 102	Cluster 79	3 base pair difference between E278 and E611	Choeras sp_3
Choeras	E611	Cluster 177	Species 35	Species 56	Species 217	Species 217	Species 102	Cluster 148		Choeras sp_4
Choeras	E613	Cluster 177	Species 35	Species 56	Species 217	Species 217	Species 102	Cluster 149		Choeras sp_4
Choeras	E418	Cluster 141	Species 161	Species 186	Species 133	Species 133	Species 103	Cluster 109		Choeras sp_5
Choeras	HYAS375-11	Cluster 223	Species 39	Species 51	Species 227	Species 219	*	*		Choeras sp_6
Choeras	MCCAA154-12	Cluster 223	Species 39	Species 51	Species 227	Species 219	*	*		Choeras sp_6
Choeras	MCCAA178-12	Cluster 223	Species 39	Species 51	Species 227	Species 219	*	*		Choeras sp_6
Choeras	HYAT400-11	Cluster 230	Species 164	Species 184	Species 214	Species 214	*	*		Choeras sp_7
Choeras	E270	Cluster 104	Species 38	Species 50	Species 226	Species 18	Species 57	Cluster 75		Choeras sp_8
Choeras	E276	Cluster 104	Species 38	Species 50	Species 226	Species 18	Species 57	Cluster 75		Choeras sp_8
Choeras	GMATR1295-16	Cluster 104	Species 38	Species 50	Species 226	Species 18	*	*		Choeras sp_8
Choeras	GMATT3228-16	Cluster 104	Species 38	Species 50	Species 226	Species 18	*	*		Choeras sp_8
Choeras	GMATT3510-16	Cluster 104	Species 38	Species 50	Species 226	Species 18	*	*		Choeras sp_8
Choeras	GMATT3519-16	Cluster 104	Species 38	Species 50	Species 226	Species 18	*	*		Choeras sp_8
Choeras	GMATT3806-16	Cluster 104	Species 38	Species 50	Species 226	Species 18	*	*		Choeras sp_8
Choeras	GMATV2548-16	Cluster 104	Species 38	Species 50	Species 226	Species 18	*	*		Choeras sp_8
Choeras	GMATS2612-16	Cluster 104	Species 38	Species 50	Species 226	Species 18	*	*		Choeras sp_8
Choeras	GMATV2575-16	Cluster 104	Species 38	Species 50	Species 226	Species 18	*	*		Choeras sp_8
Choeras	GMATU3015-16	Cluster 104	Species 38	Species 50	Species 226	Species 18	*	*		Choeras sp_8
Choeras	E434	Cluster 145	Species 163	Species 183	Species 213	Species 213	Species 57	Cluster 113	2 base pairs difference between E276 and E434	Choeras sp_9
Choeras	E342	Cluster 134	Species 40	Species 52	Species 155	Species 155	Species 57	Cluster 101	5 base pairs difference between E434 and E342	Choeras sp_10
Choeras	E381	Cluster 134	Species 40	Species 52	Species 155	Species 155	Species 57	Cluster 101		Choeras sp_10
Choeras	E345	Cluster 134	Species 40	Species 52	Species 155	Species 155	Species 57	Cluster 102		Choeras sp_10
Choeras	E344	Cluster 134	Species 40	Species 52	Species 155	Species 155	Species 57	Cluster 102		Choeras sp_10
Choeras	E378	Cluster 134	Species 40	Species 52	Species 155	Species 155	Species 57	Cluster 102		Choeras sp_10
Choeras	E379	Cluster 134	Species 40	Species 52	Species 155	Species 155	Species 57	Cluster 102		Choeras sp_10
Choeras	E377	Cluster 134	Species 40	Species 52	Species 155	Species 155	Species 57	Cluster 105		Choeras sp_10
Choeras	E62	Cluster 134	Species 40	Species 52	Species 155	Species 155	Species 57	Cluster 105		Choeras sp_10
Choeras	E197	Cluster 70	Species 162	Species 185	Species 36	Species 36	Species 56	Cluster 44		Choeras sp_11

Choeras	E621	Cluster 9	Species 33	Species 49	Species 37	Species 37	Species 56	Cluster 44	No base pair difference between E197 and E621	Choeras sp_12
Choeras	E640	Cluster 9	Species 33	Species 49	Species 37	Species 37	Species 56	Cluster 44		Choeras sp_12
Choeras	E638	Cluster 9	Species 33	Species 49	Species 37	Species 37	Species 56	Cluster 44		Choeras sp_12
Choeras	E441	Cluster 9	Species 33	Species 49	Species 37	Species 37	Species 55	Cluster 44	Wingles identical to E638??	Choeras sp_12
Choeras	AUSMG170-14	Cluster 9	Species 33	Species 49	Species 37	Species 37	*	*		Choeras sp_12
Choeras	E235	Cluster 90	Species 160	Species 187	Species 38	Species 38	Species 58	Cluster 63		Choeras sp_13
	48	13	13	13	13	13	8	15		
Dolichogenidea	E747	Cluster 207	Species 143	Species 182	Species 70	Species 70	Species 14	Cluster 174		Dolichogenidea sp_1
Dolichogenidea	HYCNE967-11	Cluster 234	Species 127	Species 150	Species 198	Species 198	*	*		Dolichogenidea sp_2
Dolichogenidea	HYAT393-11	Cluster 229	Species 128	Species 151	Species 165	Species 165	*	*		Dolichogenidea sp_3
Dolichogenidea	HYAS632-11	Cluster 226	Species 155	Species 174	Species 78	Species 78	*	*	BOLD identification is Parapanteles	Dolichogenidea sp_4
Dolichogenidea	E127	Cluster 30	Species 141	Species 180	Species 94	Species 94	Species 13	Cluster 18		Dolichogenidea sp_5
Dolichogenidea	E128	Cluster 30	Species 141	Species 180	Species 94	Species 94	Species 13	Cluster 18		Dolichogenidea sp_5
Dolichogenidea	E333	Cluster 30	Species 141	Species 180	Species 94	Species 94	Species 13	Cluster 18		Dolichogenidea sp_5
Dolichogenidea	E748	Cluster 208	Species 150	Species 168	Species 77	Species 77	Species 62	Cluster 175	1 bp difference with E3	Dolichogenidea sp_6
Dolichogenidea	E75	Cluster 208	Species 150	Species 168	Species 77	Species 77	Species 62	Cluster 180		Dolichogenidea sp_6
Dolichogenidea	E3	Cluster 125	Species 32	Species 48	Species 76	Species 76	Species 62	Cluseter 108		Dolichogenidea sp_7
Dolichogenidea	E558	Cluster 125	Species 32	Species 48	Species 76	Species 76	Species 62	Cluseter 108		Dolichogenidea sp_7
Dolichogenidea	E699	Cluster 125	Species 32	Species 48	Species 76	Species 76	Species 62	Cluseter 108		Dolichogenidea sp_7
Dolichogenidea	E749	Cluster 209	Species 154	Species 170	Species 128	Species 128	Species 62	Cluster 176	8 bp difference with E748	Dolichogenidea sp_8
Dolichogenidea	E428	Cluster 144	Species 153	Species 169	Species 129	Species 129	Species 62	Cluster 111	4 bp difference with E748, 4 bp difference with E749	Dolichogenidea sp_9
Dolichogenidea	E610	Cluster 176	Species 148	Species 166	Species 111	Species 111	Species 62	Cluster 147	2 bp differnce with E748, 8 with E749, 4 with E428	Dolichogenidea sp_10
Dolichogenidea	E102	Cluster 13	Species 145	Species 164	Species 90	Species 90	Species 62	Cluster 3	6 bp difference with E428, 4 with E748, 8 with E749	Dolichogenidea sp_11
Dolichogenidea	E568	Cluster 163	Species 147	Species 167	Species 110	Species 110	Species 112	Cluster 137		Dolichogenidea sp_12
Dolichogenidea	E442	Cluster 149	Species 149	Species 171	Species 112	Species 112	Species 111	Cluster 119		Dolichogenidea sp_13
Dolichogenidea	E752	Cluster 126	Species 151	Species 172	Species 127	Species 127	Species 92	Cluster 93		Dolichogenidea sp_14
Dolichogenidea	E316	Cluster 126	Species 151	Species 172	Species 127	Species 127	Species 92	Cluster 93		Dolichogenidea sp_14
Dolichogenidea	E700	Cluster 126	Species 151	Species 172	Species 127	Species 127	Species 92	Cluster 93		Dolichogenidea sp_14
Dolichogenidea	E230	Cluster 87	Species 146	Species 165	Species 109	Speces 109	Species 93	Cluster 59		Dolichogenidea sp_15
Dolichogenidea	E745	Cluster 205	Species 152	Species 173	Species 126	Species 126	*	*		Dolichogenidea sp_16
