ABSTRACT

Title of Thesis: MOLECULAR PHYLOGENETICS IN THE FAMILY SPHINGIDAE (LEPIDOPTERA: BOMBYCOIDEA)

Andre Arthur Mignault, Master of Science, 2004

Thesis directed by: Professor Charles W. Mitter

Department of Entomology

Moths in superfamily Bombycoidea (Lepidoptera) exhibit a range of strongly divergent life history traits, especially concerning larval herbivory and adult feeding. Building on Regier *et al.* (2001), this study aimed to provide a context for investigation of life history evolution by reconstructing molecular phylogenetic hypotheses of relationships within one bombycoid family, Sphingidae. Coding nucleotide sequence data were collected from two genes, Elongation Factor 1-alpha (1,274bp) and Dopa Decarboxylase (1,373bp), across 65 & 67 sphingids and 40 & 51 lepidopteran outgroups, respectively. Variation in both genes was concentrated in third codon positions, and phylogenetic signal between them proved discordant. Analyses under criteria of Maximum Parsimony and Maximum Likelihood generated six unique hypotheses of sphingid relatedness, each of which was evaluated for concordance with Kitching & Cadiou's (2000) classification. Given weak bootstrap support within and conflicting basal relationships among these topologies, they are best viewed as novel hypotheses subject to further testing via collection of new molecular data.

MOLECULAR PHYLOGENETICS IN THE FAMILY SPHINGIDAE (LEPIDOPTERA: BOMBYCOIDEA)

By

Andre Arthur Mignault

Thesis submitted to the Faculty of the Graduate School of the
University of Maryland, College Park, in partial fulfillment
of the requirements for the degree of
Master of Science
2004

Advisory Committee:
Professor Charles W. Mitter, Chair
Professor Jerome C. Regier
Professor Charles F. Delwiche

To Kimberly

ACKNOWLEDGMENTS

Charlie Mitter nurtured and guided the progress of this work and my general intellectual development with boundless wisdom and patience. Jerry Regier fostered a stimulating laboratory environment, making possible effective collection of these molecular data. My understanding of molecular systematic principles and methods is traced with gratitude to Chuck Delwiche. Members of the Regier Lab, especially Diane Shi, Chris Desjardins and Chris Cook, provided invaluable support during wet-bench work. I feel fortunate to have tapped Ian Kitching's exceptional reserve of knowledge on matters of sphingid taxonomy and natural history. Paul Somers and Jerry Regier contributed valuable comments on the manuscript. This research was made possible by the indispensable support of a network of sphingid collectors and enthusiasts, including: James Adams, Martin Andree, Manuel Balcazar Lara, Ed Ballard, George Balogh, Charles Bordelon, Jr., David Boucher, Don Bowman, Tom Burbidge, Ken Davenport, John DeBenedictis, Bob Denno, Willy DePrins, Duke Elsner, Chuck Ely, Les Ferge, Pete Haggard, Chuck Harp, Dan Janzen, Bill Kelly, Ian Kitching, Ed Knudson, Jim Kruse, Pete Landolt, Ron Leuschner, Mark Mello, Julio & Charyn Micheli, Bill & Byrne Mooney, Marcela More, James Mouw, John Nelson, Mike Nelson, Mogens Nielsen, John Noble, Jim Oberfoell, Paul Opler, Ric Peigler, Owen Perkins, Rob Raguso, John Richards, Kelly Richers, Craig Rudolph, Glen Smart, Dick Smith, Mike Smith, Fred Stehr, Paul Thompson, Jim Tuttle, Bruce Walsh, Reggie Webster and Kirby Wolfe. Finally, this study was inspired and motivated by the comprehensive research programme of Dan Janzen, whose enthusiasm and passion for bombycoid life history evolution provided relevance for a phylogenetic perspective.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

INTRODUCTION

Extraordinary numerical, morphological and behavioral diversity within insects (Arthropoda: Hexapoda) has made them potent model systems for examining the connection between ecological phenomena and evolutionary history (Dobler & Farrell 1999; Farrell 1993, 1998, 2001; Farrell *et al.* 2001; Hufbauer & Via 1999; Kelley & Farrell 1998; Kelley *et al.* 2000; Mitter *et al.* 1988; Pierce 1987, 1995; Powell *et al.* 1999; Sequeira *et al.* 2000; Shaw 1996a,b). Studies on insect ecology and evolution are complementary and synergistic, and can be viewed broadly from two perspectives: (i) short-term interactions between an organism and its environment (ecology) can influence long-term patterns and processes of stasis or change in organismal traits (evolution) (e.g., Costa *et al.* 1996; Hawthorne & Via 2001); and (ii) evolutionary history constrains the genesis of novel ecological habits (e.g., Farrell *et al.* 1992; Farrell & Mitter 1994; Mitter *et al.* 1991; Mitter & Farrell 1991; Wiegmann *et al.* 1993). Application of an evolutionary perspective to long-standing ecological questions may provide insight into the origin and maintenance of traits considered key elements of an organism's natural history. By comparing the observed distribution of ecologically relevant characters with independently derived estimates of organismal evolutionary history, the link between pattern and process can be inferred (Harvey & Pagel 1991). Refinement of molecular phylogenetic methodology has made available robust and novel tools for inferring evolutionary history. In conjunction with traditional and contemporary ecological studies, these methods have made feasible the examination of natural history within an evolutionary context.

Moths in the superfamily Bombycoidea (Lepidoptera: Macrolepidoptera) represent a potent study system for exploration of the connection between ecology and life history evolution. Bombycoidea is one of 43 superfamilies in the hyper-diverse Ditrysia, a lepidopteran clade characterized by explosive diversity in life history strategies which accounts for approximately 98.5% of the over 200,000 species of Lepidoptera (Wagner 2001). As currently delimited, Bombycoidea consists of 3,554 described species distributed across nine families, and is presumed monophyletic on the basis of at least four robust morphological synapomorphies (Lemaire & Minet 1999; Minet 1991 & 1994; Wagner 2001): (a) ultimate instar prothoracic coxae anteriorly fused, each having lost its independent mobility; (b) larval abdominal segment VIII with D1 setae arising from middorsal protuberance, usually a scolus; (c) flexors in valvae of male genitalia originate on the tegumen, not the vinculum; and (d) forewing with Rs1+Rs2 closely parallel to or fused to stem Rs3+Rs4. Bombycoid moths and their close relatives have a cosmopolitan distribution, are among the largest and most conspicuous Lepidoptera (e.g., *Hyalophora*, the cecropia silkmoth; *Actias*, the luna moth) and have in some cases even acquired cultural significance (e.g., *Acherontia*, the death's head sphinx). They have served as model systems for studies in insect biochemistry and physiology (Bartholomew & Casey 1978; Casey 1976; Fink 1995; Goldsmith & Wilkins 1995; Gopfert & Wasserthal 1999; Heinrich 1971a,b; Heinrich & Bartholo 1971; Liu *et al.* 1998; O'Brien 1999 ; Ojeda-Avila *et al.* 2001, 2003; Raguso *et al.* 1996; Raguso & Light 1998; Raguso & Willis 2002; Scriber 1979; Wasserthal 2001; Willmott & Ellington 1997a,b; Wilmott *et al.* 1997), development (Hatzopoulos & Regier 1987; Leclerc & Regier 1993; Mazur *et al.* 1989; Regier *et al.* 1993, 1995; Regier & Kafatos 1991) and

functional morphology (Bullock & Pescador 1983; Buttiker *et al.* 1996; Fanger 1999; Fleming 1968; Fullard & Yack 1993; Ghiradella 1998; Gopfert *et al.* 2002; Gopfert & Wasserthal 1999; Grant & Eaton 1973; Grodnitsky 1999; Krenn 1990; Miller 1997a,b; Robinson & Robinson 1972; Roeder 1972; Roeder *et al.* 1968, 1970; Roeder & Treat 1970; Schmitz & Wasserthal 1999; Scoble 1992; Wannenmacher & Wasserthal 2003; Yack & Fullard 1993a,b, 2000), with special attention focused on agricultural pests (e.g., *Manduca*, the tobacco & tomato hornworms; *Erinnyis*, a potent euphorb crop pest in the New World, see Dillon *et al.* 1983 and Winder 1976) and species of economic significance (e.g., *Bombyx*, the silkmoth; also see Batra 1983; Coffelt & Schultz 1990, 1991, 1993). Furthermore, bombycoid moths have assumed central roles in studies of insect community ecology (Bernays & Janzen 1988; Janzen 1981,1984,1988; Janzen & Waterman 1984; Young 1972), nutritional ecology (O'Brien *et al.* 2000) and pollination biology (Darwin 1862; Eisikowitch & Galil 1971; Grant & Grant 1983a,b; Haber 1984; Haber & Frankie 1982, 1989; Kitching 2002; Miller 1981; Nilsson 1988,1998; Nilsson *et al.* 1985, 1987; Paige & Whitham 1985; Raguso & Willis 2002; Wasserthal 1996,1997,1998; White et al 1994).

In a paper entitled "Two ways to be a tropical big moth: Santa Rosa saturniids and sphingids", Janzen (1984) highlighted and reformulated interest in bombycoid natural history in the context of tropical ecology. Janzen identified stark contrasts in life history strategies between and among moths in two prominent lepidopteran components of a Costa Rican tropical forest community: the bombycoid families Sphingidae and Saturniidae. Superficially, Sphingidae and Saturniidae share many similarities. Both families contain large, conspicuous moths whose larvae struggle to meet demanding

metabolic requirements to support their size. As a result, the larvae of both families can be quite large and feed externally on plant tissues, making them prime targets for suites of predators and parasites (Dyer 1995; Janzen 1988; Price 1997; Stamp & Casey 1993). The biogeographic distribution of both families overlaps both within the Santa Rosa forest and at broader spatial scales. Finally, the sexes in both families pursue common strategies: adult males strive to locate reproductively viable females, and mated females strive to locate suitable plants and/or microhabitats for oviposition. Despite these shared attributes, however, members of the Sphingidae and Saturniidae have adopted starkly divergent life history strategies (Table 1).

A critical difference between sphingid and saturniid moths, which broadly impacts many aspects of their life histories, is the ability for the adult moths to feed (Miller 1996). Sphingidae are renowned for their impressive proboscises (Krenn 1990,1997,1998,2000; Krenn & Kristensen 2000), which permit penetration into sometimes deep and morphologically specialized flower corolla tubes to extract nutrient-rich nectar, and indeed have been prominent figures in studies of pollination biology (Nilsson 1998; Nilsson *et al.* 1985, 1987; Raguso & Willis 2002; Wasserthal 1997). In his treatise, *On the Various Contrivances by which British and Foreign Orchids are Fertilised by Insects*, Darwin (1862) predicted that "in Madagascar there must be moths with proboscises capable of extension to a length of between ten and eleven inches", based on his knowledge of the deep-nectary orchid *Angraecum sesquipedale*. Forty-one years later, Rothschild & Jordan (1903) described the hawkmoth *Xanthopan morgani praedicta* (with a proboscis of length 300 mm or 11.8 inches) as a confirmed pollinator of this orchid (Kritsky 1991). This case illustrates the impressive development of

specialized mouthpart morphology associated with evolution of the feeding habit in Sphingidae. In stark contrast, all adult Saturniidae have reduced or functionally vestigial mouthparts, and the adults are relatively ineffective or incapable feeders.

Potential for adult nutrient intake has been recognized as a critical trait affecting almost every classically important parameter of insect life history, including life span, metabolic rate, activity level, sexual dimorphism and reproduction (Price 1997; see Table 1). For example, sphingid moths which feed continuously throughout their adult stage live much longer than saturniids of comparable size (Janzen 1984). Adult Sphingidae also sustain much higher activity levels and are capable of more controlled and sustained flight maneuvers than saturniids (O'Brien 1999; O'Brien & Suarez 2001). Sphingid male and female adults both share the ability to feed, and they exhibit dampened sexual dimorphism in size and behavior relative to saturniid males and females (Janzen 1984). This drastically affects both the mating habits of the adults and the ways in which female energy is allocated to reproduction. Sphingid males actively court females and are susceptible to female choice and male-male competition (Price 1997), while saturniid females mate indiscriminately with the first male encountered (Janzen 1984). Sphingid females steadily produce eggs throughout their adult lives and oviposit selectively in small clutches, while saturniid females possess their full complement of mature eggs at eclosion and oviposit in large clutches relatively indiscriminately (Janzen 1984).

Notable contrasts in life history strategies are not confined to just the adult stage of Sphingidae and Saturniidae. Janzen (1984) observed a striking series of life history correlates during sphingid and saturniid larval development. For example, sphingid larvae eat a much more restricted set of hostplants and develop much faster than

saturniids of comparable size (Janzen 1984). Characteristics of an insect herbivore's hostplants have long been regarded as central aspects of their biology. Sphingid larvae feed on inconspicuous but nutrient-rich plant materials with highly specific and toxic defensive compounds, including: Asteridae (Asteraceae, Asclepiadaceae, Apocynaceae, Bignoniaceae, Boraginaceae, Convolvulaceae, Lamiaceae, Rubiaceae, Solanaceae, Verbenaceae); Dilleniidae (Dilleniaceae, Euphorbiaceae, Flacourtiaceae); Hamamelidae (Moraceae); Magnoliidae (Lauraceae); and Rosidae (Anacardiaceae, Vitaceae) (Bernays & Janzen 1988; Janzen 1981; Janzen & Waterman 1984; Mabberley 1997; also see Table 4 in Janzen 1984). In contrast, saturniid larvae feed on more readily apparent plant materials (e.g., trees) which are nutrient-poor and rich in simpler and less toxic defensive chemicals (e.g., >50% of saturniids in Santa Rosa feed on Fabaceae [Rosidae]; see Table 3 in Janzen 1984). Finally, the larvae adopt strongly contrasting strategies for defense: sphingids by passive crypsis and mimicry, saturniids with more aggressive chemical and morphological defenses.

Janzen (1984) provided not only insightful recognition of bombycoid life history contrasts, but also a translation of those ecological patterns into a series of questions exploring insect evolution. For example, he framed the question of character evolution polarity by asking whether the sphingid "caricature" arose from a saturniid precursor, or *vice versa* (Janzen 1984, p.130)? Given that both families are members of the same putatively monophyletic superfamily, this question of directionality in life history evolution can be framed as a hypothesis testable via phylogenetic methods (Harvey & Pagel 1991, Farrell & Mitter 1990; Mitter *et al.* 1988, 1991; Wiegmann *et al.* 1993). Phylogenetic inference of relationships within the Bombycoidea may reveal which of the

two syndromes more closely represents the ancestral condition, and which is derived. Assessing such long term evolutionary trends would likewise shed light on a battery of accompanying questions also raised by Janzen. For example, what factors have contributed to much stronger intra- and inter-specific polymorphism in Saturniidae vs. Sphingidae (Janzen 1984, p.113)? Also, what factors (e.g., oviposition constraints, physiological constraints, top-down and bottom-up regulation) have influenced the distinct and nonoverlapping patterns of larval hostplant use between these families, especially when assessed by degree of polyphagy and differential exploitation of various plant growth forms (Janzen 1984, p.122)? Finally, have the selection pressures favoring non-feeding in saturniid adults been imposed by environments unfavorable to those adults, or in habitats conducive to heavy resource accumulation in the larval stage (Janzen 1984, p.130)? Reconstruction of character evolution on a robust phylogenetic hypothesis would assign direction to the contrasting syndromes (i.e., sphingid vs. saturniid) of bombycoid life history evolution, and permit assignment of one habit to the ancestral condition. This would contribute to a more complete understanding of characters impacting the notable diversification of this superfamily.

Importance of a historical perspective in this system is heightened by consideration of one of the three sphingid subfamilies, the Smerinthinae. Though these moths share morphological synapomorphies which position them resolutely in the Sphingidae (see below), smerinthines exhibit striking similarity in many aspects of their life history strategies to saturniids (Janzen 1984; see Table 1). Thus, broad interfamilial contrasts (i.e., Sphingidae vs. Saturniidae) described in Janzen's (1984) study can be considered evolutionarily "replicated" within the Sphingidae (i.e., Smerinthinae vs.

Sphinginae / Macroglossinae). Depending on the relative orientation of the three subfamilies in a tree of Sphingidae, Smerinthinae may provide an independent contrast to test the impact of divergent life history traits on diversification rates. Alternatively, a basal smerinthine position would indicate that the sphingid "caricature" (*sensu* Janzen 1984) arose once in bombycoid evolution. Regardless of the scenario, robust determination of sphingid subfamily relationships will provide a critical clue to investigate the proximate and ultimate factors responsible for the origin and maintenance of such discrepant life histories in the Bombycoidea.

Construction of a robust phylogenetic hypothesis for the Bombycoidea, subsuming all taxa in Janzen's Santa Rosa study system, would provide a powerful evolutionary backdrop against which to interpret such vast ecological differences between component families. Such a phylogeny may permit reconstruction of the presumed ancestral condition, suggesting possible character transformation pathways by which these relatively closely related families underwent ecological diversification. Ecological polarity implied by this reconstruction may greatly enhance our understanding of the opportunities and constraints governing broad scale evolution of insect life history strategies, with implications for understanding patterns of herbivory, sexual dimorphism, reproduction, population dynamics and the origin of morphological & behavioral novelty.

The bombycoid system offers a rare opportunity for significant progress in *both* construction of a robust molecular phylogeny and application of that phylogenetic hypothesis to interpretation of the connection between ecology and evolution. Initial attempts to assess phylogenetic relationships within the Bombycoidea have focused on the two most prominent members of the superfamily: the Saturniidae and Sphingidae.

The latter has recently benefited from an intersection of comprehensive morphological (Kitching & Cadiou 2000) and molecular (Regier *et al.* 2001) systematic treatments.

Kitching & Cadiou (2000) proposed an exhaustive genus-level systematic revision of Sphingidae based on unpublished cladistic analyses of morphological and behavioral characters conducted by Kitching (Table 2). Their revision exposed and resolved many layers of nomenclatural violations and proposed an approximately phylogenetic arrangement of taxa. However, this coarse treatment left unresolved many of the relationships across every taxonomic level within the family, including many of prime ecological relevance. Of greatest relevance to interpretation of contrasting life history strategies is the monophyly of and relative position among the three subfamilies recognized by Kitching & Cadiou (2000). Monophyly of the family is considered extremely well-supported on the grounds of at least nine morphological synapomorphies: (a) lateral oblique stripes on larval abdominal segments I-VII; (b) exposed hindwings not reaching pupal abdominal segment IV; (c) ventral arm of adult laterocervicale ending abruptly in a thin rod; (d) prescutal clefts of the adult mesonotum very close or fused dorsally; (e) mostly unsclerotized ventral process in tegula; (f) adult forewing vein M2 arising slightly closer to M3 than to M1; (g) adult hindwing margin produced or angulate at the tip of vein 1A+2A; (h) strong sclerotized lobe on metafurcula secondary arms reinforcing the thoraco-abdominal intersegmental membrane close to abdominal sternite II; and (i) cavity broadly open in 'tergal rim' (Minet 1994, p. 85). However, comparable morphological support has not been established for subfamily concepts, prompting Minet (1994) to state the "monophyly of each of these three subfamilies is, obviously, less convincingly established than that of the Sphingidae" (p. 85). It is hoped that a robust

phylogeny based on molecular data will both corroborate the recent classification of Kitching & Cadiou (2000) and offer clarification in the search for strict morphological synapomorphies characterizing clades at all levels within the Sphingidae.

In a pilot study, Regier *et al.* (2001; hereafter called 'Regier 2001') established the efficacy of two unlinked protein-coding nuclear markers in resolving relationships among sphingid genera. Elongation factor 1-alpha (EF) is involved in the initial stages of peptide elongation, and promotes GTP-dependent binding of aminoacyl tRNA to the ribosome A-site during protein biosynthesis (Hovemann *et al.* 1988; Kamiie *et al.* 1993). Dopa decarboxylase (DDC) catalyzes conversion of dopa into dopamine, and ninety percent of DDC activity occurs in epidermal tissues where dopamine derivatives are involved in sclerotization and melanization of insect cuticle (Hiruma *et al.* 1995; Tatarenkov *et al.* 1999). Regier 2001 found comparable information content and no significant conflict in signal between 1,240 bp of EF and 709 bp of DDC across assayed taxa. After partitioning the data into codon positions, they found that 88% of all variable sites occurred at third codon positions (nt3). Despite that 96% of all nucleotide changes were inferred to be synonymous, pairwise divergences at first and second codon positions (nt1&nt2) increased with increasing taxonomic depth, suggesting character state saturation at those positions had not yet occurred. Phylogenetic inference was conducted under two optimality criteria: (i) maximum parsimony (MP) with differential weightings across partitions; and (ii) maximum likelihood (ML) under general time reversible models with and without parameters accounting for unequal base frequency. Each analysis was performed on a variety of partition schemes, including genes and codon positions both alone and in conjunction. Differential performance of each analytical

method was assessed via a bootstrap taxon bipartition table, which itemized bootstrap support for clades of interest across the entire range of bombycoids sampled (see Table 1 of Regier 2001). A single fully dichotomous topology derived from MP analysis on the nt1&nt2 partition was selected as the best estimate of relationships among taxa sampled (Figure 1). This fully resolved topology revealed no significant conflict with Kitching's morphological hypotheses, however branches of special interest (especially the position of the "saturniid-like" Smerinthinae) were poorly supported by the data.

The current study was designed as the next step toward ultimately building a robust phylogenetic hypothesis of the entire superfamily Bombycoidea, to provide an evolutionary context for interpretation of ecological characters (e.g., those highlighted by Janzen 1984) as determinants of insect life history evolution. Specifically, this study aimed to expand taxon and character sampling as a means to improve resolution of relationships among genera in systematic analyses of the family Sphingidae. While this work touched on the orientation of Sphingidae within the superfamily, obtaining greater support for the position of the family relative to other bombycoids was left for future studies. Establishing a robust hypothesis of genealogical relatedness within the family Sphingidae has two immediate applications: (1) testing existing hypotheses of sphingid classification based on analysis of non-molecular characters (viz. Kitching & Cadiou 2000); and (2) interpreting correlations between a diverse suite of morphological and behavioral traits from an explicitly phylogenetic perspective.

Immediate goals for this work included: (a) testing the broadly accepted concept of Sphingidae monophyly by exploring robustness of the sphingid node under different suites of outgroups; (b) building on the pilot analyses conducted in Regier 2001 by

augmenting their taxon sampling and extending the range of nucleotides collected from DDC; (c) assessing the degree of corroboration between sphingid phylogenetic hypotheses derived from molecular versus morphological data, especially the monophyly of and relationships among subfamilies, tribes & sections delimited by Kitching & Cadiou (2000); (d) confirming the utility of EF and DDC, both separately and in conjunction, for providing robust phylogenetic resolution within Sphingidae; (e) investigating degree of concordance or conflict in phylogenetic signal between EF and DDC; (f) exploring effects of different taxon samples, character partitions and optimality criteria employed in phylogeny reconstruction.

Broader goals to which this study is expected to contribute include: (a) testing Minet's (1991, 1994) morphologically derived taxonomic hypotheses about relationships in Bombycoidea, including monophyly of and interrelationships among his nine recognized families; (b) contributing a robust phylogenetic component toward resolution of a long-standing polytomy at the base of Macrolepidoptera; (c) establishing a connection between ecology and evolution of life history strategies across Bombycoidea, especially through identification of independent contrasts (e.g., adult feeding, reproductive strategies, sexual dimorphism, larval diet breadth) among bombycoid sister lineages across all taxonomic levels.

MATERIALS & METHODS

Taxon Sampling

A prime focus of the present study was to expand the diversity of taxon sampling beyond that in Regier 2001. That pilot study included representatives of 7 genera across all three tribes in Macroglossinae, 2 genera in only one of the three tribes in Smerinthinae, and 5 genera in only one of the three tribes in Sphinginae (Figure 1 and Table 2). While results of that study were compelling, the current work aimed to improve the breadth of Sphingidae species in the University of Maryland (UMD) Lepidoptera Collections available for collection of nucleotide sequence data. To this end, a global network of collectors was assembled through directed correspondence and the systematic revision by Kitching & Cadiou (2000) was used as the basis for assigning target taxa to different collectors.

Choice of outgroups for systematic analyses of the Sphingidae was relatively straightforward, given the systematic classification of Bombycoidea proposed by Minet, in which nine families, including Sphingidae, were arranged into putatively monophyletic groups (Minet 1991, 1994; Lemaire & Minet 1999). Corroboration of Minet's broader systematic hypotheses by analysis of molecular evidence is forthcoming (Mitter, pers. comm.); thus, for the purposes of this study all non-sphingid bombycoids were considered viable candidates for outgroups to root the tree of Sphingidae. This study was designed primarily to explore relatedness among genera within Sphingidae, and conclusions regarding genealogical relatedness across the broader Bombycoidea were treated only provisionally.

Specimen Acquisition

To build a grassroots network of sphingid collectors, a list of self-identified sphingid enthusiasts was compiled from The Lepidopterists' Society Membership Directory for years 2000 and 2002 (J.P. Donohue, editor; Los Angeles, CA). In addition, names of registered collectors of sphingid taxa were compiled from The Lepidopterists' Society Season Summary for years 1992-2002 (J.P. Tuttle, editor; Tucson, AZ). A letter summarizing the goals of this project within the context of broader arthropod systematic research at the Maryland Center for Systematic Entomology (MCSE) was mailed to each potential collector, soliciting their help in procuring specimens for the upcoming season and/or providing leads for other collectors. Responses to these solicitations were compiled and correlated against the list of target taxa. Special emphasis was placed on enlisting geographically dispersed collectors to maximize sampling diversity across the North American fauna (see genera shaded in Table 2).

After establishing a collaboration with these parties, collecting kits consisting of the following items were assembled and mailed to interested collectors:

(a) 15mL and/or 50mL screw-cap centrifuge tubes (Corning Life Sciences, catalog nos. 430790 & 430291) filled with 100% (200 proof) ethanol and labeled internally and externally, for preservation of tissues;

(b) 5.9cm x 9.2cm side-opening glassine envelopes (Bioquip Products, catalog no. 1131B) for collection of wing vouchers and/or whole dried voucher specimens;

(c) preformatted specimen information data sheets, for recording specimen information;

(d) a one-page instruction sheet detailing proper field preservation of insect tissue for use in molecular systematic studies (Figure 2);

(e) permanent (ethanol-resistant) felt-tip markers;

(f) parafilm sheets, for sealing vial lids after specimen storage;

(g) pre-paid overnight return postage labels.

Special emphasis was made in preparation of the kits to simplify both the specimen collection/processing and the data recording steps for each collector. The number and size of vials shipped was customized to the anticipated collecting load and taxa commonly encountered by each collector. Individual vials were labeled internally with laser-printed four-digit serial numbers on strips of 65 lb. 96 brightness acid-free archival quality paper (Wausau Bright White, catalog no. 92101), and externally with the same serials hand-written in permanent marker. Specimen data sheets accompanying each kit were pre-labeled with the collectors' name, the series of numbers for corresponding tubes, and ample space for recording collection information was provided.

Field-collected specimens were transferred immediately into 100% ethanol in the provided vials, and kept cool and dark until shipment back to College Park. Ethanol was selected for specimen preservation in this study for several reasons: (a) low toxicity, (b) low melting point to facilitate storage at cryogenic temperatures, (c) rapid evaporation upon removal of specimen tissue for examination, and (d) slow rate of DNA degradation relative to aqueous solutions. Dessauer *et al.* (1996) remarked that prolonged storage of tissue in at low temperatures and in the absence of oxygen retarded the rate of degradation. Post *et al.* (1993) confirmed that samples stored in any medium at room

temperature, or in aqueous solution at any temperature, exhibited very poor yields in DNA extraction.

Specimen Curation

Upon receipt, shipped specimens were processed immediately and curated for end storage in the UMD Lepidoptera Collections. Spent ethanol preservative was decanted and the vials were refilled to capacity with fresh 100% ethanol. Extremely large specimens (e.g., *Cocytius*, *Eumorpha*, *Manduca*, *Pachysphinx*, etc.) were sectioned or slit to ensure proper penetration of the preservative into internal tissues. Extremely small specimens (e.g., *Agrius*, *Erinnyis*, *Hemaris*, *Proserpinus*, etc.) were transferred to appropriately sized vials, making every effort to maximize volume of free ethanol while conserving freezer space. If necessary, wings submersed in ethanol were separated from the specimen at the basal sclerites, blotted dry on Kimwipes and stored in glassine envelopes labeled with the same four-digit serial number. Similarly, serial numbers of wing vouchers processed by the collectors prior to shipment were checked against the specimen from which they were separated.

Both the pickled tissue specimen and the dried wing voucher were reassigned a revised UMD Lepidoptera Collections accession number consisting of the original four-digit random number with a prefix composed of the collector's initials and a two digit code for the year in which the specimen was received [e.g., "WJK-02-1941" denotes a specimen collected by William J. Kelly into vial #1941 and received at College Park in 2002]. Laser-printed labels with these final accession numbers were swapped for the original vial labels, and wing voucher labels summarizing key collection information for

each specimen were inserted into corresponding glassine envelopes. Curated specimens in 100% ethanol were archived into permanent storage at –80 degrees C in the Regier Laboratory at the University of Maryland Biotechnology Institute (UMBI) Center for Biosystems Research (CBR), College Park, MD. Wing vouchers were sorted by accession number and stored in Cornell drawer insect cabinets in the Mitter Laboratory at UMD Entomology, College Park, MD.

After specimen processing, detailed collections information was compiled from collectors' data sheets and entered into a specimen database custom-designed in FileMaker Pro (version 3.1 and 6.0; FileMaker, Inc.) for management and tracking of molecular tissues specimens in the UMD Lepidoptera Collections. Species identification was determined in all cases by the collector and was *not* independently verified prior to curation. Other key pieces of information entered into designated fields in the UMD database included: accession number, collector & determiner name(s), collection date & time, collection locality, number of specimens, life stage, preservation method, higher taxonomic assignment of each genus, wing voucher information and freezer storage location (Figure 3). In addition, specimen physical condition and any oddities in the collection/curation process were recorded in a notes field. Every effort was made to compile exhaustive collection records for each specimen, and in many cases collectors were consulted to *post facto* verify or clarify specific collection or identification data.

Sequence Collection de novo

Congruence between independent data sets has long been recognized to lend power to any phylogenetic hypothesis (Brown *et al.* 1994; Cunningham 1997; Eernisse &

Kluge 1993; Funk *et al.* 2000; Mickevich & Farris 1981; Miyamoto & Fitch 1995; Penny & Hendy 1986; Yeates & Wiegmann 1999). In this spirit, nucleotide sequence data was gathered from a portion of the coding regions of two separate and unlinked nuclear genes: (a) Elongation Factor 1-alpha (EF) and (b) Dopa Decarboxylase (DDC). Generation of novel DNA sequence was a three-tiered process: (A) genomic nucleic acid extraction; (B) amplification of the region of the genome of interest; and (C) sequencing of the bases comprising that amplified gene product.

A. Whole Nucleic Acid Extraction

Whole nucleic acids were obtained from insect tissue according to the SV Total RNA Isolation System (catalog no. Z3100, Technical Manual no. 048; Promega Corporation). While this kit was intended for extraction of RNA free of genomic DNA contamination, slight protocol modifications permitted precipitation of both genomic DNA and RNA from all samples (Otto, 1998). Extractions were conducted in batches of less than eight specimens, to ensure adequate attention was paid to each sample and to minimize opportunities for cross-contamination.

Specimen vials were removed from –80C storage to a wet ice bath, and allowed to equilibrate to ice temperature. Clean forceps were used to transfer the specimen from the ethanol preservative to a sterile disposable petri dish. A sterile disposable scalpel blade was used to section the specimen at the head, prothorax, and/or mesothorax, until approximately 10-30mg of tissue was obtained. Internal tissues were scraped out of these sectioned fragments, and antennae, ommatidia, the proboscis, and heavy chitinous structures (e.g., mandibles, tergites, proleg basal sclerites) were excluded. Ethanol-

moistened dissected tissue was air dried for several minutes before it was transferred to a 1.5mL eppendorf tube containing 178.5uL of SV RNA Lysis Buffer (4M guanidine thiocyanate, 0.01M tris, 0.97% beta-mercaptoethanol; pH7.5). Remaining unused specimen tissue was immediately returned to its original vial and refilled with fresh 100% ethanol for long-term storage at –80C.

Dissected tissue in Lysis Buffer was homogenized inside the eppendorf tube by pulverization using a pre-sterilized polypropylene pestle. Pestle pulverization on ice for 2-5 minutes yielded a brown/red homogenate with some insoluble chitin fragments. After all samples in a batch had been homogenized, 350uL of blue SV RNA Dilution Buffer (containing 25-50% guanidinium thiocyanate) was added to each tube and all tubes were inverted to mix contents gently without mechanically shearing genomic DNA macromolecules. Tubes were incubated in a 70C water bath for exactly 3 minutes, then centrifuged at 14,000g for 10 minutes in a fixed-angle rotor centrifuge (Eppendorf AG, model no. 5417C) to precipitate cellular debris. Supernatant containing dissolved whole nucleic acids was transferred to fresh 1.5mL eppendorf tubes, taking care not to disturb the debris pellet; when in doubt, supernatant was left behind rather than introducing contamination from a loose pellet. Exactly 200uL of 95% ethanol (containing 5% DEPC water) was added to this supernatant and all tubes were inverted to mix. The entire volume of fluid was loaded onto a labeled Promega Spin Column Assembly, and assemblies were spun at 14,000g for 60 seconds. Eluate was discarded, and 600uL of SV RNA Wash Solution (60mM potassium acetate, 10mM tris-hydrochloride, 60% ethanol; pH7.5) was loaded onto the dry spin column. After another centrifugation at 14,000g for 60 seconds, eluate was discarded and another 250uL of SV RNA Wash Solution was

added to the dry spin column. The manufacturer's protocol was modified at this stage in order to preserve genomic DNA bound to the spin column, as digestion of gDNA "contaminants" with DNAse I was not performed. Centrifugation at 14,000g for 2 minutes completely flushed the SV RNA Wash Solution, and the dry spin column was transferred to the permanent 1.5mL eppendorf collection tube. Exactly 100uL of Promega Nuclease-Free Water (catalog no. P119E) was added to the dry spin column and allowed to incubate at room temperature for approximately five minutes. A final centrifugation at 14,000g for 60 seconds resulted in approximately 100uL of eluate containing dissolved whole nucleic acids (RNA & DNA), which was stored immediately at –80C until further processing.

To minimize the amount of sample manipulation and to conserve extract volume, aliquots were not loaded onto an agarose gel to assess the yield of RNA and DNA. Instead, extract quality was assessed indirectly through the success of downstream RT-PCR reactions.

B.1 Reverse-Transcription Amplification

Products from the genomic whole nucleic acid extraction protocols described above served as template for selective amplification of target mRNA using the reverse transcription polymerase chain reaction (RT-PCR; Edwards *et al.* 1995; Larrick & Siebert 1995; Siebert 1999). This process entailed two stages: (i) hybridization of a single oligonucleotide primer to the 3' end of single-stranded mRNA actively transcribed *in vivo*, with subsequent reverse transcription (RT) *in vitro* of those mRNA transcripts into a double-stranded species; and (ii) polymerase-mediated synthesis of the strand

complementary to the cDNA, followed by annealing of two primers permitting selective amplification of target regions (PCR). For the purposes of this study, the key advantage of RT-PCR relative to direct PCR on genomic whole nucleic acid templates was the amplification of only coding regions. Because post-transcriptionally modified mRNA containing only spliced exons acts as template for cDNA synthesis and subsequent amplification, all amplicons generated in this study were free of intronic sequence and were readily translated to amino acids.

Oligonucleotide primers used in this study had been designed previously by members of the Regier Lab for use in amplifying both EF and DDC in taxa across Arthropoda (Regier & Shultz 1997; Cho *et al.* 1995; Fang *et al.* 1997, 2000; Friedlander *et al.* 1992, 1998, 2000; Mitchell 1998; Mitchell *et al.* 1997, 2000; Regier *et al.* 2000, 2002). Historically, amplification of EF had been trivial in these taxa and the primers and amplification strategies developed in the Regier Lab were correspondingly relatively standardized. In contrast, DDC amplification was technically much more problematic, and almost every primer developed for this gene had been redesigned multiple times, sometimes on a taxon-specific basis. A comprehensive review of all documented EF and DDC primers generated in the Regier Lab was undertaken to compile all known viable primer sites in the design of amplification strategies for each of these two genes.

Table 3 presents primer pairs used to amplify regions of EF in two studies from the Regier Lab: an investigation of the utility of this gene in resolving relationships across Arthropoda (Regier & Shultz 1997) and their original study employing EF to explore systematic relationships within Heliothinae [Lepidoptera: Noctuoidea: Noctuoidae] (Cho *et al.* 1995). Strategies developed in the arthropod work are currently

standard practice in the Regier Lab, and the four fragments labeled “p”, “A’”, “E” and “C” were amplified in this study (Table 3). Figure 4 depicts the relative orientation of these primers along the mRNA molecule of the reference sequence from *Bombyx mori* [Bombycoidea: Bombycidae] (GenBank accession no. D13338; Kamiie *et al.* 1993). A single primer, m41.21rc, was used to generate cDNA the length of the desired EF fragment during the RT phase, with the terminal primer pair 30f/m41.21rc used for subsequent PCR amplification of that cDNA. Internal primer pairs were then used to generate smaller amplicons via nested PCR on the purified cDNA template.

Table 4 presents primer pairs used to amplify regions of DDC in four studies, as well as unpublished oligonucleotides currently used in the Regier Lab to amplify this gene. These primers are sorted by site along the DDC mRNA molecule, and different versions of a given primer a re grouped together. Since the complete coding sequence of DDC for a sphingid, *Manduca sexta* (Bombycoidea: Sphingidae), had been published (GenBank accession no. U03909; Hiruma *et al.* 1995; Figure 5) and was used as the reference sequence for alignment of this gene, the most stringent (i.e., longest and least degenerate) primers were assayed first for utility in RT-PCR amplification of DDC from Sphingidae. In an ideal scenario, a single primer (7.5sR) was used to generate cDNA the entire length of DDC during the RT phase, and the terminal primer pair 1.0F/7.5sR was used to PCR amplify that cDNA. However, this primer did not yield adequate product for all taxa and in these cases a smaller cDNA fragment was generated by use of 4dnR or 4sR (two variants of a primer site upstream of 7.5sR) during the RT phase. Early attempts were made to evaluate the relative performance of alternative primer variants listed in Table 4 for both RT (especially [7.5R vs. 7.5sR]) and PCR (especially [1.0F vs.

1.1vF vs. 1.2F], [1.7F vs. 1.7dF vs. 1.7sF], [1.9dF vs. 1.9sF] and [3.2dF vs. 3.2sF]) phases by assessing amplification efficiency in ethidium-bromide stained agarose gels (data not shown). Primers eventually selected for use in this study are indicated with an asterisk (** for RT primers) in Table 4 and are presented in their corresponding pairings in Table 5a. In contrast, primers preferred by the Regier Lab for amplification from non-sphingid taxa (Regier, pers. comm.) are labeled with a † (‡ for RT primers) in Table 4 and are presented in their corresponding pairings in Table 5b.

Reagent components and relative concentrations for RT reaction mixtures are presented in Table 6a. An individual RT reaction consisted of a 10uL volume, mixed in the order presented in the table. To help control for intersample variability in reaction success, the RT reagents were mixed as a "cocktail" consisting of the same ratio of components multiplied by a factor of (n+1), where n=the number of samples in a batch. This cocktail was then aliquotted into individual 0.2mL thin-walled reaction tubes prior to addition of genomic nucleic acid extract template to each. Magnesium Chloride ($MgCl_2$; 25mM stock solution) and GeneAmp PCR Buffer II (10X stock solution; catalog no. N8080010) were obtained from Applied Biosystems. Reverse Transcriptase (50 units/uL stock; catalog no. N8080018) with accompanying RNase Inhibitor (20 units/uL; catalog no. N8080119) was also obtained from Applied Biosystems, and both reagents were stored at –20C until immediately before addition as the final components in the RT cocktail. A single oligonucleotide was included (stock 20uM) to hybridize with the 3' end of targeted mRNA. Water was obtained from Regier Lab stock and was DEPC-treated, deionized and autoclaved.

After aliquotting 9.9uL of RT cocktail into each reaction tube, individual nucleic acid extracts were retrieved from –80C storage and quick-thawed in a room-temperature water bath for less than 60 seconds. Exactly 0.1uL of raw extract was added to corresponding reaction tubes and the tubes were centrifuge-pulsed to gather contents into the bottom. Reaction tubes were loaded onto a precooled (4C) 48-well block of a DNA Engine thermal cycler (model no. PTC-200; MJ Research, Inc.) and incubated at 42C for 35 minutes, followed by 99C for 5 minutes. During this RT cycling, cocktails for PCR reactions were prepared so that time between RT and PCR reactions was minimized.

Reagent components and relative concentrations for the PCR reaction mixtures are presented in Table 6b. An individual PCR reaction consisted of a 50uL volume, 40uL of which was fresh "cocktail" added to the 10uL RT reaction immediately after RT thermal cycling was complete. Magnesium Chloride, PCR Buffer II and water were as above. AmpliTaq thermostable DNA polymerase was obtained from Applied Biosystems (5 units/uL stock; catalog no. N8080156), and was kept cold at –20C until addition to the cocktail as the last component. This AmpliTaq solution contained 0.07uM of TaqStart neutralizing monoclonal antibody (7uM stock; BD Biosciences Clontech, catalog no. 639251) to enable hot-start PCR by inhibiting AmpliTaq activity below 70C. In addition, two oligonucleotide primers (20uM stock each) bookending the fragment of interest were included to bind to the 3' ends of opposite strands in the cDNA synthesized during the RT reaction. No additional dNTP were added to the PCR cocktail.

Immediately upon completion of the RT cycle, samples were transferred to an ice bath and 40uL of PCR cocktail was added to each. Tubes were briefly shaken to mix, centrifuge-pulsed to gather contents in the bottom, and reincubated on a room-

temperature MJ DNA Engine block. Touchdown thermal cycling was employed in the PCR amplification of *in vitro* synthesized cDNA (Table 6c), in order to minimize amplification of competitively superior nontarget smaller amplicons (Don *et al.* 1991). For the first 25X cycles, annealing temperature was iteratively decreased by 0.4C per cycle, while extension time was iteratively increased by 2 seconds per cycle. After these 25X touchdown cycles, traditional PCR at a static annealing temperature was conducted for an additional 13X cycles, increasing the extension time by 3 seconds each cycle. A final extension at 72C for 10 minutes completed the thermal cycling, followed by indefinite incubation at 4C.

Amplification conditions for fragments of EF and DDC were very similar, but in consultation with Regier Lab personnel some modifications were introduced to accommodate the more troublesome DDC amplifications. All components of the RT phase were identical between genes, except that stringency was reduced for DDC by increasing the concentration of reverse primer from 2uM to 3uM. In the PCR phase, changes to the DDC protocol were more extensive: $MgCl_2$ concentration was increased from 2.5mM to 3.0mM; forward primer concentration was doubled from 0.5uM to 1.0uM; and reverse primer was increased by 50%, from 0.6uM to 0.9uM. These relaxations permitted more consistent RT-PCR amplification of DDC fragments from the same extracts as had been assayed for EF under more stringent conditions. In fact, because the extracts were never assayed via electrophoresis, presence/absence of EF amplicons through the above procedure served as a *de facto* check on the quality of the extraction procedure for a given sample.

Upon completion of the PCR phase, samples were transferred to ice and exactly 10uL of 60% glycerol loading dye (w/w in 1X TAE) containing trace bromophenol blue was added to each sample. After brief vortexing, 10uL of this sample was loaded onto a 1.4% agarose analytical gel (w/v in 1X TAE; Fisher DNA Grade High Melting Electrophoresis Grade, catalog no. BP164-500). This amounted to destructively sampling 15% of RT-PCR product at a final glycerol concentration of 10%(v/v). Samples were electrophoresed at approximately 120V for approximately 90 minutes, until the bromophenol dye band had traveled to approximately 2.5cm from the gel edge. Transillumination under UV light revealed whether viable RT-PCR product had been produced, and intensity of bands relative to known bands in a comigrating DNA ladder permitted rough quantification of product size and concentration.

B.2 Gel Purification of RT-PCR Products

RT-PCR products, which themselves served as template for downstream nested PCR (see below), were gel purified to insure that the desired fragments and only the desired fragments were retained. Once analytical gel electrophoresis confirmed successful RT-PCR amplification, the remaining 50uL of product containing glycerol loading dye was loaded onto a large well of a 1.1% agarose purification gel (w/v in 1X TAE; Continental Lab Products AgarGel Low Melt Medium Fragment Agarose, catalog no. 5413.100). Samples were electrophoresed in fresh 1X TAE, in a cleaned gel apparatus covered with an opaque dark cloth to prevent UV damage from ambient light, at approximately 100V for approximately 2 hours. The entire gel was transferred on plastic wrap to a UV plate, and under brief UV illumination cubes containing the

fragment of interest were excised from the gel using an autoclaved steel spatula. Signature banding patterns for each sample in these purification gels were directly compared against the original RT-PCR analytical gel photos to verify that samples had not been crossed. These gel cubes were transferred to sterile 1.5mL eppendorf tubes and massed to quantify the amount of agarose containing the RT-PCR product of interest.

Double-stranded DNA within this excised gel slice was purified via the Promega Wizard PCR Preps DNA Purification System, exactly according to manufacturer suggested protocols (Promega Technical Bulletin No. 118). Instead of elution in TE, however, purified products were incubated at room temperature for approximately 5 minutes and eluted in 50uL of Promega Nuclease Free Water (part no. P119E). A 7.5uL aliquot of each purified eluate was transferred to a new eppendorf tube containing 2.5uL of 60% glycerol loading buffer (w/w in 1X ABI 10X PCR Buffer II and 2.5mM $MgCl_2$) containing trace bromophenol blue. This loading buffer more closely mimicked background composition of all other amplification products run on agarose gels. All 10uL of the gel purification/loading buffer mixture was loaded onto a 1.4% agarose analytical gel; amounting to destructive sampling of 15% of gel-pure RT-PCR product at a final glycerol concentration of 15%(v/v). One or both of two DNA ladders was loaded into an adjacent well: (i) MBI Fermentas pUC Mix Marker 8 (catalog no. SM0302); or (ii) BioRad Precision Molecular Mass Standard (catalog no. 170-8207). Incorporation of these ladders permitted finer simultaneous assessment of both gel-purified fragment size and product concentration. The total mass of DNA in each band of the ladders was calculated under various loading volumes and used to calibrate an estimation of purified product concentration by comparing bands of similar intensity. In lieu of other

quantitation methods (e.g., spectrophotometry, fluorimetry), this approach permitted calculation of product concentration and tailoring of template amount contributed to downstream applications (i.e., nested PCR and direct sequencing).

B.3 Nested PCR Amplification

In ideal cases, a primer binding to the 3' end of targeted mRNA (e.g., m41.21rc for EF; 7.5sR for DDC) yielded viable RT-PCR amplification through much of the gene's coding region. Because this product was large (>1kb) and often extremely weak in electrophoretic assays, a round of nested PCR amplification based on those purified RT-PCR templates was pursued to generate fragments of manageable lengths (approximately 500bp) at sufficiently high-copy number for direct DNA sequencing. Nested PCR provided a powerful technique to amplify desired subsequence from even extremely weak RT-PCR amplicons, because those products had been gel purified and were guaranteed to contain the sequence of interest if the RT-PCR had been at all effective.

Nested PCR was most often used to amplify subsequence from within larger RT-PCR products, using pairs of primers oriented approximately 500bp apart on the molecule (for EF, see Table 3 & Figure 4; for DDC, see Table 4 & Figure 5). Reagent compositions for nested PCR reactions are presented in Table 6d; contrary to conditions for RT-PCR, reagent compositions were identical between EF and DDC fragments. Ideally, nested PCR reactions received 1.0uL of template (2% of the final RT-PCR gel purification elution), but this amount was varied per sample to between 0.5-5.0uL for especially strong or weak RT-PCR templates, respectively. Thermal cycling parameters for nested PCR were very similar between the two genes, except that the annealing

temperature for EF was elevated 10C higher than for DDC; this higher annealing temperature created much more stringent binding conditions between the EF cDNA and nested primers, but with little reduction in yield.

A related reamplification strategy was used for smaller amplicons for which recovery of tangible nested PCR product had been difficult. All primers in this study incorporated 18bp M13 tails for compatibility with sequencing chemistry (see bottom of Tables 3 &4), so the termini of all nested PCR products were effectively end-labeled with M13. In cases where insufficient nested product was obtained from RT-PCR template for sequencing, gel purified nested PCR products were subjected to the same nested PCR conditions with M13 primers. Reactions of this type generated high copy numbers of entire nested fragments, and only failed when nested PCR had itself failed.

B.4 Gel Purification of Nested PCR Products

Subsequence amplification via nested PCR with internal primers or terminal M13 primers usually yielded amplification in high copy number. These products were gel purified using exactly the same protocol as detailed above for RT-PCR products. After electrophoretic concentration estimation, these products were submitted for direct DNA sequencing.

C. Automated Sequencing

Electrophoretic assay of purified PCR products against the mass ladders described above resulted in concentration estimates for every fragment, ranging from 0.67-

10.67ng/uL. DNA sequencing along both strands was performed on an Applied Biosystems DNA Sequencer (model 3100) at the UMBI CBR core sequencing facility. This facility recommended submission of 15uL of purified template at concentrations between 5-20ng/uL. Despite these guidelines, template concentrations estimated electrophoretically as low as 0.67ng/uL by the above method returned viable sequencing reactions. Templates spanning the range of concentrations were submitted to the core facility in trial reactions, and a correlation was drawn between template concentration and sequencing signal intensity for each of the four bases (data not shown). This permitted prediction of sequencing success on the basis of electrophoretic intensity, and confirmed that viable sequence could be obtained from 15uL of any template yielding a band comparable in intensity with even the lightest ladder bands.

D. Sequence Editing

Despite efficient base-calling algorithms in the ABI 3100 analysis software, each chromatogram was inspected visually to confirm proper translation of electrophoretic data into a nucleotide text string. Oddities during sequencing reactions or electrophoresis caused disturbances in the chromatograms which were remedied on a case-by-case basis. All raw ABI chromatogram files were imported into Sequencher (version 4.1.2; Gene Codes Corporation 2000) for alignment. Conflicting signal in a particular chromatogram (e.g., overlapping peaks) was assigned the appropriate binary IUPAC ambiguity code, and tertiary and quaternary ambiguities were assigned 'N'. Both forward and reverse strands of a given PCR product were edited independently in this way. Forward and reverse-complemented reverse sequences of a given fragment were then aligned at high

match percentage thresholds to generate a consensus "double stranded" sequence. Ambiguities were resolved where possible and ambiguity codes were preserved if the base could not be resolved. Any gaps inserted by Sequencher's alignment algorithms during comparison of forward and reverse strands were resolved by direct inspection of the opposing chromatograms, and were usually attributed to poor quality in one chromatogram (e.g., at the end of a sequence) which was readily resolved by the other. Sequencing single fragments in both directions provided a layer of redundancy which improved confidence in the deduced consensus sequences.

Gene contigs were assembled by aligning both forward and reverse strands of all fragments for a sample at high match threshold, anchoring both strands of a single fragment at regions of overlap with neighboring fragments. Any gaps inserted by Sequencher's alignment algorithms during contig assembly were resolved by direct inspection of overlapping chromatograms. Oligonucleotide primer motifs were tagged in each alignment, and primer sequence was deleted from all internal fragments to create a seamless consensus sequence. Terminal primer sites (30f and m41.21rc for EF; 1.0F and 7.5sR for DDC) were retained in the consensus only to provide bookend sequences for the bounds of mRNA investigated in this study. These primer sequences were truncated prior to phylogenetic analyses.

For EF, the same four fragments (p, A', E, C; Table 3 & Figure 4) were obtained from all 54 ingroup samples and contig assembly resulted in a consensus sequence of 1,274bp, including terminal primers. A single exception applied to *Neococytius cluentius* (UMD accession WJK-03-1949), for which viable purified RT-PCR and nested PCR

products were assayed electrophoretically, but for which every forward and reverse sequence was illegible due to uniformly and prohibitively high background noise.

For DDC, three fragments (X, Y, Z; Table 4 & Figure 5) were obtained from each of 42 ingroup samples and contig assembly resulted in a consensus sequence of 1,373bp, including terminal primers. Interestingly, *Neococytius cluentius* was among these "well-behaved" samples, indicating the intractable sequencing for EF in this sample was particular to that gene. For the remaining 12 samples, a fourth fragment (W; Table 4 & Figure 5) was sequenced to compensate for difficulty obtaining strong amplification in the middle of the DDC fragment. This strategy provided effective sequence through the entire range of a homologous DDC fragment for all 54 ingroup samples.

E. Sequence Alignment

The double stranded consensus sequence from each gene was aligned independently against an orthologous reference sequence obtained from *Bombyx mori* for EF (Figure 4; GenBank accession no. D13338; Kamiie *et al.* 1993) and from *Manduca sexta* for DDC (Figure 5; GenBank accession no. U03909; Hiruma *et al.* 1995). Instances in which novel sphingid sequences contained gaps with respect to the reference sequences were interpreted as artifacts of the chromatogram editing process. In these cases, corresponding positions in the original chromatograms were re-examined under the null hypothesis that the reference sequence contained the "correct" number of bases. In all cases, reconciliation was possible on the basis of the chromatogram traces, so no artifactual N's were introduced to achieve proper sequence length. While this procedure introduced an obvious bias toward the reference sequences, it was expected that in coding

regions of genes of such critical biochemical importance, insertions and deletions altering the entire reading frame for protein translation would be extremely improbable.

After each sample's consensus sequence had been aligned against the reference sequence, a final whole-family alignment across 54 samples was performed in Sequencher. This was a trivial procedure, as each sequence had already been standardized against the reference sequences and no gaps were inserted by Sequencher.

Sequence Data Collection in silico

In addition to original nucleotide sequence data collected for 54 novel sphingid samples described above, the National Center for Biotechnology Information (NCBI) Nucleotides Database (GenBank) was mined for all representatives of Lepidoptera for which orthologous nucleotide sequence fragments of both nuclear genes had been submitted. The set of results from each of several search strings submitted to the NCBI Entrez search engine on 06 April 2004 was downloaded and the union of all unique sequence accessions was compiled into a master list. This list was filtered for a nonredundant set of taxa containing both novel sphingid ingroup sequences and a range of potential outgroup candidates for phylogenetic analyses.

