The evolutionary origin of parasitoid flies in the suborder Brachycera

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Abstract

Parasitoidy is a life-history strategy demonstrated by organisms that develop on or within a host organism, using the host as an essential trophic resource which is killed as a consequence of parasitoid development. Parasitoids represent over 3% of eukaryotes and have been shown to play an important role in structuring natural communities. However, we know very little about the evolutionary origins of parasitoidy including (i) how many independent shifts to parasitoidy have occurred, (ii) from what ancestral feeding habits parasitoids are most often derived and (iii) whether evolutionary pathways to parasitoidy differ between endo- and ectoparasitoid lineages. I investigated the evolutionary origin of parasitoid lineages in the suborder Brachycera (Order Diptera) using a supermatrix approach to estimate a proportionally sampled molecular phylogeny that is robust to model violations and appropriate for hypothesis testing. The resulting alignment sampled 565 taxa and 17 genetic loci using sequence data mined from the NCBI's Nucleotide database. I then used Bayesian inference to reconstruct the ancestral larval feeding habits of all major brachyceran lineages, and estimate the number of transitions to parasitoidy within the Brachycera. In total, twenty-two transitions were recovered, seventeen gains and five losses. Parasitism was found to be the most common larval feeding habit directly preceding shifts to parasitoidy. The evolutionary history of endo- and ectoparasitoids could not be reconstructed independently due to limitations on parameter estimation given the available data. The results of this thesis contribute to our overall understanding of the origin of parasitoid flies and contribute to their continued study by producing a phylogeny which is more suitable for further hypothesis testing.

Résumé

La parasitoïdie est un mode de vie de certains organismes qui se développent sur ou dans un organisme hôte, utilisant l'hôte comme ressource trophique essentielle qui est tuée en conséquence du développement du parasitoïde. Les parasitoïdes représentent plus de 3% des eucaryotes et il a été démontré qu'ils jouent un rôle important dans la structuration des communautés naturelles. Cependant, nous savons très peu de choses sur les origines évolutives de la parasitoïdie, y compris (i) combien de changements indépendants vers la parasitoïdie se sont produits, (ii) à partir de quelles habitudes alimentaires ancestrales les parasitoïdes sont le plus souvent dérivés et (iii) si les voies évolutives vers la parasitoïdie diffèrent entre endo - et les lignées ectoparasitoïdes. J'ai étudié l'origine évolutive des lignées de parasitoïdes dans le sous-ordre des Brachycères (ordre des diptères) en utilisant une approche de supermatrice pour estimer une phylogénie moléculaire échantillonnée proportionnellement qui est robuste aux violations du modéle et appropriée pour les tests d'hypothèses. L'alignement résultant a échantillonné 565 taxons et 17 locus génétiques à l'aide de données de séquence extraites de la base de données Nucleotide du NCBI. J'ai ensuite utilisé l'inférence bayésienne pour reconstruire les habitudes alimentaires ancestrales des larves de toutes les principales lignées de brachycères et estimer le nombre de transitions vers l'ecto- et l'endoparasitoïde au sein des Brachycères. Au total, vingt-deux transitions ont été récupérées, dix-sept gains et cinq pertes. Le parasitisme s'est avéré être l'habitude alimentaire larvaire la plus courante précédant directement le passage à la parasitoïdie. L'histoire évolutive des parasitoïdes n'a pas pu être reconstruite indépendamment en raison des limites de l'estimation des paramètres compte tenu des données disponibles. Les résultats de cette thèse contribuent à notre compréhension globale de l'origine des mouches

parasitoïdes et contribuent à leur étude continue en produisant une phylogénie qui est plus appropriée pour d'autres tests d'hypothèses.

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Thesis Format

This thesis is prepared in monograph format. All tables are presented at the end of the chapter subsection in which they are first mentioned, apart from appendices which are presented as supplementary material after the *Literature Cited*. Due to their size, all figures are placed at the end of the text, after the *Literature Cited* and before the appendices.

Contribution of Authors

Linley Sherin collected the data, performed all data analysis, and wrote this thesis. Christopher Buddle contributed scientific mentorship and guidance during planning and writing phases. Jessica Gillung contributed significantly to the concept and design of this project and provided critical suggestions throughout the data collection and data analysis phases. Christopher and Jessica both provided constructive comments on multiple drafts of this thesis. Morgan Jackson provided mentorship on many aspects of the project, most notably during phylogeny estimation and interpretation.

1. Introduction

1.1 Thesis rationale

A parasitoid is any organism that develops on or within a host organism, using the host as an essential trophic resource that is killed as a consequence of parasitoid development (Eggleton & Gaston, 1990). Parasitoids can be categorized into ectoparasitoids, which develop on the external surface of their hosts, and endoparasitoids, which develop within the body cavity of their host (Feener & Brown, 1997). The parasitoid life-history strategy (parasitoidy) is observed in more than 3% of eukaryote species across multiple phyla (Eggleton & Belshaw, 1992; Mora *et al.*, 2011). However, few studies have investigated patterns of parasitoid evolution beyond strict systematic treatments. Those that have center overwhelmingly on the parasitoid wasps (order Hymenoptera; e.g. Murray *et al.*, 2013; Sharanowski *et al.*, 2021; Tschopp *et al.*, 2013), and to a lesser extent other individual parasitoid lineages (e.g., Stireman III, 2005; Winkler *et al.*, 2015; Yeates and Greathead, 1997). By focussing on specific parasitoid lineages, these studies provide insights on the evolution of various parasitoid traits, including host breadth, time of attack, and ancestral host shifts. However, they are limited in their ability to draw conclusions about the origin of parasitoidy and consequently, many fundamental questions regarding the repeated evolutionary origins of parasitoidy remain outstanding (Feener & Brown, 1997). For instance, there is currently no accurate estimate of the number of independent shifts to parasitoidy across the tree of life, and we do not know from what ancestral feeding habits parasitoid most parasitoid lineages are derived, though this is thought to inform the host use and physiology of extant species (Eggleton & Belshaw, 1993; Eggleton & Gaston, 1990). In addition, many previous studies have not differentiated between endo- and ectoparasitoid lineages despite key differences in their biology. By broadening the scope of our research efforts to investigate the evolution of

multiple diverse parasitoid lineages, we can begin to address these knowledge gaps concerning the evolutionary origin of parasitoidy.

True flies (order Diptera) have been proposed as an alternative model for quantitative studies of parasitoid evolution due to the repeated convergent evolution of parasitoidy within the group, which has been conservatively estimated at 21 independent shifts (Eggleton & Belshaw, 1992; Feener & Brown, 1997). As nearly all parasitoid flies reside in the suborder Brachycera (Godfray, 1994; Wiegmann *et al.*, 2011), I propose this clade as an appropriate model for the testing of evolutionary hypotheses regarding parasitoid evolution. A limitation on the use of Brachycera as an evolutionary model is the lack of a well-supported phylogenetic framework to act as a foundation for the reconstruction of ancestral character states (Pagel *et al.*, 2004). Thus, the estimation of a new phylogeny of the Brachycera which addresses previous limitations is an essential precursor to confronting unresolved questions about the origin of parasitoidy within the group.

1.2 Research objectives

My thesis expands our knowledge of the evolutionary origins of parasitoidy by addressing the following three research questions, using the suborder Brachycera as a model study system:

1) How many independent shifts to parasitoidy have occurred within Brachycera?
2) From what ancestral larval feeding habit are parasitoid lineages most often derived?
3) Do evolutionary pathways to parasitoidy differ between endoparasitoid and ectoparasitoid lineages?

To address these questions, I estimated a phylogeny of the Brachycera with higher taxonomic coverage than previous phylogenetic estimates. I accomplished this by mining published DNA sequence data from multiple studies on a large scale and combining them into a single concatenated dataset (supermatrix) using a largely reproducible *R*-based workflow. Brachycera were sampled proportionally with the goal of including 0.5% of described diversity for each family within the suborder. This included the targeted sampling of parasitoid lineages to ensure that the dataset was suitable for testing the proposed hypotheses. Sequence data was harvested only for loci deemed informative in previous phylogenetic studies of dipteran evolution, including a mix of nuclear, mitochondrial, and ribosomal genes. Using the newly estimated phylogeny, I reconstructed the larval feeding habit of all ancestral nodes using Bayesian inference to evaluate the previously stated hypotheses, thus contributing to our growing knowledge of parasitoid evolution. The estimation of this phylogeny has the additional benefit of providing a foundation for the further study of parasitoid flies in the suborder Brachycera, as well as the study of parasitoids more broadly.

2. Literature review

2.1 Why parasitoids?

A parasitoid is any species that develops on or within a single host organism, using the host as a primary trophic resource that is killed due to parasitoid development. Previous research on parasitoidy has focused largely on the ecology and physiology of parasitoid insects (Feener & Brown, 1997; Godfray, 2016). These studies highlight the role that parasitoids occupy in structuring natural communities through indirect interactions (Godfray, 1994; Hassell, 2000; Morris, Lewis & Godfray, 2004; Settle & Wilson, 1990), as well as their applied use as biocontrol agents of crop and forestry pests (DeBach & Rosen, 1991; Godfray, 2016; Jervis, 2005; Pijnakker *et al.*, 2020; Pimentel *et al.*, 1997). Despite considerable scientific interest in parasitoids, many parasitoid taxa remain undescribed or biologically unknown, and parasitoids are often neglected by conservation efforts despite exhibiting many traits of extinction-prone groups (Hochberg, 2000; Shaw & Hochberg, 2001). To increase our knowledge of parasitoids, the continued study of all aspects of parasitoid biology and diversity has been highly recommended (Lasalle and Gauld 1991).

2.2 Defining parasitoidy

Previous estimates suggest that parasitoids represent ~3% of all eukaryote species. This value was calculated following Eggleton and Belshaw (1992), who state that parasitoids represent 10% of all insects, and Mora *et al.*, (2011), who estimate that insects represent nearly 30% of all eukaryotes. However, higher estimates of these values have been proposed. For instance, Godfray (1994) suggests that the proportion of parasitoids within Insecta could be as high as 20-25%, thus shifting the percentage of parasitoids within eukaryotes to above 7%.

LaSalle and Gould (1991) suggest that parasitoid wasps alone could represent 20% of all insects when accounting for undescribed species. Most recently, Sharanowski *et al*. (2021) state that parasitoid wasps alone represent 3% of all life. Thus, it appears that the proportion of parasitoids continues to grow with their continued study. However, despite discrepancies between these values, even the largest of these estimates can be considered highly conservative as they all ignore non-insect parasitoids, which are often excluded from classification as parasitoids despite meeting the requirements under a functional definition.

A functional definition of parasitoidy states that a parasitoid is any organism which develops on or within a single host organism, using the host as an essential trophic resource which is killed, either directly or indirectly, due to parasitoid development (following Eggleton & Gaston, 1990). Optionally, this definition can be further expanded to add that parasitoids all possess a free-living reproductive stage that occupies a niche that is different from their developmental stage (following Yeates & Greathead, 1997). Using the functional definition, nematodes and fungi can be classified as parasitoid taxa. This challenges alternative definitions which define parasitoidy as taxonomically constrained to insects (reviewed in Eggleton & Gaston, 1990). In fact, some definitions further limit parasitoidy to only insects which target arthropod hosts (Gauld & Bolton, 1988), having largely been informed by the biology of parasitoid wasps (order Hymenoptera; Eggleton & Belshaw, 1993). By adhering to a functional definition of parasitoidy, we ensure that parasitoidy is comparable with other life-history strategies such as phytophagy, predation and parasitism, which are defined functionally. Under the functional definition, it becomes clear that parasitoids represent a much higher proportion of eukaryote life than calculated under a taxonomically constrained definition as above. An actual estimate of this value is difficult to ascertain due to the lack of research on fungi and nematodes

within a parasitoid framework. However, there is no doubt that parasitoids represent a significant proportion of Earth's biodiversity. Thus, the study of lineages beyond parasitoid wasps can challenge traditional perspectives on parasitoid biology and provide a more holistic view of parasitoid evolutionary and ecological patterns.

2.3 Brachycera as a model

Parasitoid wasps are the most frequently studied parasitoid group primarily because they are highly species-rich, representing approximately 78% of all parasitoid insects (Eggleton & Belshaw, 1992). However, they have been criticized as an evolutionary model due to several features of the group (Eggleton & Belshaw, 1992; Feener & Brown, 1997). Namely, they represent a single evolutionary lineage and thus do not exhibit the convergence required to test certain hypotheses about repeated patterns of parasitoid evolution. Furthermore, parasitoid wasps display several unique physiological and genetic characteristics (ex. haplodiploidy) which are not generalizable to other parasitoid groups. Feener and Brown (1997) suggest true flies (order Diptera) as an alternative evolutionary model for parasitoid studies as parasitoid flies are also highly species-rich, representing 20% of parasitoid insects, and exhibit repeated convergence on parasitoidy across the order. Eggleton and Belshaw (1992) estimate that the number of transitions to parasitoidy within flies is at least 21 based on comparison at the family level. However, this is a highly conservative estimate, and they suggest the number could be as high as 100 when accounting for shifts within families. Parasitoid flies are also an ideal model for evolutionary investigations due to the extreme ecological diversity demonstrated throughout the order, including high diversity in feeding habits (Feener & Brown, 1997; Marshall, 2012). However, a limitation of the order Diptera is the large number of species that are essentially

biologically unknown, as these species cannot contribute life-history data to studies of trait evolution. Certain groups are disproportionately impacted by this issue due to a dearth of scientific experts and a large number of cryptic species (Borkent *et al.*, 2018; Savage *et al.*, 2019). In Diptera, both major suborders exhibit this limitation, but the paraphyletic Nematocera is more dramatically affected due to the small size and cryptic nature of many nematoceran flies which remain poorly known at the species level (Marshall, 2012). Furthermore, the majority of parasitoid flies reside in suborder Brachycera, a lineage comprising approximately 66% of total dipteran diversity and over 99% of known parasitoid flies (Eggleton & Belshaw, 1992; Godfray, 1994; Kirk-Spriggs & Sinclair, 2017; Pape *et al.*, 2011). Thus, by focussing on the suborder Brachycera as a parasitoid model rather than all flies, we can limit missing data and noise and achieve proper conditions for hypothesis testing. Another limitation of Brachycera as an evolutionary model is the lack of a well-supported and proportionately sampled molecular phylogeny, which is required to meet the model assumptions of phylogenetic comparative methods like ancestral character state reconstruction (Pagel *et al.*, 2004; Young & Gillung, 2020). Consequently, the estimation of a robustly sampled phylogeny of the Brachycera is a necessary first step towards addressing outstanding questions concerning parasitoid evolution.

2.4 A phylogeny of Brachycera

The monophyly of the Brachycera, which are also termed ‘short-horned flies’ due to their reduced antennal flagellomeres, has been confirmed in multiple molecular and morphological investigations of the Diptera (Lambkin *et al.*, 2013; Wiegmann *et al.* 2003, 2011; Yeates & Wiegmann, 1999). The infraorder Bibionomorpha, marsh flies and gall midges, has also been repeatedly recovered as monophyletic and sister to the Brachycera in the same studies. Multiple

phylogenetic hypotheses exist for Brachycera, however higher-level relationships within the suborder remain contentious (Bayless *et al*., 2021; Lambkin *et al.*, 2013; Shin *et al.* 2018; Song *et al.*, 2022; Wiegmann *et al.*, 2011). Difficulty recovering these relationships is thought to stem from multiple rapid radiations which occurred in deep time and are therefore difficult to recover with limited taxon sampling and discordant molecular data (Shin *et al.*, 2018; Wiegmann *et al.*, 2011). Despite varying levels of genetic coverage, previous molecular estimates of the Brachycera have included a similar range of taxonomic coverage. Wiegmann *et al.* (2011) sampled 160 brachyceran species in their phylogeny of the entire Diptera, which combined data from 14 nuclear loci, mitochondrial genomes and morphological data into an incomplete data matrix. More recently, Song *et al.* (2022) estimated a phylogeny of Brachycera by sampling 171 ingroup taxa using complete mitochondrial genomes. It could be argued that both studies had low taxonomic sampling given the suborder Brachycera presently contains 122 families and nearly 105,000 species. Taxon sampling has been shown repeatedly to impact the results of phylogenetic inference, so it has been suggested that greater sampling can aid in the resolution of deep phylogenies even when this results in a higher proportion of missing data (though the percentage of acceptable missing data remains a topic of debate; Heath *et al*., 2008; Hedtke *et al.*, 2006; Nabhan & Sarkar, 2011; Roure *et al*., 2013). Accordingly, a phylogeny estimated with a higher number of taxa that are evenly distributed across families is a viable approach to resolving recalcitrant nodes, thus resulting in a strong phylogenetic framework with which to test hypotheses.

Another limitation of previous estimates is sampling methodology. Previous studies have approached phylogenetic estimation from a systematics perspective, thus focusing primarily on the resolution of relationships between major clades, and sampling taxa disproportionately based

on the relationships being tested. This method is at odds with the model assumptions of phylogenetic comparative methods, which assume proportional sampling of taxa based on real world diversity (reviewed in Young and Gillung, 2020). Thus, to address specific hypotheses about parasitoid evolution, taxon sampling should aim to be proportional and should also include sufficient sampling of parasitoid lineages to test the proposed hypotheses. In particular, there are multiple parasitoid lineages which returned low support in previous phylogenetic estimates that should be targeted in future estimations (ex. Anthomyiidae, Conopidae, Nemestrinidae, Piophilidae and Sciomyzidae; Wiegmann *et al.*, 2011).

Supermatrix analyses, which are concatenated datasets produced by combining data from multiple sources, make it possible to harness publicly available data to address untested hypotheses without additional sequencing (de Queiroz & Gatesy, 2007). Therefore, modern advances in bioinformatics and models of sequence evolution make it is more attainable than ever to generate new datasets which are larger and more evenly sampled than previous iterations, and to use these datasets to produce well-supported phylogenetic hypotheses. This approach has become widely adopted for the reconstruction of a diverse range of taxonomic lineages (summarized in Shin *et al.*, 2018). Using this supermatrix approach, it is thus possible to address the sampling limitations of previous brachyceran phylogenetic studies while also estimating a phylogeny which is suitable for the testing of specific hypotheses regarding parasitoid evolution.

2.5 The origin of parasitoidy

Central to the question of how parasitoids evolve and diversify is the issue of their evolutionary origin. Under a functional definition of parasitoidy, parasitoids are distinguished by the feeding habit of their developmental stage which results in the death of their host (Eggleton

& Gaston, 1990; Godfray, 1994). Thus, by reconstructing the ancestral larval feeding habit of parasitoid lineages we can uncover common evolutionary pathways to parasitoidy. Previous qualitative work has proposed saprophagy as the most common pathway to parasitoidy within the flies, with fewer lineages derived from predatory or mycophagous ancestors (Eggleton & Belshaw, 1992). However, this work was conducted largely at the family level and entirely by outgroup comparison (Madison *et al.*, 1984) rather than with the use of statistical methods for ancestral character state reconstruction. Therefore, this hypothesis remains to be quantitatively tested. Furthermore, Eggleton and Belshaw (1992) did not differentiate between ectoparasitoids and endoparasitoids when inferring their origin, despite clear differences in the ecological, functional, and morphological constraints imposed on each group.

Gauld (1988), working with parasitoid wasps, proposed that endoparasitoidy is the derived state, and that transitions to endoparasitoidy may occur as a result of shifts to cocooned hosts by ectoparasitoid ancestors. Sharanowski *et al.* (2021) investigated this hypothesis in the wasp superfamily Ichneumonoidea and found some support for multiple transitions between endo- and ectoparasitoidy, though results were largely inconclusive due to limited taxon sampling. Posing the same question in bee flies (Diptera, Bombyliidae), Yeates and Greathead (1997) found support for the hypothesis that endoparasitoidy is derived. However, both Ichneumonoidea and Bombyliidae possess similar characteristics in that they are both single parasitoid lineages with a mix of endo- and ectoparasitoid species. In contrast, most parasitoid fly lineages consist entirely of endoparasitoids with no close ectoparasitoid relatives (Eggleton & Belshaw, 1992; Feener & Brown, 1997). This could suggest that endoparasitoidy can arise directly from life-history strategies other than ectoparasitoidy, or that endoparasitoidy is derived

from ectoparasitoidy but that ectoparasitoidy often acts as a transient life-history strategy and thus may not be recovered by ancestral character state reconstruction.

It is also worth investigating whether we observe shifts away from parasitoidy when investigating life-history transitions within a clade that contains both parasitoid and non-parasitoid lineages, such as Brachycera. Due to the highly specialized nature of the parasitoid life-history strategy, we could predict that parasitoidy is an evolutionary dead-end (Day *et al.*, 2016; Futuyuma & Moreno, 1988; Siddall *et al.*, 1993). This implies that the adaptations acquired by parasitoids could be irreversible from an evolutionary perspective. This is arguably more likely of endoparasitoidy, as many more specialized adaptations are required to survive inside the tissue of a host versus externally, which may be more comparable to a predatory life-history. Eggleton and Belshaw (1992) suggest that shifts away from parasitoidy are rare in both flies and beetles (order Coleoptera) but have been observed in wasps – most notably in the ants, bees and stinging wasps (Aculeata, non-parasitoids) which are thought to have derived from the same parasitoid ancestor as all parasitoid wasps (Peters *et al.*, 2017). These outstanding questions underline the importance of investigating the evolutionary history of multiple parasitoid lineages in order to draw conclusions on the origin of parasitoidy, as well as any other broad evolutionary patterns.

3. Methods

3.1 Data mining

Before mining any sequence data, I compiled a working list of families in the suborder Brachycera following Wiegmann *et al.*, 2011 and Pape *et al.*, 2011. This list was then corroborated with current literature to determine the status of contentious taxa. The final list of 122 brachyceran families with taxonomic notes and all sources used is available in Appendix 1.

All sequence data included in this study were mined from the publicly available National Center for Biotechnology (NCBI) Nucleotide database (NCBI Resource Coordinators, 2018) using the *R* package *rentrez* (Winter, 2017). This package acts as a wrapper for NCBI's Entrez Utilities API, providing an *R* interface with which to query all NCBI databases on a large scale. Using the *entrez_search()* command, I queried the NCBI Nucleotide database for all brachyceran species records for each gene of interest (see *3.2 Gene selection*). For the mitochondrial gene *cytochrome c oxidase subunit I* (COI), the number of records at the suborder level exceeded the limit I could pull using *rentrez* (n=418,632, limit is 10,000 [Accessed April 03 2022]). Therefore, I queried for COI using only the list of species that had returned results from at least one of the other gene searches. I also queried the NCBI Taxonomy database to extract family and genus level classifications for each species. These queries returned 157,370 sequence records from 8,085 species. All records were summarized in a data frame by the number of sequence records available per gene per species, along with taxonomic data. A small number of records were edited manually to correct for changes in family level classifications (noted in Appendix 1). This data frame was then used as the basis for taxon selection (see *3.3 Taxon sampling*).

After taxa were chosen, I conducted sequence selection. This was necessary as many species had multiple sequences available for commonly sequenced genes such as COI. To address

this, I automated the selection of sequences by using *R* to filter sequence records by length (bp) and select the longest sequence. A new data frame was then populated with the accession numbers of all selected sequences. Using these accession numbers and the *entrez_fetch()* command (*rentrez* package), I downloaded all sequences in fasta file format. Sequences were then concatenated into a single file for each gene using the *bash* command *cat* in preparation for DNA alignment.

3.2 Gene selection

Target genes were selected by first compiling a master list of 38 candidate genes that were considered informative in previous studies (Caravas & Friedrich, 2013; Han *et al.* 2002; Shin *et al.*, 2018; Simon *et al.*, 2010; Wahlberg & Johanson, 2018; Wiegmann *et al.*, 2011; Winkler *et al.*, 2015; Yang *et al.*, 2019). I then conducted preliminary searches within NCBI's Nucleotide database using *rentrez* to estimate the taxonomic coverage of each gene at the family level. To limit missing data, only the 18 genes which returned hits for >20% of brachyceran families were included in this study. The original list of candidate genes and the results of this search are included in Table 1. Again, COI was excluded from this search as the number of results returned exceeded the search limit. However, due to the extensive usage of COI for species barcoding, I assumed taxonomic coverage would be evenly distributed and thus COI is included as one of the final 18 genes. Despite passing this initial search, the gene ND5 was later excluded due to issues with correct identification and alignment (see *3.5 DNA alignment*). The final 17 genes include eight nuclear protein-coding genes (AATS, CAD, EF1A, PER, PGD, SINA, SNF, TPI), five mitochondrial protein-coding genes (COI, COII, CYTB, ND1, ND3), two nuclear ribosomal RNA genes (18S, 28S), and two mitochondrial ribosomal RNA genes (12S, 16S).

Table 1: List of candidate genes and results of preliminary searches within NCBI's Nucleotide database to estimate the taxonomic coverage of each gene at the family level. Only the 18 genes which returned hits for >20% of brachyceran families were included in this study. Genes which returned hits for >40% of brachyceran families are highlighted in blue; genes which returned hits for <40% and >20% of brachyceran families are highlighted in green.

Gene	Type	# Families	% Families (/134)	Taxonomic breadth
COI	mito	NA	NA	*could not compute (see note in text)*
28S	nuc ribo	116	86.57%	evenly distributed throughout
CAD	nuc	105	78.36%	evenly distributed throughout
AATS	nuc	102	76.12%	evenly distributed throughout
TPI	nuc	98	73.13%	evenly distributed throughout
PGD	nuc	84	62.69%	evenly distributed throughout
16S	mito ribo	74	55.22%	evenly distributed throughout
12S	mito ribo	68	50.75%	evenly distributed throughout
COII	mito	62	46.27%	evenly distributed throughout
EF1A	nuc	57	42.54%	evenly distributed throughout
18S	nuc ribo	56	41.79%	no Opomyzoidea
cytB	mito	55	41.04%	evenly distributed throughout
ND5	mito	32	23.88%	sparse coverage throughout (missing many superfamilies)
ND3	mito	30	22.39%	sparse coverage throughout (missing many superfamilies)
ND1	mito	29	21.64%	sparse coverage throughout (missing many superfamilies)
SINA	nuc	28	20.90%	no Opomyzoidea or Tephritoidea
PER	nuc	27	20.15%	sparse coverage (lots of Tephritids)
SNF	nuc	27	20.15%	no Opomyzoidea or Tephritoidea
COIII	ribo	25	18.66%	sparse coverage throughout (missing many superfamilies)
G6PD	nuc	24	17.91%	sparse coverage throughout
ND2	mito	23	17.16%	sparse coverage throughout (missing many superfamilies)
PEPCK	nuc	24	17.91%	sparse coverage throughout
ATP6	mito	23	17.16%	sparse coverage throughout (no Opomyzoidea, lots of Drosophilidae)
ND4L	mito	22	16.42%	sparse coverage throughout (missing many superfamilies)
ND6	mito	19	14.18%	sparse coverage throughout (missing many superfamilies)
SYX	nuc	19	14.18%	sparse coverage throughout (more Calyptratae)
ATP8	mito	18	13.43%	sparse coverage throughout (no Opomyzoidea, lots of Drosophilidae)
GART	nuc	18	13.43%	very sparse coverage throughout
PUG	nuc	18	13.43%	very sparse coverage throughout
WG	nuc	13	9.70%	very sparse coverage throughout
MAC	nuc	11	8.21%	mostly Calyptratae
MCS	nuc	9	6.72%	mostly Calyptratae
LGL	nuc	8	5.97%	mostly Calyptratae
ace	nuc	6	4.48%	only sparse coverage in Orthorrhapha
RH1	nuc	5	3.73%	very sparse coverage throughout
H3	nuc	4	2.99%	mostly Drosophilidae
DDC	nuc	3	2.24%	mostly Drosophilidae
LW-opsin	nuc	0	0.00%	no coverage

3.3 Taxon sampling

To meet model assumptions, lineages were proportionally sampled based on described diversity at the family level. In total, I aimed to sample 0.5% of suborder diversity (total number of described brachyceran species = 104,977, derived from summing the number of species per family, see Appendix 1 for citations). I calculated this for each family by first gathering an estimate of described species from primary literature, and then multiplying that value by 0.005 to produce sampling targets. These targets were rounded to the nearest whole number, except when this value was zero. In those cases, I assigned targets a value of one to avoid excluding smaller families entirely. Sampling targets for each family are presented in Appendix 1.

Selection of individual species was done manually using the sequence record data mined from NCBI's Nucleotide database (see *3.1 Data mining*). This was structured as a presence/absence matrix that displayed the number of genes with sequences available per species. Within each family, species with the most genetic data available were selected preferentially to minimize missing data. When more than one species had the same level of genetic coverage, I sought to select species from a diversity of genera and subfamilies. This was particularly important in families that display a wide range of larval feeding habits, as these characters are often shared at the generic or subfamily levels. For some families, it was not possible to sample a large variety of genera due to limited available data. In some instances, I generated chimera taxa by combining sequences from two species within the same genus to minimize missing data. In those cases, taxa are clearly labelled (Appendix 1). Some families had no data available to sample and are thus not represented in the phylogeny.

3.4 Outgroup rooting

To root the phylogeny by outgroup rooting, I sampled an additional five taxa from the Bibionomorpha, a monophyletic infraorder which is sister to the Brachycera. This included one representative each from the following families: Scatopsidae, Anisopodidae, Keroplatidae, Cecidomyiidae, and Diadocidiidae. As a large clade, Bibionomorpha was not proportionally sampled as this would have minimally added an additional 75 taxa to the sampling effort (# of species = 15,000, Ševčík *et al.*, 2016). Instead, the five outgroup taxa were included for phylogeny estimation but excluded from ancestral character state reconstruction to meet the assumption of proportional sampling.

3.5 DNA alignment

Sequences were aligned using the multiple sequence alignment program MAFFT version 7 (Online version) with strategy set to 'iterative refinement method E-INS-I' (Katoh *et al.*, 2013; Katoh *et al.*, 2019). Quality control of alignments was conducted by eye using the alignment viewing software AliView (Larsson, 2014) and Mesquite (Maddison & Maddison, 2021). This allowed unalignable sequences to be easily flagged and investigated further. I used the Basic Local Alignment Search Tool (BLAST; Boratyn *et al.*, 2013) website at NCBI to verify the identity of flagged sequences against confirmed sequences from the same gene. This often uncovered mislabeled or contaminated sequences which were then removed from the alignment. When possible, removed sequences were replaced with others from the same gene and species. As the majority of ND5 sequences were mislabeled and could not be reliably replaced, ND5 was excluded from the final alignment.

Alignments were then concatenated into a single phylip file with all genes and species using the *concat* command from the *Python* program AMAS (Borowiec, 2016). This command also output a partition file which was then manually edited. Ambiguously aligned regions, where positional homology could not be inferred with a reasonable level of confidence were excluded from the phylogenetic analyses. Sites where data was only available for a single species were also removed.

3.6 Testing model assumptions

Before phylogeny estimation, DNA sequence data were partitioned by gene (Chernomor *et al.*, 2016). I then performed three maximum matched-pair tests of symmetry in IQ-TREE version 2 (Minh *et al,*. 2020; Nguyen *et al.*, 2015) to test for the presence of model violations in the partitioned alignment (Naser-Khdour *et al.*, 2019). These tests assess whether each partition meets the model assumptions of stationarity and homogeneity by comparing their most divergent sequences. IQ-TREE then output a 'badremoved' alignment by excluding partitions which rejected model assumptions.

3.7 Phylogeny estimation

Phylogenies for both the full nucleotide alignment ('complete') and the alignment with only those partitions which did not reject model assumptions ('badremoved') were estimated under maximum likelihood (ML) using IQ-TREE. Starting trees were set to 'random' and seed was set to '12345' for reproducibility. Partition model was set with command -p so that branch lengths were linked across partitions (edge-linked), but substitution rates were allowed to vary. Substitution rate and nucleotide frequency parameters were estimated for each partition under the

GTR+G nucleotide substitution model with 4 discrete rate categories (default; Yang, 1994). Branch support was evaluated by implementing ultrafast bootstraps (Minh *et al.*, 2013; Hoang *et al.*, 2018) and the Shimodaira–Hasegaw approximate likelihood ratio test (SH-aLRT; Guindon *et al.*, 2010; Anisimova *et al.*, 2011), which were both set to 2,000 replicates. I also attempted to implement the GHOST mixture model (Crotty *et al.*, 2020), however there was insufficient data for parameter estimation (see *5.3 Model selection and assumption violations*).
Following phylogeny estimation, tree files were imported into *R* and rooted with outgroup taxa using the package *ape 5.0* (Paradis & Schliep, 2019) with command *root()*.

3.8 Topology test

To test whether topologies differ significantly between the 'badremoved' tree and the 'complete' tree, I ran an approximately unbiased (AU) topology test (Shimodaira, 2002) with 10,000 RELL replicates. The approximately unbiased (AU) topology test calculates the log-Likelihood values for multiple input trees to find the single 'best' tree, and then assesses whether the other tree topologies differ significantly from the best tree ($p<0.05$). If the other tree(s) are found to be significantly different, they are rejected in favour of the best tree. The best supported tree was then used as the basis of ancestral state reconstruction.

