THE STREPSIPTERA PROBLEM: PHYLOGENY OF THE HOLOMETABOLOUS INSECT ORDERS INFERRED FROM 18S AND 28S RIBOSOMAL DNA SEQUENCES AND MORPHOLOGY

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Abstract.—Phylogenetic relationships among the holometabolous insect orders were inferred from cladistic analysis of nucleotide sequences of 18S ribosomal DNA (rDNA) (85 exemplars) and 28S rDNA (52 exemplars) and morphological characters. Exemplar outgroup taxa were Collembola (1 sequence), Archaeognatha (1), Ephemerida (1), Odonata (2), Plecoptera (2), Blattodea (1), Mantodea (1), Dermaptera (1), Orthoptera (1), Phasmatodea (1), Embioptera (1), Psocoptera (1), Phthiraptera (1), Hemiptera (4), and Thysanoptera (1). Exemplar ingroup taxa were Coleoptera: Archostemata (1), Adephaga (2), and Polyphaga (7); Megaloptera (1); Raphidioptera (1); Neuroptera (sensu stricto = Planipennia): Mantispoidea (2), Hemerobioidea (2), and Myrmeleontoidea (2); Hymenoptera: Symphyta (4) and Apocrita (19); Trichoptera: Hydropsychoidea (1) and Limnephiloidea (2); Lepidoptera: Ditrysia (3); Siphonaptera: Pulicoidea (1) and Ceratophylloidea (2); Mecoptera: Meropeidae (1), Boreidae (1), Panorpidae (1), and Bittacidae (2); Diptera: Nematocera (1), Brachycera (2), and Cyclorrhapha (1); and Strepsiptera: Corioxenidae (1), Myrmecolacidae (1), Elenchidae (1), and Sylopidae (3). We analyzed \sim 1 kilobase of 18S rDNA, starting 398 nucleotides downstream of the 5' end, and \sim 400 bp of 28S rDNA in expansion segment D3. Multiple alignment of the 18S and 28S sequences resulted in 1,116 nucleotide positions with 24 insert regions and 398 positions with 14 insert regions, respectively. All Strepsiptera and Neuroptera have large insert regions in 18S and 28S. The secondary structure of 18S insert 23 is composed of long stems that are GC rich in the basal Strepsiptera and AT rich in the more derived Strepsiptera. A matrix of 176 morphological characters was analyzed for holometabolous orders. Incongruence length difference tests indicate that the 28S + morphological data sets are incongruent but that 28S + 18S, 18S + morphology, and 28S + 18S + morphology fail to reject the hypothesis of congruence. Phylogenetic trees were generated by parsimony analysis, and clade robustness was evaluated by branch length, Bremer support, percentage of extra steps required to force paraphyly, and sensitivity analysis using the following parameters: gap weights, morphological character weights, methods of data set combination, removal of key taxa, and alignment region. The following are monophyletic under most or all combinations of parameter values: Holometabola, Polyphaga, Megaloptera + Raphidioptera, Neuroptera, Hymenoptera, Trichoptera, Lepidoptera, Amphiesmenoptera (Trichoptera + Lepidoptera), Siphonaptera, Siphonaptera + Mecoptera, Strepsiptera, Diptera, and Strepsiptera + Diptera (Halteria). Antliophora (Mecoptera + Diptera + Siphonaptera + Strepsiptera), Mecopterida (Antliophora + Amphiesmenoptera), and Hymenoptera + Mecopterida are supported in the majority of total evidence analyses. Mecoptera may be paraphyletic because Boreus is often placed as sister group to the fleas; hence, Siphonaptera may be subordinate within Mecoptera. The 18S sequences for Priacma (Coleoptera: Archostemata), Colpocaccus (Coleoptera: Adephaga), Agulla (Raphidioptera), and Corydalus (Megaloptera) are nearly identical, and Neuropterida are monophyletic only when those two beetle sequences are removed from the analysis. Coleoptera are therefore paraphyletic under almost all combinations of parameter values. Halteria and Amphiesmenoptera have high Bremer support values and long branch lengths. The data do not support placement of Strepsiptera outside of Holometabola nor as sister group to Coleoptera. We reject the notion that the monophyly of Halteria is due to long branch attraction because Strepsiptera and Diptera do not have the longest branches and there is phylogenetic congruence between molecules, across the entire parameter space, and between morphological and molecular data. [Alignment; insect orders; molecular systematics; phylogeny; sensitivity analysis; Strepsiptera; taxon sampling.]

Holometabola (=Endopterygota), consisting of more than half of the world's described animal species (Wilson, 1988) and more than 80% of insect species (Kristensen, 1991), is comprised of the orders Coleoptera (beetles), Raphidioptera (snakeflies), Megaloptera (alderflies, dobsonflies), Neuroptera (sensu stricto = Planipennia; lacewings), Hymenoptera (bees, wasps, and ants), Trichoptera (caddisflies), Lepidoptera (moths and butterflies), Mecoptera (scorpionflies), Siphonaptera (fleas), Diptera (flies), and Strepsiptera (twistedwinged parasites). Although the monophyly of Holometabola and the included orders are relatively well established, relationships among the orders are unclear, and only a few sister-group relationships are unambiguously supported by morphological evidence. A major obstacle in establishing a robust phylogenetic hypothesis for these orders has been the problem of homology assessment across such morphologically diverse and ancient groups, whose radiations date back to the Permian (Hennig, 1981; Kukalová-Peck, 1991). A well-supported hypothesis of phylogenetic relationships for these orders has eluded entomologists for two centuries and remains one of the most basic needs of systematic entomology.

Holometabolous Relationships

Hennig (1981) and Kristensen (1991, 1995) suggested four synapomorphies uniting Holometabola: (1) immatures having larval eyes (stemmata) that do not increase in number in successive instars and are not carried over to adult stages, true ocelli absent, and adult compound eyes developed de novo in the adult (Paulus, 1986); (2) wing rudiments and external genitalia first developing below the body surface, evaginating only in the penultimate (larva–pupa) molt; (3) last immature instars nearly always inactive and nonfeeding (=pupae); and (4) tricondylic coxa-body articulation (Kristensen, 1975; Boudreaux, 1979). Hennig (1969, 1981) recognized the supraordinal groups Neuropteroidea (Megaloptera + Neuroptera + Raphidioptera), Mecopteroidea (Trichoptera

+ Lepidoptera + Mecoptera + Diptera), Amphiesmenoptera (Trichoptera + Lepidoptera), and Antliophora (Diptera + Mecoptera), although he did not specify relationships among these groups. The position of Strepsiptera and Siphonaptera—two "highly derived" groups—was problematic, and Hennig presented evidence to associate them with several different orders. Ross (1965) suggested a sister-group relationship between Hymenoptera and the other holometabolous insect orders. Boudreaux (1979) divided Holometabola into "Coleopterida" (Coleoptera + Strepsiptera) and "Telomerida" (remaining orders), although the characters supporting this division have been called into question (Kinzelbach, 1971; Kristensen, 1975; Baccetti, 1989; Kathirithamby et al., 1993).

The most widely accepted notion of insect ordinal relationships is attributable to Kristensen's extensive reviews of insect phylogeny (1975, 1981, 1991, 1995). In his most recent work, Kristensen (1995) divided Holometabola into three major clades: Neuropterida (=Hennig's Neuropteroidea) + Coleoptera, Hymenoptera + Mecopterida, and Mecopterida (=Hennig's Mecopteroidea) (Fig. 1). Kristensen (1995) considered the monophyly of Amphiesmenoptera and Mecopterida well established but had some reservations in placement of Hymenoptera as sister group to Mecopterida.

Strepsiptera Problem

The "Strepsiptera problem" (Kristensen, 1981) remains the most enigmatic question in ordinal-level insect phylogenetics. The Strepsiptera are a small (549 species; Kathirithamby, 1989) monophyletic order of insects with extremely modified morphological and life history features associated with their insect parasitoid lifestyle. Adult strepsipteran females are neotenic and lack antennae, mouthparts, eyes, wings, legs, and genitalia. Adult male Strepsiptera are morphologically extremely derived. Some of their unusual features include antennae bearing lateral flabellar segments, compound eyes with 15–150 ommatidia separated by strips of cuticle or setae, mandi-



FIGURE 1. Kristensen's (1991) phylogeny of insect orders based on morphology, including common supraordinal names. Dotted lines mark areas of questionable relationships.

bles that function as sensory organs and bear setae, absence of a trochanter in the fore and middle legs, absence of a tentorium, and forewings reduced to structures that resemble the halteres of dipterans. There are at least 25 synapomorphies supporting the monophyly of Strepsiptera (Hennig, 1969; Kinzelbach, 1971; Kathirithamby, 1989). This perplexing amalgamation of morphological reduction in the females and extreme modification in the males, combined with unusual biology and larval characteristics, has challenged systematic placement of this group for over two centuries.

Strepsiptera were first recorded by Rossi (1793), who described *Xenos vesparum* and placed it in Hymenoptera near Ichneumonidae. Kirby (1802) described *Stylops melittae* from an andrenid bee but failed to associate his species with Rossi's species. Latreille (1809) moved *Xenos vesparum* to the tribe Phthiromyae within Diptera, and later Kirby (1815) provided the first diagnosis of the anomalies of these insects and proposed the order Strepsiptera. Lamarck (1816) placed these species within the dip-

teran family Rhipidoptera, and then Latrielle (1817) removed them from Diptera and placed them within their own order, Rhipiptera. By the end of the 19th century, Strepsiptera had been placed between Odonata and Ephemerida, Hymenoptera and Lepidoptera, Suctoria (Siphonaptera) and Diptera, and again within Diptera (Pierce, 1909).

More recently, phylogenetic placement of Strepsiptera has revolved around three major hypotheses: inclusion within Coleoptera, placement as sister group to Coleoptera, and placement outside of Holometabola. Lameere (1900), Kolbe (1901), and Ganglbauer (1903) placed Strepsiptera within Coleoptera but were uncertain as to its position relative to other beetle families. Arnett (1963), Crowson (1960, 1981), and Ross et al. (1984) placed Strepsiptera as the family Stylopidae within Coleoptera. Crowson (1960, 1981) favored placement of Stylopidae within Lymexeloidea based upon a questionable scenario requiring soft plant boring as a prerequisite to insect endoparasitism. The most popular polyphagan placement for Strepsiptera is as sister group to Rhipiphoridae, based on presumed similarity of the rhipiphorid reduced elytron and strepsipteran forewing, flabellate antennae, hypermetamorphosis with a triungulin stage, and insect endoparasitism (Crowson, 1960). However, closer examination of these characters reveal that these similarities are based upon erroneous interpretations of strepsipteran morphology and biology (Kathirithamby, 1989; Stehr, 1987; Pix et al., 1993).

Handlirsch (1903), Boerner (1904), and Shipley (1904) placed Strepsiptera as an independent order closely allied to Coleoptera. Kinzelbach (1971, 1990) and Kathirithamby (1989) concurred with this hypothesis but noted that this relationship is supported by a single character: the ability to power flight with the hind wings (posteromotorism). The interpretation of presence of a gula and absence of the prothoracic notopleural suture as a Coleoptera-Strepsiptera synapomorphy (Crowson, 1954, 1960) is not tenable because Strepsiptera are primitively hypognathous (Kinzelbach, 1990) and lack a gula (Kinzelbach, 1971; Kathirithamby, 1989). The interpretation of the strepsipteran forewing as a reduced and modified elytron does not hold up under close scrutiny because the wing does not possess the characteristics of elytron morphology (Kathirithamby, 1989) or function (Pix et al., 1993).

Kristensen (1991) suggested that Strepsiptera may belong outside of Holometabola based on the presence of external wing buds on the second instar larvae and the possession of larval stemmata (Kinzelbach, 1990; Kathirithamby, 1989). However, it is not clear whether these are carried over to the adult stage as in nonholometabolous insects or regenerated during pupation as in Holometabola. Neither of the characters argue specifically against the placement of Strepsiptera within Holometabola, however, because they may be the retention of (or reversion to) a plesiomorphic condition. Research on spermatozoa (Baccetti, 1989; Kathirithamby et al., 1993) has demonstrated the uniqueness of these structures in Strepisptera but does not argue for any particular phylogenetic placement. Because of these unresolved morphological questions, Kristensen (1991) gave "these strangely aberrant insects" a tenative placement as Neoptera *incertae sedis*.

Molecular Evidence

There have been a few attempts to establish relationships within Holometabola through the use of molecular data. Wheeler (1989) found tentative support for the clades Neuroptera + Coleoptera, Holometabola, and Insecta based on a limited sample of sequence and restriction map data. Liu and Beckenbach (1992) sequenced the mitochondrial cytochrome oxidase II gene for 13 insects, 7 representing holometabolous taxa. Under both their phenetic and parsimony analyses, Holometabola were paraphyletic, and the only group congruent with ordinal level morphology was the termite–cockroach clade.

Carmean et al. (1992) assessed holometabolan relationships by sequencing a portion of 18S ribosomal DNA (rDNA). They analyzed 17 sequences representing six holometabolous insect orders (Hymenoptera: 10 sequences, Neuroptera: 2, Mecoptera: 1, Siphonaptera: 1, Diptera: 2, and Coleoptera: 1), one insect outgroup (aphid), and two noninsect arthropods (brine shrimp and bird spider). In their bootstrap consensus tree, Holometabola are paraphyletic because Diptera are placed outside of the clade including the aphid and other holometabolous orders (Fig. 2a). The authors suggested that this "misleading result" could be explained by long-branch attraction (Felsenstein, 1978) between the aphid and flies, and consequently they excluded Diptera from any subsequent analyses. From subset analyses of eight taxa, the authors concluded that Hymenoptera are sister group to Mecopterida, which in turn are sister group to Neuroptera.

Pashley et al. (1993) sequenced multiple conserved regions of 18S rDNA from Holometabola and one outgroup. Although they sampled more holometabolous orders than had any previous researchers, they did not sequence Strepsiptera and Mega-

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FIGURE 2. Prior phylogenetic hypotheses for Holometabola based on molecular data. (a) Carmean et al.'s (1992) bootstrap consensus tree (bootstrap values not included on tree) with Diptera placed outside of Holometabola. (b) Pashley et al.'s (1993) strict consensus of 10 most-parsimonious trees with monophyletic Amphiesmenoptera and Mecopterida; dipteran taxa within Mecopterida.

loptera, used few exemplars from each order, and relied on a single outgroup sequence (aphid) and so could not test for the monophyly of Holometabola. Their analysis supported a monophyletic Amphiesmenoptera and Mecopterida (Fig. 2b). In their analysis, the dipteran sequences are not attracted to the aphid sequence.

MATERIALS AND METHODS Specimens Examined

Taxa were selected for sequencing based on previous hypothesis of relationships within and between orders, with an emphasis on those groups whose phylogenetic placement is most problematic (Table 1). Eighteen outgroup taxa from 14 insect orders were sequenced in an attempt to provide rooting for Holometabola and to test adequately for holometabolan monophyly. These outgroup sequences represent all major nonholometabolous lineages within the insects, with the bulk of them from Paraneoptera (Hemiptera + Thysanoptera + Phthiraptera + Psocoptera), the hypothesized sister group to Holometabola (Kristensen, 1995). Sequences were generated from every holometabolous order. Within each order, an effort was made to select at least one representative from major suborders and multiple representatives from the larger and more diverse lineages. Three of the four coleopteran suborders are represented: Archostemata (1 sequence), Adephaga (2), and Polyphaga (7). Within Neuroptera, the three major superfamilies are present: Mantispoidea (2 sequences), Hemerobioidea (2), and Myrmeleontoidea (2). Representatives from half of the mecopteran families, two major flea lineages (Pulicoidea, Ceratphylloidea), and two major trichopteran lineages (Limnephiloidea, Hydropsychoidea) and three exemplars from Lepidoptera were sequenced. Because the sister-group relationship between Lepidoptera and Trichoptera is considered well established (Kristensen, 1995), fewer exemplars were sequenced from these groups. For Hymenoptera, we have representatives of Symphyta and Apocrita, and within Apocrita we have Parasitica and Aculeata. Dipteran sequences originated from Nematocera, Brachycera, and Cyclorrhapha, and six sequences originate from four strepsipteran families. Although fewer 28S sequences were generated in this study, they still represent all the major groups as outlined above. Important taxa we were unable to include in this collection are exemplars from Mengenillidae (Strepsiptera) and Nannochoristidae (Mecoptera).

To this collection of sequences were added all applicable GenBank sequences (as of March 1995). To be considered applicable, the sequences must sufficiently overlap the regions already sequenced to avoid the in-

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OrthopteraArcfildaeMelanoplus sp.U65115U65116XX	Dermaptera	Labiduridae	Labidura riparia	U65114		Х	Х	Х	Х	
Phasmatodea Phasmatidae Anisomorpha buprestoides U65116 V X X X X X X Pacoptera Psocidae Crastipsocus venosus U65118 X X X X X X X Psocptera Psocidae Crastipsocus venosus U65118 X X X X X X X Psocptera Psocidae Dennyus hirudensis U65119 X X X X X X X Psocpta Aphidae Acyrthosiphon pisum X62623 X X X X X X Saldida Palidee Dennyus hirudensis U65121 U55175 X X X X X X X Saldidae Saldula palipes U65121 U55175 X X X X X X X Saldidae Copocacus posticatus U65123 U55177 X X X X X X X Coleoptera Thripidae Teneiothrips inconsequents U65123 U55177 X X X X X X X Coleoptera Curpedidae Coptocacus posticatus U65125 U55179 X X X X X X Coleoptera Curpedidae Coptocacus posticatus U65125 U55179 X X X X X X Elateridae Octinodes sp. U65126 U55180 X X X X X X Elateridae Octinodes sp. U65126 U55180 X X X X X X Elateridae Octinodes sp. U65128 U55182 X X X X X X Elateridae Octinodes sp. U65128 U55182 X X X X X X X Rhipiphoridae Therbinolatus U65130 U55183 X X X X X X X Corrabacidae Tenebrio molitor X07801 U55183 X X X X X X X Pheloidae Tenebrio molitor X07801 U55184 X X X X X X X Pheloidae Tenebrio molitor X07801 U55184 X X X X X X X Pheloidae Corydalias cognatus U56131 U55185 X X X X X X X Pacoptera Raphidioptera Rapidelae Lolomyia texana U56131 U55187 X X X X X X X Pacoptera Dividae Hemerobius stigmata U56133 U55187 X X X X X X X X Papilionidae Myrmeleon timaculatus U56137 U55191 X X X X X X X X X Papilionidae Hemerobius stigmata U56137 U55191 X X X X X X X X X X Papilionidae Papilionidae Myrmeleon Sp. L10182 X X X X X X X X X X X X X X X X X X X	Orthoptera	Acrididae	Melanoplus sp.	U65115	U65173	X	X	X	X	Х
Embindina Oligotomidae Oligotoma saundersii U65117 U65174 X X X X X X X X Phthiraptera Psocidae Cerastipsocus venosus U65118 X X X X X X X Phthiraptera Menoponidae Demyus hirudensis U65119 X X X X X X X Phthiraptera Aphidae Acyrthosiphon pisum X62623 X X X X X X X Saudidae Saldula pallipes U65121 U65175 X X X X X X X Thysanoptera Thripidae Taeniothrips inconsequents U65122 U65177 X X X X X X X Coleoptera Cupedidae Priacma serrata U65124 U65178 X X X X X X X Carabidae Cybrister finbriolatus U65125 U65179 X X X X X X X Carabidae Cybrister finbriolatus U65125 U65179 X X X X X X X Carabidae Cybrister finbriolatus U65127 U55181 X X X X X X X Carabidae Cybrister finbriolatus U65127 U55181 X X X X X X X Carabidae Cybrister finbriolatus U65127 U55181 X X X X X X X Carabidae Cybrister finbriolatus U65127 U55181 X X X X X X X Carabidae Aloopcas posticatus U65129 X X X X X X X X X X Carabidae Aloopcas posticatus U65129 X X X X X X X X Carabidae Aloopcas pensylvanicus U65129 X X X X X X X X Carabidae Aloopcas pensylvanicus U65130 U55182 X X X X X X X Rhipiphoridae Rhipiphorus fasciatus U65130 U55183 X X X X X X X Republicade Coryadus cognatus U55131 U55185 X X X X X X X X X X X X X X X X X X X	Phasmatodea	Phasmatidae	Anisomorpha buprestoides	U65116		X	X	X	X	
Pscoptera Pscoidae Crastipsocus venosus U65118 X X X X X Phthriaptera Menoponidae Demyus hirudensis U65119 X X X X X Hemiptera Aphidae Acyrthosiphon pisum X62623 X X X X X Saldidae Buenos sp. U65121 U65175 X X X X X X Saldidae Lygus lineolaris U65121 U55175 X X X X X X Thysanoptera Thripidae Taeniothrips inconsequents U65122 U55177 X X X X X X Coleoptera Cupedidae Priacma serrata U65124 U55178 X X X X X X Carabidae Colpocaccus posticatus U65125 U55179 X X X X X X Elateridae Colpocaccus posticatus U65126 U55180 X X X X X X Elateridae Colpocaccus sp. U65129 U55181 X X X X X X Rhipiphoridae Rhipiphorus fascitus U65129 U55181 X X X X X X Megaloptera Raphidiae Rhipiphorus fascitus U65129 U55183 X X X X X Carabidae Meloe proscarabaeus X77766 X X X X X X Megaloptera Raphididae Corydalus cognatus U65132 U55185 X X X X X Rhipiphoridae Rhipiphorus fascitus U65130 U55185 X X X X X X Megaloptera Raphididae Corydalus cognatus U65131 U55185 X X X X X X Raphididoptera Raphididae Corydalus cognatus U65132 U55187 X X X X X X Raphididae Mateprotecarabaeus X77766 X X X X X X X Megaloptera Raphididae Corydalus cognatus U65131 U55185 X X X X X X Raphididoptera Raphididae Agulla sp. U65132 U55187 X X X X X X X Myrmeleontidae Martispa pulchella U55135 U55189 X X X X X X X Myrmeleontidae Martispa pulchella U55135 U55189 X X X X X X X Myrmeleontidae Martispa pulchella U55137 U55191 X X X X X X X X X X X X X X X X X X	Embiidina	Oligotomidae	Oligotoma saundersii	U65117	U65174	Х	Х	Х	Х	Х
Phthiraptera Menoponidae Demnyus hirudensis U65119 X X X X X X Hemiptera Aphidae Acythosiphon pisum X62623 X X X X X X X X Saldidae Guythosiphon pisum X62623 X X X X X X X X X Saldidae Saldula palipes U65121 U65175 X X X X X X X X Thysanoptera Thripidae Taeniohrips inconsequens U65122 U65177 X X X X X X X X Coleoptera Cupedidae Priacma serrata U65124 U55178 X X X X X X X X Carabidae Colpocaccus posticatus U65125 U65179 X X X X X X X X X Dytiscidae Colpoters U65125 U65179 X X X X X X X X X X X X X X X X X Dytiscidae Colpoters u65125 U65179 X X X X X X X X X X X X X X X X X X X	Pscoptera	Psocidae	Cerastipsocus venosus	U65118		X	X	X	X	
HemipteraAphidaeAcyrthosiphon pisunX62623XXXXNotonectidaeSaldula pallipesU65120U65176XXXXXSaldidaeLygus lincolarisU65121U65177XXXXXXThysanopteraThripidaeTaeniothrips inconsequensU65123U65177XXX <td>Phthiraptera</td> <td>Menoponidae</td> <td>Dennyus hirudensis</td> <td>U65119</td> <td></td> <td>X</td> <td>X</td> <td>X</td> <td>X</td> <td></td>	Phthiraptera	Menoponidae	Dennyus hirudensis	U65119		X	X	X	X	
Notonectidae Buenoa sp. U65120 U65176 X X X X X X X X X X X X X Miridae Lygus lineolaris U65121 U65177 X X X X X X X Colecoptera Thripidae Taeniohrips inconsequens U65123 U65177 X X X X X X Z Colecoptera Cupedidae Colpocaccus posticatus U65124 U65178 X X X X X X Dytiscidae Colpocaccus posticatus U65125 U65179 X X X X X X X X S Carabaeidae Colpocaccus posticatus U65125 U65180 X X X X X X X X S Carabaeidae Quiores funnos U65127 U65181 X X X X X X X X X X X S Carabaeidae Quiores funnos U65127 U65181 X X X X X X X X Lampyridae Photuris pernsylvanius U65129 U65182 X X X X X X X Lampyridae Photuris pernsylvanius U65129 U65183 X X X X X X X Melvidae Melvidae Tenebrio molitor X07801 U65183 X X X X X X X X X X X X X X X X X Melvidae Tenebroindae Corganus U65131 U65185 X X X X X X X X X X X X X X X X X X X	Hemiptera	Aphidae	Acyrthosiphon pisum	X62623		X	X	X	Х	
SaldidaeSaldida gallipesU65121U65175XX <t< td=""><td></td><td>Notonectidae</td><td>Buenoa sp.</td><td>U65120</td><td>U65176</td><td>X</td><td>X</td><td>Х</td><td>Х</td><td>Х</td></t<>		Notonectidae	Buenoa sp.	U65120	U65176	X	X	Х	Х	Х
MiridaeLysanopterU65123XXXXXColeopteraCupedidaePriacma serrataU65124U65178XXXXColeopteraCupedidaePriacma serrataU65124U65178XXXXXXDytiscidaeColpocaccus posticatusU65126U65180XXX		Saldidae	Saldula pallipes	U65121	U65175	X	Х	X	X	X
ThysanopteraIhripidaeTaenothrips inconsequensU65124U65127XXX <t< td=""><td></td><td>Miridae</td><td>Lygus lineolaris</td><td>U65122</td><td>U65177</td><td>X</td><td>X</td><td>X</td><td>X</td><td>Х</td></t<>		Miridae	Lygus lineolaris	U65122	U65177	X	X	X	X	Х
ColeopteraCupedidaePriacma seriataU65124U65178XX <th< td=""><td>Thysanoptera</td><td>Thripidae</td><td>Taeniothrips inconsequens</td><td>U65123</td><td></td><td>X</td><td>X</td><td>X</td><td>X</td><td>• /</td></th<>	Thysanoptera	Thripidae	Taeniothrips inconsequens	U65123		X	X	X	X	• /
Carabidae Colpocaccus positcatus U65125 U65179 X	Coleoptera	Cupedidae	Priacma serrata	U65124	U65178	X	X	X	X	X
DytiscidaeCybister fumbriolatusU65127U65181XX		Carabidae	Colpocaccus posticatus	U65125	U65179	X	X	X	X	X
ScarabaeidaeXyloryctes funnusU65127U65181XX </td <td></td> <td>Dytiscidae</td> <td>Cybister fimbriolatus</td> <td>U65126</td> <td>U65180</td> <td>X</td> <td>X</td> <td>X</td> <td>X</td> <td>X</td>		Dytiscidae	Cybister fimbriolatus	U65126	U65180	X	X	X	X	X
Lateridae Octimodes sp. U65128 U55182 X X X X X X X X X X X X X X X X X X X		Scarabaeidae	Xyloryctes faunus	U65127	U65181	X	X	X	X	X
LampyridaePhoturis pennsylvanicusU65129XXX <td></td> <td>Elateridae</td> <td>Octinodes sp.</td> <td>U65128</td> <td>U65182</td> <td>X</td> <td>X</td> <td>X</td> <td>X</td> <td>Х</td>		Elateridae	Octinodes sp.	U65128	U65182	X	X	X	X	Х
KhipphoridaeKhipphoridaeKhipphoridaeKhipphoridaeKhipphoridaeKi kXX<		Lampyridae	Photuris pennsylvanicus	U65129	11/5400	X	X	X	X	
MeloidaeMeloidaeMeloidaeTenebrionidaeTenebrionidaeTenebrionidaeTenebrionidaeTenebrionidaeTenebrionidaeTenebrionidaeXXX <td></td> <td>Rhipiphoridae</td> <td>Rhipiphorus fasciatus</td> <td>U65130</td> <td>U65183</td> <td>X</td> <td>X</td> <td>X</td> <td>X</td> <td>Х</td>		Rhipiphoridae	Rhipiphorus fasciatus	U65130	U65183	X	X	X	X	Х
IerebrionidaeIerebrioX0/801U65184XXX		Meloidae	Meloe proscarabaeus	X77786	TICE104	X	X	X	X	v
MegalopteraCorydalicaCorydalus cognatusU65132U65186XX <td></td> <td>Ienebrionidae</td> <td>lenebrio molitor</td> <td>X0/801</td> <td>U65184</td> <td>X</td> <td>X</td> <td>X</td> <td>X</td> <td>X</td>		Ienebrionidae	lenebrio molitor	X0/801	U65184	X	X	X	X	X
Megaloptera Coryadindae Coryadius cognatus Uobi32 Uobi86 X X X X X X X Raphidioptera Raphidiidae Agulla sp. Uobi32 Uobi86 X X X X X X X Neuroptera Berothidae Lolomyia texana Uobi33 Uobi88 X X X X X X Mantispidae Mantispa pulchella Uobi34 Uobi88 X X X X X X Hemerobiidae Hemerobius stigmata Uobi35 Uobi80 X X X X X X Chrysopidae Chrysoperla plorabunda Li0183 X X X X X X Myrmeleontidae Myrmeleon immaculatus Uobi37 Uobi90 X X X X X X Myrmeleontidae Myrmeleon immaculatus Uobi37 Uobi91 X X X X X X Papilionidae Papilio troilus Uobi38 Uobi99 X X X X X X Nocctuidae Ascalapha odorata Uobi39 Uobi99 X X X X X X Limniphilidae Pycnopsyche sparna Uobi40 Uobi200 X X X X X X Leptoceridae Ocetis axara Uobi40 Uobi200 X X X X X X Mecoptera Bittacidae Bittacus strigosus Uobi44 Uobi200 X X X X X X Meropeidae Decetis axara Uobi44 Uobi200 X X X X X X Mecoptera Bittacidae Bittacus strigosus Uobi44 Uobi200 X X X X X X Meropeidae Merope tuber Uobi44 Uobi200 X X X X X X Meropeidae Merope tuber Uobi44 Uobi200 X X X X X X Meropeidae Merope tuber Uobi45 Uobi200 X X X X X X Meropeidae Merope tuber Uobi45 Uobi200 X X X X X X Meropeidae Merope tuber Uobi45 Uobi200 X X X X X X Meropeidae Merope tuber Uobi46 Uobi200 X X X X X X Meropeidae Merope tuber Uobi46 Uobi200 X X X X X X Meropeidae Merope tuber Uobi48 Uobi200 X X X X X X Meropeidae Merope tuber Uobi48 Uobi200 X X X X X X Meropeidae Merope tuber Ubbi48 Uobi47 Uobi200 X X X X X X Meropeidae Merope tuber Ubbi48 Uobi48 X X X X X Meropeidae Merope tuber Ubbi48 Uobi48 Uobi48 X X X X X Meropeidae Merope tuber Ubbi48 Uobi48 X X X X X X Meropeidae Merope tuber Ubbi48 Uobi47 X X X X X X X X X X X X X X X X X X X	M (1) (1) (1)	Cerambycidae	letraopes tetropthalmus	U65131	U65185	X	X	X	X	X
RapindiopteraRapindioaAguila sp.U65133U65134U65188XXXXXNeuropteraBerothidaeLolomyia texanaU65134U65188XX <td>Negaloptera</td> <td>Corydalidae</td> <td>Coryaalus cognatus</td> <td>U65132</td> <td>U65186</td> <td>X</td> <td>X</td> <td>X</td> <td>X</td> <td>X</td>	Negaloptera	Corydalidae	Coryaalus cognatus	U65132	U65186	X	X	X	X	X
NeuropteraDerontidaeLotomyta texanaU65134U65188XXXXXMantispidaeMantispa pulchellaU65135U65189XXX<	Kaphidioptera	Raphialiaae	Aguita sp.	U65133	U6518/					
MaintsplateMaintsplat	Neuroptera	Mantionidae	Lolomyla texana Mantiana mulahalla	U03134	U00100	Ŷ	Ň	Ň	Ň	A V
TrichopteraPremerobildaePlemerobilas signalaCosisionXXX<		Hamarahiidaa	Mantispa puichella	U05155	U00109	Ŷ	Ň	Ň	Ň	A V
ChrysophdaeChrysophdaeChrysophdaeNXXXXMyrmeleontidaeMyrmeleon immaculatusU65137U65191XXXXXLepidopteraPyralidaeGalleria mellonellaU65138U65198XX </td <td></td> <td>Chrussenidas</td> <td>Churconorda nlonahuuda</td> <td>U00100</td> <td>063190</td> <td>Ŷ</td> <td>$\hat{\mathbf{v}}$</td> <td>^ v</td> <td>~</td> <td>Λ</td>		Chrussenidas	Churconorda nlonahuuda	U00100	063190	Ŷ	$\hat{\mathbf{v}}$	^ v	~	Λ
MyrmeleontidaeMyrmeleon sp.L10182XXXXXLepidopteraPyralidaeGalleria mellonellaU65138U65198XX <td></td> <td>Murmoloontidaa</td> <td>Chrysoperia pioradunaa Magmalaon immagulatus</td> <td>L10105</td> <td>1145101</td> <td>Ŷ</td> <td>Ň</td> <td>Ŷ</td> <td>v</td> <td>v</td>		Murmoloontidaa	Chrysoperia pioradunaa Magmalaon immagulatus	L10105	1145101	Ŷ	Ň	Ŷ	v	v
LepidopteraPyralidaeGalleria mellonellaUf5132XXXXPapilionidaePapilio troilusU65139U65199XXXXXXNoctuidaeAscalapha odorataU65140U65200XXX<		Myrmeleontidae	Mumalaon op	L 10182	003191	Ŷ	Ŷ	v	л	Λ
LephdopieraFyiandaeOdate in in intrinsitionObsisionObsisionXXX	Lenidontera	Pyralidae	Calleria mellonella	L10102	LI65108	x	X	x	x	Y
TrichopteraNoctuidaeAscalapha odorataU60107U605200XX <td>Lepidopiera</td> <td>Papilionidae</td> <td>Demilio troibus</td> <td>U65130</td> <td>U05198</td> <td>Ŷ</td> <td>x</td> <td>Ŷ</td> <td>Ŷ</td> <td>Ŷ</td>	Lepidopiera	Papilionidae	Demilio troibus	U65130	U05198	Ŷ	x	Ŷ	Ŷ	Ŷ
TrichopteraHydropsychidaeHydropsyche sparnaU65141U65201XXXXXXLimniphilidaePycnopsyche lepidaU65141U65202XXXXXXLeptoceridaeOccetis avaraU65142U65203XX		Noctuidae	Ascalapha odorata	U65140	U65200	Ŷ	x	Ŷ	Ŷ	Ŷ
HickopfeldHydropsydia bpanaGostifiGostifiGostifiKK<	Trichontera	Hydronsychidae	Hudronsuche sparna	U65141	U65200	x	x	x	x	x
Initial InformationIn	maioptera	Limninhilidae	Pucuonsuche lenida	U65142	U65202	x	x	x	x	x
MecopteraBittacidaeBittacus strigosusU65144U65204XXXXXBittacidaeBittacus chlorostigmusL10184XXXXXXXBoreidaeBoreus coloradensisU65145U65205XX <t< td=""><td></td><td>Lentoceridae</td><td>Oecetis mara</td><td>U65143</td><td>U65203</td><td>x</td><td>x</td><td>x</td><td>x</td><td>x</td></t<>		Lentoceridae	Oecetis mara	U65143	U65203	x	x	x	x	x
NiccopicitalDiminationDiminationDisplayDisplayDisplayDisplayDisplayNiccopicityNickopicity	Mecontera	Bittacidae	Rittacus strigosus	U65144	U65204	x	x	x	x	x
BoreidaeBoreus coloradensisU65145U65205XX <td>mecopieru</td> <td>Bittacidae</td> <td>Bittacus chlorostigmus</td> <td>L10184</td> <td>000201</td> <td>x</td> <td>x</td> <td>x</td> <td>~</td> <td>~</td>	mecopieru	Bittacidae	Bittacus chlorostigmus	L10184	000201	x	x	x	~	~
MeropeidaeMerope tuberU65146U65206XXXXXPanorpidaePanorpa latipennisU65147U65207XXXXXXSiphonapteraPulicidaeCtenocephalides canisU65148U65208XX<		Boreidae	Boreus coloradensis	U65145	U65205	x	x	x	х	х
PanorpidaePanorpia latipennisU65147U65207XXXXXSiphonapteraPulicidaeCtenocephalides canisU65148U65208XXXXXXHystrichopsyllidaeHystrichopsylla schefferiL10185XXX		Meropeidae	Merone tuber	U65146	U65206	x	x	x	x	x
SiphonapteraPulicidaeCtenocephalides canisU65148U65208XXXXXHystrichopsyllidaeHystrichopsylla schefferiL10185XXXXXCeratophyllidaeOrchopeas leucopusU65149U65209XXXXXXHymenopteraCephidaeHartigia cressoniiL10173XXXXXOrussidaeOrussus thoracicusL10174XXXXXTenthredinidaeHemitaxonus sp.U65150U65192XXXXXTigonalidaeBareogonalos canadensisL10176XXXXXEvaniidaeEvania appendigasterL10175XXXX		Panorpidae	Panorpa latipennis	U65147	U65207	X	X	X	X	X
HystrichopsyllidaeHystrichopsylla schefferiL10185XXXCeratophyllidaeOrchopeas leucopusU65149U65209XXXXHymenopteraCephidaeHartigia cressoniiL10173XXXXOrussidaeOrussus thoracicusL10174XXXXTenthredinidaeHemitaxonus sp.U65150U65192XXXXTenthredinidaePericlista lineaL10172XXXXTrigonalidaeBareogonalos canadensisL10176XXXEvaniidaeEvania appendigasterL10175XXX	Siphonaptera	Pulicidae	Ctenocephalides canis	U65148	U65208	X	X	X	X	X
CeratophyllidaeOrchopeas leucopusU65149U65209XXXXXHymenopteraCephidaeHartigia cressoniiL10173XXXXXOrussidaeOrussus thoracicusL10174XXXXXXTenthredinidaeHemitaxonus sp.U65150U65192XXXXXTenthredinidaePericlista lineaL10172XXXXXTrigonalidaeBareogonalos canadensisL10176XXXXEvaniidaeEvania appendigasterL10175XXX		Hystrichopsyllidae	Hystrichopsylla schefferi	L10185		х	х	х		
HymenopteraCephidaeHartigia cressoniiL10173XXXOrussidaeOrussus thoracicusL10174XXXTenthredinidaeHemitaxonus sp.U65150U65192XXXXTenthredinidaePericlista lineaL10172XXXXTrigonalidaeBareogonalos canadensisL10176XXXEvaniidaeEvania appendigasterL10175XXX		Ceratophyllidae	Orchopeas leucopus	U65149	U65209	x	X	x	х	х
OrussidaeOrussus thoracicusL10174XXXTenthredinidaeHemitaxonus sp.U65150U65192XXXXTenthredinidaePericlista lineaL10172XXXXTrigonalidaeBareogonalos canadensisL10176XXXEvaniidaeEvania appendigasterL10175XXX	Hymenoptera	Cephidae	Hartigia cressonii	L10173		х	Х	Х		
TenthredinidaeHemitaxonus sp.U65150U65192XXXXXTenthredinidaePericlista lineaL10172XXXXTrigonalidaeBareogonalos canadensisL10176XXXEvaniidaeEvania appendigasterL10175XXX	<i>, , , , , , , , , ,</i>	Orussidae	Orussus thoracicus	L10174		Х	Х	х		
TenthredinidaePericlista lineaL10172XXXTrigonalidaeBareogonalos canadensisL10176XXXEvaniidaeEvania appendigasterL10175XXX		Tenthredinidae	Hemitaxonus sp.	U65150	U65192	Х	х	х	Х	х
Trigonalidae Bareogonalos canadensis L10176 X X X Evaniidae Evania appendigaster L10175 X X X		Tenthredinidae	Periclista linea	L10172		Х	х	х		
Evaniidae <i>Evania appendigaster</i> L10175 X X X		Trigonalidae	Bareogonalos canadensis	L10176		х	х	х		
		Evaniidae	Evania appendigaster	L10175		х	Х	Х		

TABLE 1. List of insect taxa used in the analysis and GenBank accession numbers (where available).