Kristensen (1999) established rigorous systematic hypotheses of monophyly for lepidopteran families based on analyses of morphological synapomorphies. While the monophyly of Sphingidae has been regarded as firmly established on morphological grounds (Lemaire & Minet 1999; Minet 1991, 1994), this study sought an independent test of that premise using molecular data and modern systematic methods. The aim of mining GenBank for lepidopteran sequences was to permit multiple phylogenetic

analyses conducted under different taxon samples. Of special interest was the robustness of a node depicting monophyletic Sphingidae in trees for which outgroups consisted of either all other available lepidopteran sequences or all non-sphingid bombycoid sequences. The classical concept of a monotypic superfamily Sphingoidea has been collapsed as a single family within superfamily Bombycoidea (Brock 1971; Common 1990; Minet 1986), suggesting the latter may be profitably explored for the sister lineages to Sphingidae.

Sampling variation in the GenBank Nucleotide Database prevented compilation of both EF and DDC sequences for a single broad set of lepidopteran taxa. Instead, sequences were compiled separately for each gene across as broad a taxon set as possible, according to the following choice hierarchy:

(i) at least one EF and one DDC accession per subfamily across all Lepidoptera was selected;

(ii) less than five accessions per gene per family were retained to avoid gross taxonomic overweighting and tree imbalance (especially for Noctuoidea: Noctuidae and Papilionoidea: Nymphalidae);

(iii) one accession per tribe throughout Bombycoidea (Lemaire & Minet 1999; Minet 1991, 1994) was selected, these taxa being regarded as most closely related to the ingroup and representing the best outgroup candidates;

(iv) any sequence from Sphingidae which did not exactly overlap species sequenced *de novo* in this study was retained;

(v) accessions for which both EF and DDC sequences were derived from a single species or specimen were preferred, if possible, to accessions requiring sampling from multiple specimens or taxa;

(vi) accessions containing nominate genera of any given tribe, subfamily or family were preferred over other taxa;

(vii) GenBank accessions containing the longest unambiguous sequences were preferred to improve data richness;

(viii) if all above criteria did not yield a single unambiguous choice, a GenBank accession was selected randomly from the remaining candidates.

Even after implementing criterion (vii) above, almost all retrieved GenBank sequences were shorter than the novel sequences generated in this study. All sequences were aligned against the *Bombyx* (EF) or *Manduca* (DDC) reference sequences under the same null hypothesis that the reference sequences contained the "correct" number of bases. Gaps suggested by Sequencher were inspected across all lepidopteran sequences and persistent indel events were marked with missing data characters (i.e., 'N' ambiguity codes). In addition, terminal ends of sequences were filled with missing characters until every sequence agreed in length with the reference sequences.

An exception to the above alignment strategy applied to the two DDC sequences from Nepticuloidea [Glossata: Heteroneura] (GenBank contained no EF sequences for this superfamily). These sequences aligned against each other and all other Lepidoptera only at very low match thresholds (approximately 60%). Alignment via the MATCHER utility of the European Molecular Biology Open Software Suite (EMBOSS) package through the Nationale Genomforschungsnetz (NGFN) web interface revealed numerous

gaps relative to all other Lepidoptera, as well as a multi-base indel event near DDC primer 3.3sF (Figure 5). While an intriguing finding, exploration of these alignment difficulties was beyond the scope of the current study, so both representatives of Nepticuloidea were excluded from phylogenetic analyses owing to their difficult homology assessment. Because sequence sampling from GenBank was an inherently biased process with broad fluctuations in breadth and depth of taxon sampling across the Lepidoptera, it was assumed that omission of these sequences would have miniscule effects on the inclusion of Lepidoptera outgroup sequences to address questions of Sphingidae monophyly.

Data Matrix Construction

Global alignments of consensus sequences were conducted for each gene, separately for ingroup Sphingidae (Table 8; 67 samples for EF, 65 samples for DDC) and outgroup Lepidoptera (Table 9; 51 samples for EF, 40 samples for DDC). These alignments were then combined into a single master Sequencher file for each gene, followed by a final round of inspection of suggested gaps. Upon completion, all sequences were exported into a NEXUS file (Maddison *et al.* 1997) in preparation for phylogenetic analyses in PAUP* (version 4.0b10; Swofford 2003). In this way, three separate nucleotide matrices were assembled for phylogenetic analyses: (a) all EF data; (b) all DDC data; (c) combined EF&DDC data.

After these nucleotide matrices had been assembled, corresponding amino acid sequences were derived by conceptual translation in three forward frames using the standard genetic code. Terminal oligonucleotide sequences were trimmed from each

sequence and the resulting internal fragment was imported to the TRANSEQ utility of EMBOSS. Amino acid output was reimported into a parallel set of NEXUS files in PAUP*.

Character Information Content

Nucleotide data matrices were examined to determine the number of positions at which character states were invariant (constant) across taxa, were unique to only a single taxon (autapomorphic), or were suggestive of a taxon bipartition (parsimony informative). Values were tabulated for each gene individually and for the combined EF&DDC data matrix, and across four partitions by codon position (ntall, nt1, nt2, nt3). This operation was repeated separately for each of four taxon sets: (i) All Lepidoptera; (ii) All Bombycoidea; (iii) Ingroup Sphingidae only; and (iv) Sphingidae with two outgroups (Bombycidae and Saturniini; see below). This scheme was intended to provide a first approximation of agreement in the nature of character state change across different partitions and taxa sets.

Mean empirical nucleotide base frequencies, adjusted for missing data, were calculated in PAUP* as a first step to investigate the potential that base composition bias could be responsible for perceived phylogenetic signal. Empirical base frequencies were calculated for every sequence to provide a direct assessment of base compositional bias. Counts of ambiguous (IUPAC codes) and missing ('N') data were also provided to gauge the variance in data content for each sequence, and was especially important for heterogeneous accessions obtained from GenBank.

Parsimony-Based Preliminary Analyses

Analyses based on the criterion of Maximum Parsimony (MP) were conducted across all four taxon sets on each of four data partitions: (a) ntall for EF; (b) ntall for DDC; (c) ntall for combined EF&DDC, (d) nt1&nt2 for combined EF&DDC. EF and DDC data were analyzed separately to tease apart potentially subtle differences in phylogenetic signal contributed by each gene, as well as to shed light on the robustness of phylogenetic signal to minor changes in taxon sampling due to nonoverlapping taxa sampled from GenBank. For the combined data set, ntall versus nt1&nt2 partitions were analyzed separately to compare the effects of excluding hypervariable third codon positions, as advocated by Regier 2001. All MP analyses were conducted on unordered and equally weighted characters, with constant characters excluded (i.e., autapomorphies and parsimony informative sites both included).

A. PTP Test of Information Content

The Permutation Tail Probability (PTP) test as implemented in PAUP* was conducted as a crude indicator of the presence of phylogenetic signal in each nucleotide data matrix (Faith 1991; Faith & Cranston 1991). Distribution of character states across taxa might be correlated due to either shared ancestry (i.e., phylogenesis has imposed order on the data) or stochasticity (i.e., order in the data is an artifact of random nucleotide substitutions independent of evolutionary history). The PTP test was designed to quantify the degree to which order in character state distributions has an evolutionary versus a stochastic basis.

Pseudoreplicate data matrices were constructed by randomly permuting character states within each nucleotide position across taxa. Using tree length as an indicator of phylogenetic structure in the fit of data to a topology, the length of the MP topology obtained under the empirical data was used as the test statistic. A null distribution was constructed by calculating the lengths of the MP trees recovered under each pseudoreplicate data set. Under the null hypothesis that character states in the empirical data matrix were correlated due to chance alone, it was expected that each randomly permuted data set would result in a tree length comparable to the original test statistic. The P value gave the proportion of all pseudoreplicated data matrices yielding an MP tree comparable in length. Small P values indicate that the structure in the empirical data is not a product of chance, refuting the null hypothesis of no phylogenetic structure. All PTP tests were calculated with at least 1,000 pseudoreplicates. In addition, the number of steps separating the original MP tree from the next most parsimonious tree derived from all permuted data was recorded as an indication of severity in parsimony penalty imposed by randomizing character states.

B. Parsimony-Based Searches

Phylogenetic analysis under the criterion of Maximum Parsimony (MP) was conducted across four taxon sets for the four data partitions listed above. There are $\Pi(2i-5)$ unrooted bifurcating trees depicting patterns of relatedness among T terminal taxa, where i varies from 3 to T (Swofford *et al.* 1996). For the number of taxa investigated in each data set in this study (ntax $\geq$ 64), the number of possible topologies in treespace rendered exhaustive MP search algorithms untenable. Therefore, heuristic search

algorithms implemented in PAUP* were employed to sample tree and data space for optimal topologies.

Starting topologies were computed heuristically via at least 1,000 furthest stepwise addition sequence replicates, holding 10 trees at each step (hold=5 for more computationally intensive analyses). These starting topologies were permuted via the tree-bisection-reconnection (TBR) branch-swapping algorithm, employing steepest descent. All minimal trees were saved ("MulTrees" option) and zero branch lengths were collapsed.

After each analysis, the set of saved trees was filtered for shortest length. In addition to tree length, number of MP trees recovered from each search and the number of islands encountered during the search was also recorded, as an indication of heterogeneity in data space (Maddison 1991; Page 1993). Existence of multiple islands of closely related topologies indicates a danger of becoming trapped on a local optimum when non-exhaustive search algorithms (e.g., heuristic search methods) are used. Small numbers of encountered islands were taken as a suggestion of uniformity in tree space pointing to a single globally optimal topology.

To explore the effects of tree space heterogeneity on the ability for heuristic algorithms to identify globally optimal topologies, four trials of identical heuristic searches (including the same random number seed) were launched differing only in number of replicates: 10, 100, 1,000 and 10,000. Results from each trial were filtered for topologies of shortest length, and the set of recovered trees compared across trials. Trials completing higher numbers of stepwise addition sequence replicates were expected to more adequately explore a highly stratified and complex tree space and be more likely to

locate globally optimal topologies. For simpler, more homogeneous tree space, trials completing only 10 or 100 heuristic search replicates were expected to perform equally well at locating globally optimal topologies.

C. Nonparametric Bootstrap Analysis

Trees recovered from MP heuristic searches depicted taxon relatedness in a series of nested taxon bipartitions. Branch lengths of individual taxon bipartitions indicated the number of inferred synapomorphies supporting those relationships, but offered little information about the robustness of or confidence in the branches. Under the assumption that an empirical data matrix represents a finite sample from an underlying character space for the taxa being compared, nonparametric boostrapping is a method developed to approximate the underlying distribution from which those data arose by random resampling with replacement from the empirical data (Felsenstein 1985; Harshman 1994; Sanderson 1989, 1995; Wilkinson 1996). Pseudoreplicate data matrices were constructed via bootstrap resampling and each was subjected to the same MP heuristic analysis (except only 10 or 100 random addition sequence replicates were conducted per bootstrap pseudoreplicate). Optimal trees derived from heuristic searches on each bootstrap pseudoreplicate were compared across pseudoreplicates and each taxon bipartition was assigned a percentage indicating the proportion of instances it was recovered. The resulting percentages do not represent strict confidence statements about the accuracy of the taxon bipartition, but indicate the relative degree of internal consistency in the data suggesting that bipartition.

At least 1,000 pseudoreplicates were constructed for each bootstrap analysis in an effort to increase the *precision* of the bootstrap proportion, although this had no impact the *accuracy* of the taxon bipartition (Felsenstein & Kishino 1993; Hillis & Bull 1993). Bootstrap values below 50% were interpreted as insufficient evidence for the inference method to make an assertion about a particular taxon bipartition given the data at hand. The number of internal branches in the topology receiving bootstrap support >50% was tabulated and compared to the total possible number of internal branches in a fully dichotomous rooted tree: (T-2), where T is the number of terminal taxa.

D. Incongruence Length Difference (ILD) Test

Phylogenetic inferences were drawn from two separate sources of information (EF vs. DDC), whose patterns of evolutionary change may or may not be congruent. The Incongruence Length Difference (ILD; also called the partition homogeneity) test was implemented in PAUP* in an attempt to explore interactions between phylogenetic information in these data (Darlu & Lecointre 2002; Dowton & Austin 2002; Mason-Gamer & Kellogg 1996; Swofford 2003). The null hypothesis for the ILD test ignored the functional distinction between EF and DDC as separate genes, and assumed that both independent data partitions were derived from the same underlying pool of homogeneous characters. Assuming that EF and DDC data represent effectively random subpartitions of a single underlying distribution lead to the expectation that information regarding taxon relationships contained in both partitions would be fundamentally the same.

Assuming perfect agreement between partitions, the MP score of a tree derived from a combination of both genes into a single data set (L_{EF+DDC}) should be

approximately equal to the sum of lengths of the two trees derived from each partition separately ($L_{EF} + L_{DDC}$). In contrast, the MP score of a tree derived from a combination of two perfectly disagreeing genes should result in a tree much longer than the sum of their individual trees, since conflicting (homoplasious) signal will interact negatively to inflate overall length.

The original EF and DDC components of the combined EF &DDC data matrix were randomly repartitioned by scrambling characters between genes to produce two pseudoreplicate data matrices of the same size as the originals. The MP tree of each pseudoreplicate was determined heuristically and the tree length scores were added together ($L_1 + L_2$). If this sum was no greater than the sum of MP trees derived from EF and DDC individually ($L_{EF} + L_{DDC}$), then characters within each original partition were interpreted as not providing significantly conflicting signal. The proportion of pseudoreplicates for which random repartitions resulted in MP trees with a better sum of scores than the original was reported as the test's P value. Large P values suggest the ILD test failed to reject the null of partition homogeneity, suggesting the data partitions contain compatible phylogenetic signal. Small P values refute the null hypothesis, suggesting the two partitions are in significant conflict. Outcomes of the ILD test have been used as evidence to argue both for and against combining data into a single analysis (Bull *et al.* 1993; Chippindale & Wiens 1994; DeQueiroz *et al.* 1995; Huelsenbeck *et al.* 1996a; Mitchell *et al.* 2000; Olmstead & Sweere 1994; Weller *et al.* 1994; Wiens 1998).

ILD tests were conducted with at least 1,000 pseudoreplicates, each of which was subjected to 10 random stepwise addition replicates, holding 5 trees at each step and TBR branch swapping. The number of steps difference between the original ($L_{EF} + L_{DDC}$) and

the best pseudoreplicate ($L_1 + L_2$) was tabulated; negative values of this difference were taken as support for the null hypothesis of data homogeneity (i.e., some random repartitions generated *better* sums of MP tree scores), although the P value may not reflect this.

Evaluating Alternative Parsimony Topologies

In addition to generating a strongly supported phylogenetic hypothesis of relationships within the Sphingidae ingroup, the preliminary parsimony analyses described above were also intended to pare down the broad range of potential outgroup taxa from the candidate lepidopteran sequences obtained from GenBank. Once a pair of appropriate outgroup sequences had been selected by the MP criterion, topologies consisting of the Sphingidae ingroup and 2 outgroups were then used to establish initial conditions for iterative parameter and topology estimation in Maximum Likelihood (ML) analyses. Employing a ML model-based approach to phylogenetic analysis was expected to more accurately reflect the underlying processes of nucleotide substitution producing the empirical patterns observed in the data matrices (Felsenstein 1973, 1981a; Fukami & Tateno 1989; Gaut & Lewis 1995; Goldman 1990; Huelsenbeck & Crandall 1997; Kishino & Hasegawa 1989; Rogers 1997; Saitou 1988, 1990). In addition, it has been demonstrated that ML-based phylogenetic analyses are both more appropriate than MP under a wide range of conditions and are also more robust than MP with respect to minor violations in their underlying models of sequence evolution (Felsenstein 1978, 1981b; Felsenstein & Sober 1986; Huelsenbeck 1995; Sober 1984; Tateno *et al.* 1993; Yang 1994, 1996).

MP analyses on each data matrix generated a set of equally optimal topologies, so selection of a single tree from among these alternatives was imperative to reduce the potential number of starting points from which computationally intensive ML searches would be launched. Each topology was assessed for congruence across data partitions according to the criterion of maximum parsimony, and the most universally compatible trees were selected as input starting topologies for maximum likelihood analyses. Using MP trees as input strongly biased the initial conditions of ML searches in the direction of MP tree space, but significantly reduced the range of taxon bipartition parameter space required for evaluation relative to ML searches starting from completely random topologies.

Character state changes inferred from MP for each partition were mapped onto all candidate topologies from each data set, and a set of parsimony metrics was calculated to describe the performance of that topology as an explanation of the character state distributions for that partition. Raw tree length provided a relative measure of the penalty imposed by forcing character state distributions from one data set onto another partition's MP tree. This penalty was also expressed as a percentage increase in tree length (%diff) relative to the shortest length score obtained for that partition across all candidate MP trees; thus, the topology yielding the lowest %diff averaged across all partitions was selected as the best MP tree for that data set. Similarly, consistency (ci) and retention (ri) indices (Farris 1989a,b; Kluge & Farris 1969) were calculated for each instance of character state mapping and the topology with highest mean ci and ri values across all partitions was selected as the best MP tree for that data set.

Those MP trees with lowest tree length & %diff, and high ci & ri averaged across all data partitions were selected as MP-optimal topologies upon which subsequent ML parameter estimation was conducted. Thus, three "best-guess" topologies were selected from results of MP analyses on EF, DDC and combined EF&DDC data for a 66-taxon set (iv) consisting of all 64 sphingid taxa shared between these genes as well as two selected bombycoid outgroup taxa.

Selection of a Model of Nucleotide Substitution

The key "disadvantage" of conducting phylogenetic analyses under the optimality criterion of maximum likelihood is decreased feasibility in computing tree scores when using parameter rich models of nucleotide substitution. At the expense of evaluating a broad range of more simplistic ML models which may have yielded equally viable topologies, the present study employed the most generalized and parameter rich model of nucleotide substitution for ML analysis of these data.

The general time reversible (GTR) model is founded upon a separate instantaneous relative rate parameter (expressed as number of substitutions per site per unit branch length) for each of the twelve possible transformations among the four character states (A,C,G,T) in these nuclear protein coding genes (Lanave *et al.* 1984; Rodriguez *et al.* 1990; Swofford *et al.* 1996). This model is time-reversible, however, so forward and backward transformations are assumed to occur at equal rates, reducing the total number of relative rate parameters to six. In addition, the GTR model assumes that the four nucleotide bases occur in the data matrix at separate equilibrium frequencies (i.e., $\pi_A \neq \pi_C \neq \pi_G \neq \pi_T$), and these frequencies remain unchanged over time. Probability of

change from nucleotide i to j is assumed to be a Markov process independent of i, and proportional to the equilibrium frequency of j.

This nucleotide substitution model makes no allowance for differences in patterns of character state change between independent sites along the molecule. For example, different portions of a gene may be subject to variable functional constraints, effectively altering the degree to which nucleotides in those positions are likely to change. An extreme example of such among-site rate heterogeneity is the special case where some sites are constrained to *never* vary. Ignoring the phenomenon that some sites may never change while others do effectively biases inference of character state change to underestimate branch lengths (Churchill *et al.* 1992; Hasegawa *et al.* 1985; Reeves 1992; Sidow *et al.* 1992). Therefore, a parameter was included in the GTR model to account for these invariant sites (I) by assigning a probability that any particular character is free to vary. Furthermore, characters which are assumed to vary may do so at different rates, and a parameter can be added to the model to account for these differences in the rates of character change. A discrete approximation to the gamma distribution provides a range of potential nucleotide change probabilities, conveniently defined by a single shape parameter (G). Addition of single shape parameter to the GTR model explicitly accounted for differences in the propensity for nucleotide change between presumably independent nucleotide positions along the molecule (Buckley *et al.* 2001; Felsenstein 1981a; Gaut & Lewis 1995; Gu *et al.* 1995; Hasegawa *et al.* 1991; Sorhannus & van Bell 1999; Steel 1993; Sullivan *et al.* 1999; Sullivan & Swofford 1997; Yang 1993, 1994).

Character states which are identical between taxa at a given site may have never changed in the time since those taxa diverged, or they may have changed repeatedly and

randomly converged on the same state. Incorporation of I and G parameters was intended to explicitly account for both scenarios generating observed nucleotide distributions. This highlighted a key distinction between MP and ML analyses, because likelihood-based inference engines were permitted to make use of all characters, even those which parsimony deems uninformative (i.e., constant and autapomorphic characters).

Likelihood-Based Analyses

MP topologies selected from analyses of each data partition were used as independent starting hypotheses for estimation of GTR+I+G nucleotide substitution model parameters. The likelihood score for a fixed starting topology was calculated after parameters for a GTR model (5 relative rate parameters of a 6-class substitution matrix and 3 of the 4 equilibrium nucleotide frequencies), with assumed proportion of invariable sites (I) and among-site rate heterogeneity (G; i.e., the alpha shape parameter in a discrete approximation with 8 categories to the gamma distribution), were all estimated from the data. Initial branch lengths on the starting topology were estimated via the Rogers-Swofford approximation method suite of default options in PAUP*. These initial ML parameter estimates were then fixed in the GTR+I+G model to permit calculation of likelihood scores during a heuristic search ('MulPars' option in effect, steepest descent off, collapsing branches with length less than or equal to 10^{-8}) employing TBR branch swapping based on the starting MP topology. This heuristic search resulted in a first-pass ML topology, the taxon bipartitions of which were then fixed in order to re-estimate model parameters. Re-estimated parameters were again fixed in a revised GTR+I+G

model used to calculate likelihood scores on trees generated during 10 random stepwise addition heuristic searches with SPR branch-swapping, holding 1 tree per step, with all other settings as above. The topology from these heuristic searches with highest likelihood (i.e., the second-pass ML topology) was then fixed for parameter re-estimation. This iterative parameter estimation / ML search cycle was continued through four passes, and GTR+I+G model parameter values were checked for convergence after each pass.

The ML search scheme detailed above was conducted nine times: for each of the three data sets (i.e., EF, DDC, combined EF&DDC) based on each of the three independently derived MP starting trees. Parameter values and ML topologies for a given data set derived after four iterations on each of the starting trees were then compared across starting trees to check for global convergence. The set of all unique ML topology/parameter values from a given data set was selected as the optimal ML estimate of relationships within Sphingidae.

Finally, in an attempt to select a single globally optimal topology of relatedness among sphingid genera, ML scores for every candidate MP and ML topology were calculated for each data set after convergent GTR+I+G model parameters particular to those data had been fixed. These likelihood score calculations were performed as above, except that the discrete approximation to the gamma distribution consisted of 16 categories.

RESULTS

Taxon Sampling

As of fall 2003, the UMD Lepidoptera Collections Database (FileMaker Pro, version 6.0) contained 3,608 records containing collections information for more than 5,600 specimens with known determination data across 34 superfamilies, 89 families, 945 genera and 1,477 species of Lepidoptera. A total of 350 specimens across all three subfamilies of Sphingidae was collected expressly for this research and accessioned into the UMD Lepidoptera Collections (Table 10). Of these freshly obtained specimens, 55 were processed for genomic nucleic acid extraction, RT-PCR amplification of EF and DDC fragments and sequencing (Table 8). One specimen [UMD accession number IJK-02-0107: *Compsulyx cochereaui* (Smerinthinae: Ambulycini)] failed to produce any viable RT-PCR products after multiple attempts at extraction from freshly dissected tissue. Failure to obtain amplification products from this specimen collected in New Caledonia in April 2001 was attributed to poor preservation conditions, as the detailed history for this specimen could not verified. One other specimen [accession number WJK-03-1949: *Neococytius cluentius* (Sphinginae: Sphingini)] yielded exceptionally strong RT-PCR products for both EF and DDC, but failed to produce clean sequence for any EF fragment despite multiple rounds of gel purification; DDC sequence for this specimen was excellent.

In addition to the 54 ingroup Sphingidae sequenced *de novo* in this study, EF sequence for another 14 species and DDC sequence for another 11 species was obtained from the NCBI GenBank nucleotides database. Almost all of these (13 species for EF, 10 species for DDC) were obtained from the Regier 2001 pilot study. The *Manduca sexta*

(Sphinginae: Sphingini) DDC sequence from Regier 2001 was replaced by GenBank accession number U03909 (Hiruma *et al.* 1995) and used as the reference sequence against which all others were aligned. Sequences for the remaining three species in Regier 2001 [*Hyles lineata* (Macroglossinae: Macroglossini: Choerocampina), *Paonias myops* (Smerinthinae: Ambulycini), *Lapara coniferarum* (Sphinginae: Sphingini)] were generated *de novo* in this work because original specimens from which the sequences had been derived could not be verified. Finally, EF sequence for *Proserpinus clarkiae* (Macroglossinae: Macroglossini: Macroglossina) was obtained from Caterino *et al.* (2001), but comparable DDC sequence from the same species could not be obtained.

Sphingid genera sampled in this study are marked in Table 2, distributed across the complete genus-level classification scheme provided by Kitching & Cadiou (2000). Forty-eight (24%) of the 201 recognized genera in Sphingidae were sampled, distributed heterogeneously across the family. In Smerinthinae 11 (14%) of 78 genera were sampled overall: 8 genera (14%) inside the Smerinthini, 2 genera (20%) from Ambulycini and a single genus (*Hopliocnema*) from Sphingulini. Sampling was much more dense inside Sphinginae, where 13 (34%) of 38 genera were sampled overall: 10 genera (30%) inside the Sphingini and 3 genera (60%) from Acherontiini. For the most diverse subfamily, Macroglossinae, 24 (28%) of 85 genera were sampled overall: 12 genera (46%) from Dilophonotini, 5 genera (12%) from Macroglossina (Macroglossini), 6 genera (40%) from Choerocampina (Macroglossini) and a single genus (*Eumorpha*) from Philampelini.

Homologous sequences from outgroup taxa were obtained by mining the NCBI GenBank Nucleotides Database under the search parameters and selection criteria described above. Table 7 presents the number of hits and their distribution across

taxonomic levels within Lepidoptera for several similar search strings targeting both EF and DDC sequence. For EF, a single search string ("elongat* AND lepidopt*[organism]") yielded the most inclusive set of 419 hits distributed across only 9 (20%) of the 46 lepidopteran superfamilies. Many other permutations of "<gene> AND <taxon>" search strings were attempted, but none retrieved any hits not already captured by this top query (data not shown). Two examples are given to demonstrate that subtle changes in text strings submitted to the Entrez Browser can have substantial impacts on the extent of database space explored by the search engine. For example, the slightly more specific query "elong* fact* AND lepidopt*[organism]" returned all but two hits from the original 419. In contrast, a relatively simple search string "EF AND lepidopt*[organism]" returned only 259 (62%) of the hits from the original 419. Similar results were observed for DDC, for which a single search string ("dopa AND lepidopt*[organism]") returned the most inclusive set of 238 hits distributed across 13 (28%)of the 46 lepidopteran superfamilies. No other DDC search strings were found to return hits not already subsumed by this original query.

Accessions in GenBank for EF and DDC in Lepidoptera were extremely sparsely distributed across the 46 superfamilies. Table 11 illustrates this distribution by assigning the number of hits for EF and DDC to each family within a classification of Lepidoptera compiled from multiple sources (Arnett 2000; Borror 1989; Kristensen 1999; Scoble 1992; Wagner 2001). While there were 76% more accessions for EF than DDC (419 vs. 238), those hits were concentrated in 4 fewer superfamilies. In fact, 89% of all EF lepidopteran accessions were concentrated in only three superfamilies: 165 (39%) of the 419 hits inside the Papilionoidea (106 in the Nymphalidae alone), 113 (27%) in the

Bombycoidea, and 94 (22%) in the Noctuoidea. DDC accessions were distributed across a wider range of superfamilies, especially the ancestral lineages (see top of Table 11), but 75% of all DDC lepidopteran accessions were concentrated in only two superfamilies: 103 (43%) of the 238 hits inside the Noctuoidea (91 in the Noctuidae alone), and 76 (32%) in the Bombycoidea.

Obtaining a broad cross-section of Lepidoptera for which EF and DDC sequences had both been sampled was challenging, a consequence of the patchy distribution of GenBank accessions for these markers across superfamilies. This finding was especially important for outgroup analyses in this study, and was illustrated by the paucity of superfamilies (5 of 46) and families (12 of 125) for which hits were registered in both EF and DDC columns in Table 11. Thus, while EF and DDC sequences could be obtained for 20% and 28% of superfamilies and 16% and 21% of families, respectively, the intersection of taxa for which both genes were available was only 11% of superfamilies and 10% of families. This resulted in a significant decrease in taxonomic diversity available for the combined EF&DDC data set (see below), but was not unexpected given the wide sampling variance in nucleotide databases such as GenBank.

Working from the master lists used to compile Tables 7 and 11, selection criteria were applied as described above and resulted in collection of 51 potential outgroups for EF and 40 potential outgroups for DDC (Table 9). Not surprisingly, 31% (16) of EF outgroups came from the Noctuoidea, 24% (12) from the Papilionoidea and 22% (11) from the Bombycoidea. Similarly, 40% (16) of DDC outgroups came from the Noctuoidea and 20% (8) from the Bombycoidea. Also as expected, DDC outgroups covered a wider range superfamilies (11) than EF (9), but both sequences could be

compiled for members of only 5 superfamilies. Also of interest was that 40 (57%) of the 70 taxa for which at least one sequence was collected had been submitted to GenBank by the Regier Lab (see all taxa for which specimen collection information was available in Table 9).

Data Matrix Construction

GenBank accession numbers for all publicly available EF and DDC sequences used in this study are presented in Tables 8 and 9. Alignment of both nuclear protein coding genes against the reference sequences and against all other taxa was unambiguous: no insertions, deletions or hypervariable regions were detected in either gene. Introns were neither detected nor expected, as all of the novel sequences and many of the publicly available sequences were synthesized via reverse-transcription from native mRNA. Variation in sequence length for GenBank accessions necessitated filling the ends of almost every GenBank sequence with missing data characters ('N') to standardize length across the matrix. For EF, all 14 ingroup and 50 of 51 outgroup sequences collected from GenBank were shorter than the novel sequences generated in this study (1,223bp and 1,136bp average lengths were 4% and 11% shorter for ingroups and outgroups, respectively). For DDC, 10 of 11 ingroup and 39 of 40 outgroup GenBank sequences were shorter than the final matrix length (805bp and 697bp average lengths were 41% and 49% shorter for ingroups and outgroups, respectively).

Final assembly resulted in three nucleotide data matrices for phylogenetic analyses with the following dimensions in [number of nucleotides] x [number of taxa]: (a) EF: [1,274nt] x [118 taxa]; (b) DDC: [1,373nt] x [105 taxa]; and (c) combined

EF&DDC: [2,647nt] x [91 taxa]. The combined nucleotide matrix represented the strict intersection of taxa for which both EF and DDC sequences had been gathered, and was obtained by deleting 27 and 14 taxa from the EF and DDC data matrices, respectively. This represented a significant loss in taxon density (23% reduction for EF; 13% reduction for DDC), but provided the largest taxon set for which both markers could be concatenated into a single analysis.

Prior to amino acid translation and all nucleotide-based phylogenetic analyses, terminal primer sequences were stricken from the matrices (for EF, see Table 3 & Figure 4; for DDC, see Table 4 & Figure 5). This reduced the total number of nucleotides to 1,228 for EF, 1,329 for DDC and 2,557 for the combined data set. Conceptual translation to amino acids produced three protein data matrices: (a) EF: [409aa] x [118 taxa]; (b) DDC: [443aa] x [105 taxa]; and (c) combined EF&DDC: [852aa] x [91 taxa].

Information Content

Table 12 itemizes the number (and percentage) of nucleotide positions at which character states were constant, autapomorphic or parsimony informative, as well as the mean nucleotide base frequencies for all three matrices: (a) EF; (b) DDC; and (c) combined EF&DDC. These calculations were repeated for four taxon sets within each matrix: (i) all Lepidoptera; (ii) all Bombycoidea (i.e., entire Sphingidae ingroup with all bombycoid outgroups); (iii) all Sphingidae (i.e., ingroup only); and (iv) Sphingidae&2OG (i.e., 66-taxon final set). This last taxon set included all 64 Sphingidae ingroup taxa for which EF and DDC sequence had both been collected, plus two bombycoid outgroups: "Bombycidae" (*Bombyx mori*) and "Saturniini" (*Saturnia*

albofasciata for EF and *S. naessigi* for DDC). Values in Table 12 are raw uncorrected measures of variation, which ignore the possibility that multiple substitutions may have occurred at a given site. Thus, these values underestimate actual amount of evolutionary change which may have occurred in these markers across the taxa sampled.

Echoing the findings of Regier 2001, the vast majority of nucleotide variability (autapomorphic *and* parsimony informative changes) in both genes was harbored in the third codon position. In the EF matrix, 85.9%, 78.0%, 60.2% and 64.6% of nt3 were parsimony informative in taxon sets (i), (ii), (iii) and (iv), respectively. This accounted for 90% (352nt3/393allnt), 92% (320nt3/349allnt), 92% (247nt3/269allnt) and 92% (265nt3/287allnt) of all parsimony informative character state change in these taxon sets for EF. This trend in high indices of nt3 change was robust across taxon sets, lending support to Regier *et al.*'s (2001) assertion that nt3 in these data were saturated and might be productively ignored for the purposes of phylogenetic analysis. Also echoing a pattern uncovered in the Regier 2001 pilot data, nt1 were approximately three times as parsimony informative as nt2 for EF. Looking across taxon sets within EF, the percentage of parsimony informative character state changes increased and the percentage of invariant character states decreased with increasing taxonomic depth, as more ancestral Lepidoptera were added. Autapomorphic character state change was consistently approximately 5% across taxon sets, although nt3 autapomorphies increased from 5.4% to 15.1% from sets (i) to (iii).

The proportion of parsimony informative characters in DDC was approximately 50% greater than within EF, but a similar trend in excessive nt3 variation was observed. For example, 95.5%, 95.3%, 94.4% and 95.0% of nt3 were parsimony informative in

taxon sets (i), (ii), (iii) and (iv), respectively. This accounted for 67% (423nt3/649allnt), 73% (422nt3/576allnt), 77% (418nt3/544allnt) and 76% (421nt3/557allnt) of all parsimony informative character state change in these taxon sets for DDC. Similarly, there were approximately twice as many parsimony informative nt1 characters as there were for nt2 in DDC. As with EF, the percentage of parsimony informative character state changes in DDC increased and the percentage of invariant character states decreased with increasing taxonomic depth. Autapomorphic character state change in DDC was consistently approximately 5% across taxon sets, similar to EF, however nt3 autapomorphies were more consistent (~1%).

Similar trends were observed in the combined data set constructed by concatenating EF and DDC sequences for the set of taxa possessing both sequences. One difference between this study and the pilot work of Regier 2001 was that the novel DDC fragment (1,329bp) sequenced across Sphingidae in this study was 620bp longer than the fragment in Regier 2001 and 101bp longer than the EF fragment. Thus, while the contribution of characters from each gene to the combined matrix was balanced (48% EF vs. 52% DDC), the systemic increased nucleotide variation in DDC relative to EF may have shifted the relative contribution of information from each gene in this study from that in Regier 2001.

Relative nucleotide variability between the genes was also reflected in proportions of variable amino acids observed after conceptual translation. For EF, 12.2%, 6.1%, 3.9% and 4.4% of amino acids were variable (parsimony informative or autapomorphic) in taxon sets (i), (ii), (iii) and (iv), respectively. These values were much higher for DDC: 42.2%, 31.1%, 25.7% and 28.9% variable amino acids in taxon sets (i), (ii), (iii)

and (iv), respectively. Alignment of all variable amino acid characters for EF are presented in Table 13 and for DDC in Table 14. Contrasting patterns of variation between EF and DDC could be observed by searching for common "amino acid haplotypes" in the alignments in Tables 13 and 14. Across all 105 taxa in DDC matrix (i), 104 amino acid sequences were unique, and 64 of 65 Sphingidae sequences were unique (both *Cautethia* sequences were identical). In contrast, only 81 of 118 EF amino acid sequences were unique across all Lepidoptera, and 34 of 67 EF amino acid sequences were unique across Sphingidae. Even after reducing matrix sizes by culling duplicate EF haplotypes, MP phylogenetic analyses via random addition heuristic searches on amino acid data across these taxa proved too computationally intensive and could not be completed.

Mean empirical base frequencies averaged across all codon positions and adjusted for missing data hovered between 20-30% for each nucleotide across genes and taxon sets (Table 12). For EF ntall, frequencies ranged from: A(.2478-.2526), C(.2852-.2935), G(.2510-.2548), T(.2039-.2112) across taxon sets. For DDC ntall, frequencies ranged from: A(.2499-.2555), C(.2245-.2309), G(.2521-.2579), T(.2613-.2681) across taxon sets. This apparent base composition homogeneity was deconstructed by inspecting EF and DDC codon positions individually. For example, taxon set Sphingidae (iii) within the EF matrix harbored extreme fluctuations in base composition: nt1 ranged from 14.94% for T vs. 37.61% for G; nt2 ranged from 15.84% for G vs. 32.52% for A; nt3 ranged from 12.79% for A vs. 44.61% for C. Such base composition heterogeneity was less pronounced in every nucleotide position for the Sphingidae taxon set (iii) in DDC: nt1

ranged from 20.58% for T vs. 34.56% for G; nt2 ranged from 19.73% for G vs. 29.66% for T; nt3 ranged from 21.34% for G vs. 30.18% for T.

Tables 15 (Ingroup) and 16 (Outgroups) present raw empirical base frequencies calculated for all codon positions across every sequence collected in this study, including percentage of missing or ambiguous character states. As expected from above, because these values combined data from codon positions, base composition homogeneity appeared to hold as a working assumption within these genes. For example, base composition across all ingroup taxa for EF ranged from: A(.1971-.2598), C(.2288-.3143), G(.2174-.2622), T(.1669-.2182), with standard deviations of .0078(A), .0125(C), .0054(G), .0090(T) [see Table 15]. For DDC, comparable values ranged from: A(.1272-.2694), C(.1106-.2476), G(.1362-.2603), T(.1362-.2852), with standard deviations of .0418(A), .0342(C), .0362(G), .0427(T) [see Table 15]. In contrast, base composition across all outgroup taxa for EF extended over much broader ranges: A(.0969-.2826), C(.1189-.3021), G(.0993-.2630), T(.0717-.2492), with standard deviations of .0334(A), .0364(C), .0277(G), .0321(T) [see Table 16]. For DDC, comparable values ranged from: A(.0429-.2536), C(.0504-.2340), G(.0451-.2521), T(.0459-.2724), with standard deviations of .0403(A), .0336(C), .0374(G), .0438(T) [see Table 16]. While these contrasts in minimum and maximum mean base frequencies revealed no systematic trend toward base composition bias in these genes, frequencies in Tables 12, 15 & 16 highlighted two phenomena evident in these data: (a) inspection of all codon positions as a single data set suggested only minor fluctuations around base composition homogeneity; (b) inspection of individual codon positions revealed more extreme base composition heterogeneity; and (c) quantitative differences in patterns of base

composition between EF and DDC across all taxon sets may be expected to affect patterns of observed nucleotide change in these genes.

Pairwise distance matrices calculated in PAUP* based on raw uncorrected pairwise divergence estimates from amino acids and separately for the three nucleotide codon positions across EF and DDC are presented in Tables 17 and 18, respectively.

Parsimony-Based Preliminary Analyses

Results of preliminary parsimony analyses contributing to conclusions below are compiled in Table 19. Results from only a single series of analyses from each matrix are presented in Figures 6, 7 & 8.

A. Testing for Information Content

All four PTP tests conducted separately on EF and DDC returned extremely low P values, implying significant rejection of the null hypothesis that observed character state distributions in taxon sets of both matrices were the result of purely stochastic processes. For the EF matrix, 1,125 PTP replicates were completed on the ingroup Sphingidae taxon set (iii), returning a P value of 0.000889 and the next most parsimonious tree 871 steps longer than the MP tree (length=1,525 steps). In addition, 1,316 PTP replicates were completed on the Sphingidae&2OG taxon set (iv), returning a P value of 0.00076 and the next MP tree 898 steps longer than the MP tree (length=1,736 steps). For the DDC matrix, 3,821 PTP replicates were completed on the Sphingidae taxon set (iii), returning a P value of 0.000262 and the next MP tree 3,305 steps longer than the MP tree

(length=4,117 steps). In addition, 3,984 PTP replicates were completed on the Sphingidae&2OG taxon set (iv), returning a P value of 0.000251 and the next MP tree 3,336 steps longer than the MP tree (length=4,566 steps). These results were taken as evidence of phylogenetic structure within both EF and DDC, as interpreted via the maximum parsimony criterion. PTP tests were not conducted on the combined EF&DDC data matrix.

B. Parsimony Searches

The first MP analyses conducted were heuristic searches on the EF, DDC and combined EF&DDC data matrices for the All Lepidoptera (i) taxon set. These trial exploratory searches were intended primarily to pare down the list of potential outgroups in Table 9, not to generate viable hypotheses of relationships among all Lepidoptera. Two hundred random sequence addition replicates on EF data yielded 680 equally parsimonious trees confined to a single island, the strict consensus of which displayed excellent resolution in non-sphingid groups but produced many polytomies in the Sphingidae. Similarly, one thousand replicates on DDC data yielded 240 equally parsimonious trees across two islands, the strict consensus of which displayed excellent resolution throughout both ingroup and outgroups. One thousand replicates on combined EF&DDC data yielded 2 equally parsimonious trees on a single island, differing only in the relative placement of subfamilies within Noctuidae. Finally, codon position nt3 was excluded from matrix EF&DDC and taxa with identical EF amino acid haplotypes were deleted; 421 replicates on the resulting matrix returned 243 MP trees distributed across

43 islands, the strict consensus of which suggested an almost completely unresolved but monophyletic Sphingidae.

Many taxon bipartitions from the initial MP analyses agreed with well-established morphological taxonomic hypotheses, while others were nonsensical. For example, the EF MP tree suggested a polyphyletic Bombycoidea, and placed a papilionoid (Lycaenidae: Polyommatinae) next to the base of the tree with Micropterigoidea. The DDC MP tree also suggested a polyphyletic Bombycoidea and paired Papilionoidea with Gracillarioidea. Bootstrap support across all trees was very poor. Importantly, all three of these searches generated trees containing a monophyletic Sphingidae with modest bootstrap support, and all analyses suggested at least some combination of macrolepidopteran taxa as sister lineages to Sphingidae.

In an attempt to reduce heuristic search computation time, all non-bombycoid taxa were pruned from the three matrices and the above analyses repeated. All analyses again yielded trees with a monophyletic Sphingidae supported by moderate bootstrap values, but they differed in their suggestion of the most basal sphingid lineages, those most closely recently derived from the bombycoid outgroups. As with the Lepidoptera taxon set, EF data across All Bombycoidea (ii) yielded the largest set of equally parsimonious trees (n=280) and the least resolution in strict consensus. In contrast, DDC returned a manageable number of MP trees (n=20) and the combined EF&DDC matrix returned a single optimal topology.

These preliminary analyses confirmed that the sphingid taxa sampled in this study probably comprised a monophyletic group and that some members of Macrolepidoptera, usually Bombycoidea, were the most closely related outgroup(s). For this reason, an

effort was made to further decrease computation time by minimizing the number of taxa required to be informative about sphingid ingroup. The list of potential outgroups was pruned down to two ('Bombycidae' and 'Saturniini' in Table 9) to provide a means of rooting a tree of the 64 Sphingidae for which DDC and EF sequences had both been obtained. This resulted in the 66-taxon set Sphingidae&2OG (iv), on which further MP analyses for the EF, DDC and EF&DDC matrices was based. These outgroups were selected because they had demonstrated a "near-sister" relationship with the sphingid ingroup in all analyses based on the Lepidoptera (i) and Bombycoidea (ii) taxon sets, and because these two sequences collected *in silico* had the least number of missing characters relative to the 1,228bp of EF and 1,329bp of DDC sequences collected *de novo*. The EF sequence for 'Bombycidae' was in fact complete and had served as the reference sequence during all EF alignments.

Parallel MP analyses of the original nonoverlapping EF and DDC matrices tested the effects of adding three (ProserpinusGB, PachysphinxGB, PaoniasGB) and one (Neococytius1949) ingroup taxa to the Sphingidae&2OG (iv) analyses, respectively (see Table 8). Results of these analyses were unremarkable in the sense that inclusion of a few additional taxa had very little impact on global topological arrangements (data not shown). Supplementary EF sequences in the Regier 2001 pilot study from the smerinthine genera *Pachysphinx* and *Paonias* paired with their newly sequenced congeners (Pachysphinx1528 and Paonias1540, respectively) with extremely strong bootstrap support in all EF trees. While genus monophyly was preserved, however, inclusion of these taxa did impact the basal intergenus relationships in a clade consisting of *Smerinthus*, *Paonias* and *Pachysphinx*. The EF sequence for the macroglossine genus

Proserpinus (Caterino *et al.* 2001) consistently formed a clade with *Sphecodina* in analyses of the EF matrix, confirming their close orientation in Kitching & Cadiou's (2000) classification (see Table 2). Similarly, the novel DDC sequence obtained for *Neococytius* consistently proved most closely related to *Cocytius*, confirming a grouping explicitly predicted by Kitching & Cadiou (see vertical bar joining these taxa in Table 2).

The occasionally large number of equally parsimonious trees distributed across many islands encountered by the trial heuristic searches suggested the possibility of significant heterogeneity in the data space for the Bombycoidea taxon set (iii). Under these conditions, the heuristic search strategy (even with many random addition sequence replicates followed by TBR) may have had difficulty locating globally optimal topologies. To explore this phenomenon, a series of four heuristic searches with identical starting conditions (including random seed) but differing in number of replicates was performed for each of the three matrices (Table 19). As the number of random addition sequence replicates was increased, the heuristic search algorithms investigated more rearrangements and continued to find more equally MP trees distributed across more and more islands. However, when a filter was applied to retain only those topologies with optimal score, the same set of MP trees across the same few islands was retained regardless of the number of replicates. This suggested that the heuristic search settings (starting from a random addition sequence, employing TBR, with MulPars active, holding 10 trees at each step and steepest descent on) in this study generated a high-performance algorithm capable of identifying optimal solutions, in many cases even with just 10 replicates.

C. Nonparametric Bootstrap Analysis

Maximum parsimony nonparametric bootstrap analyses across all taxon sets and data matrices revealed significant variation in internal consistency for these data. Majority rule bootstrap consensus topologies consistently included moderate bootstrap proportions (i.e., greater than or equal to 50%) for a small percentage of internal discussed below. EF&DDC analyzed without nt3 consistently resulted in the weakest bootstrap support measures, probably a result of the relatively low number of parsimony informative characters in this partition.

D. ILD Test

A single test was performed to evaluate homogeneity of phylogenetic signals from EF vs. DDC across all nucleotides for just the ingroup Sphingidae taxon set (iii). The ILD test implemented in PAUP* (1,164 replicates) revealed statistically significant heterogeneity in signal between these genes within Sphingidae (P=0.000859), suggesting that the two genes were contributing conflicting phylogenetic signal. To test whether intergene conflict was a consequence of the extremely high variability and possible saturation in nt3, an attempt was made to repeat this test with only nt1&2. However, the progress of computations prevented accumulation of enough replicates to make a robust inference about statistically significant heterogeneity between the genes when nt3 was eliminated from the analysis.

Evaluating Alternative Parsimony Topologies

Having settled on a standard taxon set (Sphingidae&2OG, ntax=66), all three matrices were analyzed according to the criterion of maximum parsimony with the aim of selecting a single optimal MP topology from each for use in seeding iterative model parameter estimation / heuristic searches under the criterion of maximum likelihood.

For the Sphingidae&2OG taxon set (iv), MP analyses on the EF matrix resulted in 161 equally parsimonious trees distributed across three islands. The strict consensus of these equally viable trees was a poorly resolved topology retaining just 43 (67%) of a possible 64 nodes in a rooted, fully bifurcating tree with 66 taxa. Because the iterative ML parameter estimation / heuristic search strategy required as input a fully resolved (bifurcating) starting topology, it was important to determine a way to select a single tree from among the 161 MP alternatives. A much less stringent consensus tree building algorithm, the 50% majority rule, was employed to generate a more well-resolved topology consisting of 61 (95%) nodes. This topology was imported as a constraint tree, and filtering the original set of 161 MP trees for compatibility with it resulted in retention of only 2 MP trees. The strict consensus of these two trees was selected for input into ML analyses, with the understanding that starting tree algorithms in PAUP* would randomly resolves polytomies to produce a fully bifurcating topology. Both trees were also evaluated more rigorously according to the parsimony-based selection criteria described below.

MP analyses on the DDC matrix were much less difficult to interpret and resulted in only 10 equally parsimonious trees confined to a single island. The strict consensus of these equally viable trees was well-resolved, retaining 61 (95%) of a possible 64 nodes.

Polytomies were confined to two terminal groups: [Ceratomia1870, CeratomiaGB, Paratrea1939] and [Lapara1670, Sphinx1532, SphinxGB, Sphinx1938]. MP analyses on the combined EF&DDC matrix yielded only 3 equally parsimonious trees confined to a single island. The strict consensus of these trees was also well-resolved, retaining 62 (97%) of a possible 64 nodes, with all polytomies confined to a single clade, Dilophonotina: [Aellopos2399, AelloposGB, Nyceryx2378, Perigonia2191, Callionima0966, Erinnyis1542, Isognathus1646, Pachylia1644].

Table 20 itemizes the parsimony scores obtained by mapping each data matrix's character state distribution onto every candidate MP topology recovered by independent heuristic searches across the separate matrices. Parsimony penalty incurred by constraining one data set onto a suboptimal topology was assessed by increase in length (expressed as % of the original), CI and RI, and mean values of each measure averaged across all data matrices for a given topology were used to select the optimal candidate MP tree for each data matrix. For example, of the 161MP trees generated from analyses of the EF matrix for the Sphingidae&2OG taxon set, 2 MP trees (i, ii; length=1705, CI=0.300, RI=0.549) were retained after filtering for compatibility with the 50% majority rule consensus topology. When DDC data and combined EF&DDC data were mapped onto each of these topologies, topology (ii) had a lower mean % increase in parsimony score (%diff=3.31), while both topologies had identical mean CI (0.261) and mean RI (0.565) when averaged across all three data matrices. On this basis, tree (ii) was chosen as the optimal topology generated from the EF data (marked with a * in Table 20 and shown in Figure 6). Neither topology could be distinguished on the basis of these criteria when the same cross-mapping exercise was performed after excluding nt3.

In similar fashion, topology (v) was chosen as the optimal candidate from among the 10 MP trees (i-x; length=4484, CI=0.249, RI=0.611) produced by the MP analyses of DDC data matrix (see * in Table 20 and Figure 7). When EF data and combined EF&DDC data were mapped onto each of these topologies, topology (v) had the lowest mean % increase in parsimony score (%diff=1.83) and one of the four highest RI (0.571), while all ten topologies had identical mean CI (0.264) when averaged across all three data matrices. In addition to tree (v), trees (vi) and (ix) emerged as equally optimal choices when nt3 was excluded from cross-mapping exercises.

Finally, topology (i) was chosen as the optimal candidate from among the 3 MP trees (i,ii,iii; length=6280, CI=0.259, RI=0.588) produced by the combined EF&DDC data matrix (see * in Table 20 and Figure 8). When EF data were mapped onto each of these topologies, topology (ii) was one step shorter than the original EF tree, while this same topology was one step longer than the DDC tree when DDC data were mapped. All three indices (%diff, CI, RI) were similarly unconvincing, so topology (i) was selected randomly. None of the three topologies could be distinguished by these criteria when nt3 was excluded from the cross-mapping.

Qualification of Parsimony-Based Topologies

The optimal topology selected from MP analyses of EF for the Sphingidae&2OG taxon set is presented in Figure 6. Two subfamilies (Sphinginae and Macroglossinae) were recovered as monophyletic, though neither had bootstrap support greater than 50%, nor were they supported by many synapomorphies (4 and 6, respectively). The phylogram illustrates how widely branch lengths varied both between and within clades,

raising concern over artifacts stemming from long branch attraction (Felsenstein 1978; Hendy & Penny 1989). For example, one of the shortest branches in the tree (7 synapomorphies) separated the ingroup from the sister outgroup lineages. Since the most basal sphingid (Marumba0118) and both bombycoid outgroups have accumulated at least ten times as many autapomorphies as the branch separating them, the position of *Marumba* as the most ancestral sphingid must be interpreted cautiously. In addition, only 32 (50%) of 64 internal nodes had bootstrap support greater than 50%, with 19 of those nodes consisting of sister terminal lineages. In other words, bootstrap support for internal nodes was extremely poor and this topology can be considered only suggestive of relationships among super-generic taxonomic groups within the Sphingidae. Despite this, EF seemed efficient at placing taxa in proper subfamilial orientation, rendering only Smerinthinae paraphyletic and inserting monophyletic Ambulycini between Sphinginae and Macroglossinae.

The optimal topology selected from MP analyses of DDC is presented in Figure 7. Two subfamilies (Sphinginae and Smerinthinae) were recovered as monophyletic, with excellent and modest bootstrap support, respectively. Both subfamilies were also supported by many synapomorphies (57 and 93, respectively), and all of the deep branches within the family were longer than the more derived lineages. Derived groups within the Sphinginae and Macroglossinae formed clusters of especially short branches, highlighting potential hotspots for accelerated evolution among those lineages (e.g., *Sphinx*, *Xylophanes*). As with EF, branch lengths varied widely across the tree, but generally became shorter from the root toward the tips. One glaring exception was the branch separating ingroup from outgroup (13 synapomorphies), again suggesting long

branch attraction may have resulted in an artifactual placement of the [*Hemaris*, *Cephonodes*] clade as the most basal sphingid lineages. As with EF, the branch leading to this most basal sphingid clade and both terminal branches of the bombycoid outgroups had accumulated at least ten times as many autapomorphies as the branch separating them, suggesting the interpretation of [*Hemaris*, *Cephonodes*] as the most ancestral sphingid may be incorrect. Bootstrap support for the DDC tree was more impressive than for EF, with 46 (72%) of 64 internal nodes receiving bootstrap support greater than 50%, and 17 of those nodes uniting sister terminal lineages. In an absolute sense, bootstrap support was again extremely poor and this topology can be considered only suggestive of relationships among super-generic taxonomic groups within the Sphingidae. However, like EF, DDC retained proper expected subfamilial orientations, rendering only Macroglossinae paraphyletic and inserting *Hopliocnema* between Sphinginae and other Smerinthinae.

Not unexpectedly, the optimal topology selected from MP analyses of the combined EF&DDC data set contained elements found in both the EF and DDC trees (Figure 8). The same two subfamilies (Sphinginae and Macroglossinae) were recovered as monophyletic as for EF, this time with excellent and modest bootstrap support, respectively. Both subfamilies were also supported by many synapomorphies (59 and 110, respectively), and like the DDC tree the deep branches within the family were generally longer than the more derived lineages (with the exception of some macroglossines). Derived groups within the Sphinginae and Macroglossinae (e.g., *Sphinx*, *Xylophanes*, respectively) again formed clusters of especially short branches, but many of these also received modest bootstrap support. Interpretation of the root suffered

from the same potential long branch attraction pitfall, as the branch separating ingroup from outgroup was supported by only 23 synapomorphies. Consistent with the EF data, *Marumba* reassumed the role of most basal sphingid, with the most basal sphingids from DDC analyses (*Cephonodes* and *Hemaris*) instead constituting a very long branch nested terminally within a monophyletic Macroglossinae. Bootstrap support for the combined tree was as poor as for EF, with only 31 (48%) of 64 internal nodes receiving bootstrap support greater than 50%, and 18 of those nodes uniting sister terminal lineages. This lack of internal consistency was surprising, given that heuristic searches settled on only very few MP trees, in stark contrast to heuristic searches on the EF data. Such weak bootstrap support suggests that resolution of deeper relationships among sphingid genera will continue to be only speculative when relying on phylogenetic analysis of these markers under the criterion of maximum parsimony.