3.9 Fossil calibration

The reconstruction of ancestral character states requires an ultrametric phylogeny, where all tips are equal distance to the root. Therefore, the 'best tree' as determined by the AU topology test was time-calibrated using five fossil calibration points and the *chronos()* command in *R* (*ape 5.0*; Paradis & Schliep, 2019).

Chronos() uses the penalized maximum likelihood method (Sanderson, 2002) to estimate divergences times under multiple models of substitution rate variation (Paradis, 2013). I tested both the correlated and relaxed models of molecular evolution with smoothing parameter λ=1. Note that the *chronos()* 'relaxed model' refers to a model which allows tree branches to have variable substitution rates and makes no assumption of correlation between neighbouring branches. This may not correspond to other 'relaxed' models of molecular evolution in the literature, including those implemented under a Bayesian framework. For both the relaxed and correlated models, the maximum number of function evaluations (eval.max) was set to $1e^5$, maximum number of iterations (iter.max) was set to $5e^4$, and maximum number of alternative iterations (dual.iter.max) was set to 500. All other optimization parameters were set to defaults. During model testing, the correlated model returned a larger log-Likelihood score and a smaller ΦIC score (log-Lik = -229.5416, ΦIC = 3843.08) than the relaxed model (log-Lik = -239.6968, ΦIC = 3875.44), and was appropriately accepted as the better fitting model.

Fossil calibration points were selected following two previous estimations of a brachyceran phylogeny (Song *et al.*, 2022; Wiegmann *et al.*, 2011). In total, five fossils representing major clades across the Brachycera were used with minimum and maximum age limits set in millions of years (my): Brachycera crown, age.min = 189.6, age.max = 196.5; Stratiomyomorpha crown, age.min = 141.27, age.max = 166.73; Empidoidea crown, age.min = 112, age.max = 163, Eremoneura crown, age.min = 155.14, age.max =167.86; and Hippoboscoidea crown, age.min = 53.96, age.max = 61.04.

After calibration, the five outgroup taxa were removed in *R* using the *drop.tip()* command in *ape* in preparation for ancestral state reconstruction analyses.

3.10 Life history data

To inform the reconstruction of ancestral states, larval feeding habit data for extant taxa were collected from the literature. Species-level data were collected preferentially, but generic-level data were often included when feeding habit was unknown at the species-level and could be reliably assumed to be shared within a genus based on the literature.

I attempted to record only primary or obligate feeding habits; however, it was not always clear whether habits were obligate or facultative, especially among polyphagous species. This was specifically an issue in the calyptrate families Calliphoridae, Muscidae, and Sarcophagidae which are well-known to exhibit polyphagy, with multiple observations of saprophagy, predation and myiasis exhibited by single species. All feeding habits for these species which were observed outside of laboratory conditions were recorded and included. The species *Megaselia scalaris* (Phoridae) is also known for its flexible feeding habits that include observations of saprophagy, mycophagy, phytophagy, predation, and myiasis, in addition to facultative predation, parasitism and parasitoidy observed solely in restrictive conditions. I included all primary/obligate feeding habits for *M. scalaris* following the review by Disney (2008).

For the classification of parasitoid taxa, I did not classify all species as parasitoids, which are defined as such in the literature based on varying definitions. I instead followed the functional definition laid out in *2.2 Defining parasitoidy*: A parasitoid is any organism which develops on or within a single host organism, using the host as an essential trophic resource which is killed, either directly or indirectly, due to parasitoid development (following Eggleton & Gaston, 1990). This resulted in multiple difficult classification decisions which raised further questions on the relationship between predation, parasitoidy and parasitism. This is revisited in the *Discussion* section *5.2 Parasitoidy on a continuum*.

3.11 Ancestral state reconstruction

The program BayesTraits V4.0.0 (Pagel *et al.*, 2004) was used for ancestral state reconstruction (ASR) within a Bayesian framework. The time calibrated 'best' tree, as determined by the AU topology test, was used as an input tree. Posterior probability distributions for all internal nodes were estimated using Markov chain Monte Carlo (MCMC) and the MultiState option for reconstructing traits with more than two discrete states. The directionality of transitions was not restricted, meaning that states were assumed to be unordered, and rates were estimated for each between-state transition independently. All priors were set to an exponential distribution with mean=1. The analysis was run for 20,000,000 generations with a burn-in of 20,000 generations.

Larval feeding habit data were initially categorized into seven states coded as follows: (0) predator, (1) phytophage, (2) saprophage, (3) parasite, (4) endoparasitoid, (5) ectoparasitoid, and (6) non-feeding. Where; 'phytophage' is inclusive of palynivore, malivore, and mycophage species; 'saprophage' is inclusive of detritivore, scavenger, and coprophage species; and hyperparasitoids were classified as either endo- or ectoparasitoids depending on their feeding location. Myiasis, which is the infection and consumption of the tissue of a living animal by dipteran larvae, was classified as parasitism. However, it was sometimes unclear in the literature whether the infection of existing wounds should be classified as parasitism or saprophagy. Unknown data were coded as (-) and interpreted as having an equal probability of each trait state. Taxa with polyphagous feeding habits were coded with multiple states (i.e. '02' for a species which is both a predator and a saprophage).

However, this coding scheme resulted in the estimation of too many parameters given the available data, producing a fatal error in BayesTraits. Therefore, data were recategorized to limit the number of states being reconstructed, as the number of parameters estimated is approximately equal to the number of states to the 2^{nd} power (Pagel *et al.*, 2004). As a result, parasitoid taxa were combined into a single category and non-feeding taxa were lumped with unknowns. I justified the lumping of non-feeding taxa with unknowns as only seven non-feeding taxa were recovered during the literature search, which represented all seven taxa sampled from the monophyletic superfamily Hippoboscoidea. Thus, the exclusion of this clade from ASR was unlikely to impact the interpretation of parasitoid evolutionary transitions. These adjustments yielded five states: (0) predator, (1) phytophage, (2) saprophage, (3) parasite, and (4) parasitoid.

4. Results

4.1 Supermatrix

In total, 562 ingroup taxa and five outgroup taxa were sampled from NCBI's Nucleotide database to construct a concatenated supermatrix. However, two taxa were later excluded during the maximum tests of symmetry and were thus removed from all datasets to facilitate statistical comparison of tree topologies (see *4.2 Maximum tests of symmetry* and *4.5 Approximately unbiased topology test*). For that reason, the final supermatrix consists of 560 ingroup taxa and five outgroup taxa (Appendix 2). This failed to meet the 584-taxon sampling target representing 0.5% of described brachyceran diversity due to insufficient molecular data in NCBI's Nucleotide database. The following families were impacted by data scarcity: Chloropidae, Gobryidae, Homalocnemiidae, Milichiidae, and Nothybidae. Consequently, Chloropidae and Milichiidae were underrepresented in the final alignment, and the families Homalocnemiidae, Gobryidae, and Nothybidae were excluded entirely. The two taxa removed during tests of symmetry were both chloropids (*Cryptonevra nigritarsis* and *Lasiosina albipila*), further reducing their representation in the dataset.

4.2 Maximum tests of symmetry

The results of the maximum tests of symmetry removed three of the 17 gene partitions in the full nucleotide alignment after rejecting the assumption of stationarity ($p<0.05$; COII, SINA, SNF). Consequently, two taxa which were only represented by COII sequence data were removed from the alignment entirely and excluded from subsequent phylogeny estimation (*Cryptonevra nigritarsis* and *Lasiosina albipila* (both Chloropidae)). As topology tests require that all trees

include the same taxa, I also excluded *Cryptonevra nigritarsis* and *Lasiosina albipila* from the 'complete' 17 partition alignment before phylogeny estimation.

4.3 Phylogeny estimation

Two phylogenies were estimated using subsets of the full nucleotide alignment with 565 taxa (560 ingroup, five outgroup);

(i) the 'complete' tree estimated with all 17 gene partitions (including: 12S, 16S, 18S, 28S, AATS, CAD, COI, COII, CYTB, EF1A, ND1, ND3, PER, PGD, SINA, SNF, and TPI). This alignment contained 23,671 total sites with 52.1% missing data. The full annotated tree with bootstrap and SH-aLRT support is available in Fig.1.

(ii) the 'badremoved' tree estimated with only the 14 partitions which were not rejected by the tests of symmetry (including: 12S, 16S, 18S, 28S, AATS, CAD, COI, CYTB, EF1A, ND1, ND3, PER, PGD, and TPI; excluding: COII, SINA, and SNF). This alignment contained 22,210 total sites with 50.1% missing data. The full annotated tree with bootstrap and SH-aLRT support is available in Fig.2.

After initial phylogeny estimation, I flagged several taxa as potential 'rogue taxa' if they were both (i) placed far outside their anticipated family or superfamily clades based on existing systematic hypotheses and (ii) variably placed between tree estimates. Rogue taxa are often attributed to systematic error caused by missing data or long branch lengths (Sanderson & Shaffer, 2002). However, the observed pattern could also be the product of contaminated or mislabeled samples. Therefore, I used BLAST to verify all sequences from taxa flagged as potential rogues and all were found to be uncontaminated. As a result, no further taxa were removed from either the 'complete' or 'badremoved' alignment. However, these taxa are noted

with red text in the full tree figures (Fig.1 and Fig.2) and are referred to during discussions of topology and parasitoid transitions due to their impact on the perceived monophyly of multiple groups. In total, six taxa in the 'complete' tree met the above criteria and were thus flagged, and eleven taxa in the 'badremoved' tree were flagged. Notably, six of the taxa flagged in the 'badremoved' tree were parasitoids, whereas only two parasitoids were flagged in the 'complete' tree, and only one of these species (*Lixophaga latigena* (Tachinidae)) was flagged in both trees.

4.4 Placement of major groups

Topologies of both trees are discussed below with key similarities and differences as summarized in Fig.3 (excluding flagged taxa for readability). Existing superfamily and higher-level classifications following Pape *et al.* 2011 and Wiegmann *et al.* 2011 are used to highlight and discuss these differences (classifications defined in Appendix 1).

The 'complete' tree recovered a monophyletic Tabanomorpha as sister to the remaining Brachycera. After Tabanomorpha, the following clades were recovered as monophyletic in decreasing proximity to the root: Nemestrinidae, Xylophagaidae, Stratiomyoidea, Acroceridae, and an Asiloidea+Hilarimorphidae grouping. However, these clades each received low bootstrap support (<80%) compared with later diverging nodes. Empidoidea was recovered as non-monophyletic with respect to *Nanodromia narmkroi* (Hybotidae) and *Sybistroma obscurellum* (Dolichopodidae), which were both placed within the Schizophora and flagged as potential rogues following the criteria laid out in *4.3 Phylogeny estimation*. After the empids, a monophyletic Apystomyiidae diverged, followed by a non-monophyletic Phoroidea with respect to *Megaselia abdita* (Phoridae), which was also flagged for its placement within Schizophora. A monophyletic Syrphidae diverged after Phoroidea, followed by a non-monophyletic Pipunculidae

with respect to *Neophrocerus daeckei* (Pipunculidae) placed within the Schizophora. Excepting *N. daeckei*, this Pipunculidae group was recovered as sister to the Schizophora.

Though Schizophora has been repeatedly recovered as monophyletic in molecular investigations of the Diptera, relationships within the Schizophora have remained largely unresolved (Bayless *et al*., 2021; Shin *et al.* 2018; Song *et al.*, 2022; Wiegmann *et al.*, 2011). Specifically, the acalyptrates, a designation referring to all schizophoran taxa excluding the monophyletic Calyptratae, have been variably placed in all previous hypotheses, including those using genomic data (Bayless *et al.*, 2021) Therefore, it is not entirely surprising that the 'complete' tree did not recover the majority of proposed schizophoran superfamilies, and instead recovered two large clades I designated 'Schizophora clade #1' and 'Schizophora clade #2, which consisted of a mix of all acalyptrate families excluding those within the Agromyzidae, Odiniidae, Hippoboscoidea and Calyptratae. These clades also included many of the flagged taxa I expected to recover elsewhere based on existing systematic hypotheses. Diverging after 'Schizophora clade #2', an Agromyzidae+Odiniidae clade was recovered as non-monophyletic with respect to the flagged *Scaptomyza crassifemur* (Drosophilidae), followed by a monophyletic Hippoboscoidea. Finally, the Calyptratae were recovered as non-monophyletic with respect to the aforementioned hybotid *Nanodromia narmkroi* and the flagged *Lixophaga latigena* (Tachinidae), which was placed within Schizophora.

In contrast, the 'badremoved' tree recovered the parasitoid family Acroceridae as sister to the remaining Brachycera. This was followed by Nemestrinidae, Tabanomorpha (non-monophyletic with respect to the flagged *Adersia oestroides* (Rhagionidae)), Xylophagaidae, Stratiomyoidea (non-monophyletic with respect to the flagged *Microchyrsa polita* (Stratiomyidae)), and an Asiloidea+Hilarimorphidae clade which was non-monophyletic with

respect to three bombyliid species recovered within the Schizophora (*Neosardus principius, Comptosia quadripennis, Thraxan acutus*). Overall, this section of the tree, before the divergence of Eremoneura, received higher bootstrap support along the backbone of the phylogeny than the 'complete' tree, despite recovering fewer clades as monophyletic (3/6, vs. 6/6). Empidoidea was recovered as non-monophyletic with respect to a flagged chloropid recovered within the group (*Elachiptera bimaculata*) as well as a dolichopodid (*Dolichopus ungulates*) placed in the Schizophora. A monophyletic Apystomyiidae diverged after the empids, followed by a monophyletic Phoroidea and Syrphidae. For a second time, a non-monophyletic Pipunculidae was recovered as sister to the Schizophora, this time with respect to *Cephalops cochleatus* (Pipunculidae) which was flagged for its placement in the Schizophora. Similar to the 'complete' tree, acalyptrate groups were largely unrecovered, apart from Ephydridae and Hippoboscoidea. Again, these unplaced Schizophora fell into two ambiguously defined clades – however the composition of these clades did not match those from the 'complete' tree and thus they received their own designations, 'Schizophora clade #3' and 'Schizophora clade #4' respectively (see Fig.2). Notably, in the 'badremoved' tree, Ephydridae is recovered as monophyletic and sister to the Hippoboscoidea and Calyptratae, diverging after 'Schizophora clade #4'. This contrasts with the 'complete' tree, where the family Ephydridae was recovered as monophyletic but nested within 'Schizophora clade #1'. Additionally, the Agromyzidae+Odiniidae group recovered as sister to the Hippoboscoidea and Calyptratae in the 'complete' tree (non-monophyletic with respect to a flagged drosophilid) was recovered as non-monophyletic and split within both 'Schizophora clade #3' and 'Schizophora clade #4' in the 'badremoved' tree. Following the monophyletic Ephydridae, Hippoboscoidea was recovered as non-monophyletic with respect to Streblidae (*Trichobius longipes*), which was placed in 'Schizophora clade #3'. The resulting

Hippoboscidae+Nycterbiidae+Glossinidae clade was nested with a flagged tachinid *Lixophaga latigena* as sister to the Calyptratae. Finally, the Calyptratae were recovered as non-monophyletic with respect to several flagged taxa. Two chloropids (*Meromyza columbi*, *Oscinella frit*), two bombyllids (*Comptosia quadripennis*, *Thraxan acutus*), and one stratiomyid *Mircochyrsa polita* were recovered within the Calyptratae, and one tachinid which was anticipated within the Calyptratae was instead recovered within 'Schizophora clade #4'.

The results of both trees are plausible given the placement of major clades in existing phylogenetic hypotheses of the Brachycera (summarized in Fig.4), excluding the acalyptrates which were poorly recovered (though this also aligns with the results of previous dipteran explorations). The placement of major groups before the divergence of Eremoneura is variable between existing hypotheses, however the placement of major clades within the Eremoneura recovered in both the 'complete' and 'badremoved' trees supports previous work by Shin *et al.*(2018), Song *et al.* (2022) and Wiegmann *et al.* (2011). Though the placement of major clades is conceivable, many brachyceran families were recovered as non-monophyletic below the superfamily level in one or both phylogenies, as seen in the full tree figures. The impact the non-monophyly of these lineages had on the reconstruction of ancestral larval feeding habits is considered later in the *Results* and *Discussion.*

4.5 Approximately unbiased topology test

The AU test with the 'complete' and 'badremoved' tree inputs recovered the 'complete' tree as the best tree and found that the 'badremoved' tree had a significantly worse likelihood score ($p=1.64e^{-4}$) and could therefore be rejected. Consequently, only the 'complete' tree is used for the ancestral character state reconstruction of larval feeding habits.

4.6 Reconstruction of ancestral larval feeding habits

The reconstruction of ancestral larval feeding habits in BayesTraits estimated the transition rate between each state (larval feeding habit; see Appendix 3) in both directions and used these parameter values to output the posterior probability of each state occurring at each internal node over millions of iterations. These posterior probabilities were then averaged across all iterations and plotted as pie charts at each respective node using the *ggtree* package in *R* (Yu *et al.,* 2017; mapped on the 'complete' tree in Fig.5). The pie charts communicate uncertainty in the reconstruction of ancestral character states given the results of all BayesTraits iterations. Consequently, there is inherent ambiguity in determining in which node a transition has taken place. However, it is necessary to make assumptions about where transitions occur to draw conclusions regarding the ancestral character state of parasitoid lineages. Thus, I considered a 'gain' between two nodes when the posterior probabilities showed an **increase** in the probability of parasitoidy from an ancestral node to a derived node, such that parasitoidy became the state with the largest probability when it had not been before. To assess what state parasitoidy derived from during each gain, I recorded the state with the highest probability at the most recent ancestral node. Conversely, I considered a 'loss' between two nodes when the posterior probabilities showed a **decrease** in the probability of parasitoidy from an ancestral node to a derived node, such that a non-parasitoid state became the state with the largest probability where parasitoidy had been before. To assess what state was derived from parasitoidy at each loss, I recorded the state with the highest probability at the derived node.

Using these criteria, I recorded a total of 22 transitions to and from parasitoidy across the Brachycera, which comprised 17 gains and five losses (listed in Table 2, transitions are also

labelled on Fig.5 following the same numbering scheme). Of the 17 transitions to the ‘Parasitoid’ state (gains); nine were transitions from the ‘Parasite’ state, five were from ‘Saprophage’, two were from ‘Phytophage’ and one was from ‘Predator’. Of the five transitions away from the ‘Parasitoid’ state (losses); three were to the ‘Parasite’ state, and two were to the ‘Predator’ state. All rate parameters estimated by BayesTraits are reported in Table 3.

Table 2: Transitions to (gain) and from (loss) parasitoidy recovered during ancestral state reconstruction of larval feeding habits in the Brachycera.

Transition #	Major clade (as labelled on Figure)	Family	Gain/Loss	Transition from	Transition to	Note
1	Nemestrinidae	Nemestrinidae	Gain	Saprophage	n/a	
2	Acroceridae	Acroceridae	Gain	Saprophage	n/a	
3	Asiloidea+Hilarimorphidae	Bombyliidae	Gain	Predator	n/a	
4	Asiloidea+Hilarimorphidae	Bombyliidae	Loss	n/a	Predator	
5	Asiloidea+Hilarimorphidae	Bombyliidae	Gain	Parasite	n/a	Parasite used as a transition state (Predator)
6	Phoroidea	Phoridae	Gain	Parasite	n/a	Parasite used as a transition state (Saprophage)
7	Phoroidea	Phoridae	Loss	n/a	Parasite	Parasite used as a transition state (Saprophage)
8	Phoroidea	Phoridae	Gain	Parasite	n/a	Parasite used as a transition state (Parasitoid)
9	Phoroidea	Phoridae	Loss	n/a	Parasite	
10	Phoroidea	Phoridae	Gain	Parasite	n/a	
11	Pipunculidae	Pipunculidae	Gain	Saprophage	n/a	
12	Schizophora clade #1	Pyrgotidae+Conopidae	Gain	Parasite	n/a	Parasite used as a transition state (Saprophage)
13	Schizophora clade #1	Pipunculidae	Gain	Saprophage	n/a	Species flagged as potential rogue
14	Schizophora clade #2	Sciomyzidae+Conopidae	Gain	Parasite	n/a	Parasite used as a transition state (Saprophage)
15	Schizophora clade #2	Sciomyzidae	Loss	n/a	Predator	
16	Schizophora clade #2	Pyrgotidae	Gain	Phytophage	n/a	
17	Schizophora clade #2	Tephritidae	Gain	Phytophage	n/a	
18	Schizophora clade #2	Tachinidae	Gain	Parasite	n/a	Parasite used as a transition state (Saprophage/Phytophage), Species flagged as potential rogue
19	Schizophora clade #2	Cryptochetidae	Gain	Saprophage	n/a	
20	Calyptratae	Tachinidae	Gain	Parasite	n/a	Parasite used as a transition state (Saprophage)
21	Calyptratae	Hybotidae	Loss	n/a	Parasite	Parasite used as a transition state (Predator), Species flagged as potental rogue
22	Calyptratae	Tachinidae	Gain	Parasite	n/a	Parasite used as a transition state (Parasitoid), Sister species flagged as potential rogue

Table 3: Transition rates between larval feeding habit states, as estimated in BayesTraits. The presented rates are the average over 20,000,000 iterations. Transition rates away from parasitism are highlighted to draw attention to the much higher estimates when compared to all other rates.

From	To	Rate (averaged across iterations)
Predator	Phytophage	0.000133
Predator	Saprophage	0.000149
Predator	Parasite	0.000239
Predator	Parasitoid	0.000246
Phytophage	Predator	0.001079
Phytophage	Saprophage	0.00239
Phytophage	Parasite	0.002384
Phytophage	Parasitoid	0.001715
Saprophage	Predator	0.001329
Saprophage	Phytophage	0.002371
Saprophage	Parasite	0.00571
Saprophage	Parasitoid	0.001249
Parasite	Predator	0.80505
Parasite	Phytophage	0.629989
Parasite	Saprophage	1.299277
Parasite	Parasitoid	0.664851
Parasitoid	Predator	0.001207
Parasitoid	Phytophage	0.000427
Parasitoid	Saprophage	0.000682
Parasitoid	Parasite	0.00102

5. Discussion

5.1 Parasitoid evolutionary history

The results of this study were largely unexpected given previous investigations into parasitoid life-history transitions and my stated hypotheses. The number of total transitions to and from parasitoidy recovered within the Brachycera was only 22, with 17 gains and five losses (Table 2, Fig.5). This is less than the previous estimate made by Eggleton & Belshaw (1992) who proposed a minimum of 18 independent gains within the Brachycera (21 within the Diptera) reported solely on qualitative outgroup comparison at the family level. Based on previous knowledge of the group, my results are likely a significant underestimate of the actual number of transitions that have occurred. I propose that this underestimation is the result of several sampling limitations that hindered the reconstruction of the true evolutionary history of brachyceran parasitoids:

(i) Several known parasitoid lineages could not be sampled due to a dearth of molecular data (Anthomyiidae, Asilidae, Calliphoridae, Chloropidae, Muscidae, Sarcophagidae, and Syrphidae). Under the conservative assumption that parasitoids within each of these families are members of a single lineage (rather than multiple lineages within a single family), I propose that an additional seven potential transitions to parasitoidy could be recovered if sampling limitations were removed.

(ii) At least one family (Sciomyzidae), which exhibits a diversity of larval feeding habits, including parasitoidy, was not extensively sampled due to restrictions imposed by proportional sampling. It is not clear whether expanding the sampling of sciomyzid flies would return multiple transitions below the family level.

However, if multiple transitions did occur, they would not have been recovered in this study due to limitations of the sampling and thus, this hypothesis remains to be tested.

(iii) At least one family (Bombyliidae), which is thought to exhibit a diversity of larval feeding habits, including parasitoidy, was largely excluded from the reconstruction of ancestral feeding habits due to a scarcity of species or generic level larval feeding data in the literature. This resulted in predominantly unrecovered nodes in this section of the tree where we might expect to see multiple transitions to parasitoidy.

(iv) At least one other family (Ctenostylidae), which is thought to exhibit parasitoid larval feeding habits, was excluded from analysis due to a lack of confirmed larval feeding habit data in the literature at any level (species, genera, family).

(v) Finally, given the general limitations of our knowledge regarding brachyceran flies and life in general, it would not be surprising to learn that there are multiple unknown parasitoid lineages (either undescribed or biologically unknown) within the Brachycera that were excluded from this reconstruction, but that would represent independent shifts to parasitoidy if we were able to successfully reconstruct their evolutionary history.

The results of rate estimation during ancestral state reconstruction in BayesTraits were also unexpected. Notably, the transition rates estimated for transitions from the ‘Parasite’ state to other states were consistently multiple orders of magnitude higher than transitions to and from other states. This resulted in an unexpected pattern of transitions being observed across internal nodes, where the ‘Parasite’ state was repeatedly reconstructed as a transitionary state even in

clades where there were few or no reported parasite taxa. This was observed during ten of the 22 observed transitions to or from the 'Parasitoid' state (Table 2, Fig.5). For example, Transition #20 shows a transition from 'Saprophage' to 'Parasite' to 'Parasitoid' at the root of a large parasitoid clade in the Calyptratae consisting of mostly tachinid flies. Within the same clade, transition #21 records a second transition where the 'Parasitoid' state is lost and the most recent common ancestor of *Nanodromia narmkroi* (Hybotidae; predator) and *Euthera tentatrix* (Tachinidae; parasitoid) is recovered as a 'Parasite'.

Though it is possible that this is a biologically accurate reconstruction, and that parasitism represents a transitionary state between various larval feeding habits, it seems highly unrealistic given the constraints of the parasite biology. This feels particularly doubtful in the Brachycera given the number of parasites found in the group, which represented only 14 of the 560 taxa sampled, many of which were polyphagous. Instead, I propose that this is an artefact produced by a large amount of missing data unevenly distributed across the tree, which is interacting poorly with the way that BayesTraits interprets unknown states. It is likely that additional larval feeding habit data is necessary to resolve this anomaly (or verify it's legitimacy).

Though it is not statistically supported, I present the transitions to and from parasitoidy again, this time while ignoring the 'Parasite' transition state to assess the impact of this pattern on the final results. I produced these estimates by simply ignoring the posterior probability of the 'Parasite' state at these transition nodes and focussing only on the proportion of the other four states. Consequently, I recorded only 14 transitions to the 'Parasitoid' state (gains): nine transitions from 'Saprophage', two transitions from 'Predator', two transitions from 'Phytophage', one transition from an ancestor ambiguously reconstructed as

‘Saprophage/Phytophage’, and one legitimate transition from the ‘Parasite’ state (transition #10). Two additional transitions are eliminated, given that the ‘Parasite’ state was acting as a transition state between two ‘Parasitoid’ nodes (transition #8 and transition #22). I also record three transitions away from the ‘Parasitoid’ state (losses): two transitions to ‘Predator’, and one transition to ‘Parasite’. Again, two additional transitions are eliminated (transition #7 and transition #21). It is impossible to say conclusively whether the transitionary ‘Parasite’ states are inaccurate in any or all cases without further investigation, however the transition pattern observed when the ‘Parasite’ transition state is ignored is much closer to that suggested by Eggleton & Belshaw (1992), who proposed saprophagy as the most common ancestral feeding habit of parasitoid taxa with the Diptera, with transitions from predation, phytophagy and mycophagy (considered separately) also present.

It is also notable that transitions from parasitoidy to other states were recovered multiple times, whether the ‘Parasite’ transition state was ignored or not. Looking exclusively at the losses maintained when ignoring the ‘Parasite’ state, each occurred within a family which is known for containing species with a diversity of larval feeding habits alongside parasitoidy: Phoridae, Bombyliidae, and Sciomyzidae. Therefore, I propose that future studies that aim to reconstruct the evolutionary history of parasitoidy on a finer scale focus on these three families, as they display the highest potential for recovering multiple transitions below the family level. However, as Bombyliidae was plagued by large amount of missing larval feeding habit data, it is likely that a family level reconstruction would face the same limitations described here.

In addition to issues with the estimation of rate parameters, the reliability of several transitions is questioned given uncertainty in the input topology. Specifically, the presence of

taxa flagged as potential rogues contributed to the presence of at least four transitions which I consider unreliable;

(i) Transition #13 counts a transition from saprophage to parasitoid due to the placement of the pipuculid species *Nephrocerus daeckei* within Schizophora clade #1 rather than with the remaining Pipunculidae.

(ii) Transition #17 counts a transition from parasite to parasitoid due to the presence of the tachinid species *L. latigena* placed far outside its expected clade (Calyptratae), within a clade that is otherwise largely saprophagous and nested within the unresolved Schizophora clade #2;

(iii) Transition #20 counts a transition from parasitoid to parasite due to the presence of the hybotid species *N. narmkroi* far outside its expected clade (Empidoidea), within a clade of parasitoid Calyptratae;

(iv) Transition #21, following Transition #20, counts a transition from parasite to parasitoid in the sister species to the hybotid *N. narmkroi*.

One way to mitigate the impact of potential rogues in future reconstructions would be to identify and exclude them either before or after phylogeny estimation (methods for doing so are addressed in *5.4 Inconsistent topologies and flagged taxa*). However, another approach is to input multiple trees into BayesTraits to incorporate uncertainty in the estimated topology within the reconstruction analysis (Pagel *et al.* 2004). This is easily accommodated if phylogeny estimation is implemented within a Bayesian framework.

5.2 Parasitoidy on a continuum

A scientific consensus on the definition of parasitoidy does not currently exist. I adhered to the functional definition of parasitoidy following Eggleton & Belshaw (1990; 1992) to classify taxon larval feeding habits in this study. This definition states that a parasitoid is any organism which develops on or within a single host organism, using the host as an essential trophic resource which is killed, either directly or indirectly, due to parasitoid development. Using this definition led to multiple instances where my classification of specific taxa did not agree with the literature. In addition, there were multiple difficult classification decisions which I summarize here, and which highlight the ambiguity still present in this definition and the limitations of existing life history data.

Following Eggleton & Belshaw (1992), I did not classify egg predators, which develop within an egg sac and consume multiple eggs as parasitoids, though they are sometimes referred to as egg parasitoids in the literature. In addition, species within the family Sciomyzidae (snail-killing flies), which are specialized mollusc feeders, are often classified as predator/parasitoids by sciomyzid researchers due to the flexibility they exhibit in the number of prey consumed. Meaning that an individual larva may be classified as an ectoparasitoid if they receive all their nourishment from a single individual rather than multiple, even if other larvae in the same species feed on multiple prey. This behaviour is commonly observed within the sciomyzids due to the size of their prey, which are often many orders of magnitude larger than the larvae consuming them, and which could easily provide all the nourishment required for larval development. Eggleton & Belshaw (1990) address this confusion by adding a clause to their definition that parasitoidy is always an obligate life history strategy. Thus, excluding any polyphagous species which exhibit facultative predation, saprophagy, or other larval feeding

habits in addition to ‘parasitoid like behaviour’. Therefore, I classified these species as predators within my analysis. However, whether that exclusion is biologically justifiable remains unclear. The family Sciomyzidae also contains multiple obligate parasitoid species, which raises questions regarding the nature of parasitoidy and its relationship to the predator life-history strategy. For this reason, I reiterate my recommendation from *5.2 Proportional sampling and missing data* that the evolutionary history of parasitoids in the family Sciomyzidae should be investigated more extensively at the family-level, as further study could provide novel insight into parasitoid/predator transitions.

Another example of difficult classification concerns the species *Pollenia rudis* (Polleniidae) which is classified as both an ecto- and endoparasitoid in the literature depending on the larval instar. However, this species has been observed moving to a new host if its current host dies and begins decomposing, thus excluding it from a functional definition of parasitoidy for not meeting the requirement of having a ‘single host’. Consequently, I classified *P. rudis* as a predator during ASR. However, it remains an ambiguous case, as *P. rudis* also displays many characteristics of parasitoids including specialized host-seeking behaviour and a dependence on the host body cavity for survival during early instars.

The example of *P. rudis* also brought forward the issue with classifying larval feeding habits when they are not shared across larval instars. For instance, there are species in the family Muscidae which are known to proceed from saprophagy to predation during larval development, which we could call an example of obligate polyphagy (Marshall, 2012). However, making this classification requires a thorough knowledge of the life history of a species, and our knowledge of the feeding habits of many dipteran larvae are extremely limited at both the generic and species levels (and sometimes family level, as noted with Ctenostylidae). Thus, it is highly likely

that even when larval feeding habit data is present in the literature, that it is an incomplete picture of the actual species biology. In a parasitoid example, Robinson (1971) found that repeated rearing of *Megaselia* (Phoridae) led to a decrease in the number of species recorded as obligate parasitoids – which would remove them from classification as parasitoids at all under the current definition. It is important to acknowledge that errors in classification are possible as they could have a profound impact on the reconstruction of larval feeding habits and transition estimates. Unfortunately, these errors are nearly impossible to detect without extensive investigation of all species included in a study—which is entirely unrealistic at the suborder scale or in any study where the sampling exceeds ~20 species.