Dolichogenidea	E449	Cluster 150	Species 157	Species 177	Species 80	Species 80	*	*		Dolichogenidea sp_17
Dolichogenidea	E77	Cluster 150	Species 157	Species 177	Species 80	Species 80	*	*		Dolichogenidea sp_17
Dolichogenidea	HYAS671-11	Cluster 150	Species 157	Species 177	Species 80	Species 80	*	*		Dolichogenidea sp_17
Dolichogenidea	E289	Cluster 115	Species 158	Species 175	Species 81	Species 81	Species 158	Cluster 85		Dolichogenidea sp_18
Dolichogenidea	E115	Cluster 21	Species 129	Species 152	Species 93	Species 93	Species 86	Cluster 8		Dolichogenidea sp_19
Dolichogenidea	E88	Cluster 214	Species 130	Species 153	species 92	species 92	Species 86	Cluster 182	3 bp difference with E115	Dolichogenidea sp_20
Dolichogenidea	E37	Cluster 136	Species 134	Species 157	Species 91	Species 91	Species 87	Cluster 106		Dolichogenidea sp_21
Dolichogenidea	E324	Cluster 128	Species 125	Species 148	Species 204	Species 204	Species 79	Cluster 96		Dolichogenidea sp_22
Dolichogenidea	E711	Cluster 10	Species 26	Species 42	Species 205	Species 205	*	*		Dolichogenidea sp_23
Dolichogenidea	E581	Cluster 10	Species 26	Species 42	Species 203	Species 203	*	*		Dolichogenidea sp_23
Dolichogenidea	E440	Cluster 10	Species 26	Species 42	Species 205	Species 205	Species 79	Cluster 18	1 bp difference with E324	Dolichogenidea sp_23
Dolichogenidea	E540	Cluster 10	Species 25	Species 41	Species 206	Species 206	Species 79	Cluster 18		Dolichogenidea sp_23
Dolichogenidea	E438	Cluster 10	Species 25	Species 41	Species 206	Species 206	Species 79	Cluster 115	4 bp difference with E324, 1 bp difference with E440	Dolichogenidea sp_23
Dolichogenidea	E444	Cluster 10	Species 25	Species 41	Species 206	Species 206	Species 79	Cluster 115		Dolichogenidea sp_23
Dolichogenidea	E443	Cluster 10	Species 25	Species 41	Species 206	Species 206	Species 79	Cluster 115		Dolichogenidea sp_23
Dolichogenidea	E468	Cluster 10	Species 25	Species 41	Species 206	Species 206	*	*		Dolichogenidea sp_23
Dolichogenidea	CNCHW200-09	Cluster 10	Species 25	Species 41	Species 206	Species 206	*	*		Dolichogenidea sp_23
Dolichogenidea	E708	Cluster 10	Species 27	Species 43	Species 235	Species 243	Species 79	Cluster 164	2 bp difference with E324, 4 bp with E438, 1 bp with E440	Dolichogenidea sp_23
Dolichogenidea	E710	Cluster 10	Species 27	Species 43	Species 232	Species 242	Species 79	Cluster 165		Dolichogenidea sp_23
Dolichogenidea	E608	Cluster 10	Species 126	Species 149	Species 233	Species 235	Species 79	Cluster 146	3 bp difference with E710	Dolichogenidea sp_23
Dolichogenidea	E298	Cluster 122	Species 28	Species 44	Species 199	Species 199	*	*		Dolichogenidea sp_24
Dolichogenidea	E597	Cluster 122	Species 28	Species 44	Species 199	Species 199	*	*		Dolichogenidea sp_24
Dolichogenidea	E690	Cluster 122	Species 28	Species 44	Species 199	Species 199	*	*		Dolichogenidea sp_24
Dolichogenidea	HYAS353-11	Cluster 122	Species 28	Species 44	Species 199	Species 199	*	*		Dolichogenidea sp_24
Dolichogenidea	HYAT274-11	Cluster 122	Species 28	Species 44	Species 199	Species 199	*	*		Dolichogenidea sp_24
Dolichogenidea	E125	Cluster 29	Species 29	Species 45	Species 207	Species 207	Species 68	Cluster 17		Dolichogenidea sp_25
Dolichogenidea	E126	Cluster 29	Species 29	Species 45	Species 207	Species 207	Species 68	Cluster 17		Dolichogenidea sp_25
Dolichogenidea	E349	Cluster 29	Species 29	Species 45	Species 207	Species 207	Species 68	Cluster 17		Dolichogenidea sp_25
Dolichogenidea	E347	Cluster 29	Species 29	Species 45	Species 207	Species 207	*	*		Dolichogenidea sp_25
Dolichogenidea	E350	Cluster 29	Species 29	Species 45	Species 207	Species 207	Species 68	Cluster 17		Dolichogenidea sp_25
Dolichogenidea	E346	Cluster 29	Species 29	Species 45	Species 207	Species 207	Species 68	Cluster 17		Dolichogenidea sp_25
Dolichogenidea	E231	Cluster 88	Species 131	Species 154	Species 208	Species 208	Species 68	Cluster 60	2 bp difference with E346, E349, 350	Dolichogenidea sp_26
Dolichogenidea	E145	Cluster 37	Species 132	Species 155	Species 115	Species 115	*	*		Dolichogenidea sp_27
Dolichogenidea	E275	Cluster 107	Species 133	Species 156	Species 113	Species 113	*	*		Dolichogenidea sp_28
Dolichogenidea	GMATV2324-16	Cluster 107	Species 133	Species 156	Species 113	Species 113	*	*		Dolichogenidea sp_28
Dolichogenidea	GMATV2240-16	Cluster 107	Species 133	Species 156	Species 113	Species 113	*	*		Dolichogenidea sp_28
Dolichogenidea	E582	Cluster 167	Species 135	Species 158	Species 114	Species 114	*	*		Dolichogenidea sp_29
Dolichogenidea	E179	Cluster 56	Species 136	Species 159	Species 148	Species 148	Species 69	Cluster 35	1 bp difference with E253	Dolichogenidea sp_30
Dolichogenidea	E253	Cluster 95	Species 30	Species 46	Species 147	Species 147	Species 69	Cluster 68		Dolichogenidea sp_31
Dolichogenidea	E696	Cluster 95	Species 30	Species 46	Species 147	Species 147	Species 69	Cluster 162		Dolichogenidea sp_31
Dolichogenidea	E697	Cluster 95	Species 30	Species 46	Species 147	Species 147	Species 69	Cluster 163		Dolichogenidea sp_31
Dolichogenidea	E698	Cluster 95	Species 30	Species 46	Species 147	Species 147	Species 69	Cluster 163		Dolichogenidea sp_31
Dolichogenidea	E256	Cluster 97	Species 138	Species 161	Species 210	Species 210	Species 67	Cluster 70	Identical to E695	Dolichogenidea sp_32
Dolichogenidea	E695	Cluster 195	Species 139	Species 162	Species 209	Species 209	Species 67	Cluster 70		Dolichogenidea sp_33
Dolichogenidea	E269	Cluster 102	Species 140	Species 163	Species 173	Species 173	*	*		Dolichogenidea sp_34
Dolichogenidea	E323	Cluster 103	Species 31	Species 47	Species 149	Species 149	Species 88	Cluster 95		Dolichogenidea sp_35
Dolichogenidea	E26	Cluster 103	Species 31	Species 47	Species 149	Species 149	*	*		Dolichogenidea sp_35
Dolichogenidea	E92	Cluster 215	Species 137	Species 160	Species 150	Species 150	Species 89	Cluster 183		Dolichogenidea sp_36
Dolichogenidea	E93	Cluster 215	Species 137	Species 160	Species 150	Species 150	Species 89	Cluster 183		Dolichogenidea sp_36
Dolichogenidea	E620	Cluster 181	Species 142	Species 181	Species 69	Species 69	Species 40	Cluster 152		Dolichogenidea sp_37
Dolichogenidea	E165	Cluster 50	Species 159	Species 178	Species 71	Species 71	Species 41	Cluster 31		Dolichogenidea sp_38
Unknown	E675	Cluster 191	Species 176	Species 202	Species 169	Species 169	*	*		Dolichogenidea sp_39
Dolichogenidea	HYAT466-11	Cluster 232	Species 177	Species 203	Species 168	Species 168	*	*		Dolichogenidea sp_40
Dolichogenidea	HYCNE959-11	Cluster 233	Species 156	Species 176	Species 79	Species 79	*	*		Dolichogenidea sp_41
Dolichogenidea	E317	Cluster 127	Species 144	Species 179	Species 72	Species 72	Species 12	Cluster 94		Dolichogenidea sp_42
	78	42	45	45	47	47	19	34		
Iconella	E598	Cluster 171	Species 175	Species 201	Species 52	Species 52	Species 10	Cluster 141		Iconella sp_1
Iconella	E592	Cluster 154	Species 46	Species 63	Species 53	Species 53	Species 9	Cluster 126		Iconella sp_2