			GenBank		18S regions ^a				
Order	Family	ily Species	18S	28S	Α	D	В	С	28S
	Ichneumonidae	Ichneumon sp.	L10178		X	Х	Х		
	Ichneumonidae	Ophion sp.	U65151	U65193	Х	Х	Х	Х	Х
	Pteromalidae	Mesopolobus sp.	L10177		Х	Х	Х		
	Chrysididae	Caenochrysis doriae	L10179		Х	Х	Х		
	Bethylidae	Epyris sepulchralis	L10180		Х	Х	Х		
	Pompilidae	Priocnemus oregana	L10181		Х	Х	Х		
	Mutillidae	Dasymutilla gloriosa	U65152	U65194	Х	Х	Х	Х	Х
	Vespidae	Apoica sp.	U65153	U65195	Х	Х	Х	Х	Х
	Vespidae	Monobia quadridens	U65154	U65196	Х	Х	Х	Х	Х
	Vespidae	Polistes fuscatus	U65155	U65197	Х	Х	Х	Х	Х
	Vespidae	Polistes dominulus	X74762		Х	Х	Х		
	Formicidae	Camponotus ligniperda	X73270		Х	Х	Х		
	Formicidae	Chalepoxenus muellerianus	X73271		Х	Х	Х		
	Formicidae	Doronomyrmex kutteri	X73274		Х	Х	Х		
	Formicidae	Leptothorax acervorum	X73235		Х	Х	Х		
	Formicidae	Temnothorax recedens	X73273		Х	Х	Х		
	Formicidae	Harpagoxenus sublaevis	X73272		Х	Х	Х		
Diptera	Tipulidae	Tipula sp.	U65156	U65210	Х	Х	Х	Х	Х
-	Drosophilidae	Drosophila melanogaster	M21017	U65211	Х	Х	Х	Х	Х
	Asilidae	Laphria sp.	U65157	U65212	Х	Х	Х	Х	Х
	Bombyliidae	Mythicomyia atra	U65158		Х	Х	Х	Х	
Strepsiptera	Corioxenidae	Triozocera mexicana	U65159		Х	Х	Х	Х	
	Myrmecolacidae	Caenocholax fenyesii	U65160	U65213	Х	Х	Х	Х	Х
	Elenchidae	Elenchus japonica	U65162	U65214	Х	Х	Х	Х	Х
	Stylopidae	Crawfordia n.sp.	U65163	U65215	Х	Х	Х	Х	Х
	Stylopidae	Xenos pecki	U65164	U65216	Х	Х	Х	Х	Х
	Stylopidae	Xenos vesparum	X77784		Х	х	Х	Х	

TABLE 1. Continued.

^a See Figure 3.

troduction of large amounts of missing data. Pashley et al.'s (1993) sequences were excluded because they had less than 50% overlap with our sequences and are missing the 18S D region and a portion of the C region (Fig. 3), which contain many of the characters important for phylogenetic resolution. The 18S sequence for Aedes al*bopictus* was removed from the analysis because it appears to be replete with sequencing artifacts. (Upon alignment with all other insect sequences, positions 642, 885, 905–908, 930, 936, 999, 1008, 1009, 1024, 1054, 1059, 1065, 1088, 1094, 1101, 1102, 1114, 1117, 1118, 1123–1125, 1130, 1131, 1158–1163, 1189, 1230, 1281, 1284– 1288, 1320–1324, 1329, and 1357 do not appear to be insect sequence and are typically single indels in regions highly conserved in all other insects; positions 712-788 and 834–841 are also highly suspect [position numbers relative to GenBank X57172]). There were 26 18S sequences and

1 28S sequence added to give a total of 85 18S and 52 28S sequences in the molecular data sets.

Amplification and Sequencing of Ribosomal DNA

Total genomic DNA was isolated from fresh, ETOH-preserved, and dried insect specimens by homogenization in an extraction buffer (10 mM Tris, 25 mM EDTA, 0.5% SDS, 100 mM NaCl, 0.1 mg/ml proteinase K). After 12+ hr of incubation with agitation at 55°C, the DNAs were cleaned with a standard series of phenol/chloroform extraction followed by ethanol precipitation and resuspension in water. If tissues were rare, the precipitation step was replaced by purification of the supernatant in separation columns (Centricon 100) to increase the total DNA yield and quality.

Double-stranded template suitable for sequencing was prepared for 18S and 28S rDNA via polymerase chain reaction



FIGURE 3. Regions of insect 18S rDNA sequenced in this study compared with those sequenced in other studies. Regions are labeled according to the respective authors' nomenclature, and the position of 18S primers used in our study are presented. Position numbers are relative to the sequence for *Drosophila melanogaster* (Tautz et al., 1988).

(PCR) amplification with conserved primers (Table 2). For most 18S sequences, the entire region was amplified and sequenced with internal primers (Fig. 3). If DNA was degraded, sets of primers flanking the A, D, and B + C regions were used to amplify smaller fragments with the program 94°C denaturation (1 min), 50°C annealing (1 min), and 72°C extension (1.5 min) for 35 cycles (Perkin-Elmer Cetus 9600 cycler). Because Strepsiptera have large insert regions in the 18S D fragment with a secondary structure resistant to denaturation, the PCR denaturation times were doubled on every cycle. For 28S, the amplified region corresponds to the D3 expansion segment of 23 S-like ribosomal RNA segment (Michot and Bachellerie, 1987; Michot et al., 1990). Magnesium concentrations had to be decreased for the DNA from aquatic and semiaquatic insects, presumably because they retain heavy metals in their tissues, which interferes with the PCR reactions. Potential insect host contamination in Strepsiptera was avoided by sequencing the free-living males and designing a primer specific to Strepsiptera. Every set of PCR reactions included negative controls to screen for contaminated reagents and amplification products. If PCR product yield was low or particularly difficult to direct sequence, it was ligated to a vector

TABLE 2. Primer sequences (5' to 3') used to generate the 18S and 28S rDNA sequences. Positions for 18S are based on the sequence for *Drosophila melanogaster* (Tautz et al., 1988).

Primer	Sequence	Position
	CCTGAGAAACGGCTACCACATC	398
18S b5.0	TAACCGCAACAACTTTAAT	627
18S a0.7	ATTAAAGTTGTTGCGGTT	609
18S b3.9	TGCTTTRAGCACTCTAA	856
18S a0.79	TTAGAGTGCTYAAAGC	840
18S b3.0	GACGGTCCAACAATTTCACC	1007
18S StrepB	CATACTGTCGARMTAT	≈932
18S a1.0	GGTGAAATTCTTGGACCGTC	988
18S b0.5	GTTTCAGCTTTGCAACCAT	1222
18S a2.0	ATGGTTGCAAAGCTGAAAC	1202
18S bi	GAGTCTCGTTCGTTATCGGA	1421
285 a	GACCCGTCTTGAAACACGGA	
28S b	TCGGAAGGAACCAGCTACTA	

and transformed into a host bacterial cell (Invitrogen, TA cloning kit). The cells were grown and the product removed and sequenced following the manufacturer's protocols. Four to six clones were sequenced to screen for possible variation due to artifacts of amplification or cloning.

The 18S rDNA sequencing was carried out using ³⁵S-ATP, the primers used for PCR amplification and internal primers, the modified T7 DNA polymerase Sequenase[®] (version 2.0, U.S. Biochemical Corp.), and the accompanying reagents following standard protocols (Hillis et al., 1990). For the 28S samples, sequencing was carried out with the PRISM cycle sequencing kit (ABI) and run on the ABI 373A automated sequencer. In all cases, complementary strands of all fragments were independently amplified and sequenced to assure accurate results. If complementary strands disagreed, the product was reamplified and sequenced to resolve any discrepancies.

Morphological Characters

Quantitative cladistic analysis has not previously been applied to morphological data in the study of holometabolan relationships. Hennig (1969, 1981), Boudreaux (1979), Kristensen (1975, 1981, 1991, 1995), and others based their phylogenetic conclusions on morphology without a formal parsimony analysis of character data. Moreover, all previous molecular studies have simply compared molecular trees with a morphological topology without considering how conflict within the morphological data may influence the interpretation of molecular data. This study presents the first published morphological matrix and the first attempt to combine directly molecular and morphological evidence for insect interordinal relationships.

Our morphological matrix was derived from the literature, chiefly from the work of Kristensen (1975, 1981, 1991, 1995), Hennig (1969, 1981), and Boudreaux (1979). The matrix is a compilation of all ordinallevel phylogenetically informative characters for the holometabolous insect orders and insect outgroups, and as such these

characters represent what is considered to be the ground-plan states for each order. We did not attempt to code morphological characters for resolution of relationships below the ordinal level because the determination of these relationships is not the thrust of this paper. The matrix includes many, but by no means all, of the ordinal autapomorphies for each insect order. The morphological data were combined with the molecular data by extrapolating the ordinal scores to each sequenced exemplar. Hence, all resolution within orders is entirely the result of the molecular data. This methodology biases our results by making it less likely that the monophyly of an order will be rejected. However, this bias is not problematic because the monophyly of the holometabolous insect orders is generally not disputed.

Alignment

The 18S and 28S sequences were aligned using the multiple alignment program MALIGN (parallel version 1.93, Wheeler and Gladstein, 1994). This parsimonybased program selects among all possible multiple alignments by determining the order of sequence accretion that minimizes the phylogenetic cost for a given set of parameter values. Algorithmic alignment was preferred over manual alignment to avoid introducing bias based on preconceived notions of phylogeny and to assure optimal alignments. The heuristic algorithm "Build" with SPR branch swapping on multiple alignments was performed on 10 Hewlett-Packard workstations operating in parallel (change cost = 3, gap cost = 5, leading and trailing gap $\cos t = 8$). A change/gap cost ratio of 3:5 was selected because this ratio minimizes incongruence among aligned data sets in arthropods (Wheeler, 1995). The leading and trailing gap costs were set to 8 to cause the flanking primer regions to align. Based on the initial results of alignment, the 28S and 18S sequences were subdivided into multiple contiguous fragments, and more rigorous searches were then performed on the variable regions requiring multiple gaps. When the initial alignment presented evidence of a large insertion in a single taxon or subset of taxa, the region was removed to facilitate alignment of positions flanking the insert.

Phylogenetic Analysis

Multiple alignments were analyzed using NONA 1.15 (Goloboff, 1994) and PAUP 3.1.1. (Swofford, 1991). Primer regions were excluded, and all ambiguous nucleotides were treated as missing data. The data sets were analyzed with NONA under the options "mult*10" (10 random addition sequences with TBR swapping), "max" (TBR swapping on the trees found by mult*), and "hold 5,000" (save up to 5,000 trees). Additional swapping on up to 5,000 trees that are up to 10% longer than the shortest tree ("jump") was performed to help the swapper move between multiple "islands" of trees (Goloboff, 1994). If more than 5,000 trees were found, the search was repeated with a value for "hold," which retained the entire set of trees. For the morphology and one representative each of 18S, 28S, total molecular, and total data trees, the minimum and maximum branch lengths were calculated with PAUP. For these trees, Bremer support values (Bremer, 1994) were calculated by importing the set of most-parsimonious trees found by NONA into PAUP and then TBR branch swapping on the trees while constraining nonmonophyly of the group of interest. If Bremer support values were large (>25), the number was recalculated using heuristic search options of PAUP and the smaller value was taken. The number of steps required to force monophyly was calculated in NONA by constraining the monophyly of a group while swapping on all other terminals (force +n; max/) and taking the difference between the tree lengths.

Sensitivity analysis was performed on these data to test the robustness of clades. Sensitivity analysis is based on the premise that there are parameter values essential for data analysis in a phylogenetic context that cannot be empirically determined prior to phylogenetic analysis (Wheeler, 1995). These values might include charac-

ter weights, transition/transversion ratios, and gap/change ratios. Sensitivity analysis is not concerned with estimating the "true" value of these parameters but rather concentrates on assessing the relative robustness of clades to perturbations of values across a parameter space. If a group appears monophyletic only under a very specific combination of parameter values, less confidence may be placed in the supposition that the data robustly support the monophyly of that group. If, however, a group appears monophyletic under a wider range and combination of parameter values, more confidence may be placed in the conclusion that the data support the monophyly of that clade. In this analysis, we attempted specifically to determine the influence of gap and character weighting schemes, regions of sequence alignments, different methods of combining data, and the effect of combining multiple data sets on the robustness of holometabolous insect clades.

It has been suggested that only those regions of an alignment that can be unambiguously aligned by eye should be used in phylogenetic reconstruction because these regions are more likely to reflect true homology statements among nucleotides, particularly for deeper phylogenetic relationships (Dixon and Hillis, 1993; Van de Peer et al., 1993; Smothers et al., 1994). To determine the influence of presumed alignment conservation on nodal stability, the 18S and 28S alignments were divided into conserved and variable regions. The conserved regions correspond roughly to those that can be aligned unambiguously by eye (or regions that do not change under a wide range of alignment parameter values). The variable regions correspond to those that required more aggressive alignment routines. For 18S, the variable regions are positions 281–361 and for 28S they are 47-59, 88-118, 135-179, and 198-220 (Appendices 1, 2). In the "conserved" analyses, the variable regions were excluded during phylogenetic reconstruction; in the "entire" analyses all regions were used. Characters marking the positions of major insertions were treated as missing data in the entire analyses. Recoding these shared insert regions into multistate nonadditive characters and appending them to the data matrices does not change tree topology.

Data sets relying on multiple genes often have unequal numbers of sequences because certain taxa are only present for a subset of genes. These data sets may be combined either by removing the taxa that have not been sequenced for all gene regions (merging) or by introducing missing values for the absent sequence region (splicing; Nixon and Carpenter, 1996). Purging a data set of taxa with many missing values may reduce the total number of most-parsimonious trees found because taxa with many missing values may attach themselves to multiple positions, resulting in decreased resolution in the consensus. However, purging missing values may also have the negative effect of removing taxa that may be critical for polarity determinations. We have examined the effects of both methods of data combination in this analysis.

Matrices were generated for the conserved and entire regions of 18S and 28S and were then combined with the corresponding regions in 18S and 28S (e.g., 18S conserved + 28S conserved = molecularconserved) by the methods of merging and splicing. Each of the molecular matrices were then combined with morphological data to form a total evidence matrix (Kluge, 1989). Finally, every data set was analyzed with gaps treated as missing, given the same weight as nucleotide data, and given twice the weight of nucleotide data (the 2:1 weighting approximates the gap/ change ratio used during alignment). For the simultaneous analysis of all data sets (=total evidence analysis; Nixon and Carpenter, 1996), morphology data were given the same or twice the weight of nucleotide changes. This procedure yielded 48 matrices, which were analyzed using NONA (Goloboff, 1994) with the same approximate searches as outlined above. The strict consensus of the set of most-parsimonious trees from each matrix was calculated and used as the tree of reference in the sensitivity analyses. The morphological matrix

is given in Appendix 3 and tree statistics are given in Appendix 4.

Incongruence among the 18S, 28S, and morphology data sets was tested by calculating the difference between the length of trees from the combined data set and the sum of the lengths of trees from the partitioned data set (the incongruence length difference [ILD]; Mickevich and Farris, 1981; Farris et al., 1994). The advantage of ILD over topology-based measures is that it is character based and can take into account the relative support for a particular topology. The ILD was tested for statistical significance against a distribution of ILD values that was generated by randomly partitioning the combined data set into subsets the size of the original partitions. Each test consisted of 10,000 random partitions. The calculation of these values and tests for significance were automated by using the "arn" program of Farris et al. (1994), and test statistics were adjusted for multiple tests using the Bonferroni correction (Holm, 1979; Rice, 1989).

RESULTS

Sequence Alignment

Multiple alignment of the 18S data produced 1,116 nucleotide positions with 24 inserts; alignment of the 28S data produced 398 positions with 14 inserts (Appendices 1, 2). Of these positions, 671 for 18S and 290 for 28S contained phylogenetically informative base substitutions and/or gaps (excluding primers and insert regions). Of the 18S informative characters, two base substitutions and seven gap characters have identical distributions throughout the taxa. Of the 28S informative characters, four base substitutions and no gap characters have identical distribution throughout the taxa.

Of the 18S inserts, 6 are autapomorphic for individual taxa (inserts 1, 6, 8, 9, 14, 24), 2 are aligned at the generic level (18, 22), 10 are aligned at the ordinal level (2, 3, 12, 13, 16, 17, 19, 20, 21, 23), and 5 are aligned at the interordinal level (4, 5, 10, 11, 15). The two inserts that appear phylogenetically informative at the interordiSYSTEMATIC BIOLOGY

nal level within Holometabola (11, 15) are entirely congruent with relationships supported in all 18S analyses. The majority of the 18S inserts occur in the 5' portion of the D fragment, beginning at position 330 and extending as far as position 385, although Strepsiptera and Diptera each have an insert starting at position 268 (these inserts correspond to loop regions in the secondary structure of the molecule).

Strepsiptera have another clearly defined insert region at positions 497-520 (insert 23). Although the primary alignment of this insert appears ambiguous, the secondary structure is well supported with long stems, and the secondary structure appears conserved at least among the more morphologically derived strepsipteran taxa (Fig. 4). Insert 23 is unique in that multiple classes of inserts occur within a single strepsipteran individual. Nucleotides outside of the insert region were identical from clone to clone, but within the insert there were many differences in sequence length and nucleotide composition. We found two major classes of inserts in the more derived Strepsiptera: the "long" and "short" inserts of Xenos and Caenocholax. Stylopidae (Crawfordia and Xenos) have longer stems and a higher percentage of AT matches than do the more basal taxa (Triozocera and Caenocholax; see Fig. 4). In Xenos pecki, the long insert (386 bp) is extremely AT rich (92%), and different clones showed variation in the string length of A's and T's involved in stem pairing. The short insert is 340 bp long and lacks the AT-rich regions (44%). In Caenocholax, the long insert is 126 bp, the short is 97 bp, and neither is AT rich. The sequence from Xenos vesparum (364 bp) is AT rich (89%) and probably homologous to the long insert of X. pecki. More careful sequencing of this taxon should yield the shorter insert.

Of the 28S inserts, five are autapomorphic for individual taxa (inserts 3, 5, 9, 10, 11), seven are aligned at the ordinal level (1, 2, 4, 7, 8, 12, 13), and two are aligned at the interordinal level (6, 14). The two inserts aligned at the interordinal level support phylogenetic relationships that are



FIGURE 4. Secondary structures for strepsipteran 18S rDNA insert 23. This insert is expanded (232-394 bp) in Strepsiptera and forms long thermostable stems but is a simple loop in all other insects (21-25 bp). The more derived Strepisptera (Stylopidae: Crawfordia and Xenos) have longer stems and a higher percentage of AU matches than do the more basal taxa (Triozocera and Caenocholax). Structure computation was based on thermodynamic stability at 37°C using the default heat curve calculations as implimented in RNAdraw 1.0 (Matzura, 1995). Arrows mark the 5' end of the insert. Number of base pair matches are given. (a) Triozocera mexicana (-294.807 kJ): 48 GC, 23 AU, 12 GU. (b) Caenocholax fenyesi (-280.487 kJ): 44 CG, 26 AU, 15 GU. (c) Crawfordia n. sp. (-206.712 kJ): 16 CG, 54 AU, 15 GU. (d) Xenos vesparum (-202.19kJ): 12 CG, 102 AU, 2 GU. (e) Xenos pecki (-247.954 kJ): 10 CG, 134 AU, 2 GU. (f) Drosophila melanogaster (0 kJ): no matches.

entirely congruent with relationships supported in all 28S analyses. Once again, Strepsiptera have a large insert region within the 28S sequences.

Data Set Incongruence

Significance tests using the "arn" program of Farris et al. (1994) with a Bonferroni correction indicate that for 2 of 24 comparisons, there is sufficient evidence to reject congruence relative to the alternative hypothesis of data set incongruence (Table 3; $\alpha < 0.002$). The only cases of incongruence are found when the entire alignment of the 28S data is combined with the morphological data. There is no evidence to suggest that 18S and morphological data are incongruent; these comparisons result in α values of 1.0. Overall, these tests sug-

gest that for most data set comparisons there is insufficient evidence to reject the hypothesis of congruence and that most of the incongruence appears to originate from the entire 28S alignment.

Phylogenetic Relationships

Parsimony analysis of the morphological data with all characters weighted equally generated one most-parsimonious tree of 279 steps, a consistency index (CI) of 0.74, and a retention index (RI) of 0.82 (Fig. 5). The relationships within Holometabola are congruent with those of Kristensen (1995) except for the placement of Strepsiptera as sister to (Diptera + (Mecoptera + Siphonaptera)). This relationship is supported by 4 nonhomoplastic character changes under a modified DELTRAN optimization and 10 nonhomoplastic and 1 reversal character under a modified ACCTRAN optimization (Fig. 6a; Nixon, 1995). The difference in these branch lengths is due to the different manner in which these methods optimize the states coded as missing in Strepsiptera and Siphonaptera. The relationships among the nonholometabolous neopterans do not conflict with Kristensen's hypothesis except for the paraphyly of Paleoptera (Ephemerida + Odonata), with Ephemerida as the more basal clade. Forcing the Strepsiptera as sister group to Coleoptera increases the length of the tree by five steps by adding one extra step to characters 5, 80, 95, 117, 188, and 164 (all homoplastic on the branch subtending Strepsiptera) and removing a step from character 101 (Fig. 6b; modified DEL-TRAN). Flight by posteromotorism (character 101) is the only morphological character supporting Coleoptera + Strepsiptera when these taxa are forced together.

Parsimony analysis of the entire 18S alignment with gaps coded as missing yielded 162 trees of 1,965 steps (CI = 0.41, RI = 0.63), the strict consensus of which is

TABLE 3. Results of tests for data set incongruence using "arn" (Farris et al., 1994). Both the conserved and entire alignments were tested. Autapomorphic and uninformative characters were removed prior to performing the test, and for each test the repetition number for determining the null distribution was set at 10,000. For the two combination methods, spliced was used with 85 taxa and merged was used with 52 taxa.

_	Gaps	Alpha
Data set	weighted	value ^a
Total		
Entire spliced	?	0.079
	1	0.576
Entire merged	?	0.592
	1	0.012
Conserved spliced	?	1.000
	1	1.000
Conserved merged	?	1.000
	1	0.017
	-	
Molecular		
Entire spliced	?	1.000
	1	0.033
Entire merged	?	0.022
	1	0.004
Conserved spliced	?	1.000
-	1	0.371
Conserved merged	?	0.061
	1	0.056
18S + morphology		
Entire spliced	2	1.000
Entire spiced	: 1	1.000
Conserved spliced	2	1.000
conserved spinced	1	1.000
	1	1.000
28S + morphology		
Entire spliced	?	0.001*
*	1	0.001*
Conserved spliced	?	0.006
	1	0.006

^a Asterisks mark those values that reject the hypothesis of data set congruence.

given in Figure 7. This tree was rooted to *Hypogastrura*. Among the outgroups, the 18S data support the monophyly of Odonata, Plecoptera, Heteroptera, Dictyoptera, and Psocodea. The basal placement of *Trigoniopthalmus* and the placement of Paleoptera as sister group to Neoptera is congruent with Kristensen's hypothesis (1991, 1995). Holometabola are monophyletic and sister group to the clade including Hemiptera and Thysanoptera, members of Paraneoptera. Paraneoptera are paraphyletic because of the more basal placement of



Psocodea, and with this one exception, the overall rooting of the tree appears appropriate relative to the position of Holometabola. All orders within Holometabola are monophyletic except for Coleoptera and Mecoptera. The polyphagous beetles are monophyletic, but the basal Priacma (suborder Archostemata) and Colpocaccus (suborder Adephaga) are not associated with Polyphaga but rather form a sister group with Megaloptera + Raphidioptera (this clade is so commonly encountered in subsequent analyses that it will be abbreviated as MRPC). The other adephagan, Cybister, is associated with Polyphaga instead of *Colpocaccus*. The paraphyly of Mecoptera is due to the placement of Boreus as sister group to Siphonaptera. The monophyly of Megaloptera + Raphidioptera, Mecoptera + Siphonaptera, and Amphiesmenoptera is congruent with Kristensen's hypothesis (1991, 1995); however, Kristensen's Mecopterida and Neuropterida + Coleoptera are not supported in this analysis. The 18S data strongly support the placement of Strepsiptera as sister group to Diptera (hereinafter called Halteria). The root branches of Diptera and Strepsiptera have the greatest lengths and Bremer support values, although these are comparable to those of Trichoptera and Lepidoptera, which form Amphiesmenoptera, a group considered well established based on morphological data (Kristensen, 1991, 1995).

Parsimony analysis of the entire 28S alignment with gaps weighted as 2 and rooted to *Trigoniopthalmus* yielded 12 trees of 1,404 steps (CI = 0.36, RI = 0.62), the strict consensus of which is given in Figure 8. Among the outgroups, this analysis supports the monophyly of Plecoptera, Odonata, and Heteroptera, although the rela-

tionships among these groups are only partially congruent with morphology. Neoptera are paraphyletic because the Mantis and Oligotoma sequences are sister group to Odonata. Melanoplus and the Plecoptera sequences group with Heteroptera and, rather than Paraneoptera, form the sister group to Holometabola. Holometabola, and all included orders, are monophyletic except for Coleoptera and Mecoptera. As was seen in the 18S analysis, mecopteran paraphyly is due to the placement of *Boreus* as sister group to Siphonaptera. Coleopteran paraphyly, however, is due to the placement of Colpocaccus, rather than the MRPC grouping as described in the 18S analysis, at the base of Holometabola. Priacma is sister group to the remaining beetles, and Polyphaga are paraphyletic because Cybister is nested within the group. The 28S data are congruent with the other data sets in supporting the monophyly of Mecoptera + Siphonaptera, Megaloptera + Raphidioptera, Amphiesmenoptera, and Halteria. Again, Amphiesmenoptera and Halteria are composed of orders with long branches and high Bremer support values. The smaller CI and RI values for 28S relative to 18S indicate a greater degree of internal character conflict, especially when the smaller number of taxa and characters for the 28S is taken into consideration.

The combined molecular data were analyzed by scoring the taxa absent in the 28S data set with missing values for the 18S data (splicing) and combining the data sets. The complete 28S and 18S alignments were included, gaps were treated as missing characters, and the tree was rooted to *Hypogastrura*, and the analysis resulted in 168 trees of 2,939 steps (CI = 0.39, RI =

FIGURE 5. Insect morphology tree with mapped characters (length = 279, CI = 0.74, RI = 0.82). All characters were weighted equally, and the analysis generated one most-parsimonious tree. Mapped characters were optimized using a modified DELTRAN optimization (Nixon, 1995). Numbers next to boxes refer to character numbers as given in Appendix 3. \blacksquare = nonhomoplastic change; \square = homoplastic change; \square = reversal. Bremer support values for holometabolous relationships are Amphiesmenoptera: 9; Holometabola: 6; Neuropteroidea: 3; Mecopterida + Hymenoptera, Mecopterida, and Antliophora: 2; remaining: 1. This tree is congruent with that of Kristensen (1991) except for the placement of Strepsiptera as sister group to (Diptera + (Mecoptera + Diptera)) and a paraphyletic Paleoptera (Odonata + Ephermerida).



FIGURE 6. Holometabolous portion of morphology tree. Characters were optimized using a modified DEL-TRAN optimization (Nixon, 1995). Numbers next to boxes are the character numbers as given in Appendix 3. = nonhomoplastic change; \Box = homoplastic change; \Box = reversal. (a) Characters mapped under a modified ACCTRAN optimization (Nixon, 1995). This optimization yields a tree with 10 nonhomoplastic characters and 1 character reversal supporting the antliophoran node including Strepsiptera (arrow), in contrast to the 4 nonhomoplastic characters supporting the same node under modified DELTRAN optimization (Fig. 5). This difference is a result of how the missing values in Strepsiptera and Siphonaptera are optimized. (b) Strepsiptera forced as sister group to Coleoptera (length = 284, CI = 0.73, RI = 0.81). All characters were weighted equally, and the analysis generated one most-parsimonious tree. Forcing Strepsiptera into this position adds one step to characters 5, 80, 95, 117, 188, and 164 (all homoplastic on the branch subtending Strepsiptera) and removes a step from character 101 (relative to Fig. 5).



FIGURE 7. Insect 18S tree (length = 1,965, CI = 0.41, RI = 0.63). This is the strict consensus of 162 trees with gaps coded as missing. The entire portion of the 18S alignment was used in the analysis. Numbers above and below branches are maximum/minimum branch lengths; circled numbers are Bremer support values. The alignment is presented in Appendix 1.

0.61), the strict consensus of which is presented in Figure 9. This analysis supports the monophyly of Odonata, Paleoptera, Psocodea, Heteroptera, Plecoptera, and Dictyoptera. Psocodea are again placed basally and do not group with Hemiptera and Thysanoptera, and the sister group to Holometabola is a clade composed of Ple-



FIGURE 8. Insect 28S tree (length = 1,404, CI = 0.36, RI = 0.62). This is the strict consensus of 12 mostparsimonious trees with a gap weight of 2. The entire portion of the 28S alignment was used in the analysis. Numbers above and below branches are maximum/minimum branch lengths; circled numbers are Bremer support values. The alignment is presented in Appendix 2.

coptera, Dictyoptera, and Dermaptera. Holometabola are monophyletic, and all orders within Holometabola are monophyletic except for Mecoptera and Coleoptera. Again, the paraphyly of Mecoptera is due to the grouping of *Boreus* as sister group to Siphonaptera, and the paraphyly of Coleoptera is due to the presence of MRPC.



FIGURE 9. Insect molecular tree (length = 2,939, CI = 0.39, RI = 0.61). This is the strict consensus of 168 trees with gaps treated as missing. The entire portions of the 28S and 18S alignments were used in the analysis, and taxa not sequenced for 28S were given missing values prior to data set combination (splicing). Numbers above and below branches are maximum/minimum branch lengths; circled numbers are the Bremer support values.

This combined molecular analysis supports the monophyly of Halteria, Mecoptera + Siphonaptera, Megaloptera + Raphidioptera, and Amphiesmenoptera. Again, the monophyly of the orders comprising Halteria and Amphiesmenoptera is well supported with large branch lengths and Bremer support values. Neuroptera are sister group to Halteria, which, as a clade, are sister group to MRPC. Hymenoptera are the most basal holometabolous order.

A simultaneous analysis of all data was accomplished by scoring each taxon with the morphological data for the order to which it belongs and then combining these data with the spliced molecular data set. Gaps were treated as missing values, nucleotide and morphological characters were weighted equally, and the tree was rooted to *Hypogastrura*. Parsimony analysis resulted in 10 trees of 3,339 steps (CI = 0.42, RI = 0.67), the strict consensus of which is presented in Figure 10. Among the outgroups, this analysis supports the monophyly of Odonata, Dictyoptera, Plecoptera, Psocodea, Hemiptera, Heteroptera, Neoptera, and Paraneoptera. Relationships among these outgroups are congruent with our morphological tree except for the placement of Psocodea as sister group to Thysanoptera (rather than as sister group to Thysanoptera + Hemiptera), Dermaptera as sister group to Plecoptera (rather than Dictyoptera), and Embioptera as sister group to Phasmida (rather than Plecoptera). Paraneoptera are sister group to Holometabola, and Holometabola are a well-supported clade. All orders within Holometabola are monophyletic except for Mecoptera and Coleoptera. As seen in previous analyses, Boreus groups with the fleas, and the paraphyly of Coleoptera is due to MRPC. This simultaneous analysis supports the monophyly of Siphonaptera + Mecoptera, Megaloptera + Raphidioptera, Amphiesmenoptera, and Halteria. In addition, Mecopterida and Antliophora (with the inclusion of Strepsiptera) are both monophyletic, and Hymenoptera is sister group to Mecopterida. Once again, the Bremer support values and branch lengths for Amphiesmenoptera and Halteria are large. The placement of Amphiesmenoptera as sister group to Antliophora is congruent with our morphological analyses.

Sensitivity Analysis

Matrices for the sensitivity analysis were generated and analyzed as described above. Results from the sensitivity analyses are given in Figures 11–13, the consensus trees are shown in Figure 14, and tree statistics are presented in Appendix 4. For interordinal comparisons of topologies, if all terminals of an order were monophyletic in the strict consensus tree, the multiple terminals were replaced by the ordinal name at the node subtending those terminals. Where the representatives of an order are unresolved, the node subtending the order is illustrated by a thick bar in the figures. Paraphyletic orders are represented by an asterisk next to the name of the order, with the positions where the terminals appear on the tree labeled. A majority rule (>50%) consensus of each of these resulting sets of trees was taken. For example, the consensus tree for 18S (Fig. 14) is the majority-rule consensus of trees in Figures 11a-f. Numbers on the nodes (nodal values) represent the percentage of times a clade is monophyletic across the sensitivity analyses and were computed by dividing the number of times a group is monophyletic by the sum of the number of times it is monophyletic, paraphyletic, and polyphyletic. Unresolved groupings were ignored in this calculation because it is not clear whether they should be considered congruent or incongruent with the hypothesis of monophyly.

185 data.—In these analyses (Figs. 11a– f), all holometabolous orders are monophyletic (or unresolved) except for Coleoptera and Mecoptera (for the same reasons as discussed above) and one instance of hymenopteran paraphyly (Fig. 11c). The monophyly of Halteria, Amphiesmenoptera, Polyphaga, Mecoptera + Siphonaptera, Megaloptera + Raphidioptera, *Priacma* + *Colpocaccus*, and MRPC is supported in all 18S analyses. When only the con-



FIGURE 10. Tree from simultaneous analysis of all insect data (length = 3,339, CI = 0.42, RI = 0.67). This is the strict consensus of 10 most-parsimonious trees. The complete 18S and 28S alignments were used in this analysis, gaps were coded as missing, morphological characters were weighted by 1, and taxa not sequenced for 28S were given missing values prior to combination with the morphological data (splicing). Numbers above and below branches are maximum/minimum branch lengths; circled numbers are Bremer support values.



FIGURE 11. Results of sensitivity analysis for 18S (a–f) and 28S (g–l) matrices for holometabolous insect relationships. Sensitivity parameters are alignment region (conserved or entire) and gap weighting scheme (missing [?], 1, or 2). Relationships among outgroups are not included. Unresolved clades are shown as thick bars, and paraphyletic groups are marked by asterisks. Amp = Amphiesmenoptera (Lepidoptera + Trichoptera); *Colpo.* = *Colpocaccus*; Halt = Halteria (Diptera + Strepsiptera); Hym = Hymenoptera; M+R = Megaloptera + Raphidioptera; Mec = Mecoptera excluding *Boreus*; Neur = Neuroptera (sensu stricto = Planipennia); PC = *Priacma* + *Colpocaccus*; Plec = Plecoptera; C+P = *Cybister* nested in Polyphaga; Poly = Polyphaga; Pol + Cyb = Polyphaga + *Cybister*; Siph = Siphonaptera. Tree statistics are given in Appendix 4.

served portion of the alignment is included in tree reconstruction, the outgroup Labidura is placed within Holometabola as sister group to Halteria (Figs. 11a, 11b), Cybister is sister group to MRPC, and Neuroptera is sister group to Polyphaga. When the entire portion of the alignment is included in tree reconstruction, *Cybister* is sister group to Polyphaga, MRPC is sister group to Mecoptera + Siphonaptera, and Halteria is sister group to Amphiesmenoptera. Boreus is sister group to Siphonaptera with the entire alignment and unresolved with respect to Mecoptera and Siphonaptera with the conserved alignment.

285 data.—In all 28S analyses, Strepsiptera, Diptera, Lepidoptera, Trichoptera, Hymenoptera, Halteria, Amphiesmenoptera, and Megaloptera + Raphidioptera are monophyletic (Figs. 11g-l). Holometabola are paraphyletic in two analyses because of the grouping of Plecoptera with Halteria (Figs. 11g, 11h). When gaps are coded as missing, Polyphaga, Mecoptera, and Siphonaptera are paraphyletic (Figs. 11g, 11j). When only the conserved regions of the alignment are included in the tree reconstruction, Hymenoptera are basal to the other holometabolous orders; when the entire alignment is used, Hymenoptera are placed either basally in Holometabola (Fig. 11j) or as sister group to (Priacma + (Polyphaga + Cybister)). Boreus is placed within Siphonaptera (Figs. 11g, 11j), as sister group to Siphonaptera (Figs. 11k, 11l), or as sister group to Amphiesmenoptera (Fig. 11i) or is unresolved (Fig. 11h). Panorpa is sister group to Plecoptera + Halteria (Figs. 11g, 11h) and Colpocaccus (Fig. 11j); in the remaining analyses it groups with the other mecopteran taxa. Unlike with the 18S data, Priacma is never sister group to Colpocaccus, and although Megaloptera + Raphidioptera are monophyletic, the MRPC clade is not supported. *Priacma* is generally placed near the other beetles, but Colpocaccus does not group with the other beetles, and its position changes in each analysis, probably in part because of its unusual sequence, which includs AT-rich regions (e.g., 28S insert 5, Appendix 3).