5.3 Model selection and assumption violations

Nucleotide substitution models are based on assumptions about sequence evolution that are frequently violated by actual biological data (Naser-Khdour *et al.*, 2019; Young and Gillung, 2020). These violations can have a large influence on the inferred tree topology. Therefore, it is important to understand the assumptions and parameters of any substitution model used to avoid violating model assumptions or introducing systematic error. In this section, I discuss the results of my investigations into model selection, parameterization, and assumption violations using the brachyceran supermatrix.

The selection of a nucleotide substitution model for phylogeny estimation can have profound impacts on the resulting tree. Frequently, the most parameter-rich model is selected, especially when using popular model selection tools such as ModelFinder (IQ-TREE; Kalyaanamoorthy *et al.*, 2017) and PartitionFinder2 (Lanfear *et al.*, 2016), as this is often assumed to be the best option when data is not a limiting factor. However, this is not always the

case, as the estimation of some parameters can introduce systematic error if they are confounded with others. During tree estimation, I implemented the GTR+G substitution model, which accounts for variation in substitution rates across sites following a gamma distribution with shape parameter α (Yang, 1994). This model was selected over the more parameter rich GTR+G+I model, which incorporates an additional parameter permitting a proportion of invariable sites (p_{inv}; Gu *et al.*, 1995). Though the GTR+G+I model is widely used, it has been criticized due to fundamental flaws in parameter assumptions (Jia *et al.*, 2014; Mayrose *et al.* 2005; Sullivan *et al.*, 1999). As the +G α parameter already accounts for a proportion of sites which evolve at such a slow rate as to appear invariable, α and p_{inv} parameters under the GTR+G+I model are correlated and cannot be independently optimized. Therefore, the GTR+G model has been recommended as an alternative which accounts for both rate variation across sites and a proportion of invariable sites without introducing systematic error (Young and Gillung 2020).

In addition to the GTR+G, I tested the GHOST heterotachy mixture model (Crotty *et al.*, 2020). Heterotachy refers to the variability of substitution rates at a given site across time or across lineages, which can impact the estimation of frequency and rate parameters, and thus phylogenetic inference (Lopez *et al.*, 2002). Heterotachy is not accounted for by most widely used substitution models, including the GTR+G, which instead allows data to be partitioned *a priori* to allow for variability in rate between partitions. However, this does not accommodate rate variability within partitions, and relies entirely on data being partitioned in a biologically relevant way (Crotty *et al.*, 2020). Unfortunately, the GHOST model was unable to estimate a phylogeny with the given dataset due to numerical instability. This suggests that the supermatrix alignment has too many taxa and not enough sites to estimate parameters reliably. However, this

could also be the result of limitations of the current version of the GHOST model, which has not been reliably tested on datasets as large as the one used in this study. This is a common problem with mixture models, which are so parameter-rich that they become computationally unreliable or inaccessible, and thus have not been widely adopted for ML inference (Crotty *et al.*, 2020).

I also investigated the presence of model assumption violations in the supermatrix alignment before phylogeny estimation by conducting three maximum matched-pair tests of symmetry as implemented in IQ-TREE. These tests removed three partitions for rejecting the assumption of stationarity, where stationarity assumes that marginal frequencies of nucleotides are constant over time. This is the most common cause of model violation according to Naser-Khdour *et al.* (2019). Notably, the three genes removed (COII, SINA, SNF) were all genes with fewer than average number of sites (1,461 total, 6% of the full alignment), and higher proportions of missing data when compared to the non-rejected gene partitions. A 'badremoved' tree was then estimated with the reduced 14-partition alignment. However, when compared with the 'complete' tree estimated with all 17 partitions, this 'badremoved' tree presented more taxa flagged as potential 'rogues' due to uncertain placement. The 'complete' tree also better supported previous hypotheses of a brachyceran phylogeny based on mitochondrial genomes (Song *et al.*, 2022). Finally, the results of an AU topology test on the two trees rejected the 'badremoved' tree as having a log-Likelihood score that was significantly worse than the 'complete' tree, and thus the 'complete' tree was used for further hypothesis testing. However, these results do not conclusively resolve the question of which topology is better supported statistically given the discordant results of the symmetry tests, topology tests and comparisons to previous phylogenetic hypotheses.

In summary, many of my attempts to avoid model assumption violations with proper model selection or statistical tests resulted in inconclusive results. In the case of the GHOST mixture model, I propose that more molecular data (loci) are needed to permit accurate estimation of model parameters. The successful implementation of this model would accommodate the presence of heterotachy in the supermatrix alignment, which we may anticipate given the broad taxonomic and temporal scale that the data currently samples. Additionally, the use of non-stationarity models could present another option for addressing the results of the symmetry tests without excluding phylogenetically relevant data (Naser-Khdour *et al.* 2019). However, there is not currently an accessible way to implement these models under ML and thus a Bayesian framework must be adopted, which may introduce new computational constraints.

5.4 Inconsistent topologies and flagged taxa

The results presented here provide a plausible hypothesis for the divergence of major clades within the Brachycera, though the two presented trees differ in the placement of some groups. Furthermore, the monophyly of many families were not recovered, which in some cases conflicts with the current scientific consensus. For example, the Bombyliidae (bee flies) have been recovered as monophyletic in previous investigations of the group (e.g. Trautwein *et al.*, 2010), but were not recovered as monophyletic in either of the presented phylogenies. There are multiple potential explanations for this, the simplest being that the topologies presented here are more biologically accurate than previous estimates and that these families are non-monophyletic. However, this seems unlikely (or at least unverifiable) given the variable placement of taxa between estimates, and the topology of the largely unplaced acalyptrates. In this section, I

present future steps for resolving these ambiguities, including increased sampling and tests to assess the legitimacy of potential rogue taxa.

It is tempting to suggest that more data is the answer to resolve poorly supported or unrecovered clades. In the case of the Brachycera, I suspect the inclusion of more genetic loci would increase overall support for the resultant topology. However, more loci were not included in this alignment due to a lack of available data. Some 'available' loci were also excluded when it was considered doubtful that their inclusion would present a net positive, given the amount of missing data they would introduce and the uneven distribution of that missing data across taxonomic groups (see Table 2). An option not pursued in this thesis is the inclusion of genomic scale data available through NCBI's Sequence Read Archive (SRA) database. The availability of this data is highly restricted to specific groups which have been the target of previous investigation (Bayless *et al.*, 2021; Buenaventura *et al.*, 2020; Gillung *et al.*, 2018; Kutty *et al.*, 2019; Li *et al.*, 2020; Pauli *et al.*, 2018; Yan *et al.*, 2020), however it is possible that even the inclusion of limited genomic data would provide increased support for the backbone of the tree(s) by providing stronger phylogenetic signal for divergences in deep time and thus, further resolving the placement of major clades which did not receive high bootstrap support in the presented trees (Fig.3, see clades diverging before the Eremoneura in the 'complete' tree). However, working with genomic data introduces new challenges, including high computational and temporal requirements, which is why the inclusion of SRA data was not pursued in the presented thesis. It is also not definitively clear whether genomic data would resolve topological ambiguities given the results of a recent transcriptomic investigation into the Schizophora—which did not greatly improve the resolution of the group (Bayless *et al.*, 2021). Another approach to increasing genetic coverage is the incorporation of full mitochondrial genomes into

the current supermatrix, as the most recent phylogenetic study of brachycera presented promising results using only mitochondrial genomes (Song *et al.,* 2022). This study had limited sampling (187 species across 40 families) and excluded several major groups due to missing data (Fig.4). However, it was largely successful in recovering major groups without the inclusion of nuclear genomic data. This study also produced six new mitochondrial genomes, including two from the family Milichiidae and one from the family Chloropidae, both of which were underrepresented in my brachyceran supermatrix. Thus, the combination of data in that study and the current presented thesis may produce a better supported topology that is suited for the testing of evolutionary hypotheses.

A complement to the increased sampling of genetic loci is increased taxon sampling. However, I am not convinced that additional taxon sampling would result in a better resolved topology of the Brachycera given the constraints discussed in the next section *5.5 Proportional sampling and missing data*. Nevertheless, changes in the composition of taxa sampled may resolve the monophyly of certain groups which were recovered as non-monophyletic with respect to taxa flagged as potential rogues. Rogue taxa are often attributed to either missing data, or long branch attraction, which is a type of systematic error where distantly related taxa are inferred to be closely related due to the large amount of change exhibited by a lineage (long branch) rather than genuine shared descent (Sanderson & Shaffer, 2002). Thus, the identification and removal of true ‘rogues’ can address systematic error in an alignment and lead to an overall increase in branch support and phylogenetic confidence. There are multiple ways to approach the assessment and removal of rogues. Trautwein *et al.* (2011) proposed a method for the identification of rogue taxa in their Bayesian inferred phylogeny of the Bombyliidae using consensus networks. They subsequently pruned rogue taxa, resulting in increased posterior

probabilities at impacted nodes. Alternatively, Song *et al.* (2022) conducted a test of compositional heterogeneity on their brachyceran dataset using pairwise Euclidean distances, and then removed taxa deemed heterogeneous from their dataset prior to phylogeny estimation. Between these two methods, the identification and removal of potential rogues prior to phylogeny estimation seems to be the more principled approach. However, the test of compositional heterogeneity implemented by Song *et al.* (2022) was conducted using unpublished *Perl* scripts from a colleague rather than a test implemented in existing inference software like IQ-TREE. Consequently, there are obstacles to the widespread implementation of this method by the scientific community.

5.5 Proportional sampling and missing data

The assumption of proportional sampling made by phylogenetic comparative methods such as ancestral state reconstruction is largely ignored in phylogenetic studies (Young and Gillung, 2020). However, even when proportional sampling is attempted, there are limitations on the level of accuracy that can be achieved due to missing data.

I aimed for proportional sampling at the family-level as there exists some level of taxonomic consensus with respect to the classification of brachyceran families that is not present at the subfamily- or generic-level for most groups. This decision was also informed by the data available, which was already extremely limited for certain families and thus, proportional sampling of finer-scale taxonomic units was considered unrealistic. Even so, three families were excluded from the final alignment due to unavailable data (Homalocnemiidae, Gobryidae, and Nothybidae), and two families were severely underrepresented in the final alignment for the same reason (Chloropidae and Milichiidae). Apart from Homalocnemiidae (Empidoidea), these

families are all acalyptrates, which were largely unplaced in both presented phylogenies. It is unclear how the proportional inclusion of these families would have impacted the resultant topologies. Given the inconclusive placement of acalyptrate groups in previous studies, I am doubtful that supplementary sampling of these families would further resolve the placement of any major groups in either the 'complete' or 'badremoved' trees. However, the Chloropidae are a family with a few known parasitoid species – thus the inclusion of those species may have impacted the results of ancestral state reconstruction.

Furthermore, I suspect that the sampling constraints imposed by proportional sampling resulted in the exclusion of additional parasitoid lineages from certain families which may have recovered further independent shifts to parasitoidy below the family level had they been more broadly sampled. Specifically, the family Sciomyzidae, which consists of a mixture of predator, ectoparasitoid, and endoparasitoid species, was sampled with only three species (1 parasitoid, 1 predator, 1 unknown). Thus, only one transition was recovered above the family level, though the current hypothesis is that multiple transitions have occurred within the group (Knutson and Vala, 2012). It is certainly possible that this single transition is biologically accurate, however given the sampling limitations imposed in this study, it is not yet possible to reject the hypothesis that there are multiple transitions within the group that would be recovered upon more targeted sampling. However, the results presented here suggest that the limit is already being met regarding the amount of available data that can be sampled without further violating the assumption of proportional sampling.

5.6 Data mining and reliability

Data mining facilitates the repurposing of existing data to answer novel scientific questions, either exclusively or as a complement to newly generated data. In this thesis, data mining of NCBI's Nucleotide database was the sole sampling method used to construct a supermatrix alignment with more comprehensive sampling than previous phylogenetic studies of the Brachycera. However, combining data from multiple sources, made available through an inconsistently maintained online database, introduced several problems with data reliability which were difficult to counteract without the implementation of non-reproducible quality control measures. In this section, I discuss the limitations of data mining given the reality of online databases, with specific commentary on the structure of NCBI's Nucleotide and Taxonomy databases.

An example of data unreliability is the presence of bycatch (non-target results), during queries for specific loci. In NCBI'S Nucleotide database, bycatch is nearly impossible to avoid entirely due to how genetic loci are reported, as sequence record metadata does not include a mandatory field for designating which gene is included in a sequence. Instead, authors often communicate the genes included in a sequence by referencing them in the title of the sequence record. Consequently, it is easy for non-target sequences to be returned if the title is ambiguous. i.e. a title that reads "Genus_sp1, mitochondrial genome excluding COI" will be returned when the database is queried for "Genus_sp1 AND COI" even though COI is not present in this sequence. It is also relatively easy for sequences to be mislabelled at the time of input due to human error. Together, these features of the NCBI database system introduce multiple issues when trying to scale up the mining of sequence data, as misidentified or contaminated sequences are nearly impossible to detect prior to sequence alignment and verification in BLAST.

Of the 3,458 sequences initially selected for inclusion in the brachyceran supermatrix, roughly 4.5% of sequences were replaced or removed due to mislabeling or contamination flagged during sequence alignment (total: n=155; by gene: 16S, n=18; 18S, n=14; 28S, n=10; AATS, n=19; CAD, n=4; COII, n=23; CYTB, n=23; EF1A, n=2; ND1, n= 3; ND3, n=4; ND5, n=30 (all); PER, n=1; PGD, n=2; SINA, n=1; SNF, n=1). I found mislabeled sequences were more common for mitochondrial genes, especially *cytochrome c oxidase subunit II* (COII), *cytochrome B* (CYTB), and *NADH dehydrogenase subunit 5* (ND5). As a result, many COII and CYTB sequences (n=23 for both) had to be removed or replaced, and ND5 was completely removed from the alignment (n=30). Using BLAST, I found many of the mislabeled sequences from these genes corresponded to other portions of the mitochondrial genome. This underlines a specific issue with how mitochondrial genes are uploaded to the Nucleotide database, as they appear to be grouped together more often than nuclear or ribosomal genes, and uploaded under single records with shared titles.

Another source of data unreliability is the assumption of correct taxonomic classification. This assumption is made at multiple levels, it is assumed that: (i) species were correctly identified before sequencing, (ii) no errors were made during sequence submission, and that (iii) NCBI's Taxonomy database (which is linked to the Nucleotide database to provide associated taxonomic data for sequence records) represents the current taxonomic consensus. The first two instances are often impossible to verify, however the correct classification of species at the family or genus level within the Taxonomy database is possible to confirm by referencing recent literature (provided a taxonomic consensus exists). However, performing this due diligence at scale is time-consuming and the manual reclassification of hundreds of species is beyond the scope of most large-scale phylogenetic studies, including this one. For taxa included in this

study, I manually updated any incorrect classifications at the family level, which became apparent during the collection of described species counts from the literature. However, it is still highly likely that the classifications of some species have been revised since their initial submission to the Nucleotide database and that a baseline level of error exists within the data which could be impacting interpretation of the resultant topology.

It is clear that the public availability of sequence data is a positive scientific advancement, as the production of new molecular data is a costly and time-consuming endeavor. However, the current structure and curation of the NCBI databases does not guarantee reliable data and thus presents an obstacle to fully reproducible data mining without reliance on manual adjustments to sequence metadata. In some ways, this is unavoidable when sourcing data from a myriad of sources. However, the implementation of a few key changes to how data is stored in this database could greatly improve user experience and facilitate the use of this data for larger scale phylogenetic studies without the introduction of systematic or human error.

6. Thesis summary and conclusion

The primary objective of this thesis was to expand our knowledge of the evolutionary origins of parasitoid species by answering the following questions using the suborder Brachycera as a model system:

1) How many independent shifts to parasitoidy have occurred?
2) From what ancestral larval feeding habit are parasitoid lineages most often derived?
3) Do evolutionary pathways to parasitoidy differ between endoparasitoid and ectoparasitoid lineages?

To address these questions, I estimated two proportionally sampled phylogenies of the Brachycera with subsets of a supermatrix alignment that I compiled using sequence data mined entirely from the NCBI's Nucleotide database. The final alignment samples 17 genetic loci and 560 ingroup taxa, representing 119 of the 122 brachyceran families currently recognized. This constitutes the largest sampling effort of the Brachycera to date. Both recovered topologies were considered plausible given existing phylogenetic hypotheses, however the Schizophora were largely unrecovered in both trees. Several ambiguously placed taxa were flagged as potential rogues and considered with caution. I conducted statistical tests to determine the best supported tree and reconstructed the larval feeding habit of all internal nodes (559) using Bayesian inference to unravel the evolutionary origin of parasitoidy.

In total, 17 independent gains of parasitoidy, and five independent losses were identified within the Brachycera. Parasitism was recovered as the most common ancestral state preceding shifts to parasitoidy. However, there is evidence that this is an artifact caused by the uneven distribution of missing data on the tree. It was not possible to reconstruct the evolutionary origins

of ecto- and endoparasitoidy separately given limitations on the number of parameters that could be reliably estimated from the data.

The results of this study greatly contribute to our understanding of the evolutionary history of parasitoidy within the Brachycera. Namely, these results support previous studies which found that multiple transitions to parasitoidy have occurred within the Brachycera, and that these convergent events are distributed evenly across the Brachycera tree of life, making them an ideal model for the continued study of parasitoid evolution. Additionally, this study recovered multiple shifts away from parasitoidy, suggesting that parasitoidy is not an evolutionary dead-end and that parasitoids may not be as morphologically or ecologically constrained as has been previously suggested. Finally, the results presented here underline the need for more extensive studies of parasitoid taxa, to overcome limitations imposed by missing or insufficient data.

Future studies should seek to increase sampling of genetic loci to address the constraints presented here, where certain methods were rendered inaccessible or unreliable when attempting to estimate parameters with insufficient molecular data. Increasing genetic coverage should also improve topological resolution and branch support in future estimations of a brachyceran phylogeny. I suggest the incorporation of mitochondrial genomes and genomic-scale nuclear data to address these issues.

Additionally, the following families should be the subject of targeted sampling of parasitoid species so that they may be included in future reconstructions of the parasitoid evolutionary history: Anthomyiidae, Asilidae, Calliphoridae, Chloropidae, Muscidae, Sarcophagidae, and Syrphidae. Bombyliidae should also be the subject of studies of natural history to further elucidate their larval feeding habits at the species level in order to reconstruct

the history of parasitoidy within the group more accurately, and to limit the concentration of missing data during future reconstructions.

The results of this study also suggest that there are limitations to working at the suborder level, given the restrictions of proportional sampling and available data. Thus, future studies should also investigate the evolutionary history of parasitoid lineages below the family level to acquire finer-scale resolution of parasitoid transitions. I suggest the family Sciomyzidae as an ideal starting point for such investigations as it is a mid-size group which is relatively well-known ecologically. It is also composed of a mixture of predator and obligate parasitoid species that could provide unique insights into the transitions between these two life-history strategies.

In conclusion, this study contributes novel insights into the evolutionary history of parasitoids within the suborder Brachcyera and confirms that they are a suitable model system for the continued study of parasitoid evolution. The results presented here also bring attention to specific areas in need of further investigation and underline the importance of the continued study of parasitoids, which remain largely unknown despite being an ecologically important and diverse group.

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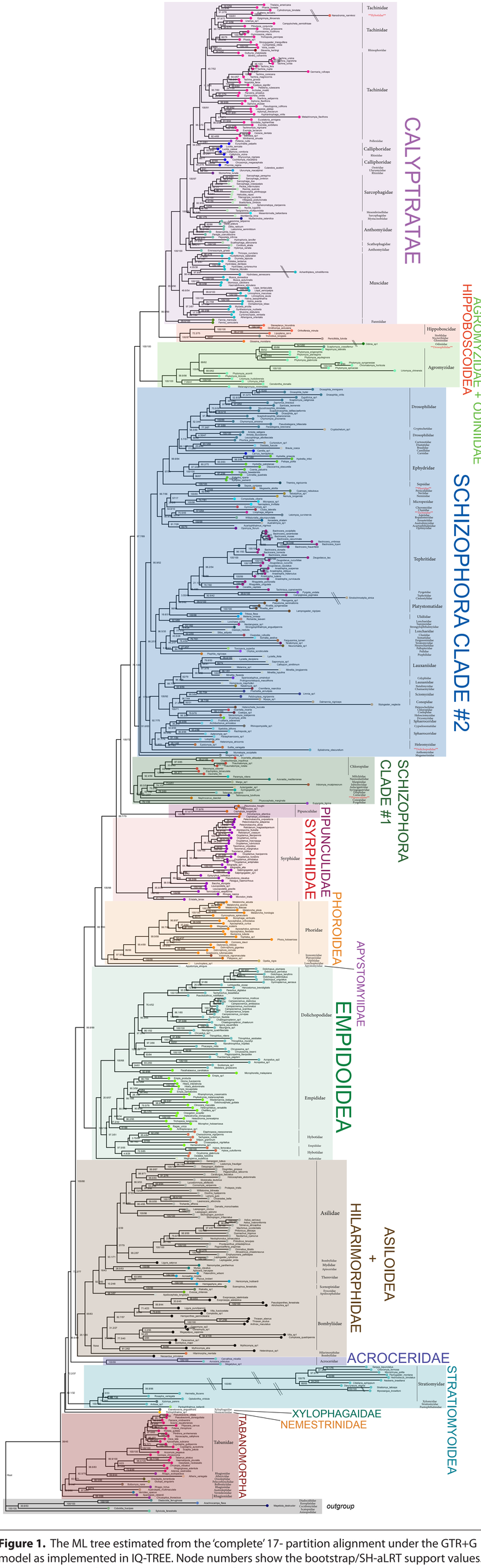

Figure 1. The ML tree estimated from the 'complete' 17- partition alignment under the GTR+G model as implemented in IQ-TREE. Node numbers show the bootstrap/SH-aLRT support values. Points at the end of branches are coloured by family to make distinguishing lineages more accessible.

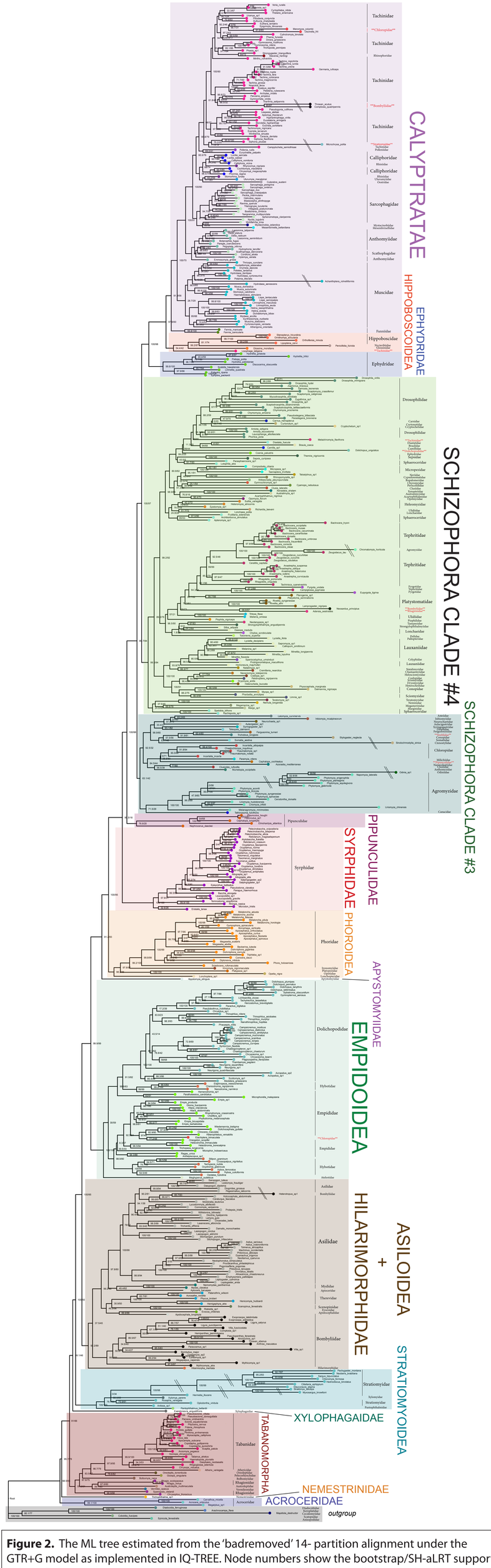

Figure 2. The ML tree estimated from the 'badremoved' 14- partition alignment under the GTR+G model as implemented in IQ-TREE. Node numbers show the bootstrap/SH-aLRT support values. Points at the end of branches are coloured by family to make distinguishing lineages more accessible.

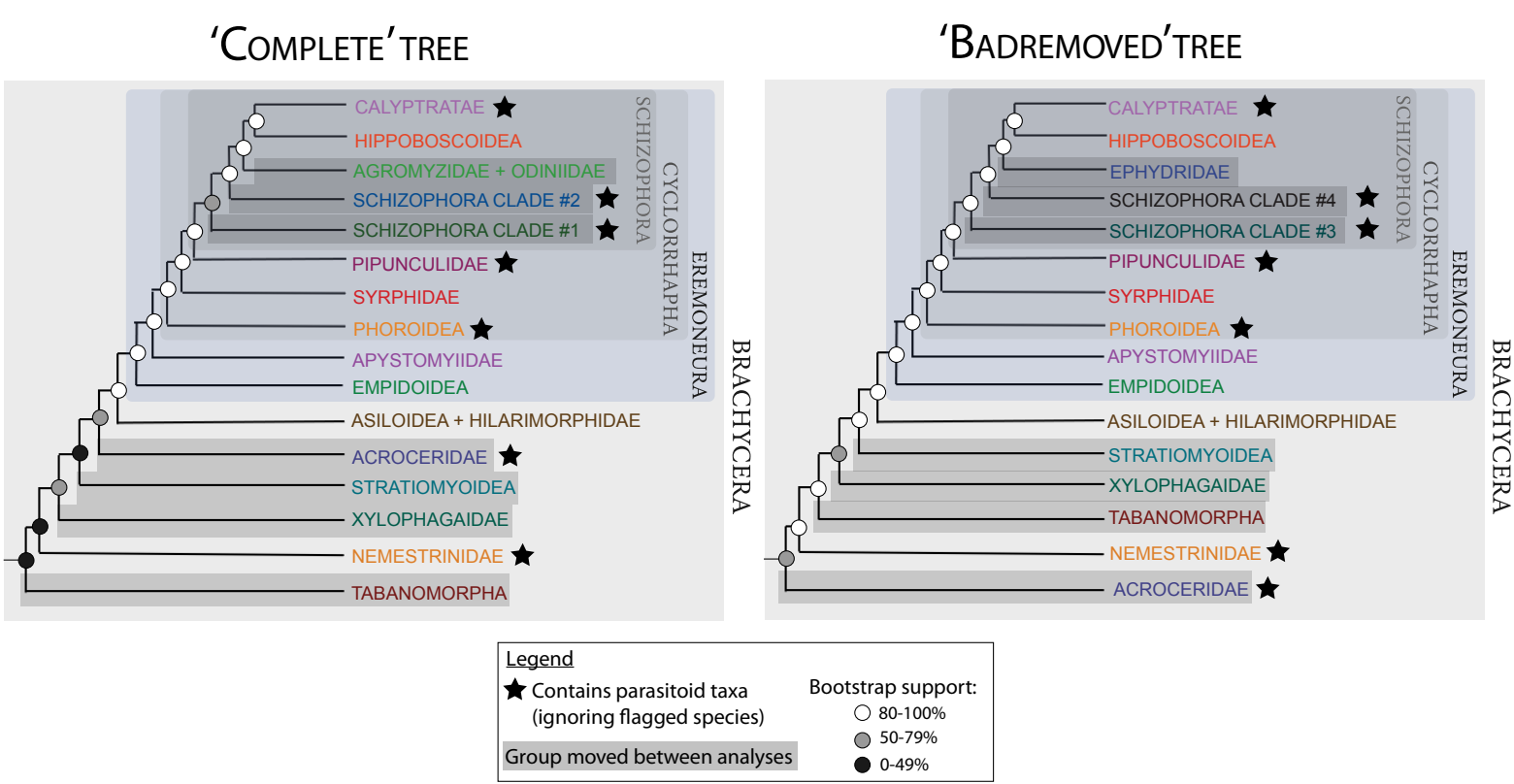

Figure 3. Topological summary of the relationships between major groups in the suborder Brachcyera as recovered in this study. **A**, 'Complete' tree, estimated from the full 17-partition alignment; **B**, 'Badremoved' tree, estimated from the14-partition subset alignment.

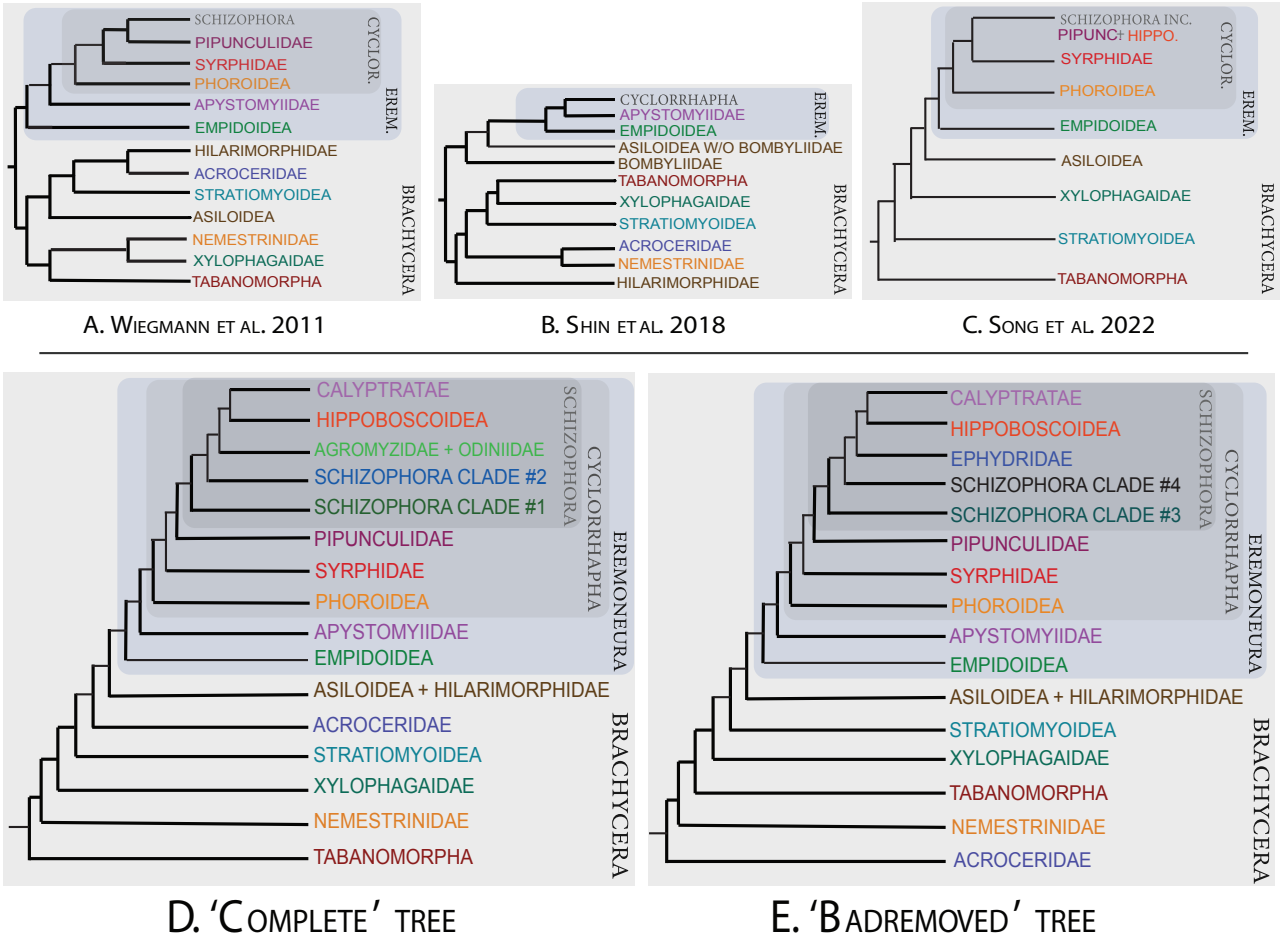

Figure 4. Topological summary of phylogenetic hypotheses for the relationships among major groups in the suborder Brachycera (Diptera) based on molecular data. **A**, Wiegmann *et al.*, 2011; **B**, Shin *et al.*, 2018; **C**, Song *et al.*, 2022; **D**, 'Complete' tree, newly presented. Estimated from the full 17-partition alignment; **E**, 'Badremoved' tree, newly presented. Estimated from the14-partition subset alignment.