Despite poor bootstrap support, a few themes emerged consistently across the suite of parsimony analyses described above. A monophyletic Sphinginae was recovered by all three analyses, with strong bootstrap support from DDC and the combined EF&DDC data. In addition, the sister group to Sphinginae in all analyses was *Hopliocnema*, the sole representative of the smerinthine tribe Sphingulini. This unexpected result was supported by very high bootstrap proportions in the DDC and combined trees. The sphingine tribe Acherontiini was also recovered with strong support, however the position of *Coelonia* was malleable across trees. Despite the paraphyly of Smerinthinae in the EF and combined trees, all three analyses returned an extremely strongly supported monophyletic smerinthine tribe Ambulycini. Similarly, Macroglossinae was rendered paraphyletic in EF and combined analyses, yet several of

its subgroups were consistently retained with high support. Section Choerocampina and its sister relationship with *Darapsa* was very highly supported in all analyses. Section Hemarina was also consistently recovered at high support values. Some form of section Dilophonotina was also consistently recovered in all analyses, although the positions of *Cautethia*, *Enyo*, *Sphecodina* and *Unzela* were extremely unstable and occasionally rendered the tribe polyphyletic. In addition, the tribe Philampelini (represented by only three *Eumorpha* species) was consistently nested within the dilophonotine assemblage. Finally, the majority of congeneric samples did in fact form monophyletic groups. Exceptions occurred in the three hyperdiverse sphingid genera for which four species each were included in this study: (a) while the four included species of *Sphinx* (56 species worldwide) were consistently monophyletic, the single representative of *Lapara* (4 species worldwide) was always inserted among them; (b) the four included species of *Manduca* (88 species worldwide) were monophyletic in all trees except EF, but in every case the monotypic *Dolba* was always inserted among them; (c) the four included species of *Xylophanes* (96 species worldwide) were monophyletic in every MP tree, but for DDC and the combined analyses one of two sampled species of *Darapsa* (Darapsa1778) was inserted among them.

Likelihood-Based Parameter Estimation

The three MP topologies selected and described above (* in Table 20) and depicted in Figures 6, 7 & 8 were used as starting topologies for estimating nucleotide substitution model parameters for the Sphingidae&2OG taxon set (ntax=66). Maximum likelihood scores of these initial trees were estimated under the GTR+I+G model, and

resulting parameter estimates were used to heuristically search for an ML tree via branch swapping on the initial MP tree. Iterative parameter re-estimation and ML heuristic searches resulted in convergence to equilibrium parameter values in most cases after only the second of four iterations. Table 21 presents the results from every iteration for likelihood estimation of every data matrix on every starting topology. Rapid convergence to equilibrium parameter values (see boldface lines in Table 21) was taken to indicate relative simplicity of the likelihood surface and high accuracy in parameter estimates. In the fourth and final iteration of each analysis, converged parameter values were fixed and more extensive heuristic searches with more replicates were launched to locate the globally ML tree.

Of special interest was not only the efficient parameter convergence within a given series of iterations of one data matrix on any given starting topology, but the global convergence of parameter values for a given data matrix across all three starting topologies. Table 21 demonstrates that for the EF and DDC data matrices, starting topology had an effect on the rapidity of parameter convergence but *not* on the final parameter values themselves. The EF data converged after only two iterations when the EF MP tree was used to seed the iterative searches; these same data converged after three iterations when the combined EF&DDC MP tree was the start topology, and after four iterations when the DDC MP tree was the start topology. In contrast, the DDC data converged to stable parameter values after only two iterations regardless of the starting topology. The combined EF&DDC data behaved slightly differently, converging to identical sets of parameter values after two iterations on the DDC starting topology and after three iterations on the EF starting topology. However, likelihood optimization of

the same data on the EF&DDC MP tree resulted in convergence after two iterations to a *different* set of parameters. While very similar, these values varied enough that the iterative ML searches on the EF&DDC data based on the EF&DDC MP starting topology produced a ML tree of slightly different topology and slightly higher likelihood than when EF or DDC starting topologies were used.

Equilibrium base frequencies estimated under the GTR+I+G model (Table 21) deviated slightly from base composition homogeneity (i.e., $\pi_A = \pi_C = \pi_G = \pi_T \approx 0.25$), reflecting the trend of empirical base frequencies in the three original data matrices (Tables 12, 15 & 16). For EF, globally convergent base frequency parameters suggested a slight excess in adenine and deficiency in guanine: 27.2%(A), 26.1%(C), 22.4%(G), 24.3%(T). Globally convergent base frequency parameters revealed a more symmetrical and greater AT bias in DDC than for EF: 27.4%(A), 21.9%(C), 21.6%(G), 29.1%(T). The greatest differences between gene base composition was in proportions of C (4.2% greater in EF) and T (4.8% greater in DDC), and not unexpectedly the convergent parameter values for the combined EF&DDC data set reflected this with intermediate values for these bases (Table 21).

Global relative rate parameter estimates of the 6-class GTR substitution model revealed a stark contrast in molecular evolution of these two genes. Relative rate parameters for EF were extremely varied across substitution classes, with an enormous excess in transitions (AG: 13.998, CT: 25.062) and transversion rates which varied fivefold between classes (AC: 2.262, AT: 5.386, CG: 2.310, GT: 1.0). In contrast, relative rate parameters for DDC were of both lower magnitude and greater homogeneity across classes. DDC revealed a more modest excess in transition substitutions (AG:

5.571, CT: 6.839) with more homogeneous transversion rates across classes (AC: 1.503, AT: 1.333, CG: 1.151, GT: 1.0). Given the widely differing pictures these values suggested about molecular evolution of EF and DDC, it was perhaps not unexpected that the convergent relative rate parameter values for the combined data set could not be predicted from the two genes independently (Table 21).

Two parameters of the nucleotide substitution model augmenting the 6-class GTR framework were the proportion of sites assumed to be invariant (I) during evolution and the one-parameter descriptor of the gamma distribution (G) describing among-site rate heterogeneity along each molecule. Values of I varied from 0.616 for EF and 0.510 for DDC to 0.574 for the combined data. These values were each lower than the empirical proportion of invariant sites calculated in Table 12, demonstrating the deviation from observation often encountered when likelihood parameters are optimized to an explicit model of nucleotide substitution. While this value suggested DDC is a slightly more variable and perhaps less evolutionarily constrained molecule than EF, the magnitude of invariant sites between them did not in itself suggest these genes are evolving under grossly different regimes. In contrast, there was a two-fold difference in alpha shape parameter of the gamma distribution between these genes (G=0.680 for EF, G=1.400 for DDC). A difference of this magnitude indicated gamma distributions with very different shapes against which the substitution model for each gene assumed independent sites were likely to vary, suggesting strongly that these two genes have accumulated variation under very different evolutionary scenarios. The value of the gamma shape parameter for the combined EF&DDC data (G=1.039-1.044) was intermediate between these two extremes, suggesting that concatenation of data caused the model to effectively average

the patterns of two separate genes experiencing very different regimes of among-site rate heterogeneity.

Evaluating Topologies from Likelihood Analyses

In addition to providing a means of efficient convergence to stable nucleotide substitution model parameter values, the ML iterative estimation / search routine discussed above was also very effective at identifying convergent topologies optimized under the criterion of maximum likelihood. Individual trees were saved after each iteration and the topologies compared for concordance after the analysis was complete. Identical topologies are indicated in Table 21 with shared symbols under the 'Tree' column. Similar to results of parameter estimation, ML topologies not only converged within iterations of a given analysis but converged globally across all analyses for a given data matrix. Optimizing the GTR+I+G substitution model for the EF data matrix on the starting topology derived from the MP EF analyses resulted in four identical trees across all iterations. This tree also matched those derived from the last two and last three iterations when the EF data was fit to the DDC and EF&DDC MP starting trees, respectively (Figure 9). Global convergence to a single ML topology was even more impressive for the DDC data set, for which every ML tree across every iteration was identical (Figure 10). For the combined data, EF and DDC MP starting topologies resulted in convergence to the same tree ('c1', -lnL = 31221.47311). However, when the EF&DDC MP tree was used as the starting topology, a slightly different topology was found to be optimal ('c2', -lnL = 31221.29642). These two topologies differed only in arrangements within the [*Paonias*, *Pachysphinx*, *Smerinthus*] clade, mirroring results of

MP analyses under nonoverlapping taxon sampling. Strictly speaking, topology'c2' was selected as the optimal tree because it had higher likelihood (Figure 11).

Analyses based on the EF data matrix produced a ML tree which retained only a single subfamily (Macroglossinae) as monophyletic. Similar to MP analyses for this gene, super-generic groups within this subfamily were preserved, including Hemarina, Choerocampina and Dilophonotina with nested Philampelini. Smerinthinae was rendered paraphyletic because Ambulycini was suggested as the sister lineage to the macroglossines, with a monophyletic Smerinthini the sister lineage to that group. Members of the Sphinginae were the among the most basal lineages in the family, with the smerinthine *Hopliocnema* assuming the most basal position. In contrast to the MP analyses, the length of the branch separating outgroup from ingroup was the longest internode in the entire tree, with extremely long terminal branches for each outgroup taxon. After the *Hopliocnema* split, branch lengths throughout the remainder of the ingroup appeared to become longer toward more derived taxa and almost every terminal branch was longer than the internode from which it arose.

Analyses based on the DDC data matrix produced a ML tree much more appealing from a taxonomic point of view, as all three subfamilies were retained as monophyletic. Two exceptions included: (a) *Hopliocnema*, oriented as sister to Sphinginae, with the remaining smerinthines sister to that lineage; and (b) the sphingine *Coelonia* was embedded on a long branch inside Macroglossinae. The same super-generic groups within all subfamilies were also preserved, except that only a subset of Dilophonotina remained monophyletic. Branch lengths within and between subfamilies were heterogeneous, with no global trends like those in the EF ML tree. Sphinginae

branches were more often short, Macroglossinae branches were more often long, and Smerinthinae branches were intermediate. Unlike the EF ML tree, not every terminal branch was longer than the internode from which it arose. Similar to the EF ML tree, the length of the branch separating outgroup from ingroup was the longest internode in the entire tree, with extremely long terminal branches for each outgroup taxon. Because all three subfamilies were monophyletic, the DDC ML tree permitted the first assessment of genealogical relationships among subfamilies. Macroglossinae was the most diverse and most basal subfamily in the tree, with the sister lineages Sphinginae and Smerinthinae more derived.

Analyses of the combined EF&DDC data matrix produced a ML tree globally similar to the DDC ML tree, with some extensive differences in fine structure. All three subfamilies were again retained as monophyletic in the same orientation: [Macroglossinae,(Sphinginae, Smerinthinae)], with *Hopliocnema* and *Coelonia* the same two exceptions. A broader monophyletic Dilophonotina consistent with the EF ML tree was retained. Unlike either single-gene analysis, Smerinthinae was broken into two monophyletic sister tribes Ambulycini and Smerinthini. Branch lengths within and between subfamilies were heterogeneous: Sphinginae branches were often short, Macroglossinae branches were often long, and Smerinthinae branches were intermediate. Every terminal branch was longer than in the DDC tree, though not always longer than the internode from which it arose. Finally, consistent with both individual gene trees, the branch separating outgroup from ingroup and the terminal branches of both outgroup taxa were the longest in the entire tree.

Evaluating the Likelihood of All Candidate Topologies

Table 22 presents the results of ML cross-calculations obtained after fixing both the model parameters optimized for each data set and each candidate topology recovered from MP and ML analyses. Four distinct versions of the GTR+I+G model of nucleotide sequence evolution were evaluated, corresponding to the globally convergent parameter values presented in Table 21d. For each unique GTR+I+G model, corresponding data were fit to every MP and ML candidate topology presented in Tables 20 & 21. Comparison of likelihood scores across topologies within a given data & model parameter set (i.e., down each column of Table 22) provided a probabilistic evaluation of the relative effectiveness of each topology at explaining the observed distribution of character states, in the context of the assumed underlying model of nucleotide sequence evolution.

Among the four alternative ML topologies presented in Table 21, likelihood scores under the EF GTR+I+G model were optimal for the EF ML topology and worst for the DDC ML topology (-lnL difference = 197.47847). The converse was true for the DDC GTR+I+G model (-lnL difference = 515.23907), underscoring the trend toward discordant phylogenetic information between the EF and DDC data sets. Interestingly, likelihood scores under both combined EF&DDC GTR+I+G models were slightly better for ML topology 'c2' than for 'c1' in Table 21 (mean -lnL difference = 0.16639), and in both cases were worst for the EF ML topology (-lnL difference = 361.24008).

Among the fifteen alternative MP topologies presented in Table 20, likelihood scores under the EF GTR+I+G model were optimal for the EF MP topology presented in Figure 6 and were worst for the DDC MP topologies (max -lnL difference = 161.07546).

For all other GTR+I+G models, likelihood scores were optimal for the second MP topology derived from combined EF&DDC data, and in every case were worst for the first EF MP topology (mean -lnL difference = 425.04928).

When the fifteen MP topologies and four ML topologies were pooled into a single set of alternative hypotheses, the ML topologies had superior likelihood scores under all four sets of GTR+I+G model parameters. For the EF model, the EF ML topology was better than the MP tree with highest likelihood (-lnL difference = 24.2507), but both EF MP topologies were better than the three other ML topologies. In contrast, under the DDC model, the MP tree with highest likelihood was worse than three of the four ML topologies (mean -lnL difference = 25.581). The same held true when MP and ML trees were compared under both combined EF&DDC models.

DISCUSSION

Building on pilot work of Regier *et al.* (2001), the present study offered some important contributions in the next phase toward more fully resolving the phylogeny of the Bombycoidea and using those phylogenetic hypotheses to interpret life history evolution in this diverse group of Lepidoptera. Confirming earlier findings in studies employing EF and DDC in phylogenetic resolution of macrolepidopteran groups (Cho *et al.* 1995; Fang *et al.* 1997, 2000; Friedlander *et al.* 1992, 1998, 2000; Mitchell 1998; Mitchell *et al.* 1997, 2000; Regier *et al.* 2000, 2002), the present work demonstrated that EF and DDC, both separately and in combination, harbored significant phylogenetic information for the resolution of relationships among genera of Sphingidae. However, both genes differed in signatures of variation and in the phylogenetic hypotheses drawn

from them, providing distinct glimpses into the molecular evolutionary history of Sphingidae.

The vast majority of nucleotide variation in both genes was concentrated in the third codon position, and of the remaining variation nt1 was thrice and twice as variable as nt2 in EF and DDC, respectively. Nucleotides in DDC were approximately 50% more variable than in EF, an observation paralleled by an ML estimate of invariant sites approximately 20% lower for DDC than EF. Amino acids in DDC were several fold more variable than the protein sequences for EF. Differences in nucleotide base composition between these genes were more subtle, but both empirical nucleotide frequencies and maximum-likelihood estimates of equilibrium base composition suggested that EF harbored an excess of adenine (27.2%) with a deficiency in guanine (22.4%), while DDC demonstrated a more classic signature of AT bias (27.4% and 29.1%, respectively, versus 21.9% C and 21.6% G).

Maximum likelihood estimates of nucleotide substitution relative rate parameters also provided a powerful means to contrast the differences in molecular evolution between these two genes. The estimated increase in rates of transition versus transversion substitutions was much higher for EF (14.0 purine transitions and 25.1 pyrimidine transitions, versus 2.7 average transversion rate) than for DDC (5.6 purine transitions and 6.8 pyrimidine transitions, versus 1.2 average transversion rate), as was the degree of variation in rates of change among the 6 substitution classes (standard deviation in rate parameters: 9.5 for EF and 2.6 for DDC). The twofold difference (DDC: 1.4 > EF: 0.7) in ML estimates of the shape parameter for a gamma distribution modeling among-site rate heterogeneity also revealed striking differences in patterns of substitution

between these genes. While the amount of data, in number of nucleotides, contributed by each gene in this study was balanced (48.1% EF and 51.9% DDC), taken together the above observations suggested strongly that patterns of nucleotide substitution and resulting information content of both genes seemed to be strongly heterogeneous.

Differences between EF and DDC in signatures of molecular evolution were mirrored by differences in phylogenetic information content from each of these genes. Parsimony-based permutation tail probability (PTP) tests revealed highly significant phylogenetic structure for both genes, confirming their utility in phylogenetic studies in insect groups. This was not surprising, given that their utility had already been demonstrated experimentally in previous studies employing one or both genes in resolution of lepidopteran groups (Cho *et al.* 1995; Fang *et al.* 1997, 2000; Friedlander *et al.* 1992, 1998, 2000; Mitchell 1998; Mitchell *et al.* 1997, 2000; Regier *et al.* 2000, 2002). However, despite their proven utility in phylogenetic analyses, consistent generation of congruent gene trees from EF and DDC had not been conclusively demonstrated. In this study, across all taxon samples, data partitions, optimality criteria and methods of analysis, the phylogenetic hypotheses inferred from EF and DDC were strikingly discordant. Disagreement in suggested relationships extended across all taxonomic levels, including monophyly and relative orientation of the three subfamilies, monophyly and relative composition of individual tribes and sections, and even patterns of relatedness among congeneric species. Consistent and reliable phylogenetic patterns from analyses of one gene were seldom both consistently and reliably recovered from analyses of the other gene. Thus, distillation of a universal genus-based family

phylogeny from these two divergent individual gene phylogenies was a formidable challenge.

Broad discordance in phylogenetic hypotheses drawn from EF and DDC simultaneously increased the relevance of a whole-data approach (i.e., constructing a phylogenetic estimate from a combined data set), and also challenged the notion that concatenation of two such conflicting genes into a single analysis was theoretically justified (Bull *et al.* 1993; Chippindale & Wiens 1994; DeQueiroz *et al.* 1995; Huelsenbeck *et al.* 1996; Mitchell *et al.* 2000; Olmstead & Sweere 1994; Weller *et al.* 1994; Wiens 1998). MP analyses on the combined data matrices in this study were noticeably more analytically efficient and less ambiguous than for either gene separately, generating fewer equally parsimonious trees in shorter computation times. Results from these analyses incorporated elements of both EF and DDC topologies, as well as novel rearrangements not viewed in either independent tree. At the deepest levels, the topology in Figure 8 suggested a sister relationship between Sphinginae and Macroglossinae, consistent with the EF MP tree. However, Figure 8 also placed Ambulycini as the most derived lineage within a paraphyletic Smerinthinae grade, more consistent with smerinthine monophyly illustrated by the DDC tree. At terminal levels, the combined EF&DDC tree demonstrated greater fidelity to the DDC MP topology, especially in relationships among species of the three included hyperdiverse genera: *Manduca*, *Sphinx* and *Xylophanes*.

Difficulty interpreting the stark differences in suggested genealogical relatedness among sphingid lineages stemming from these two independent markers was diminished somewhat when viewed in the context of support for individual nodes in each topology.

Nonparametric bootstrapping, a technique designed to quantify the internal consistency of the data on the basis of individual taxon bipartitions, was the prime means of assessing node support in this study. Bootstrap values on all three parsimony trees suggested strongly that these data alone were grossly insufficient to establish strongly supported, phylogenetically robust nodes against which existing taxonomic hypotheses could be rigorously evaluated. EF, DDC and combined EF&DDC data were able to generate topologies with only 50%, 72% and 48% of all possible nodes receiving even moderate (i.e., values greater than or equal to 50%) bootstrap support, respectively. Even more telling was that the majority of the sparse bootstrap support was concentrated among relatively "obvious" terminal nodes, for example, those uniting congeneric species into a single monophyletic genus. The most critical nodes for a systematic study of the family, those deep nodes describing the interrelationships between sections, tribes and subfamilies, were in fact the most weakly supported. While there were consistent patterns to be gleaned from MP analyses (see below), results of this study made it clear that EF and DDC in conjunction provided insufficient information to adequately and robustly resolve the phylogeny of the Sphingidae. While improved taxon sampling beyond that employed here remains a viable possibility to extract more robust phylogenetic hypotheses from these markers, pursuit of other independently evolving gene sequences seems a justified and promising line of further research for this group.

Given the poor performance of these genes to produce strongly support nodes under the criterion of maximum parsimony, pursuit of optimal topologies according to the criterion of maximum likelihood proved productive. Discordance between the three MP trees in Figures 6, 7 & 8 became an asset in a sense, as these topologies expanded the

range of treespace used to seed three independent cycles of maximum likelihood parameter estimation and heuristic searches. Using the MP trees as initial conditions biased the likelihood search toward taxon bipartitions recovered in MP analyses, but permitted more efficient model parameter estimation than would have been possible if starting from random trees. For all three data sets, convergence to a stable set of model parameters was striking for two reasons. First, parameters converged to stable values after only the second iteration in 6 out of 9 estimation/search cycles listed in Table 21. This demonstrated the efficacy of MP topologies as starting points to launch ML searches determining model parameters and globally optimal topologies. Second, in all but one case, parameter values converged globally for a given data set regardless of the MP starting topology used to seed the searches. This suggested that, while discordant in relationships among subgroups, the differences among the three MP starting topologies were not so vast as to extend the ML searches into widely dispersed areas of parameter and tree space. Alternatively, global convergence of this sort suggested a relatively smooth likelihood surface efficiently traversed by SPR branch swapping in the heuristic search algorithm.

It was not clear why the combined EF&DDC data globally converged to parameter values when seeded by the EF or DDC MP trees, but converged to a distinct set of parameters when the combined EF&DDC MP tree was the seed topology. While both sets of parameters were similar in absolute values, the latter set resulted in a ML tree with slightly higher likelihood (Figure 11 and Tree 'c2' in Table 21). This topology differed from that obtained by seeding with the EF or DDC MP trees in the orientation of a single terminal lineage: the smerinthine clade [*Paonias*, *Pachysphinx*, *Smerinthus*].

Minor rearrangements among these genera (though each remained monophyletic) were encountered throughout every analysis using both optimality criteria, demonstrating these relationships have yet to be adequately defined and suggesting an area in which increased taxon sampling may be warranted.

Exploration of topological differences between trees derived from a given data set via maximum likelihood versus maximum parsimony provided a glimpse into the ways these data were differentially interpreted under different optimality criteria. Most noticeably, ML analyses incorporating an underlying model of nucleotide substitution did a much better job of reconstructing a reasonable scenario between Sphingidae and their bombycid and saturniid outgroups. While MP trees separated these outgroups from basal sphingid lineages (*Marumba* or Hemarina) by short internal and long terminal branches, ML trees reconstructed outgroup branches as the longest in the entire tree, with a comparably long branch leading to the monophyletic Sphingidae. This stark difference provided another empirical example of the ability for maximum likelihood to more reasonably reconstruct evolutionary history in scenarios of long-branch attraction when maximum parsimony could be positively misleading (Felsenstein 1978, 1985). Another consistent difference between MP and ML trees was relocation of the root from within a paraphyletic assemblage (in MP) to the base of a monophyletic assemblage (in ML). In every case, this had dramatic consequences on the overall tree structure and especially on interpretation of relationships among the three subfamilies. In fact, only the ML trees in Figures 10 and 11 suggested concepts of three strictly monophyletic subfamilies, in the orientation [Macroglossinae, (Smerinthinae, Sphinginae)]. All three MP analyses and even the EF ML analysis rendered at least one subfamily as a basal paraphyletic grade

leading to a sister relationship between the other two subfamilies. Interestingly, at some point in all six trees presented in Figure 6-11 every subfamily assumed that basal paraphyletic position! Given the vast disagreement between trees regarding an issue as basic as subfamily relatedness, the trees presented in this study should be viewed as a new set of phylogenetic hypotheses derived from molecular data, subject to further testing through collection of novel data and implementation of novel analytical techniques.

Despite the fundamental discordance between trees, there were a few areas of agreement which gained some strong support in this study. First, all trees except one (the EF ML topology) suggested a monophyletic Sphinginae whose closest relative was *Hopliocnema*, a single taxon from the smerinthine tribe Sphingulini. The consistency with which this hypothesis recurred suggested the assignment of Sphingulini to the Smerinthinae warrants further scrutiny. However, because this finding was based on sampling a single species, future studies should focus on including several sphingulines before a taxonomic revision is undertaken. Second, the sphingine tribe Acherontiini was reconstructed as monophyletic in every analysis. However, of the three genera sampled in this study, *Coelonia* was part of the tribe only in the EF analyses and switched subfamilies (to Macroglossinae) in analyses involving DDC. Third, the smerinthine tribe Ambulycini was recovered as a monophyletic pair of sister genera in every analysis. However, the position of this tribe relative to other smerinthines was malleable, and its placement often rendered the tribe Smerinthini and/or the entire subfamily Smerinthinae paraphyletic. Fourth, the macroglossine tribe Philampelini, sampled for three species of only one genus (*Eumorpha*), was recovered as monophyletic in every analysis. This was

in fact the only tribe in Macroglossinae supported by phylogenetic analysis in this study. While members of Dilophonotini and Macroglossini consistently clustered together, they never formed monophyletic clades. The dilophonotine section Hemarina was recovered within every analysis, and large portions of Dilophonotina were often recovered, but these were never in a sister relationship. The most stable assemblage in Macroglossinae was section Choerocampina, recovered in every analysis. Interestingly, taxa in this section are characterized by a morphological synapomorphy involving development of functionally viable sound detection apparati on their mouthparts (Roeder 1972; Roeder *et al.* 1968, 1970; Roeder & Treat 1970). The other macroglossine section, Macroglossina, was never recovered as a monophyletic group in any analysis, echoing findings from the Regier 2001 study and calling into question its taxonomic legitimacy. Finally, with the exception of *Darapsa*, all congeneric species sampled in this study grouped together in monophyletic assemblages in almost every analysis. While *Darapsa* was reconstructed as monophyletic in EF, all analyses involving DDC not only embedded Darapsa1778 within *Xylophanes* (i.e., in a different section), but consistently separated it from its congener and a sample sequenced in Regier 2001, DarapsaGB. Given this extreme behavior, a reidentification of specimen GS-02-1778 and clarification of the specimen(s) used in Regier 2001 seems warranted.

In addition to redefining and solidifying the classically recognized taxonomic groups in the Sphingidae, Kitchin & Cadious's (2000) classification provided a handful of finer grain hypotheses of relationships among sphingid genera (see vertical bars in Table 2). Of sixteen such hypotheses, nine were testable given the taxon sample used in this study and six provisional support by analyses from all three data matrices:

a. within Smerinthini: (*Pachysphinx*, *Smerinthus*, *Paonias*), but see above for difficulty interpreting the arrangement among these genera;

b. within Ambulycini: (*Protambulyx*, *Adhemarius*), as discussed above;

c. within Acherontiini: (*Agrius*, *Acherontia*), with confusing placements of *Coelonia*, as discussed above;

d. within Dilophonotina: (*Nyceryx*, *Perigonia*, *Aellopos*);

e. Hemarina, within Dilophonotini: (*Hemaris*, *Cephonodes*), as discussed above;

f. Choerocampina, within Macroglossini, as discussed above.

Kitching & Cadiou's (2000) larger assemblage within Dilophonotina received support with all analyses involving DDC, but EF trees also included *Unzela*, *Cautethia* and Philampelini (*Eumorpha*) in this clade, rendering such a delimitation too restrictive. As with many groupings, the two markers sampled in this study were discordant with respect to this group, so it warrants further investigation.

DIRECTIONS FOR FURTHER ANALYSIS

The suite of analyses in this study represented only a sample of the available analytical tools which could use the EF and DDC data to shed new light on phylogenetic relatedness within the Sphingidae. Other approaches which might be productively applied to these data include:

(1) A comprehensive molecular evolutionary analysis of nucleotide substitution in these genes. Corrected estimates of transition vs. transversion and synonymous vs. nonsynonymous nucleotide changes would help refine relative rate parameter estimates. In addition, model-based distance corrections would permit pairwise

divergence plots to assess degree of saturation across all codon positions in a quantitative fashion.

(2) Differences in empirical base frequencies and uncorrected empirical information content between codon positions suggest they may evolve at different rates. ML relative rate parameter estimates and topology searches could be conducted for each codon position separately as another way to assess the congruence and reliability of phylogenetic signal from each partition.

(3) Topologies derived from ML analyses suffered for having no rigorous assessment of robustness for taxon bipartitions. Convergent model parameters could be fixed and used to generate simulated data sets for use in parametric bootstrapping (Huelsenbeck *et al.* 1996b).

(4) ML estimates of relative rate parameters could be converted to a step matrix for use in 6-parameter parsimony, capitalizing on the differences between optimality criteria and analytical methods to strengthen each approach.

(5) Increased diversity in starting topologies input for ML iterative parameter estimation/searching. Corrected distance-based topologies, morphological hypotheses, and a broader range of MP trees would seed ML analyses in more extensive areas of tree space and permit more exhaustive exploration of the dependence of parameter estimate convergence on initial conditions.

(6) Application of the likelihood ratio tests to assess partition incongruence between various data partitions, especially EF vs. DDC and nt1 vs. nt2 vs. nt3, and combinations thereof.

(7) Expansion of taxon and character sampling, through continued collection of rare sphingid taxa and selection of novel nuclear coding genes informative at lepidopteran family levels.

REFERENCES

Arnett, Jr., R.H. 2000. *American Insects: A Handbook of the Insects of America North of Mexico*. Second Edition. CRC Press LLC, Boca Raton, FL.

Bartholomew, G.A. and T.M. Casey. 1978. Oxygen consumption of moths during rest, pre-flight warm-up, and flight in relation to body size and wing morphology. *Journal of Experimental Biology*, 76: 11-25.

Batra, S.W.T. 1983. Establishment of *Hyles euphorbiae* (L.) (Lepidoptera: Sphingidae) in the United States for control of the weedy spurges *Euphorbia esula* L. and *E.cyparissias* L.. *New York Entomological Society*, 91(4): 304-311.

Bernays, E.A. and D.H. Janzen. 1988. Saturniid and sphingid caterpillars: two ways to eat leaves. *Ecology,* 69(4): 1153-1160.

Borror, D.J., C.A. Triplehorn and N.F. Johnson. 1980. *An Introduction to the Study of Insects*. Saunders College Publishing.

Brock, J.P. 1971. A contribution towards the understanding of the morphology and phylogeny of the Ditrysian Lepidoptera. *Journal of Natural History*, 5: 29-102.

Brown, J.M., O. Pellmyr, J.N. Thompson and R.G. Harrison. 1994. Phylogeny of *Greya* (Lepidoptera: Prodoxidae), based on nucleotide sequence variation in mitochondrial cytochrome oxidase I and II: congruence with morphological data. *Molecular Biology and Evolution*, 11(1): 128-141.

Buckley, T.R., C. Simon and G.K. Chambers. 2001. Exploring among-site rate variation models in a maximum likelihood framework using empirical data: effects of model assumptions on estimates of topology, branch lengths, and bootstrap support. *Systematic Biology*, 50(1): 67-86.

Bull, J.J., J.P. Huelsenbeck, C.W. Cunningham, D.L. Swofford and P.J. Waddell. 1993. Partitioning and combining data in phylogenetic analysis. *Systematic Biology*, 42(3): 384-397.

Bullock, S.H. and A. Pescador. 1983. Wings and proboscis dimensions in a sphingid fauna from western Mexico. *Biotropica*, 15(4): 292-294.

Buttiker, W., H.W. Krenn and J.F. Putterill. 1996. The proboscis of eye-frequenting and piercing Lepidoptera (Insecta). *Zoomorphology*, 116: 77-83.

Casey, T.M. 1976. Flight energetics of sphinx moths: power input during hovering flight. *Journal of Experimental Biology*, 64: 529-543.

Caterino M.S., R.D. Reed, M.M. Kuo and F.A. Sperling. 2001. A partitioned likelihood analysis of swallowtail butterfly phylogeny (Lepidoptera: Papilionidae). *Systematic Biology*, 50(1): 106-127.

Chippindale, P.T. and J.J. Wiens. 1994. Weighting, partitioning and combining characters in phylogenetic analysis. *Systematic Biology*, 43: 278-287.

Cho, S., A. Mitchell, J.C. Regier, C. Mitter, R.W. Poole, T.P. Friedlander and S. Zhao. 1995. A highly conserved nuclear gene for low-level phylogenetics: Elongation Factor-1a recovers morphology-based tree for Heliothine moths. *Molecular Biology and Evolution*, 12(4): 650-656.

Coffelt, M.A. and P.B. Schultz. 1993. Quantification of an aesthetic injury level and threshold for an urban pest management program against orangestriped oakworm (Lepidoptera: Saturniidae). *Journal of Economic Entomology*, 86(5): 1512-1515.

Coffelt, M.A. and P.B. Schultz. 1991. Citizen attitudes toward orangestriped oakworm: impact, control, host aesthetics, and IPM practices. *Journal of Arboriculture*, 17(11): 298-302.

Coffelt, M.A. and P.B. Schultz. 1990. Development of an aesthetic injury level to decrease pesticide use against orangestriped oakworm (Lepidoptera: Saturniidae) in an urban pest management project. *Journal of Economic Entomology*, 83(5): 2044-2049.

Common, I.F.B. 1990. *Moths of Australia*. Melbourne University Press, Carlton, Victoria.

Costa, J.T., J.H. McDonald and N.E. Pierce. 1996. The effect of ant association on the population genetics of the Australian butterfly *Jalmenus evagoras* (Lepidoptera: Lycaenidae). *Biological Journal of the Linnean Society*, 58: 287-306.

Cunningham, C.W. 1997. Is congruence between data partitions a reliable predictor of phylogenetic accuracy? Empirically testing an iterative procedure for choosing among phylogenetic methods. *Systematic Biology*, 46(3): 464-478.

Darlu, P. and G. Lecointre. 2002. When does the incongruence length difference test fail?. *Molecular Biology and Evolution*, 19(4): 432-437.

Darwin, C. 1862. *On the Various Contrivances by which British and Foreign Orchids are Fertilised by Insects, and On the Good Effects of Intercrossing*. John Murray, London, England.

de Queiroz, A., M.J. Donoghue and J. Kim. 1995. Separate versus combined analysis of phylogenetic evidence. *Annual Review of Ecology and Systematics*, 26: 657-681.

Dessauer, H.C., C.J. Cole and M.S. Hafner. 1996. Collection and storage of tissues. Chapter 3, pp. 29-47 *in* Hillis, D.M., C. Moritz and B.K. Mable (Editors), *Molecular Systematics*. Second Edition. Sinauer Associates, Inc., Sunderland, MA.

Dillon, P.M., S. Lowrie and D. McKey. 1983. Disarming the "Evil Woman": petiole constriction by a sphingid larva circumvents mechanical defenses of its host plant, *Cnidoscolus urens* (Euphorbiaceae). *Journal of the Lepidopterists' Society*, 24(4): 267-270.

Dobler, S. and B.D. Farrell. 1999. Host use evolution in Chrysochus milkweed beetles: evidence from behaviour, population genetics and phylogeny. *Molecular Ecology,* 8: 1297-1307.

Don, R.H., P.T. Cox, B.J. Wainwright, K. Baker and J.S. Mattick. 1991. 'Touchdown' PCR to circumvent spurious priming during gene amplification. *Nucleic Acids Research*, 19(14): 4008.

Dowton, M. and A.D. Austin. 2002. Increased congruence does not necessarily indicate increased phylogenetic accuracy: the behavior of the incongruence length difference test in mixed-model analyses. *Systematic Biology*, 51(1): 19-31.

Dyer, L.A. 1995. Tasty generalists and nasty specialists? Antipredator mechanisms in tropical lepidopteran larvae. *Ecology,* 76(5): 1483-1496.

Edwards, J.B.D.M., P. Ravassard, C. Icard-Liepkalns and J. Mallet. 1995. cDNA cloning by RT-PCR. Chapter 6, pp. 89-118 *in* McPherson, M.J., B.D. Hames and G.R. Taylor (Editors), *PCR2: A Practical Approach*. Oxford University Press, Oxford, England.

Eernisse, D.J. and A.G. Kluge. 1993. Taxonomic congruence versus total evidence, and amniote phylogeny inferred from fossils, molecules, and morphology. *Molecular Biology and Evolution*, 10(6): 1170-1195.

Eisikowitch, D. and J. Galil. 1971. Effect of wind on the pollination of *Pancratium maritimum* L. (Amaryllidaceae) by hawkmoths (Lepidoptera: Sphingidae). *Journal of Animal Ecology*, 40: 673-678.

Faith, D.P. 1991. Cladistic permutation tests for monophyly and nonmonophyly. *Systematic Zoology*, 40(3): 366-375.

Faith, D.P. and P.S. Cranston. 1991. Could a cladogram this short have arisen by chance alone?: Permutation tests for cladistic structure. *Cladistics*, 7: 1-28.

Fang, Q.Q., A. Mitchell, J.C. Regier, C. Mitter, T.P. Friedlander and R.W. Poole. 2000. Phylogenetic utility of the nuclear gene Dopa Decarboxylase in Noctuid moths (Insecta: Lepidoptera: Noctuoidea). *Molecular Phylogenetics and Evolution*, 15(3): 473-486.

Fang, Q.Q., S. Cho, J.C. Regier, C. Mitter, M. Matthews, R.W. Poole, T.P. Friedlander and S. Zhao. 1997. A new nuclear gene for insect phylogenetics: Dopa Decarboxylase is informative of relationships within Heliothinae (Lepidoptera: Noctuidae). *Systematic Biology*, 46(2): 269-283.

Fanger, H. 1999. Comparative morphology of tergal phragmata occurring in the dorsal thoraco-abdominal junction of ditrysian Lepidoptera (Insecta). *Zoomorphology*, 119: 163-183.

Farrell, B.D. 2001. Evolutionary assembly of the milkweed fauna: cytochrome oxidase I and the age of *Tetraopes* beetles. *Molecular Phylogenetics and Evolution*, 18(1): -.

Farrell, B.D. 1998. "Inordinate Fondness" explained: why are there so many beetles?. *Science*, 281: 555-559.

Farrell, B.D. 1993. Phylogenetic determinants of insect/plant community diversity. *In* Ricklefs, R.E. and D. Schluter (Editors). *Species Diversity in Ecological Communities: Historical and Geographical Perspectives*. University of Chicago Press, Chicago, IL.

Farrell, B.D., A. Sequeira, B. O'Meara, B. Normark, J. Chung and B. Jordal. 2001. The evolution of agriculture in beetles (Curculionidae: Scolytinae and Platypodinae). *Evolution*, 55(10): 2011-2027.

Farrell, B.D. and C. Mitter. 1994. Adaptive radiation in insects and plants: time and opportunity. *American Zoologist*, 34: 57-69.

Farrell, B.D. and C. Mitter. 1990. Phylogenesis of insect/plant interactions: have *Phyllobrotica* leaf beetles (Chrysomelidae) and the Lamiales diversified in parallel?. *Evolution*, 44(6): 1389-1403.

Farrell, B.D., C. Mitter and D.J. Futuyma. 1992. Diversification at the insect-plant interface: insights from phylogenetics. *Bioscience*, 42(1): 34-42.

Farris, J.S. 1989a. The retention index and homoplasy excess. *Systematic Biology*, 38: 406-407.

Farris, J.S. 1989b. The retention index and the rescaled consistency index. *Cladistics*, 5: 417-419.

Felsenstein, J. 1973. Maximum likelihood and minimum-steps methods for estimating evolutionary trees from data on discrete characters. *Systematic Zoology*, 22: 240-249.

Felsenstein, J. 1978. Cases in which parsimony or compatibility methods will be positively misleading. *Systematic Zoology*, 27: 401-410.

Felsenstein, J. 1981a. A likelihood approach to character weighting and what it tells us about parsimony and compatibility. *Biological Journal of the Linnean Society*, 16: 183-196.

Felsenstein, J. 1981b. Evolutionary trees from DNA sequences: a maximum likelihood approach. *Journal of Molecular Evolution*, 17: 368-376.

Felsenstein, J. 1985. Confidence limits on phylogenies: an approach using the bootstrap. *Evolution*, 39(4): 783-791.

Felsenstein, J. and E. Sober. 1986. Parsimony and likelihood: an exchange. *Systematic Zoology*, 35(4): 617-626.

Felsenstein, J. and H. Kishino. 1993. Is there something wrong with the bootstrap on phylogenies? A reply to Hillis and Bull. *Systematic Biology*, 42: 193-200.

Fink, L.S. 1995. Foodplant effects on colour morphs of *Eumorpha fasciata* (Lepidoptera: Sphingidae). *Journal of the Linnaean Society*, 56(3): 423-437.

Fleming, R.C. 1968. Head musculature of sphinx moths (Lepidoptera: Sphingidae). *Contributions of the American Entomological Institute*, 3(3): 1-32.

Friedlander, T.P., J.C. Regier and C. Mitter. 1992. Nuclear gene sequences for higher phylogenetic analysis: 14 promising candidates. *Systematic Biology*, 41(4): 483-490.

Friedlander, T.P., J.C. Regier, C. Mitter and D.L. Wagner. 2000. Evolution of heteroneuran Lepidoptera (Insecta) and the utility of dopa decarboxylase for Cretaceous-age phylogenetics. *Zoological Journal of the Linnean Society*, 130: 213-234.

Friedlander, T.P., K.R. Horst, J.C. Regier, C. Mitter, R.S. Piegler and Q.Q. Fang. 1998. Two nuclear genes yield concordant relationships within Attacini (Lepidoptera: Saturniidae). *Molecular Phylogenetics and Evolution*, 9(1): 131-140.

Fukami, K. and Y. Tateno. 1989. On the maximum likelihood method for estimating molecular trees: uniqueness of the likelihood point. *Journal of Molecular Evolution*, 28: 460-464.

Fullard, J.H. and J.E. Yack. 1993. The evolutionary biology of insect hearing. *Trends in Ecology and Evolution*, 8(7): 248-252.

Funk, D.J., L. Helbling, J.J. Wernegreen and N.A. Moran. 2000. Intraspecific phylogenetic congruence among multiple symbiont genomes. *Proceedings of the Royal Society of London, Series B Biological Sciences*, 267: 2517-2521.

Gaut, B.S. and P.O. Lewis. 1995. Success of maximum likelihood phylogeny inference in the four-taxon case. *Molecular Biology and Evolution*, 12(1): 152-162.

Ghiradella, H. 1998. Hairs, Bristles, and Scales. Chapter 11, pp. 257-287 *in* Harrison, F.W. and M. Locke (Editors), *Microscopic Anatomy of Invertebrates. Volume 11A: Insecta*. Wiley-Liss, Inc., New York, NY.

Goldman, N. 1990. Maximum likelihood inference of phylogenetic trees, with special reference to a poisson process model of DNA substitution and to parsimony analyses. *Systematic Zoology*, 39: 345-361.

Goldsmith, M.R. and A.S. Wilkins. 1995. *Molecular Model Systems in the Lepidoptera*. Cambridge University Press, Cambridge, England.

Gopfert, M.C., A. Surlykke and L.T. Wasserthal. 2002. Tympanal and atympanal 'mouth-ears' in hawkmoths (Sphingidae). *Proceedings of the Royal Society of London, Series B Biological Sciences*, 269: 89-95.

Gopfert, M.C. and L.T. Wasserthal. 1999a. Auditory sensory cells in hawkmoths: identification, physiology and structure. *Journal of Experimental Biology*, 202: 1579-1587.

Gopfert, M.C. and L.T. Wasserthal. 1999b. Hearing with the mouthparts: behavioural responses and the structural basis of ultrasound perception in acherontiine hawkmoths. *Journal of Experimental Biology*, 202: 909-918.

Grant, V. 1983. The systematic and geographical distribution of hawkmoth flowers in the temperate North American fauna. *Botanical Gazette*, 144(3): 439-449.

Grant, V. and K.A. Grant. 1983a. Behavior of hawkmoths on flowers of *Datura meteloides*. *Botanical Gazette*, 144(2): 280-284.

Grant, V. and K.A. Grant. 1983b. Hawkmoth pollination of *Mirabilis longiflora* (Nyctaginaceae). *Proceedings of the National Academy of Sciences*, 80: 1298-1299.

Grant, G.G. and J.L. Eaton. 1973. Scent brushes of the male tobacco hornworm *Manduca sexta* (Lepidoptera: Sphingidae). *Annals of the Entomological Society of America*, 66(4): 901-904.

Grodnitsky, D.L. 1999. Wing morphology and evolution in the Amphiesmenoptera. Chapter 4.2, pp. 125-143 *in* Grodnitsky, D.L. (Editor), *Form and Function of Insect Wings: The Evolution of Biological Structures*. The Johns Hopkins University Press, Baltimore, MD.

Gu, X., Y.-X. Fu and W.-H. Li. 1995. Maximum likelihood estimation of the heterogeneity of substitution rate among nucleotide sites. *Molecular Biology and Evolution*, 12: 546-557.

Haber, W.A. 1984. Pollination by deceit in a mass-flowering tropical tree *Plumeria rubra* L. (Apocynaceae). *Biotropica*, 16(4): 269-275.

Haber, W.A. and G.W. Frankie. 1989. A tropical hawkmoth community: Costa Rican dry forest Sphingidae. *Biotropica*, 21(2): 155-172.

Haber, W.A. and G.W. Frankie. 1982. Pollination of *Luehea* (Tiliaceae) in Costa Rican deciduous forest. *Ecology,* 63(6): 1740-1750.

Harshman, J. 1994. The effect of irrelevant characters on bootstrap values. *Systematic Biology*, 43(3): 419-424.

Harvey, P.H. and M.D. Pagel. 1991. *The Comparative Method in Evolutionary Biology*. Oxford Press, Oxford, England.

Hasegawa, M., H. Kishino and N. Saitou. 1991. On the maximum likelihood method in molecular phylogenetics. *Journal of Molecular Evolution*, 32: 443-445.

Hasegawa, M., H. Kishino and T. Yano. 1985. Dating of the human-ape splitting by a molecular clock of mitochondrial DNA. *Journal of Molecular Evolution*, 22: 160-174.

Hatzopoulos, A.K. and J.C. Regier. 1987. Evolutionary changes in the developmental expression of silkmoth chorion genes and their morphological consequences. Proceedings of the National Academy of Sciences, 84: 479-483.

Hawthorne, D.J. and S. Via. 2001. Genetic linkage of ecological specialization and reproductive isolation in pea aphids. Nature, 412: 904-907.

Heinrich, B. 1971a. Temperature regulation of sphinx moth, *Manduca sexta*. 1. Flight energetics and body temperature during free and tethered flight. *Journal of Experimental Biology*, 54(1): 141-.

Heinrich, B. 1971b. Temperature regulation of sphinx moth, *Manduca sexta*. 2. Regulation of heat loss by control of blood circulation. *Journal of Experimental Biology*, 54(1): 153-.

Heinrich, B. and G.A. Bartholo. 1971. Analysis of pre-flight warm-up in sphinx moth, *Manduca sexta*. *Journal of Experimental Biology*, 55(1): 223.

Hendy, M.D. and D. Penny. 1989. A framework for the quantitative study of evolutionary trees. *Systematic Zoology*, 38(4): 297-309.

Hillis, D.M., C. Moritz and B.K. Mable (Editors). 1996. *Molecular Systematics*. Second Edition. Sinauer Associates, Inc., Sunderland, MA.

Hillis, D.M. and J.J. Bull. 1993. An empirical test of bootstrapping as a method for assessing confidence in phylogenetic analysis. *Systematic Biology*, 42(2): 182-192.

Hiruma, K., M.S. Carter and L.M. Riddiford. 1995. Characterization of the Dopa Decarboxylase gene of *Manduca sexta* and its suppression by 20-hydroxyecdysone. *Developmental Biology*, 169: 195-209.

Hodges, R.W. 1971. *The Moths of North America North of Mexico. Fascicle 21: Sphingoidea (Hawkmoths)*. E.W. Classey Limited & R.B.D. Publications, Inc., London, England.

Hovemann, B., S. Richter, U. Walldorf and C. Cziepluch. 1988. Two genes encode related cytoplasmic elongation factors 1alpha (EF-1alpha) in *Drosophila melanogaster* with continuous and stage specific expression. *Nucleic Acids Research*, 16(8): 3175-3194.

Huelsenbeck, J.P. 1995. The robustness of two phylogenetic methods: four-taxon simulations reveal a slight superiority of maximum likelihood over neighbor joining. *Molecular Biology and Evolution*, 12: 843-849.

Huelsenbeck, J.P. and K.A. Crandall. 1997. Phylogeny estimation and hypothesis testing using maximum likelihood. *Annual Review of Ecology and Systematics*, 28: 437-466.

Huelsenbeck, J.P., D.M. Hillis and R. Jones. 1996. Parametric bootstrapping in molecular phylogenetics: applications and performance. Chapter 2, pp. 19-45 *in* Ferraris, J.D. and S.R. Palumbi (Editors), *Molecular Zoology: Advances, Strategies, and Protocols*. Wiley-Liss, Inc., New York, NY.

Huelsenbeck, J.P., J.J. Bull and C.W. Cunningham. 1996. Combining data in phylogenetic analysis. *Trends in Ecology and Evolution*, 11(4): 152-157.

Hufbauer, R.A. and S. Via. 1999. Evolution on an aphid-parasitoid interaction: variation in resistance to parasitism among aphid populations specialized on different plants. *Evolution*, 53(5): 1435-1445.

Janzen, D.H. 1988. Ecological characterization of a Costa Rican dry forest caterpillar fauna. *Biotropica*, 20(2): 120-135.

Janzen, D.H. 1984. Two ways to be a tropical big moth: Santa Rosa saturniids and sphingids. Pp. 85-140 *in* Dawkins, R. and M. Ridley (Editors), *Oxford Surveys in Evolutionary Biology*. Volume 1. Oxford University Press, Oxford, England.

Janzen, D.H. 1981. Patterns of herbivory in a tropical deciduous forest. *Biotropica*, 13(4): 271-282.

Janzen, D.H. and P.G. Waterman. 1984. A seasonal census of phenolics, fibre and alkaloids in foliage of forest trees in Costa Rica: some factors influencing their distribution and relation to host selection by Sphingidae and Saturniidae. *Journal of the Linnaean Society*, 21(4): 439-454.

Kamiie, K., H. Taira, H. Ooura, A. Kakuta, S. Matsumoto, S. Ejiri and T. Katsumata. 1993. Nucleotide sequence of the cDNA encoding silk gland elongation factor 1a. *Nucleic Acids Research*, 21(3): 742-742.

Kelley, S.T., B.D. Farrell and J.B. Mitton. 2000. Effects of specialization on genetic differentiation in sister species of bark beetles. *Heredity*, 84: 218-227.

Kelley, S.T. and B.D. Farrell. 1998. Is specialization a dead end? The phylogeny of host use in *Dendroctonus* bark beetles (Scolytidae). *Evolution*, 52(6): 1731-1743.

Kishino, H. and H. Hasegawa. 1989. Evaluation of the maximum likelihood estimate of the evolutionary tree topologies from DNA sequence data, and the branching order in Hominoidea. *Journal of Molecular Evolution*, 29: 170-179.

Kitching, I.J. 2002. The phylogenetic relationships of Morgan's Sphinx, *Xanthopan morganii* (Walker), the tribe Acherontiini, and allied long-tongued hawkmoths (Lepidoptera: Sphingidae, Sphinginae). *Zoological Journal of the Linnean Society*, 135: 471-527.

Kitching, I.J. and J.-M. Cadiou. 2000. *Hawkmoths of the World: An Annotated and Illustrated Revisionary Checklist (Lepidoptera: Sphingidae)*. The Natural History Museum, London, England.

Kluge, A.G. and J.S. Farris. 1969. Quantitative phyletics and the evolution of anurans. *Systematic Zoology*, 18: 1-32.

Krenn, H.W. 2000. Proboscis musculature in the butterfly *Vanessa cardui* (Nymphalidae, Lepidoptera): settling the proboscis recoiling controversy. *Acta Zoologica*, 81: 259-266.

Krenn, H.W. 1998. Proboscis sensilla in *Vanessa cardui* (Lepidoptera: Nymphalidae): functional morphology and significance in flower-probing. *Zoomorphology*, 118: 23-30.

Krenn, H.W. 1997. Proboscis assembly in butterflies: a once in a lifetime sequence of events. *European Journal of Entomology*, 94: 495-501.

Krenn, H.W. 1990. Functional morphology and movements of the proboscis of Lepidoptera (Insecta). *Zoomorphology*, 110: 105-114.

Krenn, H.W. and N.P. Kristensen. 2000. Early evolution of the proboscis of Lepidoptera (Insecta): external morphology of the galea in basal glossotan moths lineages, with remarks on the origin of the pilifers. *Zoologischer Anzeiger*, 239: 179-196.

Kristensen, N.P. (Editor). *Lepidoptera, Moths and Butterflies, Volume 1: Evolution, Systematics, and Biogeography*. *In* M. Fischer (Ed.), *Handbook of Zoology: A Natural History of the Phyla of the Animal Kingdom, Volume IV Arthropoda: Insecta*, Part 35. Walter de Gruyter, Inc., Hawthorne, NY.

Kritsky, G. 1991. Darwin's Madagascan hawkmoth prediction. *American Entomologist*, 37: 206-210.

Lanave, C., G. Preparata, C. Saccone and G. Serio. 1984. A new method for calculating evolutionary substitution rates. *Journal of Molecular Evolution*, 20: 86-93.

LeClerc, R.F. and J.C. Regier. 1993. Choriogenesis in Lepidoptera: morphogenesis, protein synthesis, specific mRNA accumulation and primary structure of a chorion cDNA from the gypsy moth. *Developmental Biology*, 160(1): 28-38.

Lemaire, C. and J. Minet. 1999. The Bombycoidea and their Relatives. Chapter 14, pp. 321-353 *in* Kristensen, N.P. (Editor), *Lepidoptera, Moths and Butterflies, Volume 1: Evolution, Systematics, and Biogeography*. Walter de Gruyter, Inc., Hawthorne, NY.

Liu, H., C.P. Ellington, K. Kawachi, C. Van den Berg and A.P. Willmott. 1998. A computational fluid dynamic study of hawkmoth hovering. *Journal of Experimental Biology*, 201(4): 461-477.

Mabberley, D.J. 1997. *The Plant Book: A Portable Dictionary of the Vascular Plants*. Second Edition. Cambridge University Press, Cambridge, England.

Maddison, D.R. 1991. The discovery and importance of multiple islands of most-parsimonious trees. *Systematic Zoology*, 40(3): 315-328.

Maddison, D.R., D.L. Swofford and W.P. Maddison. 1997. NEXUS: An extensible file format for systematic information. *Systematic Biology*, 46(4): 590-621.