Combined molecular data.—All combined molecular analyses support the monophyly of Diptera, Strepsiptera, Halteria, Megaloptera + Raphidioptera, Mecoptera (excluding *Boreus*), Mecoptera + Siphonaptera, Neuroptera, Lepidoptera, Trichoptera, Amphiesmenoptera, Priacma + Colpocaccus, and MRPC (Fig. 12). There are two instances of holometabolan paraphyly due to the placement of Labidura as sister group to Halteria (Figs. 12a, 12b); this result parallels that of the 18S analyses under the same parameter values (Figs. 11a, 11b). The one instance of siphonapteran paraphyly (Fig. 12a) is due to the 28S data and is congruent with the results of that analysis (Fig. 11g). Hymenoptera are sister group to Halteria when gaps are weighted as 2, are unresolved basally when gaps are weighted as 1, and are the most basal order when gaps are coded as missing, although Hymenoptera are paraphyletic in one analysis (Fig. 12a). Boreus is sister group to Siphonaptera in all analyses except that of the merged conserved molecular data, where it is sister group to Mecoptera (Figs. 12h, 12i) or unresolved (Fig. 12g); but even when Siphonaptera are paraphyletic (Fig. 12a), Boreus is associated with a flea sequence. Amphiesmenoptera is sister group to (Mecoptera + (Siphonaptera + Boreus)) in all analyses except one (Fig. 12c), where it is sister group to MRPC. *Cybister* is placed as sister group to Polyphaga in most analyses, although it is unresolved twice (Figs. 12g, 12h) and sister group to MRPC twice (Figs. 12a, 12b).

Total data.—The two molecular and the morphological data sets were combined into "total" data sets by splicing and merging as explained above. In addition to the parameter values used in the other sensitivity analyses, the morphological characters were given a weight of 1 (trees on the left side of the taxon names in Fig. 13) or 2 (trees on the right side). All 24 simultaneous analyses of the total data set support the monophyly of Strepsiptera, Diptera, Halteria, Lepidoptera, Trichoptera, Amphiesmenoptera, Megaloptera + Raphidioptera, *Colpocaccus + Priacma*, and Mecopterida. Within Mecopterida, Antli-



FIGURE 12. Results of sensitivity analysis of combined molecular data for holometabolous relationships. Sensitivity parameters are alignment region (conserved or entire), gap weighting scheme (missing [?], 1, or 2), and method of data set combination (merged or spliced). Relationships among outgroups are not included. Unresolved clades are shown by thick bars, and paraphyletic groups are marked by asterisks. Amp = Amphiesmenoptera (Lepidoptera + Trichoptera); Halt = Halteria (Diptera + Strepsiptera); Hym = Hymenoptera; M+R = Megaloptera + Raphidioptera; Mec = Mecoptera excluding *Boreus*; Neur = Neuroptera (sensu stricto = Planipennia); PC = *Priacma* + *Colpocaccus*; Poly = Polyphaga; Siph = Siphonaptera. Tree statistics are given in Appendix 4.



FIGURE 13. Results of sensitivity analysis from the simultaneous analysis of all insect data. Sensitivity parameters are alignment region (conserved or entire), gap weighting scheme (missing [?], 1, or 2), method of data set combination (merged or spliced), and weight of morphological data (1 [left trees] or 2 [right trees]). Relationships among outgroups are not included. Unresolved clades are shown as thick bars. Amp = Amphiesmenoptera (Lepidoptera + Trichoptera); *Bor = Boreus; Cyb = Cybister;* Halt = Halteria (Diptera + Strepsiptera); Hym = Hymenoptera; M+R = Megaloptera + Raphidioptera; Mec = Mecoptera excluding *Boreus;* Neur = Neuroptera (sensu stricto = Planipernia); PC = *Priacma* + *Colpocaccus;* C+P = *Cybister* nested in Polyphaga; Poly = Polyphaga; Siph = Siphonaptera. For tree 1 the group ((PC, M+R)Neur)C+P) is the most basal clade. Tree statistics are given in Appendix 4.

ophora are monophyletic in every analysis except one (Fig. 13u), where Amphiesmenoptera are sister group to Halteria. In most analyses, Halteria are sister group to Mecoptera + Siphonaptera. Boreus is sister group to Siphonaptera when the entire alignment region is included in the reconstruction and morphology is weighted as 1 (except for Fig. 13u). Under all other combinations of parameter values, *Boreus* is placed as sister group to Mecoptera (i.e., most basal member of Mecoptera) or unresolved with respect to Mecoptera and Siphonaptera. Hymenoptera is sister group to Mecopterida in all analyses except one (Fig. 13k), where it is basal to the remainder of Holometabola. Mecoptera + Siphonaptera (Fig. 13m), Coleoptera + Neuropteroidea (Fig. 13g), and MRPC (Fig. 13j) are each paraphyletic in one analysis.

Sensitivity consensus trees.—Trees that summarize results of the sensitivity analysis are presented in Figure 14. The greater resolution and higher frequency values in the 18S summary tree as compared with the 28S data indicate that, overall, there are more clades identical in the 18S analysis than in the 28S analysis. The greater sensitivity of the 28S data to parameter perturbations may be due to greater internal conflict among the characters, although the fact that the 28S data set consists of fewer taxa across a shorter length of sequence may also influence sensitivity. When the 18S and 28S data are combined, the combined molecular topology is congruent with the 18S topology and is more resolved. With the exception of the basal placement of Hymenoptera, the 28S topology is also congruent with but much less resolved than the molecular topology. The 18S data force the monophyly of MRPC for any analysis that includes 18S (with one exception, Fig. 13j). When the morphological data are added to the molecular data, the resulting topology is far more resolved than the molecular topology. This topology from the total data is congruent with the morphology tree (Fig. 5) except for the placement of Strepsiptera as sister group to Diptera and the monophyly of MRPC. The total data summary tree disagrees with the prior analyses in placing *Boreus* as sister group to Mecoptera (i.e., as the basal member of Mecoptera) rather than as sister group to Siphonaptera. This placement results because when the morphological data are given a weight of 2 there are sufficient mecopteran autapomorphies to force the monophyly of Mecoptera; if the morphology were only given a weight of 1 in the sensitivity analyses, the summary tree would place *Boreus* as sister group to Siphonaptera with a nodal value of 56.

In every sensitivity analysis, Strepsiptera, Diptera, Halteria, Trichoptera, Lepidoptera, Neuroptera, Amphiesmenoptera, and Megaloptera + Raphidioptera are monophyletic. This result suggests that confidence can be placed in the conclusion that the data presented in this study truly support these relationships. In most analyses, Hymenoptera, Siphonaptera, Mecoptera (excluding *Boreus*), Siphonaptera + Boreus + Mecoptera, Priacma + Colpocaccus, Polyphaga, MRPC, and Holometabola are monophyletic. The most borderline case is the position of Boreus, which moves between Siphonaptera and Mecoptera as discussed above.

Taxon Removal

The paraphyly of Coleoptera, Neuropterida, and Neuropterida + Coleoptera is due to the strongly supported MRPC clade in the analyses that include the 18S data. For these taxa, the 18S sequences are nearly identical for the regions sequenced (average distance = 0.01975), and even insert regions that are typically highly variable among orders (e.g., 18S insert 11) are identical across these taxa. To be certain this identity was not an artifact of amplification or sequencing, the 18S sequences for these taxa were generated multiple times from independent PCR products generated from different genomic extractions. There are base differences in the 18S sequences and marked differences in the 28S sequences, indicating that the genomic DNAs do not appear to be contaminated with the same foreign DNA. This result is surprising because the Coleoptera / Neuropterida split is presumed to be one of the oldest diver-



FIGURE 14. Sensitivity analysis consensus trees. Majority rule consensus trees were calculated for the sensitivity analysis trees presented in Figures 11–13. Nodal values represent the percentage of times a particular node is present in the sensitivity analysis; as calculated by m/m + p, where m = number of times a clade is monophyletic and p = number of times it is paraphyletic and polyphyletic. Mecoptera excludes *Boreus* (denoted by an asterisk).

gences within Holometabola (Kukalová-Peck, 1991), and it is remarkable that the nucleotide diversity between these two orders is less than that between other orders assumed to be of more recent origin (such as in Amphiesmenoptera). These results clearly indicate that the 18S molecule is not behaving in a clocklike manner in the insects and that this is a case of evolutionary stasis for 18S in these taxa.

If the MRPC clade appears to be preventing the monophyly of Coleoptera and Neuropterida, what happens when the taxa comprising this clade are removed prior to phylogenetic analysis? This question was investigated by rerunning the 18S, combined molecular, and total data sets generated for the sensitivity analyses in three additional ways: (1) with Priacma and Colpocaccus removed (PC), (2) with Agulla and Corydalus removed (M+R), and (3) with Priacma, Colpocaccus, Agulla, and Corydalus removed (MRPC). Because the 28S data do not support MRPC, the results of the removal of these taxa were not investigated. Trees were constructed using the same phylogenetic searching routines as outlined above, and their overall topology is described here in comparison with the trees generated from the all-taxa sensitivity analyses.

18S data.—When Priacma and Calpocaccus were removed from the 18S data sets, Agulla + Corydalus became sister group to Neuroptera (=Neuropterida) in four analyses (conserved gaps = 2; entire gaps = ?, 1, 2) and was unresolved with respect to Neuroptera in one analysis (conserved gaps = ?), and in one case the relative topology was unaltered (conserved gaps = 1). The removal of these taxa does not change the relationships of other orders, with three exceptions: (1) *Cybister* becomes sister group to Polyphaga (conserved gaps = 2), (2) Neuropterida becomes sister group to (Mecoptera (Boreus + Siphonaptera)) (entire gaps = 1), and (3) Coleoptera becomes the most basal taxon, followed by Neuroptera then Hymenoptera (entire gaps = 2). These results suggest that 18S provides some support for neuropterid monophyly when these two beetle taxa are

removed, and the other relationships in the tree are only slightly sensitive to the deletion of these taxa.

When the Agulla and Corydalus sequences are deleted from the 18S analyses, MRPC collapses to Priacma + Colpocaccus, and this clade remains in the same relative position as MRPC (conserved gaps = ?, 1,2; entire gaps = 1) or collapses to the base of Holometabola to give a paraphyletic Coleoptera (entire gaps = ?, 2). All other relationships are congruent or unresolved with respect to the all-taxa analyses except for a paraphyletic Hymenoptera (conserved gaps = ?) and Coleoptera becoming the most basal taxon, followed by Neuroptera and then Hymenoptera (entire gaps = 2; same topology as when the beetles were removed). Polyphaga + Neuroptera is present in the conserved analyses, and Polyphaga are placed at the base of Holometabola and just basal to Neuroptera in the entire analyses. These results suggest that the 18S data do not provide much support for a monophyletic Coleoptera, even with the removal of the megalopteran and raphidiopteran taxa.

Removal of all four sequences from the 18S data sets results in more drastic changes in topology. Halteria are placed as sister group to Psocodea (conserved gaps = 2) or at the base of the insects (conserved gaps = ?), Hymenoptera are paraphyletic (conserved gaps = 1) or nested further within Holometabola with Coleoptera at its base (entire gaps = 1, 2), and Polyphaga and Neuroptera are paraphyletic (conserved gaps = ?, 1, 2).

Combined molecular data.—When *Priacma* and *Colpocaccus* were deleted from the molecular spliced analyses, Neuropterida became monophyletic, except for in two analyses when *Agulla* and *Corydalus* form a clade in the same position as MRPC (conserved gaps = 1; entire gaps = ?). Other relationships in these trees are sensitive to the deletion of these beetle taxa: Holometabola are unresolved (conserved gaps = 1), primarily because of the movement of Halteria to the outgroup; Amphiesmenoptera become sister group to Mecoptera + Si-

phonaptera (conserved gaps = 2), and Hymenoptera + Halteria moves to the base of the tree (entire gaps = 2). The deletion of *Priacma* and *Colpocaccus* from the merged molecular data does not change relative topology; hence Neuropterida remain paraphyletic (conserved gaps = ?, 1, 2; entire gaps = ?), although they are once unresolved (entire gaps = 1) and once monophyletic (entire gaps = 2). These results suggest that the combined molecular data are less supportive of a monophyletic Neuropterida than are the 18S data alone, presumably because the 28S data do not support this grouping.

When Agulla and Corydalus are deleted from the molecular spliced analyses, Coleoptera are unresolved (conserved gaps = ?), monophyletic (entire gaps = 2), or paraphyletic (conserved gaps = 1, 2; entire gaps = ?, 1). Holometabola collapse in one instance (conserved gaps = ?) or are paraphyletic due to Halteria grouping with Psocodea (conserved gaps = 1). The clade *Priacma* + *Colpocaccus* becomes the most basal clade in two analyses (conserved gaps = 1; entire gaps = 1), and Hymenoptera are unresolved rather than paraphyletic (conserved gaps = ?). For the molecular merged data, removal of these taxa does not change relative topology, except for one case of a monophyletic Neuropterida (entire gaps = 2). These results suggest that there is little evidence from the combined molecular data to support the monophyly of Coleoptera.

When all four taxa are deleted from the combined molecular analyses (whether spliced or merged), most relationships remain the same or are less resolved than in the all-taxa analyses. One exception is the placement of Halteria in the outgroup in three analyses (conserved gaps = ?, 1, 2). The clade Amphiesmenoptera + Mecoptera + Boreus + Siphonaptera is present in all analyses, and this result is in agreement with the all-taxa analyses.

Total data.—Removal of Colpocaccus and Priacma, Agulla and Corydalus, and all four taxa from the simultaneous analyses of the total data results in trees largely congruent with the all-taxa analyses. The major ex-



FIGURE 15. Results of removing various insect taxa from the total data sensitivity matrices. Analysis parameters are given in Table 4. The analyses resulted in four general topologies for relationships among major holometabolous groups (a–d) and three less resolved topologies (e–g), with the majority rule consensus given in h. Coleoptera and Neuropterida are always monophyletic. Col = Coleoptera; NEUR = Neuropterida (=Neuroptera + Raphidioptera + Megaloptera); MEC = Mecopterida (=Trichoptera + Lepidoptera + Siphonaptera + Mecoptera + Diptera + Strepsiptera); Hym = Hymenoptera.

ception is that in all partial-taxa analyses, the monophyly of Coleoptera and the monophyly of Neuropterida are supported (in contrast to the all-taxa analyses where there is never support). Relationships among the remaining orders can be described in terms of four fully resolved general topologies (Figs. 15a–d) and three partially resolved general topologies (Figs. 15e–g; Table 4). In most cases (72%), Coleoptera and Neuropterida are sister groups. The placement of Coleoptera as the most basal taxon (topology b) is supported only in the spliced data sets of the entire alignment, most frequently when Corydalus and Agulla are removed (six times) and less frequently when Priacma and *Colpocaccus* are removed (twice) and when all four taxa are removed (three times). In most cases (93%), Hymenoptera are placed as sister group to Mecopterida, in agreement with our morphological analysis and that of Kristensen (1975, 1991, 1995).

Overall, these results suggest (1) the presence of the MRPC clade is masking some molecular evidence for a monophyletic Neuropterida and less evidence for a monophyletic Coleoptera; (2) the total data analysis with the deletion of these taxa most frequently supports ((Coleoptera + Neuropterida) + (Mecopterida + Hyme-

	Gap weights ^a					
	?			1		2
Taxa removed from analysis	M = 1	M = 2	M = 1	M = 2	M = 1	M = 2
Agulla and Corydalus						
Spliced						
Conserved	а	а	f	а	а	а
Entire	b	b	b	b	b	b
Merged						
Conserved	а	а	а	а	а	а
Entire	e	e	e	а	а	e
Priacma and Calpocaccus						
Spliced						
Conserved	g	а	d	а	а	а
Entire	Ď	b	d	g	g	а
Merged				-	-	
Conserved	d	а	g	а	а	а
Entire	d	а	d	а	а	а
Calpocaccus, Agulla, Priacma, and C	orydalus					
Spliced						
Conserved	e	e	а	a	а	а
Entire	b	b	а	а	b	а
Merged						
Conserved	а	а	а	а	а	а
Entire	с	а	с	а	а	а

TABLE 4. Results of removing various insect taxa from the total data sensitivity matrices. The analysis resulted in four general topologies (a–d) and three less resolved topologies (e–g) for relationships among major holometabolous groups. Topologies are given in Figure 15.

^a Morphological characters (M) were given a weight of 1 or 2.

noptera)); and (3) clades present on the sensitivity consensus trees (Fig. 14) are also present in the analyses with the MRPC taxa removed. The relationships among the other orders are more sensitive to the removal of *Agulla* and *Corydalus* than to the removal of *Priacma* and *Colpocaccus*, presumably because the beetles are well represented by other sequences but Megaloptera and Raphidioptera are not. The spliced analyses are more sensitive to the removal of these taxa than are the merged analyses, which may be the result of an increase in the relative amount of missing data in the spliced analyses.

DISCUSSION

Holometabolous Relationships

Holometabola.—The monophyly of Holometabola was tested with 19 insect sequences and 1 entognath outgroup sequence. Our results provide strong evidence for the monophyly of Holometabola. Although the individual 18S and 28S Bremer support values calculated for Holometabola are rather low (1 and 2, respectively), in the combined molecular analysis and the total data analysis these values are relatively high (12 and 16, respectively). The same trend is seen in branch lengths, with the shortest branch from the 18S analysis (minimum of 6) and the longest from the analysis of all data (maximum of 50). Of the 48 all-taxa sensitivity analyses, Holometabola are paraphyletic in only five instances. In three cases when 18S is included in the analysis, the Labidura sequence is placed as sister group to Halteria (Figs. 11a, 11b, 12a); in two cases when 28S is included in the analyses, Megarcys + Cultus (Plecoptera) is placed as sister group to Halteria (Figs. 11g, 11h). We do not think these few cases argue very strongly against the monophyly of Holometabola because this paraphyly occurs under very specific parameter values that

	No				Totalª		Average	
Forced groupings	constraints	185	285	Molecular	M = 1	M = 2	% steps	
Strepsiptera in Polyphaga								
Conserved Entire	1 1	0.76 0.65	0.44 1.31	1.04 0.83	0.96 0.88	1.22 0.94	$\begin{array}{c} 1.08 \\ 0.88 \end{array}$	
Strepsiptera + Coleoptera								
Conserved Entire	3 3	1.38 1.97	0.13 1.51	0.86 1.55	0.60 1.17	0.94 0.89	0.88 1.26	
Monophyletic Coleoptera								
Conserved Entire	1 1	2.18 1.17	0.43 0.91	2.21 0.80	$\begin{array}{c} 1.40\\ 0.41 \end{array}$	0.12 0.16	1.27 0.53	
Monophyletic Neuropterida								
Conserved Entire	1 1	1.33 1.02	0.09 0.17	1.09 0.74	0.59 0.49	0.12 0.16	0.63 0.48	
Coleoptera + Neuropterida								
Conserved Entire	3 3	1. 42 1.35	0.16 0.97	1.30 1.00	0.59 0.54	0.12 0.16	0.71 0.63	
Monophyletic Mecoptera								
Conserved Entire	1 1	0.33 0.09	0.07 0.68	0.23 0.18	0.05 0.04	0.00 0.00	0.12 0.10	
Monophyletic Mecopterida								
Conserved Entire	1 1	0.10 0.15	0.16 0.26	$\begin{array}{c} 0.06 \\ 0.14 \end{array}$	0.05 0.00	$0.00 \\ 0.00$	0.06 0.06	

TABLE 5. Average percentage of extra steps required to enforce group monophyly with each insect data set. The actual number of steps required to force monophyly was calculated in NONA by constraining the monophyly of a group while swapping on all other terminals (force +n; max/) and taking the difference between tree lengths. Exact counts of extra steps are given in Appendix 4.

^a Morphological characters (M) were given a weight of 1 or 2.

must include only the conserved portions of the alignment in the analysis. Moreover, the placement of the Plecoptera and Labidura sequences relative to the other outgroup taxa is highly sensitive to parameter values of tree reconstruction, hence they are behaving somewhat as "wildcard" taxa on the tree, even when placed outside of Holometabola (Nixon and Wheeler, 1992). Overall, the relationships among the outgroup taxa are mostly congruent with those based on morphology, and the rooting for Holometabola appears appropriate (Kristensen, 1995). Because the sampling of outgroup taxa was not as exhaustive as sampling of the ingroup, we had no expectation of full congruence. A more exhaustive study of nonholometabolous insect relationships is in preparation.

Neuropterida.—The monophyly of Neuropterida is never supported in our all-taxa sensitivity analyses. A higher per-

centage of steps is required to force monophyly for the 18S data (1.33% [conserved analysis] and 1.02% [entire analysis]; Table 5) than for the 28S data (0.09% [conserved analysis] and 0.17% [entire analysis]; Table 5); most of these additional steps are required to break up MRPC. There is some indication from the partialtaxa analyses that 18S provides evidence for neuropterid monophyly when Priacma and Colpocaccus are removed. In agreement with Kristensen (1991, 1995) and Achtelig (for summary, see Hennig, 1981), our results appear to strongly support the monophyly of Megaloptera + Raphidioptera; this clade is present in every analysis and is also supported by 28S insert 6. Because our analysis only included a single exemplar from both orders, we are unable to address the question of megalopteran paraphyly (see Kristensen, 1995). Our results support the monophyly of Neuroptera,

which were monophyletic in every analysis. In addition, some of the largest inserts for 18S (insert 13) and 28S (inserts 2, 7, 12) occur in this group, and these inserts could be considered further synapomorphies for these groups. In all the analyses, the *Myrmeleon* species cluster together, and the other Neuroptera are generally unresolved with respect to *Myrmeleon*.

Coleoptera.—Our all-taxa analyses never support a monophyletic Coleoptera. In the 28S analysis, coleopteran paraphyly is primarily due to the disassociation of Colpo*caccus* with the other beetles. Polyphaga are either unresolved or paraphyletic in these analyses because of the nesting of *Cybister* within the other beetles (Figs. 11i, 11k, 11l) or the multiple placements of the beetles on the tree (Figs. 11g, 11j). In all the analyses including the 18S data, coleopteran paraphyly is due to MRPC. The average percentages of extra steps required to force a monophyletic Coleoptera (Table 5) for 18S are 1.17 (entire analyses) and 2.18 (conserved analyses) compared with 0.91 (entire) and 0.43 (conserved) for 28S. Even when Agulla and Corydalus are removed from the analyses, Coleoptera are paraphyletic in the majority of analyses.

Although the molecular data do not support monophyletic Coleoptera, there is strong support for monophyletic Polyphaga. In the 18S analyses, Polyphaga are generally monophyletic and associated with either Neuroptera (Figs. 11a–c) or the adephagan *Cybister* (Figs. 11d, 11e). The molecular analyses and the simultaneous analyses reflect what is seen in the 18S analyses: Polyphaga are monophyletic (except Fig. 12a) and most commonly sister group to *Cybister*. The 18S insert 12 also has synapomorphies for Polyphaga.

Coleoptera + *Neuropterida*.—This clade was not supported in any of the all-taxa analyses (the percentage of extra steps required to force monophyly ranges from 0.16 to 1.42 [Table 5]) but was occasionally supported when *Colpocaccus/Priacma* or *Agulla/Corydalus* were removed and was supported 74% of the time when all four taxa were removed from the data set (Fig. 15). It is intriguing that the basal beetles

are sister group to Megaloptera + Raphidioptera in all analyses that include the 18S data. These basal taxa, which have retained primitive morphological features (such as vein remnants in the elytra of *Priacma*), may have also retained the primitive Coleoptera-Neuropterida nucleotide states for 18S. Hence, the similarity between these taxa might be attributed to symplesiomorphy rather than synapomorphy. The more derived Coleoptera and Neuroptera are not grouped with their more basal counterparts, but this may be a result of sampling: Coleoptera are an enormously diverse group, and although Neuroptera are less speciose, their 18S sequences are more autapomorphic than those found in most insects.

Hymenoptera.—Hymenoptera were the most well-represented order in terms of the overall number of sequenced exemplars. In nearly all analyses (96%, Fig. 14), Hymenoptera are monophyletic, the branch lengths and Bremer support values are fairly high (Fig. 10), and they share 18S insert 19. Some of the relationships within Hymenoptera are congruent with other phylogenetic hypotheses: ants are always monophyletic, ichneumonid wasps are always monophyletic, tenthredinid sawflies are usually monophyletic, and vespid wasps are usually monophyletic, although the two *Polistes* species are not sister taxa.

Our analyses do not support a definitive placement for Hymenoptera. For 28S, 17 of 24 analyses (including the partial-taxa analyses) place Hymenoptera at the base of Holometabola, but for 18S and the combined molecular data the support is weaker: 4 of 24 and 14 of 48 analyses support this placement. When only the combined molecular data are considered, the placement of Hymenoptera is quite sensitive to the analytical parameters, and this clade is placed in different positions across the combined molecular sensitivity analyses. In the simultaneous analyses of all data, Hymenoptera are sister group to Mecopterida in 82 of 96 analyses, in accord with the morphological tree.

Mecopterida.—The molecular evidence for a monophyletic Mecopterida (Trichop-

tera + Lepidoptera + Diptera + Siphonaptera + Mecoptera) is sparse, even with the inclusion of Strepsiptera. This group is never present in any of the 28S or combined molecular analyses and is only present in the 18S partial-taxa analyses when gaps = 2 and the entire alignment region is included. This grouping is present in our morphology tree (Fig. 5) and supported in all of the total data analyses with the inclusion of Strepsiptera (Fig. 12).

Amphiesmenoptera.—Under every set of parameters used in the analyses, Trichoptera, Lepidoptera, and Amphiesmenoptera are monophyletic. These groups are supported by long branch lengths and high Bremer support values, with the highest values occurring in Lepidoptera. The 18S insert 16 supports the monophyly of Lepidoptera; 18S insert 17 and 28S insert 13 support the monophyly of Trichoptera. Amphiesmenoptera are considered the best supported sister-group pair among insect orders (Hennig, 1969, 1981; Kristensen, 1995), and both the 18S and 28S data are entirely congruent with this hypothesis.

Antliophora.—The monophyly of Antliophora (Siphonaptera + Mecoptera + Diptera; with the inclusion of Strepsiptera) is not supported by the molecular data but is supported in nearly all simultaneous analyses (Fig. 14). The Mecoptera + Siphonaptera clade is monophyletic in nearly all analyses, and this clade has relatively large branch lengths and Bremer support values. The 18S insert 15 is a striking synapomorphy for this group in that the last 13 bases are identical across these taxa. Overall, our data appear to support strongly the monophyly of Mecoptera + Siphonaptera.

Siphonaptera are monophyletic in every 18S and simultaneous analysis but are paraphyletic in two 28S analyses (Figs. 11g, 11j) because of the grouping of *Boreus* with *Ctenocephalides* and in one combined molecular analysis (Fig. 12a) because of the groupings of *Boreus* + *Ctenocephalides* and *Orchopeas* + other mecopteran taxa. The monophyly of Mecoptera has been disputed, particularly in regard to the placement of Boreidae ("Neomecoptera"; Hinton, 1958) and Nannochoristidae (Wood and Borkent, 1989; Kristensen, 1995). Our analyses present some evidence for the exclusion of boreids from Mecoptera (or the inclusion of Siphonaptera as subordinate within Mecoptera). Boreus is never placed within Mecoptera (see Willman, 1987) but is found as sister group to Ctenocephalides, sister group to Siphonaptera, or sister group to the remaining Mecoptera (i.e., the most basal member). In two 28S analyses and one combined molecular analysis, Bo*reus* is placed as sister group to *Ctenocephalides* and Siphonaptera are paraphyletic. The 18S, 28S, and combined molecular analyses most frequently place Boreus as sister group to Siphonaptera (Fig. 14). In the simultaneous analyses, Boreus + Siphonaptera occurs 5 times, Boreus + remaining Mecoptera occurs 12 times, and Boreus is unresolved 7 times. The morphological data include three mecopteran autapomorphies that force *Boreus* as the most basal mecopteran member when morphology is weighted more than 1. The percentage of extra steps required to force a monophyletic Mecoptera is greatest for the 28S entire and 18S conserved analyses (Table 5), but this percentage is relatively small, indicating that a monophyletic Mecoptera is only a few steps away from the shortest tree. The hypothesis that Siphonaptera may be phylogenetically subordinate within Mecoptera is also supported by the recent finding that they share with Boreidae a suite of ovariole characters (Kristensen, 1995). Boreus aside, the remaining Mecoptera are monophyletic in every analysis except for the grouping of *Panorpa* with Plecoptera + Halteria (Figs. 11g, 11h) and Colpocaccus (Figs. 11j) in three of the six 28S sensitivity analyses. Across the remainder of the analyses, the most basal member of Mecoptera is almost always Merope, followed by the Bittacus sequences and then Panorpa.

Halteria.—The difficulty in placing Strepsiptera among the other insect orders has been discussed. In every sensitivity analysis, Strepsiptera, Diptera, and Strepsiptera + Diptera are monophyletic. The

monophyly of these orders is supported by large Bremer support values and long branch lengths, and there can be no doubt that the molecular data support this relationship. Strepsiptera and Diptera have large insertion regions in the same positions for both the 18S (inserts 2 and 3, 20 and 21) and 28S (inserts 4 and 8) alignments. These results agree with those of Chalwatzis et al. (1995), who found Xenos vesparum associated with Drosophila + Aedes in a seven-taxon analysis of 18S rDNA sequences. The average percentage of extra steps required to place Strepsiptera within Polyphaga or as sister group to Coleoptera was calculated; it requires an increase in tree length of approximately 1% to force the monophyly of these assemblages (Table 5). Our analyses do not support a placement of Strepsiptera near Rhipiphoridae as Crowson (1960) suggested, nor do they support a placement as sister group to Coleoptera.

For Diptera, *Tipula* is always the most basal taxon, and the trichotomy of *Laphria– Drosophila–Mythicomyia* is inconsistently resolved across the sensitivity analyses. For Strepsiptera, the stylopid clade (*Crawfordia* (*X. pecki* + *X. vesparum*)) is supported in every analysis, and *Caenocholax* is the most basal strepsipteran taxon. Because a formal phylogenetic analysis of groups within Strepsiptera is still forthcoming, it is not clear whether these relationships are congruent with morphology.

Only one morphological character associates Strepsiptera with Coleoptera: flight motored by the hind wings (posteromotorism). All other characters suggested to support such an association (e.g., insect endoparasitism, planidial larvae, gula, prothoracic notopleural sutures, absence of a telomere, and wing venation; Crowson, 1960; Boudreaux, 1979; Kukalová-Peck and Lawrence, 1993) have been thoroughly examined and rejected (Kathirithamby, 1989; Kinzelbach, 1990; Kristensen, 1991; Whiting and Kathirithamby, 1995). Likewise, Strepsiptera do not possess any of the supraordinal characters of Coleoptera-Neuropterida, as this hypothesis would entail. However, some morphological evidence

supports the placement of Strepsiptera within the supraordinal groups to which Diptera belong. The majority of characters supporting a monophyletic Mecopterida (characters 104-106; Appendix 3) are inapplicable to Strepsiptera because the larval mouthparts and associated musculature are too severly reduced to be scored. The lack of an ovipositor (even in the partially free-living Mengenillidae; Kathirithamby, 1989) and the absence of the outer tergal coxal remotor muscle (Kristensen, 1995) are characters that Strepsiptera share with Mecopterida. According to Kristensen (1995), Strepsiptera lack the insertion of the pleural muscle on the first axillary sclerite, the presence of which is considered a mecopterid synapomorphy.

Many of the characters supporting Antliophora (characters 118, 121-124; Appendix 3) are likewise inapplicable to Strepsiptera because of the morphological reduction of the larvae and adults. Strepsiptera do share with Antliophora the slender mandibles with weak anterior articulations (Kristensen, 1995) and prelabium (prementum) without endite lobes and associated muscles (Kristensen, 1991) but do not have a pleural ridge/scutum muscle insertion on the posterior notal wing process (Kristensen, 1995). In addition, in male Antliophora, abdominal segment IX is ringlike, enlarged, and fused along the pleuron. Kristensen (1991) treated the fusion of the gonopod bases above and below the phallic apparatus as an autapomorphy for the order Mecoptera, but this fusion clearly is also present in Strepsiptera (Kinzelbach, 1971). All nematocerous Diptera have this character, which may be the basal condition in Diptera (Wood and Borkent, 1989), although Kristensen (1995: 104) contended that "it remains uncertain whether the male segment IX was 'ringlike' in the dipteran groundplan." In Siphonaptera, sternum IX is modified to form an L-shaped clasping organ, and tergum IX is modified into a complex clasping organ consisting of a pair of manubria and articulating claspers that occupies the posterior tip of the abdomen and encloses the genitalia (Dunney and Mardon, 1991).



FIGURE 16. Scanning electron mircorgraph, dorsal view, *Caenocholax fenyesi* Pierce $(40\times)$. The forewings of male Strepsiptera are modified into structures that morphologically and functionally resemble the halteres of Diptera.

This character may be an autapomorphic modification of the enlargement of abdominal segment IX, which is seen in the other antliophoran orders. If so, this character supports the monophyly of Antliophora inclusive of Strepsiptera. Currently, there is more morphological evidence for the placement of Strepsiptera with the antliophoran orders than for an association with Coleoptera.

The most striking similarity between Diptera and Strepsiptera involves the microstructure and function of the dipteran halteres (reduced metathoracic wings) and strepsipteran pseudohalteres (Fig. 16; reduced mesothoracic wings). Kathirithamby (1989) challenged the long-held notion that pseudohalteres are modified elytra and listed a number of similarities between halteres and pseudohalteres. Pix et al. (1993) concluded that Strepsiptera use their pseudohalteres as gyroscopic balancing organs during flight in the same manner as Diptera, and our observations of Strepsiptera in flight agree with this conclusion. Whiting and Wheeler (1994) hypothesized that a homeotic mutation could be responsible for the apparent shift of the halteres from the metathorax in Diptera to the mesothorax in Strepsiptera. Research into the development of the strepsipteran thoraces is currently underway to test for this suggested homeotic shift.

Long-Branch Attraction

Whiting and Wheeler (1994) concluded that 18S rDNA data support the monophyly of Strepsiptera and Diptera and suggested implications of this phylogenetic conclusion for the role of homeosis in the evolution of Strepsiptera. Carmean and Crespi (1995) argued that halterian monophyly is an artifact of long-branch attraction (Felsenstein, 1978); they demonstrated that Strepsiptera and Diptera have a higher substitution rate than any other taxa included in their phylogenetic analysis and that these two taxa are well supported as sister groups in that analysis. There are four reasons why we believe that long-

VOL. 46

branch attraction is not a plausible explanation for the grouping of Strepsiptera and Diptera in our phylogeny.

First, 28S and 18S are congruent in strongly supporting the monophyly of Halteria; thus the occurrence of longbranch attraction would need to be postulated for both molecules. The majority of ordinal relationships on the molecular trees are congruent with other hypotheses of insect phylogeny, particularly in the mecopterid portion of the tree. Strepsiptera and Diptera are always monophyletic, and if long-branch attraction were a problem these orders occasionally would be paraphyletic because of the random grouping of an individual strepsipteran sequence with an individual dipteran sequence. Halteria are often positioned within Mecopterida (even in the Carmean and Crespi [1985] tree), and this grouping is also congruent with the morphological data. Hence there appears to be some signal in these data that is not masked by long-branch attraction and that allows ordinal monophyly (Strepsiptera and Diptera) and supraordinal placement (Mecopterida) congruent with that indicated by morphology.

Second, the branch lengths for Diptera, Strepsiptera, and Halteria are comparable to those of other insects groups in this analysis. For instance, the 18S branch lengths for Diptera (52–82) and Strepsiptera (33–63) are not far out of range of those for Lepidoptera (28–45) and Trichoptera (19–35); the branch lengths for Halteria (11–48) and Amphiesmenoptera (10–32) are even more comparable (Fig. 7). For 28S, the situation is reversed: in Lepidoptera the branch length (23–48) is greater—and with higher Bremer support—than that in Diptera (14–27) and Strepsiptera (20–24); likewise the branch length for Amphiesmenoptera (10–37) is greater than that for Halteria (9–21). This trend occurs throughout the sensitivity analyses regardless of whether the entire or only the conserved portions of the alignment are used for tree reconstruction. The mapping of characters on a tree generated from the analysis of 18S + 28S (conserved alignment, gaps = ?, merged data sets) and on a total evidence analysis tree (conserved alignment, gaps = ?, morphology = 1; Fig. 17) demonstrates that a portion of these branch lengths consists of nonhomoplastic characters. The molecular data for these trees are taken only from the unambiguous regions of the sequence alignment and are thus conservative estimates of relationships. The two orders comprising Amphiesmenoptera are considered to have the most firmly established sister-group relationship among all insect orders (Kristensen, 1995). Thus, if the association of the amphiesmenopteran sequences is also due to long-branch attraction, it is fortuitous that it is congruent with morphology.

Third, the greatest sequence diversity between any two taxa is not between Strepsiptera and Diptera. A pairwise percent difference for 18S and 28S was computed by considering only those alignment positions with any nucleotide variation to determine whether any two sequences appeared saturated relative to each other (data not shown). The result indicates that the greatest distance between any two taxa for 18S is between *Tipula* and *Lygus* (0.287) and for 28S is between Lygus and Galleria (0.300). Because the suspected long-branch attraction is between two orders, the average distance between a single order and all other orders was calculated for the 18S data. Diptera have the greatest average distance relative to all other orders (133.81/ 530 base changes), but the average number of base changes for Strepsiptera (96.26) is within three base changes of the values for Phthiraptera (99.11), Thysanoptera (96.51), Lepidoptera (96.13), Siphonaptera (95.38), Collembola (95.33), and Epheremoptera (95.27). Thus, in terms of simple average distance calculations, the substitution rate for Strepsiptera is not uniquely high relative to that for other taxa. This point is further confirmed by computing the average number of base changes for 18S between Diptera and all other orders. Strepsiptera rank somewhere in the middle, with 13 orders having higher distance values and 8 orders having lower distance values. Hence relative to Diptera, there are 13 other or-





FIGURE 17. Summary character mapping of molecular (a) and total evidence (b) trees for Holometabola. The molecular tree is the holometabolous portion of the strict consensus (conserved alignment, 18S + 28S, merged, gaps = ?). The total evidence tree is the holometabolous portion of the strict consensus (conserved alignment, 28S + 18S + morphology, merged, gaps = ?, morphological characters = 1). Symbol shapes on the nodes refer to the data set from which a character originated: \Box = morphology; \bigcirc = 28S; \triangle = 18S. Coloring represents homoplastic changes (shaded), reversals (open), and nonhomoplastic changes (solid). Numbers beneath symbols represent the number of times that class of characters was present on a node. Characters were mapped using a modified DELTRAN optimization (Nixon, 1995).

ders with higher substitution rates than Strepsiptera.