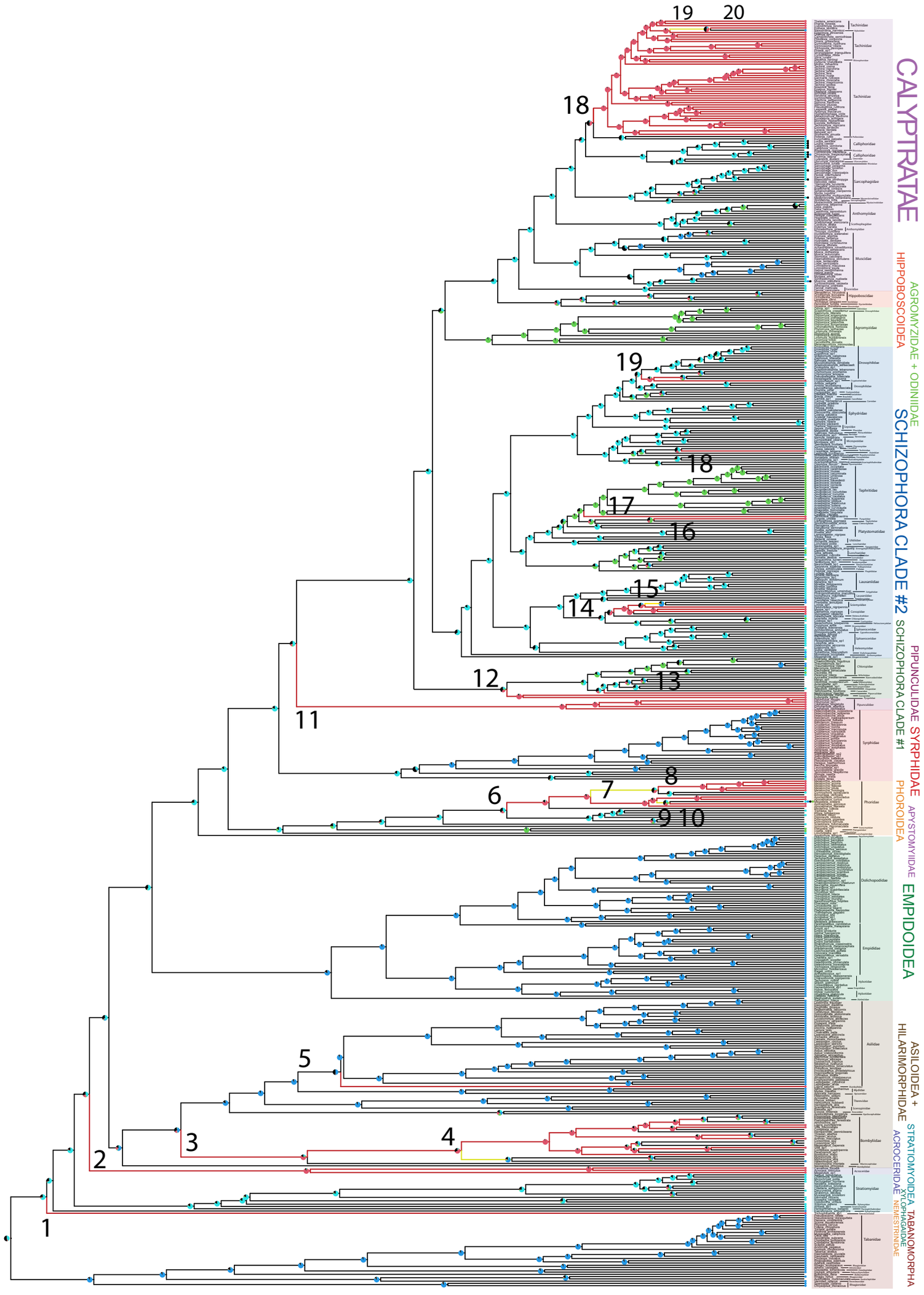

Figure 5. Bayesian ancestral state reconstruction of larval feeding habits. Pie charts on each node and terminal indicate posterior probability of state being present in the ancestor at that node: blue indicates predator, green indicates phytophage; cyan indicates sarprophage, black indicates parasite, and red indicates parasitoid. Branch colours indicate transitions to and from parasitoidy: red indicates a gain (and all parasitoid lineages derived from that gain); yellow indicates a loss. Transitions are numbered following Table 6.

Appendix 1: List of families currently recognized in the suborder Brachycera with number of described species and sampling targets for the current study (0.5% of described species, plus 1 for all families where 0.5% rounds to zero).

Unranked taxon	Unranked taxon	Infraorder	Unranked taxon	Superfamily	Family	Described species (#)	Sampling targets	Source	Classification notes
				Nemestrinoidea	Nemestrinidae	275	1	Kirk-Spriggs & Sinclair, 2017	
				Nemestrinoidea	Acroceridae	530	3	Gillung & Winterton, 2019	
					Hilarimorphidae	36	1	Pape *et al.*, 2011	
					Vermileonidae	61	1	Kirk-Spriggs & Sinclair, 2017	
				Asiloidea	Bombyliidae	4500	23	Kirk-Spriggs & Sinclair, 2017	Includes Mythicomyiidae (not supported as a family in Trautwein *et al.*, 2010), all Mythicomyiidae records manually changed to Bombyliidae
				Asiloidea	Asilidae	7600	38	Kirk-Spriggs & Sinclair, 2017	
				Asiloidea	Mydidae	476	2	Kirk-Spriggs & Sinclair, 2017	
				Asiloidea	Apioceridae	143	1	Kirk-Spriggs & Sinclair, 2017	
				Asiloidea	Evocoidae	1	1	Winterton & Ware, 2015	Includes records classified within Ocoidae, which is the name that predates Evocoidae (Yeates *et al.*, 2003), all Ocoidae records manually changed to Evocoidae
				Asiloidea	Apsilocephalidae	4	1	Winterton & Ware, 2015; Zhang *et al.*, 2018	
				Asiloidea	Scenopinidae	420	2	Kirk-Spriggs & Sinclair, 2017; Winterton & Ware, 2015	
				Asiloidea	Therevidae	1170	6	Kirk-Spriggs & Sinclair, 2017; Winterton & Ware, 2015	
				Stratiomyoidea	Pantophthalmidae	20	1	Pape *et al.*, 2011	Also spelled Panthophthalmidae
				Stratiomyoidea	Stratiomyidae	2,850	1	Kirk-Spriggs & Sinclair, 2017	
				Stratiomyoidea	Xylomyidae	138	4	Woodley, 2017	
		Tabanomorpha		Rhagionoidea	Austroleptidae	8	1	Pape *et al.*, 2011	
		Tabanomorpha		Rhagionoidea	Bolbomyiidae	4	14	Pape *et al.*, 2011	In NCBI's Nucleotide database as Bolbomyia (Rhagionidae) but has since been elevated from Rhagionidae (Kerr, 2010), all Bolbomyia records manually changed to Bolbomyiidae
		Tabanomorpha		Rhagionoidea	Rhagionidae	700	1	Kirk-Spriggs & Sinclair, 2017	
		Tabanomorpha		Tabanoidea	Athericidae	100	1	Woodley, 2017	
		Tabanomorpha		Tabanoidea	Oreoleptidae	1	1	Pape *et al.*, 2011; Zloty *et al.*, 2005	
		Tabanomorpha		Tabanoidea	Pelecorhynchidae	49	1	Pape *et al.*, 2011	
		Tabanomorpha		Tabanoidea	Tabanidae	4500	23	Kirk-Spriggs & Sinclair, 2017	
				Xylophagoidea	Xylophagaidae	133	1	Brown *et al.*, 2010	Often spelled Xylophagidae
Eremoneura				Empidoidea	Atelestidae	22	1	Pape *et al.*, 2011; Kirk-Spriggs & Sinclair, 2017	
Eremoneura				Empidoidea	Dolichopodidae	7700	39	Kirk-Spriggs & Sinclair, 2017	
Eremoneura				Empidoidea	Empididae	5000	25	Brown *et al.*, 2010	
Eremoneura				Empidoidea	Homalocnemiidae	7	1	Pape *et al.*, 2011	
Eremoneura				Empidoidea	Hybotidae	2005	10	Pape et al., 2011; Kirk-Spriggs & Sinclair, 2017	
Eremoneura				Apystomyioidea	Apystomyiidae	1	1	Pape *et al.*, 2011	In NCBI's Nucleotide database as Hilarimorphidae, all Apystomyia (single extant genus) records manually changed to Apystomyiidae
Eremoneura	Cyclorrhapha			Phoroidea	Lonchopteridae	65	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha			Phoroidea	Opetiidae	10	1	Pape *et al.*, 2011	In NCBI's Nucleotide database as Opetiinae (Platypezidae) but referenced as Opetiidae in (Stahls, 2014) and (Bayless et al. 2020), all Opetiinae records manually changed to Opetiidae
Eremoneura	Cyclorrhapha			Phoroidea	Platypezidae	277	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha			Phoroidea	Ironomyiidae	17	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha			Phoroidea	Phoridae	4202	21	Pape *et al.*, 2011	Includes Sciadoceridae (rejected as a family in Disney, 2001), all Sciadoceridae records manually changed to Phoridae
Eremoneura	Cyclorrhapha			Syrphoidea	Pipunculidae	1428	7	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha			Syrphoidea	Syrphidae	6200	31	Young et al. 2016	
Eremoneura	Cyclorrhapha	Schizophora		Conopoidea	Conopidae	831	4	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Carnoidea	Australimyzidae	9	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Carnoidea	Canacidae	323	2	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Carnoidea	Carnidae	92	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Carnoidea	Chloropidae	2885	14	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Carnoidea	Inbiomyiidae	11	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Carnoidea	Milichiidae	360	2	Swann, 2016	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Carnoidea	Nannodastiidae	5	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Ephydroidea	Ephydridae	1994	10	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Ephydroidea	Drosophilidae	4017	20	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Ephydroidea	Braulidae	7	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Ephydroidea	Cryptochetidae	34	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Ephydroidea	Camillidae	42	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Ephydroidea	Curtonotidae	65	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Ephydroidea	Diastatidae	59	1	Pape *et al.*, 2011	Includes Campichoetidae (not supported in Brown *et al.*, 2010), all Campichoetidae records manually changed to Diastatidae
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Lauxanioidea	Celyphidae	115	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Lauxanioidea	Chamaemyiidae	351	2	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Lauxanioidea	Lauxaniidae	1900	10	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Nerioidea	Cypselosomatidae	35	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Nerioidea	Micropezidae	583	3	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Nerioidea	Neriidae	112	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Opomyzoidea	Acartophthalmidae	6	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Opomyzoidea	Agromyzidae	3017	15	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Opomyzoidea	Anthomyzidae	95	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Opomyzoidea	Asteiidae	138	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Opomyzoidea	Aulacigastridae	19	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Opomyzoidea	Clusiidae	363	2	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Opomyzoidea	Fergusoninidae	29	1	Pape *et al.*, 2011; Scheffer *et al.*, 2017	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Opomyzoidea	Marginidae	3	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Opomyzoidea	Megamerinidae	16	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Opomyzoidea	Neminidae	14	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Opomyzoidea	Neurochaetidae	22	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Opomyzoidea	Odiniidae	65	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Opomyzoidea	Opomyzidae	61	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Opomyzoidea	Pallopteridae	71	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Opomyzoidea	Periscelididae	91	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Opomyzoidea	Teratomyzidae	8	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Opomyzoidea	Xenasteiidae	13	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Sciomyzoidea	Coelopidae	35	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Sciomyzoidea	Dryomyzidae	30	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Sciomyzoidea	Helcomyzidae	12	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Sciomyzoidea	Helosciomyzidae	23	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Sciomyzoidea	Heterocheilidae	2	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Sciomyzoidea	Natalimyzidae	1	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Sciomyzoidea	Ropalomeridae	33	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Sciomyzoidea	Sciomyzidae	618	3	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Sciomyzoidea	Sepsidae	345	2	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Sphaeroceroidea	Chyromyidae	139	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Sphaeroceroidea	Heleomyzidae	738	4	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Sphaeroceroidea	Heteromyzidae	7	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Sphaeroceroidea	Mormotomyiidae	1	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Sphaeroceroidea	Sphaeroceridae	1571	8	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Tanypezoidea	Diopsidae	194	1	Pape *et al.*, 2011	

Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Tanypezoidea	Gobryidae	5	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Tanypezoidea	Nothybidae	8	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Tanypezoidea	Psilidae	322	2	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Tanypezoidea	Somatiidae	7	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Tanypezoidea	Syringogastridae	10	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Tanypezoidea	Strongylophthalmyiidae	45	1	Barber, 2006	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Tanypezoidea	Tanypezidae	68	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Tephritoidea	Richardiidae	178	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Tephritoidea	Lonchaeidae	504	3	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Tephritoidea	Piophilidae	83	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Tephritoidea	Ulidiidae	678	3	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Tephritoidea	Platystomatidae	1164	6	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Tephritoidea	Ctenostylidae	10	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Tephritoidea	Pyrgotidae	351	2	Brown *et al.*, 2010; Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Acalyptratae	Tephritoidea	Tephritidae	4716	24	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Calyptratae	Hippoboscoidea	Glossinidae	25	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Calyptratae	Hippoboscoidea	Hippoboscidae	782	4	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Calyptratae	Hippoboscoidea	Nycteribiidae	274	1	Brown *et al.*, 2010	
Eremoneura	Cyclorrhapha	Schizophora	Calyptratae	Hippoboscoidea	Streblidae	237	1	Soares *et al.*, 2013	
Eremoneura	Cyclorrhapha	Schizophora	Calyptratae	Muscoidea	Fanniidae	359	2	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Calyptratae	Muscoidea	Muscidae	5000	25	Kutty *et al.*, 2014	
Eremoneura	Cyclorrhapha	Schizophora	Calyptratae	Muscoidea	Anthomyiidae	1941	10	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Calyptratae	Muscoidea	Scathophagidae	419	2	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Calyptratae	Oestroidea	Calliphoridae	1525	8	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Calyptratae	Oestroidea	Mesembrinellidae	36	1	Marinho *et al.*, 2017	In NCBI'S Nucleotide database as Mesembrinellinae (Calliphoridae) but family supported in (Buenaventura *et al.*, 2020), all Mesembrinellinae records manually changed to Mesembrinellidae
Eremoneura	Cyclorrhapha	Schizophora	Calyptratae	Oestroidea	Mystacinobiidae	1	1	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Calyptratae	Oestroidea	Oestridae	176	1	Brown *et al.*, 2010; Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Calyptratae	Oestroidea	Polleniidae	145	1	Cerretti *et al.*, 2019	
Eremoneura	Cyclorrhapha	Schizophora	Calyptratae	Oestroidea	Rhiniidae	376	2	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Calyptratae	Oestroidea	Rhinophoridae	174	1	Brown *et al.*, 2010; Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Calyptratae	Oestroidea	Sarcophagidae	3094	15	Pape *et al.*, 2011	
Eremoneura	Cyclorrhapha	Schizophora	Calyptratae	Oestroidea	Tachinidae	10000	50	Stireman *et al.*, 2006; Stireman *et al.*, 2019	
Eremoneura	Cyclorrhapha	Schizophora	Calyptratae	Oestroidea	Ulurumyiidae	1	1	Michelsen & Pape, 2017	

Appendix 2: Taxa and genes sampled with accession numbers corresponding to sequence records in NCBI's Nucleotide database.

Family	Binomial name	Chimera	12S	16S	18S	28S	AATS	CAD	COI	COII	cytB	EF1A	ND1	ND3	PER	PGD	SINA	SNF	TPI
Scatopsidae	Coboldia fuscipes	NA	KJ136692	KJ136727	KC177282	KJ136764	KC178154	FJ040623	MZ723346	KC192986	NA	NA	KC176854	NA	NA	FJ040730	KC178367	KC177054	FJ040678
Anisopodidae	Sylvicola fenestralis	NA	KC177473	NA	KC177287	KC177637	KC178141	FJ040627	HM432769	AF547667	NA	NA	NA	KC176814	KC178048	FJ040729	KC178329	KC177059	FJ040677
Keroplatidae	Arachnocampa flava	NA	KC177467	AY576351	KC177277	KC177644	NA	FJ040615	NA	AY575705	NA	NA	NA	KC176808	NA	FJ040725	KC178335	KC177051	KC177874
Cecidomyiidae	Mayetiola destructor	NA	AY460205	LC228121	KC177284	KC177649	KC178152	MN191457	JN638239	NA	AF488423	NA	NA	NA	NA	FJ040727	NA	NA	FJ040679
Diadocidiidae	Diadocidia ferruginosa	NA	KC435526	MG554126	KP288786	KC177641	KC178145	KC178394	MZ632888	NA	KC435680	NA	NA	NA	NA	FJ040694	NA	NA	FJ040688
Nemestrinidae	Trichophthalma sp1	NA	NA	NA	NA	KC177695	KC178198	KC177140	NA	NA	NA	NA	NA	NA	NA	KC177363	NA	NA	KC177925
Acroceridae	Acrocera orbiculus	NA	NA	AY140863	NA	AY144414	NA	AF539893	DQ631983	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Acroceridae	Carvalhoa micella	NA	NA	MH793692	NA	MH793700	NA	MK002243	MK002274	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Acroceridae	Megalybus sp1	NA	NA	AY140874	NA	AY144429	NA	AF539885	DQ631974	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Hilarimorphidae	Hilarimorpha mentata	NA	NA	NA	NA	KC177709	KC178211	KC177145	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	KC177938
Vermileonidae	Vermileo opacus	NA	NA	NA	NA	KC177686	KC178189	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	KC177916
Bombyliidae	Bombylius major	NA	KC177474	KC177450	EF650090	KC177708	KC178210	AY280675	KC192961	KC192985	KC177585	EU414683	KC176838	KC176815	KC178051	NA	KC178366	KC177062	KC177937
Bombyliidae	Neosardus principius	NA	NA	NA	NA	HM183042	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Bombyliidae	Villa sp1	NA	NA	AF456846	NA	AF456858	NA	NA	NA	NA	NA	NA	NA	AF484027	NA	NA	NA	NA	NA
Bombyliidae	Hemipenthes jaennickeana	NA	NA	AY325005	AY325036	AY325067	NA	NA	NA	AY325098	NA	NA	NA	NA	NA	NA	NA	NA	NA
Bombyliidae	Mythicomyia sp1	NA	NA	NA	NA	KC177706	KC178208	KC177143	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	KC177935
Bombyliidae	Paracosmus sp1	NA	NA	NA	NA	KC177707	KC178209	NA	NA	NA	NA	NA	NA	NA	NA	KC177371	NA	NA	KC177936
Bombyliidae	Megapalpus capensis	NA	NA	NA	NA	NA	NA	NA	KC562074	KC562107	NA	KC562140	NA	NA	NA	NA	NA	NA	NA
Bombyliidae	Corsomyza sp1	NA	NA	NA	NA	NA	NA	NA	KC562069	KC562102	NA	KC562135	NA	NA	NA	NA	NA	NA	NA
Bombyliidae	Corsomyza sp2	NA	NA	NA	NA	NA	NA	NA	KC562070	KC562103	NA	KC562136	NA	NA	NA	NA	NA	NA	NA
Bombyliidae	Pseudopenthes fenestrata	NA	NA	AJ391527	NA	NA	NA	NA	NA	NA	NA	NA	AJ391527	NA	NA	NA	NA	NA	NA
Bombyliidae	Ligyra satyrus	NA	NA	AJ391526	NA	NA	NA	NA	NA	NA	NA	NA	AJ391526	NA	NA	NA	NA	NA	NA
Bombyliidae	Heterotropus sp1	NA	NA	NA	NA	AY279198	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Bombyliidae	Thraxan acutus	NA	NA	AJ391516	NA	NA	NA	NA	NA	NA	NA	NA	AJ391516	NA	NA	NA	NA	NA	NA
Bombyliidae	Exoprosopa latelimbata	NA	NA	AJ391518	NA	NA	NA	NA	NA	NA	NA	NA	AJ391518	NA	NA	NA	NA	NA	NA
Bombyliidae	Atrichochira sp1	NA	NA	AJ391528	NA	NA	NA	NA	NA	NA	NA	NA	AJ391528	NA	NA	NA	NA	NA	NA
Bombyliidae	Ligyra punctipennis	NA	NA	AJ391523	NA	NA	NA	NA	NA	NA	NA	NA	AJ391523	NA	NA	NA	NA	NA	NA
Bombyliidae	Villa fuscicostata	NA	NA	AJ391529	NA	NA	NA	NA	NA	NA	NA	NA	AJ391529	NA	NA	NA	NA	NA	NA
Bombyliidae	Mythicomyia atra	NA	NA	NA	U65158	U65212	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Bombyliidae	Anthrax maculatus	NA	NA	AJ391514	NA	NA	NA	NA	HQ945435	NA	NA	NA	AJ391514	NA	NA	NA	NA	NA	NA
Bombyliidae	Comptosia quadripennis	NA	NA	AJ391511	NA	NA	NA	NA	NA	NA	NA	NA	AJ391511	NA	NA	NA	NA	NA	NA
Bombyliidae	Thraxan ebenus	NA	NA	AJ391517	NA	NA	NA	NA	NA	NA	NA	NA	AJ391517	NA	NA	NA	NA	NA	NA
Bombyliidae	Exoprosopa adelaidica	NA	NA	AJ391519	NA	NA	NA	NA	NA	NA	NA	NA	AJ391519	NA	NA	NA	NA	NA	NA
Asilidae	Lasiopogon cinctus	NA	NA	NA	EF650102	EF650189	MG189305	EF650341	KT733400	NA	NA	EF650415	NA	NA	NA	NA	NA	NA	NA
Asilidae	Machimus occidentalis	NA	NA	NA	EF650157	EF650250	EF650278	EF650395	JN289688	NA	NA	EF650466	NA	NA	NA	NA	NA	NA	NA
Asilidae	Philonicus albiceps	NA	NA	NA	EF650124	EF650216	EF650279	EF650368	KT733427	NA	NA	EF650440	NA	NA	NA	NA	NA	NA	NA
Asilidae	Asilus crabroniformis	NA	KC177475	KC177451	KC177289	KC177704	KC178206	EF650383	KC192962	KC192983	KC177586	EF650454	KC176839	KC176816	KC178050	KC177507	KC178340	KC177061	KC177933
Asilidae	Diogmites grossus	NA	NA	AY324988	AY325019	EF650246	EF650282	EF650391	MG967752	AY325081	NA	EF650475	NA	NA	NA	NA	NA	NA	NA
Asilidae	Stichopogon trifasciatus	NA	NA	AY324989	EF650175	EF650256	KY906302	EF650399	KY914518	AY325082	NA	EF650471	NA	NA	NA	NA	NA	NA	NA
Asilidae	Afroestricus chiastoneurus	NA	NA	NA	EF650120	EF650210	EF650301	EF650360	KT733200	NA	NA	EF650434	NA	NA	NA	NA	NA	NA	NA
Asilidae	Asilus sericeus	NA	NA	NA	EF650138	EF650236	EF650276	EF650384	JN289750	NA	NA	EF650455	NA	NA	NA	NA	NA	NA	NA
Asilidae	Choerades bella	NA	NA	NA	EF650110	EF650198	EF650290	EF650348	KT733173	NA	NA	EF650424	NA	NA	NA	NA	NA	NA	NA
Asilidae	Connomyia varipennis	NA	NA	NA	EF650128	EF650220	EF650304	EF650369	KT733202	NA	NA	EF650444	NA	NA	NA	NA	NA	NA	NA
Asilidae	Damalis monochaetes	NA	NA	NA	EF650149	EF650260	EF650318	EF650403	KT733097	NA	NA	EF650473	NA	NA	NA	NA	NA	NA	NA
Asilidae	Dasypogon diadema	NA	NA	NA	EF650103	EF650190	EF650281	EF650342	NC_045239	NA	NA	EF650416	NA	NA	NA	NA	NA	NA	NA
Asilidae	Dioctria hyalipennis	NA	NA	NA	EF650143	EF650244	KY906300	EF650390	KY914516	NA	NA	EF650461	NA	NA	NA	NA	NA	NA	NA
Asilidae	Dysmachus trigonus	NA	NA	NA	EF650156	EF650214	EF650277	EF650366	KT733425	NA	NA	EF650438	NA	NA	NA	NA	NA	NA	NA
Asilidae	Emphysomera pallidapex	NA	NA	NA	EF650139	EF650239	EF650300	EF650387	KT733227	NA	NA	EF650457	NA	NA	NA	NA	NA	NA	NA
Asilidae	Holcocephala abdominalis	NA	NA	AY324999	EF650131	EF650224	NA	KM879072	MN411228	AY325092	NA	NA	NA	NA	NA	NA	NA	NA	NA
Asilidae	Lamyra gulo	NA	NA	NA	EF650161	EF650258	EF650291	EF650401	KT733095	NA	NA	EF650476	NA	NA	NA	NA	NA	NA	NA
Asilidae	Lasiopogon aldrichii	NA	NA	NA	EF650174	EF650248	MG189364	EF650393	MG189011	NA	NA	EF650464	NA	NA	NA	NA	NA	NA	NA
Asilidae	Laxenecera albicincta	NA	NA	NA	EF650118	EF650208	EF650292	EF650358	KT733429	NA	NA	EF650432	NA	NA	NA	NA	NA	NA	NA
Asilidae	Leptogaster arida	NA	NA	NA	EF650135	EF650229	EF650298	EF650362	KT733213	NA	NA	EF650451	NA	NA	NA	NA	NA	NA	NA
Asilidae	Leptogaster cylindrica	NA	NA	NA	EF650101	EF650188	EF650299	EF650339	MN411149	NA	NA	EF650414	NA	NA	NA	NA	NA	NA	NA
Asilidae	Lestomyia fraudiger	NA	NA	NA	EF650132	EF650226	EF650283	EF650376	KT733207	NA	NA	EF650448	NA	NA	NA	NA	NA	NA	NA
Asilidae	Lycostommyia albifacies	NA	NA	NA	EF650116	EF650205	EF650306	EF650356	KT733185	NA	NA	EF650430	NA	NA	NA	NA	NA	NA	NA

Asilidae	Molobratia teutonus	NA	NA	NA	EF650136	EF650234	EF650284	EF650382	MN868906	NA	NA	EF650453	NA	NA	NA	NA	NA	NA	NA
Asilidae	Neoitamus cyanurus	NA	NA	NA	EF650176	EF650263	EF650327	EF650405	KT733195	NA	NA	EF650479	NA	NA	NA	NA	NA	NA	NA
Asilidae	Neolophonotus bimaculatus	NA	NA	NA	EF650107	EF650195	EF650271	EF650345	KT733127	NA	NA	EF650421	NA	NA	NA	NA	NA	NA	NA
Asilidae	Ommatius tibialis	NA	NA	NA	EF650147	EF650253	EF650302	EF650397	KT733263	NA	NA	EF650469	NA	NA	NA	NA	NA	NA	NA
Asilidae	Pegesimallus laticornis	NA	NA	NA	EF650111	EF650200	EF650285	EF650350	KT733414	NA	NA	EF650425	NA	NA	NA	NA	NA	NA	NA
Asilidae	Philodicus tenuipes	NA	NA	NA	EF650152	EF650213	EF650272	EF650364	KT733421	NA	NA	EF650437	NA	NA	NA	NA	NA	NA	NA
Asilidae	Pogonioefferia pogonias	NA	NA	NA	EF650153	EF650230	EF650273	EF650378	KT733435	NA	NA	EF650452	NA	NA	NA	NA	NA	NA	NA
Asilidae	Proctacanthus philadelphicus	NA	NA	NA	EF650154	EF650225	EF650274	EF650375	KT733434	NA	NA	EF650447	NA	NA	NA	NA	NA	NA	NA
Asilidae	Prolepsis tristis	NA	NA	NA	EF650168	EF650243	EF650308	EF650389	KT733448	NA	NA	EF650478	NA	NA	NA	NA	NA	NA	NA
Asilidae	Saropogon luteus	NA	NA	NA	EF650133	EF650227	EF650286	EF650377	KT733210	NA	NA	EF650449	NA	NA	NA	NA	NA	NA	NA
Asilidae	Stichopogon punctum	NA	NA	NA	EF650121	EF650211	EF650315	EF650361	KT733193	NA	NA	EF650435	NA	NA	NA	NA	NA	NA	NA
Asilidae	Tolmerus atricapillus	NA	NA	NA	EF650123	EF650215	EF650280	EF650367	KT733426	NA	NA	EF650439	NA	NA	NA	NA	NA	NA	NA
Asilidae	Trichardis effrena	NA	NA	NA	EF650113	EF650202	EF650296	EF650352	KT733179	NA	NA	EF650427	NA	NA	NA	NA	NA	NA	NA
Asilidae	Willistonina bilineata	NA	NA	NA	EF650173	EF650257	EF650312	EF650400	MN411139	NA	NA	EF650472	NA	NA	NA	NA	NA	NA	NA
Asilidae	Ceraturgus fasciatus	NA	NA	NA	EF650165	EF650252	NA	EF650396	MG967773	NA	NA	EF650468	NA	NA	NA	NA	NA	NA	NA
Mydidae	Mydas clavatus	NA	NA	AY324983	AY325014	KC177702	EF650269	KM879079	KM923945	KU890287	NA	EF650413	NA	NA	NA	KC177368	NA	NA	NA
Mydidae	Nemomydas pantherinus	NA	NA	NA	NA	AF266255	NA	KU890526	KU889868	KU890217	NA	NA	NA	NA	NA	KU890669	NA	KU890631	NA
Apioceridae	Apiocera haruspex	NA	NA	NA	NA	KC177703	KC178205	KC178399	KU890096	KU890250	NA	NA	NA	NA	NA	KC177369	NA	NA	KC177932
Evocoidae	Evocoa chilensis	NA	NA	KM878914	KM878989	KC177700	KC178202	KM879049	KM923934	NA	NA	NA	NA	NA	NA	KC177366	NA	NA	KC177930
Apsilocephalidae	Apsilocephala longistyla	NA	NA	KM878901	EF650092	EF650179	NA	KM879048	KM923929	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Scenopinidae	Riekiella sp1	y	NA	KM878956	KM879028	NA	NA	KM879100	KM923957	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Scenopinidae	Scenopinus fenestralis	NA	NA	AY325007	AY325038	AY325069	NA	KM879108	KM923961	AY325100	NA	NA	NA	NA	NA	NA	NA	NA	NA
Therevidae	Acrosathe novella	NA	NA	DQ250815	KC177296	KC177699	NA	KC178397	NA	NA	NA	NA	NA	NA	KC178056	KC177506	KC178354	KC177067	KC177929
Therevidae	Henicomyia hubbardi	NA	NA	KM878916	KM878991	AF147828	NA	KM879114	KM923935	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Therevidae	Patanothrix wilsoni	NA	NA	KM878941	KM879014	KT290118	NA	KM879086	KM923949	NA	NA	AF150975	NA	NA	NA	NA	NA	NA	NA
Therevidae	Hemigephyra atra	NA	NA	KM878915	EF650097	EF650184	EF650266	KM879113	NA	NA	NA	EF650410	NA	NA	NA	NA	NA	NA	NA
Therevidae	Phycus kroberi	NA	NA	NA	NA	KC177698	KC178201	KC177142	NA	NA	NA	NA	NA	NA	NA	KC177365	NA	NA	KC177928
Austroleptidae	Austroleptis multimaculata	NA	NA	NA	NA	DQ415524	NA	NA	MG968215	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Bolbomyiidae	Bolbomyia nana	NA	NA	NA	NA	KC177689	KC178192	KC177137	KT606311	NA	NA	NA	NA	NA	NA	NA	NA	NA	KC177919
Rhagionidae	Spaniopsis clelandi	NA	NA	NA	NA	DQ415537	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Rhagionidae	Chrysopilus thoracicus	NA	NA	NA	NA	KC177688	KC178191	KC177136	MG967784	NA	NA	NA	NA	NA	NA	KC177359	NA	NA	KC177918
Rhagionidae	Rhagio hirtus	NA	NA	NA	NA	KC177687	KC178190	KC177135	NA	NA	NA	NA	NA	NA	NA	KC177358	NA	NA	KC177917
Rhagionidae	Rhagio scolopaceus	NA	NA	NA	NA	NA	NA	MG823547	MG823462	NA	MG823632	MG823694	NA	NA	NA	NA	NA	NA	NA
Pantophthalmidae	Pantophthalmus bellardii	NA	NA	NA	NA	KC177680	KC178183	NA	NA	NA	NA	NA	NA	NA	NA	KC177355	NA	NA	KC177910
Stratiomyidae	Myxosargus knowltoni	NA	NA	NA	NA	DQ168745	NA	NA	MG967899	NA	NA	DQ168676	NA	NA	NA	NA	NA	NA	NA
Stratiomyidae	Hermetia illucens	NA	KC177478	KC177455	KC177295	KC177682	KC178185	NA	NC_035232	KC192996	KC177589	DQ168685	KC176842	KC176819	KC178055	KC177496	KC178353	KC177066	KC177912
Stratiomyidae	Chloromyia formosa	NA	GU947418	GU947385	NA	DQ168802	NA	NA	MN411274	NA	NA	DQ168733	NA	NA	NA	NA	NA	NA	NA
Stratiomyidae	Clitellaria ephippium	NA	GU947432	GU947399	NA	DQ168777	NA	NA	NA	NA	NA	DQ168708	NA	NA	NA	NA	NA	NA	NA
Stratiomyidae	Sargus bipunctatus	NA	GU947409	GU947376	NA	NA	NA	NA	KR433261	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Stratiomyidae	Microchrysa polita	NA	GU947408	GU947375	NA	NA	NA	NA	JN302035	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Stratiomyidae	Antissa sp1	NA	NA	AY140891	NA	NA	NA	AF539870	DQ631992	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Stratiomyidae	Dieuryneura stigma	NA	NA	NA	NA	DQ168768	NA	NA	MG968217	NA	NA	DQ168699	NA	NA	NA	NA	NA	NA	NA
Stratiomyidae	Pachygaster montana	NA	NA	NA	NA	DQ168803	NA	NA	JF871863	NA	NA	DQ168734	NA	NA	NA	NA	NA	NA	NA
Stratiomyidae	Neoberis brasiliana	NA	NA	NA	NA	DQ168789	NA	NA	MN410983	NA	NA	DQ168720	NA	NA	NA	NA	NA	NA	NA
Stratiomyidae	Stratiomys laticeps	NA	NA	NA	NA	DQ168767	NA	NA	JF877307	NA	NA	DQ168698	NA	NA	NA	NA	NA	NA	NA
Stratiomyidae	Hedriodiscus binotatus	NA	NA	NA	NA	DQ168748	NA	NA	JF868538	NA	NA	DQ168679	NA	NA	NA	NA	NA	NA	NA
Stratiomyidae	Rosapha variegata	NA	GU947428	GU947395	NA	NA	NA	NA	MG967830	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Stratiomyidae	Oplodontha viridula	NA	GU947410	GU947377	NA	NA	NA	NA	AB907186	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Xylomyidae	Xylomya parens	NA	NA	NA	NA	KC177681	KC178184	NA	NA	NA	NA	NA	NA	NA	NA	KC177356	NA	NA	KC177911
Athericidae	Atherix variegata	NA	NA	NA	NA	KC177692	KC178195	NA	KM243490	NA	NA	NA	NA	NA	NA	KC177361	NA	NA	KC177922
Oreoleptidae	Oreoleptis torrenticola	NA	NA	NA	NA	KC177691	KC178194	KC177139	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	KC177921
Pelecorhynchidae	Glutops singularis	NA	NA	NA	NA	KC177690	KC178193	KC177138	KM243522	NA	NA	NA	NA	NA	NA	KC177360	NA	NA	KC177920
Tabanidae	Scaptia patula	NA	NA	NA	NA	NA	NA	KC593183	KC592653	KC593056	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tabanidae	Fidena rhinophora	NA	NA	NA	NA	KC592470	KC592818	KC593160	KC592658	KC593061	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tabanidae	Haematopota pluvialis	NA	KC177479	KC177454	KC177294	KC177694	KC178197	NA	KC192969	KC192995	KC177593	NA	KC176846	KC176823	KC178054	NA	KC178358	NA	KC177924
Tabanidae	Tabanus atratus	NA	NA	NA	NA	KC177693	KC178196	NA	KM243513	NA	NA	NA	NA	NA	NA	KC177362	NA	NA	KC177923
Tabanidae	Rhigioglossa edentula	NA	NA	NA	NA	KM243456	KC592837	DQ983564	KT733553	KC593065	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tabanidae	Chrysops viduatus	NA	NA	HM132115	NA	NA	NA	MG823549	MN868882	NA	MG823634	MG823696	NA	NA	NA	NA	NA	NA	NA
Tabanidae	Apocampta subcana	NA	NA	NA	NA	KC592496	KC592800	KC592719	KC592580	KC593026	NA	NA	NA	NA	NA	NA	NA	NA	NA