Iconella	E7	Cluster 154	Species 46	Species 63	Species 53	Species 53	Species 9	Cluster 126		Iconella sp_2
Iconella	E80	Cluster 154	Species 46	Species 63	Species 53	Species 53	Species 9	Cluster 126		Iconella sp_2
Iconella	E505	Cluster 154	Species 46	Species 63	Species 53	Species 53	*	*		Iconella sp_2
Iconella	E504	Cluster 154	Species 46	Species 63	Species 53	Species 53	*	*		Iconella sp_2
Cotesia	E740	Cluster 204	Species 120	Species 144	Species 187	Species 187	Species 47	Cluster 172		Cotesia sp_1

Cotesia	E265	Cluster 101	Species 119	Species 143	Species 186	Species 186	Species 47	Cluster 74	4 bp difference with E740	Cotesia sp_2
Cotesia	E207	Cluster 74	Species 117	Species 141	Species 167	Species 167	Species 47	Cluster 49	2 bp difference with E740	Cotesia sp_3
Cotesia	E751	Cluster 210	Species 116	Species 140	Species 160	Species 160	Species 47	Cluster 177	4 bp difference with E740, 2 bp difference with E207	Cotesia sp_4
Cotesia	E216	Cluster 82	Species 115	Species 139	Species 159	Species 159	Species 47	Cluster 55	4 bp difference with E740, 4 bp difference with E751	Cotesia sp_5
Cotesia	E261	Cluster 100	Species 19	Species 34	Species 172	Species 172	Species 47	Cluster 73	3 bp difference with E740	Cotesia sp_6
Cotesia	E524	Cluster 100	Species 19	Species 34	Species 172	Species 172	Species 47	Cluster 73		Cotesia sp_6
Cotesia	E481	Cluster 100	Species 19	Species 34	Species 172	Species 172	*	*		Cotesia sp_6
Cotesia	E177	Cluster 55	Species 18	Species 33	Species 251	Species 237	Species 48	Cluster 34		Cotesia sp_7
Cotesia	HYAS621-11	Cluster 55	Species 18	Species 33	Species 250	Species 236	*	*		Cotesia sp_7
Cotesia	E702	Cluster 196	Species 118	Species 145	Species 161	Species 161	*	*		Cotesia sp_8
Cotesia	E13	Cluster 32	Species 112	Species 137	Species 193	Species 193	Species 45	Cluster 21		Cotesia sp_9
Cotesia	E14	Cluster 32	Species 112	Species 137	Species 193	Species 193	Species 45	Cluster 21		Cotesia sp_9
Cotesia	GE2	Cluster 32	Species 112	Species 137	Species 193	Species 193	Species 45	Cluster 21		Cotesia sp_9
Cotesia	GE4	Cluster 32	Species 112	Species 137	Species 193	Species 193	Species 45	Cluster 21		Cotesia sp_9
Cotesia	GE5	Cluster 32	Species 112	Species 137	Species 193	Species 193	Species 45	Cluster 21		Cotesia sp_9
Cotesia	E737	Cluster 32	Species 112	Species 137	Species 193	Species 193	Species 45	Cluster 21		Cotesia sp_9
Cotesia	E736	Cluster 32	Species 112	Species 137	Species 193	Species 193	Species 45	Cluster 21		Cotesia sp_9
Cotesia	E617	Cluster 179	Species 114	Species 138	Species 194	Species 194	*	*		Cotesia sp_10
Cotesia	E287	Cluster 43	Species 113	Species 31	Species 232	Species 230	Species 49	Cluster 83		Cotesia sp_11
Cotesia	E338	Cluster 43	Species 113	Species 31	Species 232	Species 230	Species 49	Cluster 83		Cotesia sp_11
Cotesia	E550	Cluster 43	Species 16	Species 31	Species 231	Species 229	Species 49	Cluster 133	3 bp difference with E338	Cotesia sp_11
Cotesia	E644	Cluster 43	Species 16	Species 31	Species 231	Species 229	*	*		Cotesia sp_11
Cotesia	E156	Cluster 43	Species 15	Species 30	Species 228	Species 228	*	*		Cotesia sp_11
Cotesia	HYQTB326-12	Cluster 43	Species 15	Species 30	Species 228	Species 228	*	*		Cotesia sp_11
Cotesia	E11	Cluster 18	Species 110	Species 135	Species 156	Species 156	Species 46	Cluster 11		Cotesia sp_12
Cotesia	E12	Cluster 18	Species 110	Species 135	Species 156	Species 156	Species 46	Cluster 11		Cotesia sp_12
Cotesia	E482	Cluster 18	Species 110	Species 135	Species 156	Species 156	Species 46	Cluster 11		Cotesia sp_12
Cotesia	E21	Cluster 77	Species 20	Species 35	Species 151	Species 151	Species 78	Cluster 56		Cotesia sp_13
Cotesia	E264	Cluster 77	Species 20	Species 35	Species 151	Species 151	Species 78	Cluster 56		Cotesia sp_13
Cotesia	E258	Cluster 77	Species 20	Species 35	Species 151	Species 151	*	*		Cotesia sp_13
Cotesia	E529	Cluster 77	Species 20	Species 35	Species 151	Species 151	*	*		Cotesia sp_13
Cotesia	E34	Cluster 77	Species 20	Species 35	Species 151	Species 151	Species 78	Cluster 56		Cotesia sp_13
Cotesia	E6	Cluster 77	Species 20	Species 35	Species 151	Species 151	Species 78	Cluster 56		Cotesia sp_13
Cotesia	E5	Cluster 77	Species 20	Species 35	Species 151	Species 151	Species 78	Cluster 56		Cotesia sp_13
Cotesia	E85	Cluster 77	Species 20	Species 35	Species 151	Species 151	Species 78	Cluster 56		Cotesia sp_13
Cotesia	E619	Cluster 77	Species 20	Species 35	Species 151	Species 151	*	*		Cotesia sp_13
Cotesia	E681	Cluster 77	Species 20	Species 35	Species 151	Species 151	*	*		Cotesia sp_13
Cotesia	E268	Cluster 77	Species 20	Species 35	Species 151	Species 151	Species 78	Cluster 56		Cotesia sp_13
Cotesia	E683	Cluster 77	Species 20	Species 35	Species 151	Species 151	Species 78	Cluster 56		Cotesia sp_13
Cotesia	E569	Cluster 77	Species 20	Species 35	Species 151	Species 151	Species 78	Cluster 56		Cotesia sp_13
Cotesia	HYAT275-11	Cluster 77	Species 20	Species 35	Species 151	Species 151	*	*		Cotesia sp_13
Cotesia	E651	Cluster 186	Species 21	Species 36	Species 238	Species 244	*	*		Cotesia sp_14
Cotesia	HYAS454-11	Cluster 186	Species 21	Species 36	Species 238	Species 244	*	*		Cotesia sp_14
Cotesia	HYAT095-11	Cluster 186	Species 122	Species 36	Species 239	Species 245	*	*		Cotesia sp_14
Cotesia	E422	Cluster 143	Species 23	Species 37	Species 152	Species 152	Species 77	Cluster 110		Cotesia sp_15
Cotesia	E76	Cluster 143	Species 23	Species 37	Species 152	Species 152	Species 77	Cluster 110		Cotesia sp_15
Cotesia	E427	Cluster 143	Species 23	Species 37	Species 152	Species 152	Species 77	Cluster 110		Cotesia sp_15
Cotesia	E474	Cluster 143	Species 23	Species 37	Species 152	Species 152	*	*		Cotesia sp_15
Cotesia	E467	Cluster 198	Species 123	Species 146	Species 185	Species 185	Species 91	Cluster 121		Cotesia sp_16
Cotesia	E712	Cluster 198	Species 123	Species 146	Species 185	Species 185	*	*		Cotesia sp_16
Cotesia	E299	Cluster 123	Species 24	Species 39	Species 154	Species 154	Species 90	Cluster 91		Cotesia sp_17
Cotesia	E590	Cluster 123	Species 24	Species 39	Species 154	Species 154	Species 90	Cluster 91		Cotesia sp_17
Cotesia	GBAH3018-07	Cluster 123	Species 24	Species 39	Species 154	Species 154	*	*		Cotesia sp_17
Cotesia	GBAH3019-07	Cluster 123	Species 24	Species 39	Species 154	Species 154	*	*		Cotesia sp_17
Cotesia	GBAH3009-07	Cluster 123	Species 24	Species 39	Species 154	Species 154	*	*		Cotesia sp_17
Cotesia	HYQTB107-11	Cluster 238	Species 124	Species 147	Species 184	Species 184	*	*		Cotesia sp_18
Cotesia	HYAS623-11	Cluster 225	Species 22	Species 38	Species 153	Species 153	*	*		Cotesia sp_19
Cotesia	HYAS645-11	Cluster 225	Species 22	Species 38	Species 153	Species 153	*	*		Cotesia sp_19
Cotesia	HYAS700-11	Cluster 225	Species 22	Species 38	Species 153	Species 153	*	*		Cotesia sp_19
Cotesia	GBAH1626-06	Cluster 218	Species 17	Species 32	Species 195	Species 195	*	*		Cotesia sp_20