Mason-Gamer, R.J. and E.A. Kellogg. 1996. Testing for conflict among molecular data sets in the tribe Triticeae (Gramineae). *Systematic Biology*, 45(4): 524-545.

Mazur, G.D., J.C. Regier and F.C. Kafatos. 1989. Morphogenesis of silkmoth chorion: sequential modification of an early helicoidal framework through expansion and densification. *Tissue and Cell*, 21: 227-242.

Mickevich, M.F. and J.S. Farris. 1981. The implications of congruence in *Menidia*. *Systematic Zoology*, 30(3): 351-370.

Miller, R.B. 1981. Hawkmoths and the geographic patterns of floral variation in *Aquilegia caerulea*. *Evolution*, 35(4): 763-774.

Miller, W.E. 1997a. Body weight as related to wing measure in hawkmoths (Sphingidae). *Journal of the Lepidopterists' Society*, 51(1): 91-92.

Miller, W.E. 1997b. Diversity and evolution of tongue length in hawkmoths (Sphingidae). *Journal of the Lepidopterists' Society*, 51(1): 9-31.

Miller, W.E. 1996. Population behavior and adult feeding capability in Lepidoptera. *Environmental Entomology*, 25(2): 213-226.

Minet, J. 1994. The Bombycoidea: phylogeny and higher classification (Lepidoptera: Glossata). *Entomologica Scandinavica*, 25: 63-88.

Minet, J. 1991. Tentative reconstruction of the ditrysian phylogeny (Lepidoptera: Glossata). *Entomologica Scandinavica*, 22: 69-95.

Minet, J. 1986. Ebauche d'une classification moderne de l'ordre des Lepidopteres. *Alexanor*, 14: 291-313.

Mitchell, A., C. Mitter and J.C. Regier. 2000. More taxa or more characters revisited: combining data from nuclear protein-encoding genes for phylogenetic analyses of Noctuoidea (Insecta: Lepidoptera). *Systematic Biology*, 49(2): 202-224.

Mitchell, A., S. Cho, J.C. Regier, C. Mitter, R.W. Poole and M. Matthews. 1997. Phylogenetic utility of Elongation Factor-1a in Noctuoidea (Insecta: Lepidoptera): the limits of synonymous substitution. *Molecular Biology and Evolution*, 14(4): 381-390.

Mitter, C.M. and B.D. Farrell. 1991. Macroevolutionary aspects of insect-plant relationships. Chapter 2, pp. 35-78 *in* Bernays, E. (Editor), *Insect Plant Interactions*, Volume 3. CRC Press, Boca Raton, FL.

Mitter, C., B.D. Farrell and D.J. Futuyma. 1991. Phylogenetic studies of insect-plant interactions: insights into the genesis of diversity. *Trends in Ecology and Evolution*, 6(9): 290-293.

Mitter, C., B.D. Farrell and B. Wiegmann. 1988. The phylogenetic study of adaptive zones: has phytophagy promoted insect diversification?. American Naturalist, 132(1): 107-128.

Miyamoto, M.M. and W.M. Fitch. 1995. Testing species phylogenies and phylogenetic methods with congruence. *Systematic Biology*, 44(1): 64-76.

Nilsson, L.A. 1998. Deep flowers for long tongues. *Trends in Ecology and Evolution*, 13(11): 259-260.

Nilsson, L.A. 1988. The evolution of flowers with deep corolla tubes. *Nature*, 334: 147-149.

Nilsson, L.A., L. Jonsson, L. Ralison and E. Randrianjohany. 1987. Angraecoid orchids and hawkmoths in central Madagascar: specialized pollination systems and generalist foragers. *Biotropica*, 19(4): 310-318.

Nilsson, L.A., L. Jonsson, L. Rason and E. Randrianjohany. 1985. Monophily and pollination mechanisms in *Angraecum arachnites* Schltr. (Orchidaceae) in a guild of long-tongued hawk-moths (Sphingidae) in Madagascar. *Biological Journal of the Linnaean Society*, 26: 1-19.

O'Brien, D. 1999. Fuel use in flight and its dependence on nectar feeding in the hawkmoth *Amphion floridensis*. *Journal of Experimental Biology*, 202: 441-451.

O'Brien, D.M. and R.K. Suarez. 2001. Fuel use in hawkmoth (*Amphion floridensis*) flight muscle: enzyme activities and flux rates. *Journal of Experimental Zoology*, 290: 108-114.

O'Brien, D.M., D.P. Schrag and C. Martinez del Rio. 2000. Allocation to reproduction in a hawkmoth: a quantitative analysis using stable isotopes. *Ecology,* 81(10): 2822-2831.

Ojeda-Avila, T., H.A. Woods and R.A. Raguso. 2003. Effects of dietary variation on growth, composition, and maturation of *Manduca sexta* (Sphingidae : Lepidoptera). *Journal of Insect Physiology*, 49(4): 293-306.

Ojeda-Avila, T., H.A. Woods and R.A. Raguso. 2001. Effects of dietary variation on growth, composition, and maturation of *Manduca sexta*. *American Zoologist*, 41(6): 1545-1545.

Olmstead, R.G. and J.A. Sweere. 1994. Combining data in phylogenetic systematics: An empirical approach using three molecular data sets in the Solanaceae. *Systematic Biology*, 43(4): 467-481.

Otto, P., D. Kephart and R. Bitner. 1998. Separate isolation of genomic DNA and total RNA from single samples using the SV Total RNA Isolation System. *Promega Notes*, 69: 19-24.

Page, R. D. M. 1993. On islands of trees and the efficacy of different methods of branch swapping in finding most-parsimonious trees. *Systematic Biology*, 42: 200-210.

Paige, R.T. and T.G. Whitham. 1985. Individual and population shifts in flower color by scarlet gilia: a mechanism for pollinator tracking. *Science*, 227: 315-317.

Penny, D. and M.D. Hendy. 1986. Estimating the reliability of evolutionary trees. *Molecular Biology and Evolution*, 3: 403-417.

Pierce, N.E. 1995. Predatory and parasitic Lepidoptera: carnivores living on plants. *Journal of the Lepidopterists' Society*, 49(4): 412-453.

Pierce, N.E. 1987. The evolution and biogeography of associations between lycaenid butterflies and ants. Pp. 89-116 *in* Harvey, P. and L. Partridge (Editors), *Oxford Surveys in Evolutionary Biology*. Volume 4. Oxford University Press, Oxford, England.

Post, R.J., P.K. Flook and A.L. Millest. 1993. Methods for the preservation of insects for DNA studies. *Biochemical Systematics and Ecology,* 21(1): 85-92.

Powell, J.A., C. Mitter and B.D. Farrell. 1999. Evolution of Larval Food Preferences in Lepidoptera. Chapter 20, pp. 403-422 *in* Kristensen, N.P. (Editor), *Lepidoptera, Moths and Butterflies, Volume 1: Evolution, Systematics, and Biogeography*. Walter de Gruyter, Inc., Hawthorne, NY.

Price, P.W. 1997. *Insect Ecology*. Third Edition. John Wiley & Sons, New York, NY.

Raguso, R.A and M.A. Willis. 2002. Synergy between visual and olfactory cues in nectar feeding by naive hawkmoths, *Manduca sexta*. *Animal Behavior*, 64: 685-695.

Raguso, R.A and D.M. Light. 1998. Electroantennogram responses of male *Sphinx perelegans* hawkmoths to floral and 'green-leaf volatiles'. *Entomologia Experimentalis et Applicata*, 86(3): 287-293.

Raguso, R.A., D.M. Light and E. Pickersky. 1996. Electroantennogram responses of Hyles lineata (Sphingidae: Lepidoptera) to volatile compounds from *Clarkia breweri* (Onagraceae) and other moth-pollinated flowers. *Journal of Chemical Ecology,* 22(10): 1735-1766.

Reeves, J.H. 1992. Heterogeneity in the substitution process of amino acid sites of proteins coded for by mitochondrial DNA. *Journal of Molecular Evolution*, 35: 17-31.

Regier, J.C., C. Mitter, R.S. Piegler and T.P. Friedlander. 2002. Monophyly, composition, and relationships within Saturniinae (Lepidoptera: Saturniidae): evidence from two nuclear genes. *Insect Systematics and Evolution*, 33(1): 9-21.

Regier, J.C., C. Mitter, T.P. Friedlander and R.S. Peigler. 2001. Phylogenetic relationships in Sphingidae (Insecta: Lepidoptera): initial evidence from two nuclear genes. *Molecular Phylogenetics and Evolution*, 20(2): 311-325.

Regier, J.C., C. Mitter, R.S. Piegler and T.P. Friedlander. 2000. Phylogenetic relationships in Lasiocampidae (Lepidoptera): initial evidence from elongation factor 1-alpha sequences. *Insect Systematics and Evolution*, 31(2): 179-186.

Regier, J.C. and J.W. Shultz. 1997. Molecular phylogeny of the major arthropod groups indicates polyphyly of crustaceans and a new hypothesis for the origin of hexapods. *Molecular Biology and Evolution*, 14(9): 902-913.

Regier, J.C., T.P. Friedlander, R.F. Leclerc, C. Mitter and B. Wiegmann. 1995. Lepidopteran phylogeny and applications to comparative studies of development. Chapter 4, pp. 107-137 *in* Goldsmith, M.R. and A.S. Wilkins (Editors), *Molecular Model Systems in the Lepidoptera*. Cambridge University Press, Cambridge, England.

Regier, J.C., C. Cole and R.F. LeClerc. 1993. Cell specific expression in the silkmoth follicle: developmental characterization of a major chorion protein, its mRNA and gene. *Developmental Biology*, 160: 236-245.

Regier, J.C. and F.C. Kafatos. 1991. Molecular genetics in the study of development and evolution: the insect chorion. Pp. 98-132 *in* Vinson, S.B. and R.L. Metcalf (Editors), *Entomology Serving Society: Emerging Technologies and Challenges*. Entomological Society of America, Lanham, MD.

Robinson, G.S. and H.S. Robinson. 1972. Genital stridulation in male *Psilogramma jordana* Bethune-Baker (Lepidoptera, Sphingidae). *The Entomologist's Record and Journal of Variation*, 84: 212-215.

Rodriguez, F., J.L. Olizer, A. Marin and J.R. Medina. 1990. The general stochastic model of nucleotide substitution. *Journal of Theoretical Biology*, 142: 485-501.

Roeder, K.D. 1972. Acoustic and mechanical sensitivity of the distal lobe of the pilifer in choerocampine hawkmoths. *Journal of Insect Physiology*, 18: 1249-1264.

Roeder, K.D., A.E. Treat and J.S. Vandeberg. 1970. Distal lobe of the pilifer: an ultransonic receptor in choerocampine hawkmoths. *Science*, 170: 1098-1099.

Roeder, K.D. and A.E. Treat. 1970. An acoustic sense in some hawkmoths (Choerocampinae). *Journal of Insect Physiology*, 16: 1069-1086.

Roeder, K.D., A.E. Treat and J.S. Vandeberg. 1968. Auditory sense in certain sphingid moths. *Science*, 159: 331-333.

Rogers, J.S. 1997. On the consistency of maximum likelihood estimation of phylogenetic trees from nucleotide sequences. *Systematic Biology*, 46(2): 354-357.

Rothschild, L.W. and K. Jordan. 1903. A revision of the lepidopterous family Sphingidae. *Novitates Zoologicae*, 9: 1-972.

Saitou, N. 1990. Maximum likelihood methods. *Methods in Enzymology*, 183: 584-598.

Saitou, N. 1988. Property and efficiency of the maximum likelihood method for molecular phylogeny. *Journal of Molecular Evolution*, 183: 261-273.

Sanderson, M.J. 1995. Objections to bootstrapping phylogenies: A critique. *Systematic Biology*, 44(3): 299-320.

Sanderson, M.J. 1989. Confidence limits on phylogenies: the bootstrap revisited. *Cladistics*, 5: 113-129.

Schmitz, A. and L.T. Wasserthal. 1999. Comparative morphology of the spiracles of the Papilionidae, Sphingidae, and Saturniidae (Insecta: Lepidoptera). *International Journal of Insect Morphology*, 28: 13-26.

Scoble, M.J. 1992. *The Lepidoptera. Form, Function and Diversity*. Oxford University Press, Oxford, England.

Scriber, J.M. 1979. Effects of leaf water supplementation upon post-ingestive nutritional indices of forb-, shrub-, vine-, and tree-feeding Lepidoptera. *Entomologia Experimentalis et Applicata*, 25: 240-252.

Sequeira, A., B.B. Normark and B.D. Farrell. 2000. Evolutionary assembly of the conifer fauna: distinguishing ancient from recent associations in bark beetles. *Proceedings of the Royal Society of London, Series B Biological Sciences*, 267: 2359-2366.

Shaw, K.L. 1996a. Polygenic inheritance of a behavioral phenotype: interspecific genetics of song in the Hawaiian cricket genus *Laupala*. *Evolution*, 50(1): 256-266.

Shaw, K.L. 1996b. Sequential radiations and patterns of speciation in the Hawaiian cricket genus *Laupala* inferred from DNA sequences. *Evolution*, 50(1): 237-255.

Sidow, A., T. Nguyen and T.P. Speed. 1992. Estimating the fraction of invariable codons with a capture-recapture method. *Journal of Molecular Evolution*, 35: 253-260.

Siebert, P.D. 1999. Quantitative RT-PCR. Chapter 4, pp. 61-85 *in* Kochanowski, B. and U. Reischl (Editors), *Quantitative PCR Protocols*. Humana Press, Totowa, NJ.

Siebert, P.D. and J.W. Larrick. 1995. Introduction and Overview. Chapter 1, pp. 1-20 *in* Larrick, J.W. and P.D. Siebert (Editors), *Reverse Transcriptase PCR*. Ellis Horwood, Ltd., London, England.

Sober, E. 1984. A likelihood justification of parsimony. *Cladistics*, 1: 209-233.

Sorhannus, U. and C. Van Bell. 1999. Testing for equality of molecular evolutionary rates: a comparison between a relative-rate test and a likelihood ratio test. *Molecular Biology and Evolution*, 16(6): 849-855.

Stamp, N.E. and T.M. Casey. 1993. *Caterpillars: Ecological and Evolutionary Constraints on Foraging*. Chapman & Hall Press, New York, NY.

Steel, M.A., L. Szekely, P.L. Erdos and P.J. Waddell. 1993. A complete family of phylogenetic invariants for any number of taxa under Kimura's 3ST model. *New Zealand Journal of Botany*, 31: 289-296.

Sullivan, J., D.L. Swofford and G.J.P. Naylor. 1999. The effect of taxon sampling on estimating rate heterogeneity parameters of maximum-likelihood models. *Molecular Biology and Evolution*, 16(10): 1347-1356.

Sullivan, J. and D.L. Swofford. 1997. Are guinea pigs rodents? The importance of adequate models in molecular phylogenies. *Journal of Mammalian Evolution*, 4(2): 77-86.

Swofford, D.L. 2003. *PAUP*: Phylogenetic Analysis Using Parsimony (* and Other Methods)*. Version 4.0b10. Sinauer Associates, Inc., Sunderland, MA.

Swofford, D.L., G.J. Olsen, P.J. Waddell and D.M. Hillis. 1996. Phylogenetic Inference. Chapter 11, pp. 407-514 *in* Hillis, D.M., C. Moritz and B.K. Mable (Editors), *Molecular Systematics*. Second Edition. Sinauer Associates, Inc., Sunderland, MA.

Tatarenkov, A., J. Kwiatowski, D. Skarecky, E. Barrio and F.J. Ayala. 1999. On the evolution of Dopa Decarboxylase (Ddc) and Drosophila systematics. *Journal of Molecular Evolution*, 48: 445-462.

Tateno Y, Takezaki N, Nei M. 1993. Relative efficiencies of the maximum likelihood, maximum parsimony, and neighbor-joining methods for estimating protein phylogeny. *Molecular Phylogenetics and Evolution*, 2: 1-5.

Wagner, D.L. 2001. Moths. Pp. 249-270 in *Encyclopedia of Biodiversity*. Volume 4 Academic Press, London, England.

Wannenmacher, G. and L.T. Wasserthal. 2003. Contribution of the maxillary muscles to proboscis movement in hawkmoths (Lepidoptera : Sphingidae) - an electrophysiological study. *Journal of Insect Physiology*, 49(8): 765-776.

Wasserthal, L.T. 2001. Flight-motor-driven respiratory air flow in the hawkmoth *Manduca sexta*. *Journal of Experimental Biology*, 204(13): 2209-2220.

Wasserthal, L.T. 1998. Deep flowers for long tongues. *Trends in Ecology and Evolution*, 13(11): 459-460.

Wasserthal, L.T. 1997. The pollinators of the Malagasy star orchids *Angraecum sesquipedale*, *A.sororium* and *A.compactum* and the evolution of extremely long spurs by pollinator shift. *Botanica Acta*, 110: 343-359.

Weller, S.J., D.P. Pashley, J.A. Martin and J.L. Constable. 1994. Phylogeny of noctuoid moths and the utility of combining independent nuclear and mitochondrial genes. *Systematic Biology*, 43(2): 194-211.

White, R.H., R.D. Stevenson, R.R. Bennet, D.E. Cutler and W.A. Haber. 1994. Wavelength discrimination and the role of ultraviolet vision in the feeding behavior of hawkmoths. *Biotropica*, 26(4): 427-435.

Wiegmann, B.M., C. Mitter and B.D. Farrell. 1993. Diversification of carnivorous parasitic insects: extraordinary radiation or specialized dead end? *American Naturalist*, 142(5): 737-754.

Wiens, J.J. 1998. Combining data sets with different phylogenetic histories. *Systematic Biology*, 47(4): 568-581.

Wilkinson, M. 1996. Majority-rule reduced consensus trees and their use in bootstrapping. *Molecular Biology and Evolution*, 13(3): 437-444.

Willmott A.P. and C.P. Ellington. 1997a. The mechanics of flight in the hawkmoth *Manduca sexta* .1. Kinematics of hovering and forward flight. *Journal of Experimental Biology*, 200(21): 2705-2722.

Willmott A.P. and C.P. Ellington. 1997b. The mechanics of flight in the hawkmoth *Manduca sexta* .2. Aerodynamic consequences of kinematic and morphological variation. *Journal of Experimental Biology*, 200(21): 2723-2745.

Willmott A.P., C.P. Ellington and A.L.R. Thomas. 1997. Flow visualization and unsteady aerodynamics in the flight of the hawkmoth, *Manduca sexta*. *Philosophical Transactions of the Royal Society of London, Biology*, 352(1351): 303-316.

Winder, J.A. 1976. Ecology and control of *Erinnyis ello* and *E.alope*, important insect pests in the new world. *PANS*, 22(4): 449-466.

Yack, J.E. and J.H. Fullard. 2000. Ultrasonic hearing in nocturnal butterflies. *Nature*, 403: 265-266.

Yack, J.E. and J.H. Fullard. 1993a. Proprioceptive activity of the wing-hinge stretch receptor in *Maduca sexta* and other atympanate moths: a study of the noctuoid moth ear B cell homologue. *Journal of Comparative Physiology*, 173: 301-307.

Yack, J.E. and J.H. Fullard. 1993b. What is an insect ear?. *Annals of the Entomological Society of America*, 86(6): 677-682.

Yang, Z. 1996. Phylogenetic analysis using parsimony and likelihood. *Journal of Molecular Evolution*, 42: 294-307.

Yang, Z. 1994. Statistical properties of the maximum likelihood method of phylogenetic estimation and comparison with distance matrix methods. *Systematic Biology*, 43: 329-342.

Yang, Z. 1993. Maximum-likelihood estimation of phylogeny from DNA sequences when substitution rates differ over sites. *Molecular Biology and Evolution*, 10(6): 1396-1401.

Yeates, D.K. and B.M. Wiegmann. 1999. Congruence and controversy: toward a higher-level phylogeny of Diptera. *Annual Review of Entomology*, 44: 397-428.

Young, A.M. 1972. Notes on a community ecology of adult sphinx moths in Costa Rican lowland tropical rain forest. *Caribbean Journal of Science*, 12(34): 151-163.

Table 1. Selected life history contrasts between Sphingidae and Saturniidae (Lepidoptera: Bombycoidea). Compiled from observations cited in Janzen (1984) and Bernays & Janzen (1988). Members of Smerinthinae generally share many life history traits with Saturniidae, despite strong morphological evidence for their inclusion in Sphingidae.

Life History Parameter	SPHINGIDAE (Sphinginae&Macroglossinae)	SATURNIIDAE & SPHINGIDAE (Smerinthinae)
adult foraging & feeding	- constant diet of nectar and water (male & female)	- no adult feeding; nutrition from larval fat and water reserves
proboscis	- functional	- vestigial
neural capacity	- large head and eyes - memory	- small head and eyes
adult lifespan	- weeks	- days
adult flight	- streamlined wing shape - powerful, agile, sustained flight - speed dash escape behavior - seasonal migration - diurnal, matinal, crepuscular, nocturnal	- broad ornate wing shape - weak flight - varied avoidance maneuvers - no seasonal migration - crepuscular, nocturnal
adult coloration	- crypsis - hindwing flash coloration	- crypsis - mimetic & aposematic coloration
intra/interspecific polymorphism	- low (color, size, wing shape)	- high (color, size, wing shape)
adult sexual dimorphism (size & behavior)	- reduced - female larger at eclosion, weights eventually equalize	- pronounced - female larger at eclosion and throughout development
attraction to light	- females arrive all night - male & female loosely attracted, stray - 10 males : 1 female	- females arrive before midnight - male and female tightly attracted, sessile - >100 males : 1 female
mating	- courtship & female choice mediated by male secondary sex organs - multiple female matings, days after female eclosion	- indiscriminate mating - single female mating, immediately after eclosion
egg maturation in female	- continuous maturation - eggs 3X smaller than saturniids	- full complement at eclosion - eggs 3X larger than sphingids
oviposition	- single egg per oviposition event - weeks/months	- large egg clutch per oviposition - approx. 50% egg load in first night; remainder within 1 week
time to egg hatch	- fast: 4-8 days	- slow: 6-15 days
larval development	- fast: 2-5 weeks	- slow: 4-10 weeks
larval defense	- crypsis - eyespot mimicry - no sequestration	- crypsis - aposematic coloration - urticating spines and urticator mimicry
larval mandibles	- intricate morphology - masticating action	- simple morphology - snipping action
larval relative head mass	- twice that of saturniids	- half that of sphingids
larval gut contents	- intense processing of little material - heterogeneous, macerated particles - effectively digested into slurry	- light processing of ample material - large, homogeneous, intact particles - only edges effectively digested
larval diet breadth	- oligophagous - diverse range of growth forms	- polyphagous - few growth forms, especially trees
larval hostplant syndrome	- low density, low apparency - small, immature - high nutrition and water content - small toxic qualitative defensive chemicals	- high density, high apparency - large, mature - low nutrition and water content - large nontoxic quantitative defensive chemicals

Table 2. Taxonomic classification and phylogenetic sequence of genera in Sphingidae (Lepidoptera: Bombycoidea) presented by Kitching & Cadiou (2000). Order of genera is approximately phylogenetic and matches that reported in Kitching & Cadiou 2000 (pp. 16-19); putative clades advocated by these authors indicated by nested vertical bars to the left of the genus name. Number of worldwide recognized species units within each genus, including distinct subspecies, indicated in 'ssp' column; single species names given for monotypic genera only. Genera for which specimens have been accessioned in the UMD Lepidoptera Collections and are available for molecular sequence collection marked with 'X' in the 'Coll' column. Genera for which EF and DDC sequence have been obtained indicated in the 'EF' and 'DDC' columns: asterisks mark sequences collected de novo in this study; 'R' marks sequences submitted to GenBank by Regier, et al. (2001); 'C' marks the sequence submitted to GenBank by Caterino, et al. (2001). Genera containing species which occur in North America (not necessarily endemics) are shaded, and were determined by consulting Hodges (1971) and Ferguson & Opler (1999).

Taxonomy	ssp	*Genus*	*species*	Genus Author	Synonyms	Coll	EF	DDC
Lepidoptera>Heteroneura>Ditrysia>Apoditrysia>Obtectomera>Macrolepidoptera>Bombycoidea>SPHINGIDAE								
SMERINTHINAE								
Smerinthini	4	***Langia***		Moore, 1872				
	8	***Laothoe***		Fabricius, 1807	Amorpha	X	*	*
	4	***Pachysphinx***		Rothschild & Jordan, 1903		X	*	*
	12	***Smerinthus***		Latreille, [1802]	Bebroptera,Bellia,Bellinca,Copismerinthus,Daddia,Dilina,Eusmerinthus,Merinthus,Nicholsonia,Niia	X	*R	*R
	5	***Paonias***		Hubner, [1819]	Calasymbolus	X	*R	*R
	1	***Poliodes***	***roseicornis***	Rothschild & Jordan, 1903				
	1	***Xenosphingia***	***jansei***	Jordan, 1920				
	3	***Ceridia***		Rothschild & Jordan, 1903				
	2	***Craspedortha***		Mell, 1922				
	1	***Parum***	***colligata***	Rothschild & Jordan, 1903				
	1	***Anambulyx***	***elwesi***	Rothschild & Jordan, 1903				
	38	***Marumba***		Moore, [1882]	Burrowsia,Kayeia,Sichia	X	*	*
	2	***Daphnusa***		Walker, 1856	Allodaphnusa			
	6	***Gynoeryx***		Carcasson, 1968				
	2	***Likoma***		Rothschild & Jordan, 1903				
	2	***Phyllosphingia***		Swinhoe, 1897	Clarkia,Clarkunella			
	1	***Amorpha***	***juglandis***	Hubner, [1819]	Cressonia	X	*	*
	2	***Mimas***		Hubner, [1819]	Lucena	X	*	*
	4	***Lophostethus***		Butler, 1876	Euclea			
	3	***Andriasa***		Walker, 1856	Devitzia,Pseudosmerinthus	X		
	1	***Microclanis***	***erlangeri***	Carcasson, 1968				
	4	***Falcatula***		Carcasson, 1968				
	2	***Chloroclanis***		Carcasson, 1968		X		
	8	***Platysphinx***		Rothschild & Jordan, 1903				
	1	***Neoclanis***	***basalis***	Carcasson, 1968				
	1	***Afrosphinx***	***amabilis***	Carcasson, 1968				
	1	***Viriclanis***	***kingstoni***	Aarvik, 1999				
	7	***Rufoclanis***		Carcasson, 1968				
	2	***Coequosa***		Walker, 1856	Metamimas			
	2	***Rhodambulyx***		Mell, 1939				
	6	***Rhodoprasina***		Rothschild & Jordan, 1903				
	1	***Cypoides***	***chinensis***	Matsumura, 1921	Amorphulus			
	13	***Cypa***		Walker, [1865]				
	7	***Smerinthulus***		Huwe, 1895				
	2	***Degmaptera***		Hampson, 1896				
	1	***Grillotius***	***bergeri***	Rougeot, 1973				
	1	***Opistoclanis***	***hawkeri***	Jordan, 1929				
	2	***Agnosia***		Rothschild & Jordan, 1903				
	11	***Callambulyx***		Rothschild & Jordan, 1903				
	6	***Sataspes***		Moore, [1858]	Myodezia			
	1	***Afrosataspes***	***galleyi***	Basquin & Cadiou, 1986				
	1	***Pseudopolyptychus***	***foliaceus***	Carcasson, 1968				
	2	***Afroclanis***		Carcasson, 1968				
	2	***Malgassoclanis***		Carcasson, 1968				
	1	***Pseudandriasa***	***mutata***	Carcasson, 1968				
	2	***Rhadinopasa***		Karsch, 1891				
	5	***Leucophlebia***		Westwood, 1847	Rasphele			
	1	***Leptoclanis***	***pulchra***	Rothschild & Jordan, 1903				
	10	***Phylloxiphia***		Rothschild & Jordan, 1903	Acentropoclanis,Libyoclanis, Typhosia			
	18	***Clanis***		Hubner, [1819]	Basiana,Metagastes			
	1	***Clanidopsis***	***exusta***	Rothschild & Jordan, 1903				
	1	***Acanthosphinx***	***guessfeldti***	Aurivillius, 1891				
	10	***Neopolyptychus***		Carcasson, 1968				
	18	***Pseudoclanis***		Rothschild, 1894	Larunda	X	*	*
	7	***Polyptychoides***		Carcasson, 1968		X		
	44	***Polyptychus***		Hubner, [1819]		X		
	3	***Polyptychopsis***		Carcasson, 1968				
	1	***Lycosphingia***	***hamatus***	Rothschild & Jordan, 1903				
	1	***Avinoffia***	***hollandi***	Clark, 1929				

Table 2. (continued)

Taxonomy	ssp	Genus	species	Genus Author	Synonyms	Coll	EF	DDC
Sphingulini	1	*Synoecha*	*marmorata*	Rothschild & Jordan, 1903				
	1	*Coenotes*	*eremophilae*	Rothschild & Jordan, 1903				
	1	*Hopliocnema*	*brachycera*	Rothschild & Jordan, 1903		X	*	*
	1	*Tetrachroa*	*edwardsi*	Rothschild & Jordan, 1903				
	3	*Pentateucha*		Swinhoe, 1908				
	3	*Kentrochrysalis*		Staudinger, 1887	Centrochrysalis			
	7	*Dolbina*		Staudinger, 1877	Dolbinopsis,Elegodolba			
	1	*Sphingulus*	*mus*	Staudinger, 1887				
	1	*Monarda*	*oryx*	Druce, 1896				
Ambulycini	63	*Ambulyx*		Westwood, 1847	Oxyambulyx			
	1	*Barbourion*	*lemaii*	Clark, 1934				
	6	*Amplypterus*		Hubner, [1819]	Calymnia,Compsogene			
	1	*Compsulyx*	*cochereaui*	Holloway, 1979		X		
	1	*Akbesia*	*davidi*	Rothschild & Jordan, 1903				
	6	*Batocnema*		Rothschild & Jordan, 1903				
	8	*Protambulyx*		Rothschild & Jordan, 1903	Ambulyx	X	*	*
	5	*Orecta*		Rothschild & Jordan, 1903				
	16	*Adhemarius*		Oiticica Filho, 1939		X	*	*
	1	*Trogolegnum*	*pseudambulyx*	Rothschild & Jordan, 1903				
SPHINGINAE								
Sphingini	1	*Sagenosoma*	*elsa*	Jordan, 1946	Dictyosoma			
	2	*Dolbogene*		Rothschild & Jordan, 1903				
	1	*Dolba*	*hyloeus*	Walker, 1856		X	R	R
	7	*Ceratomia*		Harris, 1839	Autogramma,Daremma,Isogramma	X	*R	*R
	1	*Paratrea*	*plebeja*	Grote, 1903	Atreides,Atreus	X	*	*
	56	*Sphinx*		Linnaeus, 1758	Gargantua,Herse,Hyloecus,Lethia, Lintneria,Mesosphinx,Spectrum	X	*R	*R
	1	*Thamnoecha*	*uniformis*	Rothschild & Jordan, 1903				
	4	*Lapara*		Walker, 1856	Ellema,Exedrium	X	*R	*R
	1	*Isoparce*	*cupressi*	Rothschild & Jordan, 1903				
	3	*Nannoparce*		Rothschild & Jordan, 1903				
	9	*Neogene*		Rothschild & Jordan, 1903				
	88	*Manduca*		Hubner, [1807]	Chlaenogramma,Diludia,Macrosila, Phlegethontius,Protoparce,Syzygia	X	*R	*R
	8	*Euryglottis*		Boisduval, [1875]		X	*	*
	1	*Apocalypsis*	*velox*	Rothschild & Jordan, 1903				
	3	*Pseudodolbina*		Rothschild, 1894				
	3	*Praedora*		Rothschild & Jordan, 1903				
	1	*Ellenbeckia*	*monospila*	Rothschild & Jordan, 1903				
	1	*Litosphingia*	*corticea*	Jordan, 1920				
	2	*Hoplistopus*		Rothschild & Jordan, 1903				
	1	*Oligographa*	*juniperi*	Rothschild & Jordan, 1903				
	2	*Dovania*		Rothschild & Jordan, 1903		X		
	1	*Lomocyma*	*oegrapha*	Rothschild & Jordan, 1903				
	4	*Panogena*		Rothschild & Jordan, 1903				
	6	*Macropoliana*		Carcasson, 1968				
	5	*Poliana*		Rothschild & Jordan, 1903	Taboribia			
	14	*Meganoton*		Boisduval, [1875]				
	5	*Psilogramma*		Rothschild & Jordan, 1903		X	*	*
	1	*Leucomonia*	*bethia*	Rothschild & Jordan, 1903				
	3	*Pantophaea*		Jordan, 1946				
	2	*Xanthopan*		Rothschild & Jordan, 1903				
	1	*Amphimoea*	*walkeri*	Rothschild & Jordan, 1903				
	1	*Neococytius*	*cluentius*	Hodges, 1971		X		*
	6	*Cocytius*		Hubner, [1819]	Amphonyx,Ancistrognathus	X	*	*
Acherontiini	2	*Megacorma*		Rothschild & Jordan, 1903				
	6	*Agrius*		Hubner, [1819]	Timoria	X	*	*
	1	*Callosphingia*	*circe*	Rothschild & Jordan, 1916				
	5	*Coelonia*		Rothschild & Jordan, 1903		X	*	*
	4	*Acherontia*		[Laspeyres], 1809	Atropos,Brachyglossa,Manduca	X	*	*
MACROGLOSSINAE								
Dilophonotini								
Dilophonotina	9	*Cautethia*		Grote, 1865	Braesia,Oenosanda	X	*	*
	1	*Himantoides*	*undata*	Butler, 1876				
	7	*Pachygonidia*		Fletcher, 1982	Pachygonia			
	11	*Enyo*		Hubner, [1819]	Epistor,Triptogon	X	*	*
	7	*Aleuron*		Boisduval, 1870	Callenyo,Gonenyo,Tylognathus			
	4	*Unzela*		Walker, 1856	Cornipalpus	X	*	*
	15	*Callionima*		Lucas, 1857	Calliomma,Eucheryx	X	*	*
	7	*Madoryx*		Boisduval, [1875]				
	2	*Stolidoptera*		Rothschild & Jordan, 1903				
	1	*Protaleuron*	*rhodogaster*	Rothschild & Jordan, 1903				
	4	*Pachylia*		Walker, 1856		X	*	*
	1	*Kloneus*	*babayaga*	Skinner, 1923	Oberthuerion			
	1	*Pachylioides*	*resumens*	Hodges, 1971				
	2	*Oryba*		Walker, 1856				
	4	*Hemeroplanes*		Hubner, [1819]	Leucorhampha			

Table 2. (continued)

Taxonomy	ssp	Genus	species	Genus Author	Synonyms	Coll	EF	DDC
	21	*Nyceryx*		Boisduval, [1875]		X	*	*
	1	*Baniwa*	*yavitensis*	Lichy, 1981				
	16	*Perigonia*		Herrich-SchŠffer, [1854]	Stenolophia	X	*	*
	3	*Eupyrrhoglossum*		Grote, 1865				
	9	*Aellopos*		Hubner, [1819]		X	*R	*R
	1	*Pseudosphinx*	*tetrio*	Burmeister, 1855	Macrosila			
	18	*Isognathus*		Felder & Felder, 1862	Tatoglossum	X	*	*
	16	*Erinnyis*		Hubner, [1819]	Anceryx,Dilophonota	X	*	*
	1	*Phryxus*	*caicus*	Hubner, [1819]	Grammodia			
Hemarina	20	*Hemaris*		Dalman, 1816	Aege,Chamaesesia,Cochrania, Haemorrhagia,Hemaria,Jilinga, Mandarina,Saundersia	X	*R	*R
	24	*Cephonodes*		Hubner, [1819]	Potidaea	X	*	*
Philampelini	32	*Eumorpha*		Hubner, [1807]	Argeus,Dupo,Philampelus,Pholus	X	*R	*R
	1	*Tinostoma*	*smaragditis*	Rothschild & Jordan, 1903				
Macroglossini								
Macroglossina	2	*Sphecodina*		Blanchard, 1840	Brachynota,Maredus,Thyreus	X	R	R
	7	*Proserpinus*		Hubner, [1819]	Dieneces,Lepisesia,Pogocolon, Pterogon,Pteropogon	X	C	
	1	*Amphion*	*floridensis*	Hubner, [1819]				
	1	*Arctonotus*	*lucidus*	Boisduval, 1852				
	3	*Euproserpinus*		Grote & Robinson, 1865				
	7	*Neogurelca*		Hogenes & Treadaway, 1993				
	8	*Sphingonaepiopsis*		Wallengren, 1858	Pterodonta			
	1	*Microsphinx*	*pumilum*	Rothschild & Jordan, 1903				
	2	*Odontosida*		Rothschild & Jordan, 1903				
	9	*Antinephele*		Holland, 1889				
	4	*Hypaedalea*		Butler, 1877				
	1	*Pseudenyo*	*benitensis*	Holland, 1889				
	72	*Temnora*		Walker, 1856	Aspledon,Diodosida,Eulophura, Gurelca,Lophura,Lophuron,Ocyton	X		
	1	*Temnoripais*	*lasti*	Rothschild & Jordan, 1903				
	26	*Nephele*		Hubner, [1819]	Orneus,Zonilia	X		
	3	*Maassenia*		Sallmuller, 1884				
	5	*Angonyx*		Boisduval, [1875]				
	8	*Rethera*		Rothschild & Jordan, 1903	Borshomia			
	2	*Cizara*		Walker, 1856	Abrisa,Microlophia			
	2	*Hayesiana*		Fletcher, 1982	Rhodosoma			
	7	*Eurypteryx*		R. Felder, [1874]	Indiana			
	1	*Giganteopalpus*	*mirabilis*	Huwe, 1895				
	6	*Gnathothlibus*		Wallengren, 1858	Chromus			
	1	*Philodila*	*astyanor*	Rothschild & Jordan, 1903				
	14	*Daphnis*		Hubner, [1819]	Histriosphinx,Regia	X	*	*
	5	*Ampelophaga*		Bremer & Grey, 1853				
	2	*Clarina*		Tutt, 1903	Berutana			
	4	*Darapsa*		Walker, 1856	Ampeloeca,Otus	X	*R	*R
	30	*Eupanacra*		Cadiou & Holloway, 1989				
	3	*Enpinanga*		Rothschild & Jordan, 1903				
	2	*Elibia*		Walker, 1856				
	1	*Acosmerycoides*	*harterti*	Mell, 1922				
	1	*Deidamia*	*inscriptum*	Clemens, 1859	Tricholon			
	16	*Acosmeryx*		Boisduval, [1875]				
	1	*Micracosmeryx*	*chaochauensis*	Mell, 1922				
	1	*Lepchina*	*tridens*	Oberthur, 1904				
	1	*Thibetia*	*niphaphylla*	Joicey & Kaye, 1917				
	6	*Gehlenia*		Bryk, 1944				
	1	*Dahira*	*rubiginosa*	Moore, 1888				
	1	*Atemnora*	*westermannii*	Rothschild & Jordan, 1903				
	111	*Macroglossum*		Scopoli, 1777	Bombylia,Macroglossa,Psithyros, Rhamphoschisma,Rhopalopsyche	X	*	*
	2	*Leucostrophus*		Rothschild & Jordan, 1903				
Choerocampina	96	*Xylophanes*		Hubner, [1819]	Deilonche,Dilonche,Isoples	X	*R	*R
	1	*Phanoxyla*	*hystrix*	Rothschild & Jordan, 1903				
	42	*Hyles*		Hubner, [1819]	Celerio,Danneria,Eremohyles,Hawaiina,Hippohyles,Rommeliana,Surholtia,Thaumas,Tumeria,Weismannia	X	*R	*R
	2	*Rhodafra*		Rothschild & Jordan, 1903				
	5	*Deilephila*		[Laspeyres], 1809	Choerocampa,Cinogon,Dilephila, Elpenor,Eumorpha,Metopsilus	X	*	*
	5	*Basiothia*		Walker, 1856		X	*	*
	4	*Chaerocina*		Rothschild & Jordan, 1903		X		
	3	*Euchloron*		Boisduval, [1875]	Chlorina	X		
	43	*Hippotion*		Hubner, [1819]	Lilina,Panacra	X	*	*
	2	*Centroctena*		Rothschild & Jordan, 1903				
	1	*Pergesa*	*acteus*	Walker, 1856	Rhyncholaba			
	59	*Theretra*		Hubner, [1819]	Florina,Gnathostypsis,Hathia,Oreus	X	*	*
	2	*Griseosphinx*		Cadiou & Kitching, 1990				
	19	*Rhagastis*		Rothschild & Jordan, 1903				
	11	*Cechenena*		Rothschild & Jordan, 1903				

Table 3. Elongation Factor 1-alpha (EF) Primers. Compilation of select oligonucleotide primers developed in the Regier Lab and used to amplify EF (i) across Arthropoda and (ii) within Lepidoptera. Primers are grouped into pairs generating overlapping fragments which have been successfully assembled to obtain continuous sequence for this gene. 'f' suffix in the Primer Name denotes forward primer, which anneals to the antisense strand and promotes synthesis of the sense strand. 'rc' prefix or suffix in the Primer Name denotes reverse primer, which anneals to the sense strand and promotes synthesis of the antisense strand. First four primer pairs were used in this study (abbreviated p, A', E and C), nested within purified templates obtained by reverse transcription with m41.21rc (marked with an asterisk). (iii) lists the forward and reverse M13 primers used in sequencing reactions. 'Position in Figure 4' denotes coordinate of the *5' end of the primer* relative to the sense strand in the *Bombyx mori* EF reference sequence shown in Figure 4; coordinate '1' corresponds to the 66th nucleotide in the original GenBank accession D13338. Oligonucleotide primer sequence is written 5' to 3', irrespective of orientation in Figure 4 (i.e., reverse primers can be oriented by taking their reverse complement). 'Notes': (a) 30f is a more degenerate version of M3; (b) replacing m40.71f with m40.6f generates an amplicon 42 bp longer; (c) m52f is a more degenerate version of M51.9.

Primer Name	Sequence (5' ⇒ 3')	Primer Length	Position in Figure 4	Note	Fragment Size
(i) Regier & Shultz (1997)					
30f	CAY ATY AAY ATH GTS GTI ATH GG	23	1	a	**449 (p)**
m45.71rc	TCC ATY TTR TTN CAN SCN AC	20	449		
m40.6f	ATY GAR AAR TTY GAR AAR GAR GC	23	97	b	**656 (A')**
m52rc	CCD ATY TTR TAN ACR TCY TG	20	752		
m45.71f	GTN GSN GTN AAY AAR ATG GA	20	430		**656 (E)**
m53.5rc	ATR TGV GMN GTR TGR CAR TC	20	1085		
m52f	CAR GAY GTN TAY AAR ATH GG	20	733	c	**542 (C)**
*m41.21rc	TGY CTC ATR TCD CGV ACR GCR AA	23	1274		
m40.71f	TCN TTY AAR TAY GCN TGG GT	20	139	b	**na**
m52.4f	TCN GTN GAR ATG CAY CAY G	19	853		
(ii) Cho, *et al.* (1995)					
M3	CAC ATY AAC ATT GTC GTS ATY GG	23	1	a	**282**
rcM44.9	CTT GAT GAA ATC YCT GTG TCC	21	282		
M44.1	GCT GAG CGY GAR CGT GGT ATC AC	23	175		**411**
rcM51.1	CAT RTT GTC KCC GTG CCA KCC	21	585		
M46.1	GAG GAA ATY AAR AAG GAA G	19	484		**392**
rcM52.6	GCY TCG TGG TGC ATY TCS AC	20	875		
M51.9	CAR GAC GTA TAC AAA ATC GG	20	733	c	**356**
rcM53.2	GCA ATG TGR GCI GTG TGG CA	20	1088		
M52.7	GTC AAG GAR YTG CGT CGT GG	20	931		**356**
rcM4	ACA GCV ACK GTY TGY CTC ATR TC	23	1286		
(iii) M13 Sequencing Primers					
M13-21	TGT AAA ACG ACG GCC AGT	18	-		-
M13-rev	CAG GAA ACA GCT ATG ACC	18	-		-

IUPAC Ambiguity Codes: R=AG, Y=CT, M=AC, K=GT, S=CG, W=AT | H=ACT, B=CGT, V=ACG, D=AGT | N=ACGT | I=inosine

Table 4. Dopa Decarboxylase (DDC) Primers. Exhaustive compilation of oligonucleotide primers developed in the Regier Lab and used historically to amplify DDC across Arthropoda. Primers are sorted by position along the reference sequence in Figure 5, and alternate versions of a single primer are grouped together. 'F' suffix in the Primer Name denotes forward primer, which anneals to the antisense strand and promotes synthesis of the sense strand. 'R' suffix in the Primer Name denotes reverse primer, which anneals to the sense strand and promotes synthesis of the antisense strand. Primers used in this study are marked with an asterisk (*) and those used in the RT phase are marked with **. Primers preferred in Regier Lab protocols are marked with a cross (†) and those used in the RT phase are marked with ‡. Oligonucleotide primer sequence is written 5' to 3', irrespective of orientation in Figure 5 (i.e., reverse primers can be oriented by taking their reverse complement). Underlined nucleotides mark sites of mismatch with the *Manduca sexta* DDC sequence (GenBank accession U03909). Bases at these positions exhibit high variability across Lepidoptera in multiple sequence alignments, so conflict with *Manduca* was not unexpected. Italicized bases indicate cases in which degeneracy has been increased at that position in past primer orders (e.g., I substituted for N; N substituted for B). Stricken 7.5sR primer contains an error (underlined).

Primer Name	Sequence (5' ⇒ 3')	Primer Length	Position in Figure 5	Ref	Note
* 1.0F	TTY AAR GAY TTY GCW AAR RCD ATG	24	1	2	a
1.1nF	ACI GAY TAY ATH RCI GAN T	19	25	5	
M1.1F	G GAC TAY ATC GCG GAA TAT TTG G	23	27	5	b
† 1.1vF	GAY TAY ATY RCR GAR TA	17	28	5	
† 1.2F	GAR AAY ATY AGA GAY AGR CAR GT	23	49	5	
1.4F	TTT CAT GCT TAT TTT CCT ACT GC	23	211	1	c
* 1.7F	GCT ATT GCT TGT ATT GGT TTT ACT TGG AT	29	274	1	
† 1.7sF	GCH TGY ATY GGN TTY WCN TGG AT	23	280	4	d
1.7dF	GCY TGY ATY GGW TTY ACY TGG AT	23	280	1	
† 1.8R	CAT NAC NAC YTC IAR YTC IGT RCA	24	316	5	
† 1.9sF	ATG HTN GAY TGG YTV GGY CAR ATG	24	337	4	
* 1.9dF	ATG YTR GAY TGG YTR GGY CAR ATG	24	337	1	
1.9'dF	GAY TGG CTN GGN CAR ATG	18	343	2	e
‡ 1.9sR	CAT YTG RCC BAR CCA RTC NAD CAT	24	337	[4]	
* 1.9dR	CAT YTG RCC TAR CCA RTC YAR CAT	24	337	2	
† 3.2sF	TGG YTN CAY GTN GAY GCN GCN TAY GC	26	784	4	
* 3.2dF	TGG YTR CAY GTS GAY GCD GCY TAY GC	26	784	1	f
3.2dR	TAR GCH GCR TCS ACR TGY ARC CA	23	806	1	
† 3.3sF	TTY AAY TTY AAY CCN CAY AAR TGG	24	874	[4]	
3.3'F	AAY TTY AAY CCN CAY AAR TGG	21	877	2	g
*† 3.3sR	CCA YTT RTG NGG RTT RAA RTT RAA	24	874	4	
3.3R	CCA YTT RTG NGG RTT RAA RTT	21	877	2	
**‡ 4sR	GGD ATY TGC CAR TGH CKR TAR TC	23	1012	4	
4ddR	GGK ATY TGC CAR TGM CGR TAR TC	23	1012	1	h
** 4dnR	GGG ATT TGC CAR TGA CGR TAR TC	23	1012	1	
7.0sR	GTR AAN CGN GAR CAD ATN GC	20	1324	3	i
7.5R	TCC CAR GAN ACR TGV ATR TC	20	1354	2	
**‡ 7.5sR	TCC CAN GAN ACR TGV ATR TC	20	1354	3	j
~~7.5sR~~	TCC CAN GAN ACR TGV TAR TC	20	1354	x	
M13-21	TGT AAA ACG ACG GCC AGT	18	-	-	
M13-rev	CAG GAA ACA GCT ATG ACC	18	-	-	

Table 4 (continued)

IUPAC Ambiguity Codes: R=AG, Y=CT, M=AC, K=GT, S=CG, W=AT | H=ACT, B=CGT, V=ACG, D=AGT | N=ACGT | I=inosine

'Position in Figure 5' denotes coordinate of the *5' end of the primer* relative to the sense strand in the *Manduca sexta* DDC reference sequence shown in Figure 5; coordinate '1' corresponds to the 192nd nucleotide in the original GenBank accession U03909.

References: (1) Fang, *et al.* (1997); (2) Friedlander, *et al.*(1998); (3) Mitchell (1998); (4) Mitchell, *et al.*(2000); (5) Regier Lab Optimized Protocols.

Notes:

(a) 1.0F primer nt15 (W) conflicts with G at position 206 in U03909.

(b) 1.1vF is the least degenerate and most consistent version of this primer. Version 1.1nF (unknown author) includes an extra 3nt at the 5' end and excludes 1nt at the 3' end. Version M1.1F (unknown author) includes an extra 1nt at the 5' end and 5nt at the 3' end, and has five direct conflicts with U03909: G at primer nt1 with T at position 218; G's at nt11&13 with A's at positions 228&230; A at nt16 with G at position 233; and T at nt20 with C at position 237.

(c) 1.4F is anchored at position 424 (3' end), according to Table 2 (Fang 1997, p. 272). In this orientation, T's at primer nt3,6,9&15 conflict with C's at positions 404,407,410&416 in U03909; and T's at primer nt18&21 conflict with G's at positions 419&422 in U03909.

(d) Version 1.7dF is nested entirely within 1.7F (6nt shorter on the 5' end) and incorporates more degeneracy. Version 1.7sF is a more degenerate version of 1.7dF.

(e) Version 1.9sF retains a purine (V = C+R) at nt15, but R conflicts with C at position 542 in U03909. Is this possibly a carryover error from version 1.9dF (Fang 1997)? Version 1.9'dF (Friedlander 1998) is nested entirely within 1.9dF (6nt shorter on the 5' end) and slightly more degenerate. Version 1.9sRC (Mitchell 2000) slightly increases degeneracy at nt10,19&21, relative to 1.9dRC.

(f) 3.2dRC is the reverse complement of 3.2dF, excluding 3nt on the 5' end (i.e., it ends at nt997 in U03909).

(g) Version 3.3sRC includes an additional 3nt on 3' end relative to 3.3RC (Friedlander 1998). Version 3.3sF is simply the reverse complement of 3.3sRC (Mitchell 2000), and includes an additional 3nt on 5' end relative to 3.3'F (Friedlander 1998).

(h) Version 4ddRC is a slightly more degenerate version of 4dnRC, but G or K at primer nt3 in both 4dnRC and 4ddRC conflicts with the T complement at position 1223 in U03909. Version 4sRC incorporates more degeneracy, and retains the keto (D = A+K) at primer nt3 which does not complement with T at position 1223 in U03909.

(i) "Two additional DDC primers, allowing the amplification of an extra 312 bp or 342 bp of the 3'-end of DDC, became available during this study. These primers are 7.0sRC (5'-**GTR AAN CGN GAR CAD ATN GC**-3') and 7.5sRC (5'-**TCC CAN GAN ACR TGV ATR TC**-3'), respectively." (Mitchell 1998, p. ???)

(j) Version 7.5sRC replaces R with N at nt6 to slightly increase degeneracy relative to 7.5RC. Note that a typo in some versions of 7.5sRC switches **AT** to **TA** at primer nt16-nt17 (**TCC CAN GAN ACR TGV TAR TC**; unknown author).

Table 5. Amplification strategies for DDC employed (a) in this study and (b) in the Regier Lab. Primers are grouped into pairs generating overlapping fragments which have been successfully assembled to obtain continuous sequence for DDC. Primer pairs used in RT-PCR and nested PCR phases of amplification are indicated separately. 'Fragment Size' indicates the amplicon size for each primer pair along with amplicon abbreviation in parentheses, where a naming convention has been established. Table 4 describes all other notations and presents more detailed information about individual DDC primers.

(a) Primer pairs employed in this study

Primer Name	Sequence (5' ⇒ 3')	Primer Length	Position in Figure 5	Ref	Fragment Size
	RT-PCR Amplification				
1.0F	TTY AAR GAY TTY GCW AAR RCD ATG	24	1	2	**1,373**
7.5sR	CAT YTG RCC BAR CCA RTC NAD CAT	24	1354	[4]	
1.0F	TTY AAR GAY TTY GCW AAR RCD ATG	24	1	2	**1,034**
4dnR	GGG ATT TGC CAR TGA CGR TAR TC	23	1012	1	
3.2dF	TGG YTR CAY GTS GAY GCD GCY TAY GC	26	784	1	**590**
7.5sR	TCC CAN GAN ACR TGV ATR TC	20	1354	3	
	Nested PCR Reamplification				
1.0F	TTY AAR GAY TTY GCW AAR RCD ATG	24	1	2	**360 (X)**
1.9dR	CAT YTG RCC TAR CCA RTC YAR CAT	24	337	2	
1.7F	GCT ATT GCT TGT ATT GGT TTT ACT TGG AT	29	274	1	**624 (Y)**
3.3sR	CCA YTT RTG NGG RTT RAA RTT RAA	24	874	4	
3.2dF	TGG YTR CAY GTS GAY GCD GCY TAY GC	26	784	1	**590 (Z)**
7.5sR	TCC CAN GAN ACR TGV ATR TC	20	1354	3	
1.9dF	ATG YTR GAY TGG YTR GGY CAR ATG	24	337	1	**698 (W)**
4sR	GGD ATY TGC CAR TGH CKR TAR TC	23	1012	4	

(b) Primer pairs employed in Regier Lab protocols

Primer Name	Sequence (5' ⇒ 3')	Primer Length	Position in Figure 5	Ref	Fragment Size
	RT-PCR Amplification				
1.1vF	GAY TAY ATY RCR GAR TA	17	28	5	**333 (A)**
1.9sR	CAT YTG RCC BAR CCA RTC NAD CAT	24	337	[4]	
1.7sF	GCH TGY ATY GGN TTY WCN TGG AT	23	280	4	**755 (B)**
4sR	GGD ATY TGC CAR TGH CKR TAR TC	23	1012	4	
3.2sF	TGG YTN CAY GTN GAY GCN GCN TAY GC	26	784	4	**590 (C)**
7.5sR	TCC CAN GAN ACR TGV ATR TC	20	1354	3	
	Nested PCR Reamplification				
1.1vF	GAY TAY ATY RCR GAR TA	17	28	5	**312 (z)**
1.8R	CAT NAC NAC YTC IAR YTC IGT RCA	24	316	5	
1.7sF	GCH TGY ATY GGN TTY WCN TGG AT	23	280	4	**618 (y)**
3.3sR	CCA YTT RTG NGG RTT RAA RTT RAA	24	874	4	
1.9sF	ATG HTN GAY TGG YTV GGY CAR ATG	24	337	4	**698 (w)**
4sR	GGD ATY TGC CAR TGH CKR TAR TC	23	1012	4	
3.3sF	TTY AAY TTY AAY CCN CAY AAR TGG	24	874	[4]	**500 (v)**
7.5sR	TCC CAN GAN ACR TGV ATR TC	20	1354	3	

IUPAC Ambiguity Codes: R=AG, Y=CT, M=AC, K=GT, S=CG, W=AT | H=ACT, B=CGT, V=ACG, D=AGT | N=ACGT | I=inosine

Table 6. RT-PCR and Nested PCR reaction conditions. Composition of individual reverse transcription (RT) reactions and subsequent polymerase chain reactions (PCR) is presented in (a) and (b), respectively. Concentration of stock components, volume of that stock added to a single reaction, and the resulting final component concentration in each reaction is given separately for each gene. RT thermal cycling conditions were identical for both genes and consisted of a 42C incubation for 35 minutes followed by a 99C incubation for 5 minutes. Touchdown thermal cycling parameters used in the PCR portion of these RT-PCR reactions were also identical for both genes, and are presented in (c). Composition of individual Nested PCR reactions and thermal cycling conditions are presented separately for each gene in (d) and (e), respectively.