Tabanidae	Copidapha aureohirta	NA	NA	NA	NA	KC592507	KC592804	KC592730	KC592641	KC593039	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tabanidae	Dasybasis neobasalis	NA	NA	NA	NA	KM243409	KC592828	KC593157	KC592670	KC593064	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tabanidae	Goniops chrysocoma	NA	NA	NA	NA	KM243424	KC592838	KC593164	KC592648	KC593066	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tabanidae	Myioscaptia calliphora	NA	NA	NA	NA	KC592458	KC592770	KC593096	KC592589	KC592987	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tabanidae	Anzomyia pegasus	NA	NA	NA	NA	KC592419	KC592749	KC593112	KC592606	KC593005	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tabanidae	Pityocera cervus	NA	NA	NA	NA	KM243451	KC592827	KC593156	KC592649	KC593050	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tabanidae	Scione equatoriensis	NA	NA	NA	NA	KC592468	KC592817	KC593105	KC592657	KC592997	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tabanidae	Pseudoscione vittata	NA	NA	NA	NA	KC592506	KC592803	KC592729	KC592640	KC593038	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tabanidae	Triclista guttata	NA	NA	NA	NA	KM243481	KC592748	KC593158	KC592673	KC592958	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tabanidae	Osca lata	NA	NA	NA	NA	KM243444	KC592761	KC593130	KC592629	KC593027	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tabanidae	Parosca viridiventris	NA	NA	NA	NA	KC592492	KC592802	KC593128	KC592638	KC593037	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tabanidae	Plinthina arnhemensis	NA	NA	NA	NA	KC592448	KC592763	KC593090	KC592867	KC592978	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tabanidae	Adersia oestroides	NA	NA	NA	NA	KM243387	KM243597	NA	KM243486	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tabanidae	Copidapha guttipennis	NA	NA	NA	NA	KC592517	KC592756	KC593074	KC592651	KC593055	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tabanidae	Pseudoscione dorsoguttata	NA	NA	NA	NA	KM243454	KC592796	KC593127	KC592624	KC593021	NA	NA	NA	NA	NA	NA	NA	NA	NA
Xylophagaidae	Exeretonevra angustifrons	NA	KC177477	KC177453	KC177293	FJ040532	KC178188	FJ040628	KC192964	KC192992	KC177588	NA	KC176841	KC176818	KC178053	FJ040733	KC178337	KC177065	FJ040682
Atelestidae	Meghyperus sudeticus	NA	NA	NA	NA	AF503079	NA	AY280688	NA	NA	NA	AF503140	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Syntormon flexibile	NA	FJ808125	KM282992	FJ808279	FJ808345	NA	KM283180	KM282746	KM282826	FJ808484	KM362989	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Campsicnemus curvipes	NA	KM283013	EU864028	HQ449058	DQ496188	NA	DQ369278	DQ456892	KM282765	NA	KM362925	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Neurigona quadrifasciata	NA	DQ464870	EU864024	HQ449060	KC177715	KC178217	AY280690	DQ456911	NA	NA	NA	NA	NA	NA	NA	NA	NA	KC177943
Dolichopodidae	Acropsilus sp1	NA	FJ808076	FJ808151	FJ808223	FJ808301	NA	NA	FJ792973	NA	FJ808436	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Acropsilus sp2	NA	FJ808077	FJ808152	FJ808224	FJ808302	NA	NA	FJ792974	NA	FJ808437	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Campsicnemus amblytylus	NA	KM282996	KM282907	NA	NA	NA	KM283087	KM282663	KM282749	NA	KM362910	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Campsicnemus distinctus	NA	KM283016	KM282927	NA	NA	NA	KM283109	KM282681	KM282768	NA	KM362927	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Campsicnemus loripes	NA	KM283035	HQ449014	HQ449061	NA	NA	KM283129	DQ456897	NA	NA	KM362945	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Campsicnemus modicus	NA	KM283038	KM282948	NA	NA	NA	KM283131	KM282700	KM282784	NA	KM362948	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Campsicnemus mucronatus	NA	KM283051	KM282960	NA	NA	NA	KM283145	KM282703	KM282796	NA	KM362950	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Campsicnemus scambus	NA	KM283067	KM282976	NA	NA	NA	KM283161	DQ456904	KM282809	NA	KM362975	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Chaetogonopteron chaeturum	NA	FJ808081	FJ808155	FJ808229	FJ808307	NA	NA	FJ792978	NA	FJ808442	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Chaetogonopteron sp1	NA	FJ808083	FJ808157	FJ808231	FJ808309	NA	NA	FJ792979	NA	FJ808444	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Chrysosoma bearni	NA	FJ808086	FJ808160	FJ808234	FJ808311	NA	NA	FJ792980	NA	FJ808446	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Chrysosoma sp1	NA	FJ808087	FJ808161	FJ808235	FJ808312	NA	NA	FJ792981	NA	FJ808447	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Chrysotus sp1	NA	FJ808088	FJ808162	FJ808236	FJ808313	NA	NA	FJ792982	NA	FJ808448	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Dolichopus latilimbatus	NA	DQ464845	EU863916	HQ449066	FJ706111	NA	NA	AY744200	NA	AY744241	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Dolichopus pennatus	NA	DQ464862	EU863927	HQ449069	FJ706121	NA	NA	AY744209	NA	AY744250	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Dolichopus plumipes	NA	DQ464841	EU863940	HQ449048	FJ706134	NA	NA	EU847549	NA	AY744227	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Dolichopus ungulatus	NA	DQ464826	EU863962	HQ449054	FJ706157	NA	NA	EU847559	NA	AY744235	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Dolichopus tanythrix	NA	DQ464844	EU863951	HQ449065	NA	NA	NA	AY744199	NA	AY744240	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Gymnopternus aerosus	NA	DQ464827	EU863970	HQ449056	FJ706165	NA	NA	AY744194	NA	AY744236	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Hercostomus brevidigitalis	NA	FJ808100	FJ808172	FJ808249	FJ808320	NA	NA	FJ792995	NA	FJ808458	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Lichtwardtia ziczac	NA	FJ808102	FJ808174	FJ808251	FJ808322	NA	NA	FJ792996	NA	FJ808460	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Medetera grisescens	NA	FJ808104	FJ808175	FJ808253	FJ808324	NA	NA	FJ792997	NA	FJ808461	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Nanothinophilus hoplites	NA	FJ808110	FJ808181	FJ808258	FJ808330	NA	NA	FJ793003	NA	FJ808467	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Neurigona sp1	NA	FJ808114	FJ808186	FJ808264	FJ808335	NA	NA	FJ793007	NA	FJ808472	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Neurigona squamifera	NA	FJ808116	FJ808188	FJ808266	FJ808336	NA	NA	FJ793009	NA	FJ808474	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Paraclius digitatus	NA	FJ808118	FJ808190	FJ808268	FJ808338	NA	NA	FJ793010	NA	FJ808476	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Phacaspis mitis	NA	MF928549	MF928577	FJ808270	FJ808339	NA	NA	MF944166	NA	FJ808477	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Plagiozopelma flavipodex	NA	FJ808121	FJ808192	FJ808271	FJ808340	NA	NA	FJ793012	NA	FJ808478	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Poecilobothrus nobilitatus	NA	DQ464784	EU864009	HQ449085	DQ496206	NA	DQ369296	MT410808	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Scotiomyia sp1	NA	FJ808122	FJ808193	FJ808272	FJ808341	NA	NA	FJ793013	NA	FJ808479	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Sybistroma obscurellum	NA	DQ464874	EU864016	HQ449073	FJ706170	NA	NA	DQ456918	NA	AY744265	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Tachytrechus tessellatus	NA	FJ808127	FJ808199	FJ808281	FJ808348	NA	NA	FJ793021	NA	FJ808486	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Thambemyia pagdeni	NA	FJ808133	FJ808205	FJ808287	FJ808349	NA	NA	FJ793029	NA	FJ808492	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Thinophilus asiobates	NA	FJ808135	FJ808207	FJ808289	FJ808350	NA	NA	FJ793031	NA	FJ808494	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Thinophilus murphyi	NA	FJ808137	FJ808209	FJ808290	FJ808352	NA	NA	FJ793033	NA	FJ808495	NA	NA	NA	NA	NA	NA	NA	NA
Dolichopodidae	Thinophilus nitens	NA	FJ808139	FJ808210	FJ808291	FJ808353	NA	NA	FJ793035	NA	FJ808497	NA	NA	NA	NA	NA	NA	NA	NA
Empididae	Oreogeton scopifer	NA	NA	NA	KC177291	KC177711	KC178213	DQ369287	KP264784	NA	NA	NA	NA	NA	KC178052	KC177508	KC178365	KC177063	KC177940
Empididae	Empis barbatoides	NA	KC177476	KC177443	NA	NA	NA	NA	KC192963	KC192990	KC177587	NA	KC176840	KC176817	NA	NA	NA	NA	NA
Empididae	Heterophlebus versabilis	NA	HM062581	NA	NA	HM062609	HM062635	HM062728	NA	NA	NA	HM062658	NA	NA	NA	HM062752	NA	NA	HM062682

Empididae	Trichopeza longicornis	NA	NA	HQ449035	NA	DQ496207	NA	DQ369289	HQ449172	NA	MG823617	MG823685	NA	NA	NA	NA	NA	NA	NA
Empididae	Empis producta	NA	FJ808095	FJ808167	FJ808243	FJ808316	NA	NA	FJ792989	NA	FJ808453	NA	NA	NA	NA	NA	NA	NA	NA
Empididae	Empis sp1	NA	FJ808096	FJ808168	FJ808244	FJ808317	NA	NA	FJ792990	NA	FJ808454	NA	NA	NA	NA	NA	NA	NA	NA
Empididae	Gloma fuscipennis	NA	NA	NA	NA	AF503008	NA	DQ369290	MG823418	NA	MG823589	MG823669	NA	NA	NA	NA	NA	NA	NA
Empididae	Hemerodromia sp1	NA	NA	FJ808170	FJ808247	FJ808319	NA	NA	FJ792993	NA	FJ808456	NA	NA	NA	NA	NA	NA	NA	NA
Empididae	Microphor holosericeus	NA	HQ449039	HQ448954	HQ449104	NA	NA	NA	MT410831	NA	MG823657	NA	NA	NA	NA	NA	NA	NA	NA
Empididae	Ragas unica	NA	NA	NA	NA	NA	NA	MG823499	MG823412	NA	MG823583	MG823665	NA	NA	NA	NA	NA	NA	NA
Empididae	Dolichocephala guttata	NA	NA	NA	NA	NA	NA	MG823567	MG823482	NA	MG823652	MG823703	NA	NA	NA	NA	NA	NA	NA
Empididae	Heleodromia immaculata	NA	NA	NA	NA	NA	NA	MG823557	KT225295	NA	MG823642	MG823699	NA	NA	NA	NA	NA	NA	NA
Empididae	Heleodromia boreoalpina	NA	NA	NA	NA	NA	NA	MG823522	MG823435	NA	MG823606	MG823674	NA	NA	NA	NA	NA	NA	NA
Empididae	Wiedemannia bistigma	NA	NA	NA	NA	NA	NA	MG823570	MG823486	NA	MH755994	MH764291	NA	NA	NA	NA	NA	NA	NA
Empididae	Clinocera maculata	NA	NA	NA	NA	NA	NA	MG823523	MG823436	NA	MG823607	MG823675	NA	NA	NA	NA	NA	NA	NA
Empididae	Empis bicuspidata	NA	HQ449046	HQ449033	HQ449107	NA	NA	NA	HQ449170	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Empididae	Hilara interstincta	NA	NA	NA	NA	NA	NA	MG823527	MG823440	NA	MG823611	MG823678	NA	NA	NA	NA	NA	NA	NA
Empididae	Hilara abdominalis	NA	NA	NA	NA	NA	NA	MG823533	MG823446	NA	MG823616	MG823684	NA	NA	NA	NA	NA	NA	NA
Empididae	Rhamphomyia crassirostris	NA	NA	NA	NA	NA	NA	MG823532	MG823445	NA	MG823615	MG823683	NA	NA	NA	NA	NA	NA	NA
Empididae	Chelifera sp1	NA	NA	NA	NA	NA	NA	MG823554	MG823469	NA	MG823639	MG823698	NA	NA	NA	NA	NA	NA	NA
Empididae	Phyllodromia melanocephala	NA	NA	NA	NA	NA	NA	MG823558	MG823473	NA	MG823643	MG823700	NA	NA	NA	NA	NA	NA	NA
Empididae	Microphorella malaysiana	NA	FJ808108	NA	NA	FJ808328	NA	NA	FJ793001	NA	FJ808466	NA	NA	NA	NA	NA	NA	NA	NA
Empididae	Parathalassius candidatus	NA	NA	NA	NA	KC177714	KC178216	NA	KY683174	NA	NA	NA	NA	NA	NA	NA	NA	NA	KC177942
Empididae	Anthepiscopus sp1	NA	NA	NA	NA	NA	NA	MG823563	MG823478	NA	MG823648	MG823702	NA	NA	NA	NA	NA	NA	NA
Hybotidae	Stilpon graminum	NA	NA	NA	NA	NA	NA	MG823514	MG823427	NA	MG823598	MG823672	NA	NA	NA	NA	NA	NA	NA
Hybotidae	Hybos culiciformis	NA	KC699286	KC699337	NA	KC177712	KC178214	MG823562	MT410806	NA	MG823647	NA	NA	NA	NA	NA	NA	NA	NA
Hybotidae	Ocydromia glabricula	NA	NA	NA	NA	KC177713	KC178215	KC177148	MG823423	NA	MG823594	NA	NA	NA	NA	NA	NA	NA	KC177941
Hybotidae	Oedalea hybotina	NA	HQ449047	HQ449037	HQ449109	NA	NA	MG823572	HQ449173	NA	MG823656	NA	NA	NA	NA	NA	NA	NA	NA
Hybotidae	Hybos femoratus	NA	NA	HQ449036	HQ449105	NA	NA	MG823506	HQ449126	NA	MG823590	NA	NA	NA	NA	NA	NA	NA	NA
Hybotidae	Elaphropeza neesoonensis	NA	FJ808094	FJ808166	FJ808242	NA	NA	NA	FJ792988	NA	FJ808452	NA	NA	NA	NA	NA	NA	NA	NA
Hybotidae	Chersodromia nigripennis	NA	FJ808085	FJ808159	FJ808233	FJ808310	NA	NA	NA	NA	FJ808445	NA	NA	NA	NA	NA	NA	NA	NA
Hybotidae	Nanodromia narmkroi	NA	FJ808109	FJ808180	FJ808257	FJ808329	NA	NA	FJ793002	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Hybotidae	Tachypeza nubila	NA	NA	HQ449038	HQ449108	NA	NA	MG823559	HQ449174	NA	MG823644	NA	NA	NA	NA	NA	NA	NA	NA
Hybotidae	Crossopalpus nigritellus	NA	NA	NA	NA	NA	NA	MG823500	MG823413	NA	MG823584	MG823666	NA	NA	NA	NA	NA	NA	NA
Apystomyiidae	Apystomyia elinguis	NA	NA	NA	NA	KC177705	KC178207	NA	KR260204	NA	NA	NA	NA	NA	NA	KC177370	NA	NA	KC177934
Lonchopteridae	Lonchoptera sp1	y	KC177483	KC177456	KC177298	FJ040531	KC178220	FJ040630	KC192977	KC192997	KC177600	NA	KC176853	KC176828	KC178058	FJ040732	KC178343	KC177069	FJ040681
Opetiidae	Opetia nigra	NA	KC699294	AF126347	NA	KC177719	KC178221	AY280692	MN868809	NA	KC699403	AF503146	NA	NA	NA	KC177373	NA	NA	KC177946
Platypezidae	Platypeza sp1	NA	HM062590	NA	NA	HM062618	HM062644	HM062736	NA	NA	HM062563	HM062666	NA	NA	NA	HM062759	NA	NA	HM062691
Ironomyiidae	Ironomyia nigromaculata	NA	NA	NA	NA	KC177717	KC178219	KC177150	KR260222	NA	NA	NA	NA	NA	NA	KC177372	NA	NA	NA
Phoridae	Megaselia abdita	NA	NA	NA	NA	NA	NA	NA	KY836639	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Phoridae	Megaselia scalaris	NA	KC177486	KC177442	KC177299	KC177721	KC178223	NA	NC_023794	KC192998	KC177604	GU362007	KC176858	KC176833	KC178059	KC177510	KC178349	KC177070	KC177948
Phoridae	Sciadocera rufomaculata	NA	GU559903	JN196447	NA	KC177723	KC178225	KC177154	GU559946	NA	NA	NA	GU559968	NA	NA	KC177353	NA	NA	KC177950
Phoridae	Conicera dauci	NA	JN664648	NA	NA	HM062616	JN664786	HM062735	JF873345	NA	HM062562	HM062664	NA	NA	NA	HM062757	NA	NA	HM062688
Phoridae	Beckerina luteola	NA	EU068666	EU068632	NA	MH318679	NA	EU068571	KT862036	NA	NA	NA	EU068506	NA	NA	NA	NA	NA	MH318964
Phoridae	Melaloncha horologia	NA	EU068645	EU068613	NA	GU559930	NA	EU068551	GU559951	NA	NA	NA	EU068485	NA	NA	NA	NA	NA	MH318967
Phoridae	Apocephalus spinosus	NA	GU559911	MH318621	NA	MH318681	NA	MH318809	GU559954	NA	NA	NA	MH318905	NA	NA	NA	NA	NA	MH318978
Phoridae	Gymnophora spiracularis	NA	GU559905	MH318618	NA	GU559927	NA	MH318790	KT862035	NA	NA	NA	GU559970	NA	NA	NA	NA	NA	MH318962
Phoridae	Diplonevra nitidula	NA	AF126298	AF126326	NA	KX529297	NA	JN196449	HM352601	NA	NA	NA	HM357195	NA	NA	NA	NA	NA	NA
Phoridae	Phora holosericea	NA	GU361976	AY078062	NA	KX529470	NA	NA	MN597122	NA	NA	GU362001	KX775119	NA	NA	NA	NA	NA	NA
Phoridae	Dohrniphora gigantea	NA	EU068665	EU068631	NA	EU068599	NA	EU068570	HM352597	NA	NA	NA	HM357190	NA	NA	NA	NA	NA	NA
Phoridae	Triphleba sp1	NA	GU559910	JN196446	NA	GU559932	NA	JN196452	GU559953	NA	NA	NA	GU559975	NA	NA	NA	NA	NA	NA
Phoridae	Borophaga verticalis	NA	GU559899	JN196444	NA	GU559921	NA	JN196450	GU559942	NA	NA	NA	GU559964	NA	NA	NA	NA	NA	NA
Phoridae	Melaloncha acoma	NA	EU068639	GU550187	NA	GU550273	NA	EU068546	GU550340	NA	NA	NA	EU068479	NA	NA	NA	NA	NA	NA
Phoridae	Melaloncha feleoae	NA	EU068649	GU550206	NA	EU068585	NA	EU068555	EU068523	NA	NA	NA	EU068489	NA	NA	NA	NA	NA	NA
Phoridae	Melaloncha pilula	NA	EU068654	EU068621	NA	EU068590	NA	EU068560	EU068528	NA	NA	NA	EU068494	NA	NA	NA	NA	NA	NA
Phoridae	Melaloncha adusta	NA	GU550175	GU550231	NA	GU550279	NA	GU550332	GU550386	NA	NA	NA	GU550439	NA	NA	NA	NA	NA	NA
Phoridae	Dohrniphora cornuta	NA	GU361987	HM366981	NA	NA	NA	JN196448	MN832849	NA	NA	GU362009	HM357185	NA	NA	NA	NA	NA	NA
Phoridae	Apocephalus curtus	NA	NA	MH318668	NA	MH318723	NA	MH318831	MH318887	NA	NA	NA	MH318950	NA	NA	NA	NA	NA	MH319002
Phoridae	Apocephalus flexiseta	NA	NA	MH318646	NA	MH318699	NA	MH318815	MH318861	NA	NA	NA	MH318930	NA	NA	NA	NA	NA	MH318983
Phoridae	Apocephalus orthocladus	NA	NA	MH318635	NA	MH318690	NA	MH318804	MH318850	NA	NA	NA	MH318919	NA	NA	NA	NA	NA	MH318973
Pipunculidae	Pipunculus sp1	NA	HM062589	NA	NA	HM062617	HM062643	NA	NA	NA	NA	HM062665	NA	NA	NA	HM062758	NA	NA	HM062686
Pipunculidae	Cephalops longistylis	NA	NA	NA	NA	KC177724	KC178226	KC177155	NA	NA	NA	NA	NA	NA	NA	KC177374	NA	NA	KC177951

Pipunculidae	Nephrocerus daeckei	NA	AF154720	AF154796	NA	NA	NA	NA	MG295263	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Pipunculidae	Elmohardyia atlantica	NA	NA	NA	NA	AF503020	NA	NA	MG295551	NA	NA	AF503148	NA	NA	NA	NA	NA	NA	NA
Pipunculidae	Pipunculus houghi	NA	NA	NA	NA	DQ496182	NA	AY280691	DQ337706	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Pipunculidae	Cephalops cochleatus	NA	AF154682	AF154752	NA	NA	NA	NA	JF872529	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Episyrphus balteatus	NA	AY573076	AY573115	KC177297	KC177727	KC178228	NA	NC_036481	AY573151	KC177603	NA	KC176857	KC176832	KC178057	NA	KC178344	KC177068	KC177954
Syrphidae	Rhingia nasica	NA	NA	NA	NA	KC177725	KC178227	AY280697	KM571828	NA	NA	NA	NA	NA	NA	KC177375	NA	NA	KC177952
Syrphidae	Microdon tristis	NA	NA	NA	NA	KC177726	NA	KC177157	KR672698	NA	NA	NA	NA	NA	NA	KC177376	NA	NA	KC177953
Syrphidae	Toxomerus marginatus	NA	AF154745	AF154820	EU409277	HM062624	HM062649	HM062742	EU409160	NA	HM062568	HM062672	NA	NA	NA	HM062762	NA	NA	HM062690
Syrphidae	Allograpta alta	NA	KP402891	NA	NA	KP698557	KP403097	KP402951	KP402773	NA	KP402834	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Allograpta sp1	NA	KP402892	NA	NA	KP698532	KP403098	KP402952	KP402774	NA	KP402835	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Atylobaccha flukiella	NA	KP402893	NA	NA	KP698525	KP403099	KP402953	KP402775	NA	KP402836	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Baccha elongata	NA	KP402894	NA	EU431540	KP698563	KP403100	KP402954	KP402776	NA	KP402837	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Eristalis tenax	NA	AY573077	AY123344	EU431517	AY123356	NA	NA	NC_041143	AY573152	NA	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Leucopodella gracilis	NA	KP402901	NA	EU431547	KP698551	KP403107	KP402961	KP402783	NA	KP402844	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Leucopodella sp1	NA	KP402900	NA	NA	KP698566	KP403106	KP402960	KP402782	NA	KP402843	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Ocyptamus antiphates	NA	KP402904	NA	EU241847	KP698569	KP403109	KP402963	KP402786	NA	KP402847	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Ocyptamus dimidiatus	NA	KP402916	NA	EU409240	KP698527	KP403121	KP402973	KP402798	NA	KP402857	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Ocyptamus fascipennis	NA	KP402917	NA	EU409241	KP698531	KP403122	KP402974	KP402799	NA	KP402858	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Ocyptamus funebris	NA	KP402919	NA	EU409242	KP698570	KP403124	KP402976	KP402801	NA	KP402860	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Ocyptamus fuscipennis	NA	KP402920	NA	EU409243	KP698535	KP403125	KP402977	KP402802	NA	KP402861	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Ocyptamus macropyga	NA	KP402896	NA	NA	KP698571	KP403102	KP402956	KP402778	NA	KP402839	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Ocyptamus norina	NA	KP402898	NA	EU409247	KP698549	KP403104	KP402958	KP402779	NA	KP402841	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Ocyptamus rubricosus	NA	KP402899	NA	NA	KP698538	KP403105	KP402959	KP402781	NA	KP402842	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Paragus haemorrhous	NA	KP402930	NA	EU409259	KP698522	KP403134	KP402987	KP402812	NA	KP402870	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Pelecinobaccha adspersa	NA	KP402932	NA	NA	KP698565	KP403136	KP402989	KP402814	NA	KP402872	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Pelecinobaccha alicia	NA	KP402934	NA	NA	KP698521	KP403138	KP402990	KP402816	NA	KP402874	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Pelecinobaccha ovipositoria	NA	KP402940	NA	NA	KP698543	KP403143	KP402996	KP402822	NA	KP402879	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Pseudodoros clavatus	NA	KP402944	NA	KM270807	KP698568	KP403146	KP402999	KP402826	NA	KP402882	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Relictanum crassum	NA	KP402945	NA	NA	KP698537	KP403147	KP403000	KP402827	NA	KP402883	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Relictanum magisadspersum	NA	KP402946	NA	NA	KP698517	KP403148	KP403001	KP402828	NA	KP402884	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Salpingogaster sp1	NA	KP402947	NA	NA	KP698523	KP403149	KP403002	KP402829	NA	KP402885	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Salpingogaster sp2	NA	KP402948	NA	NA	KP698530	KP403150	KP403003	KP402830	NA	KP402886	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Temnostoma vespiforme	NA	NA	NA	NA	AY261746	NA	KF936845	AY261699	NA	NA	NA	NA	NA	NA	KF936135	NA	NA	KF937203
Syrphidae	Toxomerus politus	NA	KP402949	NA	EU241863	KP698554	KP403151	KP403004	EU241755	NA	KP402888	NA	NA	NA	NA	NA	NA	NA	NA
Syrphidae	Toxomerus virgulatus	NA	KP402950	NA	EU409291	KP698536	KP403152	KP403005	KP402833	NA	KP402889	NA	NA	NA	NA	NA	NA	NA	NA
Conopidae	Myopa vesiculosa	NA	JN664611	NA	NA	JN664680	JN664749	HM062721	HM417169	NA	HM062549	HM062652	NA	NA	NA	HM062746	NA	NA	HM062677
Conopidae	Physocephala marginata	NA	KC177481	KC177452	KC177304	KC177729	JN664730	HM062719	KC192973	KC193000	KC177596	HM062651	KC176849	NA	KC178063	KC177511	KC178362	KC177074	KC177956
Conopidae	Stylogaster neglecta	NA	KR262582	KR262609	NA	HM062606	HM062632	NA	KR262677	KR262708	HM062553	NA	NA	NA	NA	HM062749	NA	NA	HM062675
Conopidae	Dalmannia nigriceps	NA	JN664601	NA	NA	HM062604	HM062630	HM062725	JN664802	NA	HM062551	HM062656	NA	NA	NA	NA	NA	NA	HM062676
Australimyzidae	Australimyza sp1	NA	NA	NA	NA	KC177808	KC178304	KC177226	NA	NA	NA	NA	NA	NA	NA	KC177433	NA	NA	KC178022
Canacidae	Tethinosoma fulvifrons	NA	NA	NA	NA	KC177816	KC178312	KC177234	NA	NA	NA	NA	NA	NA	NA	KC177436	NA	NA	KC178029
Carnidae	Carnus hemapterus	NA	NA	NA	NA	NA	NA	NA	KC871417	KC871417	NA	NA	NA	NA	NA	NA	NA	NA	NA
Chloropidae	Thaumatomyia notata	NA	NA	KC177449	KC177306	KC177813	KC178309	KC177231	KC192976	KC193005	KC177599	NA	KC176852	NA	KC178065	KC177519	KC178357	KC177076	NA
Chloropidae	Incertella albipalpis	NA	NA	NA	NA	KC177812	KC178308	KC177230	NA	NA	NA	NA	NA	NA	NA	KC177435	NA	NA	KC178026
Chloropidae	Oscinella frit	NA	AF304346	NA	NA	NA	NA	NA	HQ981992	MT318997	NA	NA	NA	NA	NA	NA	NA	NA	NA
Chloropidae	Chaetochlorops inquilinus	NA	NA	NA	NA	GU299234	NA	GU299261	HQ984632	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Chloropidae	Thaumatomyia sp1	NA	NA	NA	NA	GU299235	NA	GU299280	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Chloropidae	Incertella incerta	NA	NA	NA	NA	NA	NA	NA	KM571510	NA	KP037302	NA	NA	NA	NA	NA	NA	NA	NA
Chloropidae	Meromyza columbi	NA	NA	NA	NA	NA	NA	NA	KP037172	NA	KP037359	NA	NA	NA	NA	NA	NA	NA	NA
Chloropidae	Elachiptera bimaculata	NA	NA	NA	NA	NA	NA	NA	MN868793	MT318993	NA	NA	NA	NA	NA	NA	NA	NA	NA
Chloropidae	Cryptonevra nigritarsis	NA	NA	NA	NA	NA	NA	NA	NA	MT318987	NA	NA	NA	NA	NA	NA	NA	NA	NA
Chloropidae	Lasiosina albipila	NA	NA	NA	NA	NA	NA	NA	NA	MT318991	NA	NA	NA	NA	NA	NA	NA	NA	NA
Inbiomyiidae	Inbiomyia mcalpineorum	NA	NA	NA	NA	KC177817	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Milichiidae	Paramyia nitens	NA	NA	NA	NA	KC177815	KC178311	KC177233	KR517963	NA	NA	NA	NA	NA	NA	NA	NA	NA	KC178028
Nannodastiidae	Azorastia mediterranea	NA	NA	NA	NA	KC177782	NA	KC177203	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Ephydridae	Scatella hawaiiensis	NA	NA	EU494299	NA	NA	NA	NA	EU493565	EU493697	NA	NA	EU494299	NA	NA	NA	NA	NA	NA
Ephydridae	Hydrellia tritici	NA	EU494420	EU494420	NA	NA	NA	NA	EU493564	EU493696	EU494082	NA	EU494197	EU493825	NA	NA	NA	NA	NA
Ephydridae	Hydrellia pakistanae	NA	NA	EU494298	NA	NA	NA	NA	EU493563	EU493695	EU494081	NA	EU494298	EU493824	NA	NA	NA	NA	NA
Ephydridae	Ephydra packardi	NA	EU494419	EU494297	NA	NA	NA	NA	EU493562	EU493694	NA	NA	EU494297	NA	NA	NA	NA	NA	NA