Fourth, Carmean and Crespi (1995) argued that Strepsiptera and Diptera have uniquely high substitution rates relative to the other sequences, but the number of taxa sampled in their analysis was small: 10 ingroup taxa and 2 outgroup taxa. Representatives of Lepidoptera, Trichoptera, Megaloptera, and Raphidioptera were not included. Strepsiptera were represented by a single species, Diptera were represented by Drosophila and the apparently flawed Aedes sequence, and sampling for the rest of Mecopterida consisted of a single scorpionfly sequence and a flea sequence. Other holometabolous 18S sequences available at the time of their analysis, including ones generated by Carmean et al. (1992), were inexplicably excluded from their analysis. Thorough taxon sampling is important in this context because it reduces branch lengths (Swofford and Olsen, 1990), whereas the undersampling of taxa artificially inflates branch lengths. By including multiple representatives of each order and by sampling the basal members of Strepsiptera and Diptera, we have reduced the relative distance between the terminals in our phylogeny and have found other instances of insects with high substitution rates.

A point that is often missed in longbranch attraction discussions is that relative rates of substitution are influenced by phylogeny, and thus we should not be surprised to find cases of sister groups that have high rates of nucleotide substitution; shared elevated rates could indeed be evidence of shared history. The supposition that the clades best supported by character data are the ones we should be most suspicious of has the strange result of entailing an inverse relationship between phylogenetic evidence and phylogenetic conclusions. The large amount of molecular evidence supporting the monophyly of Halteria and Amphiesmenoptera can be taken at face value as indicative of wellsupported sister-group relationships and not as foibles of the data or analytical method.

Conclusions

There are three things unique to this study. The first is the reliance on multiple independent data sources for phylogenetic inference of holometabolous relationships. By generating two molecular data sets and producing the first morphological matrix for these orders, we have compiled the largest and most comprehensive body of evidence on holometabolan interordinal relationships. The second unique aspect is the broad and thorough selection of exemplars for sequencing. Our study is the first to include exemplars from every holometabolan order, with multiple representatives from most of the major subclades and a very broad range of outgroup taxa. Other critical taxa need to be added to this study, i.e., exemplars of Nannochoristidae (Mecoptera) and Mengenillidae (Strepsiptera) and perhaps a more thorough survey of Nematocera.

Third, we tested the robustness of the phylogenetic conclusions to the assumptions used in the data analysis by performing sensitivity analyses on multiple parameters: the influence of gap costs; methods of data set combination, partitioned versus combined data sets, and the relative weights of morphological and molecular characters. Other parameters may also prove influential in interpreting these data. For instance, ranges of gap/nucleotide cost ratios, transition/transversion biases, and alignment by presumed secondary structure may result in different statements of putative homology during alignment. We anticipate, however, that variation in these other parameters would only alter the more variable regions of the alignment and that the phylogenetic results primarily from the conserved regions are not sensitive to the alignment parameters.

The summary of our best estimate of holometabolan relationships is given in Figure 18. Halteria (Diptera + Strepsiptera), Amphiesmenoptera (Trichoptera + Lepidoptera), Megaloptera + Raphidioptera, and Holometabola are strongly supported monophyletic assemblages. Further, Mecopterida, Antliophora, and Neuropterida probably are monophyletic, although the character support is not as strong as in the previous groupings. All holometabolan orders appear monophyletic, with the possible exception of Mecoptera with regards to Boreus, which may actually be the sister group to Siphonaptera (i.e., Siphonaptera are subordinate within Mecoptera). The groups that are rather am-



FIGURE 18. Overall conclusions regarding holometabolous insect phylogenetic relationships. Thick lines subtend nodes that strongly support monophyletic groups, thin lines subtend nodes for relatively well-supported monophyletic groups, and dashed lines subtend nodes that are still questionable.

biguously placed in our analyses are Hymenoptera, Coleoptera, and Neuropterida. Hymenoptera is probably the sister group to Mecopterida, although placement at the base of Holometabola is still a possibility. Neuropterida and Coleoptera certainly sit outside of Mecopterida, and there is some morphological and some molecular evidence that these two are sister groups, but they also could be placed as pectinate on the tree, with Coleoptera as (probably) the more basal order. Sequencing more genes from a wider selection of taxa and a reevaluation of the morphological characters promises to provide a more thorough understanding of insect ordinal relationships. It is somewhat ironic that our data support a phylogenetic placement for Strepsiptera that was first suggested in the early 1800s but has long since been abandoned by entomologists.

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APPENDIX 1 18S Alignment with Appended Inserts

The 85 taxa were aligned using MALIGN (parallel version 1.93; Wheeler and Gladstein, 1994). The heuristic algorithm "Build" with SBR branch swapping on multiple alignments was performed (change cost = 3, gap cost = 5, leading and trailing gap cost = 8). Primer regions were included in the alignment but were subsequently excluded in phylogenetic analyses. Variable alignment regions (positions 281–361) were excluded from phylogenetic analyses in the conserved tree reconstructions. When the initial alignment presented evidence of a large insertion in a single taxon or subset of taxa, the region was removed to facilitate alignment of positions flanking the insert. Symbols in the alignment (other than standard nucleotide codes) refer to insertions appended after the alignment.

	185 ai	100▼
Hypogastrura	CCTGAGAAACGACTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGG-AGGTAGTGACGAAAAATAACGATACGGAACTCA
Trigoniopthalmus	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCACGCAAATTACC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACAATACGGGACTCA
Ephemerella	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Agrion	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCCCAAATTACC	CACTCCCGGAACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Libellula	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGCGCGCGC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Megarcys	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGGGGGGTAGTGACGAAAAATAACGATACGGGACTCA
Cultus	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Blaberus	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Mantis	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Labidura	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGC	CACTCCCAGCACGGGGGGGGGTAGTGACGAAAAATAACGATACGGGACTCA
Melanopius	CCTGAGAAACGGCTACCACATCCTAGGAAGGCAGCAGCGCGCGAAATTACC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Anisomorpha	CCTGAGAAACGGCTACCACATCCTAGGAAGGCAGCAGCGCGCGC	
Oligotoma		CACICCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Depayue	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTOCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGGG
Acurthosiphon	CCTGAGAANCGGCTACCACATCCAAGGCAGGCAGCAGGCGCGCGAAATTACC	CACTCC-GGAACGGGGGGGGGGGGGGGGGGGGGGGGGGGG
Buence	CCTGAGAAACGGCTACCACATCCAAGGCGGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Saldula	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCAG	CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Lyaus	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCACGCAAATTACC	CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Taeniothrips	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGCGCGCGC	CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Priacma	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCCCCAAATTACC	CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Colpocaccus	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGC	CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Cvbister	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Xyloryctes	CTTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Octinodes	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Photuris	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGC	CACTCCCGGCACGGGGGGGGGGGGGGGGGCGACGAAAAATAACGATACGGGGACTCA
Meloe	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Rhipiphorus	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Tenebrio	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Tetraopes	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Corydalus	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Agulla	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Lolomyia	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Mantispa	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Hemerobius	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Chrysoperla	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
M.immaculatus	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Myrmeleon	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTAC	CACTCCCGGCACGGGGGGGGGTAGTGACGAAAAATAACGATACGGGACTCA
Galleria		CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Papilio		CACTCCCGGCACGGGGGGGGGTAGTGACGAAAAATAACGATACGGGACTCA
Ascalapha	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACC	CACTCCCGGCACGGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCT
Hydropsyche		
Pychopsyche	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACC	
B strigosus	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCCGCAAATTACC	CACTCCCAGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
B chlorostigmus	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Boreus	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGC	CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Merope	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGC	CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Panorpa	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGC	CACTCTCGGCACGAGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Ctenocephalides	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGC	CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Hystrichopsylla	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGC	CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Orchopeas	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGC	CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Hartigia	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGC	CACTCCCGGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Orussus	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Hemitaxonus	CCTGAGAAACGGCTACCACATCTAAGGAAGGCAGCAGGCGCGCGAAATTAC	CACTCCCGGCAGCGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Peridista	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Bareogonalos	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Evania	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Ichneumon	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGC	CACTCCCGGCACGGGGGGGGGGGGGGGGGCGACGAAAAATAACGATACGGGACTCA
Ophion	CCTGAGAAACGGCTACCACATCTAAGGAAGGCAGCAGGCGCGCGAAATTAC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Mesopolobus	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Caenochrysis	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTACC	CCACTCCCGGCACGGGGGGGGGGGGGGGGGGCGACGGACG
Epyris	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTAC	CCACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Priocnemus	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTAC	CACTCCCGGCACGGGGAGGTAGTGACGAAAAATAACGATACGGGACTCA
Dasymutilla	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTAC	CACTCCCGGCACGGGGAGGTAGTGTCGAAAAATAACGATACGGGACTCA
Apoica	CCTGAGAAACGGCTACCACATCTAAGGAAGGCAGCAGGCGCGCAAATTAC	CCACTCCCGGCACGGGGGGGGGTAGTGACGAAAAATAACGATACGGGACTCA
Monobia	CCTGAGAAACGGCTACCACATCTAAGGAAGGCAGCAGGCGCGCAAATTAC	CCACTCCCGGCACGGGGGGGGGTAGTGACGAAAAATAACGATACGGGACTCA
P.IUSCATUS	CCIGAGAAACGGCTACCACATCTAAGGAAGGCAGCAGGCGCGCGC	CACTCCCGGCACGGGGGGGGTAGTGACGAAAAATAACGATACGGGACTCA
Camponotus		~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
Chalepoyepus		\^^^^^^^^^
Doropomyrmey		\^^^^^^^^^^
Harpagoyepus		~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
Leptothorax		~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
Tempothorax		***************************************
Tipula	CCTGAGAAAACGGCTACCACATCTAACGAACGCACCACCACGCCTTAACCACCACGCCTACACACAC	CAATCCCAGCACGGGGAGGTAGTGACGAAAAAAAAAAAA
Laphria	CCTGAGAAACGGCTACCACATCTAAGGAAGGCAGGCAGGC	CACTCCCAGTACGGGGAGGTAGTGACGAAAAATAACAATACAGGACTCA
Mythicomvia	CCTGAGAAACGGCTACCACATCTAAGGAAGGCAGGCAGGC	CACTCCCAGCACGGGGAGGTAGTGACGAAAAATAACAATACAGGACTCA
Drosophila	CCTGAGAAACGGCTACCACATCTAAGGAAGGCAGGCGCGCGTAAATTAC	CACTCCCAGCTCGGGGAGGTAGTGACGAAAAATAACAATACAGGACTCA
Triozocera	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGGCAGGC	CACTCCCAGCACGGGGAGGTAGTGACGATAAATAACGATCCGGGACTCT
Caenocholax	CCTGAGAAACGGCTACCACATCTAAGGAAGGCAGGCAGGC	CAATCCCAGCACGGGGGGGGGGGGGGGGGGGGGGGGGGG
Elenchus	CCTGAGAAACGGCTACCACATCTAACGAAGGCAGCAGGCGCGCAAATTAC	CCACTCCCAGCACGGGGGGGGGGGGGGGGGGGGGGGGGG
Crawfordia	CCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCGAAATTAC	CCACTCCCGGCACGGGGAGGTAGTGACGATAAATAACGATCCGGAACTCT
X.pecki	CCTGAGAAACGGCTACCACATCTAAGGAAGGCAGCAGGCGCGCAAATTAC	CACTCCCGGCACGGGGAGGTAGTGACGATAAATAACGATCCGGAACTCA
X.vesparum	***************************************	***************************************

200

		200
Hypogastrura	TAC-GAGGCTCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGATCTATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Trigoniopthalmus	TCC-GAGGCCCCGTAATTGGAATGAGTACACTTTAAATCCTTT-AACGAGTATCTATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	JTAATTCCAGC
Ephemerella	TCC-GAGGCCCCGTAATCGGAATGAGAACACTTTAAATCTTTT-AACAAGTACCTAATGGAGGGCAAGTCTGGTGCCAGCAGTCGCG	STAATTCCAGC
Agrion	TCC-GAGGCCCCGTAATCGGAATGAGAACACTTTAAATCCTTT-AACGAGGATCTATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Libellula	TCC-GAGGCCCCGTAATCGGAATGAGAACACTTTAAATCCTTT-AACGAGGATCTATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	STAATTCCAGC
Megarcys	TCC-GAGGCCCCGTAATCGGAATGAGCACAACTTAAATACTTT-AACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	<i>STAATTCCAGC</i>
Cultus	TCC-GAGGCCCCGTAATCGGAATGAGCACACATTAAATACTTT-AACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCAGCCGCG	STAATTCCAGC
Blaberus		TAATTCCAGC
Mantic		STAATTCCAGC
Manuis		STAATICCAGC
Labidura		STAATICCAGC
Melanoplus	TCC-CAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGTATCTATTGGAGGGCAAGTCTGGTGCCGCAGCAGCGCGCG	JIAATICCAGC
Anisomorpha	TGC-CAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	JTAATTCCAGC
Oligotoma	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	JTAATTCCAGC
Cerastipsocus	-ATCC-GAGGCTCTGCAATCGGAATGGGTACACTCTAAATCATTT-AACGAGTATCAATTGGAGGACAAGTCTGGTGCCAGCACCCGCG	CTAATTCCAGC
Dennyus	-ATAATGAGGCTCTGCAATCGGAATGAGAAGACTCTAAATCATTT-ACCGAGTATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGG	GTAATTCCAGC
Acyrthosiphon	TCC-GAGGCCCCGTAATCGGAATGAGAACACTTTAAAACCTTTAAACGAGGATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGG	GTAATTCCAGC
Buenoa	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACAAGGATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Saldula	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAACCCTTT-AACCAGGATCTATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAACTCCAGC
Lyqus	TAT-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACAAGGATCCATTGAAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Taeniothrips	TCT-GAGGCCCTGTAATCGGAATGACTACACTTTAAATCCTTT-AACGAGTATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Priacma	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGACCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCCGC	GTAATTCCAGC
Colpocaccus	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGACCAATTGGAGGGCAAGTCTGGTGCCAGCAGCAGCCGCG	GTAATTCCAGC
Cubister		STAA-TCCAGC
Cypiscer		CTARTCCACC
Aylorycles		GIAAIICCAGC
Octinodes		GIARIICCAGC
Photuris	TCC-GAGGCCCCGTGATCGGAATGAGCACACTTTAAATCCTTT-AACGAGGGATCAATTGGAGGGCAAGTCTGGTGCCGCAGCAGCCGCG	GTAATTCCAGC
Meloe	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AGCAAGGATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Rhipiphorus	TCC-GAGGCCCGGTAATCGGAATGAGTACACITITAAATCCTTT-AACAAGGATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Tenebrio	TCC-GAGGCCCCGTAATCGGAATGAGTACACTCTAAACCCTTT-AACGAGGATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	JTAATTCCAGC
Tetraopes	TCC-GAGGCCCCGTAATCGGAATGAGTACACTCTAAACCCTTT-AACGAGGATCAATTGGAGGGCCAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Corydalus	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGACCAATTGGAGGGCCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Agulla	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGACCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
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Mantispa	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Hemerobius	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGACCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Chrysoperla	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
M immaculatus		GTAATTCCAGC
Myrmeleon		GTAATTCCAGC
Calleria		CTANTICCAGC
Galleria		CERCEECCAGC
Papilio		GIACIICCAGC
Ascalapha	TAC-GAGGCCTCGTAATCGGAATGAGTACACTTTAAATATTTT-AACGAGGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Hydropsyche	TCC-GAGGCCTCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGGATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Pycnopsyche	TCC-GAGGCCTCGTGATCGGAATGATTACACTTTAAATCCTTT-AACGAGGGATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Oecetis	TCC-GAGGCCTCGTGATCGGAATGATTACACTTTAAATCCTTT-AACGAGGGATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
B.strigosus	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTA-TACAAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCTGCG	GTAATTCCAGC
B.chlorostigmus	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Boreus	TCC-GAGGCCCCGTAATCGGAATGAGTACACCTTAAATCCTTT-AACGAGGACCCATTAGAGGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Merope	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Panorpa	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Ctenocephalides	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGATCTATTAGAGGGCCAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Hystrichopsylla	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Orchopeas	TCC-GAGGCCCCGTAATCGGAATGAGTACACTCCTTT-AACGATTAACAATTGGAGGGCAAGCCTGGTGCCAGCAGCCGCG	GTAACCCCAGC
Hartigia	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Orussus	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Hemitaxonus	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCAGCCGCG	GTAATTCCAGC
Peridista		GTAATTCCAGC
Bareogonalos		GTAATTCCAGC
Evania		GTAATICCAGC
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Ophion	- TO CARGE CONTRACTOR AND A CONTRACT TANK TO TAKE AND A CONTRACT CONTRACT OF THE AND A C	GTAATTCCAGC
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Cooportopus	- TEC - CACCOCCETA MACCEAL MACCEAL CATTAIN TO THE ANCOMPOSITICAL HORSEGUARD LEVEL ACCACCATE AND CONTRACT AND	GTARTICCAGC
Caenochrysis	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGGTCCATGGAGGGCAAGTCTGGTGCCGCG	GTAATICCAGC
Lpyr1s	rcc-gageccccgamarcgaatagetacacrittaaatccritt-aacggatccatriggagggcaagtctggtgccAgcagcgcg	GIAATTCCAGC
Priocnemus	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACAAGGATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Dasymutilla	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGATCCATTGGAGGGCAAGTCTGGTGCCATCAGCCGCG	GTAATTCCAGC
Apoica	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Monobia	TCC-GAGGCCCTGTAATCGGAATGAGTACACTTTAAATCCTTT-AACGAGGATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
P.fuscatus	TCC-GAGGCCCCGTAATCGGAATGAGTACACTTTAAATCCTTT-AACAAGGATCCATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
P.dominulus	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	GTAATACCAGC
Camponotus	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	GTAATACCAGC
Chalepoxenus	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	GTAATACCAGC
Doronomyrmex	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	GTAATACCAGC
Harpagoxenus	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	GTAATACCAGO
Leptothorax	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	GTAATACCAGO
Temnothorax	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	GTAATACCAGC
Tipula		GTAATTCCAGC
Laphria	TATC - GAGGCCCTGTGAATGGAATGACACGTTTAAATCCTTT - AACAAGACAATTGGAGGCATGTCTGGGGCAGCGCCGCGCGCG	-TAACTCCACC
Mythicomyia		GTAATTCCACC
Drosophila		GTAATTCCACC
Triozocera	TTL_GGGTTTCGTBTCGGBTTGGGTGGGTTGGGTTGGGTCGTT_ACCACCACACACACCCCCCCCCC	GTABTTCCAGE
Copportelay		CTALLICCAGE
Caenocholax	AAGAGUIIICGAAAIIGGAAIGAGUAAAIIIAAAAIITAAAAAGUIT-AACGAGGAGCAAATGGAGGGCAAGTCTGGTGCCAGCAGCAGCCGCG	GIANI PUCAGU
Lienchus	AAGAGTTTCCGTGATCGGAATGAGTGTAATTTAATCCTTA-TACGGGGGCAAATGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
Crawfordia	AA1-GAGIIICCGTAATCGGAATAGGCACAATTTAAATCCTTT-AACGGGGCAAATGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
X.peck1	AAT-GAGTTTTCCGTAATCGGAATGAGTACAATTTTAAAAGCGTT-AGCAAGTATCAAATGGAGGGCAAGTCTGGTGCCAGCAGCCGCG	GTAATTCCAGC
X.vesparum	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	GTAATACCAGC

Hypogastrura	TCCAATAGCGTATATT
Trigoniopthalmus	TCCAATAGCGTATAT
Ephemerella	TCCATTGGCGTATXXX
Agrion	TCCAATAGCGTATATT
Tabellula	TCCANTAGCGTATAT
Magazava	TCCAATAGCGTATAT
Culture	TCCANIAGCGIAIAI
Disherus	TCCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
Bladerus	TCCAATAGCGTATAT
Mantis	TUCAATAGCGTATXX
Labidura	TCCAATAGCGTATAA
Melanoplus	TCCAATAGCGTATAT?
Anisomorpha	TCCAATAGCGTATAT
Oligotoma	TCCAATAGCGTATAT
Cerastipsocus	TCCAATAGCGTATAT
Dennyus	TCCAATAGCGTATXXX
Acvrthosiphon	TCCAATCGCGTATAT?
Buenoa	TCCAATAGCGTATAT
Saldula	TCCAATAGCGTATAT
Juque	TECANTAGEGIAIAI
Lygus	TICAATAGCGTATAT
Taeniothrips	TCCAATAGCGTATXX
Priacma	TCCAATAGCGTATATT
Colpocaccus	TCCAATAGCGTATATT
Cybister	TCCTATAGCGTATAT
Xyloryctes	TCCAATAGCGTATAT
Octinodes	TCCAATAGCGTATATT
Photuris	TCCAATAGCGTATAT
Meloe	TCCAATAGCGTATATT
Rhipiphorus	TCCAATAGCGTATAT
Tenebrio	TCCAATAGCGTATAT
Tetraopes	TCCAATAGCGTATAT
Corvdalus	TCCAATAGCGTATAT
Agulla	TCCALTAGCCTATAL
nguita Lolomui o	TOTAL ACCOUNTER
цотошАта	TCIANIAGCGTATAT
mantispa	TOCAATAGCGTATAT
Hemeroblus	TCCAATAGCGTATAT
Chrysoperla	TUCAATAGCGTATAT
M.immaculatus	TCCAATAGCGTATAT
Myrmeleon	TCCAATAGCGTATAT
Gallerıa	TCCAATAGCGTATAC'
Papilio	TCCAATAGCGTATAC'
Ascalapha	TCCAATAGCGTATAC'
Hydropsyche	TCRAATAGCGTATAC'
Pycnopsyche	TCCAATAGCATATAC
Oecetis	TCCAATAGCGTATAC
B.strigosus	TCCAATAGCGTATAT
B chlorostiamus	TCCAATAGCGTATAT
Boreus	TCTAATACCCTATAI
Nereus	TCIANIAGCGIATAT
merope	TCCAATAGCGTATAT
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Hemitaxonus	TCCAATAGCGTATAT
Peridista	TCCAATAGCGTATAT
Bareogonalos	TCCAATACCCTATAT
Evanta	TCCAATACCCTATAL
Lvdliid Tahnaumar	TOCANIAGUGTATAT
1cnneumon	ICCAATAGCGTATAT
Upnion	TUCAATAGCGTATAT
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Caenochrysıs	TCCAATAGCGTATAT?
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Priocnemus	TCCAATAGCGTATAT
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Apolca	TCCAATAGCGTATAT
Monobia	TCCAATAGCGTATAT
P. fuscatus	TCCAATAGCGTATAT
P. dominulue	TCCAATAGCGTATAT
Componetus	TCCDDTACCOTATAT
Camponotus	TCCAATAGCGTATAT
Cnaiepoxenus	TUCAATAGCGTATAT
Doronomyrmex	TUCAATAGCGTATAT
Harpagoxenus	TCCAATAGCGTATAT
Leptothorax	TCCAATAGCGTAAAT
Temnothorax	TCCAATAGCGTATAT
Tipula	TCCAATAGCGTATAT
Laphria	TCCAATAGCGTATAT
Mythicomyia	TCCAATAGCGTATAT
Drosophila	TCCAATAGCGTATAT
Triozocera	TCCATTAGTATATAT
Caepocholay	TCCDTTDCTDTDTDTDT
CachOCHOIdX Elonchus	TCCATTAGIAIATAT
Lienchus Graufend	TCCATTAGCATATAT.
Crawfordia	TUCATTAGCATATAT
X.peckı	TCCATTAGTATATAT
X vesparum	TCCATTAGCATATAT

		300▼
		-Variable Region-
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TCCAATAGCGTATATTAAAGTTGTTGCGGTTA-AACGTTCGTAGTTGAATTTGTGCTC-CATACGGGTAG====		****************
TCCAATAGCGTATATTAAAGTTGTTGCGGTTA-AACGTTCGTAGTTGAATTTGTGCTT-CAAACGGGTAG====		
TCCAATAGCGTATATTAAAGTTGTTGCGGTTA-AACGTTCGTAGTTGAACTTGTGCTT-CATACGGGTAG===		***************************************
TUUATTAGTATATATTAAAGTTGTTGUGGTTAAAAAGUTUGTAGTTGAATUTGTATUC-CATAUTGTGTGAA TUUATTAGTATATATATAAGTTGTTGUGGTTAAAAAGUTUGTAGTTGAATUTGTATUC-CUTACUTGTGTGAA		
TCCATTAGCATATATTAAAGTTGTTGCGGTTAAAAAAGCTCGTAGTCGAATCTGTATCT~CGTACTTTCGA		
TCCATTAGCATATATTAAAGTTGTTGCGGTTAAAAAGCTCGTAGTTGAATCTGTATCT-CATACTGTCAG````		
TCCATTAGTATATATATAAAGTTGTTGCGGTTAAAAAGCTCGTAGTCGAATCTGTATCT-CATCATGTCAG```		• • • • • • • • • • • • • • • • • • • •
TCCATTAGCATATATAAAGTTGTTGCGTTTAAAAAGCTCGTAGTTGAATCTGTATCT-CATCATGTCAG````	• • • • • • • • •	• • • • • • • • • • • • • • • • • • • •