(a) Composition of RT reactions

		EF		DDC	
Component	**[stock]**	**Volume**	**[reaction]**	**Volume**	**[reaction]**
$MgCl_2$	25 mM	2.0uL	5mM	2.0uL	5mM
dNTP	10mM ea	2.0uL	2mM ea	2.0uL	2mM ea
PCR Buffer	10X	1.0uL	1X	1.0uL	1X
RT primer	20uM	1.0uL	2uM	1.5uL	3uM
RNase Inhibitor	20U/uL	0.5uL	1U/uL	0.5uL	1U/uL
Reverse Transcriptase	50U/uL	0.5uL	2.5U/uL	0.5uL	2.5U/uL
Purified Water	-	2.9uL	-	2.0uL	-
Nucleic Acid extract	-	0.1uL	-	0.5uL	-
total RT reaction		***10.0uL***		***10.0uL***	

(b) Composition of PCR reactions

		EF		DDC	
Component	**[stock]**	**Volume**	**[reaction]**	**Volume**	**[reaction]**
$MgCl_2$	25 mM	3.0uL	2.5mM	4.0uL	3mM
PCR Buffer	10X	4.0uL	1X	4.0uL	1X
forward primer	20uM	1.25uL	0.5uM	2.5uL	1uM
reverse primer	20uM	0.5uL	0.6uM	1.25uL	0.9uM
AmpliTaq DNA Polymerase	5U/uL	0.5uL	0.05U/uL	0.5uL	0.05U/uL
with TaqStart Antibody	7uM		0.07uM		0.07uM
Purified Water	-	30.75uL	-	27.75uL	-
RT reaction contents	-	10uL	-	10uL	-
total RT reaction		***50.0uL***		***50.0uL***	

Table 6. (continued)

(c) Touchdown PCR thermal cycling parameters

	first 25X cycles		last 13X cycles	
Phase	**Temp (°C)**	**Time (sec)**	**Temp (°C)**	**Time (sec)**
Denaturation	94	30	94	30
Annealing	55 (-0.4/cycle)	30	45	30
Extension	72	60 (+2/cycle)	72	120 (+3/cycle)

(d) Composition of nested PCR reactions

		EF or DDC	
Component	**[stock]**	**Volume**	**[reaction]**
$MgCl_2$	25 mM	4.0uL	2.0mM
PCR Buffer	10X	5.0uL	1X
dNTP	10mM (each)	1.0uL	0.2mM (each)
forward primer	20uM	1.25uL	0.5uM
reverse primer	20uM	1.25uL	0.5uM
AmpliTaq DNA Polymerase	5U/uL	0.5uL	0.05U/uL
with TaqStart Antibody	7uM		0.07uM
Purified Water	-	36uL	-
gel pure RT-PCR template	-	1.0uL	-
total RT reaction		***50.0uL***	

(e) Nested PCR thermal cycling parameters

	EF 22X cycles		DDC 22X cycles	
Phase	**Temp (°C)**	**Time (sec)**	**Temp (°C)**	**Time (sec)**
Denaturation	94	30	94	30
Annealing	60	30	50	30
Extension	72	60 (+2/cycle)	72	60 (+2/cycle)

Table 7. Survey of GenBank accessions for EF and DDC across Lepidoptera. Number of hits recovered from various search strings requesting (a) EF or (b) DDC sequences for all Lepidoptera in the NCBI GenBank Nucleotides Database, entered into the Entrez Search Engine on 06 April 2004. General format of each search string was "<gene> AND <taxon>[organism]". Distribution of hits across Superfamilies, Families and Genera indicates the range of taxonomic diversity recovered from each search string. Compiling results from several searches results in a more exhaustive exploration of database contents.

(a) GenBank hits to EF in Lepidoptera

Search String	***Hits***	**Superfamilies**	**Families**	**Genera**
"elongat* AND lepidopt*[organism]"	***419***	9	20	248
"elong* fact* AND lepidopt*[organism]"	***417***	9	20	247
"EF AND lepidopt*[organism]"	***259***	9	17	184

(b) GenBank hits to DDC in Lepidoptera

Search String	***Hits***	**Superfamilies**	**Families**	**Genera**
"dopa AND lepidopt*[organism]"	***238***	13	26	150
"decarboxylas* AND lepidopt*[organism]"	***237***	10	25	148
"dopa decarb* AND lepidopt*[organism]"	***234***	10	25	148
"DDC AND lepidopt*[organism]"	***133***	3	8	81

Table 8. Ingroup samples (Bombycoidea: Sphingidae) for which EF and/or DDC sequences were obtained. Species are listed alphabetically by higher taxonomic assignment, which was determined from Kitching & Cadiou (2000). 'UMD Accession' provides a unique serial identifier for each specimen derived from the UMD Lepidoptera Collections; parentheses denote UMD specimens for which EF and DDC sequence was obtained from previous studies; "unknown" indicates UMD sequence data which could not be traced to a particular specimen; the entry in square brackets (*Proserpinus*) is a PubMed ID citing sequence data obtained from another source. 'Taxon Label' gives the specimen name appearing in all data matrices; note sequences obtained from GenBank have a 'GB' suffix on their Taxon Label. 'Type' indicates specimen life stage: 'A' adult, 'P' pupa, 'L' larva. Tissue portion and date of nucleic acid extraction are noted in 'ExtrDate' and 'ExtrTissue', respectively. Incomplete data is indicated by 'na'. Complete specimen information can be obtained from the University of Maryland Lepidoptera Collections database (see Figure 3). Sequence source indicated in the 'EF' and 'DDC' columns: asterisks denote sequences collected de novo in this study; GenBank numbers are given for sequences obtained in silico; 'na' indicates sequence obtained for only one gene and these taxa were omitted from combined EF&DDC analyses. Brackets around U03909 (*Manduca sexta*) indicate this was the DDC reference sequence against which all other samples were aligned.

Taxonomy	Genus	species	UMD Accession	Taxon Label	type	sex	Locality	country	Date	Collector / Determiner	Notes	WingV	Extr Date	Extr Tissue	EF	DDC
Lepidoptera>Heteroneura>Ditrysia>Apoditrysia>Obtectomera>Macrolepidoptera>Bombycoidea>SPHINGIDAE																
MACROGLOSSINAE																
Dilophonotini																
Dilophonotina	***Aellopos***	***ceculus***	DHJ-02-2399	Aellopos2399	A	M	Area de Conservacion, Guanacaste	Costa Rica	27Oct02	Janzen, DH	DHJ accession no. 02-SRNP-19139 (http://janzen.sas.upenn.edu)	2399	4Feb03	head & prothorax	*	*
	A.	***tantalus***	(RSP-95-1070)	AelloposGB	L	na	N. Key Largo, Florida	USA	18Oct95	Peigler, RS	observed on Randia aculeata	na	14Mar00	anterior portion	AF234559	AF234582
	Callionima	***parce / falcifera***	RFD-96-0966	Callionima0966	A	na	Club House, Guana Island	Virgin Islands	15Oct96	Denno, RF & Mitter, CW	captured using black light; killed in 100% EtOH; stored at room temp one week	966	15Jan03	head	*	*
	Cautethia	***spuria***	CWB-02-2573	Cautethia2573	A	na	Brownsville, Cameron Co., Texas	USA	15Sep02	Bordelon, CW & Knudson, EC	eight specimens pickled together in "Everclear", transfered to 100% EtOH after 45 days at 4C	2573	6Feb03	head & prothorax	*	*
	Cau.	***undetermined***	JKA-02-1668	Cautethia1668	A	na	El Salto Falls area, San Luis Potosi	Mexico	1Aug02	Adams, JK		na	15Jan03	head	*	*
	Enyo	***ocypete***	DHJ-02-2390	Enyo2390	A	M	Area de Conservacion, Guanacaste	Costa Rica	27Oct02	Janzen, DH	DHJ accession no. 02-SRNP-29560 (http://janzen.sas.upenn.edu)	2390	4Feb03	head & prothorax	*	*
	Erinnyis	***ello***	JPT-02-1542	Erinnyis1542	A	na	Atascosa Mtns, Santa Cruz Co., Arizona	USA	30Jul02	Tuttle, JP	white granular residue in vial	1542	15Jan03	head	*	*
	Isognathus	***rimosa***	JKA-02-1646	Isognathus1646	A	na	El Lobo, Queretaro (1500m)	Mexico	8Aug02	Adams, JK		1646	25Feb03	head & prothorax	*	*
	Nyceryx	***magna***	DHJ-02-2378	Nyceryx2378	A	M	Area de Conservacion, Guanacaste	Costa Rica	27Oct02	Janzen, DH	DHJ accession no. 02-SRNP-18766 (http://janzen.sas.upenn.edu)	2378	15Jan03	head	*	*
	Pachylia	***ficus***	JKA-02-1644	Pachylia1644	A	na	El Lobo, Queretaro (1500m)	Mexico	8Aug02	Adams, JK		1644	25Feb03	head & prothorax	*	*
	Perigonia	***ilus / lusca passerina***	WJK-03-2191	Perigonia2191	A	na	El Anegado, Manabi Province (680m)	Ecuador	4Jan03	Kelly, WJ & Wolfe, KL		2191	25Feb03	head & prothorax	*	*
	Unzela	***japix***	DHJ-02-2376	Unzela2376	A	M	Area de Conservacion, Guanacaste	Costa Rica	27Oct02	Janzen, DH	DHJ accession no. 02-SRNP-29041 (http://janzen.sas.upenn.edu)	2376	4Feb03	head	*	*
Hemarina	***Cephonodes***	***hylas virescens***	IJK-02-5931	Cephonodes5931	A	M	unknown	unknown	1Nov00	O'Neill, M & Kitching, IJ	ex bred stock, IJK accession no. 695931 (obtained from BMNH, 18Nov02)	5931	25Feb03	cervix, prothorax	*	*
	Hemaris	***diffinis***	DCR-02-1882	Hemaris1882	A	na	SW of Waldron, Scott Co., Arkansas	USA	9Sep02	Rudolph, DC	collected live to alcohol	1882	15Jan03	head	*	*
	He.	***thysbe***	(TPF-94-1450)	HemarisGB	A	na	N. Potomac, Montgomery Co., Maryland	USA	29Jul94	Friedlander, TP & Peigler, RS		1450	2Aug94	unknown	AF234568	AF234590
Macroglossini																
Choerocampina	***Basiothia***	***medea***	IJK-02-0005	Basiothia0005	A	M	Mare de Vacoas	Mauritius	1May00	Ismay, J & Kitching, IJ	bred ex larva Jun-Jul 2000; pupal tube #241; specimen sent from BMNH, 26Nov02	na	25Feb03	head & prothorax	*	*
	Deilephila	***elpenor***	IJK-02-5866	Deilephila5866	A	M	Oxfordshire, Didcot	England	2002	O'Neill, M & Kitching, IJ	IJK accession no. 695866 (obtained from BMNH, 26Nov02)	5866	25Feb03	head & prothorax	*	*
	Hippotion	***celerio***	IJK-02-5932	Hippotion5932	A	F	unknown	Czech Republic	1Sep01	O'Neill, M & Kitching, IJ	IJK accession no. 695932 (obtained from BMNH, 26Nov02)	na	25Feb03	head & prothorax	*	*
	Hyles	***hippophaes***	IJK-02-5817	Hyles5817	A	M	Hautes Alpes, San Crépin (1000m)	France	2000	O'Neill, M & Kitching, IJ	bred ex larva on Hippophae rhamnoides; IJK acc. no. 695817 (obtained from BMNH, 26Nov02)	na	25Feb03	head & prothorax	*	*
	Hy.	***lineata***	DCR-02-1881	Hyles1881	A	na	Waldron, Scott Co., Arkansas	USA	9Sep02	Rudolph, DC	collected live to alcohol	1881	4Feb03	head & prothorax	*	*
	Theretra	***alecto***	IJK-02-5880	Theretra5880	A	M	unknown	Cyprus	1Sep01	O'Neill, M & Kitching, IJ	ex bred stock, IJK accession no. 695880 (obtained from BMNH, 18Nov02)	na	25Feb03	prothorax	*	*
	Xylophanes	***chiron nechus***	IJK-02-5904	Xylophanes5904	A	F	Tabaean	Costa Rica	24Oct01	O'Neill, M & Kitching, IJ	bred ex ovo; IJK accession no. 695904 (obtained from BMNH, 18Nov02)	na	4Feb03	head	*	*
	X.	***falco***	(JPT-xx-0838)	XylophanesGB	P	na	Copper Canyon, Cochise Co., Arizona	USA	na	Tuttle, JP		na	14Mar00	anterior portion	AF234580	AF234599
	X.	***porcus***	DHJ-02-2369	Xylophanes2369	A	M	Area de Conservacion, Guanacaste	Costa Rica	27Oct02	Janzen, DH	DHJ accession no. 02-SRNP-15885 (http://janzen.sas.upenn.edu)	2369	27Feb03	prothorax	*	*
	X.	***tersa***	DCR-02-1879	Xylophanes1879	A	na	Waldron, Scott Co., Arkansas	USA	9Sep02	Rudolph, DC	collected live to alcohol	1879	15Jan03	head	*	*
Macroglossina	***Daphnis***	***nerii***	IJK-02-5810	Daphnis5810	A	M	unknown	France	1May01	O'Neill, M & Kitching, IJ	ex bred stock, IJK accession no. 695810 (obtained from BMNH, 18Nov02)	na	25Feb03	prothorax	*	*
	Darapsa	***myron***	GS-02-1778	Darapsa1778	A	na	Cape Girardeau, Cape Girardeau Co., Missouri	USA	29Jul02	Smart, G		1778	15Jan03	head	*	*
	D.	***myron/pholus***	(unknown)	DarapsaGB											AF234563	AF234585
	Macroglossum	***stellatarum***	IJK-02-5806	Macroglossum5806	A	na	unknown	France	2002	O'Neill, M & Kitching, IJ	ex bred stock, IJK accession no. 695806 (obtained from BMNH, 18Nov02)	5806	25Feb03	thorax	*	*
	Proserpinus	***clarkiae***	[12116588]	ProserpinusGB	A	na									AF173394	na
	Sphecodina	***abbottii***	(CWM-90-1454)	SphecodinaGB	A	na	BARC, Beltsville, Maryland	USA	21Jun90	"MEE" & Mitter, CW		na	8Feb94	head & thorax	AF234575	AF234594
Philampelini	***Eumorpha***	***achemon***	JPT-02-1533	Eumorpha1533	A	na	Patagonia Mtns, Santa Cruz Co., Arizona	USA	24Jul02	Mooney, B & Byrne, H & Tuttle,		1533	15Jan03	head	*	*
	E.	***pandorus***	(CWM-95-0830)	EumorphaGB	L	na	Spring Mill State Park, Mitchell, Indiana	USA	23Aug95	Mitter, CW	on Parthenocissus quinquefolia	na	3Apr96	anterior portion	AF234565	AF234588
	E.	***typhon***	JBW-02-1504	Eumorpha1504	A	na	Pena Blanca Cyn, Santa Cruz Co., AZ (1220m)	USA	26Jul02	Walsh, B	collected at MV/UV lights	na	27Feb03	head & prothorax	*	*

Table 8. (continued)

Taxonomy	Genus	species	UMD Accession	Taxon Label	type	sex	Locality	country	Date	Collector / Determiner	Notes	WingV	Extr Date	Extr Tissue	EF	DDC
SMERINTHINAE																
Ambulycini	*Adhemarius*	*gannascus*	JKA-02-1642	Adhemarius1642	A	na	Tamaznchale, San Luis Potosi	Mexico	6Aug02	Adams, JK		1642	15Jan03	head	*	*
					A	na	Morona-Santiago Province	Ecuador	1Jan03	Kelly, WJ & Wolfe, KL		1945	25Feb03	head & prothorax	*	*
	Protambulyx	*eurycles*	WJK-03-1945	Protambulyx1945			(1270m)									
Smerinthini	*Amorpha*	*juglandis*	CWB-02-1595	Amorpha1595	A	na	Concan, Uvalde Co., Texas	USA	6Sep02	Bordelon, CW & Knudson, EC	three specimens stored together, partially submerged in EtOH	1595	15Jan03	head	*	*
	Laothoe	*populi*	UJK-02-0012	Laothoe0012	A	M	London, SE3	England	1999	Godsell, G & Kitching, IJ	emerged March 2000 (obtained from BMNH, 18Nov02)	na	25Feb03	head, portion	*	*
	Marumba	*quercus*	UJK-02-0118	Marumba0118	A	F	Provence, near Toulon	France	2000	Pittaway, AR & Kitching, IJ	head	na	25Feb03	head & prothorax	*	*
	Mimas	*tiliae*	UJK-02-5836	Mimas5836	A	M	London, Raynes Park	England	2001	Kitching, IJ	UJK accession no. 695836 (obtained from BMNH, 18Nov02)	5836	25Feb03	prothorax	*	*
	Pachysphinx	*modesta*	(RSP-96-0626)	PachysphinxGB	A	F	Denver, Colorado	USA	1Jul96	Peigler, RS		na	27Sep00	thorax	AF234573	na
	Pa.	*occidentalis*	JPT-02-1528	Pachysphinx1528	A	na	Patagonia Mtns. Santa Cruz Co., Arizona	USA	20Jul02	Tuttle, JP		1528	4Feb03	head & prothorax	*	*
	Paonias	*excaecata*	(CWM-96-0573)	PaoniasGB	A	na	Mathias, West Virginia	USA	8Jul96	Miller, CW	specimen frozen live	na	27Sep00	thorax	AF234572	na
	Pao.	*myops*	JPT-02-1540	Paonias1540	A	na	Atascosa Mtns. Santa Cruz Co., Arizona	USA	26Jul02	Mooney, B & Mouw, J & Tuttle,	white residue as vial	1540	27Feb03	prothorax	*	*
	Pseudoclanis	*postica*	UJK-02-5839	Pseudoclanis5839	A	M	unknown	South Africa	2000	Kitching, IJ	ex. bred stock, UJK accession no. 695839 (obtained from BMNH, 18Nov02)	5839	27Feb03	head & prothorax	*	*
	Smerinthus	*cerisyi*	(UJK-95-0827)	SmerinthusGB	P	na	Hull, Portage Co., Wisconsin	USA	28May95	Kruse, JJ	wild female caught at UV light, ex ovo reputed Jul-Aug1995 and frozen Sep1995	na	14Mar00	thorax	AF234576	AF234595
	Sm.	*saliceti*	JBW-02-1511	Smerinthus1511	A	na	Santa Rita Mtns. Pima Co., Arizona (1067m)	USA	2Aug02	Walsh, B	collected at MV/UV lights	1511	6Feb03	head & prothorax	*	*
Sphingulini	*Hopliocnema*	*brachycera*	MJM-96-0233	Hopliocnema0233	A	na	NT, SA or ACT	Australia	1996	Matthews, MJ	specimen killed in 100% EtOH; shipped cold but delayed in shipping for 10 days	na	6Feb03	prothorax	*	*
SPHINGINAE																
Acherontiini	*Acherontia*	*styx medusa*	UJK-02-5989	Acherontia5989	A	M	Palawan, Bataraza, Malihad	Philippines	1Jul01	Zwick, A & Kitching, IJ	bred ex. larva, UJK accession no. 695989 (obtained from BMNH, 26Nov02)	na	27Feb03	prothorax	*	*
	Agrius	*cingulata*	WJK-02-1941	Agrius1941	A	na	Blackberry Mountain, Gilmer Co., Georgia	USA	22Sep02	Kelly, WJ	collected at mercury vapor light	1941	15Jan03	head	*	*
	Cedonia	*fulvinotata*	UJK-02-5816	Cedonia5816	A	F	unknown	Zimbabwe	2002	O'Neill, M & Kitching, IJ	ex. bred stock, UJK accession no. 695816 (obtained from BMNH, 18Nov02)	na	27Feb03	head & prothorax	*	*
Sphingini	*Ceratomia*	*catalpae*	DCR-02-1870	Ceratomia1870	A	na	Waldron, Scott Co., Arkansas	USA	10Sep02	Rudolph, DC	collected live to alcohol	1870	27Feb03	prothorax	*	*
	Ce.	*undulosa*	(RSP-96-0932)	CeratomiaGB	A	na	Barr Lake, Adams Co., Colorado	USA	25Jun95	DiLorenzo, S		na	14Mar00	thorax	AF234562	AF234584
	Cocytius	*duponchel*	DHJ-02-2359	Cocytius2359	A	F	Area de Conservacion, Guanacaste	Costa Rica	27Oct02	Janzen, DH	DHJ accession no. 02-SRNP-29158 (http://janzen.sas.upenn.edu)	2359	15Jan03	head	*	*
	Dolba	*hyloeus*	(RSP-xx-1349)	DolbaGB	A	na	unknown	USA	na	unknown & Peigler, RS	"specimen badly rubbed" (RS Peigler)	1349	11Jul94	unknown	AF234579	AF234598
	Eumorpha	*achemon*	WJK-03-2891	Eumorpha2891	A	na	Morona-Santiago Province (1270m)	Ecuador	1Jan03	Kelly, WJ & Wolfe, KL		2891	4Mar03	prothorax	*	*
	Lapara	*coniferarum*	JKA-02-1670	Lapara1670	A	na	Calhoun, Gordon Co., Georgia	USA	1Aug02	Adams, JK		1670	4Mar03	head & prothorax	*	*
	Manduca	*florestan*	JPT-02-1529	Manduca1529	A	na	Patagonia Mtns. Santa Cruz Co., Arizona	USA	24Jul02	Mooney, B & Byrne, H & Tuttle,		1529	4Mar03	head & prothorax	*	*
	Ma.	*muscosa*	JBW-02-1508	Manduca1508	A	na	Santa Rita Mtns. Pima Co., Arizona (1067m)	USA	2Aug02	Walsh, B	collected at MV/UV lights	1508	4Mar03	head & prothorax	*	*
	Ma.	*quinquemaculata*	DCR-02-1876	Manduca1876	A	na	Waldron, Scott Co., Arkansas	USA	11Sep02	Rudolph, DC	collected live to alcohol	1876	6Feb03	head	*	*
	Ma.	*sexta*	(TPF-91-2004)	ManducaGB	A	na	Sugar Loaf Mtn., Montogomery Co. Maryland	USA	31Jul91	Friedlander, TP & Peigler, RS	larvae on tomato plant, previously misidentified as M.quinquemaculata; original label "2001"	na	unknown	larva	AF234571	[U03909]
	Neococytius	*cluentius*	WJK-03-1949	Neococytius1949	A	na	Tinalandia, Pichincha Province (710m)	Ecuador	31Jan03	Kelly, WJ & Wolfe, KL		1949	4Mar03	prothorax	na	*
	Paratrea	*plebeja*	WJK-02-1939	Paratrea1939	A	na	Ellijay, Gilmer Co., Georgia	USA	29Aug02	Kelly, WJ	collected at MV light	1939	6Feb03	head & prothorax	*	*
	Poliagramma	*incrota*	UJK-02-5988	Poliogramma5988	A	M	Palawan, Bataraza, Malihad	Philippines	1Jul01	Zwick, A & Kitching, IJ	bred ex. larva, UJK accession no. 695988 (obtained from BMNH, 18Nov02)	na	4Mar03	head & prothorax	*	*
	Sphinx	*chersis*	(JPT-xx-0839)	SphinxGB	P	na	Pena Blanca Lake, Santa Cruz Co., Arizona	USA	na	Tuttle, JP		na	14Mar00	anterior portion	AF234577	AF234596
	Sp.	*dollii*	JPT-02-1532	Sphinx1532	A	na	Patagonia Mtns. Santa Cruz Co., Arizona	USA	24Jul02	Mooney, B & Byrne, H & Tuttle,		1532	6Feb03	head & prothorax	*	*
	Sp.	*izar*	CWB-02-1591	Sphinx1591	A	na	Concan, Uvalde Co., Texas	USA	6Sep02	Bordelon, CW & Knudson, EC		1591	4Mar03	prothorax	*	*
	Sp.	*kalmiae*	WJK-02-1938	Sphinx1938	A	na	Ellijay, Gilmer Co., Georgia	USA	28Aug02	Kelly, WJ	collected at MV light	1938	4Mar03	head & prothorax	*	*

Table 9. Outgroup samples (Lepidoptera) for which EF and/or DDC sequences were obtained. Species are listed alphabetically by higher taxonomic assignment, determined from a superfamily classification of Lepidoptera compiled from multiple sources (Arnett 2001; Borror 1989; Kristense 1999; Scoble 1992; Wagner 2001; also see Table 11). 'UMD Accession' provides a unique serial identifier for each specimen derived from the UMD Lepidoptera Collections; "unknown" indicates UMD sequence data which could not be traced to a particular specimen; entries in square brackets provide PubMed ID or other citation information for sequence data obtained other sources. 'Taxon Label' gives the specimen name appearing in all data matrices. 'Type' indicates specimen life stage: 'A' adult, 'P' pupa, 'L' larva. Tissue portion and date of nucleic acid extraction are noted in 'ExtrDate' and 'ExtrTissue', respectively. Incomplete data is indicated by 'na'. Complete specimen information can be obtained from the University of Maryland Lepidoptera Collections database (see Figure 3). GenBank accession numbers listed in the 'EF' and 'DDC' columns: blank cells indicate sequence obtained for only one gene and these taxa were omitted from combined EF&DDC analyses. Brackets around D13338 (*Bombyx mori*) indicate this was the EF reference sequence against which all other samples were aligned (see Figure 4).

Taxon Superfamily	Family	Subfamily	Tribe	Genus	species	UMD Accession	Taxon Label	stage	sex	Locality	country	Date	Collector/Determiner	Notes	WingV	Extr Date	Extr Tissue	EF	DDC
Zeuglopter a																			
Micropterigoidea	Micropterigidae			*Epimartyria*	*auricrinella*	unknown	Micropterigoidea												AF093174
				Micropteryx	*calthella*	unknown	Micropterigoidea											AF436596	
Glossata																			
Eriocranioidea	Eriocranidae			*Eriocrania*	*semipurpurella*	xx-92-xxxx	Eriocranioidea	L	na	na	na	na	na		na	na	na		AF093175
Glossata>Coelolepida>Myoglossata>Neolepidoptera>Exoporia																			
Hepialoidea	Hepialidae			*Hepialus*	*californicus*	TPF-92-1216	Hepialoidea	A	na	Bodega Bay, California	USA	13Apr92	Friedlander,TP & Wagner,DL	specimen frozen dry at -80C, until 100% EtOH added on 7/30/98		na	na		AF093178
Glossata>Coelolepida>Myoglossata>Neolepidoptera>Heteroneura																			
Incurvarioidea	Adelidae	Adelinae		*Adela*	*purpurea*	unknown	Adelidae												
	Cecidoseidae			*Cecidoses*	*eremita*	unknown	Cecidoseidae												AF093167
	Heliozelidae			*Coptodisca*	*kalmiella*	DLW-xx-xxxx	Heliozelidae	L	na	Connecticut	USA	28Jun91	Wagner,DL	larvae in few capsules	na	4Feb94	na		AF093170
	Incurvariidae			*Vespina*	*quercivora*	unknown	Incurvariidae												AF093171
	Prodoxidae	Lamproninae		*Tetragma*	*gei*	OP-89-xxxx	Lamproninae	A	na	Wawawa grade, Washington	USA	06May89	Pellmyr,O		na	na	na		AF093195
		Prodoxinae		*Prodoxus*	*quinquepunctellus*	TPF-91-0034	Prodoxinae	A	na	Adelphi, Prince George's Co., Maryland	USA	31May91	Friedlander,TP	TPF voucher #034	na	20Feb02	na		AF093192
	Palaephatoidea	Palaephatidae		*Palaephatus*	*falsus*	unknown	Palaephatoidea												AF093183
	Tischerioidea	Tischeriidae		*Tischeria*	*baditiella*	DLW-90-0026	Tischerioidea	A	na	Connecticut	USA	28Mar90	Wagner,DL	lot #89K26	na	10Oct93	na		AF093182
Glossata>Coelolepida>Myoglossata>Neolepidoptera>Heteroneura>Ditrysia																			AF093187
Gracillarioidea	Gracillariidae	Lithocolletinae		*Lewcanthiza*	*amphicarpaeafoliella*	DRD-01-0064	Gracillarioidea	na	na	Tremont, GSMNP, Tennessee	USA	01Sep00	Davis, DR		na	na	na		AF093180
Tineoidea	Psychidae	Oiketicinae		*Thyridopteryx*	*ephemeraeformis*	TPF-90-0022	Psychidae	L	na	Rockville, Montgomery Co., Maryland	USA	26Aug90	Friedlander,TP & Friedlander,LG	TPF voucher #022; frozen 29Aug90; collected on	na	8Jun93	na		AF093190
	Tineidae	Tineinae		*Tinea*	*pellionella*	JG-96-0008	Tineidae	A	na	na	Australia	31Jan96	Giebultowicz,J	voucher #209; specimen received live as pharate adult/pupa from OSU Ent. laboratory culture	na	30Jan95	na		AF093193
Glossata>Coelolepida>Myoglossata>Neolepidoptera>Heteroneura>Ditrysia>Apoditrysia>Obtectomera																			
Pyraloidea	Crambidae			*Ostrinia*	*nubilalis*	[12116588]	Crambidae											AF173392	
	Pyralidae	Galleriinae		*Galleria*	*melonella*	[Whiting 2002]	Galleriinae											AF423811	
		Pyraustinae		*Agrioglypta*	*naralis*	[Sutrisno, H.]	Pyraustinae											AB158395	
Glossata>Coelolepida>Myoglossata>Neolepidoptera>Heteroneura>Ditrysia>Apoditrysia>Obtectomera>Macrolepidoptera																			
Bombycoidea	Bombycidae	Bombycinae	Bombycini	*Bombyx*	*mori*	xx-xx-0062	Bombycidae	P	na	lab colony	unknown	na	na		109	23Jun94	anterior portion	[D13338]	AF372836
	Brahmaeidae			*Brahmaea*	*certhia*	RSP-94-1039	Brahmaeidae	A	F	unknown	Korea	15May94	Peigler,RS	obtained from dealer in Czech Republic	1039	14Mar00	head and thorax	AF234560	AF234583
	Endromidae			*Endromis*	*versicolora*	unknown	Endromidae											AF234566	
	Lemoniidae			*Lemonia*	*dumi*	RSP-96-0623	Lemoniidae	P	F	Sverthacken, Handen, Stockholm	Sweden	18Jun05	Hyden,N	specimen darker than usual internally	na	27Sep00	na	AF234570	
	Saturniidae	Ceratocampinae		*Dryocampa*	*rubicunda*	TPF-90-xxxx	Ceratocampinae	A	na	Beltsville, Prince George's Co., Maryland	USA	1996	Friedlander,TP	collected at light	na	na	na	AF234564	AF234586
		Hemileucinae	Hemileucini	*Automeris*	*cecropa*	[Rubinoff 2002]	Hemileucini											AY040098	
				Automeris	*io*	KRH-94-1445	Hemileucini	A	na	USDA trap, Beltsville, Maryland	USA	07Jun94	Horst,KR & Mitter,CW & Peigler,RS		1445	na	na		AF373956
			Polythysanini	*Polythysana*	*apollina*	KLW-96-2007	Polythysanini	L	na	Linares	Chile	08May96	Mazry,J & Wolfe,KL	3 eggs dissected, 2 live larvae plus egg shells preserved in EtOH	na	11May00	whole specimen	AF373939	
		Saturniinae	Attacini	*Attacus*	*atlas*	xx-91-1020	Attacini	A	na	unknown	Thailand	1990	na	specimen frozen alive	na	16Dec98	thorax	AF015066	AF015045
			Bunaeini	*Cirina*	*forda*	RSP-xx-0998	Bunaeini	P	na	Pretoria	South Africa	na	Peigler,RS		na	21Mar00	anterior portion	AF373931	AF373959
			Micragonini	*Holocerina*	*smilax*	RSP-xx-1040	Micragonini	A	na	Transvaal	South Africa	na	Peigler,RS		na	21Mar00	head and thorax	AF373934	AF373963
			Saturniini	*Saturnia*	*albofasciata*	RSP-xx-1053	Saturniini	A	na	California	USA	na	Peigler,RS	specimen stored in paper	na	14Mar00	thorax	AF373940	
				Saturnia	*nassiigi*	NK-94-1026	Saturniini	A	na	Manzurtal, Tunceli Province	Turkey	01Sep94	Keil,N & Peigler,RS	eggs from Norbert Keil, reared in Colorado by R.S.Peigler	na	27Dec98	thorax		AF373974.2
Geometroidea	Geometridae	Ennominae		*Lambdina*	*fiscellaria*	[12116588]	Geometroidea											AF173391	
Hedyloidea	Hedylidae			*Macrosoma*	*undetermined*	[12116588]	Hedyloidea											AF173393	
Hesperioidea	Hesperiidae	Hesperiinae		*Hylephila*	*phyleus*	[12116588]	Hesperiinae											AF173398	
		Pyrginae		*Pyrgus*	*communis*	[12116588]	Pyrginae											AF173396	
Lasiocampoidea	Lasiocampidae	Lasiocampinae	Gastropachini	*Phyllodesma*	*americana*	RSP-96-0819	Gastropachini	L	na	Georgia	USA	24May96	Peigler,RS		na	9Oct00	whole specimen	AF234554	
			Lasiocampini	*Lasiocampa*	*quercus*	RSP-96-0862	Lasiocampini	L	na	na	Italy	1996	Peigler,RS		na	28Sep00	whole specimen	AF234550	
			Malacosomatini	*Malacosoma*	*americanum*	AM-94-0145	Malacosomatini	A	na	College Park, Maryland	USA	26May94	Mitchell,A		112	30Jun98	head and thorax	AF234551	
		Macromphalinae		*Artace*	*cribraria*	AM-94-0422	Macromphalinae	A	na	College Park, Maryland	USA	24Oct94	Mitchell,A		422	8Sep98	na	AF234545	
Noctuoidea	Arctiidae	Arctiinae	Arctiini	*Estigmene*	*acrea*	AM-93-0438	Arctiinae	A	na	BARC(East), Beltsville, Maryland	USA	09Aug93	Mitchell,A		45	13Nov93	na	U85670	AF151549
		Lithosiinae	Lithosiini	*Hypoprepia*	*miniata*	RFD-93-0437	Lithosiinae	A	na	G.Washington Natl Forest, Mathias, WV	USA	17Jul93	Denno,RF & Cho,SW	tube labeled #1	076/9	28Apr94	na	U85669	AF151547
	Lymantriidae	Lymantriinae	Orgyiini	*Dasychira*	*undetermined*	CWM-93-0440	Lymantriidae	A	na	Clarksville, Howard Co., Maryland	USA	23Jul93	Mitter,CW & Poole,RW		56	16Mar94	na	U85673	AF151545
	Noctuidae "Quadrifine"	Agaristinae		*Asota*	*caricae*	UK-94-0559	Agaristinae	A	na	Doi Suthep-Pui National Park	Thailand	01Apr94	Kitching,IJ	original tube 'A1'; genitalia dissections needed for	232	30Jul96	na	AF151607	AF151551
		Catocalinae	Group 1a	*Catocala*	*ultronia*	CWM-93-0435	Catocalinae	A	na	Clarksville, Howard Co., Maryland	USA	24Jul93	Mitter,CW & Poole,RW		22	14Jan94	na	U85677	AF151561
		Noliinae	Nolini	*Meganola*	*undetermined*	CWM-93-0434	Noliinae	A	na	Clarksville, Howard Co., Maryland	USA	24Jul93	Mitter,CW & Poole,RW		25	14Jan94	na	U85675	AF151558
		Stictopterinae		*Lophoptera*	*undetermined*	UK-94-0560	Stictopterinae	A	na	Doi Suthep-Pui National Park	Thailand	01Apr94	Kitching,IJ	original tube 'L1'; genitalia dissections needed for	233	30Jul96	na	AF151610	AF151556
	Noctuidae "Trifine"	Condicinae	Condicini	*Condica*	*videns*	RWP-94-0443	Condicinae	A	na	Rockville, Montgomery Co., Maryland	USA	16Mar94	Poole,RW		47	16Mar94	na	U85682	AF151569
		Heliothinae		*Heliothis*	*decorata*	MJM-88-0031	Heliothinae	A	na	Bamako, Mali, West Africa	Africa	07Aug88	Matthews,MJ	44 male, 44 female, 10 unknown	31	7Feb94	na		U71414
				Heliothis	*subflexa*	AS-xx-xxxx	Heliothinae	A	na	na	USA	na	Sheck,A	8 vials labeled "HS" from Florida & Missouri fines	122	7Jul93	na	U20134	
		Noctuinae	Noctuini	*Abagrotis*	*alternata*	CWM-94-0415	Noctuinae	A	na	BARC(East), Beltsville, Maryland	USA	07Oct94	Mitchell,A & Mitter,CW		225	1Jul96	na	AF151630	AF151601
		Oncocnemidinae		*Oncocnemis*	*obscurata*	EK-93-0445	Oncocnemidinae	A	na	El Paso, Texas	USA	09Oct93	Knudson,E & Poole,RW	tube #67 according to Knudson specimen log	58	4Apr94	na	U85685	AF151585
		Pantheinae		*Panthea*	*furcilla*	CWM-94-0221	Pantheinae	A	na	BARC (East), Beltsville, Maryland	USA	04Jun94	Mitter,CW & MitchellA & Poole,RW		164	23Nov94	na	U85684	AF151572
	Notodontidae	Heterocampinae		*Nerice*	*bidentata*	unknown	Heterocampinae											AF151604	AF151543
		Notodontinae	Dicranurini	*Furcula*	*cinerea*	AM-93-0430	Notodontinae	A	na	College Park, Maryland	USA	10Aug93	Mitchell,A & Poole,RW		43	13Nov93	na	U85665	AF151539
		Nystaleinae		*Symmerista*	*albifrons*	CWM-94-0347	Nystaleinae	A	na	BARC (East), Beltsville, Maryland	USA	01Apr94	Mitter,CW & MitchellA & Friedlander,TP		172	27Apr95	head and thorax	U85667	AF151541
		Phalerinae		*Datana*	*perspicua*	AM-93-0431	Phalerinae	A	na	BARC (East), Beltsville, Maryland	USA	14Aug93	Mitchell,A & Poole,RW		44	13Nov93	na	U85666	AF151540
Papilionoidea	Lycaenidae	Polyommatinae		*Euphilotes*	*bernardino*	[12116588]	Polyommatinae											AF173404	
		Riodininae		*Apodemia*	*mormo*	[12116588]	Riodininae											AF173403	
	Nymphalidae	Cyrestinae	Cyrestidini	*Cyrestis*	*thyodamas*	[12927132]	Cyrestinae											AY218260	
		Danainae		*Amauris*	*ellioti*	[12927132]	Danainae											AY218253	
		Heliconiinae		*Heliconius*	*hecale*	[12927132]	Heliconiinae											AY090168	
				Heliconius	*himera*	[Bull 2003]	Nymphalidae												AY437778
		Nymphalinae		*Nymphalis*	*antiopa*	[12927132]	Nymphalinae											AY218266	
		Satyrinae	Mycaleini	*Bicyclus*	*anynana*	[12927132]	Satyrinae											AY218258	
	Papilionidae	Baroniinae		*Baronia*	*brevicornis*	[12116588]	Baroniinae											AF173406	
		Papilioninae	Papilionini	*Papilio*	*glaucus*	[Koch 1997]	Papilionidae												AF036963
				Papilio	*troilus*	[Whiting 2002]	Papilioninae											AF423810	
		Parnassiinae	Parnassiini	*Parnassius*	*clodius*	[12116588]	Parnassiinae											AF173411	
	Pieridae	Coliadinae		*Colias*	*eurytheme*	[12116588]	Coliadinae											AF173400	
		Pierinae		*Pieris*	*napi*	[12116588]	Pierinae											AF173401	

Table 10. New Sphingidae specimens. Novel material (350 specimens) collected expressly for this study was accessioned into the University of Maryland Lepidoptera Collections and is available for molecular sequence data collection (see Figures 2 and 3). Number of specimens and their distribution across taxonomic levels was tabulated for each collector.

Collector	Series	Subfamilies	Genera	Species	Specimens
James K. Adams	JKA-02	3	11	19	21
Charles W. Bordelon	CWB-02	3	8	12	28
David Boucher	DB-03	2	4	4	4
John DeBenedictis	JAD-02	2	2	2	4
Ian J. Kitching	IJK-02&03	3	32	58	99
Daniel H. Janzen	DHJ-02	3	9	18	30
William J. Kelly	WJK-02&03	3	16	37	42
Peter J. Landolt	PJL-02	1	2	2	6
Andre A. Mignault	AAM-02	1	3	3	21
Charles W. Mitter	CWM-02	1	1	1	1
Marcela More	MM-03	2	7	13	17
Mogens C. Nielsen	MCN-03	3	4	5	5
James Oberfoell	JO-03	2	3	3	5
Richard S. Peigler	RSP-02	1	1	1	1
D. Craig Rudolph	DCR-02	2	7	9	14
Glen Smart	GS-02	3	10	14	19
James P. Tuttle	JPT-02	3	10	18	20
J. Bruce Walsh	JBW-02	3	8	10	13

Table 11 Distribution of EF and DDC sequence accessions in GenBank across Lepidoptera. Search strings querying EF and DDC sequences across Lepidoptera were submitted tot he Entrez Browser in the NCBI GenBank Nucleotides Database on 06 April 2004 (see Table 7). Hits to these queries are plotted separately for each gene across all families in a classification of Lepidoptera [Hexapoda: Ectognatha(Insecta): Dicondylia: Pterygota: Neoptera: Holometabola(Endopterygota): Panorpoidea: Amphiesmenoptera] compiled from Borror 1989, Wagner 2001, Arnett 2000, Kristensen 1999, Scoble 1992. Raw and cumulative numbers of described species per superfamily and family are also included to provide diversity measures.

#	SUPERFAMILY	spp	%	cum	cum%	Family	spp	Common Name	EF	DDC
Zeugloptera										
1	**MICROPTERIGOIDEA**	121	0.07	121	0.07	**Micropterigidae**	121	mandibulate archaic moths	2	2
Aglossata										
2	**AGATHIPHAGOIDEA**	2	0.00	123	0.07	**Agathiphagidae**	2	kauri moths		
Heterobathmiina										
3	**HETEROBATHMIOIDEA**	9	0.01	132	0.07	**Heterobathmiidae**	9	valdivian archaic moths		
Glossata										
4	**ERIOCRANIOIDEA**	24	0.01	156	0.09	**Eriocraniidae**	24	sparkling archaic sun moths		2
Glossata>Coelolepida										
5	**ACANTHOPTEROCTETOIDEA**	5	0.00	161	0.09	**Acanthopteroctetidae**	5	archaic sun moths		
6	**LOPHOCORONOIDEA**	6	0.00	167	0.09	**Lophocoronidae**	6	australian archaic sun moths		
Glossata>Coelolepida>Myoglossata										
7	**NEOPSEUSTOIDEA**	11	0.01	178	0.10	**Neopseustidae**	11	archaic bell moths		
Glossata>Coelolepida>Myoglossata>Neolepidoptera>Exoporia										
8	**HEPIALOIDEA**	569	0.32	747	0.42	**Anomosetidae**	1	australian primitive ghost moths		
						Hepialidae	550	ghost moths & swifts		2
						Neotheoridae	1	amazonian primitive ghost moths		
						Palaeosetidae	8	miniature ghost moths		
						Prototheoridae	9	african primitive ghost moths		
9	**MNESARCHAEOIDEA**	14	0.01	761	0.43	**Mnesarchaeidae**	14	new zealand primitive moths		
Glossata>Coelolepida>Myoglossata>Neolepidoptera>Heteroneura										
10	**NEPTICULOIDEA**	902	0.51	1,663	0.93	**Nepticulidae**	800	leaf miners & pygmy moths		1
						Opostegidae	102	eye-cap moths		1
11	**INCURVARIOIDEA**	594	0.33	2,257	1.27	**Adelidae**	300	long-horned fairy moths		3
						Cecidosidae	7	gall moths		2
						Crinopterygidae	1			
						Heliozelidae	106	shield bearers & leaf miners		2
						Incurvariidae	100	leaf-cutter moths		1
						Prodoxidae	80	yucca moths		7
12	**PALAEPHATOIDEA**	60	0.03	2,317	1.30	**Palaephatidae**	60	gondwanaland moths		1
13	**TISCHERIOIDEA**	80	0.04	2,397	1.35	**Tischeriidae**	80	apple-leaf trumpet miners		2
Glossata>Coelolepida>Myoglossata>Neolepidoptera>Heteroneura>Ditrysia										
14	**SIMAETHISTOIDEA**	4	0.00	2,401	1.35	**Simaethistidae**	4			
15	**TINEOIDEA**	4,350	2.45	6,751	3.79	**Acrolophidae**	270	tube moths		
						Arrhenophanidae	8	tropical lattice moths		
						Eriocottidae	71	old world spiny-winged moths		
						Lypusidae	1			
						Psychidae	1,000	bag worm moths		1
						Tineidae	3,000	fungus & clothes moths		2
16	**GELECHIOIDEA**	16,631	9.35	23,382	13.14	**Amphisbatidae**	65			
						Autostichidae	308			
						Batrachedridae	100			
						Chimabachidae	6			
						Coleophoridae	1,418	casebearer moths		
						Cosmopterigidae	1,628	cosmet moths		
						Deoclonidae	4			
						Elachistidae	3,270	grass miner moths		
						Gelechiidae	4,530	twirler moths		
						Glyphidoceridae	50			
						Lecithoceridae	875	tropical longhorned moths		
						Oecophoridae	3,150	concealer moths		
						Peleopodidae	25			
						Schistonoeidae	2			
						Xyloryctidae	1,200			
17	**GRACILLARIOIDEA**	2,316	1.30	25,698	14.44	**Bucculatricidae**	250	ribbed coccoon-maker moths		
						Douglasiidae	26	douglas moths		
						Gracillariidae	2,000	leaf miner moths		1
						Roeslerstammiidae	40			
18	**YPONOMEUTOIDEA**	1,869	1.05	27,567	15.49	**Acrolepiidae**	95	false diamond-back moths		
						Bedelliidae	18			
						Glyphipterygidae	390	sedge moths		
						Heliodinidae	55	sun moths		
						Lyonetiidae	210	lyonet moths		
						Plutellidae	380	diamond-back moths		
						Yponomeutidae	591	ermine moths		
						Ypsolophidae	130			

Table 11. (continued)

Glossata>Coelolepida>Myoglossata>Neolepidoptera>Heteroneura>Ditrysia>Apoditrysia										
19	**ALUCITOIDEA**	164	0.09	27,731	15.59	**Alucitidae**	146	many-plumed moths		
						Tineodidae	18	false plume moths		
20	**PTEROPHOROIDEA**	986	0.55	28,717	16.14	**Pterophoridae**	986	plume moths		
21	**CHOREUTOIDEA**	415	0.23	29,132	16.37	**Choreutidae**	415	metalmark moths		
22	**COSSOIDEA**	676	0.38	29,808	16.75	**Cossidae**	670	carpenter & goat moths		
						Dudgeoneidae	6	dudgeon carpenter worm moths		
23	**SESIOIDEA**	1,372	0.77	31,180	17.53	**Brachodidae**	100	little bear moths		
						Castniidae	137	giant butterfly moths		
						Sesiidae	1,135	clearwing moths		
24	**ZYGAENOIDEA**	2,783	1.56	33,963	19.09	**Aididae**	6			
						Anomoeotidae	40			
						Cyclotornidae	12	australian parasite moths		
						Dalceridae	50	tropical slug caterpillar moths		
						Epipyropidae	55	planthopper parasite moths		
						Heterogynidae	10	mediterranean burnet moths		
						Himantopteridae	40	long-tailed burnet moths		
						Lacturidae	125	tropical burnet moths		
						Limacodidae	1,080	slug & saddleback caterpillar moths		
						Megalopygidae	265	flannel moths		
						Somabrachyidae	?	mediterranean flannel moths		
						Zygaenidae	1,100	smoky moths & burnets		
25	**EPERMENIOIDEA**	83	0.05	34,046	19.14	**Epermeniidae**	83	fringe-tufted moths		
26	**GALACTICOIDEA**	17	0.01	34,063	19.15	**Galacticidae**	17			
27	**SCHRECKENSTEINIOIDEA**	5	0.00	34,068	19.15	**Schreckensteiniidae**	5	bristle-legged moths		
28	**TORTRICOIDEA**	8,000	4.50	42,068	23.65	**Tortricidae**	8,000	leafroller moths		
29	**URODOIDEA**	80	0.04	42,148	23.69	**Urodidae**	80	false burnet moths		
Glossata>Coelolepida>Myoglossata>Neolepidoptera>Heteroneura>Ditrysia>Apoditrysia>Obtectomera										
30	**COPROMORPHOIDEA**	330	0.19	42,478	23.88	**Carposinidae**	275	fruitworm moths		
						Copromorphidae	55	tropical fruitworm moths		
31	**HYBLAEOIDEA**	18	0.01	42,496	23.89	**Hyblaeidae**	18	teak moths		
32	**IMMOIDEA**	246	0.14	42,742	24.02	**Immidae**	246	imma moths		
33	**PYRALOIDEA**	17,763	9.98	60,505	34.01	**Crambidae**	11,630	close-wings & grassmoths		
						Pyralidae	6,133	snout & grass moths	27	1
34	**THYRIDOIDEA**	760	0.43	61,265	34.44	**Thyrididae**	760	picture-winged leaf moths		
35	**WHALLEYANOIDEA**	2	0.00	61,267	34.44	**Whalleyanidae**	2			
Glossata>Coelolepida>Myoglossata>Neolepidoptera>Heteroneura>Ditrysia>Apoditrysia>Obtectomera>Macrolepidoptera										
36	**BOMBYCOIDEA**	3,553	2.00	64,820	36.43	**Bombycidae**	350	silkworm moths	4	3
						Brahmaeidae	20	brahmin moths	2	2
						Carthaeidae	1	australian silkworm moths		
						Endromidae	1	glory moths	1	
						Eupterotidae	300	giant lappet moths		
						Lemoniidae	20	autumn silkworm moths	1	
						Mirinidae	2			
						Saturniidae	1,590	emperor & giant silkworm moths	76	53
						Sphingidae	1,269	hawk, hornworm & sphinx moths	29	18
37	**LASIOCAMPOIDEA**	2,125	1.19	66,945	37.63	**Anthelidae**	75	australian lappet moths		
						Lasiocampidae	2,050	tent caterpillars & lappet moths	13	
38	**MIMALLONOIDEA**	255	0.14	67,200	37.77	**Mimallonidae**	255	sack-bearer moths		
39	**NOCTUOIDEA**	70,000	39.35	137,200	77.12	**Arctiidae**	11,000	tiger, footman & wasp moths	4	4
						Ctenuchidae	?	wasp moths		
						Doidae	?			
						Lymantriidae	2,500	tussock & gypsy moths	3	3
						Noctuidae	35,000	dagger, owlet & forester moths	81	91
						Nolidae	?			
						Notodontidae	2,800	prominent moths	6	5
						Oenosandridae	?			
						Pantheidae	?			
40	**DREPANOIDEA**	815	0.46	138,015	77.58	**Drepanidae**	790	hook-tip moths		
						Epicopeiidae	25	oriental swallowtail moths		
41	**GEOMETROIDEA**	21,740	12.22	159,755	89.79	**Geometridae**	21,000	measuringworms, cankerworms	1	
						Sematuridae	40	american swallowtail moths		
						Uraniidae	700	swallowtail moths		
42	**AXIOIDEA**	6	0.00	159,761	89.80	**Axiidae**	6	gold moths		
43	**CALLIDULOIDEA**	60	0.03	159,821	89.83	**Callidulidae**	60	old world butterfly moths		
44	**HEDYLOIDEA**	40	0.02	159,861	89.85	**Hedylidae**	40	american butterfly moths	1	
45	**HESPERIOIDEA**	3,675	2.07	163,536	91.92	**Hesperiidae**	3,675	skippers	3	
46	**PAPILIONOIDEA**	14,375	8.08	177,911	100.00	**Lycaenidae**	6,575	blues, coppers, hairstreaks	2	
						Nymphalidae	6,000	brushfooted,fritillaries,checkerspots,satyrs	106	27
						Papilionidae	575	swallowtails & parnassians	41	1
						Pieridae	1,225	yellow-white & orange-tips, sulfurs	16	
		total no. species				***total no. species***			***EF***	***DDC***
		(superfamily estimates) : 177,911				***(family estimates) : 151,411***		***total GenBank hits :***	***419***	***238***

Table 12. Summary of character information content and nucleotide composition in data matrices by gene, taxon set and partition. For the (a) EF, (b) DDC and (c) EF&DDC combined data matrices, the number ('chars') and percentage ('%') of invariant, autapomorphic and parsimony informative amino acid and nucleotide characters is tabulated for each partition across four taxon sets: (i) all Lepidoptera, (ii) all Bombycoidea, (iii) all Sphingidae and (iv) shared Sphingidae (n=64) along with Bombycidae and Saturniini outgroups. Mean nucleotide base frequencies for each partition were calculated in PAUP* and are adjusted for missing data. Complete empirical nucleotide base composition for every ingroup and outgroup sequence is available in Tables 15 and 16, respectively.