Ephydridae	Hydrellia griseola	NA	NA	NA	NA	KC177806	KC178302	KC177224	MF059320	NA	NA	NA	NA	NA	NA	KC177431	NA	NA	KC178020
Ephydridae	Psilopa polita	NA	NA	NA	NA	KC177805	KC178301	KC177223	NA	NA	NA	NA	NA	NA	NA	KC177430	NA	NA	KC178019
Ephydridae	Coenia palustris	NA	NA	NA	NA	KC177807	KC178303	KC177225	NA	NA	NA	NA	NA	NA	NA	KC177432	NA	NA	KC178021
Ephydridae	Limnellia quadrata	NA	AF126305	AF126333	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Ephydridae	Ephydra riparia	NA	NA	NA	NA	GU597374	NA	NA	JF867574	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Ephydridae	Discocerina obscurella	NA	NA	NA	NA	GU597408	NA	NA	JF875838	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Drosophilidae	Drosophila sp1	y	EU494480	M37275	M21017	NR_133562	KC178299	X04813	KT174474	MH925016	M37275	X06870	M37275	M37275	X03636	KC177518	KC178331	NM_078490	X57576
Drosophilidae	Phortica picta	NA	EU494422	EU494301	NA	AY081424	NA	NA	EU493567	EU493699	NA	NA	EU494301	EU493828	NA	NA	NA	NA	NA
Drosophilidae	Drosophila immigrans	NA	EU494439	EU494320	AF348906	AB932824	NA	NA	JQ679115	EU493716	EU494102	NA	EU494320	EU493846	L06337	MK016876	MK017576	NA	MK017333
Drosophilidae	Drosophila hydei	NA	EU494459	MK659821	NA	GU597386	NA	NA	EU493606	EU493736	NA	NA	EU494230	EU493866	FJ267301	NA	JF736328	JF736388	NA
Drosophilidae	Drosophila virilis	NA	AF185058	AF508180	HG798349	GU597420	NA	NA	HQ849831	EU493751	EU494135	NA	EU494353	EU493881	AY854874	NA	M77282	JF736417	NA
Drosophilidae	Chymomyza amoena	NA	EU494425	M93986	NA	GQ244450	NA	NA	EU493570	EU493702	EU494086	NA	EU494304	EU493831	NA	NA	NA	NA	NA
Drosophilidae	Chymomyza procnemis	NA	EU494426	EU494426	NA	GU597413	NA	NA	EU493571	EU493703	EU494087	NA	EU494305	EU493832	NA	NA	NA	NA	NA
Drosophilidae	Mycodrosophila dimidiata	NA	EU494530	EU494408	NA	GU597440	NA	NA	EU493682	EU493811	EU494184	NA	EU494408	EU493939	NA	NA	NA	NA	NA
Drosophilidae	Samoaia leonensis	NA	EU494531	EU494409	NA	KC192913	NA	NA	EU493683	EU493812	EU494185	NA	EU494409	EU493940	NA	NA	NA	NA	NA
Drosophilidae	Scaptodrosophila latifasciaeformis	NA	EU494532	EU494410	NA	GU597377	NA	NA	EU493684	EU493813	EU494186	NA	EU494410	EU493941	NA	NA	NA	NA	NA
Drosophilidae	Scaptodrosophila lebanonensis	NA	EU494534	MK659851	NA	HQ110555	NA	NA	EU493686	EU493815	EU494188	NA	EU494411	EU493943	NA	NA	NA	NA	NA
Drosophilidae	Scaptomyza crassifemur	NA	EU494581	KC609614	NA	AF059860	NA	NA	EU493677	EU493806	EU494180	NA	EU494282	EU493934	NA	NA	NA	NA	NA
Drosophilidae	Amiota leucostoma	NA	EU494421	EU494300	NA	NA	NA	NA	EU493566	NA	EU494083	NA	EU494300	EU493827	NA	NA	NA	NA	NA
Drosophilidae	Amiota setigera	NA	EU494423	EU494302	NA	NA	NA	NA	EU493568	EU493700	EU494084	NA	EU494302	EU493829	NA	NA	NA	NA	NA
Drosophilidae	Leucophenga albofasciata	NA	EU494424	EU494303	NA	NA	NA	NA	EU493569	EU493701	EU494085	NA	EU494303	EU493830	NA	NA	NA	NA	NA
Drosophilidae	Scaptomyza caliginosa	NA	EU494525	EU494402	NA	NA	NA	NA	EU493676	EU493805	EU494179	NA	EU494402	EU493933	NA	NA	NA	NA	NA
Drosophilidae	Zygothrica sp1	NA	EU494539	EU494539	NA	NA	NA	NA	EU493692	EU493821	EU494194	NA	EU494417	EU493948	NA	NA	NA	NA	NA
Drosophilidae	Zaprionus lineosus	NA	EU494536	EU494414	NA	NA	NA	NA	EU493689	EU493818	EU494191	NA	EU494414	NA	NA	NA	NA	NA	NA
Drosophilidae	Parastegana brevivena	NA	NA	NA	NA	KJ813905	NA	MH372863	KJ813938	MH373057	NA	NA	NA	NA	NA	NA	NA	NA	NA
Drosophilidae	Pseudostegana bifasciata	NA	NA	NA	NA	JF313867	NA	MH372871	JF273079	MH373065	NA	NA	NA	NA	NA	NA	NA	NA	NA
Braulidae	Braula coeca	NA	NA	NA	NA	KC177809	KC178305	KC177227	NA	NA	NA	NA	NA	NA	NA	KC177434	NA	NA	KC178023
Cryptochetidae	Cryptochetum sp1	NA	NA	NA	NA	KC177814	KC178310	KC177232	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	KC178027
Camillidae	Camilla sp1	NA	NA	NA	NA	KC177800	KC178297	KC177220	NA	NA	NA	NA	NA	NA	NA	KC177429	NA	NA	KC178015
Curtonotidae	Curtonotum saheliense	NA	NA	NA	NA	NA	NA	JQ765780	JQ765818	NA	NA	NA	NA	NA	NA	NA	NA	NA	JQ765810
Diastatidae	Diastata fuscula	NA	NA	NA	NA	KC177802	KC178298	KC177221	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	KC178016
Celyphidae	Spaniocelyphus umsinduzi	NA	NA	NA	NA	KC177761	KC178261	KC177183	NA	NA	NA	NA	NA	NA	NA	KC177400	NA	NA	KC177985
Chamaemyiidae	Cremifania nearctica	NA	NA	NA	NA	KC177758	KC178258	KC177181	NA	NA	NA	NA	NA	NA	NA	KC177398	NA	NA	KC177982
Lauxaniidae	Sapromyza sexpunctata	NA	NA	KT956368	NA	KT956419	NA	NA	AJ439153	NA	NA	KU991646	NA	NA	NA	NA	NA	NA	NA
Lauxaniidae	Minettia flaveola	NA	NA	KC177448	KC177305	KC177760	KC178260	NA	KC192974	KC192999	KC177597	NA	KC176850	KC176826	KC178064	KC177515	KC178345	KC177075	KC177984
Lauxaniidae	Minettia lupulina	NA	JN664646	KT956349	NA	HM062610	HM062636	HM062729	KM571706	NA	HM062556	KU991627	NA	NA	NA	HM062753	NA	NA	NA
Lauxaniidae	Melanina sp1	NA	HM062583	NA	NA	HM062611	HM062637	HM062730	NA	NA	HM062557	HM062660	NA	NA	NA	NA	NA	NA	HM062694
Lauxaniidae	Lyciella decipiens	NA	NA	KT956334	NA	KC177759	KC178259	KC177182	NA	NA	NA	KU991613	NA	NA	NA	KC177399	NA	NA	KC177983
Lauxaniidae	Calliopum simillimum	NA	NA	KT956322	NA	KT956376	NA	NA	MN868801	NA	NA	KU991600	NA	NA	NA	NA	NA	NA	NA
Lauxaniidae	Homoneura mayrhoferi	NA	KR262566	KR262593	NA	NA	NA	NA	KR262638	KR262693	NA	NA	NA	NA	NA	NA	NA	NA	NA
Lauxaniidae	Minettia longipennis	NA	NA	KT956348	NA	KT956402	NA	NA	MN868895	NA	NA	KU991626	NA	NA	NA	NA	NA	NA	NA
Lauxaniidae	Lyciella illota	NA	NA	KT956336	NA	KT956391	NA	NA	MG673800	NA	NA	KU991614	NA	NA	NA	NA	NA	NA	NA
Lauxaniidae	Protrigonometopus maculifrons	NA	KR262579	KR262606	NA	NA	NA	NA	KR262665	KR262705	NA	NA	NA	NA	NA	NA	NA	NA	NA
Cypselosomatida	Rhinopomyzella sp1	NA	NA	NA	NA	KC177738	KC178238	KC177165	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	KC177965
Micropezidae	Micropeza sp1	NA	KM287346	NA	NA	NA	NA	KM287265	KM287301	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Micropezidae	Taeniaptera trivittata	NA	KM287371	NA	NA	HM062613	HM062639	HM062732	KM287330	NA	HM062559	HM062662	NA	NA	NA	HM062755	NA	NA	HM062693
Micropezidae	Compsobata cibaria	NA	NA	NA	NA	KC177733	KC178233	KC177161	MG823463	NA	MG823633	MG823695	NA	NA	NA	KC177381	NA	NA	KC177960
Neriidae	Telostylinus sp1	NA	NA	NA	NA	KC177734	KC178234	KC177162	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	KC177961
Acartophthalmida	Acartophthalmus nigrinus	NA	NA	NA	NA	KC177818	KC178313	KC177235	KM860533	NA	NA	NA	NA	NA	NA	KC177437	NA	NA	KC178030
Agromyzidae	Melanagromyza minimoides	y	AY573083	AY573120	NA	EF104831	NA	EF104743	KR262643	AY573158	NA	NA	NA	NA	NA	NA	NA	NA	NA
Agromyzidae	Phytomyza ilicicola	NA	NA	NA	KC177307	KC177784	KC178281	EF104814	AF276860	AF276860	NA	NA	NA	NA	KC178066	KC177517	KC178347	KC177077	NA
Agromyzidae	Liriomyza trifolii	NA	NA	MF141914	KY563323	EF104879	NA	EF104791	GU327644	AY375176	NA	KY558636	NA	MF141934	NA	NA	NA	NA	NA
Agromyzidae	Liriomyza huidobrensis	NA	NA	NA	AY842478	FJ890888	NA	EF104788	JQ862474	AY375174	NA	AY035339	NA	NA	NA	NA	NA	NA	NA
Agromyzidae	Phytomyza glabricola	NA	NA	NA	NA	EF104901	NA	EF104813	AF276838	AF276838	NA	JX658435	NA	NA	NA	EU367830	NA	NA	NA
Agromyzidae	Phytomyza syngenesiae	NA	NA	NA	NA	EF104867	NA	EF104779	KR476575	NA	NA	NA	NA	MF141930	NA	EU367821	NA	NA	NA
Agromyzidae	Cerodontha dorsalis	NA	NA	NA	NA	KC177783	KC178280	EF104771	EF104686	NA	NA	NA	NA	NA	NA	KC177415	NA	NA	KC178002
Agromyzidae	Phytomyza aconiti	NA	NA	NA	NA	EU367930	NA	EU367687	AF276828	AF276828	NA	NA	NA	NA	NA	EU367885	NA	NA	NA
Agromyzidae	Phytomyza aquilegivora	NA	NA	NA	NA	EF104899	NA	EF104811	AF276830	AF276830	NA	NA	NA	NA	NA	EU367903	NA	NA	NA
Agromyzidae	Phytomyza erigerophila	NA	NA	NA	NA	EF104900	NA	EF104812	AF276833	AF276833	NA	NA	NA	NA	NA	EU367869	NA	NA	NA

Agromyzidae	Phytomyza plantaginis	NA	NA	NA	NA	EF104903	NA	EF104815	AF276829	AF276829	NA	NA	NA	NA	NA	EU367899	NA	NA	NA
Agromyzidae	Liriomyza chinensis	NA	NA	NA	AY323212	EF104874	NA	EF104786	NC_041083	AY327823	NA	NA	NA	NA	NA	NA	NA	NA	NA
Agromyzidae	Chromatomyia horticola	NA	NA	NA	AY327824	NA	NA	LT795098	EU443642	AY884066	NA	NA	NA	NA	NA	NA	NA	NA	NA
Agromyzidae	Phytomyza spinaciae	NA	NA	NA	NA	EF104869	NA	EF104781	EF104696	NA	NA	NA	NA	NA	NA	EU367896	NA	NA	NA
Agromyzidae	Napomyza lateralis	NA	NA	NA	NA	EF104884	NA	EF104796	EF104710	NA	NA	NA	NA	NA	NA	EU367909	NA	NA	NA
Anthomyzidae	Mumetopia occipitalis	NA	KJ418443	KJ418465	NA	KJ418509	NA	NA	JN298659	KJ418632	NA	NA	NA	NA	NA	NA	NA	NA	NA
Asteiidae	Leiomyza curvinervis	NA	NA	NA	NA	GU299232	NA	GU299268	KM855347	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Aulacigastridae	Aulacigaster sp1	NA	NA	NA	NA	KC177787	KC178284	KC177206	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Clusiidae	Clusia lateralis	NA	NA	NA	NA	FJ890870	KC178285	FJ416889	FJ435907	FJ435943	NA	NA	NA	NA	NA	KC177416	NA	NA	NA
Clusiidae	Clusiodes ruficollis	NA	EU268512	EU268538	NA	KJ418495	NA	NA	KJ418546	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Fergusoninidae	Fergusonina turneri	NA	NA	NA	NA	KC177790	KC178287	KC177208	KY378336	NA	NA	NA	NA	NA	NA	KC177419	NA	NA	NA
Marginidae	Margo sp1	NA	NA	NA	NA	KC177735	KC178235	NA	NA	NA	NA	NA	NA	NA	NA	KC177382	NA	NA	KC177962
Megamerinidae	Megamerina sp1	NA	NA	NA	NA	KC177731	KC178231	KC177159	NA	NA	NA	NA	NA	NA	NA	KC177379	NA	NA	KC177958
Neminidae	Nemula longarista	NA	NA	NA	NA	GU299223	KC177010	KC177209	NA	NA	NA	NA	NA	NA	NA	KC177420	NA	NA	KC178006
Neurochaetidae	Neurochaeta sp1	NA	NA	NA	NA	KC177792	KC178289	KC177210	NA	NA	NA	NA	NA	NA	NA	KC177421	NA	NA	KC178007
Odiniidae	Odinia sp1	NA	NA	NA	NA	EF104909	NA	EF104821	EF104734	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Opomyzidae	Opomyza florum	NA	KJ418459	KJ418480	NA	KC177795	KC178292	KC177214	KJ418617	KJ418644	KJ418662	NA	NA	NA	NA	KC177424	NA	NA	KC178010
Pallopteridae	Toxonevra superba	NA	AY573106	AY573138	NA	HM062615	HM062641	HM062734	KR262684	AY573181	HM062561	HM062663	NA	NA	NA	HM062756	NA	NA	NA
Periscelididae	Cyamops nebulosus	NA	NA	NA	NA	GU299226	KC178293	KC177216	MG103787	NA	NA	NA	NA	NA	NA	KC177425	NA	NA	KC178011
Teratomyzidae	Teratomyza sp1	NA	NA	NA	NA	KC177798	KC178295	KC177218	NA	NA	NA	NA	NA	NA	NA	KC177427	NA	NA	KC178013
Xenasteiidae	Xenasteia shalam	NA	NA	NA	NA	KC177799	KC178296	KC177219	NA	NA	NA	NA	NA	NA	NA	KC177428	NA	NA	KC178014
Coelopidae	Coelopa sp1	y	NA	AF403457	NA	KC177763	KC178263	KC177185	GU672779	AF427694	NA	AY048524	NA	NA	NA	KC177402	NA	NA	NA
Dryomyzidae	Dryomyza anilis	NA	JN828149	AF403448	NA	KC177764	KC178264	KC177186	JN828346	JN828305	NA	AY048513	NA	NA	NA	KC177403	NA	NA	KC177987
Helosciomyzidae	Neosciomyza luteipennis	NA	NA	AF403447	NA	KC177766	NA	KC177188	NA	NA	NA	AY048512	NA	NA	NA	KC177405	NA	NA	NA
Heterocheilidae	Heterocheila buccata	NA	EU435518	AF403446	EU435624	KC177767	KC178266	KC177189	EU435772	EU435846	EU435904	AY048511	NA	NA	NA	KC177406	NA	NA	KC177989
Natalimyzidae	Natalimyza sp1	NA	NA	NA	NA	KC177775	KC178274	KC178405	NA	NA	NA	NA	NA	NA	NA	KC177414	NA	NA	KC177997
Ropalomeridae	Willistoniella pleuropunctata	NA	EU435519	EU435573	EU435625	KC177770	KC178269	KC177192	EU435773	EU435847	EU435905	EU435973	NA	NA	NA	NA	NA	NA	KC177992
Sciomyzidae	Limnia sp1	y	JN828161	JN828217	NA	JN828269	NA	NA	MT483658	JN828312	JN828400	JN828431	NA	NA	NA	NA	NA	NA	NA
Sciomyzidae	Pelidnoptera nigripennis	NA	JN828163	JN828218	NA	KC177769	KC178268	KC177191	JN828357	JN828313	JN828401	JN816249	NA	NA	NA	KC177408	NA	NA	KC177991
Sciomyzidae	Pherbellia annulipes	NA	JN828166	JN828220	NA	KC177771	KC178270	KC177193	JN828359	JN828315	JN828403	JN828433	NA	NA	NA	KC177409	NA	NA	KC177993
Sepsidae	Themira nigricornis	NA	AJ844302	AJ843107	EU435686	EU435761	EU436079	NA	AJ832117	AJ841762	EU435966	AJ829544	NA	NA	NA	NA	NA	NA	NA
Sepsidae	Sepsis cynipsea	NA	AF304349	EU435602	KC177309	KC177776	KC178275	KC177198	KC192966	KC193003	KC177590	EU436005	KC176843	KC176820	KC178075	KC177490	KC178333	KC177078	KC177998
Chyromyidae	Gymnochiromyia sp1	NA	NA	NA	NA	KC177777	KC178276	KC177199	NA	NA	NA	NA	NA	NA	NA	KC177413	NA	NA	KC177999
Heleomyzidae	Epistomyia sp1	NA	JX887754	NA	NA	JX887727	JX260418	NA	JX260392	NA	JX887703	NA	NA	NA	NA	NA	NA	NA	NA
Heleomyzidae	Suillia variegata	NA	NA	NA	NA	KC177778	KC178277	KC178407	MN868903	NA	NA	NA	NA	NA	NA	NA	NA	NA	KC178000
Heleomyzidae	Heteromyza atricornis	NA	NA	NA	NA	KC177789	KC178286	KC177213	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Sphaeroceridae	Spelobia bifrons	NA	NA	NA	KC177308	KC177780	KC178279	NA	KC192979	KC193004	NA	NA	KC176855	KC176830	KC178067	KC177516	KC178363	NA	NA
Sphaeroceridae	Lotophila atra	NA	AY573082	AY573119	NA	JX887730	JX260421	NA	KR262642	AY573157	JX887706	NA	NA	NA	NA	NA	NA	NA	NA
Sphaeroceridae	Rachispoda sp1	NA	HM062594	NA	NA	HM062622	HM062647	HM062740	NA	NA	HM062566	HM062670	NA	NA	NA	NA	NA	NA	HM062689
Sphaeroceridae	Frutillaria edenensis	NA	JX887756	NA	NA	JX887729	JX260420	NA	JX260394	NA	JX887705	NA	NA	NA	NA	NA	NA	NA	NA
Sphaeroceridae	Apteromyia sp1	NA	JX887743	NA	NA	JX887717	JX260416	NA	JX260390	NA	JX887692	NA	NA	NA	NA	NA	NA	NA	NA
Sphaeroceridae	Parasphaerocera sp1	NA	JX887758	NA	NA	JX887731	JX260422	NA	JX260396	NA	JX887707	NA	NA	NA	NA	NA	NA	NA	NA
Sphaeroceridae	Archiborborus annulatus	NA	JX887744	NA	NA	JX887718	JX260398	NA	JX260354	NA	JX887693	NA	NA	NA	NA	NA	NA	NA	NA
Diopsidae	Teleopsis dalmanni	NA	AY573073	AY123348	KC177302	KC177739	KC178239	NA	KC192968	AY573148	KC177592	AF303212	KC176845	KC176822	KC178061	KC177512	KC178360	KC177072	KC177966
Psilidae	Chyliza scrobiculata	NA	JN664644	NA	NA	HM062620	HM062646	HM062738	JF867180	NA	JN664892	HM062668	NA	NA	NA	NA	NA	NA	NA
Somatiidae	Somatia aestiva	NA	NA	NA	NA	KC177742	KC178242	KC177167	NA	NA	NA	NA	NA	NA	NA	KC177386	NA	NA	KC177967
Syringogastridae	Syringogaster sp1	NA	NA	NA	NA	KC177740	KC178240	KC177166	NA	NA	NA	NA	NA	NA	NA	KC177385	NA	NA	NA
Strongylophthalm	Strongylophthalmyia angustipennis	NA	JN664645	NA	NA	HM062623	HM062648	HM062741	JN291515	NA	HM062567	HM062671	NA	NA	NA	NA	NA	NA	HM062683
Tanypezidae	Neotanypeza sp1	NA	NA	NA	NA	KC177743	KC178243	KC177168	NA	NA	NA	NA	NA	NA	NA	KC177387	NA	NA	KC177968
Richardiidae	Richardia teevani	NA	NA	NA	NA	KC177751	KC178251	KC177175	NA	NA	NA	NA	NA	NA	NA	KC177393	NA	NA	KC177976
Lonchaeidae	Lonchaea polita	NA	NA	NA	NA	KC177746	KC178246	KC177170	NA	NA	NA	NA	NA	NA	NA	KC177389	NA	NA	KC177971
Lonchaeidae	Silba adipata	NA	AY573101	AY123350	NA	NA	NA	NA	KR262672	AY573176	NA	NA	NA	NA	NA	NA	NA	NA	NA
Lonchaeidae	Dasiops inedulis	NA	AY573074	AY573114	NA	NA	NA	NA	KR262625	AY573149	NA	NA	NA	NA	NA	NA	NA	NA	NA
Piophilidae	Piophila nigriceps	NA	AY573104	AY573136	U01269	NA	NA	NA	KR262676	AY573179	AM259631	KP659050	NA	NA	NA	NA	NA	NA	NA
Ulidiidae	Melieria omissa	NA	KR262570	KR262597	NA	KC177755	KC178255	KC177179	KR262645	KR262696	NA	NA	NA	NA	NA	KC177395	NA	NA	KC177980
Ulidiidae	Tritoxa flexa	NA	AY573107	AY123351	U01274	AY123363	NA	NA	KR262680	AY573182	NA	NA	NA	NA	NA	NA	NA	NA	NA
Platystomatidae	Lamprogaster nigripes	NA	HM062591	NA	NA	HM062619	HM062645	HM062737	NA	NA	HM062564	HM062667	NA	NA	NA	HM062760	NA	NA	HM062685
Platystomatidae	Rivellia syngenesiae	NA	NA	NA	NA	KC177749	KC178249	KC177173	MT410799	NA	NA	NA	NA	NA	NA	KC177392	NA	NA	KC177974
Platystomatidae	Rivellia alini	NA	AY573099	AY573132	NA	MH510224	NA	NA	KR262669	AY573174	NA	NA	NA	NA	NA	NA	NA	NA	NA

Platystomatidae	Platystoma seminationis	NA	AY573093	AY573128	NA	NA	NA	NA	KR262657	AY573168	NA	NA	NA	NA	NA	NA	NA	NA	NA
Platystomatidae	Pterogenia sp1	NA	KR262578	KR262605	NA	NA	NA	NA	KR262664	KR262704	NA	NA	NA	NA	NA	NA	NA	NA	NA
Ctenostylidae	Sinolochmostylia sinica	NA	KR262581	KR262608	NA	NA	NA	NA	KR262673	KR262707	NA	NA	NA	NA	NA	NA	NA	NA	NA
Pyrgotidae	Pyrgota undata	NA	AY573097	AY123352	U01264	JN664714	JN664781	HM062739	KR262666	AY573172	HM062565	HM062669	NA	NA	NA	HM062761	NA	NA	NA
Pyrgotidae	Eupyrgota tigrina	NA	AY573079	AY573117	NA	NA	NA	NA	KR262631	AY573154	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tephritidae	Ceratitis capitata	NA	NA	AF177123	AH006961	KC177754	KC178254	EU717163	NC_000857	DQ011889	JX500798	MG683583	AH014646	NA	AH015344	KC177514	KC178346	KC177071	KC177979
Tephritidae	Bactrocera dorsalis	NA	EU926853	EU926922	U01251	GU323792	NA	MG683277	KT343905	AB972850	NA	GU339154	NA	MG916968	KC446693	NA	NA	NA	NA
Tephritidae	Zeugodacus cucurbitae	NA	EU926852	EU926921	U01250	NA	NA	MG683199	JN635562	AB192452	DQ006904	MG683520	KC594985	NA	AB517621	NA	NA	NA	NA
Tephritidae	Bactrocera correcta	NA	AY037332	AY037375	KF246551	JQ906101	NA	MG683252	NC_018787	AB192423	KP055591	MG683572	FJ665832	NA	MG683722	NA	NA	NA	NA
Tephritidae	Bactrocera tryoni	NA	AY037345	JQ671089	XM_040115129	KC446993	NA	MG683298	HQ130030	AB192442	JQ420932	MG683620	AY037474	NA	AF480840	NA	NA	NA	NA
Tephritidae	Bactrocera carambolae	NA	AY037324	AY037367	AF033940	KC447278	NA	MG683317	MN104217	AB192421	KC439576	MG683640	AY037453	NA	KC446709	NA	NA	NA	NA
Tephritidae	Anastrepha obliqua	NA	AY037507	AF152078	NA	AJ634703	NA	KY428152	HQ677064	MG020784	NA	KY428459	HM592661	NA	NA	KY428620	NA	NA	KT594599
Tephritidae	Zeugodacus tau	NA	AY037348	FJ168028	AY209010	GU323789	NA	MG683201	MF966383	AB192461	KC439660	MG683522	AY037477	NA	MG683678	NA	NA	NA	NA
Tephritidae	Bactrocera cacuminata	NA	AY037327	JQ671096	NA	KC447052	NA	MG683310	MG683459	JQ671162	NA	MG683632	AY037456	NA	KC446489	NA	NA	NA	NA
Tephritidae	Anastrepha ludens	NA	NA	AF152074	EU179519	MH999061	NA	KU527434	HQ677057	AB192462	NA	KY428448	NA	NA	NA	KY428613	NA	NA	KT594565
Tephritidae	Anastrepha suspensa	NA	NA	U39380	U01249	DQ279855	NA	KY428163	KY428318	NA	NA	KY428470	NA	NA	MG683835	KY428626	NA	NA	NA
Tephritidae	Rhagoletis pomonella	NA	EU926900	AF177127	U01265	MH999122	MH998810	KU527451	DQ006862	U53229	DQ006893	NA	NA	NA	MG825196	NA	NA	NA	NA
Tephritidae	Anastrepha fraterculus	NA	NA	AF152067	AF187101	AY686688	NA	KY428135	NC_034912	MG020783	NA	MF028812	NA	NA	NA	KY428608	NA	NA	KT594623
Tephritidae	Bactrocera musae	NA	AY037328	JQ671086	NA	KC447012	NA	MG683312	AB192432	AB192432	NA	MG683634	AY037457	NA	KC446450	NA	NA	NA	NA
Tephritidae	Bactrocera oleae	NA	AY037337	AF164590	NA	NA	NA	MG683222	GU108467	GQ175825	NA	MG683538	AF164590	NA	KM023545	AM158090	NA	NA	NA
Tephritidae	Bactrocera occipitalis	NA	AY037343	KM023483	NA	KC447134	NA	MG683308	AB192435	AB192435	NA	MG683630	AY037472	NA	KC446579	NA	NA	NA	NA
Tephritidae	Rhagoletis cingulata	NA	EU926896	U39427	NA	KU511180	MH998796	MG825286	DQ006863	KT221479	DQ006894	NA	NA	NA	MG825197	NA	NA	NA	NA
Tephritidae	Zeugodacus cucumis	NA	AY037306	JQ671092	AF114473	NA	NA	MG683268	AB192448	AB192448	NA	MG683590	AY037435	NA	MG683741	NA	NA	NA	NA
Tephritidae	Bactrocera frauenfeldi	NA	AY037315	JQ671085	NA	NA	NA	MG683285	AB192428	AB192428	AF033906	MG683606	AY037444	NA	MG683757	NA	NA	NA	NA
Tephritidae	Bactrocera umbrosa	NA	AY037322	KM023489	NA	NA	NA	MG683200	KT881558	AB192443	DQ006899	MG683521	AY037451	NA	KM023549	NA	NA	NA	NA
Tephritidae	Campiglossa pygmaea	NA	HM062597	NA	NA	HM062625	HM062650	HM062743	NA	NA	HM062569	HM062673	NA	NA	NA	HM062763	NA	NA	NA
Tephritidae	Zeugodacus caudatus	NA	AY037320	KM023474	NA	KP694326	NA	MG683273	KT625492	MG020791	NA	MG683594	AY037449	NA	KM023535	NA	NA	NA	NA
Tephritidae	Tachinisca cyaneiventris	NA	EU926907	EU926949	NA	KC177752	KC178252	KC177177	KR262678	EU926838	NA	NA	NA	NA	NA	KC177394	NA	NA	KC177977
Tephritidae	Anastrepha curvicauda	NA	EU926910	U39381	U01273	NA	NA	KY428117	HQ677147	EU926841	NA	KY428419	NA	NA	NA	KY428594	NA	NA	NA
Glossinidae	Glossina morsitans	NA	NA	EF531110	KC177312	KC177834	KC178323	EF531178	KC192971	KR820741	KC177594	JF439518	KC176847	KC176824	KC178070	KC177524	KC178334	KC177081	KC178039
Hippoboscidae	Ortholfersia minuta	NA	NA	EF531123	NA	EF531156	NA	EF531182	EF531221	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Hippoboscidae	Ornithomya avicularia	NA	NA	MF495919	AF322421	EF531146	KC178325	EF531168	MF495992	NA	NA	MF495969	NA	NA	NA	NA	NA	NA	KC178041
Hippoboscidae	Stenepteryx hirundinis	NA	NA	EF531121	NA	KC177835	KC177046	KC177246	EF531215	NA	NA	NA	NA	NA	NA	KC177439	NA	NA	KC178040
Hippoboscidae	Lipoptena cervi	NA	NA	AF322437	AF322426	EF531139	NA	MN370852	MF496025	DQ133114	NA	MF495964	NA	NA	NA	NA	NA	NA	NA
Nycteribiidae	Penicillidia fulvida	NA	NA	EF531124	KF156697	EF531157	NA	EF531174	KF021520	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Streblidae	Trichobius longipes	NA	NA	DQ133052	DQ133088	NA	NA	NA	MH282298	DQ133124	DQ133158	NA	NA	NA	NA	NA	NA	NA	NA
Fanniidae	Fannia canicularis	NA	DQ656884	DQ648647	FJ025489	KC177820	NA	KC177237	MF511734	AJ879606	DQ657051	AJ871202	NA	NA	NA	NA	NA	NA	KC178031
Fanniidae	Fannia manicata	NA	DQ656885	FJ025435	FJ025490	DQ656962	NA	NA	DQ657038	NA	DQ657052	NA	NA	NA	NA	NA	NA	NA	NA
Muscidae	Musca domestica	NA	DQ377075	AY123346	GQ465780	KC177822	KC178316	AY280689	KM200723	KT272857	KT272857	AF503149	KT272857	KT272857	KC178071	GQ265612	KC178355	KC177082	KC178033
Muscidae	Stomoxys calcitrans	NA	DQ377080	HM245737	FJ025499	KC177824	KC178317	KC177247	DQ533708	EU029770	KU932178	AJ605062	HM245737	EU029770	NA	KC177438	NA	NA	KC178035
Muscidae	Helina evecta	NA	FJ025377	FJ025439	NA	FJ025522	KP161777	AJ867936	FJ025619	AJ879607	FJ025719	AJ871203	NA	NA	NA	NA	NA	NA	NA
Muscidae	Atherigona orientalis	NA	DQ377077	KC347602	NA	KC538817	KP161761	KP161814	EU627707	KC347607	NA	KP161729	KC524782	NA	NA	NA	NA	NA	NA
Muscidae	Muscina stabulans	NA	FJ025396	EF531117	NA	EF531145	NA	EF531167	NC_026292	EU627738	FJ025736	AJ871205	NA	NA	NA	NA	NA	NA	NA
Muscidae	Musca autumnalis	NA	FJ025394	FJ025457	NA	KJ476353	NA	FJ025590	MT410827	JQ821709	KU932173	KU932198	NA	NA	NA	NA	NA	NA	NA
Muscidae	Hydrotaea aenescens	NA	DQ377079	NA	NA	KJ439011	KP161794	KP161837	NC_042952	AY184819	KU932156	KU932183	NA	NA	NA	NA	NA	NA	NA
Muscidae	Drymeia alpicola	NA	FJ025370	FJ025430	NA	KC177823	NA	KC177239	FJ025608	NA	FJ025710	FJ025669	NA	NA	NA	NA	NA	NA	KC178034
Muscidae	Huckettomyia watanabei	NA	KJ476276	KJ476311	NA	KJ476346	KP161779	KP161824	KJ510624	NA	KJ510557	KP161738	NA	NA	NA	NA	NA	NA	NA
Muscidae	Dichaetomyia bibax	NA	KJ476267	KJ476303	NA	KJ476337	KP161771	KP161821	KJ510615	NA	KJ510549	KJ510588	NA	NA	NA	NA	NA	NA	NA
Muscidae	Polietes lardarius	NA	KJ476289	FJ025471	NA	FJ025557	KP161798	FJ025597	KF919035	NA	NA	FJ025695	NA	NA	NA	NA	NA	NA	NA
Muscidae	Thricops cunctans	NA	FJ025418	FJ025478	NA	FJ025564	NA	FJ025600	FJ025661	NA	FJ025753	FJ025700	NA	NA	NA	NA	NA	NA	NA
Muscidae	Synthesiomyia nudiseta	NA	NA	JN226649	NA	NA	KP161811	KP161849	NC_042953	DQ345099	NA	MK292743	NA	NA	NA	NA	NA	NA	NA
Muscidae	Limnophora exuta	NA	FJ025384	FJ025446	NA	FJ025530	NA	FJ025581	FJ025626	NA	FJ025725	FJ025684	NA	NA	NA	NA	NA	NA	NA
Muscidae	Lispe tentaculata	NA	KX856038	KX856044	NA	KX856039	NA	KX856018	KX856027	NA	FJ025729	KX856032	NA	NA	NA	NA	NA	NA	NA
Muscidae	Haematobosca stimulans	NA	FJ025375	FJ025437	NA	FJ025518	NA	FJ025576	MT410787	NA	FJ025716	FJ025673	NA	NA	NA	NA	NA	NA	NA
Muscidae	Mydaea ancilla	NA	FJ025398	FJ025460	NA	FJ025547	NA	FJ025592	FJ025639	NA	FJ025737	FJ025690	NA	NA	NA	NA	NA	NA	NA
Muscidae	Potamia littoralis	NA	FJ025412	FJ025472	NA	FJ025558	NA	FJ025598	KU932145	NA	KU932176	KU932201	NA	NA	NA	NA	NA	NA	NA
Muscidae	Cyrtoneuropsis veniseta	NA	KJ476266	KJ476302	NA	NA	KP161769	KP161819	KJ510614	NA	KJ510548	KP161735	NA	NA	NA	NA	NA	NA	NA
Muscidae	Achanthiptera rohrelliformis	NA	KJ476258	KJ476294	NA	KJ476331	KP161760	NA	KJ510606	NA	KJ510542	KJ510580	NA	NA	NA	NA	NA	NA	NA
Muscidae	Helina lasiophthalma	NA	FJ025379	NA	NA	FJ025524	NA	AJ605055	FJ025621	AJ627899	FJ025720	AJ605067	NA	NA	NA	NA	NA	NA	NA