Cotesia	HYCNE493-11	Cluster 218	Species 17	Species 32	Species 195	Species 195	*	*		Cotesia sp_20
Cotesia	MCCAA222-12	Cluster 2	Species 111	Species 136	Species 157	Species 157	*	*		Cotesia sp_21
Cotesia	ASQAS181-11	Cluster 2	Species 111	Species 136	Species 157	Species 157	*	*		Cotesia sp_21
Cotesia	GMATB979-15	Cluster 219	Species 121	Species 142	Species 158	Species 158	*	*		Cotesia sp_22
	65	22	25	23	26	26	9	15		
Glyptapanteles	ASQAS186-11	Cluster 3	Species 107	Species 132	Species 100	Species 100	*	*		Glyptapanteles sp_1
Glyptapanteles	ASQAS187-11	Cluster 4	Species 108	Species 133	Species 124	Species 124	*	*		Glyptapanteles sp_2
Glyptapanteles	E117	Cluster 22	Species 14	Species 40	Species 101	Species 101	Species 31	Cluster 9		Glyptapanteles sp_3
Glyptapanteles	E79	Cluster 22	Species 14	Species 40	Species 101	Species 101	Species 31	Cluster 9		Glyptapanteles sp_3
Glyptapanteles	E731	Cluster 202	Species 219	Species 240	Species 179	Species 179	Species 96	Cluster 171		Glyptapanteles sp_4
Glyptapanteles	E641	Cluster 184	Species 218	Species 239	Species 178	Species 178	Species 96	Cluster 155	1 bp difference with E731	Glyptapanteles sp_5
Glyptapanteles	E630	Cluster 182	Species 217	Species 238	Species 130	Species 130	Species 96	Cluster 153	4 bp difference with E731	Glyptapanteles sp_6
Glyptapanteles	E193	Cluster 68	Species 63	Species 80	Species 229	Species 231	*	*		Glyptapanteles sp_7
Glyptapanteles	E623	Cluster 68	Species 63	Species 80	Species 229	Species 231	Species 96	Cluster 145	2 bp difference with E731	Glyptapanteles sp_7
Glyptapanteles	E632	Cluster 68	Species 63	Species 80	Species 229	Species 231	Species 96	Cluster 145		Glyptapanteles sp_7
Glyptapanteles	E627	Cluster 68	Species 63	Species 80	Species 229	Species 231	Species 96	Cluster 145		Glyptapanteles sp_7
Glyptapanteles	E604	Cluster 68	Species 63	Species 80	Species 229	Species 231	Species 96	Cluster 145		Glyptapanteles sp_7
Glyptapanteles	E605	Cluster 68	Species 63	Species 80	Species 229	Species 231	Species 96	Cluster 145		Glyptapanteles sp_7
Glyptapanteles	MCCAA225-12	Cluster 68	Species 212	Species 233	Species 230	Species 232	*	*		Glyptapanteles sp_7
Glyptapanteles	E647	Cluster 185	Species 213	Species 234	Species 192	Species 192	*	*		Glyptapanteles sp_8
Glyptapanteles	E198	Cluster 71	Species 214	Species 235	Species 131	Species 131	Species 96	Cluster 45	3 bp difference with E731	Glyptapanteles sp_9
Glyptapanteles	E160	Cluster 46	Species 209	Species 230	Species 121	Species 121	Species 83	Cluster 29		Glyptapanteles sp_10
Glyptapanteles	HYQT050-08	Cluster 46	Species 209	Species 230	Species 121	Species 121	*	*		Glyptapanteles sp_10
Glyptapanteles	E599	Cluster 172	Species 210	Species 231	Species 122	Species 122	Species 83	Cluster 142	2 bp difference with E160	Glyptapanteles sp_11
Glyptapanteles	E601	Cluster 172	Species 210	Species 231	Species 122	Species 122	Species 83	Cluster 142		Glyptapanteles sp_11
Glyptapanteles	E600	Cluster 174	Species 215	Species 236	Species 85	Species 85	Species 84	Cluster 144		Glyptapanteles sp_12
Glyptapanteles	E602	Cluster 174	Species 215	Species 236	Species 85	Species 85	Species 84	Cluster 144		Glyptapanteles sp_12
Glyptapanteles	E282	Cluster 112	Species 216	Species 237	Species 86	species 86	Species 97	Cluster 81		Glyptapanteles sp_13
Glyptapanteles	E283	Cluster 112	Species 216	Species 237	Species 86	species 86	Species 97	Cluster 81		Glyptapanteles sp_13
Glyptapanteles	E735	Cluster 160	Species 64	Species 81	Species 87	Species 87	Species 85	Cluster 134		Glyptapanteles sp_14
Glyptapanteles	E552	Cluster 160	Species 64	Species 81	Species 87	Species 87	Species 85	Cluster 134		Glyptapanteles sp_14
Glyptapanteles	E716	Cluster 200	Species 220	Species 241	Species 17	Species 17	Species 50	Cluster 167		Glyptapanteles sp_15
Glyptapanteles	E296	Cluster 120	Species 221	Species 242	Species 18	Species 18	Species 5	Cluster 90		Glyptapanteles sp_16
Glyptapanteles	E551	Cluster 120	Species 221	Species 242	Species 18	Species 18	Species 5	Cluster 90		Glyptapanteles sp_16
Glyptapanteles	E500	Cluster 120	Species 221	Species 242	Species 18	Species 18	Species 5	Cluster 90		Glyptapanteles sp_16
Glyptapanteles	E119	Cluster 23	Species 41	Species 58	Species 137	Species 137	Species 108	Cluster 10		Glyptapanteles sp_17
Glyptapanteles	E413	Cluster 23	Species 41	Species 58	Species 137	Species 137	Species 108	Cluster 10		Glyptapanteles sp_17
Glyptapanteles	E144	Cluster 36	Species 168	Species 194	Species 145	Species 145	Species 109	Cluster 22		Glyptapanteles sp_18
Glyptapanteles	E557	Cluster 161	Species 170	Species 196	Species 134	Species 134	Species 109	Cluster 135	5 bp difference with E144	Glyptapanteles sp_19
Glyptapanteles	E609	Cluster 175	Species 171	Species 197	Species 135	Species 135	*	*		Glyptapanteles sp_20
Glyptapanteles	HYAT424-11	Cluster 231	Species 172	Species 198	Species 136	Species 136	*	*		Glyptapanteles sp_21

Glyptapanteles	HYAT425-11	Cluster 231	Species 172	Species 198	Species 136	Species 136	*	*		Glyptapanteles sp_21
Glyptapanteles	HYAT371-11	Cluster 228	Species 169	Species 195	Species 146	Species 146	*	*		Glyptapanteles sp_22
Glyptapanteles	HYAT396-11	Cluster 228	Species 169	Species 195	Species 146	Species 146	*	*		Glyptapanteles sp_22
Glyptapanteles	E260	Cluster 99	Species 42	Species 59	Species 141	Species 141	Species 110	Cluster 72		Glyptapanteles sp_23
Glyptapanteles	E565	Cluster 99	Species 42	Species 59	Species 141	Species 141	Species 110	Cluster 72		Glyptapanteles sp_23
Glyptapanteles	E59	Cluster 173	Species 43	Species 60	Species 140	Species 140	Species 110	Cluster 143	2 bp difference with E565	Glyptapanteles sp_24
Glyptapanteles	E684	Cluster 173	Species 43	Species 60	Species 140	Species 140	*	*		Glyptapanteles sp_24
Glyptapanteles	E73	Cluster 173	Species 43	Species 60	Species 140	Species 140	Species 110	Cluster 143		Glyptapanteles sp_24
Glyptapanteles	E210	Cluster 78	Species 44	Species 61	Species 34	Species 34	Species 36	Cluster 100		Glyptapanteles sp_25
Glyptapanteles	E469	Cluster 78	Species 44	Species 61	Species 34	Species 34	Species 36	Cluster 100		Glyptapanteles sp_25
Glyptapanteles	E340	Cluster 78	Species 44	Species 61	Species 34	Species 34	Species 36	Cluster 100		Glyptapanteles sp_25
Glyptapanteles	E343	Cluster 78	Species 44	Species 61	Species 34	Species 34	*	*		Glyptapanteles sp_25
Glyptapanteles	E355	Cluster 78	Species 44	Species 61	Species 34	Species 34	Species 36	Cluster 100		Glyptapanteles sp_25
Glyptapanteles	E367	Cluster 78	Species 44	Species 61	Species 34	Species 34	Species 36	Cluster 100		Glyptapanteles sp_25
Glyptapanteles	E97	Cluster 217	Species 173	Species 199	Species 33	Species 33	Species 38	Cluster 186		Glyptapanteles sp_26
Glyptapanteles	E22	Cluster 86	Species 45	Species 62	Species 32	Species 32	Species 37	Cluster 58		Glyptapanteles sp_27