(a) EF: Elongation Factor 1-alpha (1,228nt; 409aa)

			INVARIANT		AUTAP		PARS INF		BASE FREQUENCIES (%)			
TAXON SET	PART	TOTAL	chars	%	chars	%	chars	%	A	C	G	T
(i) Lepidoptera	**aa**	**409**	**359**	***87.8%***	**29**	***7.1%***	**21**	***5.1%***	.	.	.	.
ntax=118	**ntall**	**1,228**	**776**	***63.2%***	**59**	***4.8%***	**393**	***32.0%***	**25.26**	**28.52**	**25.10**	**21.12**
	nt1	409	361	*88.3%*	18	*4.4%*	30	*7.3%*	29.03	18.37	37.73	14.86
	nt2	409	379	*92.7%*	19	*4.6%*	11	*2.7%*	32.47	25.00	15.80	26.73
	nt3	410	36	*8.8%*	22	*5.4%*	352	*85.9%*	14.28	42.18	21.79	21.76
(ii) Bombycoidea	**aa**	**409**	**384**	***93.9%***	**11**	***2.7%***	**14**	***3.4%***	.	.	.	.
ntax=82	**ntall**	**1,228**	**830**	***67.6%***	**49**	***4.0%***	**349**	***28.4%***	**25.14**	**28.80**	**25.26**	**20.80**
	nt1	409	376	*91.9%*	10	*2.4%*	23	*5.6%*	29.03	18.40	37.60	14.96
	nt2	409	396	*96.8%*	7	*1.7%*	6	*1.5%*	32.51	25.00	15.84	26.65
	nt3	410	58	*14.1%*	32	*7.8%*	320	*78.0%*	13.87	42.99	22.36	20.78
(iii) Sphingidae	**aa**	**409**	**393**	***96.1%***	**5**	***1.2%***	**11**	***2.7%***	.	.	.	.
ntax=67	**ntall**	**1,228**	**890**	***72.5%***	**69**	***5.6%***	**269**	***21.9%***	**24.78**	**29.35**	**25.48**	**20.39**
	nt1	409	388	*94.9%*	4	*1.0%*	17	*4.2%*	29.03	18.43	37.61	14.94
	nt2	409	401	*98.0%*	3	*0.7%*	5	*1.2%*	32.52	25.01	15.84	26.63
	nt3	410	101	*24.6%*	62	*15.1%*	247	*60.2%*	12.79	44.61	23.01	19.59
(iv) Sphingidae	**aa**	**409**	**391**	***95.6%***	**7**	***1.7%***	**11**	***2.7%***	.	.	.	.
&2OG	**ntall**	**1,228**	**871**	***70.9%***	**70**	***5.7%***	**287**	***23.4%***	**24.85**	**29.28**	**25.41**	**20.46**
ntax=66	nt1	409	386	*94.4%*	6	*1.5%*	17	*4.2%*	29.03	18.43	37.58	14.96
	nt2	409	399	*97.6%*	5	*1.2%*	5	*1.2%*	32.53	25.03	15.83	26.61
	nt3	410	86	*21.0%*	59	*14.4%*	265	*64.6%*	13.00	44.37	22.84	19.80

(b) DDC: Dopa Decarboxylase (1,329nt; 443aa)

			INVARIANT		AUTAP		PARS INF		BASE FREQUENCIES (%)			
TAXON SET	PART	TOTAL	chars	%	chars	%	chars	%	A	C	G	T
(i) Lepidoptera	**aa**	**443**	**256**	***57.8%***	**57**	***12.9%***	**130**	***29.3%***	.	.	.	.
ntax=105	**ntall**	**1,329**	**599**	***45.1%***	**81**	***6.1%***	**649**	***48.8%***	**24.99**	**23.09**	**25.79**	**26.13**
	nt1	443	251	*56.7%*	42	*9.5%*	150	*33.9%*	22.33	22.03	35.38	20.26
	nt2	443	330	*74.5%*	37	*8.4%*	76	*17.2%*	29.15	21.7	19.72	29.43
	nt3	443	18	*4.1%*	2	*0.5%*	423	*95.5%*	23.5	25.55	22.27	28.68

Table 12. (continued)

Table 12. (continued)

(ii) Bombycoidea	**aa**	**443**	**305**	***68.8%***	**40**	***9.0%***	**98**	***22.1%***	.	.	.	.
ntax=73	**ntall**	**1,329**	**693**	***52.1%***	**60**	***4.5%***	**576**	***43.3%***	**25.55**	**22.45**	**25.24**	**26.76**
	nt1	443	302	*68.2%*	36	*8.1%*	105	*23.7%*	22.85	21.96	34.67	20.53
	nt2	443	372	*84.0%*	22	*5.0%*	49	*11.1%*	29.21	21.39	19.76	29.65
	nt3	443	19	*4.3%*	2	*0.5%*	422	*95.3%*	24.6	24	21.28	30.12
(iii) Sphingidae	**aa**	**443**	**329**	***74.3%***	**29**	***6.5%***	**85**	***19.2%***	.	.	.	.
ntax=65	**ntall**	**1,329**	**736**	***55.4%***	**49**	***3.7%***	**544**	***40.9%***	**25.48**	**22.51**	**25.21**	**26.80**
	nt1	443	326	*73.6%*	26	*5.9%*	91	*20.5%*	22.88	21.99	34.56	20.58
	nt2	443	391	*88.3%*	17	*3.8%*	35	*7.9%*	29.15	21.47	19.73	29.66
	nt3	443	19	*4.3%*	6	*1.4%*	418	*94.4%*	24.42	24.06	21.34	30.18
(iv) Sphingidae	**aa**	**443**	**315**	***71.1%***	**37**	***8.4%***	**91**	***20.5%***	.	.	.	.
&2OG	**ntall**	**1,329**	**711**	***53.5%***	**61**	***4.6%***	**557**	***41.9%***	**25.46**	**22.50**	**25.23**	**26.81**
ntax=66	nt1	443	313	*70.7%*	35	*7.9%*	95	*21.4%*	22.84	22.01	34.57	20.57
	nt2	443	379	*85.6%*	23	*5.2%*	41	*9.3%*	29.16	21.44	19.73	29.67
	nt3	443	19	*4.3%*	3	*0.7%*	421	*95.0%*	24.38	24.04	21.38	30.20

(c) EF&DDC: Combined Data (2,557nt; 852aa)

			INVARIANT		AUTAP		PARS INF		BASE FREQUENCIES (%)			
TAXON SET	PART	TOTAL	chars	%	chars	%	chars	%	A	C	G	T
(i) Lepidoptera	**aa**	**852**	**651**	***76.4%***	**76**	***8.9%***	**125**	***14.7%***	.	.	.	.
ntax=91	**ntall**	**2,557**	**1449**	***56.7%***	**148**	***5.8%***	**960**	***37.5%***	**25.19**	**26.01**	**25.30**	**23.51**
	nt1	852	646	*75.8%*	58	*6.8%*	148	*17.4%*	25.97	20.06	36.41	17.56
	nt2	852	736	*86.4%*	53	*6.2%*	63	*7.4%*	30.99	23.40	17.63	27.99
	nt3	853	67	*7.9%*	37	*4.3%*	749	*87.8%*	18.61	34.57	21.85	24.97
(ii) Bombycoidea	**aa**	**852**	**695**	***81.6%***	**47**	***5.5%***	**110**	***12.9%***	.	.	.	.
ntax=72	**ntall**	**2,557**	**1546**	***60.5%***	**108**	***4.2%***	**903**	***35.3%***	**25.28**	**25.79**	**25.27**	**23.66**
	nt1	852	687	*80.6%*	42	*4.9%*	123	*14.4%*	25.97	20.17	36.16	17.71
	nt2	852	770	*90.4%*	28	*3.3%*	54	*6.3%*	30.89	23.22	17.77	28.13
	nt3	853	89	*10.4%*	38	*4.5%*	726	*85.1%*	18.99	33.97	21.91	25.13
(iii) Sphingidae	**aa**	**852**	**723**	***84.9%***	**33**	***3.9%***	**96**	***11.3%***	.	.	.	.
ntax=64	**ntall**	**2,557**	**1630**	***63.7%***	**116**	***4.5%***	**811**	***31.7%***	**25.12**	**25.95**	**25.35**	**23.59**
	nt1	852	716	*84.0%*	29	*3.4%*	107	*12.6%*	25.93	20.23	36.07	17.77
	nt2	852	792	*93.0%*	20	*2.3%*	40	*4.7%*	30.84	23.24	17.79	28.14
	nt3	853	122	*14.3%*	67	*7.9%*	664	*77.8%*	18.57	34.39	22.20	24.84
(iv) Sphingidae	**aa**	**852**	**706**	***82.9%***	**44**	***5.2%***	**102**	***12.0%***	.	.	.	.
&2OG	**ntall**	**2,557**	**1582**	***61.9%***	**131**	***5.1%***	**844**	***33.0%***	**25.16**	**25.88**	**25.32**	**23.65**
ntax=66	nt1	852	699	*82.0%*	41	*4.8%*	112	*13.1%*	25.92	20.23	36.07	17.78
	nt2	852	778	*91.3%*	28	*3.3%*	46	*5.4%*	30.83	23.23	17.79	28.15
	nt3	853	105	*12.3%*	62	*7.3%*	686	*80.4%*	18.71	34.18	22.11	25.00

Table 13. Amino acid alignment for EF. All variable positions from the complete 409 amino acid EF matrix are presented across (a) 67 ingroup taxa and (b) 51 outgroup taxa. The amino acid sequence of Bombyx mori (obtained by conceptual translation of GenBank Nucleotides accession number D13338) was used as the standard sequence for alignment. A '.' indicates identity with the Bombyx mori reference sequence at a particular residue. The Bombyx sequence is repeated in the outgroup matrix (b) to separate representatives of Bombycoidea from all other Lepidoptera. '?' designates a missing amino acid, at residues for which missing nucleotide data ('N') prevented unambiguous conceptual translation.

Table 13 (a)

Amino Acid Position in EF Matrix (InGroup)

Taxon (IG)	7	8	9	10	32	38	54	69	70	71	78	128	138	148	149	151	190	192	194	201	202	203	209	210	213	222	231	257	263	264	270	271	280	310	317	321	324	340	369	375	378	379	384	389	391	393	396	400	403	406	
1 Bombycidae	S	T	T	T	A	G	E	S	K	Y	A	T	V	Y	S	P	P	T	M	Q	V	E	A	D	S	L	P	V	I	V	N	I	M	Y	N	K	A	S	T	V	K	S	D	N	V	S	L	S	E	P	1
52 Aellopos2399	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	52
53 Aellopos AF234559	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	.	.	.	L	?	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	53
54 Callionima0966	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	54
55 Cautethia2573	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	55
56 Cautethia1668	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	56
57 Enyo2390	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	.	.	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	57
58 Erinnyis1542	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	58
59 Isognathus1646	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	59
60 Nyceryx2378	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	60
61 Pachylia1644	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	61
62 Perigonia2191	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	A	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	62
63 Unzela2376	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	.	A	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	63
64 Cephonodes5931	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	64
65 Hemaris1882	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	65
66 HemarisAF234568	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	66
67 Basiothia0005	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	.	.	.	.	.	.	.	.	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	67
68 Deilephila5866	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	.	.	.	.	.	.	.	.	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	68
69 Hippotion5932	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	.	.	.	.	.	.	.	.	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	69
70 Hyles5817	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	.	.	.	.	.	.	.	.	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	70
71 Hyles1881	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	.	.	.	.	.	.	.	.	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	71
72 Theretra5880	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	A	.	.	.	.	.	.	.	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	72
73 Xylophanes5904	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	.	.	.	.	.	.	.	.	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	73
74 XylophanesAF2345	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	.	.	.	.	.	.	.	.	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	74
75 Xylophanes2369	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	.	.	.	.	.	.	.	.	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	75
76 Xylophanes1879	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	.	.	.	.	.	.	.	.	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	76
77 Daphnis5810	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	77
78 Darapsa1778	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	78
79 DarapsaAF234563	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	79
80 Macroglossum5806	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	A	I	V	.	.	.	.	.	.	R	.	.	.	D	.	.	.	.	.	.	.	.	.	.	80
81 ProserpinusAF173	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	?	?	?	?	?	?	?	?	?	?	?	?	?	81
82 SphecodinaAF2345	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	82
83 Eumorpha1533	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	83
84 EumorphaAF234565	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	84
85 Eumorpha1504	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	85
86 Adhemarius1642	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	86
87 Protambulyx1945	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.	.	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	87
88 Amorpha1595	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	A	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	88
89 Laothoe0012	.	.	.	.	.	.	.	G	R	.	.	.	.	.	.	S	A	.	.	.	.	.	.	.	C	.	A	.	V	.	.	.	.	.	.	R	.	.	.	D	.	.	.	.	.	.	M	.	.	.	89
90 Marumba0118	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	A	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	90
91 Mimas5836	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	.	A	.	.	L	.	.	.	E	C	.	A	I	V	.	.	.	.	.	.	R	.	.	.	D	.	.	.	.	.	.	M	.	.	.	91
92 PachysphinxAF234	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	V	.	.	L	.	.	.	E	C	.	A	.	V	.	.	.	.	.	.	R	.	.	.	D	.	.	.	.	.	.	M	.	.	.	92
93 Pachysphinx1528	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	V	.	.	L	.	.	.	E	C	.	A	.	V	.	.	.	.	.	.	R	.	.	.	D	.	.	.	.	.	.	M	.	.	.	93
94 PaoniasAF234572	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.	S	A	.	.	L	.	.	.	E	C	.	A	.	V	.	.	.	.	.	.	R	.	.	.	D	.	.	.	.	.	.	M	.	.	.	94
95 Paonias1540	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	A	.	.	A	.	.	.	.	C	.	A	.	V	.	.	.	.	.	.	R	.	.	.	D	.	.	.	.	.	.	M	.	.	.	95
96 Pseudoclanis5839	.	.	.	.	.	.	.	.	R	.	.	.	.	.	.	S	A	.	.	A	.	D	.	.	C	.	A	.	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	.	.	.	.	96
97 SmerinthusAF2345	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.	S	V	.	.	L	.	.	.	E	C	.	A	.	V	.	.	.	.	.	.	R	.	.	.	D	.	.	.	.	.	.	M	.	.	.	97
98 Smerinthus1511	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.	S	V	.	.	L	.	.	.	E	C	.	A	.	V	.	.	.	.	.	.	R	.	.	.	D	.	.	.	.	.	.	M	.	.	.	98
99 Hopliocnema0233	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	A	.	.	.	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	99
100 Acherontia5989	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	100
101 Agrius1941	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	101
102 Coelonia5816	.	.	.	.	.	.	.	.	.	.	.	.	.	.	N	S	.	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	102
103 Ceratomia1870	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	A	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	103
104 CeratomiaAF23456	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	104
105 Cocytius2359	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	105
106 DolbaAF234579	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	106
107 Euryglottis2891	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.	.	.	.	L	.	.	G	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	107
108 Lapara1670	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	A	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	108
109 Manduca1529	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	109
110 Manduca1508	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	110
111 Manduca1876	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	111
112 ManducaAF234571	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	112
113 Paratrea1939	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	.	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	113
114 Psilogramma5988	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	A	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	114
115 SphinxAF234577	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	A	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	115
116 Sphinx1532	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.	S	.	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	116
117 Sphinx1591	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.	S	A	.	.	L	.	.	.	E	C	.	A	I	V	.	.	.	.	F	.	.	.	A	.	D	.	.	.	.	.	.	M	.	.	.	117
118 Sphinx1938	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	S	A	.	.	L	.	.	.	E	C	.	A	I	.	.	.	.	.	.	.	.	.	.	.	D	.	.	.	.	.	.	M	.	.	.	118
	7	8	9	10	32	38	54	69	70	71	78	128	138	148	149	151	190	192	194	201	202	203	209	210	213	222	231	257	263	264	270	271	280	310	317	321	324	340	369	375	378	379	384	389	391	393	396	400	403	406	

Table 13. (continued)

Table 14. Amino acid alignment for DDC. All variable positions from the complete 443 amino acid DDC matrix are presented across all 40 outgroup taxa and 65 ingroup taxa. The amino acid sequence of *Manduca sexta* (obtained by conceptual translation of GenBank Nucleotides accession number U03909) was used as the standard sequence for alignment. A '.' indicates identity with the *Manduca sexta* reference sequence at a particular residue. Horizontal lines separate taxa into three blocks: Sphingidae, other Bombycoidea and all other Lepidoptera. '?' designates a missing amino acid, at residues for which missing nucleotide data ('N') prevented unambiguous conceptual translation.

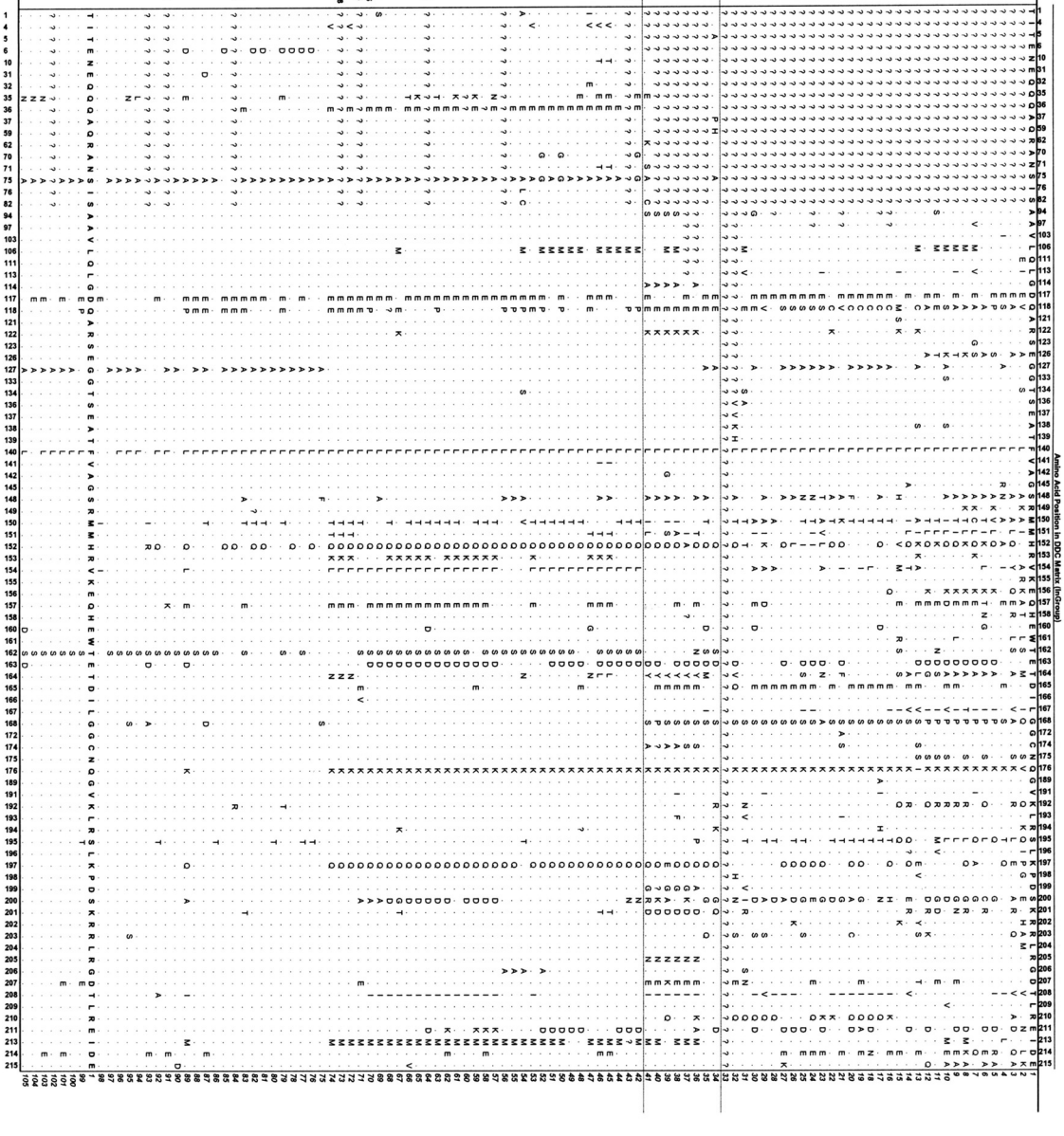

Table 14. (continued)

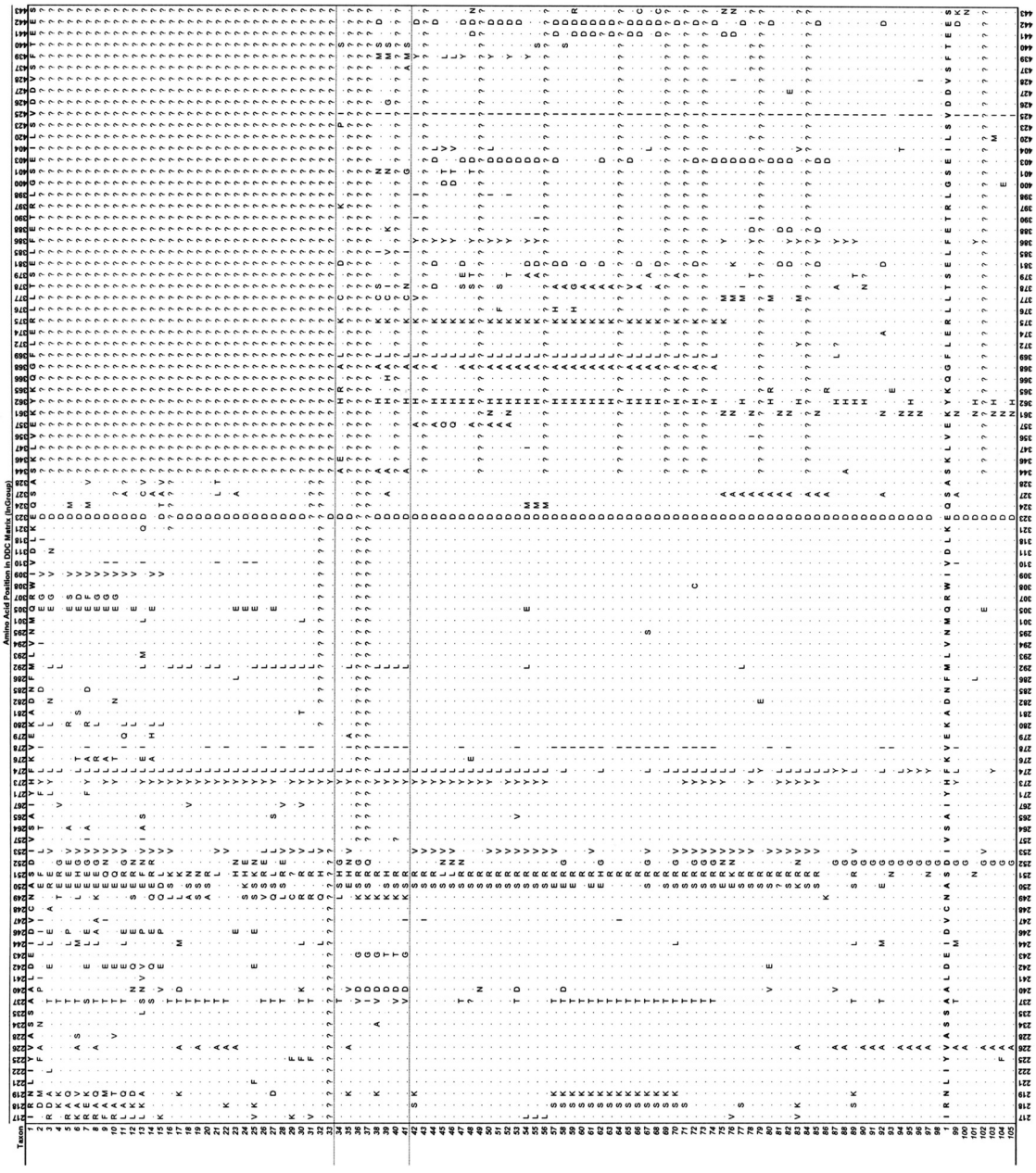

Table 15. Empirical base compositions for EF and DDC among ingroup taxa (Bombycoidea: Sphingidae). Empirical frequencies of six character state categories were calculated separately for each gene across every ingroup sequence obtained de novo or in silico in this study. Percentage adenine (A), cytosine (C), guanine (G), thymine (T), missing data (N) and ambigious data ('X', binary IUPAC ambiguity codes) was calculated by dividing the count of each category in the final aligned sequence by the matrix sequence length (1,274bp for EF; 1,373bp for DDC). In contrast to the final matrix length, 'real bp' reports the number of nucleotides collected in the native sequence, before missing data characters (N) were appended at either end to standarize length across taxa. For sequences whose 'real bp' < 'final matrix length', the 'start' column indicates the position of the first real nucleotide realtive to the reference sequences depicted in Figure 4 (EF) and Figure 5 (DDC). Values in the 'start' and 'real bp' columns are especially important descriptions of sequences collected in silico in this study (indicated by a 'GB' suffix on the Taxon Label), as GenBank accessions were extremely variable in length.

					Elongation Factor 1-alpha (EF)										Dopa Decarboxylase (DDC)									
Taxonomy		Genus	species	Taxon Label	Accession	%A	%C	%G	%T	%N	%X	start	real bp		Accession	%A	%C	%G	%T	%N	%X	start	real bp	
MACROGLOSSINAE																								
Dilophonotini	**Dilophonotina**	***Aellopos***	***ceculus***	Aellopos2399	DHJ-02-2399	24.10	30.37	25.65	19.63	0.00	0.24	1	1274		DHJ-02-2399	25.06	22.95	25.81	25.96	0.00	0.23	1	1373	
		A.	***tantalus***	AelloposGB	AF234559	23.94	30.21	25.65	20.03	0.00	0.16	24	1240		AF234582	12.72	12.72	14.07	13.69	46.73	0.08	303	709	
		Callionima	***parce / falcifera***	Callionima0966	RFD-96-0966	23.94	30.70	25.90	19.46	0.00	0.00	1	1274		RFD-96-0966	25.36	23.55	24.23	26.86	0.00	0.00	1	1373	
		Cautethia	***spuria***	Cautethia2573	CWB-02-2573	24.59	30.21	25.41	19.54	0.00	0.24	1	1274		CWB-02-2573	25.43	21.37	25.28	27.69	0.00	0.23	1	1373	
		Cau.	***undetermined***	Cautethia1668	JKA-02-1668	24.59	30.37	25.24	19.71	0.00	0.08	1	1274		JKA-02-1668	25.51	21.52	25.28	27.69	0.00	0.00	1	1373	
		Enyo	***ocypete***	Enyo2390	DHJ-02-2390	23.94	31.03	25.81	19.22	0.00	0.00	1	1274		DHJ-02-2390	24.38	22.95	25.58	27.01	0.00	0.08	1	1373	
		Erinnyis	***ello***	Erinnyis1542	JPT-02-1542	23.70	30.54	25.81	19.87	0.00	0.08	1	1274		JPT-02-1542	24.15	24.76	25.73	24.76	0.00	0.60	1	1373	
		Isognathus	***rimosa***	Isognathus1646	JKA-02-1646	24.19	30.05	25.57	20.03	0.00	0.16	1	1274		JKA-02-1646	17.76	18.89	19.49	19.34	24.08	0.45	1	1034	
		Nyceryx	***magna***	Nyceryx2378	DHJ-02-2378	24.43	30.37	25.24	19.95	0.00	0.00	1	1274		DHJ-02-2378	24.83	22.80	25.58	26.79	0.00	0.00	1	1373	
		Pachylia	***ficus***	Pachylia1644	JKA-02-1644	24.19	30.13	25.49	20.11	0.00	0.08	1	1274		JKA-02-1644	24.45	22.20	25.13	27.84	0.00	0.38	1	1373	
		Perigonia	***ilus / lusca passerina***	Perigonia2191	WJK-03-2191	23.94	30.05	25.98	20.03	0.00	0.00	1	1274		WJK-03-2191	24.76	22.87	25.51	26.79	0.00	0.08	1	1373	
		Unzela	***japix***	Unzela2376	DHJ-02-2376	23.53	31.43	26.22	18.49	0.00	0.33	1	1274		DHJ-02-2376	25.73	22.57	24.98	26.71	0.00	0.00	1	1373	
	Hemarina	***Cephonodes***	***hylas virescens***	Cephonodes5931	IJK-02-5931	24.67	29.64	25.16	20.44	0.00	0.08	1	1274		IJK-02-5931	25.66	21.75	24.98	27.61	0.00	0.00	1	1373	
		Hemaris	***diffinis***	Hemaris1882	DCR-02-1882	24.92	29.07	25.16	20.77	0.00	0.08	1	1274		DCR-02-1882	25.58	21.60	24.60	28.22	0.00	0.00	1	1373	
		He.	***thysbe***	HemarisGB	AF234568	24.92	28.83	25.16	20.93	0.00	0.16	24	1240		AF234590	12.72	11.74	14.07	14.82	46.65	0.00	303	709	
	Macroglossini	**Choerocampina**	***Basiothia***	***medea***	Basiothia0005	IJK-02-0005	24.43	30.37	25.98	19.14	0.00	0.08	1	1274		IJK-02-0005	24.53	23.18	25.36	26.94	0.00	0.00	1	1373	
			Deilephila	***elpenor***	Deilephila5866	IJK-02-5866	24.67	30.13	25.65	19.38	0.00	0.16	1	1274		IJK-02-5866	24.23	21.97	25.28	26.26	0.00	2.26	1	1373	
			Hippotion	***celerio***	Hippotion5932	IJK-02-5932	24.27	30.29	26.14	19.22	0.00	0.08	1	1274		IJK-02-5932	24.60	22.95	26.03	26.19	0.00	0.23	1	1373	
			Hyles	***hippophaes***	Hyles5817	IJK-02-5817	24.51	30.37	25.57	19.30	0.00	0.24	1	1274		IJK-02-5817	25.21	21.97	24.68	26.03	0.00	2.11	1	1373	
			Hy.	***lineata***	Hyles1881	DCR-02-1881	24.59	30.05	25.73	19.54	0.00	0.08	1	1274		DCR-02-1881	25.51	22.27	24.91	26.94	0.00	0.38	1	1373	
			Theretra	***alecto***	Theretra5880	IJK-02-5880	24.84	29.89	25.57	19.71	0.00	0.00	1	1274		IJK-02-5880	25.21	22.72	25.13	26.86	0.00	0.08	1	1373	
			Xylophanes	***chiron nechus***	Xylophanes5904	IJK-02-5904	24.59	30.29	25.57	19.38	0.00	0.16	1	1274		IJK-02-5904	24.53	23.33	25.43	26.34	0.00	0.38	1	1373	
			X.	***falco***	XylophanesGB	AF234580	24.59	30.29	25.65	19.14	0.00	0.33	24	1240		AF234599	13.02	12.04	14.60	13.69	46.65	0.00	303	709	
			X.	***porcus***	Xylophanes2369	DHJ-02-2369	25.00	30.29	25.49	19.22	0.00	0.00	1	1274		DHJ-02-2369	24.76	22.65	25.66	26.94	0.00	0.00	1	1373	
			X.	***tersa***	Xylophanes1879	DCR-02-1879	24.67	30.37	25.49	19.22	0.00	0.24	1	1274		DCR-02-1879	24.23	23.10	26.03	26.41	0.00	0.23	1	1373	
		Macroglossina	***Daphnis***	***nerii***	Daphnis5810	IJK-02-5810	24.35	29.64	25.90	20.11	0.00	0.00	1	1274		IJK-02-5810	25.73	22.20	24.91	26.79	0.00	0.38	1	1373	
			Darapsa	***myron***	Darapsa1778	GS-02-1778	24.43	30.13	25.49	19.63	0.00	0.33	1	1274		GS-02-1778	24.60	22.57	25.43	26.34	0.00	1.05	1	1373	
			Darapsa	***myron/pholus***	DarapsaGB	AF234563	24.67	30.21	25.57	19.30	0.00	0.24	24	1240		AF234585	17.31	17.83	19.86	18.81	25.73	0.45	25	987	
			Macroglossum	***stellatarum***	Macroglossum5806	IJK-02-5806	24.43	30.21	25.73	19.63	0.00	0.00	1	1274		IJK-02-5806	24.98	22.12	25.21	27.24	0.00	0.45	1	1373	
			Proserpinus	***clarkiae***	ProserpinusGB	AF173394	19.71	22.88	21.74	16.69	18.97	0.00	39	995		na									
			Sphecodina	***abbottii***	SphecodinaGB	AF234575	24.67	29.23	25.24	20.68	0.00	0.16	24	1240		AF234594	13.24	11.06	13.92	15.05	46.65	0.08	303	709	
	Philampelini		***Eumorpha***	***achemon***	Eumorpha1533	JPT-02-1533	24.10	29.80	25.73	20.36	0.00	0.00	1	1274		JPT-02-1533	26.03	21.29	24.45	28.22	0.00	0.00	1	1373	
			E.	***pandorus***	EumorphaGB	AF234565	24.10	30.29	25.65	19.79	0.00	0.16	24	1240		AF234588	13.24	11.44	13.62	15.05	46.65	0.00	303	709	
			E.	***typhon***	Eumorpha1504	JBW-02-1504	24.51	29.40	25.49	20.60	0.00	0.00	1	1274		JBW-02-1504	25.73	20.77	24.98	28.52	0.00	0.00	1	1373	
SMERINTHINAE																								
Ambulycini		***Adhemarius***	***gannascus***	Adhemarius1642	JKA-02-1642	24.76	28.99	25.33	20.93	0.00	0.00	1	1274		JKA-02-1642	26.34	20.84	24.53	28.29	0.00	0.00	1	1373	
		Protambulyx	***euryalus***	Protambulyx1945	WJK-03-1945	25.33	29.32	25.16	20.20	0.00	0.00	1	1274		WJK-03-1945	25.51	22.65	24.83	27.01	0.00	0.00	1	1373	
Smerinthini		***Amorpha***	***juglandis***	Amorpha1595	CWB-02-1595	25.08	28.26	24.92	21.74	0.00	0.00	1	1274		CWB-02-1595	25.51	22.72	25.43	26.34	0.00	0.00	1	1373	
		Laothoe	***populi***	Laothoe0012	IJK-02-0012	24.67	28.18	25.90	21.17	0.00	0.08	1	1274		IJK-02-0012	25.58	22.57	24.98	26.26	0.15	0.45	1	1351	
		Marumba	***quercus***	Marumba0118	IJK-02-0118	25.98	27.69	25.08	21.25	0.00	0.00	1	1274		IJK-02-0118	18.36	19.79	20.32	17.16	24.00	0.38	1	1034	
		Mimas	***tiliae***	Mimas5836	IJK-02-5836	25.24	28.58	25.08	20.93	0.00	0.16	1	1274		IJK-02-5836	25.06	22.50	25.43	27.01	0.00	0.00	1	1373	
		Pachysphinx	***modesta***	PachysphinxGB	AF234573	25.33	27.28	25.00	21.42	0.00	0.98	24	1240		na									
		Pa.	***occidentalis***	Pachysphinx1528	JPT-02-1528	25.33	27.69	25.24	21.74	0.00	0.00	1	1274		JPT-02-1528	25.81	22.27	24.83	27.01	0.00	0.08	1	1373	
		Paonias	***excaecata***	PaoniasGB	AF234572	25.08	28.50	25.08	20.77	0.00	0.57	24	1240		na									
		Pao.	***myops***	Paonias1540	JPT-02-1540	25.24	28.42	25.24	21.09	0.00	0.00	1	1274		JPT-02-1540	25.58	22.42	25.36	26.19	0.00	0.45	1	1373	
		Pseudoclanis	***postica***	Pseudoclanis5839	IJK-02-5839	25.08	28.83	25.49	20.52	0.00	0.08	1	1274		IJK-02-5839	25.96	23.02	25.36	25.51	0.15	0.00	1	1351	
		Smerinthus	***cerisyi***	SmerinthusGB	AF234576	25.24	27.69	25.16	21.50	0.00	0.41	24	1240		AF234595	13.47	12.49	13.77	13.62	46.65	0.00	303	709	
		Sm.	***saliceti***	Smerinthus1511	JBW-02-1511	25.33	27.52	25.24	21.74	0.00	0.16	1	1274		JBW-02-1511	25.81	22.87	24.76	26.56	0.00	0.00	1	1373	
	Sphingulini		***Hopliocnema***	***brachycera***	Hopliocnema0233	MJM-96-0233	24.92	28.75	25.41	20.52	0.00	0.41	1	1274		MJM-96-0233	26.34	21.82	24.30	27.31	0.00	0.23	1	1373	
SPHINGINAE																								
Acherontiini		***Acherontia***	***styx medusa***	Acherontia5989	IJK-02-5989	25.00	29.32	25.16	20.52	0.00	0.00	1	1274		IJK-02-5989	25.88	22.72	25.21	26.03	0.00	0.15	1	1373	
		Agrius	***cingulata***	Agrius1941	WJK-02-1941	24.92	29.32	25.16	20.36	0.00	0.24	1	1274		WJK-02-1941	26.26	20.99	24.83	27.69	0.00	0.23	1	1373	
		Coelonia	***fulvinotata***	Coelonia5816	IJK-02-5816	24.76	29.23	25.24	20.28	0.00	0.49	1	1274		IJK-02-5816	24.15	22.80	25.88	25.66	0.08	1.43	1	1373	
Sphingini		***Ceratomia***	***catalpae***	Ceratomia1870	DCR-02-1870	24.84	27.85	25.49	21.82	0.00	0.00	1	1274		DCR-02-1870	26.19	22.57	24.45	26.56	0.00	0.23	1	1373	
		Ce.	***undulosa***	CeratomiaGB	AF234562	25.00	28.34	25.49	20.60	0.00	0.57	24	1240		AF234584	20.84	17.01	19.26	21.75	20.92	0.23	303	1051	
		Cocytius	***duponchel***	Cocytius2359	DHJ-02-2359	24.67	29.15	25.24	20.77	0.00	0.16	1	1274		DHJ-02-2359	25.73	22.05	24.53	27.39	0.00	0.30	1	1373	
		Dolba	***hyloeus***	DolbaGB	AF234579	24.92	28.58	25.24	21.01	0.00	0.24	24	1240		AF234598	20.92	16.25	19.56	21.60	20.92	0.75	303	1051	
		Euryglottis	***dognini***	Euryglottis2891	WJK-03-2891	25.16	28.50	25.41	20.93	0.00	0.00	1	1274		WJK-03-2891	25.43	22.87	25.21	26.11	0.00	0.38	1	1373	
		Lapara	***coniferarum***	Lapara1670	JKA-02-1670	25.33	28.26	25.33	21.09	0.00	0.00	1	1274		JKA-02-1670	26.94	21.82	24.23	26.64	0.00	0.38	1	1373	
		Manduca	***florestan***	Manduca1529	JPT-02-1529	25.08	28.91	25.33	20.68	0.00	0.00	1	1274		JPT-02-1529	26.64	22.42	24.45	26.49	0.00	0.00	1	1373	
		Ma.	***muscosa***	Manduca1508	JBW-02-1508	25.08	28.58	25.41	20.93	0.00	0.00	1	1274		JBW-02-1508	26.71	22.27	24.68	26.19	0.00	0.15	1	1373	
		Ma.	***quinquemaculatus***	Manduca1876	DCR-02-1876	24.92	28.26	25.41	21.25	0.00	0.16	1	1274		DCR-02-1876	26.34	21.82	24.68	27.09	0.00	0.08	1	1373	
		Ma.	***sexta***	ManducaGB	AF234571	25.00	28.75	25.41	20.85	0.00	0.00	24	1240		*U03909*	25.88	22.27	25.13	26.71	0.00	0.00	1	1373	
		Neococytius	***cluentius***	Neococytius1949	na										WJK-03-1949	26.41	22.20	24.30	26.94	0.00	0.15	1	1373	
		Paratrea	***plebeja***	Paratrea1939	WJK-02-1939	25.49	28.99	24.84	20.52	0.00	0.16	1	1274		WJK-02-1939	26.79	22.35	24.15	26.71	0.00	0.00	1	1373	
		Psilogramma	***increta***	Psilogramma5988	IJK-02-5988	25.00	29.23	25.00	20.68	0.00	0.08	1	1274		IJK-02-5988	26.19	22.42	25.36	26.03	0.00	0.00	1	1373	
		Sphinx	***chersis***	SphinxGB	AF234577	25.41	28.58	25.08	20.68	0.00	0.24	24	1240		AF234596	13.24	12.42	14.07	13.62	46.65	0.00	303	709	
		Sp.	***dollii***	Sphinx1532	JPT-02-1532	25.49	28.26	25.33	20.93	0.00	0.00	1	1274		JPT-02-1532	26.34	22.27	24.76	26.64	0.00	0.00	1	1373	
		Sp.	***istar***	Sphinx1591	CWB-02-1591	24.92	28.50	25.49	21.09	0.00	0.00	1	1274		CWB-02-1591	26.64	22.20	24.45	26.56	0.00	0.15	1	1373	
		Sp.	***kalmiae***	Sphinx1938	WJK-02-1938	25.24	28.09	25.33	21.17	0.00	0.16	1	1274		WJK-02-1938	26.34	21.90	24.38	27.09	0.00	0.30	1	1373	

Table 16. Empirical base compositions for EF and DDC among outgroup taxa (Lepidoptera). Empirical frequencies of six character state categories were calculated separately for each gene across every outgroup sequence obtained in silico in this study. Percentage adenine (A), cytosine (C), guanine (G), thymine (T), missing data (N) and ambiguous data ('X', binary IUPAC ambiguity codes) was calculated by dividing the count of each category in the final aligned sequence by the matrix sequence length (1,274bp for EF; 1,373bp for DDC). In contrast to the final matrix length, 'real bp' reports the number of nucleotides collected in the native sequence, before missing data characters (N) were appended at either end to standardize length across taxa. For sequences whose 'real bp' < 'final matrix length', the 'start' column indicates the position of the first real nucleotide relative to the reference sequences depicted in Figure 4 (EF) and Figure 5 (DDC). Values in the 'start' and 'real bp' columns are especially important descriptions of outgroup sequences collected in silico in this study, as GenBank accessions were extremely variable in length.

Taxonomy	Superfamily	Family	Subfamily	Tribe	*Genus*	*species*	Taxon Label	Elongation Factor 1-alpha (EF)									Dopa Decarboxylase (DDC)								
								Accession	%A	%C	%G	%T	%N	%X	start	real bp	Accession	%A	%C	%G	%T	%N	%X	start	real bp
Zeugloptera																									
	Micropterigoidea	Micropterigidae			*Epimartyria*	*auricrinella*	Micropterigoidea	na									AF093174	12.19	13.39	15.73	12.04	46.65	0.00	303	709
					Micropterix	*calthella*	Micropterigoidea	AF436596	9.69	11.89	9.93	7.17	61.32	0.00	119	478	na								
Glossata																									
	Eriocranioidea	Eriocraniidae			*Eriocrania*	*semipurpurella*	Eriocranioidea	na									AF093175	10.08	15.80	16.78	10.68	46.65	0.00	303	709
Glossata>Coelolepida>Myoglossata>Neolepidoptera>Exoporia																									
	Hepialoidea	Hepialidae			*Hepialus*	*californicus*	Hepialoidea	na									AF093178	11.96	13.62	14.90	12.87	46.65	0.00	303	709
Glossata>Coelolepida>Myoglossata>Neolepidoptera>Heteroneura																									
	Incurvarioidea	Adelidae	Adelinae		*Adela*	*purpurea*	Adelidae	na									AF093167	10.53	15.27	16.48	11.06	46.65	0.00	303	709
		Cecidosidae			*Cecidoses*	*eremita*	Cecidosidae	na									AF093170	11.06	14.82	15.05	12.42	46.65	0.00	303	709
		Heliozelidae			*Coptodisca*	*kalmiella*	Heliozelidae	na									AF093171	9.86	15.50	17.83	10.16	46.65	0.00	303	709
		Incurvariidae			*Vespina*	*quercivora*	Incurvariidae	na									AF093195	9.78	17.08	17.61	8.88	46.65	0.00	303	709
		Prodoxidae	Lamproniinae		*Tetragma*	*gei*	Lamproniinae	na									AF093192	12.79	13.39	14.15	13.02	46.65	0.00	303	709
			Prodoxinae		*Prodoxus*	*quinquepunctellus*	Prodoxinae	na									AF093183	11.81	13.47	15.43	12.34	46.95	0.00	303	709
	Palaephatoidea	Palaephatidae			*Palaephatus*	*falsus*	Palaephatoidea	na									AF093182	10.91	15.20	16.33	10.53	47.03	0.00	303	709
	Tischerioidea	Tischeriidae			*Tischeria*	*badiiella*	Tischerioidea	na									AF093187	13.39	12.87	13.77	13.17	46.80	0.00	303	709
Glossata>Coelolepida>Myoglossata>Neolepidoptera>Heteroneura>Ditrysia																									
	Gracillarioidea	Gracillariidae	Lithocolletinae		*Leucanthiza*	*amphicarpaeafoliella*	Gracillarioidea	na									AF093180	13.32	12.64	15.20	12.11	46.73	0.00	303	709
	Tineoidea	Psychidae	Oiketicinae		*Thyridopteryx*	*ephemeraeformis*	Psychidae	na									AF093190	10.99	13.39	17.01	11.74	46.88	0.00	303	709
		Tineidae	Tineinae		*Tinea*	*pellionella*	Tineidae	na									AF093193	14.00	11.29	13.69	14.37	46.65	0.00	303	709
Glossata>Coelolepida>Myoglossata>Neolepidoptera>Heteroneura>Ditrysia>Apoditrysia>Obtectomera																									
	Pyraloidea	Crambidae			*Ostrinia*	*nubilalis*	Crambidae	AF173392	19.63	23.78	21.91	15.64	18.97	0.08	39	995	na								
		Pyralidae	Galleriinae		*Galleria*	*melonella*	Galleriinae	AF423811	22.64	22.07	19.79	22.23	13.27	0.00	187	1080	na								
			Pyraustinae		*Agrioglypta*	*naralis*	Pyraustinae	AB158395	19.38	23.86	18.97	17.02	20.77	0.00	220	1024	na								
Glossata>Coelolepida>Myoglossata>Neolepidoptera>Heteroneura>Ditrysia>Apoditrysia>Obtectomera>Macrolepidoptera																									
	Bombycoidea	Bombycidae	Bombycinae	Bombycini	*Bombyx*	*mori*	Bombycidae	*D13338*	27.61	25.57	23.21	23.62	0.00	0.00	1	1274	AF372836	24.68	23.40	25.21	26.71	0.00	0.00	1	1373
		Brahmaeidae			*Brahmaea*	*certhia*	Brahmaeidae	AF234560	26.71	26.79	24.02	22.48	0.00	0.00	24	1240	AF234583	14.45	13.24	13.09	12.49	46.65	0.08	303	709
		Endromidae			*Endromis*	*versicolora*	Endromidae	AF234566	25.90	26.47	24.59	22.39	0.00	0.65	24	1240	na								
		Lemoniidae			*Lemonia*	*dumi*	Lemoniidae	AF234570	26.47	26.38	24.35	22.80	0.00	0.00	24	1240	na								
		Saturniidae	Ceratocampinae		*Dryocampa*	*rubicunda*	Ceratocampinae	AF234564	26.47	29.32	24.35	19.14	0.08	0.65	24	1240	AF234586	8.50	6.47	8.58	8.28	68.17	0.00	361	423
			Hemileucinae	Hemileucini	*Automeris*	*cecrops*	Hemileucini	AY040098	19.30	20.60	20.11	15.64	24.35	0.00	93	932	na								
					Automeris	*io*	Hemileucini	na									AF373956	8.80	6.09	8.73	7.98	68.25	0.15	362	103
				Polythysanini	*Polythysana*	*apollina*	Polythysanini	AF373939	26.47	27.12	24.43	21.82	0.00	0.16	24	1240	na								
			Saturniinae	Attacini	*Attacus*	*atlas*	Attacini	AF015066	28.26	24.92	22.80	23.94	0.08	0.00	24	1240	AF015045	21.22	17.08	20.17	20.47	21.07	0.00	303	1051
				Bunaeini	*Cirina*	*forda*	Bunaeini	AF373931	28.26	24.59	22.88	24.27	0.00	0.00	24	1240	AF373959	21.14	16.25	20.02	21.60	20.99	0.00	303	1051
				Micragonini	*Holocerina*	*smilax*	Micragonini	AF373934	26.87	24.43	23.70	24.27	0.00	0.73	24	1240	AF373963	14.15	11.29	13.47	13.32	46.73	1.05	303	709
				Saturniini	*Saturnia*	*albofasciata*	Saturniini	AF373940	27.44	25.08	23.53	23.78	0.00	0.16	24	1240	na								
					Saturnia	*naessigi*	Saturniini	na									AF373974.2	25.36	20.47	25.06	27.24	1.88	0.00	50	1304
	Geometroidea	Geometridae	Ennominae		*Lambdina*	*fiscellaria*	Geometroidea	AF173391	20.60	22.64	20.85	16.94	18.97	0.00	39	995	na								
	Hedyloidea	Hedylidae			*Macrosoma*	*undetermined*	Hedyloidea	AF173393	20.44	22.23	21.17	17.18	18.97	0.00	39	995	na								
	Hesperioidea	Hesperiidae	Hesperiinae		*Hylephila*	*phyleus*	Hesperiinae	AF173398	20.28	23.45	21.42	15.88	18.97	0.00	39	995	na								
			Pyrginae		*Pyrgus*	*communis*	Pyrginae	AF173396	20.68	21.82	20.52	18.00	18.97	0.00	39	995	na								
	Lasiocampoidea	Lasiocampidae	Lasiocampinae	Gastropachini	*Phyllodesma*	*americana*	Gastropachini	AF234554	25.90	28.18	25.16	20.44	0.00	0.33	24	1240	na								
				Lasiocampini	*Lasiocampa*	*quercus*	Lasiocampini	AF234550	26.47	25.41	24.35	23.53	0.00	0.24	24	1240	na								
				Malacosomatini	*Malacosoma*	*americanum*	Malacosomatini	AF234551	26.06	26.47	25.16	21.99	0.00	0.33	24	1240	na								
			Macromphaliinae		*Artace*	*cribraria*	Macromphaliinae	AF234545	26.30	25.49	25.00	23.21	0.00	0.00	24	1240	na								
	Noctuoidea	Arctiidae	Arctiinae	Arctiini	*Estigmene*	*acrea*	Arctiinae	U85670	26.38	27.20	23.53	22.80	0.00	0.08	24	1240	AF151549	12.04	10.23	12.34	15.73	49.66	0.00	316	669
			Lithosiinae	Lithosiini	*Hypoprepia*	*miniata*	Lithosiinae	U85669	26.38	25.33	23.70	24.59	0.00	0.00	24	1240	AF151547	14.15	11.89	13.09	14.00	46.65	0.23	303	709
		Lymantriidae	Lymantriinae	Orgyiini	*Dasychira*	*undetermined*	Lymantriidae	U85673	26.47	25.00	23.62	24.92	0.00	0.00	24	1240	AF151545	13.24	11.89	13.02	15.20	46.65	0.00	303	709
		Noctuidae "Quadrifine"	Aganainae		*Asota*	*caricae*	Aganainae	AF151607	25.49	28.66	24.02	21.82	0.00	0.00	24	1240	AF151551	13.24	11.59	13.47	15.05	46.65	0.00	303	709
			Catocalinae	Group 1a	*Catocala*	*ultronia*	Catocalinae	U85677	24.84	28.91	24.67	21.58	0.00	0.00	24	1240	AF151561	12.87	13.92	13.24	13.32	46.65	0.00	303	709
			Nolinae	Nolini	*Meganola*	*undetermined*	Nolinae	U85675	26.22	27.44	23.94	22.31	0.00	0.08	24	1240	AF151558	11.96	13.39	14.97	12.19	47.48	0.00	314	698
			Stictopterinae		*Lophoptera*	*undetermined*	Stictopterinae	AF151610	24.76	30.21	24.84	20.03	0.00	0.16	24	1240	AF151556	13.24	14.22	14.22	11.51	46.65	0.15	303	709
		Noctuidae "Trifine"	Condicinae	Condicini	*Condica*	*videns*	Condicinae	U85682	25.24	29.15	24.67	20.68	0.00	0.24	24	1240	AF151569	12.34	12.64	14.90	13.47	46.65	0.00	303	709
			Heliothinae		*Heliothis*	*decorata*	Heliothinae	na									U71414	12.64	12.94	13.92	12.42	48.08	0.00	325	690
					Heliothis	*subflexa*	Heliothinae	U20134	25.08	29.15	24.92	20.85	0.00	0.00	24	1240	na								
			Noctuinae	Noctuini	*Abagrotis*	*alternata*	Noctuinae	AF151630	25.16	29.23	24.67	20.68	0.00	0.24	24	1240	AF151601	12.57	12.94	14.75	13.09	46.65	0.00	303	709
			Oncocnemidinae		*Oncocnemis*	*obscurata*	Oncocnemidinae	U85685	24.84	29.32	24.76	21.09	0.00	0.00	24	1240	AF151585	11.74	13.77	14.30	13.54	46.65	0.00	303	709
			Pantheinae		*Panthea*	*furcilla*	Pantheinae	U85684	26.06	28.09	24.51	21.17	0.00	0.16	24	1240	AF151572	12.87	12.72	14.30	13.39	46.65	0.08	303	709
		Notodontidae	Heterocampinae		*Nerice*	*bidentata*	Heterocampinae	AF151604	24.27	29.72	26.30	19.71	0.00	0.00	24	1240	AF151543	11.59	15.05	15.35	10.38	47.03	0.60	307	705
			Notodontinae	Dicranurini	*Furcula*	*cinerea*	Notodontinae	U85665	25.65	27.85	24.51	21.99	0.00	0.00	24	1240	AF151539	11.36	13.54	15.65	12.04	46.65	0.75	303	709
			Nystaleinae		*Symmerista*	*albifrons*	Nystaleinae	U85667	23.70	29.72	25.98	20.60	0.00	0.00	24	1240	AF151541	11.59	16.18	14.67	10.61	46.65	0.30	303	709
			Phalerinae		*Datana*	*perspicua*	Phalerinae	U85666	25.41	28.50	24.67	21.09	0.00	0.33	24	1240	AF151540	11.14	12.49	14.07	13.32	48.98	0.00	313	678
	Papilionoidea	Lycaenidae	Polyommatinae		*Euphilotes*	*bernardino*	Polyommatinae	AF173404	18.65	26.63	22.48	13.11	18.97	0.16	39	995	na								
			Riodininae		*Apodemia*	*mormo*	Riodininae	AF173403	23.21	18.81	19.22	19.79	18.97	0.00	39	995	na								
		Nymphalidae	Cyrestinae	Cyrestidini	*Cyrestis*	*thyodamas*	Cyrestinae	AY218260	20.44	22.15	19.46	18.16	19.71	0.08	187	1064	na								
			Danainae		*Amauris*	*ellioti*	Danainae	AY218253	21.82	24.43	20.68	19.71	13.36	0.00	187	1064	na								
			Heliconiinae		*Heliconius*	*himera*	Nymphalidae	na									AY437778	7.90	8.65	8.95	7.60	66.89	0.00	104	441
					Heliconius	*hecale*	Heliconiinae	AY090168	22.56	23.53	19.71	19.87	14.33	0.00	187	1052	na								
			Nymphalinae		*Nymphalis*	*antiopa*	Nymphalinae	AY218266	22.64	22.80	20.03	20.85	13.36	0.33	187	1064	na								
			Satyrinae	Mycalesini	*Bicyclus*	*anynana*	Satyrinae	AY218258	21.82	24.10	20.85	18.65	14.58	0.00	187	1052	na								
		Papilionidae	Baroniinae		*Baronia*	*brevicornis*	Baroniinae	AF173406	23.45	17.67	19.14	20.77	18.97	0.00	39	995	na								
			Papilioninae	Papilionini	*Papilio*	*glaucus*	Papilionidae	na									AF036963	4.29	5.04	4.51	4.59	81.57	0.00	790	245
					Papilio	*troilus*	Papilioninae	AF423810	22.23	24.19	21.25	19.79	12.54	0.00	178	1089	na								
			Parnassiinae	Parnassiini	*Parnassius*	*clodius*	Parnassiinae	AF173411	21.74	19.14	19.95	20.11	18.97	0.08	39	995	na								
		Pieridae	Coliadinae		*Colias*	*eurytheme*	Coliadinae	AF173400	20.44	21.91	21.09	17.43	18.97	0.16	39	995	na								
			Pierinae		*Pieris*	*napi*	Pierinae	AF173401	21.58	20.28	19.87	19.14	18.97	0.16	39	995	na								

Table 17. Empirical pairwise distance matrix for EF data. Uncorrected pairwise distances are reported for every comparison of the 1,228bp EF sequences across the 118 taxon EF data matrix. Values in each cell below the diagonal are nucleotide distances tabulated separately for each codon position, in the format 'nt1.nt2.nt3'. Values above the diagonal are amino acid distances calculated from the comparisons of the 409 residue sequences obtained after conceptual translation of nucleotide data. Intra-Sphingidae comparisons (ntax=67) are boxed in the upper left quadrant of the matrix. Intra-Bombycoidea comparisons (ntax=15) are separated from other Lepidoptera by a line after taxon #82 (Saturniini).