Muscidae	Hydrotaea cyrtoneurina	NA	FJ025380	FJ025441	NA	FJ025526	NA	FJ025578	KU932131	NA	FJ025721	KU932186	NA	NA	NA	NA	NA	NA	NA
Muscidae	Hydrotaea dentipes	NA	FJ025381	FJ025442	NA	FJ025527	NA	FJ025579	NC_047403	NA	KU932161	KU932187	NA	NA	NA	NA	NA	NA	NA
Muscidae	Limnophora maculosa	NA	FJ025385	FJ025447	NA	FJ025531	NA	FJ025582	FJ025627	NA	FJ025726	FJ025685	NA	NA	NA	NA	NA	NA	NA
Muscidae	Lispe sericipalpis	NA	KX856033	KX856047	NA	KX856042	NA	KX856019	KX856025	NA	KX856012	KX856029	NA	NA	NA	NA	NA	NA	NA
Anthomyiidae	Delia radicum	NA	KC177480	KC177444	KC177311	KC177819	KC178314	KC178409	NC_028226	KC192988	KC177595	NA	KC176848	KC176825	AB810218	NA	KC178332	KC177080	NA
Anthomyiidae	Lasiomma seminitidum	NA	DQ656893	DQ648649	NA	DQ656971	NA	NA	AF104624	AF104624	DQ657061	DQ657112	NA	NA	NA	NA	NA	NA	NA
Anthomyiidae	Lasiomma latipenne	NA	DQ656892	FJ025445	FJ025491	DQ656970	NA	NA	DQ657044	NA	DQ657060	FJ025683	NA	NA	NA	NA	NA	NA	NA
Anthomyiidae	Emmesomyia grisea	NA	FJ025372	FJ025432	FJ025487	FJ025510	NA	NA	KP412985	KP413007	FJ025712	NA	NA	NA	NA	NA	NA	NA	NA
Anthomyiidae	Delia platura	NA	DQ656894	FJ025429	FJ025486	DQ656972	NA	NA	MH013345	NA	DQ657062	NA	NA	NA	NA	NA	NA	NA	NA
Anthomyiidae	Botanophila fugax	NA	DQ656890	NA	NA	DQ656967	NA	NA	MT410801	KP413016	DQ657057	FJ025665	NA	NA	NA	NA	NA	NA	NA
Anthomyiidae	Hydrophoria lancifer	NA	DQ656891	NA	NA	EF531129	NA	EF531164	MT941919	NA	DQ657058	FJ025677	NA	NA	NA	NA	NA	NA	NA
Anthomyiidae	Hylemya variata	NA	FJ025383	FJ025444	NA	NA	NA	NA	MT483664	NA	FJ025724	FJ025682	NA	NA	NA	NA	NA	NA	NA
Anthomyiidae	Paregle coerulescens	NA	FJ025403	FJ025465	NA	NA	NA	NA	FJ025645	NA	FJ025741	FJ025693	NA	NA	NA	NA	NA	NA	NA
Anthomyiidae	Pegoplata infirma	NA	FJ025408	NA	FJ025497	FJ025554	NA	NA	NC_050312	NA	FJ025746	NA	NA	NA	NA	NA	NA	NA	NA
Scathophagidae	Scathophaga stercoraria	NA	DQ656952	KC177445	KC177315	KC177825	KC178318	AJ605051	KM200724	AF104619	KC177602	DQ657141	KC176856	KC176831	KC178073	NA	KC178361	KC177086	KC178036
Scathophagidae	Cordilura atrata	NA	DQ656903	DQ648657	NA	DQ656981	NA	NA	DQ657047	NA	DQ657071	DQ657116	NA	NA	NA	NA	NA	NA	NA
Calliphoridae	Eurychaeta palpalis	NA	FJ025374	FJ025434	GQ409180	FJ025512	NA	FJ025575	FJ025612	NA	KY749704	KY749862	NA	NA	NA	NA	NA	NA	NA
Calliphoridae	Chrysomya megacephala	NA	AF151386	GQ396704	FJ025483	AJ551435	NA	FJ169350	KT272775	JN014846	FJ025706	JF439533	DQ407491	MN594764	KC966414	NA	NA	NA	NA
Calliphoridae	Lucilia sericata	NA	NA	GQ396689	KR133393	KR133394	NA	FJ169332	NC_009733	MW266393	MW266393	KR133396	MW266393	MW266393	NA	NA	NA	NA	KP260681
Calliphoridae	Calliphora vomitoria	NA	FJ025365	AY114203	FJ025482	AJ300134	NA	FJ169335	NC_028411	GQ223336	JQ307812	FR719220	MF536078	NA	NA	NA	NA	NA	NA
Calliphoridae	Cochliomyia macellaria	NA	AF151384	NA	KC177310	KC177826	KC178319	FJ040629	KT272853	AF295555	KT272853	JF439534	NA	NA	KC178068	FJ040731	KC178352	KC177079	FJ040680
Calliphoridae	Calliphora vicina	NA	DQ056742	AY114199	NA	AJ300132	NA	JQ307804	MW266392	MW266392	MW266392	FR719219	MW266392	MW266392	KF839531	NA	NA	NA	L38975
Calliphoridae	Lucilia caesar	NA	FJ025389	GQ396699	KP940432	AJ300138	NA	JQ307801	KM657112	AJ417703	JQ307808	FR719239	MF536077	NA	KF839532	NA	NA	NA	NA
Calliphoridae	Phormia regina	NA	AF262957	KF908068	NA	JF713458	NA	FJ169331	KX853042	AF295550	KF908169	FR719264	KF225194	NA	NA	NA	NA	NA	NA
Mesembrinellidae	Mesembrinella bellardiana	NA	NA	NA	NA	JQ246635	NA	NA	KR820715	KR820777	NA	NA	NA	NA	NA	NA	NA	NA	NA
Mystacinobiidae	Mystacinobia zelandica	NA	GQ409075	GQ409136	GQ409191	JF439567	NA	NA	JF439542	NA	GQ409406	NA	NA	NA	NA	NA	NA	NA	NA
Oestridae	Cuterebra austeni	NA	NA	NA	KP954330	KP954361	NA	MF414479	MN411300	NA	NA	KP899710	NA	NA	NA	NA	NA	NA	KP260688
Polleniidae	Pollenia rudis	NA	GQ409088	GQ409146	GQ409202	AJ558192	NA	NA	MT628579	KR820755	KY749707	FR719265	NA	NA	NA	NA	NA	NA	NA
Rhiniidae	Stomorhina lunata	NA	NA	KP004739	NA	KP004547	NA	NA	KP004880	KP004802	KP004850	KY749866	NA	NA	NA	NA	NA	NA	NA
Rhiniidae	Rhyncomya nigripes	NA	GQ409092	NA	GQ409205	GQ409268	NA	NA	NA	NA	GQ409423	GQ409481	NA	NA	NA	NA	NA	NA	NA
Rhinophoridae	Stevenia hertingi	NA	GQ409109	GQ409162	GQ409221	GQ409282	NA	NA	NA	NA	GQ409440	GQ409493	NA	NA	NA	NA	NA	NA	NA
Sarcophagidae	Wohlfahrtia trina	NA	GQ409118	GQ409170	NA	NA	NA	NA	NA	NA	GQ409450	GQ409498	NA	NA	NA	NA	NA	NA	NA
Sarcophagidae	Sarcophaga peregrina	NA	KF038385	JF416600	MH576421	NA	NA	JQ290773	EF405928	EF405928	AY879246	JX027605	DQ407503	NA	KC966434	NA	NA	NA	NA
Sarcophagidae	Sarcophaga crassipalpis	NA	GQ409097	NC_026667	GQ409208	JF439572	NA	JQ290873	NC_026667	GU174024	GQ409428	JF439523	NA	NA	AB079533	NA	NA	NA	NA
Sarcophagidae	Sarcophaga dux	NA	NA	JF416590	MK861148	KU746444	NA	JQ290722	MH937748	EF405939	AY879242	KY416688	NA	NA	KC966418	NA	NA	NA	NA
Sarcophagidae	Helicobia rapax	NA	GQ409067	NA	GQ409183	KP954366	NA	KP973918	GQ223319	GQ223319	GQ409400	KP899707	NA	NA	NA	NA	NA	NA	KP260683
Sarcophagidae	Blaesoxipha plinthopyga	NA	GQ409055	GQ409120	GQ409173	GQ409232	NA	NA	GQ223341	GQ223341	GQ409387	GQ409453	NA	NA	NA	NA	NA	NA	NA
Sarcophagidae	Sphenometopa claripennis	NA	GQ409106	GQ409159	GQ409218	NA	NA	NA	KY749757	NA	KY749679	KY749836	NA	NA	NA	NA	NA	NA	NA
Sarcophagidae	Taxigramma multipunctata	NA	GQ409112	NA	GQ409224	GQ409284	NA	NA	KY749763	NA	KY749685	KY749842	NA	NA	NA	NA	NA	NA	NA
Sarcophagidae	Nyctia lugubris	NA	GQ409077	GQ409138	GQ409193	GQ409253	NA	NA	NA	NA	GQ409408	GQ409474	NA	NA	NA	NA	NA	NA	NA
Sarcophagidae	Titanogrypa luculenta	NA	GQ409113	GQ409165	GQ409225	GQ409287	NA	NA	GQ223331	GQ223331	GQ409445	GQ409495	NA	NA	NA	NA	NA	NA	NA
Sarcophagidae	Sarcophaga omikron	NA	GQ409100	GQ409156	GQ409212	GQ409275	NA	JQ290868	JQ807183	NA	GQ409432	GQ409487	NA	NA	NA	NA	NA	NA	NA
Sarcophagidae	Ravinia querula	NA	NA	KR676975	NA	KR676929	NA	NA	GQ223316	GQ223316	NA	KR608373	NA	NA	KR676857	NA	NA	NA	NA
Sarcophagidae	Peckia intermutans	NA	GQ409082	NA	GQ409196	GQ409256	NA	NA	GQ223335	GQ223335	GQ409413	GQ409475	NA	NA	NA	NA	NA	NA	NA
Sarcophagidae	Boettcheria cimbicis	NA	GQ409057	NA	GQ409174	GQ409234	NA	NA	GQ223324	GQ223324	GQ409388	GQ409455	NA	NA	NA	NA	NA	NA	NA
Sarcophagidae	Villegasia postuncinata	NA	GQ409116	GQ409168	GQ409228	GQ409289	NA	NA	JQ807217	NA	GQ409448	GQ409497	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Triarthria setipennis	NA	GQ409114	GQ409166	GQ409226	MK070813	NA	KX833263	MN868911	NA	GQ409446	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Epalpus signifer	NA	NA	NA	KP954332	JF439568	NA	AY280680	JF439543	NA	NA	JF439519	NA	NA	NA	NA	NA	NA	KP260669
Tachinidae	Gymnosoma nitens	NA	GQ409064	NA	NA	GQ409239	NA	MF414505	NA	NA	GQ409396	GQ409462	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Pseudogonia rufifrons	NA	NA	NA	NA	MK070786	NA	MK338220	MN411244	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Mintho rufiventris	NA	NA	NA	NA	MK070719	NA	MK338148	MN868871	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Exorista larvarum	NA	NA	KC177447	KC177316	KC177833	KC178322	NA	KC192967	KC192993	KC177591	NA	KC176844	KC176821	KC178074	KC177523	KC178348	KC177084	KC178038
Tachinidae	Phania funesta	NA	GQ409086	GQ409144	GQ409200	MK070759	NA	MF414536	KX844433	NA	GQ409417	GQ409477	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Tachina grossa	NA	FJ222684	GQ409163	NA	KC177830	NA	KC177242	KU146899	NA	GQ409442	GQ409494	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Gymnocheta viridis	NA	GQ409065	GQ409129	GQ409181	GQ409240	NA	NA	KX844485	NA	GQ409397	GQ409463	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Ceracia dentata	NA	NA	NA	KP954329	KP954360	NA	MF414466	HQ945093	NA	NA	AF364351	NA	NA	NA	NA	NA	NA	KP260676
Tachinidae	Hyphantrophaga virilis	NA	NA	NA	KP954337	KP954367	NA	KP973919	EF181547	NA	NA	AF364370	NA	NA	NA	NA	NA	NA	KP260675
Tachinidae	Lespesia aletiae	NA	NA	NA	KP954338	KP954368	NA	KP973920	KP189249	NA	NA	KP899695	NA	NA	NA	NA	NA	NA	KP260668
Tachinidae	Voria ruralis	NA	NA	NA	KP954354	KP954384	NA	MF414564	JN298628	NA	NA	KP899693	NA	NA	NA	NA	NA	NA	KP260666

Tachinidae	Tachina magnicornis	NA	GQ409111	GQ409164	GQ409223	GQ409283	NA	NA	MN868734	NA	GQ409443	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Peleteria rubescens	NA	GQ409085	GQ409143	GQ409199	GQ409259	NA	NA	MN868712	NA	GQ409416	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Tachinomyia nigricans	NA	NA	NA	KP954350	KP954380	NA	KP973896	JQ520147	NA	NA	KP899698	NA	NA	NA	NA	NA	NA	KP260665
Tachinidae	Cylindromyia binotata	NA	NA	NA	KP954331	KP954362	NA	MF414480	HQ583134	NA	NA	KP899699	NA	NA	NA	NA	NA	NA	KP260677
Tachinidae	Panzeria ampelus	NA	NA	NA	KP954343	KP954373	NA	MF414531	JF869094	NA	NA	KP899704	NA	NA	NA	NA	NA	NA	KP260673
Tachinidae	Ptilodexia conjuncta	NA	NA	NA	KP954346	KP954376	NA	KP973897	HQ982435	NA	NA	KP899690	NA	NA	NA	NA	NA	NA	KP260672
Tachinidae	Siphona plusiae	NA	NA	NA	KP954348	KP954378	NA	KP973927	HM417418	NA	NA	KP899705	NA	NA	NA	NA	NA	NA	KP260667
Tachinidae	Trichopoda pennipes	NA	NA	NA	KP954352	KP954382	NA	MF414560	GU803753	NA	NA	KP899700	NA	NA	NA	NA	NA	NA	KP260679
Tachinidae	Winthemia sinuata	NA	NA	NA	KP954355	KP954385	NA	MF414566	HQ984486	NA	NA	KP899696	NA	NA	NA	NA	NA	NA	KP260678
Tachinidae	Campylocheta semiothisae	NA	NA	NA	KP954326	KP954357	NA	MF414462	KR651911	NA	NA	KP899691	NA	NA	NA	NA	NA	NA	KP260671
Tachinidae	Epigrimyia illinoensis	NA	NA	NA	KP954333	KP954364	NA	MF414494	MG968077	NA	NA	KP899708	NA	NA	NA	NA	NA	NA	KP260693
Tachinidae	Thelaira americana	NA	NA	NA	KP954351	KP954381	NA	MF414557	HM417100	NA	NA	KP899692	NA	NA	NA	NA	NA	NA	KP260687
Tachinidae	Archytas nivalis	NA	AY573067	AY123345	NA	AY123357	NA	NA	KR262616	AY573142	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Nowickia ferox	NA	FJ025416	FJ025476	FJ025500	FJ025562	NA	NA	FJ025659	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Gymnosoma nudifrons	NA	NA	GQ409130	NA	KC177832	NA	KC177245	KP044778	NA	GQ409398	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Dinera grisescens	NA	FJ913874	FJ913867	NA	MK070613	NA	MK338041	HQ583161	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Blondelia hyphantriae	NA	NA	NA	KP954325	KP954356	NA	KP973910	HQ634223	NA	NA	NA	NA	NA	NA	NA	NA	NA	KP260670
Tachinidae	Dufouria chalybeata	NA	HM770470	HM770489	NA	MK070618	NA	MK338048	KX844212	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Strongygaster triangulifera	NA	NA	NA	KP954349	KP954379	NA	MF414554	HM412619	NA	NA	NA	NA	NA	NA	NA	NA	NA	KP260680
Tachinidae	Aplomya theclarum	NA	NA	NA	NA	AF366652	NA	MK337973	JF869069	NA	NA	AF364346	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Eucelatoria armigera	NA	NA	NA	NA	AF366665	NA	MK338062	JQ520141	NA	NA	AF364362	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Exorista sorbillans	NA	NA	NA	NA	NA	NA	NA	HQ322500	NA	HM192802	NA	NA	NA	NA	NA	NA	NA	AB700065
Tachinidae	Belvosia sp1	NA	NA	DQ133027	DQ133059	NA	NA	NA	NA	DQ133095	DQ133131	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Lixophaga latigena	NA	KR262568	KR262595	NA	NA	NA	NA	KR262641	KR262694	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Germaria ruficeps	NA	FJ222688	FJ222718	NA	NA	NA	NA	FJ656175	NA	FJ656187	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Cyrtophleba nitida	NA	NA	NA	NA	JF439569	NA	MK338033	JF439544	NA	NA	JF439520	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Siphona flavifrons	NA	NA	NA	NA	KC177831	KC178321	KC177244	KX844074	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Euthera tentatrix	NA	NA	NA	KP260727	KP260746	NA	MF414498	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	KP260689
Tachinidae	Phasia sp1	NA	NA	NA	NA	KP954374	NA	KP973924	NA	NA	NA	KP899701	NA	NA	NA	NA	NA	NA	KP260692
Tachinidae	Uramya sp1	NA	NA	NA	KP954353	KP954383	NA	KP973931	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	KP260674
Tachinidae	Metadrinomyia flavifrons	NA	KR262571	KR262598	NA	NA	NA	NA	KR262646	KR262697	NA	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Tachina nupta	NA	FJ222672	FJ222704	NA	NA	NA	NA	KX844134	NA	FJ656198	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Tachina corsicana	NA	FJ222667	FJ222695	NA	NA	NA	NA	FJ656182	NA	FJ656194	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Tachina fera	NA	FJ222668	FJ222697	NA	NA	NA	NA	JN298627	NA	FJ656189	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Tachina lurida	NA	FJ222680	FJ222709	NA	NA	NA	NA	MN868845	NA	FJ656190	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Tachina nigrohirta	NA	FJ222682	FJ222714	NA	NA	NA	NA	FJ656180	NA	FJ656192	NA	NA	NA	NA	NA	NA	NA	NA
Tachinidae	Tachina ursina	NA	FJ222681	FJ222712	NA	NA	NA	NA	KX843896	NA	FJ656191	NA	NA	NA	NA	NA	NA	NA	NA
Ulurumyiidae	Ulurumyia macalpinei	NA	GQ409071	GQ409133	GQ409186	KY945986	NA	KY928452	NA	NA	GQ409402	GQ409468	NA	NA	NA	NA	NA	NA	NA

Appendix 3: Larval feeding habit data for all ingroup taxa.

Family	Binomial name	Larval feeding habit	Source
Nemestrinidae	Trichophthalma sp1	Endoparasitoid	Kirk-Spriggs & Sinclair, 2017
Acroceridae	Acrocera orbiculus	Endoparasitoid	Gillung & Winterton, 2019
Acroceridae	Carvalhoa micella	Endoparasitoid	Gillung & Winterton, 2019
Acroceridae	Megalybus sp1	Endoparasitoid	Gillung & Winterton, 2019
Hilarimorphidae	Hilarimorpha mentata	Unknown	Marshall, 2012
Vermileonidae	Vermileo opacus	Predator	Kirk-Spriggs & Sinclair, 2017
Bombyliidae	Bombylius major	Ectoparasitoid	Yeates & Greathead, 1997
Bombyliidae	Neosardus principius	Unknown	
Bombyliidae	Villa sp1	Endoparasitoid	Yeates & Greathead, 1997
Bombyliidae	Comptosia sp1	Unknown	
Bombyliidae	Hemipenthes jaennickeana	Unknown	Yeates & Greathead, 1997; Kirk-Spriggs & Sinclair, 2017
Bombyliidae	Mythicomyia sp1	Unknown	
Bombyliidae	Paracosmus sp1	Unknown	
Bombyliidae	Megapalpus capensis	Unknown	
Bombyliidae	Corsomyza sp1	Unknown	Kirk-Spriggs & Sinclair, 2017
Bombyliidae	Corsomyza sp2	Unknown	Kirk-Spriggs & Sinclair, 2017
Bombyliidae	Pseudopenthes fenestrata	Unknown	
Bombyliidae	Ligyra satyrus	Ectoparasitoid	Yeates & Greathead, 1997
Bombyliidae	Heterotropus sp1	Predator	Kirk-Spriggs & Sinclair, 2017
Bombyliidae	Thraxan acutus	Unknown	
Bombyliidae	Exoprosopa latelimbata	Unknown	Yeates & Greathead, 1997; Kirk-Spriggs & Sinclair, 2017
Bombyliidae	Atrichochira sp1	Unknown	Kirk-Spriggs & Sinclair, 2017
Bombyliidae	Ligyra punctipennis	Ectoparasitoid	Yeates & Greathead, 1997
Bombyliidae	Villa fuscicostata	Endoparasitoid	Yeates & Greathead, 1997
Bombyliidae	Mythicomyia atra	Unknown	
Bombyliidae	Anthrax maculatus	Ectoparasitoid	Yeates & Greathead, 1997; Kirk-Spriggs & Sinclair, 2017
Bombyliidae	Comptosia quadripennis	Unknown	
Bombyliidae	Thraxan ebenus	Unknown	
Bombyliidae	Exoprosopa adelaidica	Unknown	Yeates & Greathead, 1997; Kirk-Spriggs & Sinclair, 2017
Asilidae	Lasiopogon cinctus	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Machimus occidentalis	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Philonicus albiceps	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Asilus crabroniformis	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Diogmites grossus	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Stichopogon trifasciatus	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Afroestricus chiastoneurus	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Asilus sericeus	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Choerades bella	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Connomyia varipennis	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Damalis monochaetes	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Dasypogon diadema	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Dioctria hyalipennis	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Dysmachus trigonus	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Emphysomera pallidapex	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Holcocephala abdominalis	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Lamyra gulo	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Lasiopogon aldrichii	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Laxenecera albicincta	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Leptogaster arida	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Leptogaster cylindrica	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Lestomyia fraudiger	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Lycostommyia albifacies	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Molobratia teutonus	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Neoitamus cyanurus	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Neolophonotus bimaculatus	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Ommatius tibialis	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Pegesimallus laticornis	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Philodicus tenuipes	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Pogonioefferia pogonias	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Proctacanthus philadelphicus	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Prolepsis tristis	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Saropogon luteus	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Stichopogon punctum	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Tolmerus atricapillus	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Trichardis effrena	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Willistonina bilineata	Predator	Kirk-Spriggs & Sinclair, 2017
Asilidae	Ceraturgus fasciatus	Predator	Kirk-Spriggs & Sinclair, 2017
Mydidae	Mydas clavatus	Predator	Kirk-Spriggs & Sinclair, 2017
Mydidae	Nemomydas pantherinus	Predator	Kirk-Spriggs & Sinclair, 2017
Apioceridae	Apiocera haruspex	Predator	Kirk-Spriggs & Sinclair, 2017
Evocoidae	Evocoa chilensis	Unknown	Marshall, 2012
Apsilocephalidae	Apsilocephala longistyla	Unknown	
Scenopinidae	Riekiella sp1	Predator	Kirk-Spriggs & Sinclair, 2017, Marshall, 2012
Scenopinidae	Scenopinus fenestralis	Predator	Kirk-Spriggs & Sinclair, 2017, Marshall, 2012
Therevidae	Acrosathe novella	Predator	Kirk-Spriggs & Sinclair, 2017, Marshall, 2012
Therevidae	Henicomyia hubbardi	Predator	Kirk-Spriggs & Sinclair, 2017, Marshall, 2012
Therevidae	Patanothrix wilsoni	Predator	Kirk-Spriggs & Sinclair, 2017, Marshall, 2012
Therevidae	Hemigephyra atra	Predator	Kirk-Spriggs & Sinclair, 2017, Marshall, 2012
Therevidae	Phycus kroberi	Predator	Kirk-Spriggs & Sinclair, 2017, Marshall, 2012
Austroleptidae	Austroleptis multimaculata	Unknown	Marshall, 2012
Bolbomyiidae	Bolbomyia nana	Unknown	Marshall, 2012
Rhagionidae	Spaniopsis clelandi	Predator	Marshall, 2012
Rhagionidae	Chrysopilus thoracicus	Predator	Marshall, 2012

Appendix 3: Larval feeding habit data for all ingroup taxa.

Family	Binomial name	Larval feeding habit	Source
Rhagionidae	Rhagio hirtus	Predator	Marshall, 2012
Rhagionidae	Rhagio scolopaceus	Predator	Marshall, 2012
Pantophthalmidae	Pantophthalmus bellardii	Saprophage	Marshall, 2012
Stratiomyidae	Myxosargus knowltoni	Unknown	
Stratiomyidae	Hermetia illucens	Saprophage	Kirk-Spriggs & Sinclair, 2021; McAlpine, 1981
Stratiomyidae	Chloromyia formosa	Saprophage	Kirk-Spriggs & Sinclair, 2021
Stratiomyidae	Clitellaria ephippium	Unknown	
Stratiomyidae	Sargus bipunctatus	Saprophage	Lessard *et al.*, 2020
Stratiomyidae	Microchrysa polita	Saprophage	Kirk-Spriggs & Sinclair, 2021
Stratiomyidae	Antissa sp1	Saprophage	Kirk-Spriggs & Sinclair, 2021
Stratiomyidae	Dieuryneura stigma	Saprophage	Kirk-Spriggs & Sinclair, 2021
Stratiomyidae	Pachygaster montana	Saprophage	Marshall, 2012
Stratiomyidae	Neoberis brasiliana	Unknown	
Stratiomyidae	Stratiomys laticeps	Unknown	
Stratiomyidae	Hedriodiscus binotatus	Unknown	
Stratiomyidae	Rosapha variegata	Saprophage	Kirk-Spriggs & Sinclair, 2021
Stratiomyidae	Oplodontha viridula	Unknown	Kirk-Spriggs & Sinclair, 2021
Xylomyidae	Xylomya parens	Saprophage	Kirk-Spriggs & Sinclair, 2017; Marshall, 2012
Athericidae	Atherix variegata	Predator	Kirk-Spriggs & Sinclair, 2017
Oreoleptidae	Oreoleptis torrenticola	Predator	Zloty *et al.*, 2005
Pelecorhynchidae	Glutops singularis	Predator	McAlpine, 1981
Tabanidae	Scaptia patula	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Fidena rhinophora	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Haematopota pluvialis	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Tabanus atratus	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Rhigioglossa edentula	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Chrysops viduatus	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Apocampta subcana	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Copidapha aureohirta	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Dasybasis neobasalis	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Goniops chrysocoma	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Myioscaptia calliphora	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Anzomyia pegasus	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Pityocera cervus	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Scione equatoriensis	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Pseudoscione vittata	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Triclista guttata	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Osca lata	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Parosca viridiventris	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Plinthina arnhemensis	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Adersia oestroides	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Copidapha guttipennis	Predator	Kirk-Spriggs & Sinclair, 2017
Tabanidae	Pseudoscione dorsoguttata	Predator	Kirk-Spriggs & Sinclair, 2017
Xylophagaidae	Exeretonevra angustifrons	Predator	Palmer & Yeates, 2000
Atelestidae	Meghyperus sudeticus	Unknown	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Syntormon flexibile	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Campsicnemus curvipes	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Neurigona quadrifasciata	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Acropsilus sp1	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Acropsilus sp2	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Campsicnemus amblytylus	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Campsicnemus distinctus	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Campsicnemus loripes	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Campsicnemus modicus	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Campsicnemus mucronatus	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Campsicnemus scambus	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Chaetogonopteron chaeturum	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Chaetogonopteron sp1	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Chrysosoma bearni	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Chrysosoma sp1	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Chrysotus sp1	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Dolichopus latilimbatus	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Dolichopus pennatus	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Dolichopus plumipes	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Dolichopus ungulatus	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Dolichopus tanythrix	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Gymnopternus aerosus	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Hercostomus brevidigitalis	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Lichtwardtia ziczac	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Medetera grisescens	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Nanothinophilus hoplites	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Neurigona sp1	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Neurigona squamifera	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Paraclius digitatus	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Phacaspis mitis	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Plagiozopelma flavipodex	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Poecilobothrus nobilitatus	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Scotiomyia sp1	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Sybistroma obscurellum	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Tachytrechus tessellatus	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Thambemyia pagdeni	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Thinophilus asiobates	Predator	Kirk-Spriggs & Sinclair, 2017
Dolichopodidae	Thinophilus murphyi	Predator	Kirk-Spriggs & Sinclair, 2017

Appendix 3: Larval feeding habit data for all ingroup taxa.