Glyptapanteles	E508	Cluster 86	Species 45	Species 62	Species 32	Species 32	Species 37	Cluster 58		Glyptapanteles sp_27
Glyptapanteles	E636	Cluser 183	Species 109	Species 134	Species 123	Species 123	Species 24	Cluster 154		Glyptapanteles sp_28
Glyptapanteles	E639	Cluser 183	Species 109	Species 134	Species 123	Species 123	Species 24	Cluster 154		Glyptapanteles sp_28
Glyptapanteles	E182	Cluster 59	Species 165	Species 188	Species 211	Species 211	Species 98	Cluster 38		Glyptapanteles sp_29
Glyptapanteles	E439	Cluster 147	Species 166	Species 189	Species 212	Species 212	Species 99	Cluster 116		Glyptapanteles sp_30
Glyptapanteles	E548	Cluster 159	Species 206	Species 190	Species 107	Species 107	Species 71	Cluster 132		Glyptapanteles sp_31
Glyptapanteles	E43	Cluster 148	Species 207	Species 191	Species 73	Species 73	Species 70	Cluster 117		Glyptapanteles sp_32
Glyptapanteles	E290	Cluster 116	Species 62	Species 57	Species 106	Species 106	Species 72	Cluster 86		Glyptapanteles sp_33
Glyptapanteles	E292	Cluster 116	Species 62	Species 57	Species 106	Species 106	Species 72	Cluster 86		Glyptapanteles sp_33
Glyptapanteles	E633	Cluster 116	Species 62	Species 57	Species 106	Species 106	*	*		Glyptapanteles sp_33
Glyptapanteles	HYQTB084-11	Cluster 237	Species 211	Species 232	Species 84	Species 84	*	*		Glyptapanteles sp_34
	63	34	35	35	35	35	21	28		
Miropotes	E746	Cluster 206	Species 106	Species 98	Species 8	Species 8	Species 7	Cluster 173		Miropotes sp_1
Miropotes	E120	Cluster 24	Species 105	Species 97	Species 42	Species 42	Species 42	Cluster 12		Miropotes sp_2
Miropotes	E251	Cluster 94	Species 13	Species 7	Species 41	Species 41	Species 42	Cluster 66	4 bp difference with E120	Miropotes sp_3
Miropotes	E375	Cluster 94	Species 13	Species 7	Species 41	Species 41	*	*		Miropotes sp_3
Miropotes	E57	Cluster 94	Species 13	Species 7	Species 41	Species 41	Species 42	Cluster 138		Miropotes sp_3
Miropotes	E436	Cluster 94	Species 13	Species 7	Species 41	Species 41	*	*		Miropotes sp_3
Miropotes	E53	Cluster 94	Species 13	Species 7	Species 41	Species 41	Species 42	Cluster 129	Has Y - cluster 138 has C, Cluster 66 has T	Miropotes sp_3
Miropotes	E69	Cluster 94	Species 13	Species 7	Species 41	Species 41	Species 42	Cluster 138		Miropotes sp_3
Miropotes	E756	Cluster 212	Species 95	Species 94	Species 16	Species 16	Species 81	Cluster 179		Miropotes sp_4
Miropotes	E96	Cluster 216	Species 96	Species 95	Species 15	Species 15	Species 81	Cluster 185	5 bp difference with E756	Miropotes sp_5
Miropotes	E100	Cluster 11	Species 97	Species 96	Species 55	Species 55	Species 81	Cluster 1	5 bp difference to E756, 4 bp with E96	Miropotes sp_6
Miropotes	E166	Cluster 51	Species 89	Species 88	Species 59	Species 59	*	*		Miropotes sp_7
Miropotes	E286	Cluster 113	Species 8	Species 5	Species 244	Species 233	Species 80	Cluster 82		Miropotes sp_8
Miropotes	HYAS646-11	Cluster 227	Species 8	Species 5	Species 245	Species 234	*	*		Miropotes sp_9
Miropotes	E180	Cluster 57	Species 90	Species 89	Species 202	Species 202	Species 80	Cluster 36	3 bp difference with E286	Miropotes sp_10
Miropotes	E595	Cluster 170	Species 93	Species 92	Species 200	Species 200	Species 80	Cluster 36	3 bp difference with E204, 1 bp difference with 72,	Miropotes sp_11
Miropotes	E543	Cluster 158	Species 94	Species 93	Species 60	Species 60	Species 80	Cluster 36	1 bp difference with E72, 3bp with E286	Miropotes sp_12
Miropotes	E204	Cluster 73	Species 92	Species 91	Species 201	Species 201	Species 80	Cluster 48	2 bp difference with E286, 3 bp with E180	Miropotes sp_13
Miropotes	E72	Cluster 190	Species 91	Species 90	Species 116	Species 116	Species 80	Cluster 170		Miropotes sp_14
Miropotes	E67	Cluster 190	Species 91	Species 90	Species 116	Species 116	Species 80	Cluster 170		Miropotes sp_14
Miropotes	E383	Cluster 138	Species 9	Species 6	Species 54	Species 54	Species 82	Cluster 107		Miropotes sp_15
Miropotes	E410	Cluster 138	Species 9	Species 6	Species 54	Species 54	*	*		Miropotes sp_15
Miropotes	AUSBC910-12	Cluster 5	Species 7	Species 4	Species 51	Species 51	*	*		Miropotes sp_16
Miropotes	AUSBC1041-12	Cluster 5	Species 7	Species 4	Species 51	Species 51	*	*		Miropotes sp_16
Miropotes	AUSBC1048-12	Cluster 5	Species 7	Species 4	Species 51	Species 51	*	*		Miropotes sp_16
Miropotes	AUSBC1173-12	Cluster 5	Species 7	Species 4	Species 51	Species 51	*	*		Miropotes sp_16
Miropotes	AUSBC1273-12	Cluster 5	Species 7	Species 4	Species 51	Species 51	*	*		Miropotes sp_16
Miropotes	AUSBC1467-12	Cluster 5	Species 7	Species 4	Species 51	Species 51	*	*		Miropotes sp_16
Miropotes	AUSBC1500-12	Cluster 5	Species 7	Species 4	Species 51	Species 51	*	*		Miropotes sp_16
Miropotes	AUSBC1635-12	Cluster 5	Species 7	Species 4	Species 51	Species 51	*	*		Miropotes sp_16
Miropotes	AUSBC1677-12	Cluster 5	Species 7	Species 4	Species 51	Species 51	*	*		Miropotes sp_16
Miropotes	AUSBC1686-12	Cluster 5	Species 7	Species 4	Species 51	Species 51	*	*		Miropotes sp_16
Miropotes	AUSBC1690-12	Cluster 5	Species 7	Species 4	Species 51	Species 51	*	*		Miropotes sp_16
Miropotes	AUSBC1692-12	Cluster 5	Species 7	Species 4	Species 51	Species 51	*	*		Miropotes sp_16
Miropotes	AUSBC2061-12	Cluster 5	Species 7	Species 4	Species 51	Species 51	*	*		Miropotes sp_16
Miropotes	AUSBC2068-12	Cluster 5	Species 7	Species 4	Species 51	Species 51	*	*		Miropotes sp_16
Miropotes	AUSBC2074-12	Cluster 5	Species 7	Species 4	Species 51	Species 51	*	*		Miropotes sp_16
Miropotes	AUSBC925-12	Cluster 5	Species 7	Species 4	Species 51	Species 51	*	*		Miropotes sp_16
Miropotes	AUSBC290-12	Cluster 5	Species 7	Species 4	Species 51	Species 51	*	*		Miropotes sp_16
	39	16	15	15	16	16	5	13		
	E709	Cluster 197	Species 85	Species 87	Species 49	Species 49	*	*		unknown sp_1
	E586	Cluster 168	Species 84	Species 84	Species 47	Species 47	*	*		unknown sp_2
	E704	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	E104	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	E105	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	E471	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	E337	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	E423	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	E247	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	E249	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	E425	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	E706	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	E585	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	E594	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	E335	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	E424	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	E707	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	E584	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	ASQAS157-11	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	MCCAA2641-12	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	HYAT465-11	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	MCCAA1444-12	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	ASQAS156-11	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	CNBAN190-13	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	MCCAA1052-12	Cluster 1	Species 1	Species 1	Species 46	Species 46	*	*		unknown sp_3