EF	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1 Acherontia5989	-.-.-	1	1	2	1	4	6	3	3	3	2	3	2	2	3	3	4	4	6	2
2 Adhemarius1642	5.0.58	-.-.-	2	1	2	3	5	2	2	2	1	2	1	1	2	2	3	3	5	1
3 Aellopos2399	2.0.53	5.0.65	-.-.-	1	2	5	5	2	2	2	1	4	3	3	4	2	3	3	5	3
4 AelloposAF234559	4.0.60	5.0.64	2.0.15	-.-.-	3	4	4	1	1	1	0	3	2	2	3	1	2	2	4	2
5 Agrius1941	1.0.23	6.0.56	3.0.47	5.0.54	-.-.-	3	5	2	4	4	3	2	1	3	2	2	3	3	5	3
6 Amorpha1595	5.1.73	6.1.83	5.1.77	5.1.82	4.1.75	-.-.-	4	3	3	3	4	1	2	2	3	3	2	2	4	2
7 Basiothia0005	5.2.65	6.2.63	5.2.49	5.2.54	4.2.59	4.1.84	-.-.-	3	3	3	4	5	4	4	5	3	2	2	0	4
8 Callionima0966	3.0.47	6.0.51	3.0.32	3.0.35	2.0.46	4.1.71	2.2.43	-.-.-	2	2	1	2	1	3	2	0	1	1	3	3
9 Cautethia2573	4.1.52	5.1.57	4.1.37	4.1.40	5.1.50	5.0.75	1.1.48	3.1.33	-.-.-	0	1	4	3	1	4	2	1	1	3	1
10 Cautethia1668	5.1.54	6.1.58	5.1.39	5.1.41	6.1.51	6.0.76	2.1.50	4.1.35	1.0.1	-.-.-	1	4	3	1	4	2	1	1	3	1
11 Cephonodes5931	4.0.52	3.0.66	4.0.48	4.0.53	5.0.51	7.1.73	3.2.56	3.0.49	2.1.46	3.1.47	-.-.-	3	2	2	3	1	2	2	4	2
12 Ceratomia1870	4.0.53	7.0.75	6.0.72	6.0.71	3.0.58	3.1.73	5.2.80	3.0.66	6.1.73	7.1.75	6.0.74	-.-.-	1	3	2	2	3	3	5	3
13 CeratomiaAF23456	3.0.43	5.0.61	5.0.56	5.0.59	2.0.42	4.1.74	4.2.65	2.0.52	5.1.57	6.1.59	5.0.62	1.0.34	-.-.-	2	1	1	2	2	4	2
14 Cocytius2359	3.1.45	6.1.62	5.1.59	3.1.66	4.1.51	4.0.75	4.1.68	4.1.54	3.0.60	4.0.62	5.1.58	5.1.69	4.1.56	-.-.-	3	3	2	2	4	0
15 Coelonia5816	2.1.19	5.1.56	4.1.54	4.1.59	1.1.26	3.2.71	3.3.63	1.1.45	4.2.52	5.2.54	4.1.56	2.1.49	1.1.41	3.2.45	-.-.-	2	3	3	5	3
16 Daphnis5810	6.0.59	5.0.67	4.0.50	4.0.51	5.0.58	5.1.78	3.2.45	3.0.49	4.1.49	5.1.50	4.0.50	6.0.77	5.0.65	7.1.61	4.1.60	-.-.-	1	1	3	3
17 Darapsa1778	5.1.62	6.1.67	5.1.49	5.1.54	4.1.63	4.0.77	0.1.46	2.1.45	1.0.55	2.0.57	3.1.52	5.1.77	4.1.67	4.0.68	3.2.61	3.1.54	-.-.-	0	2	2
18 DarapsaAF234563	5.1.64	6.1.69	5.1.49	5.1.52	4.1.63	4.0.86	0.1.38	2.1.49	1.0.50	2.0.52	3.1.53	5.1.77	4.1.65	4.0.70	3.2.61	3.1.48	0.0.29	-.-.-	2	2
19 Deilephila5866	5.2.60	6.2.60	5.2.49	5.2.56	4.2.58	4.1.86	0.0.29	2.2.42	1.1.48	2.1.48	3.2.53	5.2.76	4.2.62	4.1.68	3.3.58	3.2.46	0.1.39	0.1.37	-.-.-	4
20 DolbaAF234579	5.1.42	6.1.66	7.1.63	7.1.68	6.1.44	6.0.72	6.1.73	6.1.55	5.0.66	6.0.68	5.1.61	7.1.59	6.1.44	4.0.48	5.2.39	7.1.71	6.0.69	6.0.77	6.1.71	-.-.-
21 Enyo2390	3.1.53	6.1.57	3.1.40	5.1.41	4.1.50	6.0.74	2.1.52	4.1.26	1.0.33	2.0.35	3.1.51	7.1.70	6.1.54	4.0.54	5.2.48	5.1.47	2.0.47	2.0.48	2.1.49	6.0.56
22 Erinnyis1542	1.0.55	6.0.58	1.0.41	3.0.42	2.0.50	6.1.71	4.2.56	2.0.25	3.1.43	4.1.44	3.0.48	5.0.71	4.0.57	4.1.56	3.1.51	5.0.54	4.1.52	4.1.54	4.2.55	6.1.62
23 Eumorpha1533	1.0.58	6.0.65	1.0.49	3.0.48	2.0.60	6.1.78	4.2.63	2.0.42	3.1.48	4.1.49	3.0.57	5.0.74	4.0.62	4.1.60	3.1.55	5.0.56	4.1.55	4.1.56	4.2.59	6.1.66
24 EumorphaAF234565	1.0.57	6.0.65	1.0.43	3.0.45	2.0.57	6.1.75	4.2.57	2.0.38	3.1.47	4.1.49	3.0.56	5.0.73	4.0.61	4.1.53	3.1.53	5.0.57	4.1.53	4.1.58	4.2.57	6.1.63
25 Eumorpha1504	1.0.66	6.0.73	1.0.57	3.0.56	2.0.68	6.1.78	4.2.71	2.0.48	3.1.56	4.1.57	3.0.63	5.0.79	4.0.68	4.1.69	3.1.63	5.0.64	4.1.63	4.1.64	4.2.69	6.1.70
26 Euryglottis2891	2.1.48	7.1.72	4.1.66	6.1.68	1.1.45	3.2.85	3.3.77	3.1.62	4.2.69	5.2.67	6.1.64	4.1.56	3.1.48	3.2.63	2.2.47	6.1.71	3.2.77	3.2.79	3.3.68	5.2.49
27 Hemaris1882	5.0.56	4.0.68	5.0.57	5.0.62	4.0.55	6.1.69	2.2.63	2.0.52	3.1.53	4.1.54	1.0.17	5.0.76	4.0.65	6.1.59	3.1.60	3.0.54	2.1.60	2.1.60	2.2.60	6.1.58
28 HemarisAF234568	5.0.58	4.0.71	5.0.57	5.0.60	4.0.57	6.1.71	2.2.64	2.0.50	3.1.52	4.1.53	1.0.18	5.0.76	4.0.68	6.1.61	3.1.62	3.0.54	2.1.63	2.1.61	2.2.61	6.1.60
29 Hippotion5932	5.2.63	6.2.60	5.2.43	5.2.50	4.2.59	4.1.83	0.0.11	2.2.40	1.1.44	2.1.46	3.2.54	5.2.78	4.2.65	4.1.64	3.3.61	3.2.44	0.1.40	0.1.36	0.0.28	6.1.73
30 Hopliocnema0233	3.1.50	6.1.68	5.1.59	5.1.61	2.1.51	2.2.74	4.1.62	2.1.53	5.2.58	6.2.59	5.1.64	1.1.59	2.1.51	4.2.60	1.2.45	5.1.65	4.2.60	4.2.69	4.1.59	6.2.50
31 Hyles5817	5.2.56	6.2.58	5.2.54	5.2.61	4.2.54	4.1.78	0.0.34	2.2.42	1.1.48	2.1.50	3.2.51	5.2.70	4.2.58	4.1.63	3.3.56	3.2.49	0.1.49	0.1.45	0.0.29	6.1.67
32 Hyles1881	5.2.57	6.2.60	5.2.55	5.2.59	4.2.59	4.1.81	0.0.33	2.2.47	1.1.53	2.1.55	3.2.55	5.2.66	4.2.56	4.1.61	3.3.54	3.2.50	0.1.45	0.1.40	0.0.31	6.1.64
33 Isognathus1646	3.0.63	6.0.72	1.0.49	3.0.52	4.0.61	6.1.79	6.2.65	4.0.36	5.1.56	6.1.58	5.0.63	7.0.74	6.0.65	6.1.66	5.1.58	5.0.67	6.1.61	6.1.62	6.2.62	8.1.68
34 Laothoe0012	8.3.66	9.3.73	10.3.74	9.3.79	7.3.68	5.4.76	7.3.71	7.3.63	8.4.69	9.4.70	10.3.76	6.3.81	6.3.69	7.4.72	6.4.70	10.3.73	7.4.79	7.4.82	7.3.73	9.4.75
35 Lapara1670	5.1.55	8.1.76	7.1.67	7.1.70	4.1.57	2.0.79	4.1.72	4.1.62	5.0.71	6.0.73	7.1.72	1.1.53	2.1.45	4.0.68	3.2.48	7.1.75	4.0.70	4.0.74	4.1.71	6.0.52
36 Macroglossum5806	5.1.62	6.1.64	5.1.59	5.1.57	4.1.60	6.2.79	2.3.52	2.1.42	3.2.52	4.2.53	3.1.58	5.1.80	4.1.69	6.2.57	3.2.60	3.1.47	2.2.49	2.2.47	2.3.44	8.2.72
37 Manduca1529	4.1.45	5.1.62	6.1.67	6.1.68	3.1.48	3.0.72	3.1.73	3.1.55	4.0.66	5.0.68	4.1.66	4.1.58	3.1.52	3.0.47	2.2.41	6.1.64	3.0.72	3.0.74	3.1.71	3.0.34
38 Manduca1508	5.0.48	4.0.60	5.0.66	5.0.68	4.0.49	4.1.80	6.2.71	4.0.55	7.1.67	8.1.69	5.0.65	5.0.58	4.0.46	6.1.48	3.1.40	3.0.65	6.1.72	6.1.73	6.2.69	4.1.36
39 Manduca1876	4.0.46	5.0.71	6.0.67	6.0.68	5.0.46	7.1.74	7.2.68	5.0.59	6.1.66	7.1.68	4.0.60	6.0.56	5.0.45	5.1.54	4.1.42	6.0.68	7.1.66	7.1.70	7.2.67	3.1.33
40 ManducaAF234571	4.0.43	5.0.65	6.0.60	6.0.63	5.0.41	7.1.75	7.2.63	5.0.55	6.1.58	7.1.60	4.0.57	6.0.52	5.0.39	5.1.50	4.1.40	6.0.65	7.1.62	7.1.66	7.2.64	3.1.36
41 Marumba0118	5.1.81	8.1.93	7.1.88	7.1.97	4.1.81	2.0.89	4.1.100	4.1.81	5.0.91	6.0.92	7.1.82	3.1.91	4.1.86	4.0.83	3.2.78	7.1.92	4.0.95	4.0.99	4.1.91	6.0.78
42 Mimas5836	7.2.60	8.2.67	7.2.66	9.2.73	6.2.63	4.1.49	6.2.67	8.2.60	7.1.65	8.1.67	9.2.67	5.2.79	6.2.68	8.1.63	7.3.62	7.2.67	6.1.66	6.1.74	6.2.67	10.1.68
43 Nyceryx2378	2.0.56	5.0.63	2.0.31	2.0.38	3.0.52	5.1.78	3.2.60	1.0.37	2.1.42	3.1.44	2.0.51	4.0.70	3.0.61	3.1.58	2.1.54	4.0.54	3.1.51	3.1.53	3.2.52	5.1.64
44 Pachylia1644	1.0.51	6.0.64	1.0.39	3.0.41	2.0.44	6.1.76	4.2.56	2.0.35	3.1.39	4.1.40	3.0.46	5.0.70	4.0.57	4.1.58	3.1.52	5.0.49	4.1.52	4.1.57	4.2.52	6.1.58
45 PachysphinxAF234	7.2.71	8.2.80	9.2.81	8.2.88	6.2.79	6.3.83	6.4.82	6.2.66	7.3.78	8.3.80	7.2.85	5.2.81	6.2.80	8.3.80	5.3.74	7.2.78	6.3.81	6.3.88	6.4.82	10.3.82
46 Pachysphinx1528	7.2.77	8.2.85	9.2.86	8.2.93	6.2.84	6.3.90	6.4.86	6.2.72	7.3.85	8.3.87	7.2.92	5.2.85	6.2.87	8.3.86	5.3.81	7.2.85	6.3.89	6.3.96	6.4.90	10.3.88
47 PaoniasAF234572	9.1.66	8.1.72	11.1.74	10.1.83	8.1.68	6.2.79	6.3.73	8.1.64	7.2.72	8.2.74	9.1.81	7.1.80	7.1.72	8.2.74	7.2.69	9.1.72	6.2.77	6.2.78	6.3.77	10.2.72
48 Paonias1540	9.2.69	8.2.76	9.2.77	8.2.85	8.2.71	6.3.81	10.3.76	8.2.66	11.3.74	12.3.74	11.2.86	7.2.80	7.2.76	10.3.79	7.3.72	9.2.76	10.3.81	10.3.83	10.3.78	12.3.76
49 Paratrea1939	2.0.43	5.0.62	4.0.60	4.0.60	3.0.43	5.1.72	5.2.68	3.0.53	4.1.59	5.1.60	4.0.61	2.0.47	1.0.33	3.1.60	2.1.42	6.0.64	5.1.66	5.1.67	5.2.65	5.1.45
50 Perigonia2191	4.1.51	7.1.54	4.1.28	4.1.37	5.1.50	3.0.75	3.1.54	3.1.28	2.0.39	3.0.41	4.1.47	4.1.72	5.1.58	3.0.53	4.2.49	6.1.48	3.0.51	3.0.52	3.1.49	5.0.57
51 ProserpinusAF173	3.0.51	4.0.54	4.0.48	4.0.49	2.0.49	4.1.59	2.2.48	1.0.38	3.1.41	4.1.43	3.0.49	3.0.61	2.0.47	4.1.55	1.1.49	1.0.55	2.1.43	2.1.51	2.2.54	4.1.47
52 Protambulyx1945	3.0.54	6.0.46	5.0.61	7.0.63	4.0.53	6.1.76	4.2.58	6.0.48	3.1.56	4.1.57	5.0.65	7.0.69	6.0.60	4.1.64	5.1.54	7.0.64	4.1.64	4.1.68	4.2.58	4.1.66
53 Pseudoclanis5839	6.2.68	9.2.75	7.2.68	7.2.77	5.2.71	5.3.82	6.3.72	4.2.67	7.3.70	8.3.72	7.2.71	4.2.80	5.2.71	7.3.67	4.3.68	7.2.71	6.3.73	6.3.74	6.3.72	9.3.67
54 Psilogramma5988	3.0.40	6.0.59	5.0.67	5.0.67	2.0.39	2.1.81	4.2.67	2.0.56	5.1.58	6.1.58	5.0.54	1.0.61	2.0.49	4.1.58	1.1.39	5.0.68	4.1.66	4.1.61	4.2.65	6.1.56
55 SmerinthusAF2345	10.2.73	7.2.76	10.2.79	9.2.84	9.2.72	5.3.73	7.4.77	9.2.70	8.3.77	9.3.78	10.2.84	8.2.79	8.2.71	9.3.76	8.3.76	8.2.77	7.3.81	7.3.86	7.4.81	11.3.75
56 Smerinthus1511	9.2.79	8.2.81	11.2.81	10.2.86	8.2.80	6.3.74	6.4.82	8.2.75	7.3.80	8.3.81	9.2.90	7.2.88	7.2.81	8.3.82	7.3.80	9.2.80	6.3.85	6.3.89	6.4.87	10.3.81
57 SphinxAF234577	4.0.50	7.0.72	6.0.64	6.0.67	3.0.55	3.1.77	5.2.71	3.0.57	6.1.68	7.1.70	6.0.68	0.0.61	1.0.53	5.1.60	2.1.42	6.0.71	5.1.70	5.1.75	5.2.72	7.1.50
58 Sphinx1532	4.0.54	7.0.70	6.0.73	6.0.70	3.0.57	3.1.82	3.2.73	3.0.65	4.1.69	5.1.70	6.0.73	2.0.59	1.0.56	3.1.64	2.1.50	6.0.70	3.1.71	3.1.76	3.2.72	5.1.57
59 Sphinx1591	7.1.47	10.1.67	9.1.64	9.1.67	6.1.52	4.2.77	6.3.70	6.1.61	7.2.65	8.2.67	9.1.66	3.1.52	4.1.47	6.2.60	5.2.41	9.1.73	6.2.69	6.2.70	6.3.69	8.2.49
60 Sphinx1938	4.0.55	7.0.73	6.0.64	6.0.68	3.0.56	3.1.80	5.2.75	3.0.62	6.1.72	7.1.74	6.0.68	0.0.61	1.0.55	5.1.59	2.1.49	6.0.72	5.1.70	5.1.76	5.2.70	7.1.53
61 SphecodinaAF2345	5.1.56	8.1.72	5.1.55	5.1.64	6.1.59	6.0.79	4.1.60	4.1.49	3.0.50	4.0.52	5.1.54	5.1.71	4.1.62	4.0.64	5.2.57	5.1.57	4.0.59	4.0.62	4.1.62	4.0.63
62 Theretra5880	6.2.68	7.2.68	6.2.62	6.2.69	5.2.64	3.1.87	1.0.37	3.2.51	2.1.62	3.1.63	4.2.59	4.2.79	5.2.70	5.1.72	4.3.67	4.2.57	1.1.42	1.1.49	1.0.34	7.1.77
63 Unzela2376	4.1.57	7.1.60	4.1.34	6.1.40	5.1.55	5.0.78	3.1.46	5.1.27	2.0.41	3.0.43	4.1.49	6.1.73	7.1.56	5.0.60	6.2.53	6.1.50	3.0.54	3.0.55	3.1.48	7.0.63
64 Xylophanes5904	6.2.59	5.2.57	4.2.48	4.2.53	5.2.61	3.1.79	1.0.23	3.2.42	2.1.45	3.1.47	4.2.49	6.2.71	5.2.61	5.1.60	4.3.60	2.2.39	1.1.35	1.1.38	1.0.24	7.1.69
65 XylophanesAF2345	5.2.62	6.2.61	5.2.46	5.2.55	4.2.61	4.1.82	0.0.28	2.2.45	1.1.49	2.1.51	3.2.53	5.2.73	4.2.59	4.1.65	3.3.61	3.2.45	0.1.42	0.1.40	0.0.23	6.1.73
66 Xylophanes2369	5.2.67	6.2.65	5.2.55	5.2.62	4.2.62	4.1.81	0.0.28	2.2.50	1.1.51	2.1.53	3.2.54	5.2.80	4.2.67	4.1.67	3.3.65	3.2.54	0.1.49	0.1.43	0.0.31	6.1.74
67 Xylophanes1879	5.2.71	5.2.61	4.2.52	4.2.59	4.2.71	3.1.86	0.0.30	2.2.52	1.1.54	2.1.56	3.2.59	5.2.81	4.2.71	4.1.69	3.3.68	2.2.52	0.1.46	0.1.45	0.0.32	6.1.80
68 Attacini	5.0.136	10.0.146	5.0.141	7.0.144	6.0.135	10.1.126	8.2.143	6.0.143	7.1.140	8.1.142	7.0.135	7.0.137	6.0.137	8.1.138	7.1.136	7.0.148	8.1.138	8.1.147	8.2.144	8.1.132
69 Bombycidae	6.3.138	9.3.156	6.3.145	6.3.150	7.3.138	11.4.148	9.3.153	7.3.146	8.4.147	9.4.149	8.3.138	10.3.148	8.3.138	7.4.140	8.4.140	8.3.146	9.4.157	9.4.155	9.3.152	9.4.141
70 Brahmaeidae	5.1.120	6.1.139	5.1.130	5.1.133	4.1.121	6.2.138	2.1.134	2.1.130	3.2.121	4.2.124	3.1.118	5.1.132	4.1.131	6.2.125	3.2.124	3.1.126	2.2.134	2.2.140	2.1.133	6.2.126
71 Bunaeini	6.1.139	9.1.152	6.1.154	6.1.158	7.1.139	9.0.140	7.1.156	7.1.160	6.0.149	7.0.149	8.1.147	10.1.149	8.1.145	5.0.140	8.2.142	10.1.155	7.0.157	7.0.158	7.1.155	9.0.139
72 Ceratocampinae	5.0.111	8.0.119	5.0.109	5.0.113	4.0.110	6.1.131	4.2.119	2.0.106	5.1.111	6.1.112	5.0.116	5.0.121	4.0.118	6.1.112	3.1.104	5.0.120	4.1.114	4.1.111	4.2.115	8.1.120
73 Endromidae	6.2.114	7.2.125	6.2.113	8.2.110	5.2.111	7.1.113	3.0.114	5.2.106	4.1.119	5.1.120	6.2.109	8.2.110	6.2.112	7.1.119	6.3.117	6.2.112	3.1.107	3.1.115	3.0.113	9.1.118
74 Gastropachini	8.0.101	11.0.104	9.0.101	11.0.105	9.0.93	11.1.111	10.2.99	10.0.99	9.1.99	10.1.102	9.0.98	12.0.112	11.0.108	9.1.100	10.1.93	13.0.101	10.1.105	10.1.106	10.2.103	9.1.107
75 Hemileucini	6.1.101	9.1.100	7.1.85	7.1.87	5.1.94	7.0.95	5.1.85	6.1.83	6.0.84	7.0.85	8.1.95	8.1.99	7.1.94	5.0.92	6.2.92	8.1.96	5.0.94	5.0.101	5.1.91	9.0.95
76 Lasiocampini	5.2.119	8.2.131	6.2.127	8.2.133	6.2.116	8.3.115	7.2.128	7.2.123	6.3.127	7.3.128	6.2.123	9.2.118	8.2.114	6.3.132	7.3.115	10.2.126	7.3.127	7.3.127	7.2.129	6.3.117
77 Lemoniidae	5.1.132	6.1.140	5.1.138	5.1.138	4.1.130	6.2.131	2.1.137	2.1.137	3.2.129	4.2.131	3.1.128	5.1.127	4.1.128	6.2.131	3.2.133	3.1.128	2.2.130	2.2.135	2.1.133	8.2.132
78 Macromphaliinae	8.1.138	9.1.137	6.1.136	8.1.133	7.1.136	7.2.132	7.1.140	7.1.136	8.2.135	9.2.135	8.1.125	8.1.133	7.1.132	9.2.124	8.2.139	8.1.127	7.2.135	7.2.137	7.1.141	7.2.134
79 Malacosomatini	11.2.119	10.2.119	11.2.125	11.2.123	12.2.118	14.3.120	10.2.129	10.2.122	9.3.118	10.3.119	7.2.128	13.2.122	12.2.122	12.3.118	11.3.116	11.2.122	10.3.120	10.3.128	10.2.119	12.3.117
80 Micragonini	6.2.131	9.2.144	6.2.133	8.2.131	5.2.128	7.1.133	5.2.132	5.2.136	6.1.123	7.1.123	8.2.130	8.2.131	6.2.128	7.1.135	6.3.135	8.2.134	5.1.136	5.1.137	5.2.132	9.1.131
81 Polythysanini	6.3.121	11.3.121	6.3.120	8.3.120	5.3.119	7.4.125	5.5.128	5.3.119	6.4.122	7.4.122	8.3.122	8.3.128	7.3.123	7.4.124	6.4.120	6.3.123	5.4.123	5.4.128	5.5.116	7.4.119
82 Saturniini	8.1.123	9.1.137	7.1.126	7.1.127	7.1.123	7.2.134	8.3.132	6.1.129	9.2.129	10.2.131	9.1.128	8.1.129	7.1.127	9.2.131	6.2.131	5.1.137	8.2.128	8.2.135	8.3.135	7.2.121
83 Agaraninae	7.2.98	8.2.96	7.2.91	7.2.90	8.2.85	6.1.102	6.0.95	6.2.86	5.1.90	4.1.91	7.2.85	7.2.101	7.2.94	6.1.92	7.3.92	9.2.89	6.1.93	6.1.93	6.0.91	8.1.97
84 Arctiinae	5.1.123	8.1.125	5.1.115	4.1.114	4.1.114	6.2.117	4.1.114	2.1.110	5.2.114	4.2.115	5.1.110	5.1.130	4.1.126	6.2.116	3.2.118	5.1.118	4.2.111	4.2.118	4.1.115	8.2.114
85 Baroniinae	6.2.138	8.2.139	7.2.140	7.2.140	5.2.133	8.3.132	6.2.149	5.2.145	7.3.146	8.3.147	7.2.143	7.2.141	6.2.138	8.3.138	5.3.140	7.2.140	6.3.148	6.3.146	6.2.149	8.3.133
86 Catocalinae	7.1.94	10.1.98	7.1.95	7.1.95	6.1.95	4.0.116	4.1.96	4.1.95	5.0.93	4.0.94	7.1.86	5.1.102	6.1.101	6.0.93	5.2.99	7.1.88	4.0.90	4.0.97	4.1.97	8.0.101
87 Coliadinae	6.0.90	7.0.93	7.0.79	7.0.77	7.0.85	9.1.89	7.2.87	6.0.81	6.1.89	5.1.90	6.0.85	8.0.100	7.0.88	7.1.90	6.1.89	8.0.81	7.1.91	7.1.94	7.2.88	9.1.83
88 Condicinae	5.2.92	10.2.106	5.2.83	7.2.87	6.2.87	6.1.110	6.0.91	6.2.82	5.1.86	6.1.88	7.2.85	7.2.101	8.2.93	6.1.96	7.3.90	9.2.92	6.1.98	6.1.95	6.0.96	6.1.92
89 Crambidae	7.7.80	8.7.95	8.7.76	8.7.75	8.7.78	8.8.83	8.7.76	7.7.74	7.8.79	6.8.82	7.7.78	7.7.88	8.7.80	8.8.79	7.8.76	9.7.74	8.8.81	8.8.85	8.7.83	10.8.76
90 Cyrestinae	12.2.103	11.2.112	12.2.108	12.2.110	12.2.96	10.1.108	8.0.109	10.2.106	8.1.101	9.1.103	10.2.107	10.2.105	10.2.107	11.1.110	11.3.102	11.2.113	8.1.107	8.1.115	8.0.111	13.1.107
91 Danainae	8.4.124	11.4.129	8.4.124	10.4.120	7.4.117	9.3.128	5.2.123	7.4.127	6.3.122	7.3.123	8.4.124	10.4.126	9.4.124	9.3.112	8.5.117	8.4.122	5.3.129	5.3.130	5.2.121	11.3.121
92 Galleriinae	10.1.132	7.1.149	11.1.137	11.1.137	11.1.135	13.2.133	10.1.145	10.1.142	9.2.138	8.2.139	7.1.133	10.1.134	8.1.138	11.2.142	10.2.132	11.1.133	10.2.137	10.2.144	10.1.142	11.2.138
93 Geometroidea	8.2.105	11.2.105	9.2.92	11.2.93	7.2.106	9.1.94	7.2.94	8.2.97	8.1.99	7.1.101	10.2.97	10.2.98	9.2.97	9.1.96	8.3.105	10.2.99	7.1.96	7.1.101	7.2.101	11.1.93
94 Hedyloidea	4.1.97	7.1.99	5.1.93	7.1.89	3.1.98	7.2.90	5.3.95	4.1.93	6.2.92	7.2.92	6.1.94	6.1.103	5.1.98	7.2.99	4.2.98	6.1.92	5.2.94	5.2.102	5.3.100	9.2.95
95 Heliconiinae	11.4.114	15.4.123	11.4.122	12.4.118	10.4.113	9.3.123	9.2.121	9.4.121	10.3.119	11.3.119	12.4.120	8.4.119	9.4.120	11.3.117	10.3.111	12.4.124	9.3.122	9.3.126	9.2.122	11.3.114
96 Heliothinae	7.3.84	10.3.101	7.3.83	5.3.86	6.3.81	4.2.103	4.1.89	4.3.80	5.2.80	6.2.82	7.3.78	5.3.97	6.3.92	4.2.93	5.4.81	7.3.84	4.2.88	4.2.92	4.1.90	8.2.84
97 Hesperiinae	4.1.82	5.1.81	5.1.77	5.1.75	3.1.81	5.2.73	3.1.73	2.1.69	4.2.79	3.2.81	4.1.77	4.1.88	3.1.80	5.2.77	2.2.73	4.1.66	3.2.73	3.2.79	3.1.75	7.2.79
98 Heterocampinae	5.2.89	8.2.97	5.2.79	5.2.78	4.2.84	2.1.103	2.0.85	2.2.75	3.1.85	4.1.88	5.2.87	3.2.100	4.2.93	4.1.91	3.3.87	5.2.89	2.1.89	2.1.97	2.0.86	6.1.90
99 Lithosiinae	4.2.148	9.2.146	4.2.149	6.2.149	5.2.143	7.1.146	5.0.148	5.2.144	4.1.150	3.1.151	6.2.145	8.2.146	7.2.145	5.1.146	6.3.144	8.2.140	5.1.140	5.1.150	5.0.148	7.1.140
100 Lymantriidae	10.0.140	11.0.148	10.0.146	9.0.145	11.0.141	11.1.150	9.2.149	9.0.148	8.1.147	7.1.149	10.0.134	10.0.151	8.0.149	9.1.138	10.1.146	10.0.137	9.1.134	9.1.144	9.2.149	9.1.142
101 Micropterigoidea	4.2.62	7.2.57	5.2.52	6.2.52	4.2.56	6.1.62	4.1.57	5.2.58	4.1.50	4.1.51	6.2.64	6.2.65	5.2.58	4.1.66	5.3.58	7.2.62	4.1.61	4.1.60	4.1.58	6.1.62
102 Noctuinae	5.4.98	8.4.107	5.4.96	7.4.96	4.4.99	6.3.108	2.2.104	4.4.95	3.3.96	4.3.98	5.4.90	7.4.98	6.4.100	6.3.97	5.5.97	6.4.95	2.3.104	2.3.103	2.2.102	8.3.88
103 Nolinae	9.0.110	12.0.126	9.0.119	9.0.121	8.0.110	8.1.116	6.2.117	6.0.115	7.1.120	8.1.122	9.0.102	7.0.113	6.0.117	8.1.111	7.1.110	9.0.118	6.1.114	6.1.123	6.2.118	10.1.123
104 Notodontinae	5.2.98	6.2.113	5.2.98	5.2.98	4.2.95	4.1.97	2.0.101	2.2.97	3.1.99	4.1.101	5.2.96	5.2.101	3.2.96	4.1.96	3.3.96	5.2.98	2.1.102	2.1.106	2.0.106	6.1.88
105 Nymphalinae	12.5.130	14.5.137	12.5.132	12.5.130	11.5.124	10.4.124	8.3.125	10.5.124	9.4.128	10.4.129	11.5.122	11.5.124	12.5.123	12.4.130	11.4.126	11.5.126	8.4.130	8.4.131	8.3.125	14.4.119
106 Nystaleinae	5.1.84	8.1.96	5.1.70	7.1.74	4.1.84	6.0.93	2.1.78	4.1.65	3.0.75	4.0.77	5.1.75	7.1.90	6.1.85	6.0.80	5.2.80	5.1.76	2.0.83	2.0.82	2.1.78	8.0.91
107 Oncocnemidinae	5.2.87	8.2.92	5.2.79	5.2.82	6.2.85	6.1.99	4.0.84	4.2.80	3.1.81	4.1.82	5.2.77	7.2.101	6.2.91	4.1.90	5.3.86	7.2.74	4.1.88	4.1.84	4.0.87	6.1.88
108 Pantheinae	7.3.109	10.3.120	7.3.108	9.3.112	6.3.111	6.2.115	6.1.104	6.3.108	7.2.104	8.2.104	9.3.101	7.3.115	7.3.118	8.2.114	7.4.111	9.3.107	6.2.109	6.2.110	6.1.109	10.2.112
109 Papilioninae	6.2.102	9.2.125	7.2.112	7.2.109	5.2.104	7.3.109	6.2.110	4.2.111	7.3.103	8.3.103	7.2.94	6.2.112	5.2.111	7.3.107	4.3.98	7.2.107	6.3.111	6.3.111	6.2.110	9.3.104
110 Parnassiinae	3.2.114	4.2.112	4.2.115	3.2.115	4.2.112	6.3.111	4.2.110	3.2.117	3.3.114	4.3.115	3.2.110	5.2.113	4.2.112	4.3.117	3.3.114	5.2.103	4.3.116	4.3.110	4.2.112	6.3.115
111 Phalerinae	7.2.88	8.2.102	5.2.85	5.2.93	6.2.86	2.1.107	4.0.95	4.2.93	5.1.89	6.1.91	7.2.87	5.2.105	6.2.98	6.1.92	5.3.90	5.2.97	4.1.97	4.1.103	4.0.97	8.1.96
112 Pierinae	8.3.111	9.3.112	9.3.113	9.3.108	7.3.106	7.4.109	5.3.117	6.3.116	6.4.122	7.4.122	8.3.117	6.3.111	5.3.112	7.4.109	6.2.108	8.3.113	5.4.120	5.4.117	5.3.122	9.4.112
113 Polyommatinae	9.4.101	11.4.100	10.4.95	11.4.96	8.4.98	9.3.110	7.2.93	8.4.86	8.3.93	7.3.96	10.4.102	8.4.111	7.4.101	9.3.97	8.5.97	10.4.92	7.3.98	7.3.100	7.2.91	9.3.96
114 Pyraustinae	8.1.83	9.1.88	8.1.82	8.1.82	8.1.83	10.2.86	6.3.92	6.1.77	6.2.83	7.2.85	6.1.88	9.1.84	8.1.85	9.2.90	7.2.78	7.1.88	6.2.86	6.2.92	6.3.93	11.2.89
115 Pyrginae	4.2.98	7.2.96	5.2.95	7.2.90	3.2.97	5.1.93	3.0.102	4.2.96	4.1.98	5.1.100	6.2.99	6.2.97	5.2.99	5.1.100	4.3.98	6.2.95	3.1.101	3.1.106	3.0.102	7.1.103
116 Riodininae	11.4.129	10.4.137	10.4.130	9.4.127	12.4.127	12.3.126	12.2.134	13.4.138	11.3.135	12.3.136	11.4.128	13.4.126	12.4.131	10.3.119	13.5.128	13.4.128	12.3.139	12.3.135	12.2.134	12.3.123
117 Satyrinae	9.4.116	12.4.130	9.4.115	9.4.117	8.4.116	6.3.116	6.2.121	6.4.114	7.3.115	8.3.115	9.4.119	7.4.118	8.4.119	8.3.116	7.5.113	9.4.121	6.3.122	6.3.130	6.2.114	10.3.103
118 Stictopterinae	6.1.95	9.1.104	6.1.82	6.1.76	7.1.87	5.0.108	5.1.86	5.1.80	4.0.84	5.0.85	6.1.83	6.1.101	7.1.99	5.0.97	6.2.91	8.1.85	5.0.86	5.0.94	5.1.91	7.0.102

EF	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39
1 Acherontia5989	2	1	1	1	1	3	3	3	6	4	6	6	1	10	4	5	3	2	2
2 Adhemarius1642	3	2	2	2	2	4	2	2	5	3	5	5	2	9	3	4	2	1	1
3 Aellopos2399	1	0	0	0	0	4	2	2	5	5	5	5	0	11	5	4	4	3	3
4 AelloposAF234559	2	1	1	1	1	5	1	1	4	4	4	4	1	10	4	3	3	2	2
5 Agrius1941	3	2	2	2	2	2	2	2	5	3	5	5	2	9	3	4	2	1	3
6 Amorpha1595	4	5	5	5	5	4	3	3	4	2	4	4	5	7	0	5	1	2	4
7 Basiothia0005	4	5	5	5	5	6	3	3	0	4	0	0	5	7	4	5	3	4	6
8 Callionima0966	3	2	2	2	2	4	0	0	3	3	3	3	2	9	3	2	2	1	3
9 Cautethia2573	1	2	2	2	2	5	2	2	3	5	3	3	2	10	3	4	2	3	3
10 Cautethia1668	1	2	2	2	2	5	2	2	3	5	3	3	2	10	3	4	2	3	3
11 Cephonodes5931	2	1	1	1	1	5	1	1	4	4	4	4	1	10	4	3	3	2	2
12 Ceratomia1870	5	4	4	4	4	4	2	2	5	1	5	5	4	7	1	4	2	1	3
13 CeratomiaAF23456	4	3	3	3	3	3	1	1	4	2	4	4	3	8	2	3	1	0	2
14 Cocytius2359	2	3	3	3	3	4	3	3	4	4	4	4	3	9	2	5	1	2	2
15 Coelonia5816	5	4	4	4	4	4	2	2	5	3	5	5	4	9	3	4	2	1	3
16 Daphnis5810	3	2	2	2	2	4	0	0	3	3	3	3	2	9	3	2	2	1	3
17 Darapsa1778	2	3	3	3	3	4	1	1	2	4	2	2	3	9	2	3	1	2	4
18 DarapsaAF234563	2	3	3	3	3	4	1	1	2	4	2	2	3	9	2	3	1	2	4
19 Deilephila5866	4	5	5	5	5	6	3	3	0	4	0	0	5	7	4	5	3	4	6
20 DolbaAF234579	2	3	3	3	3	4	3	3	4	4	4	4	3	9	2	5	1	2	2
21 Enyo2390	-.-.-	1	1	1	1	4	3	3	4	6	4	4	1	11	4	5	3	4	4
22 Erinnyis1542	2.1.32	-.-.-	0	0	0	4	2	2	5	5	5	5	0	11	5	4	4	3	3
23 Eumorpha1533	2.1.35	0.0.47	-.-.-	0	0	4	2	2	5	5	5	5	0	11	5	4	4	3	3
24 EumorphaAF234565	2.1.30	0.0.43	0.0.19	-.-.-	0	4	2	2	5	5	5	5	0	11	5	4	4	3	3
25 Eumorpha1504	2.1.43	0.0.53	0.0.12	0.0.29	-.-.-	4	2	2	5	5	5	5	0	11	5	4	4	3	3
26 Euryglottis2891	3.2.66	3.1.66	3.1.67	3.1.71	3.1.75	-.-.-	4	4	6	5	6	6	4	9	4	6	3	3	5
27 Hemaris1882	4.1.54	4.0.54	4.0.59	4.0.62	4.0.62	5.1.66	-.-.-	0	3	3	3	3	2	9	3	2	2	1	3
28 HemarisAF234568	4.1.52	4.0.53	4.0.59	4.0.62	4.0.63	5.1.68	0.0.4	-.-.-	3	3	3	3	2	9	3	2	2	1	3
29 Hippotion5932	2.1.48	4.2.50	4.2.59	4.2.53	4.2.69	3.3.77	2.2.61	2.2.62	-.-.-	4	0	0	5	7	4	5	3	4	6
30 Hopliocnema0233	6.2.54	4.1.62	4.1.60	4.1.60	4.1.66	3.2.54	4.1.62	4.1.62	4.1.58	-.-.-	4	4	5	6	2	5	3	2	4
31 Hyles5817	2.1.46	4.2.50	4.2.59	4.2.55	4.2.67	3.3.71	2.2.58	2.2.59	0.0.33	4.1.62	-.-.-	0	5	7	4	5	3	4	6
32 Hyles1881	2.1.52	4.2.55	4.2.60	4.2.58	4.2.64	3.3.66	2.2.59	2.2.60	0.0.34	4.1.55	0.0.22	-.-.-	5	7	4	5	3	4	6
33 Isognathus1646	4.1.43	2.0.28	2.0.60	2.0.54	2.0.66	5.1.76	6.0.66	6.0.64	6.2.58	6.1.70	6.2.62	6.2.66	-.-.-	11	5	4	4	3	3
34 Laothoe0012	9.4.69	9.3.68	9.3.75	9.3.79	9.3.81	6.4.74	9.3.77	9.3.80	7.3.70	5.2.65	7.3.71	7.3.72	11.3.81	-.-.-	7	7	8	8	8
35 Lapara1670	6.0.67	6.1.72	6.1.75	6.1.72	6.1.83	3.2.52	6.1.74	6.1.76	4.1.68	2.2.55	4.1.71	4.1.66	8.1.73	5.4.83	-.-.-	5	1	2	4
36 Macroglossum5806	4.2.42	4.1.49	4.1.60	4.1.56	4.1.70	5.2.76	2.1.64	2.1.64	2.3.49	4.2.63	2.3.48	2.3.50	6.1.62	7.2.73	6.2.78	-.-.-	4	3	5
37 Manduca1529	5.0.56	5.1.61	5.1.64	5.1.63	5.1.66	2.2.56	3.1.63	3.1.65	3.1.71	3.2.51	3.1.69	3.1.63	7.1.65	6.4.72	3.0.56	5.2.68	-.-.-	1	3
38 Manduca1508	8.1.58	6.0.61	6.0.66	6.0.61	6.0.68	5.1.55	4.0.65	4.0.68	6.2.69	4.1.54	6.2.71	6.2.64	6.0.63	9.3.76	6.1.53	6.1.73	3.1.20	-.-.-	2
39 Manduca1876	7.1.61	5.0.62	5.0.62	5.0.62	5.0.70	6.1.43	5.0.59	5.0.62	7.2.69	5.1.45	7.2.66	7.2.62	7.0.66	8.3.76	7.1.48	7.1.70	4.1.41	3.0.43	-.-.-
40 ManducaAF234571	7.1.58	5.0.58	5.0.59	5.0.57	5.0.67	6.1.44	5.0.60	5.0.63	7.2.65	5.1.48	7.2.62	7.2.57	7.0.65	8.3.72	7.1.49	7.1.66	4.1.43	3.0.41	0.0.14
41 Marumba0118	6.0.86	6.1.85	6.1.88	6.1.90	6.1.94	3.2.87	6.1.86	6.1.84	4.1.95	2.2.82	4.1.89	4.1.98	8.1.91	5.4.83	2.0.88	6.2.99	3.0.84	6.1.85	7.1.85
42 Mimas5836	6.1.61	8.2.68	8.2.70	8.2.66	8.2.76	5.3.76	8.2.65	8.2.67	6.2.66	6.3.68	6.2.65	6.2.70	8.2.72	7.3.66	4.1.73	6.1.69	7.1.67	8.2.74	11.2.65
43 Nyceryx2378	3.1.41	1.0.41	1.0.51	1.0.47	1.0.61	4.1.69	3.0.57	3.0.57	3.2.54	3.1.59	3.2.58	3.2.61	3.0.46	8.3.73	5.1.74	3.1.56	4.1.67	5.0.65	4.0.66
44 Pachylia1644	2.1.37	0.0.42	0.0.51	0.0.47	0.0.57	3.1.65	4.0.51	4.0.49	4.2.51	4.1.55	4.2.56	4.2.60	2.0.53	9.3.68	6.1.71	4.1.52	5.1.63	6.0.63	5.0.62
45 PachysphinxAF234	8.3.77	8.2.77	8.2.80	8.2.82	8.2.87	7.3.79	6.2.87	6.2.88	6.4.77	4.3.72	6.4.78	6.4.79	10.2.85	3.3.44	6.3.78	4.1.80	7.3.79	8.2.79	7.2.79
46 Pachysphinx1528	8.3.84	8.2.83	8.2.87	8.2.89	8.2.92	7.3.86	6.2.94	6.2.95	6.4.82	4.3.79	6.4.83	6.4.85	10.2.91	3.3.50	6.3.87	4.1.87	7.3.86	8.2.83	7.2.86
47 PaoniasAF234572	8.2.69	10.1.73	10.1.76	10.1.80	10.1.81	7.2.70	8.1.82	8.1.82	6.3.72	6.2.71	6.3.67	6.3.71	12.1.81	1.2.35	6.2.79	6.0.77	7.2.74	10.1.75	9.1.76
48 Paonias1540	12.3.71	10.2.75	10.2.79	10.2.82	10.2.82	9.3.72	10.2.85	10.2.85	10.3.75	6.2.73	10.3.71	10.3.74	10.2.83	3.2.36	8.3.84	8.1.82	9.3.76	8.2.79	9.2.81
49 Paratrea1939	5.1.56	3.0.56	3.0.62	3.0.61	3.0.68	4.1.51	5.0.64	5.0.67	5.2.66	3.1.55	5.2.62	5.2.58	5.0.64	8.3.68	3.1.48	5.1.62	4.1.49	5.0.49	4.0.42
50 Perigonia2191	3.0.33	3.1.32	3.1.47	3.1.45	3.1.55	4.2.64	5.1.52	5.1.52	3.1.49	3.2.59	3.1.53	3.1.53	5.1.44	6.4.69	3.0.72	5.2.49	4.0.58	7.1.62	6.1.59
51 ProserpinusAF173	4.1.40	3.0.43	3.0.46	3.0.44	3.0.49	3.1.64	2.0.52	2.0.53	2.2.44	2.1.52	2.2.45	2.2.50	5.0.51	6.3.62	4.1.58	2.1.52	3.1.54	2.0.55	3.0.49
52 Protambulyx1945	2.1.54	4.0.60	4.0.66	4.0.62	4.0.70	3.1.72	6.0.66	6.0.68	4.2.57	6.1.64	4.2.51	4.2.55	6.0.68	9.3.64	6.1.77	6.1.64	5.1.67	8.0.68	7.0.69
53 Pseudoclanis5839	8.3.70	6.2.70	6.2.81	5.2.80	6.2.83	6.3.82	6.2.72	6.2.73	6.3.69	3.2.71	6.3.68	6.3.66	8.2.73	6.2.75	5.3.78	6.3.79	6.3.73	7.2.75	6.2.70
54 Psilogramma5988	6.1.57	4.0.59	4.0.60	4.0.62	4.0.66	3.1.53	4.0.55	4.0.56	4.2.65	0.1.59	4.2.60	4.2.59	6.0.71	5.3.77	2.1.65	4.1.67	3.1.59	4.0.59	5.0.47
55 SmerinthusAF2345	9.3.73	11.2.77	11.2.85	11.2.84	11.2.90	8.3.71	9.2.82	9.2.85	7.4.74	7.3.65	7.4.77	7.4.77	11.2.85	2.3.36	7.3.77	7.1.82	8.3.74	9.2.73	10.2.72
56 Smerinthus1511	8.3.76	10.2.83	10.2.90	10.2.87	10.2.95	7.3.77	8.2.88	8.2.91	6.4.79	6.3.73	6.4.82	6.4.81	12.2.90	1.3.40	6.3.86	6.1.87	7.3.81	10.2.81	9.2.81
57 SphinxAF234577	7.1.63	5.0.69	5.0.73	5.0.67	5.0.81	4.1.53	5.0.72	5.0.74	5.2.69	1.1.56	5.2.68	5.2.67	7.0.69	6.3.83	1.1.31	5.1.73	4.1.52	5.0.51	6.0.45
58 Sphinx1532	5.1.68	5.0.72	5.0.76	5.0.73	5.0.83	2.1.64	5.0.75	5.0.77	3.2.70	3.1.59	3.2.71	3.2.70	7.0.77	6.3.80	1.1.40	5.1.75	2.1.62	5.0.59	6.0.52
59 Sphinx1591	8.2.62	8.1.63	8.1.75	8.1.70	8.1.83	5.2.55	8.1.70	8.1.72	6.3.66	4.2.52	6.3.64	6.3.62	10.1.67	5.4.79	2.2.34	6.2.72	5.2.50	8.1.50	9.1.45
60 Sphinx1938	7.1.63	5.0.67	5.0.74	5.0.67	5.0.80	4.1.57	5.0.71	5.0.73	5.2.72	1.1.58	5.2.72	5.2.71	7.0.69	6.3.85	1.1.38	5.1.71	4.1.52	5.0.52	6.0.48
61 SphecodinaAF2345	4.0.53	4.1.63	4.1.60	4.1.60	4.1.65	5.2.75	6.1.56	6.1.56	4.1.58	6.2.65	4.1.55	4.1.67	6.1.72	9.4.79	4.0.67	6.2.69	5.0.65	6.1.68	5.1.63
62 Theretra5880	3.1.65	5.2.68	5.2.71	5.2.66	5.2.79	4.3.78	3.2.67	3.2.69	1.0.37	3.1.66	1.0.39	1.0.38	7.2.72	6.3.74	3.1.81	3.3.55	4.1.75	7.2.73	8.2.73
63 Unzela2376	1.0.37	3.1.37	3.1.54	3.1.50	3.1.64	4.2.68	5.1.53	5.1.53	3.1.45	5.2.62	3.1.44	3.1.55	5.1.47	8.4.71	5.0.70	3.3.43	6.0.67	9.1.66	8.1.66
64 Xylophanes5904	3.1.45	5.2.52	5.2.55	5.2.49	5.2.63	4.3.73	3.2.56	3.2.57	1.0.22	5.1.55	1.0.26	1.0.26	5.2.62	8.3.63	5.1.70	3.3.43	4.1.69	5.2.67	8.2.65
65 XylophanesAF2345	2.1.51	4.2.54	4.2.60	4.2.57	4.2.70	3.3.76	2.2.58	2.2.59	0.0.24	4.1.61	0.0.29	0.0.29	6.2.63	7.3.71	4.1.70	2.3.49	3.1.73	6.2.69	7.2.68
66 Xylophanes2369	2.1.57	4.2.59	4.2.69	4.2.64	4.2.77	3.3.79	2.2.60	2.2.61	0.0.32	4.1.64	0.0.34	0.0.36	6.2.68	7.3.69	4.1.76	2.3.53	3.1.75	6.2.75	7.2.73
67 Xylophanes1879	2.1.52	4.2.61	4.2.65	4.2.58	4.2.71	3.3.83	2.2.66	2.2.67	0.0.27	4.1.67	0.0.33	0.0.36	5.2.70	7.3.76	4.1.79	2.3.59	3.1.77	5.2.75	7.2.79
68 Attacini	6.1.144	4.0.142	4.0.140	4.0.141	4.0.143	7.1.143	8.0.139	8.0.138	8.2.144	8.1.130	8.2.135	8.2.130	6.0.152	13.3.135	8.1.137	8.1.137	9.1.140	8.0.142	7.0.133
69 Bombycidae	7.4.143	5.3.146	5.3.147	5.3.140	5.3.141	8.4.143	9.3.144	9.3.141	9.3.152	9.2.132	9.3.145	9.3.147	7.3.148	10.4.141	11.4.149	9.4.151	10.4.142	9.3.138	6.3.138
70 Brahmaeidae	4.2.124	4.1.130	4.1.125	4.1.127	4.1.132	5.2.126	2.1.115	2.1.114	2.1.135	4.0.126	2.1.125	2.1.129	6.1.134	9.2.133	6.2.138	2.2.131	5.2.138	6.1.135	7.1.129
71 Bunaeini	5.0.155	5.1.157	5.1.155	5.1.153	5.1.156	6.2.150	9.1.146	9.1.143	7.1.154	9.2.141	7.1.148	7.1.144	7.1.162	10.4.141	9.0.147	9.2.152	8.0.149	11.1.146	10.1.145
72 Ceratocampinae	6.1.104	4.0.107	4.0.114	4.0.111	4.0.120	5.1.117	4.0.125	4.0.121	4.2.118	4.1.110	4.2.112	4.2.110	6.0.112	7.3.126	6.1.115	2.1.114	5.1.118	6.0.119	7.0.119
73 Endromidae	3.1.113	5.2.110	5.2.116	5.2.112	5.2.120	4.3.118	5.2.115	5.2.114	3.0.112	7.1.112	3.0.115	3.0.117	7.2.112	8.3.104	7.1.116	5.3.114	6.1.116	9.2.117	10.2.116
74 Gastropachini	8.1.90	8.0.106	8.0.101	7.0.97	8.0.103	8.1.107	10.0.106	10.0.106	10.2.100	11.1.98	10.2.100	10.2.99	8.0.110	14.3.109	11.1.107	12.1.102	8.1.102	11.0.103	10.0.113
75 Hemileucini	5.0.81	6.1.87	6.1.99	6.1.92	6.1.99	4.2.99	7.1.93	7.1.93	5.1.85	7.2.86	5.1.94	5.1.90	8.1.86	7.4.98	7.0.97	5.2.93	6.0.93	9.1.93	10.1.95
76 Lasiocampini	5.3.126	5.2.126	5.2.130	4.2.126	5.2.130	5.3.127	7.2.124	7.2.121	7.2.127	8.1.124	7.2.123	7.2.125	5.2.123	11.3.116	8.3.124	9.3.127	5.3.123	8.2.125	7.2.121
77 Lemoniidae	4.2.131	4.1.140	4.1.135	4.1.132	4.1.141	5.2.133	2.1.128	2.1.127	2.1.134	4.0.128	2.1.127	2.1.132	6.1.141	9.2.138	6.2.135	2.2.134	5.2.143	6.1.137	7.1.133
78 Macromphaliinae	7.2.132	7.1.132	7.1.140	7.1.136	7.1.141	6.2.140	7.1.127	7.1.128	7.1.136	9.0.135	7.1.140	7.1.136	7.1.136	12.2.130	7.2.139	9.2.131	6.2.136	7.1.136	10.1.139
79 Malacosomatini	10.3.115	10.2.124	10.2.119	10.2.119	10.2.123	13.3.116	8.2.125	8.2.125	10.2.126	12.1.118	10.2.121	10.2.124	10.2.128	17.3.115	14.3.122	10.3.118	11.3.122	12.2.121	11.2.116
80 Micragonini	5.1.134	5.2.142	5.2.125	5.2.132	5.2.132	4.3.130	7.2.135	7.2.134	5.2.131	7.3.122	5.2.133	5.2.126	7.2.149	8.5.134	7.1.128	7.3.137	6.1.141	9.2.137	10.2.128
81 Polythysanini	5.4.119	5.3.126	5.3.126	5.3.126	5.3.129	4.4.122	7.3.118	7.3.117	5.5.124	7.4.118	5.5.119	5.5.117	7.3.137	8.4.121	7.4.129	5.4.129	6.4.124	7.3.124	8.3.129
82 Saturniini	10.2.130	8.1.132	8.1.128	7.1.132	8.1.129	8.2.133	8.1.127	8.1.124	8.3.134	7.2.119	8.3.126	8.3.123	8.1.145	12.2.131	9.2.132	8.2.139	8.2.135	5.1.133	8.1.123
83 Agaraninae	6.1.85	6.2.84	6.2.94	6.2.91	6.2.96	7.3.97	8.2.89	8.2.86	6.0.94	6.1.95	6.0.83	6.0.87	8.2.93	7.3.100	6.1.100	8.3.83	7.1.99	10.2.97	9.2.96
84 Arctiinae	6.2.117	4.1.109	4.1.117	4.1.118	4.1.119	5.2.124	4.1.111	4.1.108	4.1.113	4.0.110	4.1.112	4.1.107	6.1.116	7.2.123	6.2.126	4.2.120	5.2.121	6.1.120	7.1.117
85 Baroniinae	7.3.147	6.2.146	6.2.153	6.2.152	6.2.152	6.3.138	6.2.143	6.2.141	6.2.148	6.1.138	6.2.143	6.2.146	8.2.138	8.3.146	8.3.135	6.3.143	7.3.136	8.2.137	9.2.138
86 Catocalinae	6.0.92	6.1.97	6.1.96	6.1.92	6.1.99	5.2.100	6.1.96	6.1.93	4.1.95	4.2.101	4.1.91	4.1.85	8.1.104	7.4.102	4.0.111	6.2.91	5.0.106	8.1.107	9.1.100
87 Coliadinae	7.1.88	6.0.80	6.0.88	6.0.85	6.0.90	8.1.87	7.0.89	7.0.87	7.2.87	7.1.84	7.2.81	7.2.80	6.0.85	9.3.86	9.1.86	7.1.84	8.1.88	9.0.90	6.0.85
88 Condicinae	4.1.83	4.2.79	4.2.102	4.2.96	4.2.105	5.3.96	8.2.93	8.2.90	6.0.91	6.1.99	6.0.91	6.0.86	6.2.87	9.3.101	6.1.96	8.3.94	7.1.97	10.2.96	9.2.90
89 Crambidae	8.8.70	7.7.77	7.7.83	7.7.74	7.7.85	9.8.84	8.7.75	8.7.75	8.7.78	6.6.78	8.7.78	8.7.77	9.7.88	8.8.94	8.8.82	8.8.71	9.8.78	10.7.79	7.7.78
90 Cyrestinae	9.1.104	11.2.105	11.2.112	11.2.109	11.2.110	11.3.112	10.2.106	10.2.104	8.0.109	10.1.95	8.0.102	8.0.105	11.2.111	7.3.110	9.1.112	8.3.108	11.1.106	14.2.112	12.2.102
91 Danainae	5.3.119	7.4.113	7.4.121	7.4.118	7.4.126	6.5.120	7.4.127	7.4.123	5.2.123	9.3.119	5.2.115	5.2.113	9.4.116	10.5.122	9.3.131	7.5.118	8.3.121	11.4.120	10.4.117
92 Galleriinae	10.2.142	10.1.144	10.1.146	9.1.144	10.1.147	12.2.134	8.1.134	8.1.138	10.1.143	11.0.136	10.1.144	10.1.140	10.1.143	12.2.131	11.2.138	10.2.139	10.2.139	11.1.139	8.1.137
93 Geometroidea	7.1.95	8.2.93	8.2.102	8.2.95	8.2.98	6.3.96	9.2.99	9.2.98	7.2.94	9.3.97	7.2.99	7.2.89	8.2.101	9.5.112	9.1.96	9.3.103	8.1.100	11.2.99	10.2.97
94 Hedyloidea	5.2.88	4.1.99	4.1.98	4.1.99	4.1.99	4.2.104	5.1.95	5.1.96	5.3.94	5.2.97	5.3.98	5.3.97	4.1.104	9.4.106	7.2.100	5.2.99	6.2.98	7.1.101	8.1.98
95 Heliconiinae	10.3.114	10.4.119	10.4.126	10.4.118	10.4.127	9.5.109	11.4.116	11.4.114	9.2.123	9.3.109	9.2.117	9.2.112	12.4.120	10.5.126	7.3.114	11.5.117	10.3.117	13.4.118	12.4.106
96 Heliothinae	6.2.81	6.3.80	6.3.97	6.3.92	6.3.102	5.4.89	6.3.90	6.3.87	4.1.86	4.2.84	4.1.89	4.1.85	8.3.94	7.4.96	4.2.92	6.4.89	5.2.91	8.3.92	9.3.87
97 Hesperiinae	5.2.69	4.1.76	4.1.78	4.1.72	4.1.79	4.2.85	3.1.78	3.1.78	3.1.74	3.0.73	3.1.69	3.1.66	6.1.85	7.2.84	5.2.81	3.2.69	4.2.81	5.1.84	6.1.82
98 Heterocampinae	4.1.79	4.2.81	4.2.100	4.2.96	4.2.103	3.3.99	4.2.91	4.2.87	2.0.85	2.1.91	2.0.88	2.0.85	6.2.89	5.3.102	2.1.97	4.3.93	3.1.96	6.2.94	7.2.94
99 Lithosiinae	3.1.146	3.2.143	3.2.147	3.2.152	3.2.145	4.3.146	7.2.145	7.2.142	5.0.147	7.1.136	5.0.148	5.0.141	5.2.147	10.3.148	7.1.146	7.3.141	6.1.147	9.2.147	8.2.139
100 Lymantriidae	9.1.146	9.0.147	9.0.144	9.0.144	9.0.142	10.1.146	11.0.133	11.0.131	9.2.145	11.1.138	9.2.148	9.2.149	11.0.154	8.3.136	9.1.150	11.1.147	10.1.143	11.0.143	8.0.138
101 Micropterigoidea	3.1.59	4.2.62	4.2.60	4.2.58	4.2.61	3.2.62	6.2.61	6.2.61	4.1.57	6.2.53	4.1.59	4.1.61	4.2.64	6.3.63	5.1.62	5.2.63	5.1.61	8.2.62	7.2.62
102 Noctuinae	2.3.90	4.4.93	4.4.102	4.4.104	4.4.104	3.5.95	4.4.95	4.4.92	2.2.105	6.3.92	2.2.97	2.2.90	6.4.101	9.3.104	6.3.101	4.5.92	5.3.93	8.4.97	9.4.88
103 Nolinae	8.1.118	8.0.113	8.0.122	8.0.115	8.0.122	7.1.114	8.0.110	8.0.109	6.2.117	8.1.120	6.2.110	6.2.112	8.0.121	9.3.120	6.1.120	8.1.116	7.1.121	10.0.120	9.0.116
104 Notodontinae	4.1.97	4.2.100	4.2.104	4.2.103	4.2.107	3.3.97	4.2.95	4.2.92	2.0.101	4.1.95	2.0.93	2.0.97	6.2.105	5.3.96	4.1.94	4.3.107	3.1.94	6.2.96	7.2.83
105 Nymphalinae	9.4.125	11.5.130	11.5.131	11.5.131	11.5.127	10.6.120	10.5.123	10.5.121	8.3.129	10.4.111	8.3.127	8.3.121	11.5.132	9.6.121	10.4.126	10.6.127	11.4.124	14.5.123	13.5.120
106 Nystaleinae	2.0.72	4.1.66	4.1.78	4.1.79	4.1.84	3.2.82	4.1.81	4.1.77	2.1.74	6.2.86	2.1.77	2.1.78	6.1.79	7.4.88	6.0.84	2.2.73	5.0.93	8.1.89	9.1.85
107 Oncocnemidinae	4.1.79	4.2.75	4.2.86	4.2.88	4.2.90	5.3.95	6.2.79	6.2.76	4.0.81	6.1.88	4.0.80	4.0.76	6.2.90	7.3.97	6.1.95	6.3.82	5.1.91	8.2.90	5.2.89
108 Pantheinae	6.2.107	6.3.105	6.3.118	6.3.116	6.3.114	5.4.117	8.3.103	8.3.103	6.1.104	6.2.113	6.1.104	6.1.97	8.3.115	7.4.116	6.2.117	8.4.116	7.2.115	10.3.119	11.3.121
109 Papilioninae	8.3.115	6.2.109	6.2.113	5.2.115	6.2.118	6.3.107	6.2.98	6.2.97	6.2.111	5.1.101	6.2.107	6.2.102	6.2.110	8.1.120	7.3.103	6.1.112	6.3.103	7.2.101	6.2.95
110 Parnassiinae	4.3.115	3.2.115	3.2.123	3.2.123	3.2.119	5.3.113	4.2.114	4.2.113	4.2.110	4.1.108	4.2.105	4.2.104	5.2.115	4.1.114	6.3.119	4.1.110	5.3.119	6.2.115	3.2.116
111 Phalerinae	6.1.96	6.2.93	6.2.103	6.2.96	6.2.111	5.3.100	6.2.91	6.2.92	4.0.92	4.1.102	4.0.95	4.0.98	6.2.99	7.3.108	4.1.105	6.3.99	5.1.104	6.2.100	9.2.93
112 Pierinae	7.4.122	8.3.111	8.3.119	8.3.113	8.3.113	6.4.114	7.3.123	7.3.121	5.3.118	7.2.105	5.3.111	5.3.110	10.3.116	7.4.119	5.4.112	7.4.107	6.4.113	9.3.112	8.3.115
113 Polyommatinae	8.3.86	9.4.90	9.4.98	9.4.94	9.4.103	7.5.107	9.4.100	9.4.100	7.2.91	9.3.94	7.2.90	7.2.93	11.4.97	9.5.107	7.3.110	9.5.92	8.3.98	11.4.101	10.4.102
114 Pyraustinae	7.2.82	7.1.83	7.1.88	7.1.89	7.1.86	9.2.84	6.1.90	6.1.90	6.3.90	8.2.78	6.3.83	6.3.83	9.1.85	10.4.87	10.2.84	6.2.91	9.2.81	10.1.88	8.1.83
115 Pyrginae	3.1.91	4.2.94	4.2.102	4.2.96	4.2.100	2.3.108	5.2.104	5.2.104	3.0.102	5.1.95	3.0.92	3.0.92	6.2.104	7.3.99	5.1.95	5.3.88	4.1.96	7.2.104	8.2.99
116 Riodininae	10.3.135	11.4.134	11.4.139	11.4.136	11.4.137	11.5.125	12.4.132	12.4.130	12.2.133	14.3.117	12.2.132	12.2.125	11.4.141	10.3.126	12.3.125	12.3.131	11.3.121	12.4.127	11.4.123
117 Satyrinae	8.3.116	8.4.122	8.4.119	8.4.119	8.4.118	7.5.111	8.4.116	8.4.115	6.2.121	6.3.104	6.2.116	6.2.110	8.4.116	7.5.116	6.3.110	8.5.117	7.3.115	10.4.115	9.4.113
118 Stictopterinae	5.0.80	5.1.79	5.1.96	5.1.90	5.1.98	6.2.96	7.1.92	7.1.89	5.1.85	5.2.100	5.1.85	5.1.85	7.1.94	8.4.101	5.0.102	7.2.87	6.0.104	9.1.104	8.1.102