Family	Binomial name	Larval feeding habit	Source
Dolichopodidae	Thinophilus nitens	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Oreogeton scopifer	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Empis barbatoides	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Heterophlebus versabilis	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Trichopeza longicornis	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Empis producta	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Empis sp1	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Gloma fuscipennis	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Hemerodromia sp1	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Microphor holosericeus	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Ragas unica	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Dolichocephala guttata	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Heleodromia immaculata	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Heleodromia boreoalpina	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Wiedemannia bistigma	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Clinocera maculata	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Empis bicuspidata	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Hilara interstincta	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Hilara abdominalis	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Rhamphomyia crassirostris	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Chelifera sp1	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Phyllodromia melanocephala	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Microphorella malaysiana	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Parathalassius candidatus	Predator	Kirk-Spriggs & Sinclair, 2017
Empididae	Anthepiscopus sp1	Predator	Kirk-Spriggs & Sinclair, 2017
Hybotidae	Stilpon graminum	Predator	Kirk-Spriggs & Sinclair, 2017
Hybotidae	Hybos culiciformis	Predator	Kirk-Spriggs & Sinclair, 2017
Hybotidae	Ocydromia glabricula	Predator	Kirk-Spriggs & Sinclair, 2017
Hybotidae	Oedalea hybotina	Predator	Kirk-Spriggs & Sinclair, 2017
Hybotidae	Hybos femoratus	Predator	Kirk-Spriggs & Sinclair, 2017
Hybotidae	Elaphropeza neesoonensis	Predator	Kirk-Spriggs & Sinclair, 2017
Hybotidae	Chersodromia nigripennis	Predator	Kirk-Spriggs & Sinclair, 2017
Hybotidae	Nanodromia narmkroi	Predator	Kirk-Spriggs & Sinclair, 2017
Hybotidae	Tachypeza nubila	Predator	Kirk-Spriggs & Sinclair, 2017
Hybotidae	Crossopalpus nigritellus	Predator	Kirk-Spriggs & Sinclair, 2017
Apystomyiidae	Apystomyia elinguis	Unknown	Marshall, 2012
Lonchopteridae	Lonchoptera sp1	Saprophage	Kirk-Spriggs & Sinclair, 2017
Opetiidae	Opetia nigra	Mycophagous	Tkoc & Rohacek, 2014
Platypezidae	Platypeza sp1	Mycophagous	Kirk-Spriggs & Sinclair, 2017
Ironomyiidae	Ironomyia nigromaculata	Unknown	Li & Yeates, 2019
Phoridae	Megaselia abdita	Saprophage	Manlove & Disney, 2008
Phoridae	Megaselia scalaris	Saprophage, Predator, Parasite, Phytophage	Disney, 2008
Phoridae	Sciadocera rufomaculata	Saprophage	Kavazos *et al.*, 2011
Phoridae	Conicera dauci	Saprophage	Brown *et al.*, 2010
Phoridae	Beckerina luteola	Unknown	
Phoridae	Melaloncha horologia	Endoparasitoid	Brown *et al.*, 2010
Phoridae	Apocephalus spinosus	Endoparasitoid	Brown *et al.*, 2010
Phoridae	Gymnophora spiracularis	Saprophage	Brown *et al.*, 2010
Phoridae	Diplonevra nitidula	Unknown	Brown *et al.*, 2010
Phoridae	Phora holosericea	Unknown	Brown *et al.*, 2010
Phoridae	Dohrniphora gigantea	Unknown	
Phoridae	Triphleba sp1	Saprophage	Brown *et al.*, 2010
Phoridae	Borophaga verticalis	Unknown	
Phoridae	Melaloncha acoma	Endoparasitoid	Brown *et al.*, 2010
Phoridae	Melaloncha feleoae	Endoparasitoid	Brown *et al.*, 2010
Phoridae	Melaloncha pilula	Endoparasitoid	Brown *et al.*, 2010
Phoridae	Melaloncha adusta	Endoparasitoid	Brown *et al.*, 2010
Phoridae	Dohrniphora cornuta	Unknown	
Phoridae	Apocephalus curtus	Endoparasitoid	Brown *et al.*, 2010
Phoridae	Apocephalus flexiseta	Endoparasitoid	Brown *et al.*, 2010
Phoridae	Apocephalus orthocladus	Endoparasitoid	Brown *et al.*, 2010
Pipunculidae	Pipunculus sp1	Endoparasitoid	Marshall, 2012
Pipunculidae	Cephalops longistylis	Endoparasitoid	Marshall, 2012
Pipunculidae	Nephrocerus daeckei	Endoparasitoid	Marshall, 2012
Pipunculidae	Elmohardyia atlantica	Endoparasitoid	Marshall, 2012
Pipunculidae	Pipunculus houghi	Endoparasitoid	Marshall, 2012
Pipunculidae	Cephalops cochleatus	Endoparasitoid	Marshall, 2012
Syrphidae	Episyrphus balteatus	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Rhingia nasica	Saprophage	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Microdon tristis	Predator	Reemer, 2013
Syrphidae	Toxomerus marginatus	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Allograpta alta	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Allograpta sp1	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Atylobaccha flukiella	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Baccha elongata	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Eristalis tenax	Saprophage	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Leucopodella gracilis	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Leucopodella sp1	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Ocyptamus antiphates	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Ocyptamus dimidiatus	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Ocyptamus fascipennis	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Ocyptamus funebris	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Ocyptamus fuscipennis	Predator	Kirk-Spriggs & Sinclair, 2021

Appendix 3: Larval feeding habit data for all ingroup taxa.

Family	Binomial name	Larval feeding habit	Source
Syrphidae	Ocyptamus macropyga	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Ocyptamus norina	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Ocyptamus rubricosus	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Paragus haemorrhous	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Pelecinobaccha adspersa	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Pelecinobaccha alicia	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Pelecinobaccha ovipositoria	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Pseudodoros clavatus	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Relictanum crassum	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Relictanum magisadspersum	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Salpingogaster sp1	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Salpingogaster sp2	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Temnostoma vespiforme	Saprophage	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Toxomerus politus	Predator	Kirk-Spriggs & Sinclair, 2021
Syrphidae	Toxomerus virgulatus	Predator	Kirk-Spriggs & Sinclair, 2021
Conopidae	Myopa sp1	Endoparasitoid	Marshall, 2012
Conopidae	Physocephala marginata	Endoparasitoid	Marshall, 2012
Conopidae	Stylogaster neglecta	Endoparasitoid	Marshall, 2012
Conopidae	Dalmannia nigriceps	Endoparasitoid	Marshall, 2012
Australimyzidae	Australimyza sp1	Saprophage	Brake & Mathis, 2007
Canacidae	Tethinosoma fulvifrons	Unknown	Kirk-Spriggs & Sinclair, 2021
Carnidae	Carnus hemapterus	Saprophage	Kirk-Spriggs & Sinclair, 2021
Chloropidae	Thaumatomyia notata	Predator	Kirk-Spriggs & Sinclair, 2021
Chloropidae	Incertella albipalpis	Phytophage	Deeming & Al-Dhafer, 2012
Chloropidae	Oscinella frit	Phytophage	Kirk-Spriggs & Sinclair, 2021
Chloropidae	Chaetochlorops inquilinus	Unknown	
Chloropidae	Thaumatomyia sp1	Predator	Kirk-Spriggs & Sinclair, 2021
Chloropidae	Incertella incerta	Phytophage	Deeming & Al-Dhafer, 2012
Chloropidae	Meromyza columbi	Phytophage	Kirk-Spriggs & Sinclair, 2021
Chloropidae	Elachiptera bimaculata	Saprophage	Kirk-Spriggs & Sinclair, 2021
Chloropidae	Cryptonevra nigritarsis	Phytophage	Kirk-Spriggs & Sinclair, 2021
Chloropidae	Lasiosina albipila	Unknown	
Inbiomyiidae	Inbiomyia mcalpineorum	Unknown	Brown *et al.*, 2010
Milichiidae	Paramyia nitens	Saprophage	Kirk-Spriggs & Sinclair, 2021
Nannodastiidae	Azorastia mediterranea	Unknown	Brown *et al.*, 2010
Ephydridae	Scatella hawaiiensis	Saprophage	Kirk-Spriggs & Sinclair, 2021
Ephydridae	Hydrellia tritici	Saprophage	Kirk-Spriggs & Sinclair, 2021
Ephydridae	Hydrellia pakistanae	Saprophage	Kirk-Spriggs & Sinclair, 2021
Ephydridae	Ephydra packardi	Saprophage	Kirk-Spriggs & Sinclair, 2021
Ephydridae	Hydrellia griseola	Saprophage	Kirk-Spriggs & Sinclair, 2021
Ephydridae	Psilopa polita	Saprophage	Kirk-Spriggs & Sinclair, 2021
Ephydridae	Coenia palustris	Saprophage	Kirk-Spriggs & Sinclair, 2021
Ephydridae	Limnellia quadrata	Saprophage	Kirk-Spriggs & Sinclair, 2021
Ephydridae	Ephydra riparia	Saprophage	Kirk-Spriggs & Sinclair, 2021
Ephydridae	Discocerina obscurella	Saprophage	Kirk-Spriggs & Sinclair, 2021
Drosophilidae	Drosophila sp1	Saprophage	Kirk-Spriggs & Sinclair, 2021
Drosophilidae	Phortica picta	Unknown	Kirk-Spriggs & Sinclair, 2021
Drosophilidae	Drosophila immigrans	Saprophage	Kirk-Spriggs & Sinclair, 2021
Drosophilidae	Drosophila hydei	Saprophage	Kirk-Spriggs & Sinclair, 2021
Drosophilidae	Drosophila virilis	Saprophage	Kirk-Spriggs & Sinclair, 2021
Drosophilidae	Chymomyza amoena	Unknown	Brown *et al.*, 2010
Drosophilidae	Chymomyza procnemis	Unknown	Brown *et al.*, 2010
Drosophilidae	Mycodrosophila dimidiata	Mycophage	Brown *et al.*, 2010
Drosophilidae	Samoaia leonensis	Unknown	
Drosophilidae	Scaptodrosophila latifasciaefor	Unknown	Kirk-Spriggs & Sinclair, 2021
Drosophilidae	Scaptodrosophila lebanonensis	Unknown	Kirk-Spriggs & Sinclair, 2021
Drosophilidae	Scaptomyza crassifemur	Phytophage	Kirk-Spriggs & Sinclair, 2021
Drosophilidae	Amiota leucostoma	Saprophage	Kirk-Spriggs & Sinclair, 2021
Drosophilidae	Amiota setigera	Saprophage	Kirk-Spriggs & Sinclair, 2021
Drosophilidae	Leucophenga albofasciata	Unknown	Kirk-Spriggs & Sinclair, 2021
Drosophilidae	Scaptomyza caliginosa	Phytophage	Kirk-Spriggs & Sinclair, 2021
Drosophilidae	Zygothrica sp1	Unknown	Kirk-Spriggs & Sinclair, 2021
Drosophilidae	Zaprionus lineosus	Saprophage	Kirk-Spriggs & Sinclair, 2021
Drosophilidae	Parastegana brevivena	Unknown	
Drosophilidae	Pseudostegana bifasciata	Unknown	
Braulidae	Braula coeca	Palynivore, Malivore	Kirk-Spriggs & Sinclair, 2021
Cryptochetidae	Cryptochetum sp1	Endoparasitoid	Kirk-Spriggs & Sinclair, 2021
Camillidae	Camilla sp1	Saprophage	Kirk-Spriggs & Sinclair, 2021
Curtonotidae	Curtonotum sp1	Unknown	
Diastatidae	Diastata fuscula	Unknown	Brown *et al.*, 2010
Celyphidae	Spaniocelyphus umsinduzi	Saprophage	Kirk-Spriggs & Sinclair, 2021
Chamaemyiidae	Cremifania nearctica	Predator	Kirk-Spriggs & Sinclair, 2021
Lauxaniidae	Sapromyza sp1	Saprophage	Kirk-Spriggs & Sinclair, 2021
Lauxaniidae	Minettia flaveola	Saprophage	Kirk-Spriggs & Sinclair, 2021
Lauxaniidae	Minettia lupulina	Saprophage	Kirk-Spriggs & Sinclair, 2021
Lauxaniidae	Melanina sp1	Saprophage	Kirk-Spriggs & Sinclair, 2021
Lauxaniidae	Lyciella decipiens	Saprophage	Kirk-Spriggs & Sinclair, 2021
Lauxaniidae	Calliopum simillimum	Saprophage	Kirk-Spriggs & Sinclair, 2021
Lauxaniidae	Homoneura mayrhoferi	Saprophage	Kirk-Spriggs & Sinclair, 2021
Lauxaniidae	Minettia longipennis	Saprophage	Kirk-Spriggs & Sinclair, 2021
Lauxaniidae	Lyciella illota	Saprophage	Kirk-Spriggs & Sinclair, 2021
Lauxaniidae	Protrigonometopus maculifron	Saprophage	Kirk-Spriggs & Sinclair, 2021
Cypselosomatidae	Rhinopomyzella sp1	Saprophage	Marshall, 2012

Appendix 3: Larval feeding habit data for all ingroup taxa.

Family	Binomial name	Larval feeding habit	Source
Micropezidae	Micropeza sp1	Saprophage	Marshall, 2012
Micropezidae	Taeniaptera trivittata	Saprophage	Marshall, 2012
Micropezidae	Compsobata cibaria	Saprophage	Marshall, 2012
Neriidae	Telostylinus sp1	Saprophage	Kirk-Spriggs & Sinclair, 2021
Acartophthalmidae	Acartophthalmus nigrinus	Saprophage	Andrade *et al.*, 2015
Agromyzidae	Melanagromyza minimoides	Phytophage	Kirk-Spriggs & Sinclair, 2021
Agromyzidae	Phytomyza ilicicola	Phytophage	Kirk-Spriggs & Sinclair, 2021
Agromyzidae	Liriomyza trifolii	Phytophage	Kirk-Spriggs & Sinclair, 2021
Agromyzidae	Liriomyza huidobrensis	Phytophage	Kirk-Spriggs & Sinclair, 2021
Agromyzidae	Phytomyza glabricola	Phytophage	Kirk-Spriggs & Sinclair, 2021
Agromyzidae	Phytomyza syngenesiae	Phytophage	Kirk-Spriggs & Sinclair, 2021
Agromyzidae	Cerodontha dorsalis	Phytophage	Kirk-Spriggs & Sinclair, 2021
Agromyzidae	Phytomyza aconiti	Phytophage	Kirk-Spriggs & Sinclair, 2021
Agromyzidae	Phytomyza aquilegivora	Phytophage	Kirk-Spriggs & Sinclair, 2021
Agromyzidae	Phytomyza erigerophila	Phytophage	Kirk-Spriggs & Sinclair, 2021
Agromyzidae	Phytomyza plantaginis	Phytophage	Kirk-Spriggs & Sinclair, 2021
Agromyzidae	Liriomyza chinensis	Phytophage	Kirk-Spriggs & Sinclair, 2021
Agromyzidae	Chromatomyia horticola	Phytophage	Kirk-Spriggs & Sinclair, 2021
Agromyzidae	Phytomyza spinaciae	Phytophage	Kirk-Spriggs & Sinclair, 2021
Agromyzidae	Napomyza lateralis	Phytophage	Kirk-Spriggs & Sinclair, 2021
Anthomyzidae	Mumetopia occipitalis	Saprophage	Kirk-Spriggs & Sinclair, 2021
Asteiidae	Leiomyza curvinervis	Mycophagous	Brown et al., 2010
Aulacigastridae	Aulacigaster sp1	Unknown	Kirk-Spriggs & Sinclair, 2021
Clusiidae	Clusia lateralis	Saprophage	Kirk-Spriggs & Sinclair, 2021
Clusiidae	Clusiodes ruficollis	Saprophage	Kirk-Spriggs & Sinclair, 2021
Fergusoninidae	Fergusonina turneri	Phytophage	Scheffer *et al.*, 2017
Marginidae	Margo sp1	Unknown	Kirk-Spriggs & Sinclair, 2021
Megamerinidae	Megamerina sp1	Predator	Rohacek, 2016
Neminidae	Nemula longarista	Unknown	Kirk-Spriggs & Sinclair, 2021
Neurochaetidae	Neurochaeta sp1	Unknown	Kirk-Spriggs & Sinclair, 2021
Odiniidae	Odinia sp1	Unknown	Kirk-Spriggs & Sinclair, 2021
Opomyzidae	Opomyza florum	Phytophage	Vickerman, 1982
Pallopteridae	Toxonevra superba	Unknown	
Periscelididae	Cyamops nebulosus	Unknown	Kirk-Spriggs & Sinclair, 2021
Teratomyzidae	Teratomyza sp1	Unknown	
Xenasteiidae	Xenasteia shalam	Unknown	Kirk-Spriggs & Sinclair, 2021
Coelopidae	Coelopa sp1	Saprophage	Brown *et al.*, 2010
Dryomyzidae	Dryomyza anilis	Saprophage	Mathis & Sueyoshi, 2011
Helosciomyzidae	Neosciomyza luteipennis	Unknown	
Heterocheilidae	Heterocheila buccata	Saprophage	Mathis, 2011
Natalimyzidae	Natalimyza sp1	Saprophage	Barraclough & McAlpine, 2006
Ropalomeridae	Willistoniella pleuropunctata	Unknown	Brown *et al.*, 2010
Sciomyzidae	Limnia sp1	Unknown	Knutson & Vala, 2011
Sciomyzidae	Pelidnoptera nigripennis	Endoparasitoid	Kirk-Spriggs & Sinclair, 2021
Sciomyzidae	Pherbellia annulipes	Predator	Knutson & Vala, 2011
Sepsidae	Themira nigricornis	Saprophage	Kirk-Spriggs & Sinclair, 2021
Sepsidae	Sepsis cynipsea	Saprophage	Kirk-Spriggs & Sinclair, 2021
Chyromyidae	Gymnochiromyia sp1	Saprophage	Kirk-Spriggs & Sinclair, 2021
Heleomyzidae	Epistomyia sp1	Unknown	
Heleomyzidae	Suillia variegata	Saprophage	Rotheray, 2012
Heleomyzidae	Heteromyza atricornis	Saprophage	Rotheray, 2012
Sphaeroceridae	Spelobia bifrons	Saprophage	Kirk-Spriggs & Sinclair, 2021; Marshall, 2012
Sphaeroceridae	Lotophila atra	Saprophage	Kirk-Spriggs & Sinclair, 2021; Marshall, 2012
Sphaeroceridae	Rachispoda sp1	Saprophage	Kirk-Spriggs & Sinclair, 2021; Marshall, 2012
Sphaeroceridae	Frutillaria edenensis	Saprophage	Kirk-Spriggs & Sinclair, 2021; Marshall, 2012
Sphaeroceridae	Apteromyia sp1	Saprophage	Kirk-Spriggs & Sinclair, 2021; Marshall, 2012
Sphaeroceridae	Parasphaerocera sp1	Saprophage	Kirk-Spriggs & Sinclair, 2021; Marshall, 2012
Sphaeroceridae	Archiborborus annulatus	Saprophage	Kirk-Spriggs & Sinclair, 2021; Marshall, 2012
Diopsidae	Teleopsis dalmanni	Saprophage	Kirk-Spriggs & Sinclair, 2021
Psilidae	Chyliza scrobiculata	Phytophage	Brown *et al.*, 2010
Somatiidae	Somatia aestiva	Unknown	Brown *et al.*, 2010
Syringogastridae	Syringogaster sp1	Unknown	Brown *et al.*, 2010
Strongylophthalmyiidae	Strongylophthalmyia angustipe	Saprophage	Lonsdale, 2013
Tanypezidae	Neotanypeza sp1	Unknown	
Richardiidae	Richardia teevani	Saprophage	Brown *et al.*, 2010
Lonchaeidae	Lonchaea polita	Saprophage	Kirk-Spriggs & Sinclair, 2021
Lonchaeidae	Silba adipata	Phytophage	Kirk-Spriggs & Sinclair, 2021
Lonchaeidae	Dasiops inedulis	Phytophage	Kirk-Spriggs & Sinclair, 2021
Piophilidae	Piophila nigriceps	Saprophage	Rochefor *et al.*, 2015
Ulidiidae	Melieria omissa	Saprophage	Kirk-Spriggs & Sinclair, 2021
Ulidiidae	Tritoxa flexa	Saprophage	Kirk-Spriggs & Sinclair, 2021
Platystomatidae	Lamprogaster nigripes	Saprophage	Kirk-Spriggs & Sinclair, 2021
Platystomatidae	Rivellia syngenesiae	Saprophage	Kirk-Spriggs & Sinclair, 2021
Platystomatidae	Rivellia alini	Saprophage	Kirk-Spriggs & Sinclair, 2021
Platystomatidae	Platystoma seminationis	Saprophage	Kirk-Spriggs & Sinclair, 2021
Platystomatidae	Pterogenia sp1	Saprophage	Kirk-Spriggs & Sinclair, 2021
Ctenostylidae	Sinolochmostylia sinica	Unknown	
Pyrgotidae	Pyrgota undata	Endoparasitoid	Kirk-Spriggs & Sinclair, 2021
Pyrgotidae	Eupyrgota tigrina	Endoparasitoid	Kirk-Spriggs & Sinclair, 2021
Tephritidae	Ceratitis capitata	Phytophage	Brown *et al.*, 2010
Tephritidae	Bactrocera dorsalis	Phytophage	Brown *et al.*, 2010
Tephritidae	Zeugodacus cucurbitae	Phytophage	Brown *et al.*, 2010
Tephritidae	Bactrocera correcta	Phytophage	Brown *et al.*, 2010

Appendix 3: Larval feeding habit data for all ingroup taxa.

Family	Binomial name	Larval feeding habit	Source
Tephritidae	Bactrocera tryoni	Phytophage	Brown *et al.*, 2010
Tephritidae	Bactrocera carambolae	Phytophage	Brown *et al.*, 2010
Tephritidae	Anastrepha obliqua	Phytophage	Brown *et al.*, 2010
Tephritidae	Zeugodacus tau	Phytophage	Brown *et al.*, 2010
Tephritidae	Bactrocera cacuminata	Phytophage	Brown *et al.*, 2010
Tephritidae	Anastrepha ludens	Phytophage	Brown *et al.*, 2010
Tephritidae	Anastrepha suspensa	Phytophage	Brown *et al.*, 2010
Tephritidae	Rhagoletis pomonella	Phytophage	Brown *et al.*, 2010
Tephritidae	Anastrepha fraterculus	Phytophage	Brown *et al.*, 2010
Tephritidae	Bactrocera musae	Phytophage	Brown *et al.*, 2010
Tephritidae	Bactrocera oleae	Phytophage	Brown *et al.*, 2010
Tephritidae	Bactrocera occipitalis	Phytophage	Brown *et al.*, 2010
Tephritidae	Rhagoletis cingulata	Phytophage	Brown *et al.*, 2010
Tephritidae	Zeugodacus cucumis	Phytophage	Brown *et al.*, 2010
Tephritidae	Bactrocera frauenfeldi	Phytophage	Brown *et al.*, 2010
Tephritidae	Bactrocera umbrosa	Phytophage	Brown *et al.*, 2010
Tephritidae	Campiglossa pygmaea	Phytophage	Brown *et al.*, 2010
Tephritidae	Zeugodacus caudatus	Phytophage	Brown *et al.*, 2010
Tephritidae	Tachinisca cyaneiventris	Endoparasitoid	Brown *et al.*, 2010
Tephritidae	Anastrepha curvicauda	Phytophage	Brown *et al.*, 2010
Glossinidae	Glossina morsitans	Non-feeding	Marshall, 2012
Hippoboscidae	Ortholfersia minuta	Non-feeding	Marshall, 2012
Hippoboscidae	Ornithomya avicularia	Non-feeding	Marshall, 2012
Hippoboscidae	Stenepteryx hirundinis	Non-feeding	Marshall, 2012
Hippoboscidae	Lipoptena cervi	Non-feeding	Marshall, 2012
Nycteribiidae	Penicillidia fulvida	Non-feeding	Marshall, 2012
Streblidae	Trichobius longipes	Non-feeding	Marshall, 2012
Fanniidae	Fannia canicularis	Saprophage	Marshall, 2012
Fanniidae	Fannia manicata	Saprophage	Marshall, 2012
Muscidae	Musca domestica	Saprophage, Parasite	Brown *et al.*, 2010
Muscidae	Stomoxys calcitrans	Saprophage	Brown *et al.*, 2010
Muscidae	Helina evecta	Predator	Brown *et al.*, 2010
Muscidae	Atherigona orientalis	Saprophage	Brown *et al.*, 2010
Muscidae	Muscina stabulans	Saprophage, Parasite, Predator	Brown *et al.*, 2010
Muscidae	Musca autumnalis	Saprophage	Brown *et al.*, 2010
Muscidae	Hydrotaea aenescens	Saprophage	Brown *et al.*, 2010
Muscidae	Drymeia alpicola	Predator	Brown *et al.*, 2010
Muscidae	Huckettomyia watanabei	Unknown	
Muscidae	Dichaetomyia bibax	Unknown	
Muscidae	Polietes lardarius	Saprophage, Predator	Skidmore, 1985
Muscidae	Thricops cunctans	Unknown	
Muscidae	Synthesiomyia nudiseta	Saprophage	Ivorra *et al.*, 2021
Muscidae	Limnophora exuta	Predator	Brown *et al.*, 2010
Muscidae	Lispe tentaculata	Predator	Brown *et al.*, 2010
Muscidae	Haematobosca stimulans	Saprophage	Skidmore, 1985
Muscidae	Mydaea ancilla	Saprophage, Predator	Brown *et al.*, 2010
Muscidae	Potamia littoralis	Predator	Skidmore, 1985
Muscidae	Cyrtoneuropsis veniseta	Unknown	
Muscidae	Achanthiptera rohrelliformis	Predator	Skidmore, 1985
Muscidae	Helina lasiophthalma	Predator	Brown *et al.*, 2010
Muscidae	Hydrotaea cyrtoneurina	Saprophage	Brown *et al.*, 2010
Muscidae	Hydrotaea dentipes	Saprophage, Predator	Brown *et al.*, 2010
Muscidae	Limnophora maculosa	Predator	Brown *et al.*, 2010
Muscidae	Lispe sericipalpis	Predator	Brown *et al.*, 2010
Anthomyiidae	Delia radicum	Phytophage	Kirk-Spriggs & Sinclair, 2021; Brown *et al.*, 2010
Anthomyiidae	Lasiomma seminitidum	Saprophage	Kirk-Spriggs & Sinclair, 2021; Brown *et al.*, 2010
Anthomyiidae	Lasiomma latipenne	Saprophage	Kirk-Spriggs & Sinclair, 2021; Brown *et al.*, 2010
Anthomyiidae	Emmesomyia grisea	Saprophage	Kirk-Spriggs & Sinclair, 2021; Brown *et al.*, 2010
Anthomyiidae	Delia platura	Phytophage	Kirk-Spriggs & Sinclair, 2021; Brown *et al.*, 2010
Anthomyiidae	Botanophila fugax	Saprophage	Kirk-Spriggs & Sinclair, 2021
Anthomyiidae	Hydrophoria lancifer	Saprophage	Kirk-Spriggs & Sinclair, 2021
Anthomyiidae	Hylemya variata	Unknown	Kirk-Spriggs & Sinclair, 2021
Anthomyiidae	Paregle coerulescens	Unknown	Kirk-Spriggs & Sinclair, 2021
Anthomyiidae	Pegoplata infirma	Saprophage	Kirk-Spriggs & Sinclair, 2021; Brown *et al.*, 2010
Scathophagidae	Scathophaga stercoraria	Saprophage	Blanckenhorn *et al.*, 2010
Scathophagidae	Cordilura atrata	Phytophage	James, 1955
Calliphoridae	Eurychaeta palpalis	Saprophage	Brown *et al.*, 2010; Nasser *et al.,* 2021
Calliphoridae	Chrysomya megacephala	Saprophage, Predator, Parasite	Brown *et al.*, 2010; Nasser *et al.,* 2021
Calliphoridae	Lucilia sericata	Saprophage, Parasite	Brown *et al.*, 2010; Nasser *et al.,* 2021
Calliphoridae	Calliphora vomitoria	Saprophage, Parasite	Brown *et al.*, 2010; Nasser *et al.,* 2021
Calliphoridae	Cochliomyia macellaria	Saprophage, Parasite	Brown *et al.*, 2010; Nasser *et al.,* 2021
Calliphoridae	Calliphora vicina	Saprophage, Parasite	Brown *et al.*, 2010; Nasser *et al.,* 2021
Calliphoridae	Lucilia caesar	Saprophage, Parasite	Brown *et al.*, 2010; Nasser *et al.,* 2021
Calliphoridae	Phormia regina	Saprophage, Parasite	Brown *et al.*, 2010; Nasser *et al.,* 2021
Mesembrinellidae	Mesembrinella bellardiana	Saprophage, Parasite	Nasser *et al.*, 2021
Mystacinobiidae	Mystacinobia zelandica	Saprophage	Gleeson *et al.*, 2000
Oestridae	Cuterebra austeni	Parasite	Marshall, 2012
Polleniidae	Pollenia rudis	Predator	Nasser *et al.*, 2021
Rhiniidae	Stomorhina lunata	Predator	Marshall, 2012
Rhiniidae	Rhyncomya nigripes	Unknown	
Rhinophoridae	Stevenia hertingi	Endoparasitoid	Marshall, 2012
Sarcophagidae	Wohlfahrtia trina	Unknown	
Sarcophagidae	Sarcophaga peregrina	Saprophage	Brown *et al.*, 2010

Appendix 3: Larval feeding habit data for all ingroup taxa.

Family	Binomial name	Larval feeding habit	Source
Sarcophagidae	Sarcophaga crassipalpis	Saprophage	Brown *et al.*, 2010
Sarcophagidae	Sarcophaga dux	Saprophage, Parasite	Sukontason *et al.*, 2014
Sarcophagidae	Helicobia rapax	Unknown	
Sarcophagidae	Blaesoxipha plinthopyga	Saprophage, Parasite	Wells & Smith, 2013
Sarcophagidae	Sphenometopa claripennis	Unknown	
Sarcophagidae	Taxigramma multipunctata	Unknown	
Sarcophagidae	Nyctia lugubris	Unknown	
Sarcophagidae	Titanogrypa luculenta	Unknown	
Sarcophagidae	Sarcophaga omikron	Saprophage	Brown *et al.*, 2010
Sarcophagidae	Ravinia querula	Saprophage	Pape, 1996
Sarcophagidae	Peckia intermutans	Saprophage	Brown *et al.*, 2010
Sarcophagidae	Boettcheria cimbicis	Unknown	
Sarcophagidae	Villegasia postuncinata	Saprophage	Brown *et al.*, 2010
Tachinidae	Triarthria setipennis	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Epalpus signifer	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Gymnosoma nitens	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Pseudogonia rufifrons	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Mintho rufiventris	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Exorista larvarum	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Phania funesta	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Tachina grossa	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Gymnocheta viridis	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Ceracia dentata	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Hyphantrophaga virilis	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Lespesia aletiae	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Voria ruralis	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Tachina magnicornis	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Peleteria rubescens	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Tachinomyia nigricans	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Cylindromyia binotata	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Panzeria ampelus	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Ptilodexia conjuncta	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Siphona plusiae	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Trichopoda pennipes	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Winthemia sinuata	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Campylocheta semiothisae	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Epigrimyia illinoensis	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Thelaira americana	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Archytas nivalis	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Nowickia ferox	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Gymnosoma nudifrons	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Dinera grisescens	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Blondelia hyphantriae	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Dufouria chalybeata	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Strongygaster triangulifera	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Aplomya theclarum	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Eucelatoria armigera	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Exorista sorbillans	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Belvosia sp1	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Lixophaga latigena	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Germaria ruficeps	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Cyrtophleba nitida	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Siphona flavifrons	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Euthera tentatrix	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Phasia sp1	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Uramya sp1	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Metadrinomyia flavifrons	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Tachina nupta	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Tachina corsicana	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Tachina fera	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Tachina lurida	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Tachina nigrohirta	Endoparasitoid	Brown *et al.*, 2010
Tachinidae	Tachina ursina	Endoparasitoid	Brown *et al.*, 2010
Ulurumyiidae	Ulurumyia macalpinei	Saprophage	Michelson & Pape, 2017