	Variable Region 400▼	
Hypogastrura	TGTTTGGACGATTTTCTTGGT(((((((((((((((((((((((((((G-
Trigoniopthalmus	TGG-CCCGGACGT-CCTGTCGGT(((((((((((((((((((((((((G-
Ephemerella	CGGTT-CGGACGT-CATGCCGGTGGGACC\\\\\\\\\\\\\CTTACCCTCCGCGATG-TTCTTAACCGAGTG-GTCGGTGGGCCGGCAC	G-
Agrion	CGGT-CCRGACGT-ACTGCCGGWGGGGCC\\\\\\\\\\\\\\TTATCCTTCCTTGGTC-CTCTTCACCGAGTGCCTTGGTGGGCCGGCACC	G-
Lıbellula	CGGT-CCGGACGT-CCTGCCGGTGGGGCT\\\\\\\\\\\\\\\\\\\	G-
Megarcys	ATGTGA-GTG-GGACGT-CCAGCCGGT)))))))))))))))))))))))))))))))	G-
Cultus	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	G-
Blaberus	ATGCA-CGTGCTGACGT-CCTGCCGGTGGCCCA<<<<<<<<<<< <ata-cccctcgtggtg-ctcttaaccgagtgtctcgatgggccggcac< td=""><td>G-</td></ata-cccctcgtggtg-ctcttaaccgagtgtctcgatgggccggcac<>	G-
Mantis		XX
Labidura	ATGTTGC-AATTCGT-CCGT-CCGTCGGGATA<<<<<<<<<<<<<<<<< <tcacccattacgtgc-cgt-ccgt-ccgtcgggata<<<<></tcacccattacgtgc-cgt-ccgt-ccgtcgggata<<<<>	G-
Netanopius Netanopius		3- C
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Cerastinsocus		G-
Depayus	AGTCCCC-GAACGT-CCTCCCCGTIIIIIIIIIIIIIIIIIIIIIIIII	Ğ-
Acyrthosiphon		G-
Buenoa	ATGCCGCG-GGATGT-CCTGTCGGTGGAGGT1111111CCGCCCGATTCAATCCTGCCGCGGTG-CTCTTCACTGAGTGTCGAGTAGGCCGACACC	G-
Saldula	ATGTCGTG-GGATGT-CCTGTCGGTGGCGCGCC1111111TCGCCGACTCAATCCTG-C-CGGTG-CTCTTCACTGAGTGTCGACGACAGCCGACAC	G-
Lvaus	ATGCCGTG-GCATGT-CCTGTCGGTGGCGTT111111TCGCCTACTCTACCTACGTAGGTG-CTCTTCACCGAGTGTCGAGGTAGGCCGACACC	Ğ-
Taeniothrips	GTGTCGCG-GAACGT-CATGCCGGTGGGGTG]]]]]]TCGAGT-CGGAATCCCGCTGCGGTG-CTCTTCATTGAGTGTCGAGGTGGGCCCGGCACC	Ğ-
Priacma	ATGTT-TGTG-AGACGT-CCTGCCGGTGGATGG////////AAATCCTGTCGAAA-TCCTGTCGGGTGTGTCGAGGCGGGCCCGCACC	G-
Colpocaccus	ATGTT-TGTG-AGACGT-CCTGCCGGTGGATGG////////AAATCCTGTCGAAA-TCCTGTCGCGAGTGTCGAGGCCGGCCGGCCGCCACC	G-
Cybister	ACGTT-CGCG-AGACGT-CCTGGCGGTGGCCAC{{{{{{{{{{	G-
Xyloryctes	GTGT-CCGTG-GGACGT-CCTGCCGGTGGACTT { { { { { { { { { { { { { { { CCAACTT-CAAATCCCACCGCGGTG-CTCTTTACCGAGTGTCGAGGTGGGCCCGGCACC	G-
Octinodes	GTGTTACGCG-GGACGT-CCTGCCGGTGGGCTT { { { { { { { { { { { CCAACTTGCGAATCCCGCCGCGGTG-CTCTTCGCTGAGTGTCGAGGCGGGCCCGCACC	G-
Photuris	-CG-G-CACC-TGACGT-CCAGCCGGT{{{{{{{{{{}	AC
Meloe	GTGACATG-GGACGT-CCTGCCGGTGGGTTT { { { { { { { { { { { { { { {	A
Rhipiphorus	GTTTTGTG-GGACGT-CCTGCCGGCGGACTT { { { { { { { { {CCAATTTAATCCTGCCGCGTTG-CTCTTCATTGAGTGTCGAGGTGGGCCGGCAC!	Τ-
Tenebrio	GTGCCGCG-GGACGT-CCTGCCGGTGGGCTT { { { { { { { { { { { { { { { { { CCAACTCAATCCCGCCGCGTG-CTCTTCGTTGAGTGTCGAGGTGGGCCGGCACC	G-
Tetraopes	GTT-CCGG-GGACGT-CCTGCCGGAGGGCTT{{{{{{{{{{}}}}}}}	G-
Corycalus	ATGTT-TGTG-AGACGT-CCGCCGGTGGATGG/////////AAATCCTGTCGGGGTG-CTCTTAATTGAGTGCGAGGCGGCC-G(G-
Aguila	ATGTT-TGTG-AGACGT-CCTGCCGGTGGATGG///////////AAATCCTGTCGGGGG-CTCTTAATTGAGTGTCGAGGCGGGCC-G	
Lolomyla	ATGTTATGTG-AGACGT-CCTACCGGTGGGTGG!!!!!!CCCCAATGCAATGCAATCCTGT-CCGGTC-CCTCTTAATTGAGTGCGAGGTGGCCCGGTAC	
Hancispa		G-
Chrysoperla		G-
M.immaculatus		x-
Myrmeleon	ATGTTTTGTG-GGACGT-CCTACCGGT0000000000000000000000000000000	.G-
Galleria	ACGTTT-GCG-GAACGT-ATCGTCGGTGAGC}}}}}})}))))))	т-
Papilio	ACGTCT-GCG-GAACGT-ATCGTCGGTGAGC}}}}})})))CCAACT-CAAAATCCTATCGCGGTG-CTCTTCGGTGAGTGTCGAGGTGGGCCCGACAA	т-
Ascalapha	ACGTCT-GCG-GAACGT-ATCGTCGGTGAGC}}}}}})})))CCAACT-CAAAATCCTATCGCGGTG-CTCTTCGGTGAGTGTCGAGGTGGGCCGACAA	-T.
Hydropsyche	ACGTCT-GCG-GGCTT-CTCGCCGGT\$\$\$\$\$\$\$\$\$\$\$\$	\$-
Pycnopsyche	ACGTCT-GCG-GGGCTT-CTCGCCGGT\$\$\$\$\$\$\$\$\$\$\$\$	Ş-
Oecetis	GCGTCT-GCG-GACTT-CTCGCCNNN\$	Ş-
B.strigosus	ACGTCT-A-G-GAATGT-YTTACCGGTGGT+++++++++CCAAATTATAAATCCTATTGCGGTG-CTCTTAATCGAGTGCGTTATAGGCCGGTAC	G-
B.chlorostigmus	ATGTCT-GTG-GAACGT-CCTACCGGTGGGT+++++++CCAAATAACAAATCCTATCACGGTG-CTCTTAAACGACGTCGGGCGGGTAC	G-
Boreus		G-
Banarpa		-G-
Ctenocenhalides		G-
Hystrichonsylla		G-
Orchopeas	ATCTCT-GTG-GGA-CCT-CCTACCGGTGGGCGG########CCAACT-CAAAATCCTACCACGTG-CTCTTCACCGAGTGTCGAGGTGGCGGGCGGTAC	.G-
Hartigia	ATGA-CTGTG-GGACGT-CCTACCGGTGGGCTT%%%%%%CCAACTAATATCCCATCGCGGTG-CTCTTTACCGAGTGTCGAGGTGGGCCCGGTAC	G -
Orussus	ATGA-C-GTG-GGACGT-CCTACCGGTGGGCTC%%%%%%CCAACTAATATCCCATCGCGGTG-CTCTTCACTGAGTGCCCGAGGTGGGCCCGGTACC	.G-
Hemitaxonus	ATGATT-GTG-GGACGT-CCTACCGGTGGGCTT%%%%%%CCAACTAATATCCCATC-GGGTG-CTCTTCACTGAGTGTCGAGGTGGGCCCGGAAC	GT
Peridista	ATGATT-GTG-GGACGT-CCTACCGGTGGGCTT%%%%%%CCAACTAATATCCCATCGCGGTG-CTCTTCACTGAGTGTCGAGGTGGGCCGGTAC	G-
Bareogonalos	ATGATT-GTG-GGACGT-CCTACCGGTGGGCTT%%%%%%CCAACTAATATCCCATCGCGGTG-CTCTTAACCGAGTGTCGAGGTGGGCCCGGTAC	G-
Evanıa	ATGCCGTG-GTACGT-CCTACCGGTGGGCTT%%%%%%CCAGTCGATATCCCCGTCACGGTG-CTCTTCACTGAGTGTCGAGGTGGGCCCGGTAC	G-
Ichneumon	ATGCCGTG-AGACGT-CCTACCGGTGGGCTT%%%%%%CCAACTAATATCCCATCGCGGTG-CTCTTTATTGAGTGTCGAGGTGGGCCCGGTAC	G-
Ophion	ATGCCGTG-AGACGT-CCTACCGGTGGGCTT%%%%%CCAACTAATATCCCATC-GGGTG-CTCTTCACTGAGTGTCGAGATGGGCCCGGAAC	GT
Mesopolobus	ATGATT-GTG-GGACGT-CCTACCGGTGGGCTT%%%%%CCAGCTAATATCCCATCGCGGTG-CTCTTTACCGAGTGTCGAGGTGGGCCCGGTAC	G-
Caenochrysis	ATGTAGTG-GGACGT-CCTATCGGTGAACTC\$\$\$\$\$\$TTCTCCAA-ATCCTATCGCGGTG-CTCTTCACTGAGTGTCGAGATGGGCCGATAC	G-
Epyris	ATCA-C-GTG-GGACGT-CCTACCGGTGGCTTC%%%%%%CCAACTAATATCCCATCGCGGTG-CTCTTCATTGAGTGTCGAGGTGGGCCGGTAC	G-
Priocnemus	ACGATGTG-GGACCT-CCTACCGGTGGGCCT******CCAACT-ATACATCCCATCGCGTG-CTCTTCATTGACTGTCGAGGTGGGCCGGTAC	G-
Dasymutilla	ACGATGTG-GTAGGT-CCTACCGGTGGGCTT******CCAGCTACATCCCTCACCGTG-CTCTACGAGGCGCGGCGC	6-
Apoica		GU
P fuscatus		'GT
P.dominulus	ATGATGTGGGACGG-CCTACCGGTGGGCCTA*****CCAACTATATACCCATCGCGGGG-CTCTTCATGACGGCGGATGGGCCGGTA	:G-
Camponotus	GTGATGTG-GGACGT-CCTACCTGTGGGCTT\$\$\$\$\$\$CCAACTAATATCCCGTCGCGGGG-CTCTTTACTGAGTGTCGAGTCGGGCCGGTAC	:G-
Chalepoxenus	GTGATGTG-GGACGT-CCTACCGGTGGGCTT%%%%%%CCAACTAATATCCCGTCGCGGTG-CTCTTTACTGAGTGTCGAGTCGGGCCCGGTAC	.G-
Doronomyrmex	GTGATGTG-GGACGT-CCTACCGGTGGGCTT%%%%%%CCAACTAATATCCCGTCGCGGTG-CTCTTTACTGAGTGTCGAGTCGGGCCGGTAC	:G-
Harpagoxenus	GTGATGTG-GGACGT-CCTACCGGTGGGCTT%%%%%%CCAACTAATATCCCGTCGCGGTG-CTCTTTACTGAGTGTCGAGTCGGGCCGGTAC	:G-
Leptothorax	GTGATGTG-GGACGT-CCTACCGGTGGGCTT%%%%%CCAACTAATATCCCGTCGCGGTG-CTCTTTACTGAGTGTCGAGTCGGGCCGGTAC	G-
Temnothorax	GTGATGTG-GGACGT-CCTACCGGTGGGCTT%%%%%CCAACTAATATCCCGTCGCGGTG-CTCTTTACTGAGTGTCGGGCCGGTAC	G-
Tıpula	=TG-CTA-T-GACGT-ATTACTG-T&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&	Т-
Laphria	=TGTTATGCGAG-CGT-ATTACCGGT&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&	A-
Mythicomyia	=TGTAT-GTGAG-CGT-ATTACCGT&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&	Т-
Drosophila	=TGTAT-G-TAAG-CGT-ATTACCGGT&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&	T-
Triozocera	TGTAT-G-GGATATGC-A-GCTGGC+++++++++++++++++++++++++++++++++	T-
Caenocholax		A-
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V necki	1011 0 - 0010100-0-1010001	-^~
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Hypogastrura	TTTACTTTGAAAAAATTGGAATGCTCAAAGCAGCGC-TAC-A-GCCTGAACATTAGTGCAATGGAATAATGGAATGG
Trigoniopthalmus	TTTACTTTGACAAATTAGAGTGCTTAAAGCAGGCAGT-G-I-C-GCCTGAATGGCATGGCATAATGGAATAGGACCTCGGTTCTATTTI
Agrion	TTTACTT GAACAAATT I GAGTGCTCAAAGCAGGC=-CITATGT=CGCCTGGAATAACTGT=GTGCATGGATAATGAAAGAGGACCTTGGTTCTATTTG TTTACTTTGAACAAATTACAGGACGAAGAGCAGCC=-CGTGGAGT-C-GCCTGGAATAACTGAATAATGGAATAAGGACCTGGGTCCAATTA
Libellula	TTTXXXXXXXXXXXXTTAGAGTGCTCAAAGCAGGCCGTTGGTACAGCCTGAATACTGT-GTGCATGGAATAATAGAATAG
Megarcys	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCCAATTGC-T-GCCTGAATATTGT-GTGCATGGAATAATGGAATAGGATCTCGGTTCTATTTT
Cultus	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCCAATTGC-T-GCCTGAATATTGT-GTGCATGGAATAATGGAATAGGAATCCGGTTCTATTTT
Blaberus	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCAGC-ATC-C-GCCTGAATACTGA-GTGCAATAGGAACTAGGAACTAGGACCTCGGTTCTATTTT
Mantis	XXXXXXXXXXXXXXTTAGAGTGCTTAAAGCGGCAGC-ATC-C-GCCTGAATACCGA-GTGCATGGAATAATGGAANAGGACCTCGGTTCTATTTT TTTTCCACCAATAATGGAANAGGACCTCGGTCCTATTTTCCCCCCAATAATGGAANAGGACCTCGGTTCCAATAATGGAANAGGACCTCGGAATAATGGAANAGGACCTCGAATAATGGAANAGGACCTCGAATAATGGAANAGGACCTCGAATAATGGAANAGGACCTCGAATAATGGAANAGGACCTCGGTTCCAATAATGGAANAGGACCTCGGTTCCAATAATGGAANAGGACCTCGGTTCCAATAATAGGAANAGGACCTCGGTTCCAATAATGGAANAGGACCTCGAATAATGGAANAGGACCTCGAATAATGGAANAGGACCTCGAATAATGGAANAGGAACTAATGGAANAGGACCTCGAATAATGGAANAGGACCTCGAATAATGGAANAGGACCTCGAATAATGGAANAGGAACTTCGAATAATGGAATAATGGAANAGGACCTCGAATAATGGAATAATGGAANAGGACCTCGAATAATGGAANAGGACCTCGAATAATGGAATAATGGAANAGGACCTCGAATAATGGAATAATGGAANAGGACCTCGAATAATGGAANAGGACCTCGAATAATGGAANAGGACCTCGAATAATGGAANAGGACCTCGAATAATAATGGAANAGGAACTCGAATAATGGAANAGGAATAATGGAATAATGGAANAGGAACTTGGAATAATGGAANAGGAATAATGGAATAATGGAANAGGAACTTGGAATAATAATGGAANAGGAANAGGAACTGAATAATGGAANAGGAANAGAACTCGAATAATAATGGAANAGGAANAGGAACTGAATAATAATAATAATAATAATAATAATAATAATAATAA
Melanoplus	TTTACTTTGAACAAATTAGAGTGCTTAAAAGAGGC=A=-GCC-C-NCCTGAATAGT-GT-GTGCATGGAATAATAGGACCTGGGTCTATTTT
Anisomorpha	TTTACTTTGAACAAATTAGAGTGCTCCCACCAGGCAGTGGCC-T-GCCTGAATATTGT-GTGCATGGAATAATGGAATAGGACCTCGGTTCTATTTT
Oligotoma	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCAGT-GCT-TAGCCTGAATGCTGT-GTGCATGGAATAATGGAATAGGACCTCGGTTCTATTTT
Cerastipsocus	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCCTTCAAT-T-GCC-GAAAACTGT-GTGCATGGAATAATATAAT
Dennyus	TTTACTTTGAACAAATTGAAGGGCTCAAAGGAGGCACGTGAACGGGCTTGAAAAATGT-GCGCATGGAATAAGGACCGCGGTTCTATTT
Acyrthosiphon	TTTACTTTGAACAAATTAGAGTGCTCAAAGCAGGCTCGAATCIG-CCCTGAATACTGG-TCGCATGAATAATGGAACAAGACCCCGGT;;;;;;; mmm.cmmm.cmmm.cmm.cm.cmm.cmm.cmm.cmm.cm
Saldula	TTTRACTTCARCAATTAGAGTGCCTCARAAGCAGC=TGATTCC_CAGCTGCCTGCATGCATCARCACTAGAATAAGAACAGGAGCCTTGGCTCCAATTC
Lyqus	TTTACTTTGAACAAATTAGAGTGCTCAAAGCAGGCTGAAATCTCTGCCTGAATA-GTG-GTGCATGGAATAATAAAACAGGACCTTGGTTCTATTTT
Taeniothrips	TTTACTTTGAACAAATTTGAGTGCTCCAAGCAGGATTTCT-CGCCTGAAGA-TAA-GTGCATGGAATAATAGAATAG
Priacma	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTAAATTAAT-GCCTGAATAATTA-GTGCATGGAATAATAGAACAGGACCTTGGTTCTATTTT
Colpocaccus	TTTACTTTGAACAAATTAGAGTGCTCAAAGCAGGCTAAATTAAT-GCCTGAATAATTA-GTGCATGGAATAATAGAACAGGACCTTGGTTCTATTTT
Cybister	TTTACTTTCAACAALTTAGAGTGCTCCAACGCGGCGCGCGCGCGCGCGCGCGCGGCGGCGGCGGC
Octinodes	
Photuris	GTACTTTGAACAAATTAAAGTGCTTAAAGCAGGCTAAAT-TCC-GCTCGCATACACG-C-GCATGGAATAATCGAATAGGACCTCCGTTCTATTTT
Meloe	TTTACTTTGAACAAATTAAAGTGCTTAAAGCAGGCTAAAATTTT-GCCTGAATA-TGT-GTGCATGGAATAATGGAATAGGACCTCGGTTCTATTTT
Rhipiphorus	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTAAAATTTT-GCCTGAATACTGT-GTGCATGGAATAATAGAATAG
Tenebrio	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTAAAACTTC-GCCTGAATACTGT-GTGCATGGAATAATGGAATAGGAACCCCGGTTCTATTTT
Tetraopes	TTTACTTTGAACAAATTAGAGTGCTTAAAGGAGGCTAAAATTC-GCCTGAATACTGT-GTGCATGGAATAAGGACCTCGGTTCTATTT
Corydaius	TTTACTTICAAGAAATTAGAGIGGITAAAGCAGGGTAA-TTAAT-GCCTGAATAATTA-GIGGATGAATAATAGAACAGGACUTIGGITCTATTI TTTACTTICABGAB ATTAGAGGCGTABGABGCABGCATAA-TTAAT-GCCTGAATAATTA-GIGGABTBATAGABCAGGACCAGGACCAGGACCAAGGACCAGAGGAA
Lolomvia	TTTRACTTTGACGAAATTAGAGTGCTTAAGGCAGGCTAAAATTTC-GCCTGAATATTGT-GTGCATGGAATAATGGAATAGGAACTAGGACTCGGTTCTATTT
Mantispa	TTTACTTTGAACAAATTAGAGTGCTTAAGGCAGGCTAAAATTTT-GCCTGAATATTGT-GTGCATGGAATAATGGAATAGGACCTCGGTTCTATTTT
Hemerobius	TTT-CTTTGAACAAATTAGAGTGCTTAAAGCAGGCTAAAATTTT-GCCTAAATATTGT-GTGCATGGAATAATGGAATAGGACCTCGGTTCTATTTT
Chrysoperla	TTTACTTTGAACAAATTAGAGTGCTTAAGGCAGGCTCAAATTTT-GCCTGAATATTGT-GTGCATGGAATAATGGAATAGGACCTCGGTTCTATTT
M.immaculatus	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCT>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
Myrmeieon	TTTACTTICAACAAATTAATTAGAGTGCTTAAAGGAGGCCNANTATGCTGCAATATTGC-GTGCAATGGAATAGGAGTCCGGTTCCGTTCTATTT
Papilio	TTTACTTTGAACAAATTAGAGTGCTCAAAGGGGGCCAAAATGGG-GCCTGAATAATTC-GTGCATGGAATAATAGAATATGATCTGGGTCTAATTT
Ascalapha	TTTACTTTGAACAAATTAGAGTGCTCAAAGCGGGCCAAAATGCG-GCNTGAATATTTC-GTGCATGGAATAATAGAATATGAATCCGGTTCTATTTT
Hydropsyche	TTTACTTTGAACAAATTAGAGTGCTCAAACGGGGCTGACTCTCG-GCCTGAATATTGT-GYGCATGGAATAATRGAATAGGACCTCGGTTCAATTTT
Pycnopsyche	TTTACTTTGAACAAATTAGAGTGCTCAAACGGGGCTAACTCTCG-GCCTGAATATTGT-ACGCATGGAATAATAGAATAG
Oecetis D. stringeous	TTTACTTTACACAAATTAGAGTGCTCCAAAGGGCTAACACNCG-GCCTGAATATTG-ACGCATGGAATAATAGAACTAGGCCCTGGTTCTGTTT
B.strigosus B.chlorostigmus	111AC111GAACAAA1AAGAGIGGITAAAGCAGG——ITAATGIGGOTGIATATAI-GIGGAIGGAATAATAAGAGCUUGGUGTATTAT ####C####GAACAAATAAGAGC#GE##AAGAGGG===#########==GCC#GAA##AFGGAA##AFGGAD####################
Boreus	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCAAATTTCGCCTGAATATTGT-GTGCATGGAATAATGGAATAGGACCCGGTTCTATTT
Merope	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTAAATTTTGCCTGAATATTCT-GTGCATGGAATAATGGAATAGGACCTCGTTTCTATTT
Panorpa	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTAATCTCGCCTGTATATTGT-GTGCATGGAATAATAGAATAG
Ctenocephalides	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTUNNTCGCCTGAATATTGF-GTGGAATAATGGAACAGGACCTCGGTTCTATTTT
Hystrichopsylla Orchopeas	TTTACTTITACACAAATTAGAGTGCTTAAAGCAGGCCCATTTGCCTGAATATTG-GTGCATGGAATAATGGAACAATAGGACCTCGGTTCTAATTT TTTACTTITACA COA BATTAGGAGTGCTTAABCCAGCCCATTCGCCTGAATATTG-GTGCAATAATGGAACAATAGGACCTCGGTCCTAATATTGAATAG
Hartigia	TTTACTTTGACAAATTAGAGTGCTTAAAGCAGGCTACCTCGCCTGAATACTGC-GTGCATGAATAATGGAATAGGACTCGGTTCTATTT
Orussus	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTGTCTTCGCCTGAATACTGT-GTGCATGGAATAATGGAATAGGACCTCGGTTCTATTTI
Hemitaxonus	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTATTTTCGCCTGAATACTGT-GTGCATGGAATAATGGAATAGGACCTCGGTTCTATTT
Peridista	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTATTTTCGCCTGAATACTGT-GTGCATGGAATAATGGAATAGGACCTCGGTTCTATTTT
Bareogonalos	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTATTTTCGCCTGAATACTGT-GTGCATGGAATAATGGAACAGGCCTCGGTTCTATTTT
Evania Ichneumon	TTTACTTICAACAAATTAGAGTGGTCAAAGCAGGG——TAACTTI——GCCTGAATAGTGGTGGTGGADTAATGGAATAGGACCTGGTTCTATTTI TTTACTTICAACAAATTAGGACTAAAGCAGGGC——TAACTTI——GCCTGAATAGTGGADTAATGGADTAATGGACCTCGGTCCAATAGGACTAATAGGACCTGGTCGAATA
Ophion	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTATTTCGCCTGAATACTGT-GTGCATGAATAATGGAATAGGACCCGGGTTCTATTT
Mesopolobus	TTTACTTTGAACAAATTAGAGTGCTCAAAGCAGGCTATGTTCGCCTGAATACTGT-GTGCATGGAATAATGGAATAGGACCTCGGTTCTATTT
Caenochrysis	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTATCTTCGCCTGAATACTGT-GTGCATGGAATAATGGAATAGGACCTCGGTTCTATTTT
Epyris	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTACTTTCGCCTGAATACTGT-GTGGAATAGGAATAGGAATAGGACCTCGGTTCTATTTT
Priocnemus	TTTACTTGAACAAATTAAAGTGCTTTAAAGCAGCTACTCTCGCCTGAATATTCI-GTGCATGGAATAATGGAATAGCACCTCGGTTCTATTTT
Apolica	111 RCT116MACAMATIAGAGIGCITAAAGAGGC=TAGCCICCCCIGATACIGIGCAIGAATAAGAATAGAAATAGGACUGGGICIAATA TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
Monobia	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTAGCTTCGCCTGAATACTGT-GTGCATGGAATAGTGAATAGGAATAGGAACCCCGGTTCTATTTT
P fuscatus	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTAGCCTCGCCTGAATACTGT-GTGCATGGAATAATGGAATAGGACCTCGGTTCTATTT
P.dominulus	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTAGCCTCGCCTGAATACTGT-GTGCATGGAATAATGGAATAGGACCTCGGTTCTATTT
Camponotus	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTACCTTCGCCTGAATACTGC-GTGGAATAGGACCTCGGTTCTATTTT
Chalepoxenus	CITACITICACAACAACITAGAGIGCITTAAACCAGGCTATCCICGCCIGAATACIGC-GTGCATGGA-AATGGAATAGGACCICGGITCITATTI CITACITICACAACAACITAGAGIGCITTAAACCAGGCTATCCICGCCIGAATACIGC-GTGCATGGA-AATGGAATAGGACCICGGITCITATTIT
Harpadoxenus	CTINETTIGARTARABURAGUNARA DU AL CONTRACTARA DO LA CALONALIZZA CONTRACTA CONTRACTA DE LA CALONALIZZA CONTRACTA C
Leptothorax	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTATCCTCGCCTGAATACTGC-GTGCATGGAATAATGGAATAGGACCTCGGTTCTATTT
Temnothorax	TTTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTATCCTCGCCTGAATACTGC-GTGCATGGAATAATGGAATAGGACCTCGGTTCTATTT
Tipula	ATTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCCATTTGTGCCTGAATAATTCT-CTGCATGGAATAATGGAATAAGACGTCTGTTCTATTT
Laphria	ATTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCTTCAAATGCTCGAATATTTT-GTGCATGGAATAATGGAATAAGACCTCTGTTCTACTT
mythicomyia Drosophila	ALLACT I GANCAWATTAGAGIGUTTAAAGCAGGUTTTAGAAT $$ COTGAATATTTT-GIGCATGGAATAATGGAATAAGACCTCTGTTCTACTT
Triozocera	$\label{eq:construction} The rest of the $
Caenocholax	ATTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCAAATTTATATGCCTTGAATATCG-CAGCATGGAATAATAGAATATGATCTCGGTACCG-~~~
Elenchus	ATTACTTTGAACAAAXXXXXXXXXXXXXXXXXXXXXXXXX
Crawfordia	ATTACTTTGAACAAATTAGAGTGCTTAAAGCAGGCAAATTTATATGCCTTGAATATGATCAGCATGGAATAATAGAATAG
x pecki	ATTAUTTGAQGAATTAGAGTGCTTAAAGCAGGCAAATTTATATGCCGTGGATATAA-CAGCATGGAATAATAGAATATGATCTCGATACTG
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	ADMRTTPR(DDDD(ADMRDD(RDDD(RDDD(ADDD(RDD);RDD(RDD(RDD(RDD(RDD(RDD);RDD(RDD(RDD(RDD);RDD(RDD(RDD);RDD(RDD(RDD);RDD(RDD(RDD(RDD);RDD(RDD);RDD(RDD);RDD(RDD);RDD(RDD);RDD(RDD);RDD(RDD);RDD(RDD(RDD);RDD(RDD);RDD);RDD(RDD);RDD(RDD);RDD(RDD);RDD(RDD);RDD(RDD);RDD);RDD(RDD);RDD(RDD);RDD);RDD(RDD);RDD(RDD);RDD);RDD(RDD);RDD);RDD(RDD);RDD);RDD(RDD);RDD);RDD(RDD);RDD);RDD(RDD);RDD);RDD(RDD);RDD);RDD(RDD);RDD);RDD(RDD);RDD);RDD(RDD);RDD);RDD(RDD);RDD);RDD(RDD);RDD);RDD(RDD);RDD);RDD(RDD);RDD);RDD);RDD(RDD);RDD);RDD);RDD(RDD);RDD);RDD);RDD(RDD);RDD);RDD);RDD);RDD(RDD);RDD);RDD);RDD);RDD);RDD(RDD);RDD);RDD);RDD);RDD(RDD);RDD);RDD);RDD);RDD);RDD);RDD);RDD);RDD);RDD);RDD);RDD);RDD;RDD);RDD	ыľ (T
	ACGAACTGAAGCGTAAGCGTTTGTCAAAAACGTTTTCAT-TGATCAAGAACGTTAGAGGTTCGAAGGCGATCAGATACCGCCCCTAGTTCTAACCA	ίŢ
	ACGAACTGAAGCGAAAGCGTTTGTCAAAAACGTTTTCAT-TGATCAAGAACGAAAGTTAGAGGTTCGAAGGCGATCAGATACCGCCCTAGTTCTAACCP	١Ť
	ACGAACTGAAGCGAAAGCGTTTGTCAAAAAACGTTTTCAT-TGATCAAGAACGAAAGTTAGAGGTTCGAAGGCGATCAGATACCGCCCTAGTTCTAACCA	١T

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Hypogastrura	AAACGATGTCGACCGGCGATCCGTCGTCGTCGTTAATATTA-AT-GA-CTCGACGGGCAGCCT-CCGGGAAACCAGAGTGTTTGGATTCCAGGGGGGAGATATGC
Trigoniopthalmus	AAACGATGCCAGCCAGCCAGCGATCCCCCGAAGTTCCT-CCA-AT-GA-CTCGGCGGGCGCGCTT-CCGGCGAACCAAAGCTTTTGGGTTCCGGGGGAAGAAGTATGG
Ephemerella	AAACGATGTCAGCCAGCGATGCCGCCGATGTCCT-CCG-AT-GA-CACGGGGCGCGAACTT-CCGGGAAACCAAACGATGTGGGTCCGGGGGGAGGTTGGG
Agrion	
Menarcys	
Cultus	AAGGGATTACCTCCGGTGTTCCGCCGATGATCCG-NNN-AT-GA-CCCGACGGGCXXXXXXXXXXXXXXXXXXXXXXXXXX
Blaberus	AAACGATGCCAGCCAGCAATCCGCCGAAGTTCCT-CCG-AT-GA-CTCGGCGGGCAGCTT-CCGGGGAAACCAAAGCTTTTGGGTTCCGGGGGAAGTATGG
Mantıs	AAACGATGCCAGCCAGCAATCCGCCGAAGTTCCT-CCG-AT-GA-CTCGGCGGGCAGCTT-CCGGGGAAAGCTTTTGGGTTCCGGGGGAAGTATGG
Labıdura	AAACGATGCCAGCCAGCGATCCGCCGAAGTTCCT-CCG-AT-GA-CTTAGCGGGCAGCTT-CCGGGGAAACCAAAGCTTTTGGGTTCCGGGGGAAGTATGG
Melanoplus	AATCGATGCCAGCCAGCCGCCGCCGCAGTTCCT-CCG-AT-GA-CTCGGCGGGCAGCCT-CCGGGGAAACCAAAGCTTTTGGGTTCCGGGGGAAGTATGG
Anisomorpha	AAACGATGCCAGCTAGCGATCCGCCGAAGTTCCT-CCG-AT-GA-CTCGGCGGGCAGCTT-CCGGGAAACCAAAGCXXXXXXXXXXXXXXXXXXXXXXXX
Oligotoma Corpotingoouc	ANACGATGCCAGCTAGCGATCGCCGAGTTCCT-CCG-AT-GA-CTCGGCGGCGCGCCT-CCGGCGAACCAAAGCTTTGGGTTCCGGGGGAAGTATGG
Dennyus	
Acvrthosiphon	AAACGATGCCAGCTAGCGATCCGCCGCGTTTCA-TTA-AC-GA-CCCGGCGGCGGCAGCTT-CCGGGAAACCATTCCGGTTCCGGGGGAAGTATGA
Buenoa	AAACGATGCCAGCCAGCGATCCGCCGATGTTCCT-CCG-AT-AG-CTCGGCGGGCAGCTT-CCGGGGAAACCAAAGCTTTTGGGTTCCGGGGGGAAGTATGG
Saldula	AAACGATGTCAGCCAGCGATCCGCCGACGTTCAT-TGA-AT-GG-CTCGGCGGGCAGCTT-CCCGGAAACGAAAGCTTTCGGGTTCCGGGGGAAGTATGG
Lygus	AAACGATGCCAGCCAGCGATCCGCCGATGTTCCT-CCG-AT-GA-CTCGGCGGGGAGCTT-CCGGGGAAACCAAAGCTTTTGGGTTCCGGGGGAAGTATGG
Taeniothrips	AAACGATGTCAACTAGCAATTTGCCCCAAGGTTCT-CTG-AT-GC-CTGGGCAAGCGGCTT-CCGGGGAAACCAAAGTTTTTCGATTCCGGGGGAAGTATGG
Priacma	AAACGATGCCAGCTAGCGATCCGCCAAAGTTCCT-CCG-AT-GA-CTTGGCGGGTAGCTT-TCGGGAAACCAAAGCTTTTGGGTTCCGGGGGAAGTATGG
Colpocaccus	AAACGATGCCAGCTAGCGATCCGCCCAAAGTTCCT-CCG-AT-GA-CTTGCCGGGTAGCTT-TCGGGAAACCAAAGCTTTTGGGTTCCGGGGGAAGTATGG
Cybister	AAACGATGCCAGCTAGCGATCGGCGGCGTTCT-CCG-AT-GA-CTCGGCGGCAGCTT-CCGGGGAAACCAAAGCTTTTGGCTTCCGGGGGAAGTATGG
Octinodes	
Photuris	AAACTATGCCAGCTAGCGATCCGCCGAAGTTACT-TCT-AC-GA-CTCGGCGGGCAGCTT-CCGGGAAACCAAAGCTTTCGGGTTCCGGGGGAAGTATGC
Meloe	AAACGATGCCAGCCAGCGATCCGCCGATGTTCCT-CCG-AT-GA-CTCGGCGGGGAGCTT-CCGGGGAAACCAAAGCTTTTGGGTTCCGGGGGAAGTATGG
Rhipiphorus	AAACGATGCCAGCTAGCGATCCGCCGACGTTCCT-CAT-AT-GA-CTCGGCGGGCAGCTT-CCGGGGAAACCAAAGCTTTTGGGTTCCGGGGGAAGTATGG
Tenebrio	AAACGATGCCAGCTAGCGATCCGCCGACGTTCCT-CCG-AT-GA-CTCGGCGGGCAGCTT-CCGGGGAAACCAAAGCTTTTGGGTTCCGGGGGAAGTATGG
Tetraopes	AAACGATGCCAGCTAGCGATCCGCCGACGTTCCT-CCG-AT-GA-CTCGGCGGCAGCTT-CCGGGGAAACCAAAGCTTTTGGGTTCCGGGGGAAGTATGG
Corydalus	AAACGATGCCAGCTAGCGATCCGCCAAAGTTCCT-CCG-AT-GA-CTTGGCGGGTAGCTT-TCGGGAAACCAAAGCTTTTGGGTTCCGGGGGAAGTATGG
Agulla	AAACGATGCCAGCTAGCGATCCCCCAAAGTTCCT-CCG-T-GA-CTTGGCGGGTAGCTT-CGGGGAAACCAAAGCTTTGGGGTCCGGGGGAAGTATGG
Lolomyia	AAACGATGCCAGCTAGCGATCCGCCGAAGTTCTT-CCG-AT-GA-CTCGGCGGCCAGCTT-CCGGCAAACCAAAGCTTTTGGCTCCGGGGGAAGTATTGG
Hemerobius	
Chrvsoperla	AAAGGATGCCAGCTAGCGATCCGCCGAAGTTCCTCG-AT-GA-CTCGGCGGGCAGCXXXXXXXXXXXXXXXXXXXXXXXXXXX
M.immaculatus	AAACGATGCCAGCTAGCGATCCGCCAAAGTTCCT-CCG-AT-GA-CTTGGCGGGCAGCTT-CCGGGGAAACCAAAGCATTTGGGTTCCGGGGGGAAGTATGC
Myrmeleon	AAACGATGCCAGCTAGCGATCCGCCAAAGTTCCT-CCG-AT-GA-CTTGGTGGGCAGCXXXXXXXXXXXXXXXXXXXXXXXXXXX
Gallerıa	AAATNATGTCATCTAGCGATCCGCCGACGTTACT-ACA-AT-GG-CTCGGCGGGCAGCTT-CCGGGGAAACCAAAGATTTTGGTCTCCCGGGGGA-GTATGC
Papilio	AAATNATGTCATCTAGCGATCCGCCCGACGTTACT-ACT-AT-GG-CTCGGCGGGCAGCTT-CCGGGGAAACCAAAGATTTTGGACTCCGGGGGA-GTATGG
Ascalapha	AAATNATGTCATCTAGCGATCCGCCGACGTTACT-ACA-AT-GG-CTCGGCGGGCAGCTT-CCGGGAAACCAAAGATTTTGGTCTCCGGGGGA-GTATGG
Hydropsyche	AAATGATGCCAGCTAGCCGATCCGCCGGAGGTCCCCT-TCG-ATT-TAACCCGGGGGGCGCGCGCGCGCGCGCGGGGGCGCGCGCG
Oecetis	AAN GATGCAGCCAGGCAGGCAGCGAGGATCCGCCGAGGTTCT-TATTT-TATTT-TATCCGCTGGCAGCCAGTC-CCGGGATACCAAGCAGGCTGCGGCGGCGGGGGGGGGG
B.strigosus	AAACGATGCCAACTAGCCAATCCGCCGCAGTCCCCT-ATG-TT-GA-CTCGGTGGCCAGCTT-CTGGGAAACCAAGGTTTTTGGGTTCCGGGGAAGTATCG
B.chlorostigmus	AAACGATGCCAGCTAGCGATCCGCCGAAGTTCCTCG-AT-GA-CTCGGCGGGCAGCXXXXXXXXXXXXXXXXXXXXXXXXXXX
Boreus	AAACGATGCCAGCTAGCGATCCGCCGAAGTTCCT-CCG-AT-GA-CTCGGCGGGCAGCTT-CCGGGGAAAGCTTTTGGGTTCCGGGGGAAGTATGG
Merope	AAACGATGCCAGCTAGCGATCTGCGCACGTTCCT-CCG-AT-GA-CTCGGTAGGCAGCTT-CCGGGGAAACCAAAGCTTTTGGGTTCCGGGGGAAGTATGC
Panorpa	AAACGATGCCAGCTAGCGATCCGCCAAAGTTCCT-CCG-AT-GA-CTTGGCGGGCAGCTT-CCGGGGAAACCAAAGCTTTTGGGTTCCGGGGGAAGTATGC
Ctenocephalides	AAACGATGCCAGCTAGCGATCCGCCGAAGTTCCT-CCG-AT-GA-CTCGGCGGCAGCTT-CCGGGGAAACCAAAGCTTTTGGGTTCCGGGGGAAGTATGG
Aystrichopsylla	AAACGATGCCAGCTAGCCATCCGCCCAACTTCTCC-AT-GA-CTCGGCCGGCAGCXXXXXXXXXXXXXXXXXXXXXXXXXXX
Hartigia	
Orussus	AAAGGATGCCAGCTAGCGATCCGCCGAGTTCCT-CNG-AT-GA-CTCGGCGGGCAGCXXXXXXXXXXXXXXXXXXXXXXXXXXX
Hemitaxonus	AAACGATCCCAGCTAGCGATCCGCCGAAGTTCCT-CCG-AT-GA-CTCGGCCGGCCAGCTT-CCGGGGAAACCAAAGCTTTTGGGTTCCGGGGGAAGTATGC
Peridista	AAACGATGCCAGCTAGCGATCCGCCGAAGTTCCT-CCG-AT-GA-CTCGGCGGGCAGCXXXXXXXXXXXXXXXXXXXXXXXXXXX
Bareogonalos	AAACGATGCCAGCTAGCGATCCGCCGAAGTTCCT-CCG-AT-GA-CTCGGCGGGCAGCXXXXXXXXXXXXXXXXXXXXXXXXXXX
Evanıa	AAACGATGCCAGCTAGCGATCCGCCGAAGTTCCT-CNG-AT-GA-CTCGGCGGGCAGCXXXXXXXXXXXXXXXXXXXXXXXXXXX
Ichneumon	AAACGATGCCAGCTAGCGATCCGCCGAAGTTCCT-CCG-AT-GA-CTCGGCGGCAGCXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Ophion	AACGATGCCAGCTAGCGATCCGCCGAAGTCCCCCG-AT-GA-CTCGGCGGGCAGCTT-CCGGGGAAACCAAAGCTTTTGGGTCCCGGGGAAGTATGG
Caepochrysis	
Fouris	
Priocnemus	AAACGATGCCAGCCAGCGATCCGCCGAAGTTCCT-CCG-AT-GA-CTCGGCGGGCAGCXXXXXXXXXXXXXXXXXXXXXXXXXXX
Dasymutilla	AAACGATGCCAGCTAGCGATCCGCCGAAGTTCCT-CCG-AT-GA-CTCGGCGGGCAGCTT-CCGGGGAAACCAAAGCTTTTGGGTTCCGGGGGAAGTATGG
Apoica	AAACGATGCCAGCTAGCGATCCGCCGAAGTTCCT-CCT-AT-GA-CTCGGCGGGCAGCTT-CCGGGGAAAGCTTTTGGGTTCCGGGGGAAGTATGG
Monobia	AAACGATGCCAGCTAGCGATCCGCCGAAGTTCCT-CCG-AT-GA-CTCGGCGGGCAGCTT-CCGGGAAACCAAAGCTTTTGGGTTCCGGGGGAAGTATGG
P.fuscatus	AAACGATGCCAGCTAGCGATCCGCCGAAGTTCCT-CCG-AT-GA-CTCGGCGGGCAGCTT-CCGGGAAAACCAAAGCTTTTGGGTTCCGGGGGAAGTATGG
P.dominulus	AACGATGCCAGCTAGCGATCCGCCGAAGTICCT-CCG-AT-GA-CTCGACGGCAGCTT-CCGGGAAACCAAAGCTTTTGGGTTCCGGGGAAGTATCG
Camponotus	AAAGATGCAGCTAGCGATCGGCGAAGTCGTCGGCGCAGCGCGCGC
Doronomyrmex	
Harpagoxenus	AAACGATGCCAGCTAGCGATCCGCCGAAGTTCCT-CCG-AT-GA-CTCGGCGGCAGCTT-CCGGGAAACCAAAGCTTTGGGTTCCGGGGGAATATGG
Leptothorax	AAACGATGCCAGCTAGCGATCCGCCGAAGTTCCT-CCG-AT-GA-CTCGGCGGGCAGCTT-CCGGGAAACCAAAGCTTTTGGGTTCCGGGGGAAGTATGC
Temnothorax	AAACGATGCCAGCTAGCGATCCGCCGAAGTTCCT-CCG-AT-GA-CTCGGCGGGCAGCTT-CCGGGGAAACCAAAGCTTTTGGGTTCCGGGGGAACTATGG
Tıpula	AAACGATGCCAGCTAGCAATTGGATGGAGCTACT-TAT-AT-GG-CTCTTTCAGTCGCTTTCCGGGAAACCAAAGCTTTTGGGCTCCGGGGGAAGTATGG
Laphria	AAACGATGCCAGCTAGCAATTGGGTGTAGCTACT-ACT-AT-GG-CTTTCTCAGTCGCTTCCCGGGAAAACCAAAGCTTTTGGGCTCCGGGGGAAGTATGG
Mythicomyia	AAACGATECCAGGTAGCAATTGGGTGGTAGCTACT-TTT-AT-GG-CTTTCCAGTCGCTTCCCGGGAAACCAAAGCTTTTGGGCTCCCGGGGAAGTATGG
urosophila Triozocera	AAAUGATUUASUTASUAATTUSGTUTASUTASUTATUTTT-ATTUSGTUTCTCAGTCGCTT-CCGGGAAACCAAAGCTTTTGGGCTCCGGGGGAAGTATGG
Caepocholay	
Elenchus	AAACTATGCCGACTAGTGATCCGTCGATGTTCAT_TTAAATTGA_CTCGACGGCAACTT-CCGGGCAACCAAACTTTTTAGGTCCGGGGGAAGTAATG
Crawfordia	AAACGATGCCGACCAGCGATCGTCGATGTTCAT-TTAAATTGA-CTCGACGGCAGCTT-CCGGGGAAACCAAAGTTTTTGGGTTCCGGGGGAAGTATGG
X.peckı	AAACGATGCCGACCAGCGATCCGTCGATCTTCAT-TCAAATTGA-CTCGACGGGCAGCTT-CCGGGAAACCAAAGTTTTTGGGTTCCGGGGGAAGTATGG
X.vesparum	AAACGATGCCGACCAGCGATCCGTCGATGTTCAT-TCAAATTGA-CTCGACGGGCAGCTT-CCGGGGAAAGTTTTTAGGTTCCGGGGGAAGTATGG

Hypogastrura Trigoniopthalmus Ephemerella Agrion Libellula Megarcys Cultus Blaberus Mantis Labıdura Melanoplus Anisomorpha Oligotoma Cerástipsocus Dennyus Acyrthosiphon Buenoa Saldula Lygus Taeniothrips Priacma Colpocaccus Cybister Xyloryctes Octinodes Photuris Meloe Rhipiphorus Tenebrio Tetraopes Corydalus Agulla Lolomyia Mantispa Hemerobius Chrysoperla M ımmaculatus Myrmeleon Galleria Papilio Ascalapha Hydropsyche Pycnopsyche Oecetis B.strigosus B.chlorostigmus Boreus Merope Panorpa Ctenocephalides . Hystrichopsylla Orchopeas Hartigia Orussus Hemitaxonus Peridista Bareogonalos Evanıa Ichneumon Ophion Mesopolobus Caenochrysis Epyris Priocnemus Dasymutilla Apolca Monobia P.fuscatus P.dominulus Camponotus Chalepoxenus Doronomyrmex Harpagoxenus Leptothorax Temnothorax Tipula Laphria Mythicomyia Drosophila Triozocera Caenocholax Elenchus Crawfordia X.pecki X.vesparum

TTGCANAGCTGANACTTANAGGANTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGGCTTAATTGACTCAACACGGGANACCTCACCAGGCCCGGA TTGCANAGCTGANACTTANAGGANTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGGCTTAATTGACTCAACACGGGANACCTCACCAGGCCCGGA TTGCANAGCTGANACTTAAAGGANTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGGTTAATTGACTCAACACGGGANACCTCACCAGGCCCGGA TTGCANAGCTGANACTTAAAGGANTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGGTTAATTGACTCAACACGGGANACCTCACCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCACGAGGAGTGGAGCCTGCGGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCAGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCAGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGCGCACCACCAGGAGTGCAGCCTGCGGCTTAATTTGACTCAACACGGGAAATCTCACCAGGCCCAGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCTTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCAGGCCCAGA TTGCAAAGTTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCGCCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCAGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCAGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCAGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGTTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCAGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCG-CTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCAGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCAGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCAGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCAGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGC TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTTACCAGGCCCAGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCAGA TTGCAAAGTTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACTACAAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGTCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCCGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTG-AGC-TGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCAGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCAGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCAGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCACA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCAGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCAGA TTGCAAAGCTTAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCTTGCGGCTTAATTTGACTCAACACGGGGAAACTTACCAGGTCCGAA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCACGAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTTACCAGGTCCGAA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTTACCAGGTCCGAA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCACGAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTTACCAGGTC-GAA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCTTGCGGCTTAATTTGACTCAACACGGGAAATCTCACCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGTACCACCAGGAGTGGAGCTTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGTCAGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCTTGCGGCTTAATTTGACTCAACACGGGAAATCTCACCAGGCCAGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCTTGCGGCTTAATTTGACTCAACACGGGAAATCTCACCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCTTGCGGCTTAATTTGACTCAACACGGGAAATCTCACCAGGCCCGGA TTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCTTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCAGGCCCGGA

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Hypogastrura Trigoniopthalmus Ephemerella Agrion Libellula Megarcys Cultus Blaberus Mantis Labidura Melanoplus Anisomorpha Oligotoma Cerastipsocus Dennyus Acvrthosiphon Buenoa Saldula Lygus Taeniothrips Priacma Colpocaccus Cybister Xyloryctes Octinodes Photuris Meloe Rhipiphorus Tenebrio Tetraopes Corydalus Agulla Lolomyia Mantispa Hemerobius Chrysoperla M.immaculatus Myrmeleon Galleria Papilio Ascalapha Hydropsyche Pycnopsyche Oecetis B.strigosus B.chlorostigmus Boreus Merope Panorpa Ctenocephalides Hystrichopsylla Orchopeas Hartigia Orussus Hemitaxonus Peridista Bareogonalos Evania Ichneumon Ophion Mesopolobus Caenochrysis Epyris Priocnemus Dasymutilla Apoica Monobia P.fuscatus P.dominulus Camponotus Chalepoxenus Doronomyrmex Harpagoxenus Leptothorax Temnothorax Tipula Laphria Mythicomyia Drosophila Triozocera Caenocholax Elenchus Crawfordia X.peckı X.vesparum

185 b1→ caccegataGgattGacAgaataAgacctctttcttGattc-ggtgGgtgGtgGtgCatGgccCgttcttActtgGtgG-gcGattTgtctGgttAattccccatGgtAgAttGac-gattGadgaccttttcttTgttGttgGtGGtGGtGCatGgtCgtAgAttGac-gattGadgaccttttcttAgttGctGgtAgAttGacGattGacGgtAgAttGacGattGacGgtAgattGacGgtAgattGacGattGacGgtAgattGacGgCATTGGAAGGATTGACAGATTGATAGCTCTTTCTTGATTC-AGTGGGTAGTGGTGCATGGCCGTTCTTAGTTGGTGGAACGATTGCTGGTTGATAGCTCGTTAATTCCG CATTGGAAGGATTGACAGATTGATAGCTCTTTCTTGATTC-AGTGGGGTAGTGGTGCATGGCCGTTCTTAGTTGGTGGAACGATTGTCTGGTTGATAGCTCG $\label{eq:caccegargearter} Caccegargearter c$ CACCG-AA-GATTGACAGATTGATAGCTCTTTTCTTGATTC-GGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCCG CACCGGAAGGATTGACAGATTGATAGCTCTTTTCTTGATTC-GGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCCG CACCGGAAGGATTGACAGATTGATAGCTCTTTTCTTGATTC-GGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGCGATTGTCTGGTTGATTCCG CACCGGAAAGATTGACAGATTGATAGCTCTTTTCTTGATTC-GGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCCG CATAAATGAGTAAGACAGATTGATAAGCTCTTTTCTCGAATC-TATGGGTGGTGGTGCATGGCCGTTGTTAGTTCGTGGAGTGGATTGTCTGGTTAATTCCG CATAAGTGTGTAAGACAGATTGATAAGCTCTTTTCTCGAATC-TATGGGTGGTGGTGCATGGCCGTTCTTAGTTCGTGGAGTGGATTTGTCTGGTTAATTCCG CACCGAAAGGATTGACAGATTAATAGCTCTTTCTTGATTC-GGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCCG CACTGATAGGATTGACAGATTGATAGCTCTTTTCTTGATTC-AGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCCG CACCGAAAGGATTGACAGATTAATAGCTCTTTCTTGATTC-GGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCCG CACCGAAAGGATTGACAGATTAATAGCTCTTTTCTTGATTC-GGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCCG

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$\boldsymbol{\mathcal{O}}$	v

Hypogastrura	ATAACGAACGAGACTC
Trigoniopthalmus	ATAACGAACGAGACTC
Ephemerella	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Agrion	ATAACGAACGAGACTC
Libellula	ATAACGAACGAGACTC
Megarcys	ATAACGAACGAGACTC
Plaborus	AXAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
Mantis	ATAACGAACGAGACTC
Labidura	ATAACGAACGAGACTC
Melanoplus	ATAACGAACGAGACTC
Anısomorpha	ATAACGAACGAGACTC
Oligotoma	ATAACGAACGAGACTC
Cerastipsocus	ATAACGAACGAGACTC
Dennyus	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Ruenca	ATAACGAACGAGACTC
Saldula	ATAACGAACGAGACTC
Lyqus	ATAACGAACGAGACTC
Taeniothrips	ATAACGAACGAGACTC
Priacma	ATAACGAACGAGACTC
Colpocaccus	ATAACGAACGAGACTC
Cypister	ATAACGAACGAGACTC
Xyloryctes	ATAACGAACGAGACTC
Photurus	ATAACGAACGAGACTC
Meloe	ATAACGAACGAGACTC
Rhipiphorus	ATAACGAACGAGACTC
Tenebrio	ATAACGAACGAGACTC
Tetraopes	ATAACGAACGAGACTC
Corydalus	ATAACGAACGAGACTC
Agulla	ATAACGAACGAGACTC
Lolomyıa	ATAACGAACGAGACTC
Mantispa	ATAACGAACGAGACTC
Chrysoperla	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
M.immaculatus	ATAACGAACGAGACTC
Myrmeleon	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Galleria	ATAACGAACGAGACTC
Papilio	ATAACGAACGAGACTC
Ascalapha	ATAACGAACGAGACTC
Hydropsyche	ATAACGAACGAGACTC
Pycnopsyche	ATAACGAACGAGACTC
Decetis P. strigogue	ATAACGAACGAGACTC
B.chlorostigmus	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Boreus	ATAACGAACGAGACTC
Merope	ATAACGAACGAGACTC
Panorpa	ATAACGAACGAGACTC
Ctenocephalides	ATAACGAACGAGACTC
Hystrichopsylla	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Orchopeas	ATAACGAACGAGACTC
Hartigia	*****
Vemitaxonus	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
Peridista	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Bareogonalos	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Evania	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Ichneumon	XXXXXXXXXXXXXXXXXXX
Ophion	ATAACGAACGAGACTC
Mesopolobus	*****
Caenochrysis	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Epyris	****
Priocnemus	AXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Apolea	ATAACGAACGAGACIC
Monobia	ATAACGAACGAGACTC
P.fuscatus	ATAACGAACGAGACTC
P.dominulus	ATAACGAACGAGACTC
Camponotus	ATAACGAACGAGACTC
Chalepoxenus	ATAACGAACGAGACTC
Doronomyrmex	ATAACGAACGAGACTC
Harpagoxenus	ATAACGAACGAGACTC
Tempothorax	ATAACGAACGTGACTC
Tipula	ATAACGAACGAGACTC
Laphria	ATAACGAACGAGACTC
Mythicomyia	ATAACGAACGAGACTC
Drosophila	ATAACGAACGAGACTC
Triozocera	ATAACGAACGAGACTC
Caenocholax	ATAACGAACGAGACTC
Elenchus	ATAACGAACGAGACTC
Crawfordia V peeks	ATAACGAACGAGACTC
A.pecki Vecharum	ATAACGAACGAGACTC

VOL. 10

INSERT 1 ^^^ Acyrthosiphon	GCACGGTGCC GGACCACCCT GGCGGTCCGT CGTGTCGCGG CCGGCCGTGT CGCGGGACCA
INSERT 2 === 1	Diptera
Tipula	TACAACCG-TAACTG-GGTTCGTACATCATCTTGA
Laphria	TACAACTATTAATATTGGTTTGTACATTACCTT-A
Mythicomyia	TACACCTA-AAATATTGGTTCGTACATTACCTTTT
Drosophila	TACAACTTACAATTGTGGTTAGTACTATACCTTTA
INSERT 3 ``` s	Strepsiptera
Triozocera	-TCG-TTCGTAATTT-AATTTGCGTGGTTTGACAT-T-TT
Caenocholax	-ATT-CCCGCGATTT-ATTCGCTGTGGTTTTG-GTTAT-T-TAAT
Elenchus	-TCGTTAGTAATTTAAATTTAATTGA-GACAATT-TT
Crawfordia	CTCG-CTCGTAATTT-AATTTATGCAGTTTGATTGAC-A-T-TT
X.pecki	-TCG-CTCGTAATTT-AATTTATGTAGTTTGATTTGAC-A-T-TT
X vesparum	-TCG-CTCGTAATTT-AATTTATGTAGTTTGATTTGAC-A-T-TT
INSERT 4 (((H	Basal Hexapods
Hypogastrura	TCGTTCA
Trigoniopthali	mus ATGTCCT
INSERT 5 \\\ H	Basal Insects
Ephemerella	TCGGCGCACGGTTCCGTAA
Agrion	GCGAGGCTCCG
Libellula	GTAAAAGGCTCCG
INSERT 6 })) Megarcys	ATGTGAGTGG GACGTCCAGC CGGTGGGTCG NCAGGTCGTG AGCTATGCTG GCCGCGCCCC TTGGCGGTTC CATATCATGG CCGCGTCGTG GNGTGTGTCG GGAGGTGTTT GTGTCGNNCG TTCGCGTTCG TCGAAGNATC GCCTGGCCCG NCAATAAAAC GGCGCTGTGT TGTGGGGACC GTCTCTCACT CAGGGTGTCG CTGTGTCGGC GCACACGGTG CCGGACCCCA TG
INSERT 7 <<< 0 Blaberus Labidura Melanoplus Anisomorpha Oligotoma	Drthopterolds AGCCGGGAGCTCTTGGTGCGAGTCCCTCCAGGGTCTCCGGCCTCGAACCCGGTCTCTGGGGAGGGSCT-ACTC TGGTATG-TAATAGTTTGCTTTCGTTCTT-TTCTAAAGGCGGA-CTATTGTCAGGCGGCCTTTCTCT AGC-CGAAG-GCGC-GC-GC-CCTT-G-GCGCTGCCCGTGCGCTCCGCGCTC-CCTG GGYC-GACCG-TGGG-C-C-TC-TGGT-C
INSERT 8 [{[Dennyus	TEGCATATCC TEGGTTEGGG AATTECEGEAG TICTEGTEEG TETETTGETT ACTEGEGTEA GECETAGGTE EGGGTEGGGT TATTTETEEG TIEGGTEEGG TEEGTGGATA ETEAAAGGGA ETEAGTEEG GGGTTTEAEG GETEEGGE GEEGGAAGTG EETEEGGE GAGTTEEGGE GGEGAGTEGG GIETEGGAET TAEGGGGGEE AAAATTTEGE TGTGAECEAG EG
INSERT 9 :.	TCGGCGCGGT CGCCGTCGCG CTCGTCAGCC GTCTCGGGGT GTTAGTTACC GGCACGTCGG CCGGACGTAT TGTCGGCAGG CGGACACGTG
Acyrthosiphon	TCGTGCTTCC GGCCCGCCGT CGCGGCCACG CGTCGCGGG CCGTCGGTGT TCGACGACGG CGGCCGA
[NSERT 10]]]	Hemipteroids
Buenoa	CGGGACCACGGCG-CGTCCAGGCTCGT-CT-CAGGGC-CG-AAAC-G-CGCCGATG-TGTGTCAGG
Saldula	CGGG-GTCTTCG-GA-CAAG-TGCCCT-C-GGGT-GC-TTTCCGTCGTTC-TT-CCGG
Lygus	CGGGAGCCTCGTCTAGGTGACGGCCCTTGCCACAAGCTTGGTGTCCCGGAGGCCGGGGGTATACTCGT
Taeniothrips	TCAGCTGCG-GG-TT-T-CG-GCT-C-GCAT-GC-GG-CCGCCGAGTA-AT
INSERT 11 ///	Megaloptera, Raphidioptera, Basal Coleoptera
Priacma	TACGTAATAGTTGAGGTCTTTACGGATTTCTTCTATTGCTCATCCGACTTTTT
Colpocaccus	TACGTAATAGTTGAGGTCTTTACGGATTTCTTTGCTATCGCACCACTCTTT
Corydalus	TACGTAATAGTTGAGGTCTTTACGGATTTCTTCTTATTGCTCATCCGACTTTTT
Agulla	TACGTAATAGTTGAGGTCTTTACGGATTTCTTCTTATTGCTCATCCGACTTTTT
INSERT 12 {{{	Coleoptera
Cybister	GCGGGCCTTTCCGTAAGGTTGCGTCTC-GCGTC-
Xyloryctes	AGCCCTCGGGG-CGGT
Octinodes	AGCCCGCGAGG-CGGC
Photuris	AGCTCGTAGGGGGC
Meloe	AGCTTGCAAAAG-CGGT
Rhipiphorus	AGCTTGCAAGGG-CGGC
Tenebrio	AGCTCGTAAGGG-CGGC
Tetraopes	AGCTCGTAAGGC-GC

INSERT 13 ''' i Lolomyia Mantispa Hemerobius Chrysoperla	Neuroptera
Lolomyıa Mantıspa Hemerobıus Chrysoperla	TGAAAAACGATTATATTTCATACACACACACATTTATTAGCTGGTGTATGTGTGTG
Lolomyia Mantispa Hemerobius Chrysoperla	$\label{eq:calibratic} TCACACCGGGCTGATTTATTGGCGTGTGGAAAAATTATTTTCCAATTTTGATATGCGTCAGATTTGATATACACGCCATATATACACGCCATATTGGCCATATTATTATGAT-ACACGCGGACCTCCAATAATAAGTAAACC-GG-T-TGAGTTGGATTT-TGTG-AT-TAT-GTGGAT-TAT-GTGGAT-TAT-GTGGAT-TAT-GTGGATT-TGGATG-GTGCACATTTT$
Lolomyıa Mantıspa Hemerobıus Chrysoperla	CGCCACTTGGATTCAAATGTATATTATACGTATATGCAGTTGGGTGGATAATATACATCAAATAATTTGCCGTAAGTGTTTAGCCGTGAAGAACGGCGGC -A-AA-TTG-TTCTGTTGTTCATG-TGCG-ATTTGT-G-TGTGTGA-ACGTT-GAT-AA-T'-TTTACCGTAAGTGTTTAGCCGTAAGAACGGCGGC -ACCGTG
Lolomyia Mantispa Hemerobius Chrysoperla	A-GC AGGC C C
INSERT 14 000 Myrmeleon sp.	(note this sequence is highly suspect) GGTGAGGTAT AAATTATATA TIGTACAATA TAGTTATAAA TAAAAATTAT ACACTIGTAT TITTATITAA ATTITTATIT TATGGGTAAA TAATNAAAAT GITATITTGT TITTGGGTAT AATATTATAT TAATTITTTT NAATTTATAT GTATATATATA AAATATTATA NITTGNNITT TITTTACNIT GNAAAATTNA AAGTATACNIT ANGAAAANNN NNNNNNTATT NGGNGCINCA TANTATNCCN ATIN
INSERT 15 ### Boreus Merope Panorpa Ctenocephalide Hystrichopsyll Orchopeas	Mecoptera Siphonaptera TTAGCCCGTCAAAAGCGGC TTAGCCCGTCAAAAGGCGGC -TAGCCCGTCAAAAGGCGAC s TTAGCGTCAAAAGCGGC aGCACGTCAAAAGCGGC AGCCCGTCAAAAGGCGGC
INSERT 16 }}} Galleria Papilio Ascalapha	Lepidoptera CGCGGTAAAAGGGCGCTCAATA CGCCGGTAATAGGGCGTTCAATA CGCCGGTAATAGGTCGTTCAATA
INSERT 17 \$\$\$ Hydropsyche Pycnopsyche Oecetis	Trichoptera GGTTTCCCGCCGGTGCGTGCGTCGTCCCTCACGGTCTGGCCGTCTGGTTTGGCGACGTTGCGCTG GCGTCCACCGCCGGCGTGTGTCGGTCG-GCCTACGGTCTGGCCGTCTGGCGGACGTTGCGCTG GCGTTTTCCGCCGATGCGAGTCGGTCGGCCGCCTCGGCCGTCTGGCCGGTCGGCGGCGG
INSERT 18 +++ B.strigosus B.chlorostigmu	Bittacus ATCATGTTCACCCCACGATTTGTAGTAAACTACTAGTGGGGAATGGTGACTGAC
INSERT 19 %%% Hartigia Orussus Hemitakonus Peridista Bareogonalos Evania Ichneumon Ophion Mesopolobus Caenochrysis Epyris Priocnemus Dasymutilla Apoica Monobia Pfuscatus Pdominulus Chalepoxenus Chalepoxenus Leptohorax	Hymenoptera AGCTCC-TCACGGGGGGCGGC AGCCCCTTTC-AGAGCGGT AGCC-TTCGGGCGGC AGCC-TTCGGGCGGC AGCTCCTGCGGGGCGGT AGCTCT-TCGCGGGCGGT AGCTCT-TACAGGCGGT AGCTCT-TACAGGCGGT AGC-CCTAACGCGGT AGC-CCTTGGGCGGG AGCTCT-TTCGGGCGGG AGCTCT-TTCGGGCGGG AGC-CC-CTTGGGCGGG AGC-CC-CTTGGGCGGG AGCC-CTTCGGGCGGG AGCC-CTTCGGGCGGG AGCC-CTTCGGGCGGG AGCC-CTTCGGGCGGC AGCC-CTCGGGCGGC AGCC-CTCGGGCGGC AGCC-CTCCGGGCGGC AGCC-CTCCGGGCGGC AGCC-CTCCGGGCGGC AGCC-CTCCCGAGGGCCGC AGCC-CTCCCGAGGGCCGC AGCC-CCGCAGGGCCGC AGCC-CCGCAGGGCCGC

INSERT 20 &&& D	ptera
Tipula	- AGTGGC-AT-A-A-ACGTAA-G-T-T-TATCCGC-G-TAATAAATCTAAAT
Laphria Muthicomuia	1949 TICHAHAMAHAHAHAHAHAHAHAHAHAHAHAHAHAHAHAHAH
MyEnicomyla GGAGTI-TIA-AIGC-IGCOIGIGOITI-CACAIG-T-AGIAI-T-GGCICCIAIIAAAAACCIGCII Drosophila GGAGTICTIAIAIGCATAAATACIT-GTATITIT-CATAIGT-TCCTCCIAIT-TAAAAACCIGCII	
Diopopiiia	
INSERT 21 *** S	repsiptera
Triozocera	3GGTTACCGGT-ACGTGTCGGTAAGCCGTGTACA-A-T-AAA-AC-G-G-CACA-CTGCTGCGTTG-C-CTTTGCGC-A-A-G-TGCA-
Caenocholax	3GATGTTTAGA-A-ATCGTT-TGCT-TATA-GACG-AC-G-GACA-TCTGTTCG-CG-C-TATTCATC-G-A-T-TTCGA-
Elenchus	3GATTTTAAGTAATCAAA-ATAAAA-ATTCATTTTTTTTTGTATATAATCGATACAAAATAATTTTTTTT
Crawfordıa	;GATTTTTCAAG-GTTTTT-TTCG-TATAGTGGCG-TTT-CT-T-TTCGATTCGTTTTT-TTGCGTTTCGAAA-A-A-AGTGC-T-T-C-
X.pecki	GATTTTTCAAA-ATTGAA-ATTTATTTTT-T-TAT-AT-AT-T-TA-TT-
X.vesparum	3GATTTTTCAAA-ATTGAA-TTTTATTTA-T-T-TAT-AT-T-TTTGGT-TTTTTTTT
7-107000-13	
Caepocholay	
Elenchus	TTTTTTTAATGGAAAAATTTCAAAATTATTGCAAATTATTTTTGCTCTAAATTGTAAAAAATATATTGTTACATAAAATTAGATATTTATAAAATTTAC
Crawfordia	-A-G-AAATTA-A-TC-CTTAAA-ATC-CGA-TATGGTAGTTTTAAAAA-AAAATCGAAAAAATTTTCACA-G-TTT-ATTT-A
X.pecki	ATTTTCA-A-TTTTAAA-ATT-CGA-TATAATAATTTTTAATT-AAAAAAGTTTATTTTTT-A-ATTA-AAAA-AATATT-TTTT-
X.vesparum	AATATAA-A-TTAT-AT-AGTAA-TTTTCGATTTTAAAAT-TCGATATAATAATTTTT-A-ATCA-AAAA-AGTTTA-TCGA-
Triozocera	CAG-TG-TCCCG-AT-GGCGAC-G-GATTCGA-TTAGC-T-TCGAACTCGTA-TCGCAT-TC-TG-ATC-GAAACTCGT-G
Caenocholax	ZTG-TT-GAAG-AA-AG-CGT-TGC-TT-A-AATTCGA-TTGTA-T-TCTAAA-C-TA-T-GAAG-AA-AG-CGT-TGCGGTCAG-A
Elenchus	CAAATCAATAGTGGAGAAATTTTTTTCCATTAATGAAAAATTTTAATAAATA
Crawfordia	IAG-AA-A-IG-AGGAIT-AA-AITGAA-AAITTITIT-IGAIT-A-AICAITTC-GI-T-ITIA-AAGIG-AIT-AAAIAAAIGAA-T-T
X.pecki	
x.vesparum	4-A-AT-AA-A-TGTTATTT-TTTTAAT-AATAAATTT-TTT-
Triozocera	D-T
Caenocholax	
Elenchus	ITTTTTATATTAAATAATTTATTTAATTATCGTAAAAATATTTTGTATTCTAATAAAAATTATGTTATTTTATAAATGCATAA-TTTTTTGATT
Crawfordia	ТТТ-ТТТ-С-Т-Т-Т-Т-Т-Т-ТААА-АСТААТ-Т-АТАТТСТААТGАААААТ-ТААТТ-ТТТТТТАА-ААА-
X.pecki	Γ− Α− C−−TT−−− Α−A− −T−−T− ΑΑΑ− TT−T −Α−−T ΑTTCTAATAAAA−TTAT−TTTTT−GTAA−−T−−−T−T−T−T−T−
X.vesparum	ГАА-СТТТ-Т-А-ТТ-АААТ-АТТААТ-Т-АТАТТСТААТАААА-ТТАТ-ТТАААСGТААТТ-Т-Т-Т-Т-А
INSERT 22 >>> M	yrmeleon
INSERT 22 >>> N M.immaculatus	yrmeleon TTRARAATTARATAGT TTRARAATTARATAGT
INSERT 22 >>> N M.immaculatus Myrmeleon	y zmeleon Traaarttaantagt Traaaattaantagt
INSERT 22 >>> N M.1mmaculatus Myrmeleon	y zmeleon TTAAAATTTAAATAGT TTAAAATTTAAATAGT TTAAAATTTAAATAGT
INSERT 22 >>> N M.immaculatus Myrmeleon	y Emeleon TTAAAATTTAAATAGT TTAAAATTTAAATAGT
INSERT 22 >>> N M.immaculatus Myrmeleon INSERT 23 ~~~ S	yrmeleon ΤΡΑΑΑΥΤΤΑΛΝΤΑGΤ ΓΓΑΑΑΥΤΤΑΛΝΤΑGΤ L repsipters
INSERT 22 >>> M M.immaculatus Myrmeleon INSERT 23 ~~~ S X.vesparum X.reskillongi	γχπείοση ΤΤΑΛΑΑΤΤΤΑΛΑΤΑΘΤ ΓΤΑΛΑΑΤΤΤΑΛΑΤΑΘΤ ΓΥΡΑΛΑΥΤΤΑΛΑΤΑΘΤ LTEPS1pters ΤΤΤΑΛΑΛΑΑΘΑΑΛΑΤΤΤΤΤΤΤΤΟΤΘΑΤΤΤΤΤΤ-Τ-Τ-Τ-Τ-Τ-ΤΤΑΑ-ΑΤ-GΑ-ΤΤΑΘΑΑΑΑΑ-ΑΑΑΤΤΑΑΑΑΑΤΓGG-CTTAAAGAA7AAA-TAATTTTA ΤΤΤΑΛΑΛΑΔΒΑ-ΔΟΓΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΑΤΤΤΤΤΑ
INSERT 22 >>> M M.immaculatus Myrmeleon INSERT 23 ~~~ S X.vesparum X.peck1[long] X.peck1[short]	yrmeleon ΤΤΑΡΑΑΤΤΤΑΡΑΤΑΓ ΤΤΑΡΑΑΤΤΤΑΡΑΤΑΓ Lrepsipters ΤΤΤΑΡΑΡΑΛΑΓΑΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤ-Τ-Τ-Τ-Τ-Τ-Τ-ΤΑΡ-ΑΤ-GΑ-ΤΤΆGΑΡΑΡΑ-ΑΡΑΤΑΡΑΡΑΤΤGG-CTTAPAGAPATAPA-TAPATTTA ΤΤΤΑΡΑΡΑΛΑΓΑΡΑΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤ
INSERT 22 >>> M M.immaculatus Myrmeleon INSERT 23 ~~~ S X.vesparum X.peck1[long] X.peck1[short] Gaenocholax[loo]	yrmeleon ТГРАЛАТТТАЛАТАБС ТГРАЛАТТТАЛАТАБС trepsipters тГТАЛАЛАБАЛАБАЛАТТТТТТСТБАТТТТТ-Т-Т-Т-Т-Т-ТАЛ-АТ-GА-ТТАБАЛАЛА-АЛАТАЛАЛАТГБG-СТТАЛАБАЛАТАЛА-ТАЛТТТА ТТТАЛАЛАЛА-Л6ТТТТТТТТТТТТТТТТТТТ-Т-Т-Т-Т-Т-ТАТ-АГ-GA-ТТАБАЛАЛА-АЛАТАЛАЛАТТБG-СТТАЛАБАЛАТАЛА-ТАЛТТТ GGGCTTAЛAGC-AGG-CA-A-T-T-T-AT-ATG-C-CTTGAR-ANATAЛАЛАТАЛАЛТТТАСТТАЛАЛТТТТСАСАЛАЛАЛА G T-T
INSERT 22 >>> M M.immaculatus Myrmeleon INSERT 23 ~~~ S X.vesparum X.peck1[long] X.peck1[short] Caenocholax[sho	yrmeleon TTANAATTTANATAGT TTANAATTTANATAGT TTTANAATAGAANATTTTTTTCTGATTTTTT-T-T-T-T-T-TTAN-AT-GA-TTAGAANAA-ANATAANAATTGG-CTTANAGAANTAAA-TAATTTTA TTTANANAA-AGTTTTTTTTTTTTTTTTTTTTTTTTTTATTTTA
INSERT 22 >>> N M.immaculatus Myrmeleon INSERT 23 ~~~ S X.vesparum X.peck1[long] X.peck1[long] Caenocholax[lon Caenocholax[lon Caenocholax]Sh	<pre>yrmeleon TTRANATTTANATAGT TTRANATTTANATAGT TTRANATTTANATAGT TTANAATTTANATAGT TTTANAAGAANATTTTTTTTTGATTTTTT-T-T-T-T-T-TAA-AT-GA-TTAGAAANA-ANATAANATTGG-CTTAAAGAAATAAN-TAATTTTA TTTAAAAAA-AGTTTTTTTTTTTTTTTTTT</pre>
INSERT 22 >>> M M.immaculatus Myrmeleon INSERT 23 S X.vesparum X.peckı[long] X.peckı[long] Caenocholax[lon Caenocholax[shc Crawfordia Triozocera	<pre>yrmeleon TTRANATTTANATAGT TTRANATTTANATAGT TTRANATTTANATAGT TTRANAATTTANATAGT TTTAAAAAAAAAAATTTTTTTTTTT</pre>
INSERT 22 >>> M M.immaculatus Myrmeleon INSERT 23 ~~~ 1 X.vesparum X.peck1(long) X.peck1(short) Caenocholax(sho Crawfordia Triozocera	yrmeleon TTRANATTTANATAGT TTRANATTTANATAGT TTRANAATTTANATAGT TTTANAAATTTTTTTTTTTTTTTTT
INSERT 22 >>> N M.immaculatus Myrmeleon INSERT 23 ~~~ 2 X.vesparum X.pecki[long] X.pecki[short] Caenocholax[lol Caenocholax[lol Crawfordlax] Triozocera X.vesparum	<pre>yrmeleon TTRANATTTANATAGT TTRANATTTANATAGT TTRANATTTANATAGT GG</pre>
INSERT 22 >>> M M.immaculatus Myrmeleon INSERT 23 ~~~ S X.vesparum X.pecki[long] Caenocholax[lon Caenocholax[shc Crawfordia Triozocera X.vesparum X.pecki[long]	yrmeleon TTRANATTTANATAGT TTRANATTTANATAGT TTRANAATTTANATAGT TTTAAAAAGAAAATTTTTTTTTTTT
INSERT 22 >>> N M.immaculatus Myrmeleon INSERT 23 ~~~ 1 X.vesparum X.peck1[ang] X.peck1[ang] X.peck1[ang] Caenocholax[and Crawfordia Triozocera X.vesparum X.peck1[ang] X.peck1[ang]	<pre>yrmeleon TTRAAATTTAAATAGA TTRAAATTTAAATAGT TTRAAAATTTAAATAGT TTTAAAATTTAAATAGT TTTAAAAATAGAAAAAGAAAATTTTTTTT</pre>
INSERT 22 >>> M M.immaculatus Myrmeleon INSERT 23 2 X.vesparum X.peck1[long] X.peck1[short] Caenocholax[lon Crawfordia Triozocera X.vesparum X.peck1[long] Caenocholax[lond] Caenocholax[lond]	<pre>yrmeleon TTRAAATTTAAATAGT TTRAAATTTAAATAGT TTRAAAATTTAAATAGT TTRAAAATTTAAATAGT TTTAAAATTTAAATAGT TTTAAAATATAGT TTTAAAATATAGTTTTTTTT</pre>
INSERT 22 >>> M M.Immaculatus Myrmeleon INSERT 23 5 X.vesparum X.peck1[long] X.peck1[long] Caenocholax[shc Crawfordia Triozocera X.vesparum X.peck1[long] X.peck1[short] Caenocholax[lon Caenocholax[shc Caenocholax[shc	<pre>yrmeleon TTRANATTTANATAGT TTRANATTTANATAGT TTRANAATTTANATAGT TTTANAAATTTANATAGT TTTANAAATTTTTTTTTT</pre>
INSERT 22 >>> b M.Immaculatus Myrmeleon INSERT 23 ~~~ 2 X.vesparum X.peck1[long] X.peck1[long] Caenocholax[lon Caenocholax[lon Crawfordla Triozocera X.vesparum X.peck1[long] X.peck1[long] Caenocholax[short] Caenocholax[short] Caenocholax[short] Triozocera	<pre>yrmeleon TTRAAATTTAAATAGT TTRAAATTTAAATAGT TTRAAAATTTAAATAGT TTTAAAAATTAAATAGT GGGGCRAAGTTTTTTTTTTTTTTTTTTTTTTTTTTTAATAAAAAAA</pre>
INSERT 22 >>> b M.immaculatus Myrmeleon INSERT 23 2 X.yeeki[long] X.pecki[long] X.pecki[long] Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon	<pre>yrmeleon TTANAATTTANATAGT TTANAATTTANATAGT TTANAATTTANATAGT TTANAATTTANATAGT TTANAAATAAAAAAAAAA</pre>
INSERT 22 >>> b M.immaculatus Myrmeleon INSERT 23 ~~~ 5 X.vesparum X.peck1[long] X.peck1[long] Caenocholax[shc Crawfordia Triozocera X.vesparum X.peck1[long] X.peck1[short] Caenocholax[lon Caenocholax[lon Caenocholax[shc Crawfordia Triozocera X.vesparum	<pre>yrmeleon TTANAATTTANATAGT TTANAATTTANATAGT TTANAAATTTANATAGT TTANAAATTTANATAGT TTTAAAAAAAAAA</pre>
INSERT 22 >>> b M.immaculatus Myrmeleon INSERT 23 ~~~ 2 X.vesparum X.pecki[long] X.pecki[short] Caenocholax[lon Caemocholax[long] X.pecki[long] X.pecki[long] X.pecki[short] Caenocholax[short] Caenocholax[short] Caenocholax[short] Caenocholax[short] Caenocholax[short] Caenocholax[short] Caenocholax[short] Caenocholax[short] Caenocholax[short] Caenocholax[short] Caenocholax[short] X.vesparum X.vesparum	<pre>yrmeleon TTRAAATTTAAATAGT TTRAAATTTAAATAGT TTRAAAATTTAAATAGT TTRAAAATTTAAATAGT TTTAAAAATAGAAAAAGAAAAATAGTTTTTTTT</pre>
INSERT 22 >>> b M.immaculatus Myrmeleon INSERT 23 ~~~ 2 X.yeeki[long] X.pecki[long] X.pecki[long] Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon S.pecki[long] X.pecki[long]	<pre>yrmeleon TTANAATTTANATAGT TTANAATTTANATAGT TTANAATTTANATAGT TTANAAATATAATAGT TTANAAATATAATAGT TTANAAAAAGAAAATTTTTTTTTT</pre>
INSERT 22 >>> M M.Immaculatus Myrmeleon INSERT 23 ~~~ 1 X.vesparum X.peck1[long] X.peck1[long] Caenocholax[sho Crawfordia Triozocera X.vesparum X.peck1[long] X.peck1[short] Caenocholax[lon Crawfordia Triozocera X.vesparum X.peck1[long] X.peck1[short] X.peck1[long] X.peck1[long] X.peck1[long] X.peck1[long]	<pre>yrmeleon TTRAAATTTAAATAGT TTRAAATTTAAATAGT TTRAAAATTTAAATAGT TTTAAAATTTAAATAGT TTTAAAAATAGAAAAGTTTTTTTT</pre>
INSERT 22 >>> b M.immaculatus Myrmeleon INSERT 23 ~~~ 2 X.vesparum X.peck1[long] X.peck1[short] Caenocholax[lon Crawfordia Triozocera X.vesparum X.peck1[long] X.peck1[short] Caenocholax[shc Crawfordia Triozocera X.vesparum X.peck1[long] X.peck1[short] Caenocholax[lond] X.peck1[short] Caenocholax[shc	<pre>yrmeleon TTRAAATTTAAATAGT TTRAAATTTAAATAGT TTRAAAATTTAAATAGT TTRAAAATTTAAATAGT TTTAAAATTTAAATAGT TTTAAAATATAATAGT TTTAAAAATAGAAAAATTTTTTTT</pre>
INSERT 22 >>> M M.immaculatus Myrmeleon INSERT 23 ~~~ 3 X.yeeki[long] X.pecki[long] X.pecki[long] Gaenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[long] X.pecki[long] X.pecki[long] Caenocholax[long] Caenocholax[shott] Caenocholax[shott] Caenocholax[shott] Caenocholax[shott] Caenocholax[shott]	<pre>yrmeleon TTAAAATTTAAATAG TTAAAATTTAAATAG TTTAAAAATTTAAATAG TTTAAAAATTTTAAATAG TTTAAAAAAGAAAATTTTTTTT</pre>
INSERT 22 >>> b M.Immaculatus Myrmeleon INSERT 23 ~~~ 2 X.vesparum X.peck1[long] X.peck1[long] Caenocholax[lon Caenocholax[lon Crawfordla Triozocera X.vesparum X.peck1[long] X.peck1[short] Caenocholax[sho Crawfordla Triozocera X.vesparum X.peck1[long] X.peck1[short] Caenocholax[sho Crawfordla Triozocera	<pre>yrmeleon TTRAAAATTTAAATAGT TTRAAAATTTAAATAGT TTRAAAATTTAAATAGT TTTAAAATTTAAATAGT TTTAAAAATATAATAGT TTTAAAAATAAGGAAAATTTTTTTT</pre>
INSERT 22 >>> b M.immaculatus Myrmeleon INSERT 23 ~~~ 2 X.yesparum X.peck1[long] X.peck1[short] Caenocholax[lon Caenocholax[lon Crawfordla Triozocera X.vesparum X.peck1[long] X.peck1[short] Caenocholax[shc Crawfordla Triozocera X.yesparum X.peck1[short] Caenocholax[shc Crawfordla Triozocera X.yeck1[short] Caenocholax[shc Crawfordlax]shc Crawfordlax[shc Crawfordlax]shc Crawfordlax[shc Crawfordlax]shc Crawfordlax[shc Crawfordlax]shc Crawfordlax[shc Crawfordlax]shc Crawfordlax[shc Crawfordlax]shc Crawfordlax[shc Crawfordlax]shc Crawfordlax[shc Crawfordlax]shc Crawfordlax[shc Crawfordlax]shc Crawfordlax[shc Crawfordlax]shc Crawfordlax[shc Crawfordlax]shc	<pre>yrmeleon TTRAAATTTAAATAGT TTRAAATTTAAATAGT TTRAAAATTTAAATAGT TTRAAAATTTAAATAGT TTTAAAATTTAAATAGT TTTAAAATATAATAGT TTTAAAAAAGAAAAGTTTTTTTT</pre>
INSERT 22 >>> M M.immaculatus Myrmeleon INSERT 23 ~~~ S X.vesparum X.pecki[long] X.pecki[long] X.pecki[long] Gaenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[long] X.pecki[long] X.pecki[long] Caenocholax[lon Caenocholax[shc Crawfordia Triozocera X.vesparum Triozocera X.vesparum Y.pecki[long]	<pre>yrmeleon TTAAAATTTAAATAGT TTAAAATTTAAATAGT TTAAAAATTTAAATAGT TTAAAAATATAATAGT TTTAAAAAAGAAAATTTTTTTT</pre>
INSERT 22 >>> b M.Immaculatus Myrmeleon INSERT 23 ~~~ 2 X.vesparum X.peck1[long] X.peck1[short] Caenocholax[lon Caenocholax[lon Crawfordia Triozocera X.vesparum X.peck1[long] X.peck1[short] Caenocholax[sho Crawfordia Triozocera X.vesparum X.peck1[short] Caenocholax[long] X.peck1[short] Caenocholax[long] X.peck1[short] Caenocholax[long] X.peck1[short] X.peck1[short] X.vesparum X.vesparum X.vesparum X.vesparum X.vesparum X.vesparum X.peck1[long]	<pre>yrmeleon TTRAAATTTANATAGT TTRAAATTTANATAGT TTRAAAATTTANATAGT TTRAAAATTTANATAGT TTTAAAAATAAAGAAAATTTTTTTTGATTTTATTTA</pre>
INSERT 22 >>> b M.immaculatus Myrmeleon INSERT 23 2 X.peck1[long] X.peck1[long] X.peck1[long] Caenocholax[lon Crawfordia Triozocera X.vesparum X.peck1[long] X.peck1[short] Caenocholax[shc Crawfordia Triozocera X.vesparum X.peck1[short] Caenocholax[shc Crawfordia Triozocera X.vesparum X.peck1[short] Caenocholax[shc Crawfordia Triozocera X.vesparum X.peck1[short] Caenocholax[shc Crawfordia Triozocera X.vesparum X.peck1[long] X.peck1[short]	<pre>yrmeleon TTRAAATTTAAATAGT TTRAAATTTAAATAGT TTRAAAATTTAAATAGT TTRAAAATTTAAATAGT TTRAAAATTTAAATAGT TTTAAAAAAGAAAATTTTTTTTTT</pre>
INSERT 22 >>> M M.immaculatus Myrmeleon INSERT 23 S X.vesparum X.peck1[long] X.peck1[short] Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[short] Caenocholax[short] Caenocholax[short] Caenocholax[short] Caenocholax[short] Caenocholax[short] Caenocholax[short] Caenocholax[short] Caenocholax[short] Caenocholax[short]	<pre>yrmeleon TTRAAAATTTAAATAGT TTRAAAATTTAAATAGT TTRAAAATTTAAATAGT TTTAAAAATAAAGAAAATTTTTTTT</pre>
INSERT 22 >>> b M.immaculatus Myrmeleon INSERT 23 ~~~ 2 X.vesparum X.peck1[long] X.peck1[short] Caenocholax[lon Crawfordia Triozocera X.vesparum X.peck1[long] X.peck1[short] Caenocholax[sho Crawfordia Triozocera X.vesparum X.peck1[long] X.peck1[short] Caenocholax[sho Crawfordia Triozocera X.vesparum X.peck1[long] X.peck1[short] Caenocholax[sho Crawfordia Triozocera X.vesparum X.peck1[long] X.peck1[short] Caenocholax[sho Crawfordia Triozocera	<pre>yrmeleon TTRAAATTTANATAGT TTRAAATTTANATAGT TTRAAAATTTANATAGT TTRAAAATTTANATAGT TTTAAAAATAGAAAATTTTTTTTTATTTATTTTTTTT</pre>
INSERT 22 >>> b M.immaculatus Myrmeleon INSERT 23 2 X.vesparum X.peck1[long] X.peck1[long] X.peck1[short] Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[lon Caenocholax[shc Triozocera X.vesparum X.peck1[short] Caenocholax[shc Crawfordia Triozocera X.vesparum X.peck1[short] Caenocholax[shc Crawfordia Triozocera X.vesparum X.peck1[long] X.peck1[long] X.peck1[long] X.peck1[short] Caenocholax[shc Crawfordia Triozocera	<pre>yrmeleon TTAAAATTTAAATAGT TTAAAATTTAAATAGT TTTAAAATTTAAATAGT TTTAAAATTTAAATAGT TTTAAAATATAAGTTTTTTTT</pre>

INSERT 24 ;;; Acyrthosiphon cccgcgcatc tccgcgcacgg cgaaatcgcc tccggggcgt ttccgtgcgc gggccgccgg gccgcgggcs ccagtcgcc gccgtcccg ccgggccggt tttcgggacc ggaggtaatg atcaaca

100

Appendix 2 285 Alignment with Appended Inserts

The 52 taxa were aligned using MALIGN (parallel version 1.93; Wheeler and Gladstein, 1994). The heuristic algorithm "Build" with SBR branch swapping on multiple alignments was performed (change $\cot t = 3$, gap $\cot t = 5$, leading and trailing gap $\cot t = 8$). Primer regions were included in the alignment but were subsequently excluded in phylogenetic analyses. Variable alignment regions (positions 47–59, 88–118, 135–179, 198–220) were excluded from phylogenetic analyses in the conserved tree reconstructions. When the initial alignment presented evidence of a large insertion in a single taxon or subset of taxa, the region was removed to facilitate alignment of positions flanking the insert. Symbols in the alignment (other than standard nucleotide codes) refer to insertions appended after the alignment.