	E214	Cluster 80	Species 83	Species 85	Species 48	Species 48	Species 100	Cluster 53		unknown sp_4
	E693	Cluster 193	Species 86	Species 86	Species 50	Species 50	*	*		unknown sp_5
	E259	Cluster 98	Species 80	Species 28	Species 13	Species 13	Species 11	Cluster 71		unknown sp_6
	E266	Cluster 98	Species 80	Species 28	Species 13	Species 13	Species 11	Cluster 71		unknown sp_6
	E559	Cluster 98	Species 80	Species 28	Species 13	Species 13	Species 11	Cluster 71		unknown sp_6
	E566	Cluster 98	Species 80	Species 28	Species 13	Species 13	Species 11	Cluster 71		unknown sp_6
	E9	Cluster 98	Species 80	Species 28	Species 13	Species 13	Species 11	Cluster 71		unknown sp_6

	E734	Cluster 119	Species 222	Species 243	Species 61	Species 61	Species 22	Cluster 88		unknown sp_7
	E295	Cluster 119	Species 222	Species 243	Species 61	Species 61	Species 22	Cluster 88		unknown sp_7
	E46	Cluster 152	Species 223	Species 244	Species 62	Species 62	Species 23	Cluster 122		unknown sp_8
	E121	Cluster 25	Species 174	Species 200	Species 35	Species 35	Species 3	Cluster 13		unknown sp_9
	E47	Cluster 153	Species 167	Species 193	Species 14	Species 14	Species 4	Cluster 124		unknown sp_10
	E157	Cluster 44	Species 203	Species 227	Species 28	Species 29	Species 18	Cluster 26		unknown sp_11
	E719	Cluster 44	Species 203	Species 227	Species 28	Species 29	Species 18	Cluster 26		unknown sp_11
	E724	Cluster 201	Species 204	Species 228	Species 27	Species 27	Species 19	Cluster 169		unknown sp_12
	40	12	12	12	12	12	9	9		
Sathon	E307	Cluster 96	Species 3	Species 3	Species 177	Species 177	*	*		Sathon sp_1
Sathon	E254	Cluster 96	Species 3	Species 3	Species 177	Species 177	Species 51	Cluster 69		Sathon sp_1
Sathon	E591	Cluster 96	Species 3	Species 3	Species 177	Species 177	Species 51	Cluster 69		Sathon sp_1
Sathon	E334	Cluster 96	Species 3	Species 3	Species 177	Species 177	*	*		Sathon sp_1
Sathon	E78	Cluster 96	Species 3	Species 3	Species 177	Species 177	Species 51	Cluster 69		Sathon sp_1
Sathon	E255	Cluster 96	Species 3	Species 3	Species 177	Species 177	Species 51	Cluster 69		Sathon sp_1
Sathon	E309	Cluster 96	Species 3	Species 3	Species 177	Species 177	Species 51	Cluster 69		Sathon sp_1
Sathon	E250	Cluster 93	Species 2	Species 2	Species 176	Species 176	Species 51	Cluster 65	2 bp differences with E309	Sathon sp_2
Sathon	E376	Cluster 93	Species 2	Species 2	Species 176	Species 176	Species 51	Cluster 65		Sathon sp_2
Sathon	E58	Cluster 93	Species 2	Species 2	Species 176	Species 176	Species 51	Cluster 65		Sathon sp_2
	HYAS1268-12	Cluster 93	Species 2	Species 2	Species 176	Species 176	*	*		Sathon sp_2
	MCCAA1058-12	Cluster 93	Species 2	Species 2	Species 176	Species 176	*	*		Sathon sp_2
	HYAS1265-12	Cluster 93	Species 2	Species 2	Species 176	Species 176	*	*		Sathon sp_2
	HYAS1270-12	Cluster 93	Species 2	Species 2	Species 176	Species 176	*	*		Sathon sp_2
Sathon	E44	Cluster 108	Species 65	Species 29	Species 7	Species 7	Species 59	Cluster 78		Sathon sp_3
Sathon	E277	Cluster 108	Species 65	Species 29	Species 7	Species 7	Species 59	Cluster 78		Sathon sp_3
	GMATV2226-16	Cluster 108	Species 65	Species 29	Species 7	Species 7	*	*		Sathon sp_3
Sathon	E140	Cluster 140	Species 102	Species 100	Species 182	Species 182	*	*		Sathon sp_4
Sathon	E372	Cluster135	Species 103	Species 101	Species 183	Species 183	Species 44	Cluster 104		Sathon sp_5
Sathon	E533	Cluster 155	Species 104	Species 102	Species 108	Species 108	Species 44	Cluster 127	2 differences between 533 and 372	Sathon sp_6
Sathon	E211	Cluster 79	Species 12	Species 8	Species 5	Species 5	Species 44	Cluster 52	3 differences with 533 and 273	Sathon sp_7
Sathon	E371	Cluster 79	Species 12	Species 8	Species 5	Species 5	Species 44	Cluster 52		Sathon sp_7
Sathon	E61	Cluster 79	Species 12	Species 8	Species 5	Species 5	Species 44	Cluster 52		Sathon sp_7
Sathon	E71	Cluster 79	Species 12	Species 8	Species 5	Species 5	Species 44	Cluster 52		Sathon sp_7
Sathon	E577	Cluster 164	Species 101	Species 105	Species 120	Species 120	*	*		Sathon sp_8
Sathon	E579	Cluster 166	Species 100	Species 104	Species 224	Species 220	*	*		Sathon sp_9
Sathon	E578	Cluster 165	Species 99	Secies 103	Species 225	Species 221	*	*		Sathon sp_10
Sathon	E271	Cluster 105	Species 11	Species 9	Species 119	Species 119	Species 76	Cluster 76		Sathon sp_11
	GMATU192-16	Cluster 105	Species 11	Species 9	Species 119	Species 119	*	*		Sathon sp_11
	GMATU176-16	Cluster 105	Species 11	Species 9	Species 119	Species 119	*	*		Sathon sp_11
	GMATU3355-16	Cluster 105	Species 11	Species 9	Species 119	Species 119	*	*		Sathon sp_11
	GMATU161-16	Cluster 105	Species 11	Species 9	Species 119	Species 119	*	*		Sathon sp_11
	GMATV2265-16	Cluster 105	Species 11	Species 9	Species 119	Species 119	*	*		Sathon sp_11
	GMATU2939-16	Cluster 105	Species 11	Species 9	Species 119	Species 119	*	*		Sathon sp_11
	GMATX2213-16	Cluster 105	Species 11	Species 9	Species 119	Species 119	*	*		Sathon sp_11
	GMATX2218-16	Cluster 105	Species 11	Species 9	Species 119	Species 119	*	*		Sathon sp_11
	GMATU3019-16	Cluster 105	Species 11	Species 9	Species 119	Species 119	*	*		Sathon sp_11
	GMATU198-16	Cluster 105	Species 11	Species 9	Species 119	Species 119	*	*		Sathon sp_11
	GMATU165-16	Cluster 105	Species 11	Species 9	Species 119	Species 119	*	*		Sathon sp_11
	GMATU202-16	Cluster 105	Species 11	Species 9	Species 119	Species 119	*	*		Sathon sp_11
	GMATU2743-16	Cluster 105	Species 11	Species 9	Species 119	Species 119	*	*		Sathon sp_11
	GMATU158-16	Cluster 105	Species 11	Species 9	Species 119	Species 119	*	*		Sathon sp_11
	GMATW1405-16	Cluster 105	Species 11	Species 9	Species 119	Species 119	*	*		Sathon sp_11
	GMATU246-16	Cluster 105	Species 11	Species 9	Species 119	Species 119	*	*		Sathon sp_11
	GMATU2750-16	Cluster 105	Species 11	Species 9	Species 119	Species 119	*	*		Sathon sp_11
	GMATV2228-16	Cluster 105	Species 11	Species 9	Species 119	Species 119	*	*		Sathon sp_11
Sathon?	HYCNF356-11	Cluster 235	Species 87	Species 99	Species 9	Species 9	*	*		Sathon sp_12
	47	12	12	12	12	12	5	8		
Choeras	E89	Cluster 12	Species 10	Species 10	Species 138	Species 138	Species 75	Cluster 2		Choeras morialta
Choeras	E191	Cluster 12	Species 10	Species 10	Species 138	Species 138	Species 75	Cluster 2		Choeras morialta
morialta										
Choeras	E101	Cluster 12	Species 10	Species 10	Species 138	Species 138	Species 75	Cluster 2		Choeras morialta
morialta										
Choeras	E54	Cluster 12	Species 10	Species 10	Species 138	Species 138	Species 75	Cluster 2		Choeras morialta
morialta										