m	
Trigonioptnaimus	
Ephemerella	GACCCGTCTTGAAGCAAGGAGICTTAACATGIGCGCGCGAGICATTGGGCCCCGTCTTTTACACCGAAGGCGTATTGAACGAAAA-GGCCCGTCTG
Libellula	
Agrion	GACCCGTCTTGCABCCACCACCACCACCACCCACCCGTCCCCCCCCCC
Megarcys	
Cultus	
Malapoplus	GACCCGTCTTGARCCAGGAGTCTARAATGGCCCGGCCGGCCGGCGCGCGCGCGCGCGCAGGAGCCGAGGCGCAGGAGG
Melahopius O`lastoma	
Origotoma	
Saldula	
Buenoa	GACCCGTCTTCTA LOCACCGTCTTACA TO TO CONTROL TO TO CONTROL TO
Lygus	
Calassasas	
Corpocaccus	
Cydister	
Aylorycles	
Octinodes	
Rhipiphorus	
Tenebrio	
Tecraopes Coundalus	
Corydalus	
Aguila	
Loromyra	
Nancispa	
Hemerobius	
M.IMMaculatus	
Ophion	GACCCGTCTTCAACCGGGGCTCTAACATGTGGGGGGGGGG
Degramutable	GACCONCINGACCOCCONCINACING COCCONCICATION CONTINUES AND A CONTINUES
Dasymutilia	GACCOMMENTAL ACCORDING AND AND A CONSTRAINTS A
Manahia	Chocomenter and accompany and a construction of the construction o
P fueestue	Chocompany and a concondition of the construction of the construct
Calleria	
Banilia	GACCOMPTER A CONCENTRATION OF THE CONTRACT AND A CO
Papilio	GACCONCINGACCACCACCACCACCACCACCACCACCACCACCACCACC
Hudropaugha	GACCONCINGACCOCCONCINGCINGCONCOCCONCICATION ACCONCINGUA ACCONCINUA ACCONCIN
Rydropsyche	GROCCOTOTICA CONCORDICIA GONTIGOCOGO CONTICATION CONCORDA CONCOR
Pychopsyche	
Decetifs B strigosus	GROCOGTETERA NOROCORCENEGROUP CONTROL AND CONTROL CONTROL AND CONTROL AND CONTROL CONTROL AND CONTROL
Baseus	
Boreus	GACCONCINGACCACCONCINGCAL CONCINCING CONTROL AND A CONTRACT AND A
Danarna	GRCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Ctopocophalados	
Orehenene	Gaccompare has a concentration of the contract of the contra
Orchopeas Tapula	
Taphria	
Drosophila	
Mythicomyla	
Caepocholax	GLCCCTCTTTGLCCLCCGGGTCTLACALGTGTGCGGGTGTTGCGSSSSSSSSSSSSSSSSSSSSSSS
Flenchus	
Crawfordia	
X.pecki	GACCCGTCTTGAACCACGGAGTCTAACAAGTATGCGAGTTATTGGT\$\$\$\$\$\$\$\$\$\$

INSERT 1 ''' Odonata Libellula TCGGACACG Agrion TCGGACACG

INSERT 2 000 Neuroptera Lolomyia ---AATAAAACATTTTTCATCGGAATGTATATAAT-Mantispa ---ACTAAAACATTTTTCATCGGAATGTATATAAA-Hemerobius AATAATAT-GTATTTTTTCATCGGAATATAATAGATA ...mmaculatus ---AATAAAATATTTTTTCATTGAAATATTAATAAA-INSERT 3 ###

Mythicomyia TATATAATCA TTTTACTATG ATTGTATATT TAA

VO	L.	46	
- V U	Ľ٠.	4 C	,

	200
	Variable
Trigoniopthalmus	ATTTT-GG-CCGAACCGAGGGGGAGATCCG-C-GGTCGCTTCGCG-CGGCCCGGCGCATCCCCGGGGCGTCTCGTC
Ephemerella	CTCC-GCG-T-CGGCTGAGGGAAGATGGG-C-G-TC-C-C-CCTCG-CG-G-G-CGCCCCGCATTCCCGGGGCGTCTC(((
Lıbellula	TTCG-CG-G-G-ACCGAGGGAGGACGGA-G-G-CTC-C-TT-CG-CGAGGCTCCCGCACTCCCGGGGCGTCTGATT
Agrion	TTCT-GG-T-G-GCCCGAGGGAGGACGGG-G-T-CGTTCGCGCG-CTCCGGCG-CGC-GTCGGTCCCCGCACCCCCGGGGCGTCTGATC
Megarcys	AAGCC-CG-GCCCAAAGAGGGGAGATGTC-C-G-AGT-ATATAA-AATAT-GAA-GGACCGCATCCCCGGGGCGTCTCC-T
Cultus	AAGCC-CG-GCCCACAGAGGGGAGATGTC-C-G-TGG-CG-TCCCT-AG-TGT-CGCCGACGGACCGCATCCCCGGGGCGTCTCG-T
Mantis	TTCG-TG-C-C-CCCAAGGGAGGATGGC-T-C-TCCTCA-A-C-GGGGGAG-CCCGCACTCCCGGGGCGCCCCC)))
Melanoplus	CTTG-CG-C-GGGCCGAGGGAGGATGGG-G-C-T-TCCCCGCCCTTACA-C-GGGG-CGGT-GGCCTCCGCACTCCCGGGGCGTCTCG-T
Oligotoma	CTAG-GG-T-A-GCCGAGGGAGGAGGATGGA-G-C-AGGCA-T-T-GTCCGGCTTCCGCACTCCCGGGGCGTCTCA-C
Saldula	T-CT-GT-C-CCTTAGGGAAGATGGG-A-G-AAGTACCTTC-G-A-A-GTTG-CTCCCCGYATTCCCGGGGCGTCTCT-T
Buenoa	T-TG-GAACGCT-T-TCCTAGGGAGGATGAC-C-G-TGTCAGCCCG-A-A-AAGGCG-GCGG-TCCGCACTCCCGGGGCGTCTCT-T
Lygus	T-TT-GT-T-TTTGAGGGAGGATGGG-T-T-AGGTACCTTT-T-TTAAAGGA-CCGG-CCT-CGCACTCCCGGGGCGTCTCT-A
Priacma	CTCGTTG-C-GGACCGAGGGAGGAGGATGGC-C-G-CGTTGC-GG-CGTCGGCTCCGCACTCCCGGGGCRTCTCTCG
Colpocaccus	**************************************
Cybister	CTCG-AG-C-GGACCGAGGGAGGATGGG-CGG-CGGGCTT-TT-GT-ACGTCGCCTCGCACTCCCGGGGCGTCTCGCA
Xyloryctes	CTTG-CG-C-GAACTGAGGGAGGATGGA-CGG-TCCTTC-GA-GGCCGTCCCGCACTCCCTGGGCGTCTCGTT
Octinodes	CTCG-CG-C-GGGCTTAGGGAGGATGGG-CGA-AGCGATT-CG-TTCGTGTGTAGCCCCGCACTCCCGGGGCGTCTCGTT
Rhipiphorus	CTCG-TG-C-TTACCGAGGGAGGATGAG-TAT-AACTAA-GG-TT-ATTGCTCCGCACTCCCGGGGCGTTTCATT
Tenebrio	CTAG-CGC-C-GGACTCAGGGAGGATGGG-TGG-TCCTCT-GT-GG-ACCGCCTCGCACTCCCGGGGCGTCTCGTT
Tetraopes	CTCG-CG-C-GGACCGAGGGAGGATGGA-CGG-TCCGCGCTTTCG-CGCGCG-GCCGCCCCGCACTCCCGGGGCGTCTCGTT
Corydalus	20202020202020202020202020202020202020
Agulla	ACCOMPANY
Lolomyıa	>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
Mantispa	>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
Hemerobius	>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
M.immaculatus	>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
Hemitaxonus	C-CT-AG-C-GCTGACCGAGGGAGGA-T-G-GGCCGC-GTCGATGGCACTCCCGGGGCGTCTCGTT
Ophion	C-CT-YG-C-GCCGACCGAGGGAGGA-T-G-GGYCGC-GTCGATGGCACTCCCGGGGCGTCTCGTT
Dasymutilla	C-CT-AG-C-TCCAACCGAGGGAGGA-T-G-GGCCGC-GTTACGATGGCACTCCCGGGGCGTCTCGTT
Apoica	ACCTACT-AA-G-GTCGACCGAGGGAGGA-T-G-GGCCGC-GTTAGCGCGGCACTCYCGGGGCGTCTCGTT
Monobia	C-TT-CG-C-GTCGACCGAGGGAGGA-T-G-GGCCGC-GC-G
P.fuscatus	TACT-AA-G-GTCGACCGAGGGAGGA-T-G-GGCCGC-GT-TTACGCGGCACTCCCGGGGCGTCTCGTT
Galleria	CTCG-CCG-C-GCGCTCAGGGAGGATGGA-G-C-GTCGG-TC-TA-GG-TCGCTCGCTCTCGCACTCCCGAGGCGTCTCGTT
Papilio	CTAG-CCG-C-GCGCTCAGGGAGGATGGA-G-C-GTCGG-TCGTT-CGATCGGC-CTCTCGCACTCCCGAGGCGTCTCGTT
Ascalapha	CTAG-CCG-C-GCGCTCAGGGAGGATGGA-G-C-TTCGA-TC-TA-GG-TCGTA-CTCTCGCACTCCCGAGGCGTCTCGTT
Hydropsyche	CTTC-GG-T-GGCCGCAGGGAAGATGGC-G-G-C-CGG-TA-CG-CCCGTC-CGCC-CGCATTCCCGAGGCGTTTC===
Pycnopsyche	CTCG-AG-CCGGTCGCAGGGAAGATGCGCG-G-G-CGTCGT-CA-GACGCC-CCGCCGCATTCCCGAGGCGTTTC===
Oecetis	CTCG-CGCTCCGTCCCAGGGAAGATGCGCG-C-A-CGTCTC-CG-CACGTG-CCGCCGCATTCCCGAGGCGTTTC===
B.strigosus	******G-GG-T-GGAGGGAAGATGTG-T-A-A-TCT-ATCAT-ATTAACACCGCACTCCCGGRATGTCTCA-A
Boreus	CTTA-AG-T-GAACTCAGGGAAGACGGA-T-C-G-CGT-CTCGA-TGCGATCCCGCACTCCCGGGGCGTCTCACT
Merope	TTTG-TG-T-T-TCTAAGGGATGATGGG-T-T-G-TGC-CACAA-TATAACCCCGCAATCCCGGGACGTCTCATT
Panorpa	TACC-C-AAG-T-GAATTTAGGGAAGATGTA-T-A-A-TCC-TA-AT-GATTGTACCGCATTCCCAGGACGTCTCATA
Ctenocephalides	CTTA-AG-T-GAACTGAGGGATGACGGA-C-C-G-CATCTACGG-AT-GCGTGCTCGCAATCCCGGGGCGTCTCACT
Orchopeas	CTTA-TG-C-GGACTGAGGGATGATGGT-T-G-G-CAT-TACGG-AGCAAACTCGCAATCCCGGGGCGTCTTACT
Tipula	////www.acadaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
Laphria	\$
Drosophila	**************************************
Mythicomyia	
Caenocholax	\$
Elenchus	\$
Crawfordia	\$
X.pecki	\$

INSERT 4 \$\$\$ Caenocholax Elenchus Crawfordia X.pecki	Strepslptera CTAAA-AC-AATGTGACTT-GAGTT-T-T-G-T-T-A-CTCTAT-TTT-AAGTTTTT-GG-TT-T-TAA-T-T-CA-AA-A CTAAA-AC-AATGTGG-TG
Caenocholax	А-АВАВДАТАВСССССССССССТСТСААВТАСА-Т-ТА-ААСТАААТ-А-А-АААС-ТААААВСАА-ААТСВААА-GTGAAA-GTGAAAGAAAG-A-A-C-AGC
Elenchus	А-ATCGNAAAA-A-ATT-A-TTT-TAAAA-CCA-A-A-AGCGAAAT-G-A-AAGTAATTGAA-A-GTGGAA-GTGGAN-TAAAGTTT-TC
Crawfordia	А-ATTCGATCG-GGATTTAATATCGAAAATTTT-T-TA-TAGGAATTT-G-A-AAAC-CAAAAGCAACAAA-GTGAAAAAAAGTG-A-AT-TTG
X.pecki	АТАТТТТТАААААААТТТТGTTTTTTTTTTTTTAATTTAA
Caenocholax	АGCATT-GTGTAATAA-CGTGTTTTGGTTTTTC-TA-AAATGATGAGATCGATTTG-CTGCTGCTTTGRA-AA-AAGCG-A
Elenchus	TCCATT-TCARATGA-TGA-A-AT-TGTAGACA-AAGTGATGA-AA-AAATTTT-T-ATTTTAT-CT-ATCA
Crawfordia	TCGGGT-TCGTTTGGA-TTTGAGAAATTCACTT-TA-AAGTGATGAAATTTTTTTCAGTCT-GCA-GCGCCGCGCAGCAGCAGCAGCAGCAGCAGCAGCA
X.pecki	AGCATAAGCAAAAGTAAAAAAGAAATAATTTTTATTTATT
Caenocholax	С-GА-А-А-А-G-АGATC
Elenchus	АТТ
Crawfordia	GTGT-G-AGAGCGGCGGAATGATT
X.pecki	TTTTTTTAAAGA-ААААААААТТ

Trigoniopthalmus	CG-CATT-TACGCGG-TG-AGGCGCACCTAGAGCGCACACGTTGGGACCCGAAAGATGGTGAACTATGCCTGGCCAGGACGAAGCCAGGGGAVACCCTGG
Ephemerella	{{{{{{{{{{{{{{{{{{{{{{{{{{{{{{{{{{{{{{
Libellula	CC-TCTG-CTTGAGG-GA-AGGCGCACCCAGAGCGCACACGTTGGGACCCGAAAGATGGTGAACTATGCCTGGCCAGGACGAAGTCAGGGGAAACCCTGA
Agrion	CC-TCAT-CGCGAGG-GG-AGGCGCACCCAGAGCGCACACGTTGGGACCCGAAAGATGGTGAACTATGCCTGGCCAGGACGAAGTCAGGGGAAACCCTGA
Megarcys	TG-TCAT-TGCGACACAGTAGGCGCACCCAGAGCGTACACGTTGGGACCCGAAAGATGGTGAACTATGCCTGGCCAGGTCGAAGTCAGGGGAAACCCTGA
Cultus	TG-TCAT-TGCGACACAGTAGGCGCACCCAGAGCGTACACGTTGGGACCCGAAAGATGGTGAACTATGCCTGGTCAGGTCGAAGTCAGGGGAAACCCTGA
Mantıs))))))))))))))))))))))))))))))))))))))
Melanoplus	CC-TCAT-TGCGAGG-TG-AGGCGCACCTAGAGCGTACACGTTGGGACCCGAAAGATGGTGAACTATGCCTGGCCAGGACGAAGTCAGGGGAAACCCTGA
Oligotoma	CC-TCAT-TGCGAGG-AG-AGACGCACCTAGAGCGTACACGTTGGGACCCGAAAGATGGTGAACTATGCCTGGCCAGGACGAAGTCAGGGGAAACCCTGA
Saldula	TC-TCAT-TGCGAGT-GG-AGGCGCACCTAGAGCGCACACGTTGGGACCCGAAAGATGGTGAACTATGCCTGGCCAGGACGAAGCCAGGGGAAACCCTGG
Buenoa	TC-TC-T-TACGAGT-GG-AGGCGCACCCAGAGCGTACACGTTAGGACCCGAAAGATGGTGAACTATGCCTGGTCAGGACGAAGCCAGGGGAAACCCIGG
Lygus	TC-TCAT-TGCGAGA-GG-AGGCGCACCTAGAGCGTACACGCTGATACCCGAAAGATGGTGAACTATGCCTGGCCAGGACGAAGCCAGGGGAAACCCCTGG
Priacma	GCCTCAT-TGCGAGG-CG-AGGCGCACCCAGAGCGTACACGCTGGGACCCGAAAGATGGTGAACTATGCCTGGTCAGGACGAAGTCAGGGGAAACCCCTGA
Colpocaccus	-C-TTAT-TGCAAGT-TG-CGGCGCACCAAGAGCGTACACGCTGGGACCCCGAAAGATGGTGAACTATGCCTGGTCAGGACGAAGTCAGGGGAAACCCTGG
Cybister	-C-TCAT-CGCGAGG-CG-AGGCGCACCACGAGCGTACACGCTGGGACCCGAAAGATGGTGAACTATGCCTGGTCAGGACGAACTCAGGGGAAACCCTGG
Xyloryctes	-C-TCAT-AGCGAGA-AG-AGGCGCACCAAGAGCGTACACGCTGGGACCCGAAAGATGGTGAACTATGCCTGGTCAGGACGAAGTCAGGGGAAACCCCTGA
Octinodes	-C-TCAT-TGCGAGA-AG-AGGCGCACCTAGAGCGTACACGCTGGGACCCGAAAGATGGTGAACTATGCCTGGTCAGGACGAAGTCAGGGCGAACCCCTGA
Rhipiphorus	-C-TCAT-TGCGAGA-AG-AGGCGCACCTAGAGCGTACACGCTGGGACCCGAAAGATGGTGAACTATGCCTGGTCAGGACGAAGTCAGGGGAAACCCCTGA
Tenebrio	-C-TCAT-TGCGAGA-AG-AGGCGCACCAAGAGCGTACACGCTGGGACCCGAAAGATGGTGAACTATGCCTGGTCAGGACGAACTCAGGGGAAACCCTGG
Tetraopes	-C-TCAT-CGCGAGA-AG-AGGCGCACCAAGAGCGTACACGCTGGGACCCGAAAGATGGTGAACTATGCCTGGTCAGGACGAAGTCAGGGCGAAACCCTGA
Corydalus	-C-TCAT-CGCGAGA-CG-AGGCGCATCCGGAGCGTACACGCTGGGACCCGAAAGATGGTGAACTATGCCTGGTCAGGACGAAGTCAGGGGAAACCCCTGA
Agulla	-C-TCAT-CGCGAGA-TG-AGGCGCATCGAGAGCGTACACGCTGGGACCCGAAAGATGGTGAACTAIGCCTGGTCAGGACGAAGTCAAGGGGAAACCCTGA
Lolomyıa	+++++++++++++AG-AGGCGCACCTAGAGCGTACACGCTGGGACCCGAAAGATGGTGAACTATGCCTGGTCAGGACGAAGTCAGGGGGAAACCCCTGA
Mantispa	++++++++++++++AG-AGCGCACCCAGAGCGTATACGCTGGGACCCGAAAGATGGTGAACTATGCCTGGTCAGGACGAAGTCAGGGGGAAACCCCTGA
Hemerobius	++++++++++++AG-AGTCGCACCTAGAGCGTACACCCTGGGACCCGAAAGATGGTGAACTTAGCCTGGTCAGGACGAAGTCAGGGGAAACCCTGA
M.ımmaculatus	+++++++++++++AA-AGGCGCACCTAGAGCGTACACGCTGGGACCCGAAAGATGGTGGACTATGCCTGGTCAGGACGAAGTCAGGGGGAAGCCCTGA
Hemitaxonus	-C-TCAT-TACGAGA-AG-AGCGCACCCAGAGCGTACACGTTGGGACCCGAAAGATGGTGAACTATGCCTGGTCAGGACGAAGTCAGGGGGAAACCCCTGA
Ophion	-C-TCAT-TGCGAGA-AG-AGGCGCACCCAGAGCGTACACGTTGGGACCCGAAAGATGGTGAACTATGCCTGGTCAGGACGAAGTCAGGGGAAACCCCTGA
Dasymutilla	-C-TCAT-TGCGAGA-AG-AGGCGCACCCAGAGCGTACACCGTTGGGACCCGCAAAGATGGTGAACTGTGACCTGGACGACGACGACGACGACGACGACGACGACGACGACGAC
Apoica	-C-TCAT-TGCGAGA-AG-AGGCGCACCCAGAGCGTACACCFTGGGACCCCAGAGTGGACTGGAC
Monobia	-C-TCAT-TACGAGA-AG-AGGCGCACCCAGASCGTACACCTTGGGACCGCAAAGATGGTGAACTATGCCTGGTCAGGACGAAAGTGGCAAACCCTGA
P.fuscatus	-C-TCAT-TGCCAGA-AG-AGGCGCACCCCAGAGCGTAGGGCGCACAGATGGTGAACTATGCTGAACTATGCCCGCAAGTCASGGGCAACCCCCGA
Galleria	TCC-AATCCGTGA-A-TGTGGGCGCGCTCTGGCGCGCAGATGCTGGGGCCCGGAAGTGCTGGACTCGAAGTCGTGAACTCGTGGGCGCAAACGCGAAACGCGGAACGCGGGGCACCCTGA
Papilio	TCC-AATCGTGA-A-TGTAGGCGCGCTTGAGCAGGATGCTGGGCCCGAAAGATGGTGAGCTGCACGCGCGAGCGGAGGGGAAACCCCCG
Ascalapha	TCC-AATCTGTGA-A-TGCAGGGGCCTGAGCATAAATGCTGGGACCCGAAAGATGGTGAGCTGAAGTGGCGCGCGC
Hydropsyche	
Pycnopsyche	
Oecetis	
B.strigosus	
Boreus	
Merope	
Panorpa	
Ctenocephalides	
Urchopeas	
Tipula	
Drosophila	///////AB-C-TG-GAACGTAGCTTGAGCATATATGTTGTGACCCGAAAGATGGTGAACTATACTTGATCAGGTGAAGTCAGGGGAAACCCTGA
Mythicomyla	///////AB-C-TG-GAGCGTAGCTTGAGCATATATGTTGTGACCCGAAAGATGGTGAACTATACCTGATCAGGTTGAAGTCAGGGGAAACCCCGA
Caepocholax	////////aggt_cg-gaatatatcaacagcatacttgttgggacccgaaagatggtgaactatacctggccaggatgaagtcaggagaaatrctgggagaaatrctgg
Elepobus	///////// TAGT-CG-ANATATATATATAAGGGCATAATTGTTGGGACCCGAAGATGGTGAACTATACCTGGCCAGGGTGAAGTCAGGAGAAATTCTGA
Crawfordia	///////CAGT-CG-ADATATATCAAGAGCATACTTGTTGGGACCCGAAAGATGGTGAACTATACCTGGCCAGGATGAAGTCAGGAGAAATTCTGA
Y pecki	//////// ABGT-CG-ADATATATCAAGAGCATACTTGTTGGGACCCGAAAGATGGTGAACTATACCTGGCCAGGATGAAGTCAGGAGAAA ITCTGA
A. pecki	

INSERT 5 %%% Colpocaccus	ΤΑΤΑΤΑΤΑΑΤ ΑΤΤΤΑΤΑΤΑΤ ΤΤΤΤΑΤΑΑΑ
INSERT 6 ^^^	Megaloptera + Raphidioptera
Corydalus	AGAACGGACGTCCGCGCGCCTCACGCGCGCTCTCGTCCG-ACGTACGGGAGGATGCGCGCGTCCGTCGGGGGCGTACTACTCTCTCCGTCGACGACGCGGC
Agulla	GCGTCGTTCGTGCGCGCGCGCGCCG-TCGCGCGCGTACGTCCGACGGAGGAAGATACGCGTACG-C-TACGTGCGCGAAAATGTG-TAT-AACGTA-C
Corydalus	GCGCGCC
Agulla	GCG-T-C
INSERT 7 >>>	Neuroptera
Lolomyia	TATTATTAATTGTTTTGCGGAATTTATT-TTTATGTT-GCAAATTAAATAATAAAGGGAAGATATATTTGTATTATGTATTAAATATC
Mantispa	-ATG-TTTATTATTATATATT-G-CA-AA-ATGTA-TGG-TATT-GCA-TAAGGGAAGATATATTTTTACTATGTGTTAAATATC
Hemerobius	-TGG-TTTAATTATTGGCTT-CACG-GC-CTTTAGTTGTTAAAATCA-TAAGGGAGGAGTATATTTAAATTATGTATTAAATTGA
M.immaculatus	-ATAATTTTTTATTTGG-AAATTTYTTT-TTTATTTA-TGAATACCAAAAATTTGAGGGAGGAGTATATTTTAATTATGTATTGAATAAT
INSERT 8 &&& D	iptera
Tipula	TAA-TATATGGGATTACATGTG-AT-T-GT-ATATAATT
Laphria	TGTTA-TATATGGGATCATATATATATATGTTTATT-ATATATAT
Drosophila	TAA-TA-ATGGGATGATTTTTAGCTAT-TT-ATAGCTAATTA-AC
Mythicomyia	TGTTATTACATGGGATGA-ATATATTT-TCTGAA-ATA-TGAAATATAC

	398
	285 b1
Trigoniopthalmus	TGGAGGTCCGTAGCGATTCTGACGTGCAAATCGATCGTCGGAGCTTGGTATAGGGGCGGAAAGACTAATCGAACC-AT-C-GTAGCTGGTTCCTTCCGA
Ephemerella	TGGAGTECGTAGCGATTETGACGTGCAAATCGATCGTCAGAGCTGGGTATAGGGGCCGAAAGACTAATCGAACC-AT-C-GTAGETGGTTCCTTECGA
Libellula	TGGAGTECGTAGCATTETGACGTGCAAATCGATCGTCGGAGCTGGGTATAGGGGCGAAAGACTAATCGAACC-AT-C-GTAGCTGGTTCCTTCCGA
Agrion	TGGAGGTCCGTAGCGATTCTGACGTGCAAATCGATCGTCGGAGCTGGGTATAGGGGCGAAAGACTAATCGAAACC-AT-C-GTAGCTGGTTCCTTCCGA
Megarcys	TGGAGACCGTAGCGATTCTGACCTGCAAATCGATCGTCAGAGCTGGGTATAGGGGCGCAAAGACTAATCGAGCATCT-TAGTAGCTGGTTCCTTCCGA
Cultus	TGGAGAACCGTAGCGATTCTGACGTGCAAATCGATCGTCAGAGCTGGGTATAGGGGCGAAAGACTAATCGAGCATCT-TAGTAGCTGGTTCCTTCCGA
Mantis	TGGAGFTCCGCAGCGATTCTGACGTGCAAATCGATCGTCAGAGCTGCCTATAGGGGCGGAAAGACTAATCGAACC-AT-TAGTAGCTGGTTCCTTCCGA
Melanopius	TGGAGTCCGTAGCGATTCTGACGTGCAAATCGATCGTCGGAGCTGGGTATAGGGGCGGAAGACCAACTCATCGACCA-CT-TAGTAGCTGGTTCCTTCCGA
Oligotoma	TGGAGTCCGTAGCGATTCTGACGTGCAAATCGATCGTCAGAGCTGGTATAGGGGCGCAAAGACTAATCGAACC-ATCTAGTAGCTGGTTCCTTCCGA
Saldula	
Buenoa	
Lygus	
Priacma	
Colpocaccus	
Cydister	
Xylorycles	TGGAGTCCGTAGCGATTCTGACGTGCAAATCGATCGTCGGAACTGGTATAGGGGCGAAAGACTAATCGA-CC-ATCTAGTAGCTGGTTCCTTCCGA
Octinodes	TGGAGTCCGTAGCGATTCTGACGTGCAAATCGATCGTCGGAACTGGGTATAGGGGCGAAAGACTAATCGA-CC-ATCTAGTAGCTGGTTCCTTCCGA
Rhipiphorus	TGGAGGTCCGTAGCAATTCTGACGTGCAAATCGATTGTCGGAACTGGGTATAGGGGCGAAAGACTAATCGA-CC-ATCTAGTAGCTGGTTCCTTCCGA
Tenebrio	TGGAGT CCGTAGCGATTCTGACGTGCAAATCGATCGTCGGCACTGGGTATAGGGGCGAAGACTAATCGA-CC-ATCTAGTAGCTGGTTCCTTCCGA
Tetraopes	TGGAGGTCCGTAGCGATTCTGACGTGCAAATCGATCGTCGGCACTGGGTATAGGGGCGAAAGACTAATCGA-CC-ATCTAGTAGCTGGTTCCTTCCGA
Corydaius	TGGAGTCCGTAGCGATTCTGACGTGCAAATCGATCGTCGGCACTGGGTATAGGGGCGAAAGACTAATCGAACC-GTCTAGTAGCTGGTTCCTTCCGA
Aguila	I GGAGGTCCGTAGCGATTCTGACGTGCAAATCGATCGTGGGAACTGGGTATAGGGGCGAAAGACTAATCGAACC-GTCTAGTAGCTGGTTCCTTCCGA
LOIOMYIA	I GAGGI CUG TAGUGATTU TGACGI CAAATUGATUGI CGGAATUGGU AGAGAU TAGGGU CAAAGAU TAATUGAACU -ATUTAGTAGU GU CATU
Mantispa	I GGAGG I TI CITAGUGATTU TIGACG TGUATATUGATUGTUGGAAL TGUGTATAGUGGUGAAAGACTAATUGAACU -ATUTAGTAGUTUGTUGTUGAU
Hemerobius	I GGAGGI C CGTAGCGATTC I GACGI GCAAATCGATCGI CGGAACTGGGTATAGGGGCGGAAAGACTAATCGAACC - ATCTAGTAGCTGGTCCTTCCGA
M.IMMACUIALUS	I GAGGI CUGTAGUGATTUTGACGTGCAAATUGATUGTGGGAACTGGGTATAGGGGCGAAAGACTAATUGAACC-ATUTAGTAGUTGGTUCCTTCCGA
Hemitaxonus	TGGAGGTCCGTAGCGATTCTGACGTGCAAATCGATCGTCGGAACTGGGTATAGGGGCGAAAGACTAATCGAACC-ATCTAGTAGCTGGTTCCTTCCGA
Desumutable	
Dasymutilla	TGGAGGTCCGTAGCGATTCTGACGTGCAAATCGATCGTCGGTACTGGGTATAGGGGCGGAAAGACTAATCGAACC-ATCTAGTAGCTGGTTCCTTCCGA
Apoica	TGGAGGTCCGTAGCGATTCTGACGTGCAAATCGATCGTCGGAACTGGGTATAGGGGCGAAAGACTAATCGAACC-ATCTAGTAGCTGGTCCTTCCGA
Monobia D fieretue	TGGAGGTC/CGTAGCGATTCTGACGTGC/AAATCGATCGTCGCAAACGGCGGAGGGCGAAAGACTAATCGAACC-ATCTAGTAGCTGGTTCCTTCCGA
Calleria	TGGAGTECGTAGCGATTETGAGGTGCAAATCGATCGTCGAGAACTGGTATAGGGGCGAAAGACTAATCGAACC-ATCTAGTAGCTGGTTCCTTCCGA
Dapilia	TO BAGGACCOTACCATTCT CACGTOCATACTCATCCATACTCCATACTCCATCCATCCATCTACCATCTACTCATCAT
Papilio	TOCHOCOLOGIACCATICIANCICATICATICATICATICATICATICATICATICATICA
Ascarapha	TOBAGACCETACCETACCETACCETACTCALACTICETCALACTICETACTCALACTICETACCETACT
Byopopsyche	TOGAGACCGTACCGTACCATTCTGACGTACCATCGTCTGCAACTGGTATAGGGCGAAAGACTATCGAACT-ATCTAGTAGCTGGTCCTTCCGA
Pychopsyche	TGENGGACCEANGCGATTCTENCGTECCANTCGTCCCCANTCGCCCCANTACCTATCGAACT-ATCTAGTAGCTGGTTCCTTCCG
P strigosus	TGChGchCCChAGCCATTCTChCGTCCATATCGTCCATCCCCCCATATCCCCCCCATATCCATCTATCT
Boreus	TGGAGGACCGTAGCGATTCTGACGTCCAALGCATCGTCGAALCTGGGTATAGGGGCGAAAGACTAATCGAACC-ATCTAGTAGCTGGTTCCTACCGA
Merope	TGGAGGACCGTAGCGATTCTGACGTCCGATCGGTCGGCGGGGGGGG
Paporpa	TGGAGACGATAGCGATCTALCGTCCALATCGATCGCTAGGGTATAGGGGCGALATCGATCC-ATCTACTAGTGGTCCTTCCGA
Ctopogophaladog	TGGAGGACCGTAGCGATTCTGACGTGCAAATCGATCGTCGAAGCTGGGTATAGGGCGAAAGACTAATCGAACC-ATCTAGTAGCTGGTTCCTTCCGA
Orchopeas	TGGAGGACCGTAGCGATTCTGACGTCGALGTCGACGTCGGCGALGTCGGCGALGCCGALGCTAATCGAACATCTGAGTGCTGCTGCGACG
Tipula	TGGIGGATCGTAGCAGTCTGACGTGCAAATCGTTGGTGGAAATGGGGCTAAAGGGGCGGAAAGCC-ATCTAGTAGTGGTGCTGCTGG
Laphria	TGGAGACCGADDCAGTCTGACGTGCADDTCGATGCAGTGCAG
Drosophila	TGGABACCGABBCAGTCTGACGTGCABBTCGTTGTCAGBTTGTGAGBTGGGGCGABBGACCAFCGAFCCAFCGACC
Mythicomyia	TGGAAGACCGAAACAGTTTGACGTGCAAATCGATTGCCGATTGGGTATAGGGGCGAAAGACCAATCGAACCATCTAGTAGTGGTCCTTCCGA
Caenocholax	TGGAGGTCCGAAGCGATTCGACGTGCAAATCGACGTGGGCGGGGGGGG
Elenchus	TGGAGGCCCGTAGCGATTCTGACGTGCAAATCGACGGCGCGGGGGGGG
Crawfordia	TGGAAGTCCGTGGCGATTCTGACGTCGCAAATCGACCGTCGGGCGGAAGGCGGGGGGGG
X.pecki	TGGAAGTCCGTAGCGATTCTGACGTGCAAATCGACCGCCGGACGGGCGAAAGACTAATCGACCC_ATCTAGTAGTGGTTCCTTCCGA

INSERT 9 *** .	Bittacus
D.SCIIGOSUS	
INSERT 10 (((Ephemeroptera
Ephemerella	GTGCTACCGTCGCTCGCGGG
INSERT 11)))	Mantodea
Mantıs	GGCTTCGGCCGTG
INSERT 12 +++	Neuroptera
Lolomy1a Mantiona	A-T-ATTRC-TAT-A-TAG-A-TATT-AATTTGTAGTTGG-T-T-CTC-GTGGTGTGTGTGTGTGTGTGCC-C-TTGTGCATTC-TCCC-ACGCGCGCCCCCCACGCACGCACGCACGCACGCACG
Hemerobius	ATI-ATI-T-ATI-C-TTTTA-TA-T
M.immaculatus	A-T-ATTATT-C-TTATAA-TTA-T-T-T-T
Lolomyıa	C-TCTACAGAATATAAT-G-TTC-TATATAGT
Mantispa	CGTGTACATTGGCTTGTCGATTCGTTTATAAT
Hemerobius	
M.IMMACUIALUS	11AI-GA-I
INSERT 13 ===	Trichoptera
Hydropsyche	GAGAAATGCCCCGTGCGATT
Oecetis	GAGAAA-GTCACCGTGCGATT
INSERT 14 ///	
Tipula	-A $-A$ $-A$ $-A$ $-A$ $-A$ $-A$ $-A$
Drosophila	ATATA-GT-TATGTATAT-G-T-ATATTTATAT
Mythicomyia	AT-CA-GT-TATGTA-TAGA-T-T-GT-G-T-ATG-CTTC-GGCATGCACAT-TT-ATG-CCTCTA-A-CT-GG
Caenocholax	GGACACGTGTTTTTTGTTGGCGACTGATGACGGAGATGGCGCAAGTTGTTTTCGT-TGTTGTCAGCTGTTCACGAGGTCG
Elenchus	GG-A-C-ACGTA-T-T-T-T-ATAT-T-T-T-T-T-T-AT-AT-AT-T-T-T-T-T-A-T-GTC-GA
Crawfordia V posky	GUA-UAUGIAA-GUA-ATTI-I-ICUGAT-AITI-I-I-I-A-C-GA-AGI-05A GB_CBCGBBTMTTGTC-GA
v.becvi	

APPENDIX 3 MORPHOLOGICAL DATA

The following morphological data have been compiled from various sources, but especially from Hennig (1981), Kristensen (1975, 1981, 1991, 1995) and Boudreaux (1979), including recent contributions by Kukalová-Peck (1978, 1985) and Minet and Bourgoin (1986). The multistate characters were treated as additive, unless specified as nonadditive in the list below. These ordinal-level characters were extrapolated to each sequenced exemplar in the total evidence analyses. The data matrix is provided in Figure A1.

Character List

- 1. *Cerci.*—Absent (0); present, originating from appendages of 11th abdominal segment (1); simplified (2); unsegmented (3) [nonadditive] (Hennig, 1981). Simplified form has no more than two segments (Kristensen, 1981).
- Malphigian tubules.—Developed, many (>6) (0); lost (1); four (2) [nonadditive] (Kristensen, 1975).
- 3. Anterior tentorium.—Present (0); reduced (1) (Kristensen, 1975; Boudreaux, 1979).
- Posterior tentorium.—Absent (0); bearing arms (1); arms fused (2). The posterior arms are fused together, forming a single transverse apodeme in the ectognath insects (Kristensen, 1975; Boudreaux, 1979).
- Ovipositor.—Absent (0); present (1); vestigial (2 valve pairs) (2); modified (3); fused (4) [nonadditive]. The ovipositor is composed of valvulae from abdominal venter VIII + IX. The modified condition in this case refers to reduction in the second valvulae, the third valvulae serving as the functional components of the ovipositor (Boudreaux, 1979; Kristensen 1981).
- 6. Caudal filament.—Absent (0); present, long (1); short (2). The third single caudal filament (paracerus, terminal filament) was considered by Kristensen (1975) to be a synapomorphy of the Insecta. Sharov (1966) suggested that a long, flagellate telson was present in ancestral myriapods and that it was lost in the entognaths. Kristensen considered Sharov's proposition as entirely unfounded. The filament is suppressed in Neoptera (Boudreax, 1979; similar structures in Plecoptera and Dermaptera are of arguable homology).
- Mandibular articulation.—Monocondylic (0); dicondylic (1); anterior articulation fixed (2). A monocondylous mandible is found in Archaeognatha, two articulations being synapomorphic for Thysanura and all pterygote orders (Hennig, 1981). Kukalová-Peck (1985) discussed the difference in the anterior articulation among pterygotes.
- Gonangulum in ovipositor base.—Absent (0); present (1). Presence of a distinct gonangulum in the ovipositor base is taken as synapomorphic for Dicondylia (see summary by Hennig, 1981).
- Origin of ventral mandibular and maxillary (stipital) adductors.—On endoskeletal plates (0); on tento-

rium (1) (Chaudonneret, 1950; see also Kristensen, 1975).

- Fulturae.—Present (0); absent (1) (Francois, 1969, 1970).
- Postoccipital ridge.—Absent (0); internal ridge lateral only (1); continuous (2) (Lauterbach, 1972; see Kristensen, 1975).
- 12. *Tracheal commisures and connectives.*—Not developed in abdomen (0); developed in abdomen (1) (Stobbart, 1956; see Kristensen, 1981).
- Amniotic cavity.—Absent (0); open (1); closed (2) (Kristensen, 1991).
- Median fusion (at least basal part) of male penes.— Absent (0); present (1) (Kristensen, 1975).
- Paired female genital openings.—Absent (0); present (1). Kristensen (1975) characterized these as "retained" in Ephemerida and "lost" in Odonata and Neoptera, but they are not present in other hexapods (Snodgrass, 1933; Boudreaux, 1979).
- 16. Two pairs of wings.—Absent (0); present (1); absent in adult females (2). "Wings" constitutes a suite of characters. Also, there are synapomorphic similarities of the complicated basal articulation of the wing, the venation of the wing (including the archedictyon irregular network of cross-veins), and the flight muscles, adding several characters to the monophyly of Pterygota (whether or not Kukalová-Peck's [1985] homologies are adopted).
- Two coxal proprioreceptor organs.—Absent (0); present (1) (Lombardo, 1973, as cited by Hennig, 1981: note 132).
- Basal wing brace.—Absent (0); present (1). Anastomosis of CuP and anterior anal vein (Kukalová-Peck, 1985).
- Media stem.—Absent (0); present (1). Basal fusion of MA and MP (Kukalová-Peck, 1985).
- 20. Superlinguae.—Absent (0); present (1). Well developed in ephemerid nymphs. Reports in Dermaptera (Giles, 1963) appear actually to represent nonhomologous structures (Moulins, 1969), as may also be true of the lateral hypopharyngeal lobes of primitive Odonata (Tillyard, 1928; see Kristensen, 1975). Boudreaux's (1979) contention that superlinguae do not occur in Entognatha is not true of the ground plan (Kristensen, 1981).
- 21. Habitat of nymphs.—Terrestrial (0); aquatic (1).
- 22. Subimago.—Present (0); absent (1). This character was questioned by Sharov (1957; see also Kristensen, 1975; Hennig, 1981), who suggested that a protoperlarian had a subimago stage. Illies (1968) and Kristensen (1975), however, questioned this interpretation of the fossil record and doubted that the fossils believed to be subimagos are actually so; instead they may represent different species or sexes or morphs (but see Kukalová-Peck, 1978).
- 23. Tracheation.—Anterior only (0); arch (1). In Odonata and Neoptera each wing, like each leg, is supplied with an anterior tracheal trunk from the corresponding segmental spiracle and a posterior trunk from the spiracle behind. The two

	1	5	10	15	20	25	30	35	40	45	50	55	60
	1	1	1	1	1	1	1	1	1	1	1	1	
Collembola	010	1000?(00000	000??	2100?(00000)?0??	?0000	000000	00000)?00??	000?	00
Archaeognatha	100	211000	01011	.000??	2000?(00000)?0??	?0000	000000	00000)?00??	000?	00
Ephemerida	100	2011?1	L12120)11111	.11000	00000	10000	00000	000007	??0000	00000	00000	00
Odonata	100	212211	L12121	.01111	.01111	L11112	20000	00000	000003	??0000	00000	0000	00
Plecoptera	101	2002?1	L12120	01101	.01111	111111	11?11	.00011	110020	01000	00000	0011	00
Blattodea	100	210211	L12121	.01100	00111	111111	11111	.03111	001011	11000	02111	1100	11
Phasmida	300	230211	L12121	.01101	.00111	111111	11111	.00111	000011	.11110	10000	0000	11
Mantodea	100	210211	12121	.01100	00111	11111	11111	00111	001011	.11000	00111	1100	11
Dermaptera	100	220201	12120	01100	00111	L11111	L1?11	02111	010121	.11100	01111	.0000	1?
Orthoptera	200	230211	12121	.01101	.00111	111111	11111	00111	000011	.11100	10000	0000	11
Embioptera	200	2002?1	12121	.02101	.00111	11111	L1?10	02111	110120	01210	00100	00000	01
Psocoptera	020	210211	12121	.01100	00111	L10111	L1110	11111	000010	00001	.00000	0010	10
Pthiraptera	020	210211	12121	.001??	001?1	L11111	L?1??	?1111	000013	?0001	?00??	001?:	10
Hemiptera	020	210211	12121	01100	00111	11111	L1110	11111	000010	00001	.00000	0010:	10
Thysanoptera	020	210211	12121	01100	00111	11111	L1110	11111	000010	00001	.00000	00103	10
Coleoptera	100	210211	12121	01100	00111	11111	L1110	11111	000010	00001	.00000	0011:	10
Megaloptera	100	240211	12121	01100	01111	11111	L1110	11111	000010	00001	.00000	0011:	10
Raphidioptera	100	240211	12121	.01100	00111	11111	L1110	11111	000010	00001	.00000	0011:	10
Neuroptera	100	240211	12121	.01100	00111	11111	L1110	11111	000010	00001	.00000	0011:	10
Lepidoptera	100	2002?1	12121	.01100	00111	11111	L1110	14111	000010	00001	.00000	00113	10
Trichoptera	100	2002?1	12121	.01100	01111	11111	L1110	11111	000010	00001	.00000	0011:	10
Mecoptera	100	2002?1	12121	.01100	00111	11111	L1110	11111	000010	00001	.00000	00112	10
Siphonaptera	100	2002?1	12121	.001??	001?1	11111	L?1??	?1111	00001?	?0001	.?00??	001?2	10
Hymenoptera	100	210211	12121	.01100	00111	11111	L1110	11111	000010	00001	.00000	00112	10
Diptera	100	2002?1	12121	.01100	00111	11111	L11??	?1111	000010	?0001	.00000	00112	10
Strepsiptera	101	0002?7	212121	.02100	00111	1??11	L1?10	11111	000000	00001	.00000	00?1:	10

	61	65	70	75	80	85	90	95	100	105	110	115	120
	1	1	1	1	1	1	1	1	1	1	1	1	1
Collembola	0000	00000	00000	00000	00000	00000	00000	00000	02000	00000)?0000	00000)0
Archaeognatha	0000	00000	00000	00000	00000	00000	00000	00000	0?000	00000)?0000	00000)0
Ephemerida	0001	.00000	10000	00000	00000	00000	00000	00000	00000	00000	00000	00000)0
Odonata	0002	200000	10000	00000	00000	00000	00000	00000	00000	00000	00000	00000)0
Plecoptera	1012	200000	10010	00000	00000	00000	00000	00000	00000	00000	00000	00000)0
Blattodea	0101	10021	.21111	.00000	00000	00000	00000	00000	00000	00000	00000	00000)0
Phasmida	0011	.01100	10010	011000	00000	00000	00000	00000	00000	00000	00000	00000)0
Mantodea	0101	.10021	.21112	200000	00000	00000	00000	00000	00000	00000	00000	00000)0
Dermaptera	0102	200010	10010	01000	00000	00000	00000	00000	00000	00000	00000	00000	00
Orthoptera	0011	.00000	10010	00000	00000	00000	00000	00000	00000	00000	00000	00000)0
Embioptera	1012	201100	10010	010000	00000	00000	00000	00000	00000	00000	00000	00000)0
Psocoptera	0002	20000	10000	00111	11110	00000	00000	00000	00000	00000	00000	00000)0
Pthiraptera	0002	20000	10000	02111	11110	00000	00000	00000	0?000	00000)?0000	00000)0
Hemiptera	0002	20000	10000	00111	10001	10000	00000	00000	00000	00000	00000	00002	20
Thysanoptera	0002	20000	10000	00111	10001	10000	00000	00000	00000	00000	00000	00000)0
Coleoptera	0001	.00000	10000	00000	10000	01111	11000	01000	11000	00000	00000	00000)0
Megaloptera	0001	.00000	10000	00000	10000	01111	11000	00111	.10111	01000	00000	00000)0
Raphidioptera	0001	.00000	10000	00000	10000	01111	11000	00011	.10111	00000	00000	00000)0
Neuroptera	0001	.00000	10000	00000	10000	01111	11000	00011	.10100	01000	00000	00000)0
Lepidoptera	0001	.00000	10000	00000	00000	01111	.00111	10111	.10000	11111	.11111	12000)0
Trichoptera	0001	.00000	10000	00000	00000	01111	00111	10111	.10000	11111	.11111	11000)0
Mecoptera	0001	.00000	10000	00000	00000	01111	00111	10111	10000	11110	00000	00111	.1
Siphonaptera	0001	.00000	10000	00020	00000	01111	00111	10011	1?000	?1010)?0000	00300)1
Hymenoptera	0001	.00000	10000	00000	00000	01111	00111	00110	10000	00000	00000	00000)0
Diptera	0001	.00000	10000	00020	00000	01111	.00111	10011	10000	11110	00000	00211	.1
Strepsiptera	0001	.00000	10000	000030	00000	01001	0??00	1?0?1	.11000	0;??(00000	00112	??

FIGURE A1. Data matrix for 176 insect morphological characters.

	121 125	130	135	140	145	150	155	160	165	170	175
		1	1	1	1	1	1	1	1	1	1
Collembola	000000000	00000	00001	.00000	00000	00000	00000	00000	00000	00000	00
Archaeognatha	000000000	00100	00001	.00000	00000	00000	00000	00000	00000	00000	00
Ephemerida	000000000	00200	00000	010000	00000	00000	00000	00000	00000	00000	00
Odonata	000000000	00211	11100	10000	00000	00000	00000	00000	00000	00000	00
Plecoptera	000000000	00200	00010	00000	00000	00000	00000	00000	00000	00000	00
Blattodea	000000000	00200	00000	10000	00000	00000	00000	00000	00000	00000	00
Phasmida	000000000	00200	00000	10000	00000	00000	00000	00000	00000	00000	00
Mantodea	000000000	00200	00000	010000	00000	00000	00000	00000	00000	00000	00
Dermaptera	000000000	00200	00000	10000	00000	00000	00000	00000	00000	00000	00
Orthoptera	000000000	00200	00000	10000	00000	00000	00000	00000	00000	00000	00
Embioptera	000000000	00200	00000	10000	00000	00000	00000	00000	00000	00000	00
Psocoptera	000000000	00200	00000	10000	00000	00000	00000	00000	00000	00000	00
Pthiraptera	000000000	00200	00000	11000	00000	00000	00000	00000	00000	00000	00
Hemiptera	000000000	00200	00000	10111	00000	00000	00000	00000	000?0	00000	00
Thysanoptera	000000000	00200	00000	10000	00000	00000	00000	00000	00000	00000	00
Coleoptera	000000000	00300	00000	10000	01111	00000	00000	00000	00000	00000	00
Megaloptera	000000000	00300	00000	10000	00000	00000	00000	00000	00000	00000	00
Raphidioptera	000000000	00300	00000	10000	00000	00000	00000	00000	00000	00000	00
Neuroptera	000000000	00300	00000	10000	10000	00000	00000	00000	00000	00000	00
Lepidoptera	000000000	00300	00000	10000	00000	00000	00000	00000	00000	00001	11
Trichoptera	000000000	00300	00000	10000	00000	00000	00000	00000	0000?	11110	00
Mecoptera	111112011	.11300	00000	10000	00000	00000	00000	00111	10000	00000	00
Siphonaptera	??1111111	.11300	00000	011000	00000	00000	00011	11000	00000	00000	00
Hymenoptera	00000000	00300	00000	10000	00000	00001	11100	00000	00000	00000	00
Diptera	111111100	00300	00000	10000	00000	00000	00000	00001	01111	00000	00
Strepsiptera	00????0??	00300	00000	10000	00000	11110	00000	00001	000?0	00000	00

FIGURE A1. Continued.

alar trunks are almost always fused to form a complete arch in the wing base, and the leg trunks are similarly fused. In most ephemerids, only the anterior alar trunk is present; the arrangement is similar to the tracheization of the paranotal lobe in Zygentoma (Kristensen, 1975). For alternative interpretations, see papers cited by Kristensen (1975).

- 24. Posterior tracheation of leg.—Absent (0); present (1). Kristensen (1975) pointed out that the similar condition reported in *Epeorus* by Chapman (1918) involves a very small trachea and even if posterior may not correspond to the ground plan for Ephemerida.
- 25. Direct spiracular musculature.—Absent (0); present (1). In odonates and neopterans, muscles insert directly on the sclerotized spiracular lip (Miller, 1962; Poonawalla, 1966). In contrast, Ephemerida have no direct spiracular muscles but in their place use compression through contraction of dorsoventral body wall muscles (Ford, 1923; Birket-Smith, 1971) (see Kristensen, 1975; Boudreaux, 1979, citation of Maki [1938] on presence in Zygentoma).
- 26. Tentorio-lacinial muscle.—Present (0); absent (1). Ephemerida are the only pterygotes with this muscle. Its presence is probably plesiomorphic, because a similar muscle is found in Archaeognatha. However, this muscle is not known to be present in Zygentoma. Odonata and Neoptera do not have this muscle, and if it is part of the pterygote ground

plan then it supports their sister-group status (see Matsuda, 1965; Kristensen, 1975).

- Tentorio-mandibular muscles.—Several bundles (0); one (1). Never more than one in Odonata and Neoptera. More bundles may be retained in Ephemerida according to Matsuda (1965) and Kristensen (1975).
- Loss of pterothoracic muscles.—No (0); yes (1). Second phragma-tergum II, profurcasternum-mesobasalare, furca-first axillary muscles are present in Ephemerida (and Zygentoma) but not in Odonata or Neoptera (Matsuda, 1970; Hamilton, 1971; see Kristensen, 1975).
- Sperm transfer.—Indirect (0); copulation (1); indirect, using claspers (2) [nonadditive] (Boudreaux, 1979).
- 30. *Wing flexion.*—Absent (0); present (1). A pleural muscle inserted on the third axillary sclerite permits the wing to be flexed over the back. The basal articulation of the wing is complex and might be divided into several characters, such as described by Hennig (1981).
- 31. Third valvulae forming sheath.—Absent (0); present (1). In all Neoptera with a functional ovipositor, the third valvulae (=gonoplacs of Scudder, 1961) are primarily developed along the full length of the ovipositor, forming a protective sheath for the first and second valvulae. Absent in Odonata (Kristensen, 1975), Ephemerida, etc.
- 32. Anal furrow.—Absent (0); present (1). Forbes (1943) pointed out that an anal furrow separates

the anal lobe from the anterior portion of wing (see Hennig, 1981).

- 33. *Enlarged hind-wing vannus.*—Small (0); enlarged (1). This character refers to the size of the anal fan of the hind wings (Kristensen, 1981).
- 34. Jugal bar.—Absent (0); present (1). This character describes whether or not a sclerotization (=jugal bar) is present on the jugum (Kristensen, 1981).
- Ocelli.—Present (0); absent in immatures (1); absent in adults (2); median ocellus absent (3); median ocellus absent in adults (4) [nonadditive] (Kristensen, 1975).
- 36. *Metameric testes ducts.*—Present (0); absent (1) (Kristensen, 1975).
- Male gonocoxopidites IX.—Articulated (0); not articulated (1). Retention of articulated male gonocoxopodites IX is unique to grylloblattids within Neoptera (Kristensen, 1975).
- Metaspina.—Present (0); absent (1). Reported by Kristensen (1975) to be retained within Grylloblattaria.
- Phallomeres.—Normal (0); reduced (1). Male phallomeres are said to be reduced, in conjunction with the formation of secondary intromittent organs from the eversible ejaculatory duct (Kristensen, 1981).
- 40. *Male styli.*—Expressed (0); supressed (1). The suppression of male styli was suggested by Boudreaux (1979) to be accompanied by the formation of accessory clasping organs "from various sources" (!).
- 41. Segmental arteries.—Absent (0); present (1) (Kristensen, 1975; Boudreaux, 1979).
- 42. Female broodcare behavior.-Absent (0); present (1).
- 43. *Trochantin*.—Absent (0); present (1); trochantinepisternal sulcus present (2). This character involves the separation of the trochantin and episternum by a sulcus or membranous line (Kristensen, 1981).
- 44. *Sclerotization of forewing*.—Membranous (0); sclerotized (1). The forewings are said to be "more or less sclerotized" (see Kristensen, 1981).
- 45. Vannus pleated.—No (0); yes (1) (Kristensen, 1981).
- 46. Two cervical sclerites.—No (0); yes (1). This character is problematic (Kristensen, 1981). Once offered as a synapomorphy of "Orthopterodida," it is also present in embilds, "some" Plecoptera (coded here as present for stoneflies), and "some" Holometabola (here not coded as present for holometabolans, because its precise distribution therein is not cited).
- Prognathy.—Absent (0); present (1); gula present (2) [nonadditive]. Sometimes said to be synapomorphic in embiids and dermapterans, but earwigs do not have a gula, whereas webspinners do (Kristensen, 1991).
- Dorsal paraglossa flexor.—Normal (0); "aberrant," "peculiar" (1) (Rähle, 1970; see Kristensen, 1975).
- 49. Phallic rudiments produce gonopods.—No (0); yes (1) (Boudreaux, 1979).
- 50. Prominent precostal field.—Absent (0); present (1) (Kristensen, 1981).

- Discoid pronotum.—Absent (0); present (1); enlarged (2) (Kristensen, 1981).
- 52. Pleural sutures.—Not slanting forward (0); slanting forward (1) (Boudreaux, 1979).
- 53. Indirect wing muscles.—Developed (0); reduced (1). Pterothoracic modifications include reduction of the postnota and phragmata, associated with reduction of dorsolongitudinal and tergosternal indirect wing muscles. Functions of these muscles are, instead, assumed by direct wing depressors and tergopleural-tergocoxal muscles, respectively (see Boudreaux, 1979).
- 54. Metathoracic tergosternal wing elevators.—Present (0); weak or suppressed (1). It has been suggested (see Kristensen, 1981:147) that the initial stage of reduction of the dorsolongitudinal wing depressors and the loss of the metathoracic tergosternal wing elevators may be synapomorphies of Dermaptera and Dictyoptera. Kristensen, however, considered these conditions to be independently derived in these two orders, and variation within each may call this character into serious question.
- Coxa conical, backwards directed.—No (0); yes (1) (Boudreaux, 1979).
- 56. *Phallomeres.*—Symmetrical (0); asymmetrical (1) (Kristensen, 1981).
- Shape of mesotrochantin "holometabolan."—No (0); yes (1) (Ross, 1965; see also Kristensen, 1975:11).
- 58. First branch of Cu.-Not grooved (0); grooved (1). Adams (1958) suggested several possible synapomorphies shared by Plecoptera and Holometabola. These synapomaorphies are, collectively, largely based on Adams's conception of the holometabolan ground plan and thus are controversial. Although Adams suggested several characters in this regard (few-branched weak stem of posterior branch of M, grooved first branch of Cu, distribution of microtrichiae on wing surfaces, tendency for coalescence of S and anterior branch of M, etc.), all have been questioned by Hennig, Kristensen, and others because they are vague, imprecise, or apparently part of a broader ground plan (probably neopteran, for some characers not in list above). One representative character from Adams is registered here (see Kristensen, 1975).
- 59. Separate coxopleuron.—Yes (0); no (1) (Kristensen, 1975).
- Several male accessory glands arranged in cluster.— No (0); yes (1) (Kristensen, 1975).
- Median ventral excurrent ostia in dorsal vessel.—Absent (0); present (1) (Kristensen, 1975).
- Mesothoracic basisternal fold.—Absent (0); present (1) (Kristensen, 1975).
- 63. Premental lobes.—Free (0); fused (1). This character from Hennig was considered by Kristensen (1981) to have evolved probably more than once. It is coded here as an apomorphy found in orthopteroids (as contended by Hennig) and as also occurring in plecopterans and embilds as noted by Kristensen (1981). It is not coded for blattopteroid taxa because Kristensen believed them to be divergent (see Kristensen, 1975:13).

- 64. *Tarsi.*—Not subdivided (0); 5-segmented (1); 3-segmented (2) (Kristensen, 1975).
- 65. *Sternum I.*—Developed (0); reduced (1); absent (2) (Kristensen, 1975).
- 66. Dorsal flexor of paraglossae.—Absent (0); present (1). This refers to a secondary, dorsal flexor of the paraglossae, probably derived from one of the extrinsic prelabial muscles (Kristensen, 1975).
- 67. Second profurca-spinasternal muscle.—Absent (0); present (1). This muscle is in addition to the primitive profurca-spinasternal muscle and has a more oblique course, with posterior insertion on anterior part of (furca+) spinasternum. Kristensen (1975) considered a similar muscle in phasmids clearly convergent.
- 68. Female sternum VII.—Small (0); large (1); forming vestibulum (2). "Dictyopteran" female postabdominal structure. According to Günther and Herter (1974) and Hennig (1981), there exists a unique structural configuration of the female postabdomen in Dermaptera and Dictyoptera (=Blattaria + Mantodea + Isoptera). The genitalia have a vestibulum formed by enlargement of sternum VII and shortening of ovipositor valves (Kristensen, 1975).
- 69. Sex determination.—XX/XY (0); XX/XO (1) (see Thorne and Carpenter, 1992).
- Corporotentorium.—Absent (0); present (1); perforation through which circumesophageal connectives pass (2) (Kristensen, 1975).
- Anterior teeth of proventriculus forming ring of strongly sclerotized teeth.—Absent (0); present (1) (Kristensen, 1975).
- Proventriculus teeth with secondary denticles.—Absent (0); present (1) (see Thorne and Carpenter, 1992).
- 73. Tarsal plantulae.—Absent (0); present (1) (Minet and Bourgoin, 1986).
- Ootheca.—Absent (0); present (1); ootheca hardened after deposition (2) (see Thorne and Carpenter, 1992).
- First axillary sclerite attached close to scutal margin.—Absent (0); present (1) (Kristensen, 1975).
- Sperm axoneme sheaths.—Absent (0); present (1); two dense sheaths surround the inner and outer singlets (2) (Jamieson, 1987).
- 77. Abdominal ganglia.—Unconcentrated (0); one (1). A so-called "concentrated" nerve cord exists in paraneopterans that is defined as consisting of only two or fewer discrete abdominal ganglia (see Kristensen, 1981:148–150).
- Lacinia.—Broad (0); slender rod (1); stylets (2) [nonadditive] (Kristensen, 1981). For information on lacinial stylets, see Kristensen (1975).
- Flagella of spermatozoa.—One (0); two (1) (Kristensen, 1981).
- Gonangulum fused with tergum IX.—No (0); yes (1) (Kristensen, 1981).
- Cibarium.—Absent (0); present (1). This character is stated as a "unique complement of sclerotizations in the cibarium," attributed to Denis and Bitsch (1973) by Kristensen (1981).

- 82. Ovarioles.—Telotrophic or panoistic (0); polytrophic (1) (Kristensen, 1981).
- Basal part of antennal flagellomeres with rupture-facilitating cuticular modification.—Absent (0); present (1) (Kristensen, 1981).
- 84. Mandibles.—Broad (0); stylettiform (1) (Kristensen, 1981).
- Sclerotized rings between antennal flagellomeres.— Absent (0); present (1) (Kristensen, 1981).
- Metamorphosis.—Incomplete (0); complete (1) (Kristensen, 1981).
- Larval eyes.—Carried over to adult (0); not carried over to adult (1) (Kristensen, 1981, 1991, 1995; Paulus, 1986).
- Wing rudiments.—Evaginated prior to penultimate molt (0); evaginated at larval-pupal molt (1) (Kristensen, 1981, 1991, 1995).
- Appearance of external genitalia.—Prior to penultimate molt (0); penultimate molt (1) (Kristensen, 1981, 1991, 1995).
- 90. Cruciate cervical muscles.—Present (0); absent (1) (Kristensen, 1981, 1991).
- 91. Female genitalia.—First valvulae (gonopohyses 8) developed and separate, second valvulae (gonopophyses 9) discrete, cerci articulated (0); first valvulae strongly reduced and fused, second valvulae not discrete, cerci not articulated (1) (Kristensen, 1981, 1991).
- 92. Pretarsal claw of larval leg.—Paired (0); unpaired (1) (Kristensen, 1981, 1991, 1995).
- Silk secretion from larval labial glands.—Absent (0); present (1) (Kristensen, 1981, 1991, 1995).
- Eruciform larvae.—Absent (0); present (1) (Kristensen, 1981). Kristensen (1991) expressed doubts about this character because primitive Mecoptera (Nannochoristidae) and some primitive Amphiesmenoptera are prognathous.
- 95. Outer tergo-coxal remotor muscle.—Present (0); absent (1) (Kristensen, 1995).
- Telomere.—Present (0); absent (1). This character describes the transverse division of the male gonopod ("paramere") into basimere and telomere (Boudreaux, 1979; Kristensen, 1981). Gonopods are absent in Strepsiptera (Kristensen, 1991).
- Abdominal limb buds.—Repressed (0); "derepressed" (1) (Boudreaux, 1979). Kristensen (1981) rejected a single "derepression" event for megalopteran, hymenopteran, and panorpid larval prolegs.
- Gastric caeca.—Present (0); lost (1) (Kristensen, 1981).
- 99. *Meron.*—Absent (0); present (1) (Boudreaux, 1979). Kristensen (1981) suggested that the presence of a demarcated meron is probably a ground plan state for Holometabola and that its loss in Hymenoptera and Coleoptera is probably secondary.
- 100. Cryptosterny.—Absent (0); present (1) (Kristensen, 1981).
- Flight by posteromotorism.—No (0); yes (1) (Kristensen, 1981, 1991, 1995).
- Intrinsic musculature in (fused) third valvulae.—Absent (0); present (1) (Mickoleit, 1973; Kristensen, 1981, 1991).

- 103. Connection of metepimeron to an apophysis-bearing postepimeron pertaining to abdominal segment I.— Weakly or not connected (0); firmly connected (1) (Achtelig, 1975, 1978; Kristensen, 1991).
- 104. Reinforcement of tergum II acrotergite.—Absent (0); present (1). The reinforcement of the acrotergite accommodates the origin of strong polyintersegmental muscles. See Kristensen (1991); his source was Achtelig (1975, 1978).
- Pleural muscle inserted on first axillary sclerite.—No (0); yes (1) (Kristensen, 1981, 1991).
- Larval stipes.—Entire (0); transversely divided (1) (Kristensen, 1981, 1991).
- Larval cranial cardo-promotor, stipitolacinial, and stipitogalaeal muscles.—Present (0); absent (1) (Kristensen, 1981, 1991).
- Cranial antagonist of the primitive craniolacinial muscle in larva.—Absent (0); present (1) (Kristensen, 1981, 1991, 1995).
- 109. Female heterogamety.—Absent (0); present (1) (Kristensen, 1981, 1991, 1995).
- Double Y-shaped fusion of anal veins.—Absent (0); present (1) (Kristensen, 1975, 1981, 1991).
- 111. Achiasmatic oogenesis.—Absent (0); present (1) (Kristensen, 1975).
- Preholocentric chromosomes.—Absent (0); present (1) (Kristensen, 1975).
- 113. Pterothoracic furcal arms fused with epimeron.—Absent (0); present (1) (Kristensen, 1975).
- Pair of glands opening on sternum V.—Absent (0); present (1) (Kristensen, 1975).
- 115. Outer accessory filaments of sperm flagellum very stout (ca. 300 Å diameter).—Thin (0); stout (1) (Kristensen, 1975).
- Vestiture on wing surfaces between veins.—Absent (0); dense vestiture of long setae (1); scales (2) (Kristensen, 1975).
- Daggerlike mandible with anterior articulation reduced.—Absent (0); present (1); articulation lost (2) (Kristensen, 1975, 1991, 1995).
- Prelabium without endite lobes/ligula and associated muscles.—No (0); yes (1) (Kristensen, 1975, 1981, 1991).
- 119. Labial palp segments.—Five (0); two (1); absent (2) (Kristensen, 1975, 1991, 1995).
- Tentorial muscles of prelabium.—Present (0); lost (1). This refers to loss of some primitive labial muscles that are retained in the amphiesmenopteran ground plan (see Kristensen, 1975:34, 1981:153).
- Structure of posterior notal wing articulation.—Not modified (0); modified (1) (Kristensen, 1975, 1991, 1995).
- Pleural ridge/scutum muscle inserting on posterior notal wing process.—No (0); yes (1) (Kristensen, 1975, 1991, 1995).
- Transverse muscle between profurcal arms.—Absent (0); present (1) (Kristensen, 1975, 1991).
- Lateral labral retractor.—Present (0); absent (1) (Kristensen, 1975, 1991).
- 125. Tentorial adductors of cardo in larva.—Present (0); absent (1) (Kristensen, 1975). Hinton (1958) recorded this muscle as present for the mecopteran

family Boreidae, and Willman (1989) rejected this character for Antliophora (see Kristensen, 1991).

- 126. Hypopharyngeal muscles in larva.—Present (0); retractor of hypopharynx and ventral dilator of salivarium absent (1); loss of mouth-angle retractors and dorsal dilator of salivarium (2) (Kristensen, 1975, 1981).
- Larvae.—Podous (0); apodous (1) (Kristensen, 1975, 1991). This refers to thoracic and/or prolegs.
- 128. Extrinsic labral muscles.—Present (0); absent (1) (Kristensen, 1975, 1991).
- Proventriculus with specialized type of cuticular processes, acanthae.—Absent (0); present (1) (Kristensen, 1975, 1991).
- Flagellum of spermatozoon coiled around straight axial mitochondrion.—Absent (0); present (1) (Kristensen, 1975, 1991).
- Procoxa with condylus fitting pleural concavity.—No (0); yes (1) (Kristensen, 1991).
- Coxa-body articulation.—None (0); pleural, mobile (1); pleural, fixed (2); tricondylic (3) [nonadditive] (Kristensen, 1975; Boudreaux, 1979).
- 133. Larval labium.—Not prehensile (0); prehensile (1). A well-known autapomorphy of Odonata. Most of the following ordinal autapomorphies, which are also familiar, are not referenced; however Kristensen's (1991) listing may be consulted.
- 134. Posterior tracheal larval gills.—Absent (0); present (1) [Odonata].
- Lateral cervical sclerite in three pieces.—No (0); yes
 (1) [Odonata].
- Pteropleura tilted backward with notum small.—No (0); yes (1) [Odonata].
- Male accessory copulatory organs.—Absent (0); present (1) [Odonata].
- Tufted larval tracheal gills.—Absent (0); present, lateral (1) [Plecoptera].
- Eversible vesicle on abdominal segment I.—Absent (0); present (1) (Kristensen, 1981).
- Transverse stipital muscle.—Present (0); absent (1) (Kristensen, 1981).
- 141. Vertebrate ectoparasites.—No (0); yes (1) [Pthiraptera and Siphonaptera].
- 142. Labium ensheathing mandibular and maxillary stylets.—No (0); yes (1) [Hemiptera].
- 143. Maxillary palpi lost.—No (0); yes (1) [Hemiptera].
- 144. Maxillary and mandibular stylets piercing/sucking.—Absent (0); present (1) [Hemiptera].
- 145. *Larval piercing-sucking tubes.*—Absent (0); present (1) [Neuroptera].
- 146. Elytra.-Absent (0); present (1) [Coleoptera].
- 147. Abdominal segments VIII and IX telescoped.—No (0); yes (1) [Coleoptera].
- Abdominal sterna I and II membranous.—No (0); yes
 (1) [Coleoptera].
- 149. Mesothorax and metathorax fused.—No (0); yes (1) [Coleoptera].
- 150. Insect endoparasitism.—Absent (0); present (1) [Strepsiptera].
- 151. Forewing "halteres."—Absent (0); present (1) [Strepsiptera].
- 152. Antennae flabellate.—No (0); yes (1) [Strepsiptera].

- Male eyes protruding, with ommatidia seperated by cuticle and setae.—No (0); yes (1) [Strepsiptera].
- Hamuli.—Absent (0); present (1) [Hymenoptera].
 Notocoxal muscles.—Present (0); absent(1) [Hymenoptera].
- 156. Volsella.—Absent (0); present (1) [Hymenoptera].
- 157. Venom production by female accessory gland.—Absent (0); present (1) [Hymenoptera].
- 158. Male antennae serving as accessory clasping organs.—No (0); yes (1) [Siphonaptera].
- 159. Ctenidium on prothorax.—Absent (0); present (1) [Siphonaptera].
- Salivary channels in lacinial stylets.—No (0); yes (1) [Siphonaptera].
- 161. Body laterally compressed.—No (0); yes (1) [Siphon-aptera].
- Clypeus and labrum fused.—No (0); yes (1) [Mecoptera] (Kristensen 1975, 1981).
- 163. Stylar organ of the male claspers.—Absent (0); present (1) [Mecoptera] (Willmann, 1987).
- 164. Male abdominal segment IX ringlike.—No (0); yes (1). See Kristensen (1975), Wood and Borkent

(1989), Kinzelbach (1990). For an alternative interpretation, see Kristensen (1995).

- 165. Spermathecal opening separate from gonopore.—No (0); yes (1) [Mecoptera].
- 166. Halteres.—Absent (0); present (1) [Diptera].
- 167. Hypopharynx styletlike.—No (0); yes (1) [Diptera]. 168. Labial palpi forming labellum.—No (0); yes (1)
- [Diptera].
- 169. Larval spiracles without closing apparatus.—No (0); yes (1) [Diptera].
- 170. Larvae apneustic, respiration epidermal.—No (0); yes (1) [Trichoptera].
- 171. Anal prolegs.—Absent (0); present (1) [Trichop-tera].
- 172. *Larval antennae papillae*.—No (0); yes (1) [Trichoptera].
- 173. Adult labium and hypopharynx fused.—No (0); yes (1) [Trichoptera].
- 174. Abdominal tergum X bilobed.—No (0); yes (1) [Lepidoptera].
- 175. Corporotentorium with median posterior process.— No (0); yes (1) [Lepidoptera].
- 176. Ventral nerve cord solid.—No (0); yes (1) [Lepidoptera].

							No. extra steps ^e						
Analysis	Alignment	Gapsª	Length	No. trees ^b	CIc	RId	A	В	С	D	E	F	G
185	Conserved	?	1,571	5,032	42	64	12	26	34	28	26	3	4
		1	1,711	4,022	44	65	13	24	36	22	25	2	6
		2	1,848	504	45	66	14	21	42	18	22	0	7
	Entire	?	1,965	162	41	63	10	38	21	21	28	4	1
		1	2,257	18	43	63	10	38	21	21	28	4	1
		2	2,542	104	43	65	19	49	27	26	29	4	2
28S	Conserved	?	406	84	45	69	13	5	13	3	5	6	3
-		1	424	180	45	69	11	3	11	3	4	2	2
		2	437	4	46	70	10	2	-9	1	3	4	õ
	Entire	?	938	8	36	59	17	19	10	3	9	5	10
	Dittile	1	1 179	4	36	60	9	16	1 9	2	11	2	7
		2	1,404	12	36	62	20	18	13	ĩ	14	2	7
Molecular			,										
Enliged	Conconned	2	2 000	40	40	64	17	22	20	21	24	1	6
Spilceu	Conserveu	1	2,000	40	42	64	21	15	42	21	24	2	5
		1	2,170	0,432	42	04	21	10	42	22	24	2	5 7
	Entline	2	2,323	20	43	65	25	10	45	23	24	3	/
	Entire	{ 1	2,939	100	39	61	21	40	30	21	32	5	0
		1	3,492	1,4/6	39	62	21	45	22	23	20	3	8
14 1	C 1	2	4,016	72	40	63	32	51	24	25	30	4	6
Merged	Conserved	-	1,520	12	48	68	15	23	44	20	25	0	2
		1	1,632	2	50	69	19	19	38	19	27	1	4
	F	2	1,738	l	51	69	20	18	39	18	25	Û	3
	Entire	?	2,304	6	44	64	22	47	30	23	38	6	6
		1	2,751	28	43	64	25	46	23	23	29	4	5
		2	3,176	18	43	64	31	51	19	21	26	3	1
Morphology	y = 1												
Spliced	Conserved	?	2,401	756	46	72	17	12	29	12	12	0	0
-		1	2,561	96	47	72	21	10	31	13	13	0	0
		2	2,718	3,564	48	72	25	10	33	14	14	2	2
	Entire	?	3,333	10	42	67	23	37	15	16	18	0	2
		1	3,883	332	42	67	30	38	13	13	18	0	2
		2	4,413	12	42	67	43	44	15	18	19	0	3
Merged	Conserved	?	1,818	24	52	73	19	13	28	13	13	3	3
U		1	1,935	3	53	73	21	22	30	16	16	0	0
		2	2.045	5	54	74	24	10	31	13	13	1	1
	Entire	?	2.613	8	47	68	26	39	18	17	19	0	1
		1	3,060	1	46	68	27	37	14	17	17	0	0
		2	3,485	2	46	68	33	45	13	19	20	0	1
Morphology	v = 2 .												
Spliced	Concorred	2	2 760	78	50	76	28	23	2	2	2	0	0
Spilleu	Conserveu	1	2,700	10	50	76	20	25	2	2	2	0	0
		2	2,720	44	50	76	27	20	5	5	5	0	0
	Enting	2	2 701	900	31 4E	70	21	20	10	10	12	0	0
	Entire	{ 1	3,701	10	45	72	25	20	12	12	12	0	0
		1	4,24/	18	45	/1	35	32	1	1	1	0	0
Mar. 1		2	4,//8	12	45	/1	43	3/	9	9	9	0	0
wierged	Conserved	{ 1	2,101	6	55	//	2/	24	4	4	4	0	U
		1	2,220	12	56	77	28	27	2	2	2	U	U
	F	2	2,331	4	57	77	34	29	3	3	3	U	U
	Entire	?	2,898	3	50	72	30	32	5	5	5	U	0
		1	3,347	12	49	71	34	32	8	8	8	U	Ŭ
		2	3,/83	4	48	70	39	38	8	8	8	U	U

APPENDIX 4. Tree statistics for the sensitivity analyses of insect data.

^a Gaps were coded as missing (?) or were weighted by 1 or 2.

^b Number of most-parsimonious trees.

^c CI = consistency index.

 d RI = retention index. d RI = retention index. e A = to place Strepsiptera in Polyphaga; B = to force Strepsiptera sister group to Coleoptera; C = to force Coleoptera monophyly; D = to force Neuropteroidea monophyly; E = to force Coleoptera sister group to Neuropteroidea; F = to force Mecopterida monophyly; G = to force Mecoptera monophyly.