Choeras	E223	Cluster 12	Species 10	Species 10	Species 138	Species 138	Species 75	Cluster 2		Choeras morialta
morialta										
Choeras	E463	Cluster 12	Species 10	Species 10	Species 138	Species 138	Species 75	Cluster 2		Choeras morialta
morialta										
Choeras	GBMIN74055-17	Cluster 12	Species 10	Species 10	Species 138	Species 138	*	*		Choeras morialta
morialta										
Choeras	E224	Cluster 85	Species 98	Species 106	Species 139	Species 139	Species 75	Cluster 2	no difference between E224 and E463	Choeras morialta
morialta										
Choeras	E437	Cluster 146	Species 205	Species 229	Species 64	Species 64	Species 73	Cluster 114		Choeras sp_2
Choeras	E615	Cluster 178	Species 61	Species 79	Species 63	Species 63	Species 74	Cluster 150		Choeras sp_3
Choeras	E662	Cluster 178	Species 61	Species 79	Species 63	Species 63	*	*		Choeras sp_3
Choeras	E668	Cluster 178	Species 61	Species 79	Species 63	Species 63	Species 74	Cluster 159		Choeras sp_3
Choeras	E279	Cluster 109	Species 4	Species 11	Species 252	Species 252	*	*		Choeras sp_4
Choeras	E273	Cluster 106	Species 4	Species 11	Species 253	Species 253	Species 26	Cluster 77		Choeras sp_4
Choeras	E272	Cluster 106	Species 4	Species 11	Species 253	Species 253	*	*		Choeras sp_4
Choeras	GMATS2678-16	Cluster 221	Species 88	Species 107	Species 45	Species 45	*	*		Choeras sp_5
Choeras	GMATT3210-16	Cluster 221	Species 88	Species 107	Species 45	Species 45	*	*		Choeras sp_5
Choeras	GMATT3567-16	Cluster 221	Species 88	Species 107	Species 45	Species 45	*	*		Choeras sp_5
Choeras	GMATT3602-16	Cluster 221	Species 88	Species 107	Species 45	Species 45	*	*		Choeras sp_5
Choeras	GMATT3731-16	Cluster 221	Species 88	Species 107	Species 45	Species 45	*	*		Choeras sp_5
Choeras	GMATU2690-16	Cluster 221	Species 88	Species 107	Species 45	Species 45	*	*		Choeras sp_5
Choeras	GMATU2915-16	Cluster 221	Species 88	Species 107	Species 45	Species 45	*	*		Choeras sp_5
Choeras	GMATU2957-16	Cluster 221	Species 88	Species 107	Species 45	Species 45	*	*		Choeras sp_5
Choeras	GMATU3004-16	Cluster 221	Species 88	Species 107	Species 45	Species 45	*	*		Choeras sp_5
Choeras	GMATU3020-16	Cluster 221	Species 88	Species 107	Species 45	Species 45	*	*		Choeras sp_5
Choeras	GMATU3060-16	Cluster 221	Species 88	Species 107	Species 45	Species 45	*	*		Choeras sp_5
Choeras	GMATU3069-16	Cluster 221	Species 88	Species 107	Species 45	Species 45	*	*		Choeras sp_5
Choeras	GMATU3114-16	Cluster 221	Species 88	Species 107	Species 45	Species 45	*	*		Choeras sp_5
Choeras	GMATV2279-16	Cluster 221	Species 88	Species 107	Species 45	Species 45	*	*		Choeras sp_5
Choeras	GMATV2337-16	Cluster 221	Species 88	Species 107	Species 45	Species 45	*	*		Choeras sp_5
Choeras	GMATV2403-16	Cluster 221	Species 88	Species 107	Species 45	Species 45	*	*		Choeras sp_5
Choeras	GMATV2554-16	Cluster 221	Species 88	Species 107	Species 45	Species 45	*	*		Choeras sp_5
Choeras	GMATV2570-16	Cluster 221	Species 88	Species 107	Species 45	Species 45	*	*		Choeras sp_5
Choeras	GMATW1621-16	Cluster 221	Species 88	Species 107	Species 45	Species 45	*	*		Choeras sp_5
Choeras	GMATS2567-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*		Choeras sp_6
Choeras	GMATS2618-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*		Choeras sp_6
Choeras	GMATS2668-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*		Choeras sp_6
Choeras	GMATT3267-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*		Choeras sp_6
Choeras	GMATT3570-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*		Choeras sp_6

Choeras	GMATT3691-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*	Choeras sp_6
Choeras	GMATU2659-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*	Choeras sp_6
Choeras	GMATU2674-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*	Choeras sp_6
Choeras	GMATU2760-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*	Choeras sp_6
Choeras	GMATU2947-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*	Choeras sp_6
Choeras	GMATU3112-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*	Choeras sp_6
Choeras	GMATV2193-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*	Choeras sp_6
Choeras	GMATV2215-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*	Choeras sp_6
Choeras	GMATV2379-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*	Choeras sp_6
Choeras	GMATV2402-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*	Choeras sp_6
Choeras	GMATV2434-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*	Choeras sp_6
Choeras	GMATV2435-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*	Choeras sp_6
Choeras	GMATV2465-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*	Choeras sp_6
Choeras	GMATV2489-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*	Choeras sp_6
Choeras	GMATV2560-16	Cluster 220	Species 5	Species 12	Species 132	Species 132	*	*	Choeras sp_6
Choeras	GMATV2281-16	Cluster 222	Species 6	Species 13	Species 246	Species 250	*	*	Choeras sp_7
Choeras	GMATV2317-16	Cluster 222	Species 6	Species 13	Species 246	Species 250	*	*	Choeras sp_7
Choeras	GMATU2660-16	Cluster 222	Species 6	Species 13	Species 247	Species 251	*	*	Choeras sp_7
Choeras	GMATU2768-16	Cluster 222	Species 6	Species 13	Species 247	Species 251	*	*	Choeras sp_7
Choeras	GMATU3126-16	Cluster 222	Species 6	Species 13	Species 247	Species 251	*	*	Choeras sp_7
	59	9	8	8	10	10	4	5	
outgroup	E175								
outgroup	E339								
outgroup	E55								
outgroup	E91								
outgroup	E281								

Chapter 2: Supplementary Table S4:

Blast Results

Named species			
Species	Extraction or BOLD code	Genbank code	Percent identity
Cotesia glomerata	E11	JQ240174 (Australia)	100%
Apanteles carpatus	E174	KM897027 (Canada)	99.70%
Diolcogaster perniciosus	E112	HM430950 (New Zealand)	100%
Cotesia ruficrus	E712	KY832162 (Pakistan)	100%
Apanteles ippeus	E321, E318, E25, 480, E81, E525, E538, E8, E82, E24, E476, E83, E84, E329, E20	JQ240187 (USA lab culture)	99.4-100%
Microplitis demolitor	E616	HM904940 (USA lab culture)	100%
Cotesia rubecula	HYCNE493-11	DQ411830 (Australia)	100%
Choeras morialta	E89, E191, E101, E54, E223, E463, E224	KY359139 (Australia)	99.8-100%

Unidentified matches					
Genbank code	Extraction/BOLD codes	"Species"	Country	Percent match	Genus
HQ550329	E40	Apanteles sp_18	Costa Rica	99.8%	Apanteles
HM373820	E233, E132	Apanteles sp_32	Papua New Guinea	99.2-98.8%	Apanteles
HM374003	E330	Apanteles sp_33	Papua New Guinea	98.5%	Apanteles
HM373860	E152, E149, HYQTB094-11, HYQTB088-11	Apanteles sp_4	Papua New Guinea	99.2-99.4%	Apanteles
KX051752	E287, E338, E156, E664, E550, HYQTB326-12	Cotesia sp_11	French Polynesia	98.3-98.6%	Cotesia
JN282098	E651, HYAS454-11	Cotesia sp_14	New Zealand	98.0-98.3%	Cotesia
KX051762	HYQTB107-11	Cotesia sp_18	French Polynesia	99.8%	Cotesia
HM430530	E545	Diolcogaster sp_1	Thailand	98.0%	Diolcogaster
KY830061	E728	Diolcogaster sp_1	Pakistan	98.0%	Diolcogaster
JN659977	E289	Dolichogenidea sp_18	Thailand	98.8%	Dolichogenidea
HM420957	E597	Dolichogenidea sp_24	New Zealand	98.3%	Dolichogenidea
HM430957	HYAT274-11, HYAS353-11	Dolichogenidea sp_24	New Zealand	98.3%	Dolichogenidea
HM373817	HYCNE959-11	Dolichogenidea sp_41	Papua New Guinea	98.9%	Unidentified
HM397080	ASQAS186-11	Glyptapanteles sp_1	Sweden	99.9%	Glyptapanteles
HM373798	E602	Glyptapanteles sp_12	Papua New Guinea	98.0%	Unidentified

Chapter 2: Supporting Information S5:

Scripts for bioinformatics pipeline

```
#!/bin/bash
#
# usage: program.sh
#
# Amplicon processing pipeline
# Erinn
# June 2017

for file in *_R1.fastq.gz
do
        FILESTEM=${file%_*}
        SAMPLE=${file%%_*}

        # run all paired data through bbmap
        bbduk.sh in1=$file in2=$FILESTEM"_R2.fastq.gz"
out1=../no_adapters/$FILESTEM"_R1_clean.fq.gz"
out2=../no_adapters/$FILESTEM"_R2_clean.fq.gz"
outs=../no_adapters/$FILESTEM"_singletons.fq.gz"
literal=AGATCGGAAGAGCAC,AGATCGGAAGAGCGT ktrim=r k=15 mink=15 hdist=0 tbo qtrim=rl
trimq=20 minlength=30 usejni=t
        #collapse reads using PEAR
        pear -f ../no_adapters/$FILESTEM"_R1_clean.fq.gz" -r
../no_adapters/$FILESTEM"_R2_clean.fq.gz" -o ../no_adapters/$SAMPLE"_peared"
        #sort by primer
        bbduk.sh in=../no_adapters/$SAMPLE"_peared.assembled.fastq"
outm=../COIA/$SAMPLE"_COIA.fq" outu=../COIA/$SAMPLE"_unmatchedCOIA.fq"
restrictleft=25 k=25 hdist=0 literal=GGTCAACAAATCATAAAGATATTGG usejni=t;
        bbduk.sh in=../COIA/$SAMPLE"_unmatchedCOIA.fq"
outm=../COIB/$SAMPLE"_COIB.fq" outu=../COIB/$SAMPLE"_unmatchedCOIB.fq"
restrictleft=22 k=22 hdist=0 literal=KCWTTYCCWCGWATAAATAATA copyundefined
usejni=t;
        bbduk.sh in=../COIB/$SAMPLE"_unmatchedCOIB.fq"
outm=../WING/$SAMPLE"_WING.fq" outu=../WING/$SAMPLE"_unmatchedWING.fq"
restrictleft=26 k=26 hdist=0 literal=GARTGYAARTGYCAYGGYATGTCTGG copyundefined
usejni=t;
        bbduk.sh in=../WING/$SAMPLE"_unmatchedWING.fq"
outm=../ITS2/$SAMPLE"_ITS2.fq" outu=../ITS2/$SAMPLE"_unmatchedITS2.fq"
restrictleft=20 k=20 hdist=0 literal=TGTGAACTGCAGGACACATG usejni=t;
        #remove primers and quality trim
        bbduk.sh in=../COIA/$SAMPLE"_COIA.fq"
out=../COIA/$SAMPLE"_COIA_clean1.fq" outs=../COIA/$SAMPLE"_COIA_singletons.fq"
literal=GGTCAACAAATCATAAAGATATTGG ktrim=l k=25 hdist=0 tbo qtrim=l trimq=20
minlength=200 usejni=t;
        bbduk.sh in=../COIA/$SAMPLE"_COIA_clean1.fq"
out=../COIA/$SAMPLE"_COIA_clean2.fq" outs=../COIA/$SAMPLE"_COIA_singletons2.fq"
literal=GGNTGAACNGTNTATCCNCC ktrim=r k=20 tbo hdist=0 qtrim=r trimq=20
minlength=200 copyundefined usejni=t;
        bbduk.sh in=../COIB/$SAMPLE"_COIB.fq"
out=../COIB/$SAMPLE"_COIB_clean1.fq" outs=../COIB/$SAMPLE"_COIB_singletons.fq"
literal=KCWTTYCCWCGWATAAATAATA ktrim=l k=22 hdist=0 tbo qtrim=l trimq=20
minlength=200 copyundefined usejni=t;
        bbduk.sh in=../COIB/$SAMPLE"_COIB_clean1.fq"
out=../COIB/$SAMPLE"_COIB_clean2.fq" outs=../COIB/$SAMPLE"_COIB_singletons2.fq"
literal=TGATTTTTTGGTCACCCTGAAGTTTA ktrim=r k=26 hdist=0 tbo qtrim=r trimq=20
minlength=200 usejni=t;
        bbduk.sh in=../ITS2/$SAMPLE"_ITS2.fq"
out=../ITS2/$SAMPLE"_ITS2_clean1.fq" outs=../ITS2/$SAMPLE"_ITS2_singletons.fq"
literal=TGTGAACTGCAGGACACATG ktrim=l k=20 hdist=0 tbo qtrim=l trimq=20
minlength=200 usejni=t;
        bbduk.sh in=../ITS2/$SAMPLE"_ITS2_clean1.fq"
out=../ITS2/$SAMPLE"_ITS2_clean2.fq" outs=../ITS2/$SAMPLE"_ITS2_singletons2.fq"
literal=ACCCCCTAAATTTAAGCAT ktrim=r k=19 hdist=0 tbo qtrim=r trimq=20
minlength=200 copyundefined usejni=t;
        bbduk.sh in=../WING/$SAMPLE"_WING.fq"
out=../WING/$SAMPLE"_WING_clean1.fq" outs=../WING/$SAMPLE"_WING_singletons.fq"
```

```
literal=GARTGYAARTGYCAYGGYATGTCTGG ktrim=l k=26 hdist=0 tbo qtrim=l trimq=20
minlength=200 copyundefined usejni=t;
        bbduk.sh in=../WING/$SAMPLE"_WING_clean1.fq"
out=../WING/$SAMPLE"_WING_clean2.fq" outs=../WING/$SAMPLE"_WING_singletons2.fq"
literal=TGYACATTCCAYTGGTGYGCGHAGT ktrim=r k=25 hdist=0 tbo qtrim=r trimq=20
minlength=200 copyundefined usejni=t;
        # dereplicate using vsearch
        vsearch --derep_fulllength ../COIA/$SAMPLE"_COIA_clean2.fq" --output
../COIA/$SAMPLE"_COIA_clean2_derep.fa" --sizeout;
        vsearch --derep_fulllength ../COIB/$SAMPLE"_COIB_clean2.fq" --output
../COIB/$SAMPLE"_COIB_clean2_derep.fa" --sizeout;
        vsearch --derep_fulllength ../ITS2/$SAMPLE"_ITS2_clean2.fq" --output
../ITS2/$SAMPLE"_ITS2_clean2_derep.fa" --sizeout;
        vsearch --derep_fulllength ../WING/$SAMPLE"_WING_clean2.fq" --output
../WING/$SAMPLE"_WING_clean2_derep.fa" --sizeout;
        # remove chimeras
        vsearch --uchime_denovo ../COIA/$SAMPLE"_COIA_clean2_derep.fa" --
uchimeout ../COIA/$SAMPLE"_COIA_chimera_results" --nonchimeras
../COIA/$SAMPLE"_COIA_nonchimeras.fa";
        vsearch --uchime_denovo ../COIB/$SAMPLE"_COIB_clean2_derep.fa" --
uchimeout ../COIB/$SAMPLE"_COIB_chimera_results" --nonchimeras
../COIB/$SAMPLE"_COIB_nonchimeras.fa";
        vsearch --uchime_denovo ../ITS2/$SAMPLE"_ITS2_clean2_derep.fa" --
uchimeout ../ITS2/$SAMPLE"_ITS2_chimera_results" --nonchimeras
../ITS2/$SAMPLE"_ITS2_nonchimeras.fa";
        vsearch --uchime_denovo ../WING/$SAMPLE"_WING_clean2_derep.fa" --
uchimeout ../WING/$SAMPLE"_WING_chimera_results" --nonchimeras
../WING/$SAMPLE"_WING_nonchimeras.fa";

        # cluster
        vsearch  --cluster_size ../COIA/$SAMPLE"_COIA_nonchimeras.fa" --consout
../COIA/$SAMPLE"_COIA_cluster_consensus.fa" --sizein --sizeout --id 1;
        vsearch  --cluster_size ../COIB/$SAMPLE"_COIB_nonchimeras.fa" --consout
../COIB/$SAMPLE"_COIB_cluster_consensus.fa" --sizein --sizeout --id 1;
        vsearch  --cluster_size ../ITS2/$SAMPLE"_ITS2_nonchimeras.fa" --consout
../ITS2/$SAMPLE"_ITS2_cluster_consensus.fa" --sizein --sizeout --id 1;
        vsearch  --cluster_size ../WING/$SAMPLE"_WING_nonchimeras.fa" --consout
../WING/$SAMPLE"_WING_cluster_consensus.fa" --sizein --sizeout --id 1;

        mkdir ../COI
        mkdir ../COI/final_consensus
        mkdir ../ITS2/final_consensus
        mkdir ../WING/final_consensus

        # output biggest cluster(s) as a consensus sequence
        vsearch --sortbysize ../COIA/$SAMPLE"_COIA_cluster_consensus.fa" --
output ../COIA/$SAMPLE"_COIA_final_consensus.fa" --relabel $SAMPLE"_COIA" --
sizeout --topn 1;
        vsearch --sortbysize ../COIB/$SAMPLE"_COIB_cluster_consensus.fa" --
output ../COIB/$SAMPLE"_COIB_final_consensus.fa" --relabel $SAMPLE"_COIB" --
sizeout --topn 1;
        vsearch --sortbysize ../ITS2/$SAMPLE"_ITS2_cluster_consensus.fa" --
output ../ITS2/final_consensus/$SAMPLE"_ITS2_final_consensus.fa" --relabel
$SAMPLE"_ITS2" --sizeout --topn 3;
        vsearch --sortbysize ../WING/$SAMPLE"_WING_cluster_consensus.fa" --
output ../WING/final_consensus/$SAMPLE"_WING_final_consensus.fa" --relabel
$SAMPLE"_WING" --sizeout --topn 2;
        done
```