Table 17. (continued)

Table 17. (continued)

Table 18. Empirical pairwise distance matrix for DDC data. Uncorrected pairwise distances are reported for every comparison of the 1,329bp DDC sequences across the 105 taxon EF data matrix. Values in each cell below the diagonal are nucleotide distances tabulated separately for each codon position, in the format 'nt1.nt2.nt3'. Values above the diagonal are amino acid distances calculated from the comparisons of the 443 residue sequences obtained after conceptual translation of nucleotide data. Intra-Sphingidae comparisons (ntax=65) are boxed in the upper left quadrant of the matrix. Intra-Bombycoidea comparisons (ntax=8) are separated from other Lepidoptera by a line after taxon #73 (Saturniini).

DDC	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
1 Acherontia5989	-.-.-	26	38	22	8	23	36	31	39	39	39	13	11	24	30	38	31	28	30	19	38	35	33	22	31	15	31	21	38	20	31	32
2 Adhemarius1642	25.11.206	-.-.-	37	18	21	20	37	29	39	39	37	22	20	25	33	40	38	25	40	26	37	29	33	20	31	18	28	16	39	18	36	35
3 Aellopos2399	33.16.215	29.13.220	-.-.-	3	36	35	26	15	32	32	33	38	34	42	25	27	26	17	28	35	34	21	29	16	27	37	25	13	29	37	26	24
4 AelloposAF234582	23.9.114	19.6.125	4.0.28	-.-.-	20	19	15	3	16	16	17	21	21	23	14	18	16	16	19	20	18	7	16	15	15	18	12	12	19	18	18	16
5 Agrius1941	9.3.99	24.8.206	36.15.219	25.8.121	-.-.-	18	36	30	37	37	36	8	8	18	24	34	31	23	33	18	35	34	31	20	29	9	27	17	37	14	29	32
6 Amorpha1595	23.9.169	22.8.154	27.15.205	21.6.109	24.6.181	-.-.-	30	28	42	42	34	17	17	22	26	35	31	22	34	24	36	34	32	22	30	20	29	16	35	15	28	28
7 Basiothia0005	34.15.215	34.10.209	26.11.182	19.4.96	35.14.210	30.12.190	-.-.-	20	38	38	38	35	34	32	25	23	8	11	11	33	27	26	21	15	21	37	28	19	9	35	7	7
8 Callionima0966	28.11.230	31.8.226	17.7.158	6.2.90	31.10.218	27.9.207	28.8.165	-.-.-	27	27	26	30	30	33	27	24	22	15	23	31	25	13	19	13	19	30	18	11	27	28	22	21
9 Cautethia2573	39.17.213	34.12.219	28.17.197	17.8.100	38.14.209	36.14.216	36.14.191	28.12.206	-.-.-	0	38	40	32	44	31	33	36	22	35	35	31	32	28	14	26	38	31	16	39	40	33	32
10 Cautethia1668	39.17.215	34.12.220	28.17.198	17.8.100	38.14.210	36.14.217	36.14.192	28.12.206	0.0.0	-.-.-	38	40	32	44	31	33	36	22	35	35	31	32	28	14	26	38	31	16	39	40	33	32
11 Cephonodes5931	41.14.220	37.11.204	30.10.206	17.6.109	39.11.226	36.11.207	39.13.188	29.9.202	34.14.196	34.14.196	-.-.-	39	36	40	37	40	38	26	41	39	32	35	30	20	30	40	15	8	45	35	38	38
12 Ceratomia1870	12.6.118	25.9.186	29.16.194	19.7.111	13.3.123	19.4.172	28.13.198	26.9.214	33.15.210	33.15.212	35.12.223	-.-.-	6	19	27	34	31	25	33	14	36	33	34	24	32	8	30	20	36	13	28	31
13 CeratomiaAF23458	11.5.84	19.8.151	26.13.156	21.7.114	11.2.93	16.4.132	27.12.156	25.10.171	29.12.162	29.12.163	29.11.171	4.1.27	-.-.-	17	25	34	30	22	31	12	33	33	31	23	29	5	30	20	34	11	28	29
14 Cocytius2359	16.8.144	21.9.208	33.16.201	23.7.105	17.5.153	21.7.179	32.11.203	28.11.228	39.15.215	39.15.216	41.12.226	14.4.132	11.3.102	-.-.-	28	34	30	20	28	22	34	38	30	20	30	15	33	20	35	16	27	30
15 Coelonia5816	32.9.164	27.8.195	21.11.186	14.4.99	31.6.164	30.8.175	25.10.157	29.8.192	29.12.204	29.12.204	36.9.194	30.7.160	25.6.126	30.7.177	-.-.-	20	22	10	22	28	32	30	27	14	25	27	26	15	26	29	19	20
16 Daphnis5810	33.17.211	33.14.205	22.16.174	17.10.100	32.14.203	29.14.175	23.9.156	23.12.189	27.14.194	27.14.194	34.15.205	29.13.193	28.12.159	29.13.199	19.10.166	-.-.-	19	14	19	35	28	31	23	16	21	34	31	23	24	36	17	18
17 Darapsa1778	30.13.214	36.10.199	25.8.169	18.2.90	33.12.200	30.10.191	10.2.87	26.6.170	35.12.167	35.12.168	39.10.175	26.11.195	26.10.158	28.11.195	26.7.155	21.7.156	-.-.-	7	9	30	23	26	19	13	19	34	28	19	9	33	2	6
18 DarapsaAF234585	24.9.170	27.4.136	15.6.126	16.4.96	25.6.153	22.4.134	13.4.89	14.2.123	21.8.122	21.8.123	25.6.139	19.5.154	16.5.113	18.5.155	14.2.106	11.7.120	6.3.62	-.-.-	10	21	17	18	18	15	17	23	16	15	11	22	6	9
19 Deilephila5866	31.13.217	35.11.198	25.12.172	18.6.103	34.13.196	31.13.170	8.3.94	26.9.173	37.15.178	37.15.178	41.14.184	25.12.198	26.11.171	27.10.188	25.9.153	20.8.137	6.3.85	6.6.79	-.-.-	31	25	30	20	15	20	34	29	23	13	35	9	11
20 DolbaAF234598	13.9.97	20.11.151	26.14.164	20.8.114	12.7.107	18.7.131	27.13.156	24.11.166	30.12.160	30.12.161	29.12.173	6.6.52	6.5.51	11.6.114	25.7.144	27.13.164	25.11.161	14.6.110	27.12.171	-.-.-	36	34	33	23	31	15	34	22	34	16	29	29
21 Enyo2390	31.18.216	35.13.209	27.14.177	18.7.104	33.15.207	29.13.207	31.11.177	21.11.188	29.12.212	29.12.213	35.10.207	30.14.197	26.12.148	32.14.208	33.13.184	23.13.194	27.9.176	19.6.137	29.12.177	25.13.157	-.-.-	28	10	4	10	38	26	16	28	36	22	25
22 Erinnyis1542	33.11.210	33.6.225	21.7.167	10.2.88	35.10.215	33.10.204	35.8.177	17.2.177	27.12.221	27.12.221	34.9.213	32.11.214	27.10.172	33.11.219	26.8.193	31.11.178	32.6.185	21.2.134	32.9.172	29.11.175	22.11.186	-.-.-	26	15	24	34	27	16	24	32	26	25
23 Eumorpha1533	32.12.221	31.11.197	22.12.175	17.6.97	31.11.207	29.11.182	24.7.166	19.7.177	24.10.188	24.10.189	30.10.210	28.10.203	25.9.165	28.10.197	22.9.191	16.9.177	22.5.160	14.6.103	24.6.163	24.10.156	16.6.167	24.7.200	-.-.-	1	2	34	22	16	24	33	20	19
24 EumorphaAF234588	23.9.125	21.8.121	17.6.94	19.6.93	21.8.118	19.8.103	12.6.87	17.4.104	14.5.97	14.5.97	20.8.124	19.7.121	20.7.117	21.7.108	12.6.93	9.9.103	13.5.86	14.6.78	15.6.93	18.8.120	10.3.94	16.4.110	2.0.30	-.-.-	0	21	15	15	15	23	15	12
25 Eumorpha1504	32.12.222	31.11.196	22.12.172	17.6.98	31.11.211	29.11.179	24.7.159	19.7.177	24.10.189	24.10.191	30.10.205	28.10.201	25.9.160	28.10.199	22.9.185	16.9.183	22.5.159	14.6.107	24.6.155	24.10.153	16.6.169	24.7.200	0.0.27	2.0.31	-.-.-	32	22	15	22	31	20	17
26 Euryglottis2891	11.7.114	20.10.194	28.17.194	19.7.114	12.4.127	18.6.162	33.14.195	25.12.214	34.16.205	34.16.207	36.13.223	5.3.43	3.1.30	9.5.129	29.8.161	28.14.204	29.12.192	19.6.154	28.13.203	5.6.43	31.15.199	29.12.211	29.11.203	21.7.115	29.11.199	-.-.-	31	17	38	11	30	33
27 Hemaris1882	34.14.222	29.9.208	21.8.194	12.4.106	33.11.210	31.11.201	30.11.181	20.7.195	27.13.195	27.13.195	13.4.66	28.12.211	25.11.160	32.12.225	27.7.182	25.13.192	30.8.177	17.4.134	28.12.175	25.12.169	26.12.198	25.7.210	22.10.196	16.8.113	22.10.191	27.13.214	-.-.-	0	35	28	27	28
28 HemarisAF234590	21.11.115	17.6.114	12.4.109	12.4.106	19.8.110	19.6.107	16.8.102	10.4.111	13.8.106	13.8.106	7.2.32	15.7.120	17.7.118	19.7.118	14.4.83	16.11.101	17.6.91	14.4.98	17.10.97	16.8.125	18.7.116	14.4.122	14.8.111	16.8.114	14.8.111	15.7.122	0.0.4	-.-.-	23	17	19	18
29 Hippotion5932	36.16.213	36.11.204	30.12.181	22.4.100	37.15.215	32.12.189	4.1.58	32.8.174	38.15.197	38.15.198	43.14.191	30.13.204	28.13.159	34.12.213	27.11.169	25.10.159	9.3.109	12.4.93	8.4.110	29.14.161	29.12.192	35.9.180	24.8.174	11.6.87	24.8.167	35.15.205	34.12.183	19.8.100	-.-.-	38	9	8
30 Hopliocnema0233	14.9.155	17.8.190	29.13.206	20.4.117	13.6.161	17.4.161	32.10.217	28.8.219	35.12.201	35.12.202	35.9.229	10.5.129	7.4.95	10.5.153	30.6.182	29.12.193	30.8.201	21.2.145	31.11.203	9.5.107	32.11.210	34.8.229	28.9.202	20.6.116	28.9.202	7.6.134	28.9.206	16.4.117	34.11.220	-.-.-	30	33
31 Hyles5817	26.14.209	34.9.192	26.10.172	19.4.100	29.11.203	26.9.169	10.3.79	27.7.182	33.11.176	33.11.177	40.10.186	21.10.190	23.9.160	24.10.188	24.7.146	19.6.117	3.1.73	7.2.82	7.4.81	22.10.164	26.8.174	32.7.183	23.6.162	12.6.92	23.6.159	24.11.191	31.8.180	18.6.101	10.4.92	26.7.194	-.-.-	5
32 Hyles1881	29.14.215	35.9.192	24.11.179	17.5.95	32.13.204	27.11.192	10.2.84	27.7.178	33.13.190	33.13.192	40.12.194	25.12.197	24.11.153	27.10.191	25.9.161	21.7.161	6.2.77	10.4.79	10.3.83	23.12.155	28.10.186	34.7.184	23.6.168	11.6.88	23.6.166	28.13.198	31.10.192	17.8.106	12.3.96	29.9.199	2.3.45	-.-.-
33 Isognathus1646	22.7.157	23.5.163	13.5.122	9.3.86	21.7.161	22.5.165	21.5.127	5.1.129	20.9.148	20.9.150	21.7.169	21.6.150	18.6.109	22.6.165	21.5.148	18.10.144	18.4.130	17.3.121	18.5.128	19.7.117	17.7.142	9.1.79	17.5.138	18.5.105	17.5.135	19.7.153	13.5.169	11.5.123	22.5.133	19.3.163	19.5.130	21.5.130
34 Laothoe0012	21.7.172	18.5.149	28.11.197	18.5.106	22.4.180	14.4.123	37.12.190	23.8.202	34.12.203	34.12.203	35.9.200	17.5.169	13.4.128	15.7.172	28.6.165	29.14.174	35.10.195	20.3.128	34.13.180	15.7.126	30.13.209	29.7.205	25.11.186	18.7.104	25.11.182	12.6.163	26.7.196	14.5.105	39.13.183	15.4.163	31.9.179	32.11.189
35 Lapara1670	13.4.127	24.9.203	31.16.202	23.8.113	14.1.139	18.5.178	31.13.200	29.11.217	37.15.209	37.15.210	38.12.227	9.2.80	7.1.58	15.4.136	32.7.177	32.13.209	31.11.202	23.6.150	32.12.205	9.6.77	31.14.220	34.11.223	31.10.194	21.8.111	31.10.195	8.3.66	31.12.206	19.8.107	33.14.202	11.5.149	26.10.198	28.12.201
36 Macroglossum5806	36.12.220	35.9.193	19.10.172	15.4.104	37.9.192	31.9.186	20.7.145	25.7.181	30.13.190	30.13.191	30.8.182	30.8.193	30.7.155	34.8.203	14.3.90	16.7.164	18.4.126	10.2.91	18.6.137	31.8.163	28.10.177	31.7.187	18.6.157	13.6.98	18.6.158	31.9.193	20.6.166	15.4.91	22.8.152	32.7.197	19.4.133	20.6.133
37 Manduca1529	14.4.123	23.9.202	29.16.201	20.8.116	13.1.135	21.5.177	32.13.210	28.11.216	33.15.213	33.15.215	35.12.231	6.2.62	5.1.47	14.4.134	28.7.173	29.13.202	30.11.208	21.6.159	31.12.207	5.6.51	32.14.209	32.11.222	28.10.206	18.8.122	28.10.204	5.3.53	28.12.214	14.8.118	34.14.211	8.5.138	25.10.198	29.12.208
38 Manduca1508	13.5.118	22.10.189	28.17.201	20.9.119	12.2.136	20.6.171	31.14.204	27.12.216	32.15.211	32.15.213	34.13.230	5.3.62	4.2.48	13.5.136	27.8.172	28.14.202	29.12.206	21.7.153	30.13.205	4.5.49	31.15.204	31.12.219	27.11.208	18.9.122	27.11.206	4.4.53	27.13.215	14.9.121	33.15.206	7.6.139	24.11.195	28.13.206
39 Manduca1876	17.7.129	24.8.196	33.13.208	20.5.116	18.4.129	22.4.179	34.10.200	30.8.220	35.12.216	35.12.218	38.9.224	7.3.69	7.2.56	17.3.146	32.4.178	33.10.199	30.8.206	22.3.152	31.9.205	5.3.53	32.11.215	32.8.228	30.7.202	18.5.116	30.7.194	8.4.64	31.9.215	17.5.122	34.11.208	13.2.155	25.7.196	29.9.200
40 ManducaU03909	15.8.134	22.7.197	32.12.209	21.4.114	14.5.136	20.3.179	33.9.204	29.7.226	34.11.213	34.11.215	36.8.225	7.4.70	6.3.58	15.4.150	31.5.172	30.11.198	31.7.207	22.2.158	32.10.208	4.4.56	31.10.212	33.7.224	27.8.211	17.6.122	27.8.205	6.5.62	29.8.215	15.4.119	33.10.210	9.1.153	26.6.199	30.8.206
41 Marumba0118	17.5.147	18.6.150	22.8.163	19.6.124	18.4.152	17.4.111	23.8.137	22.4.164	27.12.159	27.12.159	28.8.163	16.5.143	10.5.107	19.7.147	20.8.96	25.13.138	21.7.153	25.6.148	22.10.137	11.8.109	28.10.160	22.4.157	25.8.155	21.8.125	25.8.153	16.6.144	22.8.158	17.8.116	24.8.146	14.4.146	21.8.142	23.8.157
42 Mimas5836	22.7.167	19.8.151	30.15.208	22.6.108	21.6.176	9.4.77	27.12.193	28.10.208	31.14.204	31.14.205	35.11.213	18.5.164	16.4.124	18.7.179	27.8.169	24.14.138	27.10.194	20.4.137	28.12.173	16.7.127	30.13.210	34.10.217	22.11.184	14.8.105	22.11.182	17.6.162	28.11.204	16.6.106	29.13.192	14.2.155	23.9.166	24.11.200
43 Neococytius1949	20.8.151	21.9.195	35.14.204	24.5.113	17.5.149	25.7.179	34.13.218	32.11.225	39.15.226	39.15.227	41.10.232	18.4.131	15.3.97	10.4.112	32.5.186	31.13.205	32.10.209	21.5.156	31.12.202	15.6.100	34.14.213	35.9.230	30.10.200	20.7.116	30.10.205	13.5.125	32.10.226	18.5.121	36.14.225	12.5.153	28.10.198	31.12.201
44 Nyceryx2378	31.14.209	28.11.204	10.2.93	3.1.50	32.13.209	28.13.201	27.11.175	9.5.167	25.15.203	25.15.204	26.8.199	27.14.206	26.11.158	29.14.205	26.9.181	22.15.180	25.8.161	15.5.116	25.12.169	26.12.165	23.12.179	17.5.174	20.10.180	16.5.98	20.10.178	26.15.206	17.8.196	9.3.109	31.12.187	27.11.210	26.10.168	26.10.171
45 Pachylia1644	25.10.209	29.7.209	17.6.139	10.2.77	25.9.194	25.9.177	27.7.150	11.1.134	25.11.180	25.11.180	27.8.174	22.10.193	21.9.149	26.10.201	25.7.173	19.11.163	25.5.149	14.2.99	25.8.144	21.10.150	20.10.166	18.1.163	19.6.142	15.4.81	19.6.140	21.11.188	20.6.169	12.4.93	31.8.164	24.7.203	24.6.147	24.6.161
46 Pachysphinx1528	18.6.178	17.7.155	27.12.201	19.4.105	17.5.180	13.3.132	36.9.185	24.7.194	33.13.211	33.13.212	35.10.205	14.4.173	9.3.136	14.6.175	29.7.168	29.13.179	34.7.186	22.4.134	33.10.183	11.6.130	30.12.208	30.7.216	26.8.184	19.6.104	26.8.183	9.5.166	26.10.201	15.6.112	38.10.183	12.3.169	30.8.173	31.8.186
47 Paonias1540	18.5.186	17.6.156	27.11.194	20.4.101	19.4.183	13.4.130	34.10.191	24.6.193	33.12.202	33.12.202	35.9.206	14.5.176	10.4.135	12.7.178	29.6.165	27.14.179	32.8.180	20.4.128	31.11.179	10.7.135	28.13.202	30.6.210	24.9.184	18.6.103	24.9.183	9.6.168	26.9.205	16.6.115	36.11.186	12.4.170	28.9.174	29.9.192
48 Paratrea1939	11.6.118	22.7.197	30.16.197	20.7.116	12.3.131	18.5.176	31.13.207	27.11.213	34.15.207	34.15.209	36.12.226	5.2.46	3.1.33	11.4.142	31.7.165	30.13.203	27.11.200	20.5.163	28.12.204	5.6.56	31.14.199	31.9.225	29.10.204	20.7.123	29.10.205	2.3.54	29.12.215	16.7.123	33.14.209	7.5.135	22.10.195	26.12.201
49 Perigonia2191	31.15.202	30.12.208	12.3.91	5.2.56	32.14.197	24.14.185	29.12.176	13.6.166	30.16.208	30.16.209	27.7.195	27.15.194	24.12.154	29.15.197	26.10.177	25.16.176	29.9.167	17.6.124	29.13.163	26.13.158	22.13.172	17.6.158	22.11.171	16.6.91	22.11.170	24.16.188	18.7.189	11.2.106	33.13.186	25.12.203	28.11.166	28.11.175
50 Protambulyx1945	27.10.201	12.5.125	33.16.207	20.7.117	28.7.206	22.5.146	36.11.201	35.11.218	40.14.220	40.14.222	41.12.213	25.6.186	18.5.154	23.6.200	33.9.189	35.15.197	38.11.195	27.5.141	37.12.188	20.6.152	39.14.208	39.9.220	35.12.186	22.9.121	35.12.184	20.7.190	32.12.211	17.7.116	38.12.203	17.5.195	36.10.191	37.10.194
51 Pseudoclanis5839	27.10.193	22.8.184	30.16.196	24.8.106	28.9.209	21.9.154	38.13.196	29.11.207	33.15.208	33.15.208	40.16.213	25.10.189	20.9.145	27.10.199	33.11.188	31.17.197	36.13.213	22.8.147	36.14.204	22.14.154	32.18.210	38.10.221	30.14.203	22.10.116	30.14.200	22.11.191	31.14.216	19.10.118	38.14.199	23.11.186	33.14.194	33.12.210
52 Psilogramma5988	10.7.128	25.6.206	31.13.210	21.6.116	9.4.136	19.4.184	34.12.215	26.8.217	37.11.213	37.11.214	39.9.223	10.5.125	8.4.91	14.7.156	32.6.183	33.14.207	30.10.203	23.4.159	31.13.199	10.5.106	30.13.218	30.8.217	32.11.227	23.8.120	32.11.225	9.6.114	32.9.221	19.6.115	36.13.213	10.4.173	26.9.198	29.11.204
53 SmerinthusAF2345	12.7.103	10.4.82	17.6.111	19.6.109	12.4.97	8.2.68	21.8.98	15.4.100	18.8.95	18.8.95	20.6.119	10.3.102	10.3.102	12.5.102	20.6.94	19.11.102	20.7.99	19.4.91	20.10.109	11.6.97	19.7.118	17.4.119	17.8.97	17.8.105	17.8.98	8.3.99	15.6.117	15.6.118	22.8.92	11.2.94	19.6.105	18.8.107
54 Smerinthus1511	16.6.182	17.5.154	29.12.205	20.5.107	17.3.193	15.3.132	36.11.182	26.7.198	33.11.203	33.11.203	37.8.201	16.4.185	11.3.141	14.6.184	29.5.173	29.13.185	34.9.188	23.3.133	33.12.179	13.6.143	30.12.204	30.7.214	26.10.193	18.7.108	26.10.193	11.5.174	28.8.205	16.5.118	38.12.178	14.3.174	30.8.173	31.10.191
55 SphinxAF234596	7.4.74	13.5.111	18.7.120	20.7.117	7.1.73	11.3.92	16.9.112	16.5.122	19.9.112	19.9.112	17.7.128	3.0.34	3.0.35	9.2.79	20.5.106	20.10.117	15.8.109	18.5.114	17.9.120	4.5.46	22.8.121	20.5.123	20.7.109	20.7.118	20.7.109	3.0.29	16.7.121	16.7.119	19.9.113	6.3.84	14.7.119	13.9.114
56 Sphinx1532	11.4.117	24.9.198	29.16.203	20.8.114	12.1.131	18.5.167	31.13.207	27.11.224	35.15.210	35.15.211	36.12.234	7.2.71	5.1.46	13.4.134	30.7.178	30.13.208	29.11.207	20.6.156	30.12.203	7.6.63	31.14.210	32.11.226	29.10.198	20.8.113	29.10.201	6.3.60	29.12.218	16.8.118	33.14.211	9.5.149	24.10.202	26.12.205
57 Sphinx1591	13.7.116	22.10.188	29.17.199	19.8.113	14.4.133	20.6.165	31.14.200	27.12.216	33.14.211	33.14.212	34.13.228	7.3.66	4.2.47	13.5.130	28.8.166	30.14.199	29.12.197	20.6.147	30.13.193	4.7.60	31.15.202	32.12.215	29.11.194	19.8.111	29.11.196	6.4.57	27.13.214	15.8.115	33.15.207	9.6.143	24.11.186	26.13.193
58 Sphinx1938	10.5.121	23.8.194	28.15.202	20.7.118	11.2.130	17.4.172	30.12.204	26.10.218	33.14.216	33.14.218	35.11.232	5.1.69	4.0.53	12.3.132	29.6.167	29.12.199	28.10.204	20.5.151	29.11.201	6.5.64	30.13.206	30.10.220	28.9.199	20.7.119	28.9.201	4.2.59	28.11.219	16.7.121	32.13.207	8.4.147	23.9.196	25.11.197
59 SphecodinaAF2345	23.7.115	23.4.107	11.2.97	13.2.90	23.6.108	21.4.102	10.4.89	14.0.103	19.6.90	19.6.90	19.6.110	19.5.110	21.5.111	21.5.107	12.4.90	10.9.92	9.3.80	12.2.73	11.6.92	18.6.108	14.5.87	17.0.112	10.4.72	12.4.74	10.4.71	21.5.112	14.4.100	14.4.100	13.4.91	20.2.106	10.4.86	10.4.88
60 Theretra5880	31.14.220	33.11.212	24.12.178	19.6.97	34.13.198	33.13.187	11.3.94	25.9.170	34.14.191	34.14.191	38.14.188	27.12.198	26.11.167	27.10.209	23.9.168	20.8.157	7.3.97	8.6.89	5.2.69	25.10.166	26.12.191	29.9.187	23.6.178	16.6.97	23.6.172	28.13.204	27.12.181	18.10.92	11.4.114	31.11.208	8.4.101	11.3.107
61 Unzela2376	29.13.214	30.11.215	17.12.165	13.6.85	30.13.215	28.11.193	23.5.166	16.7.174	23.13.182	23.13.183	29.12.180	25.12.209	22.11.166	25.12.219	19.9.188	13.9.182	19.3.171	10.4.117	19.4.166	21.12.164	15.10.178	23.7.186	5.6.163	6.6.91	5.6.164	24.13.212	19.10.178	12.8.108	25.6.180	27.9.204	20.4.172	20.4.178
62 Xylophanes5904	30.15.216	36.11.195	24.9.158	17.1.88	33.14.198	30.12.189	10.6.82	26.8.175	34.16.184	34.16.185	39.11.192	26.13.187	25.11.155	30.13.194	25.8.153	23.11.150	2.3.69	8.4.79	8.7.80	26.12.156	29.13.175	31.7.181	24.9.164	14.7.90	24.9.157	29.13.192	30.9.187	16.5.103	9.7.91	30.10.208	4.5.67	6.6.69
63 XylophanesAF2345	19.10.130	23.7.115	15.3.87	17.3.85	19.9.117	19.7.104	6.1.38	16.3.91	19.7.95	19.7.95	23.9.103	13.8.113	14.8.115	15.8.113	10.5.63	10.7.77	1.0.26	6.3.49	3.3.47	12.9.112	16.6.107	19.3.100	12.5.91	14.5.90	12.5.89	15.8.116	18.7.96	18.7.95	5.1.53	16.5.117	2.1.32	4.2.30
64 Xylophanes2369	31.14.222	37.11.197	25.10.163	18.3.84	34.13.201	33.9.192	11.3.76	25.6.181	35.13.179	35.13.180	38.12.186	27.11.202	26.11.162	29.12.205	26.9.159	22.8.151	5.1.62	9.3.70	9.4.79	25.12.164	26.10.176	30.7.184	23.6.164	15.5.86	23.6.159	30.13.203	29.10.182	17.7.92	11.3.88	31.9.209	5.2.63	7.3.64
65 Xylophanes1879	31.15.219	37.12.199	25.11.174	18.4.92	34.14.210	31.12.194	9.4.81	27.8.174	35.14.180	35.14.181	40.13.189	27.13.198	26.11.161	29.13.200	26.10.156	22.9.159	1.2.24	7.5.75	7.5.81	25.12.163	28.11.176	32.8.185	23.7.161	13.6.88	23.7.157	30.13.194	31.11.190	17.8.100	8.5.101	31.10.208	3.3.70	5.4.74
66 Attacini	46.25.184	47.24.206	44.24.197	34.16.130	42.24.191	45.21.197	47.21.187	45.21.195	42.23.192	42.23.193	50.21.192	41.22.177	44.22.175	47.23.191	44.22.182	43.20.200	45.19.193	30.13.145	45.20.187	43.21.177	44.20.187	46.22.195	39.19.210	31.15.139	39.19.202	42.23.179	46.23.191	32.17.133	45.20.188	46.20.197	44.18.196	44.19.185
67 Bombycidae	47.18.250	39.18.256	45.22.252	22.12.135	44.16.252	46.14.242	47.19.250	45.18.241	54.23.242	54.23.243	55.19.253	45.15.254	38.14.204	45.17.249	43.18.238	48.16.249	47.17.245	28.11.183	42.18.237	41.13.191	49.21.258	42.17.252	41.17.258	21.13.133	41.17.251	44.16.252	43.19.249	23.13.139	47.20.255	47.14.260	47.16.253	51.17.251
68 Brahmaeidae	24.9.126	23.11.143	24.12.122	26.12.119	24.11.129	27.11.134	23.12.128	23.11.122	26.14.127	26.14.127	29.14.125	26.10.126	26.10.129	28.10.138	26.15.114	25.18.117	24.13.129	25.13.123	24.13.132	25.11.126	27.15.134	25.11.128	23.14.132	25.14.127	23.14.132	24.10.131	23.15.126	23.15.127	26.12.129	25.11.132	25.14.130	25.11.133
69 Bunaeini	48.27.207	45.26.199	44.27.192	32.18.123	46.26.211	45.22.199	47.24.185	48.23.192	45.25.186	45.25.187	46.23.192	41.24.194	45.24.193	47.25.204	46.24.183	45.24.195	49.22.187	28.14.130	47.23.192	45.21.191	51.23.176	49.24.185	42.22.201	30.17.132	42.22.194	44.25.200	43.25.186	29.18.135	47.24.181	44.22.207	48.21.190	50.23.184
70 Ceratocampinae	22.19.84	22.21.88	19.20.81	20.20.79	22.18.84	20.18.85	21.20.73	19.19.77	17.20.70	17.20.70	21.18.93	21.18.82	22.18.84	25.18.92	21.17.89	18.17.83	19.19.78	17.17.82	20.18.84	21.17.86	20.18.79	20.19.92	17.17.74	18.17.78	17.17.73	22.18.81	18.20.88	18.20.89	18.20.76	21.17.83	20.18.81	20.19.83
71 Hemileucini	19.17.85	19.17.94	23.15.92	24.15.87	19.16.88	22.15.90	23.15.89	25.15.87	22.18.80	22.18.81	27.14.94	22.16.90	22.16.90	23.16.86	23.15.87	20.16.83	23.14.87	23.13.85	24.15.96	22.14.92	23.16.90	22.15.94	20.17.85	19.17.83	20.17.86	21.16.91	24.16.89	24.16.90	22.15.85	21.13.87	22.13.86	22.16.89
72 Micragonini	29.17.133	26.16.139	25.14.135	27.14.135	29.16.133	31.14.135	29.14.130	27.14.134	26.17.130	26.17.131	28.14.129	27.15.129	29.15.128	31.15.139	29.14.118	26.16.121	28.13.127	23.12.136	28.14.131	26.14.132	30.15.139	29.14.135	24.16.139	26.16.140	24.16.135	27.15.131	24.16.122	24.16.122	28.14.124	28.12.130	29.12.126	29.15.129
73 Saturniini	45.26.235	46.25.249	42.27.237	27.15.132	44.25.243	46.22.251	49.22.238	46.21.252	46.26.227	46.26.228	50.22.241	41.22.225	38.21.183	48.24.244	47.23.234	45.21.230	50.20.239	32.14.189	47.21.224	38.20.194	48.23.230	47.23.253	41.22.249	29.16.139	41.22.246	44.25.234	44.24.243	25.16.134	49.22.238	45.21.248	48.19.222	49.20.232
74 Adelidae	40.23.159	43.18.163	42.17.152	43.17.152	44.21.152	39.19.155	42.17.140	42.18.145	48.21.152	48.21.152	42.17.149	42.20.151	42.20.150	45.18.151	41.16.132	49.21.154	43.17.137	42.16.141	45.19.148	43.17.154	47.21.155	41.18.140	45.22.152	45.22.149	45.22.150	42.20.149	44.16.140	44.16.139	43.17.143	42.17.152	44.17.152	44.16.146
75 Aganainae	22.11.135	22.13.143	24.11.148	22.11.139	24.11.133	25.11.133	25.12.141	19.11.142	28.16.133	28.16.134	29.14.144	21.10.134	21.10.141	21.12.135	25.12.131	24.16.136	22.11.141	21.11.131	22.14.137	22.11.136	22.16.137	18.11.141	24.15.135	24.15.131	24.15.134	19.10.139	22.14.144	22.14.146	24.12.133	22.11.124	21.12.140	23.11.135
76 Arctiinae	27.11.128	22.11.124	25.8.137	23.8.134	29.11.123	28.9.120	30.9.131	24.9.128	29.14.133	29.14.133	27.11.133	28.10.128	28.10.127	27.12.125	24.10.129	26.15.130	31.8.132	28.9.129	31.11.125	29.9.133	28.14.116	23.9.137	24.13.124	24.13.118	24.13.122	26.10.130	22.11.126	22.11.129	31.9.132	26.9.125	30.9.135	29.10.128
77 Catocalinae	29.10.130	23.8.141	27.9.133	29.9.133	29.10.134	27.8.138	25.10.145	28.8.140	29.14.137	29.14.137	32.11.139	28.9.134	28.9.132	26.11.139	24.9.124	23.15.134	24.9.137	23.8.133	24.12.140	27.10.141	28.13.130	27.8.130	22.12.147	22.12.134	22.12.141	26.9.136	27.11.132	27.11.132	24.10.142	25.8.139	23.10.133	25.10.131
78 Cecidosidae	38.22.149	42.23.154	38.20.148	41.20.150	40.22.161	41.24.155	42.22.149	39.21.151	44.25.153	44.25.153	46.24.155	42.21.155	42.21.149	45.19.149	39.21.152	43.25.151	41.22.150	38.23.141	41.22.155	43.20.149	42.24.153	40.21.140	39.23.151	40.23.152	39.23.148	42.21.151	44.23.157	44.23.156	42.22.150	44.22.155	42.24.148	41.21.147
79 Condicinae	27.11.144	22.13.139	30.10.125	28.10.128	29.11.139	30.11.149	31.14.131	29.11.133	31.15.133	31.15.134	31.11.141	28.10.137	28.10.145	30.12.138	30.13.119	32.18.131	30.12.127	32.13.136	30.16.127	29.10.133	32.14.126	28.11.122	31.13.138	31.13.142	31.13.139	26.10.144	28.13.137	28.13.139	30.14.126	25.11.139	29.14.129	31.13.126
80 Eriocranioidea	48.27.151	52.25.162	47.22.145	50.22.150	52.27.143	51.25.150	51.23.150	49.22.143	53.26.151	53.26.151	51.25.157	54.26.145	53.26.148	53.25.154	44.22.128	50.28.146	49.22.146	47.22.152	49.25.151	55.23.148	53.27.154	50.22.136	48.26.167	49.26.160	48.26.164	52.26.144	52.24.153	52.24.151	52.23.148	54.23.160	50.24.160	50.23.152
81 Gracillarioidea	50.26.142	42.23.149	42.23.141	43.23.140	51.27.138	47.25.143	51.22.150	45.23.145	44.23.148	44.23.148	49.27.156	51.26.147	50.26.145	50.26.140	47.26.138	44.26.152	49.23.145	49.25.150	49.22.149	50.26.141	44.25.145	43.23.135	48.24.150	48.24.150	48.24.151	49.26.149	48.26.150	48.26.149	50.22.146	49.25.140	48.24.150	46.21.146
82 Heliothinae	29.13.143	27.10.141	28.9.124	30.9.127	31.13.139	31.11.151	31.11.126	29.11.132	33.16.140	33.16.140	33.13.145	30.12.144	30.12.144	32.12.146	27.13.128	32.19.123	30.11.127	29.13.139	30.13.126	31.10.139	35.16.136	29.11.129	29.15.144	31.15.142	29.15.145	28.12.144	29.13.140	29.13.139	30.11.125	31.11.135	31.13.133	33.12.124
83 Heliozelidae	47.26.154	48.24.157	47.22.149	50.22.152	49.25.154	51.25.162	50.22.137	49.23.147	51.25.157	51.25.157	49.23.162	51.24.156	50.24.156	51.22.154	47.22.139	49.25.156	48.22.137	46.24.143	48.22.136	50.21.155	51.25.134	48.23.135	48.23.152	49.23.147	48.23.151	49.24.158	48.22.158	48.22.156	49.22.143	51.23.164	49.23.149	49.21.142
84 Hepialoidea	33.12.139	31.11.131	29.12.132	33.12.133	37.12.136	33.12.124	31.11.122	35.12.129	37.18.134	37.18.135	39.15.130	34.11.134	33.11.137	34.11.138	26.11.107	31.15.134	26.12.124	26.12.128	26.11.122	35.11.138	37.17.123	34.12.125	31.14.128	33.14.125	31.14.124	32.11.134	36.15.117	36.15.118	28.11.120	33.12.139	27.13.128	27.10.122
85 Heterocampinae	26.11.132	25.11.141	23.7.130	25.7.125	28.11.135	23.9.132	27.7.134	26.7.133	33.13.143	33.13.143	30.11.149	28.10.127	28.10.125	26.10.131	24.9.124	28.13.138	26.6.128	23.7.137	26.9.137	27.9.124	31.12.130	25.7.127	25.11.137	27.11.136	25.11.135	26.10.123	29.11.142	29.11.142	28.7.134	27.7.131	27.7.136	27.8.131
86 Incurvariidae	39.22.149	47.23.151	43.20.141	46.20.145	43.22.155	46.24.154	45.22.148	45.21.143	45.25.154	45.25.155	47.24.156	45.21.151	44.21.149	47.19.156	38.21.136	42.25.150	43.22.145	41.23.144	43.22.149	46.20.148	46.26.138	41.21.140	42.23.164	43.23.161	42.23.160	43.21.149	44.23.157	44.23.155	44.22.140	48.22.155	44.24.155	44.21.157
87 Lamproniinae	36.18.150	39.15.148	37.12.145	34.12.148	40.18.150	40.16.147	41.14.149	33.13.134	39.18.148	39.18.150	38.16.145	40.17.150	41.17.153	44.15.149	38.15.135	40.20.156	39.14.150	37.15.156	39.16.147	41.14.157	34.18.138	33.13.141	39.17.144	40.17.151	39.17.145	40.17.154	37.15.145	37.15.145	40.14.148	45.14.152	40.16.152	40.13.147
88 Lithosiinae	26.12.141	24.15.139	27.12.142	27.12.136	26.13.132	30.13.139	31.13.136	31.13.139	30.18.157	30.18.157	29.16.135	27.12.143	27.12.154	27.14.135	26.14.135	29.17.132	30.12.132	29.13.133	30.13.132	28.13.152	29.18.133	28.12.144	27.17.133	27.17.134	27.17.130	25.12.153	26.16.132	26.16.135	30.13.132	24.13.150	29.13.134	29.14.130
89 Lymantriidae	27.11.134	25.11.132	26.9.129	24.9.129	27.11.133	29.9.124	30.10.138	24.9.131	29.14.137	29.14.138	28.12.144	26.10.140	26.10.145	26.12.145	26.10.122	26.14.143	29.9.131	26.9.136	29.12.135	27.9.144	26.14.134	21.9.131	24.13.135	24.13.129	24.13.132	24.10.145	25.12.135	25.12.135	29.10.135	25.9.139	28.10.126	28.9.127
90 Micropterigoidea	57.36.130	60.36.164	62.33.141	61.33.146	60.37.147	61.35.152	61.32.145	60.34.139	63.36.149	63.36.149	61.37.146	61.36.153	60.36.146	58.34.148	59.35.130	61.38.137	61.33.141	58.34.140	59.34.146	60.37.150	59.38.146	60.33.129	60.37.149	59.37.148	60.37.149	59.36.145	61.37.140	61.37.139	59.32.137	62.35.148	60.34.145	61.33.144
91 Noctuinae	35.13.150	33.12.147	33.10.140	37.10.147	37.13.152	35.11.152	35.14.136	36.11.141	36.15.149	36.15.149	36.12.160	36.12.147	36.12.155	36.14.149	30.13.131	35.18.150	34.12.141	32.13.148	34.16.148	37.10.150	40.15.147	36.11.138	34.14.151	36.14.152	34.14.153	34.12.150	33.13.161	33.13.161	34.14.138	35.11.148	35.14.140	37.13.135
92 Nolinae	28.14.136	25.15.149	27.12.138	29.12.138	32.13.132	28.13.141	32.13.123	32.12.137	29.13.135	29.13.136	32.13.145	30.12.130	30.12.127	30.12.135	29.12.119	30.16.133	31.12.114	30.11.129	31.15.130	31.12.135	31.15.119	29.12.118	28.15.135	28.15.135	28.15.135	28.12.128	29.14.137	29.14.138	33.13.127	29.11.135	30.12.123	30.12.127
93 Notodontinae	29.13.144	23.13.129	25.10.139	29.10.139	31.13.140	27.11.126	31.11.120	30.9.136	31.15.132	31.15.133	30.12.142	31.12.139	30.12.139	31.12.132	26.10.120	30.16.135	30.10.121	27.9.129	30.13.120	32.10.145	35.14.131	30.9.130	27.13.141	29.13.137	27.13.137	29.12.135	29.12.141	29.12.140	30.11.120	28.9.140	31.11.130	31.11.127
94 Nymphalidae	24.15.95	17.13.95	20.9.83	21.9.78	25.15.98	21.13.86	27.12.88	24.10.82	23.13.85	23.13.85	22.13.100	23.14.94	23.14.93	24.15.95	24.13.96	25.16.93	27.11.90	26.12.87	27.14.95	24.12.98	28.14.88	23.10.79	24.13.87	23.13.86	24.13.89	21.14.94	21.12.101	21.12.101	28.12.89	21.12.93	26.12.96	24.13.93
95 Nystaleinae	30.12.145	31.13.145	31.11.126	33.11.126	34.13.144	31.11.141	33.11.131	34.11.137	39.17.142	39.17.143	38.15.158	34.12.136	33.12.140	34.14.137	30.13.130	34.17.132	32.10.133	31.11.137	32.11.140	33.13.133	33.16.126	33.11.115	29.15.147	29.15.143	29.15.147	32.12.137	37.15.150	37.15.151	32.11.133	35.11.138	33.11.137	33.12.137
96 Oncocnemidinae	27.12.140	22.10.140	23.8.134	25.8.142	29.10.137	26.8.144	22.10.129	26.10.136	27.14.131	27.14.133	28.10.143	28.9.144	28.9.147	26.11.143	21.8.116	23.14.136	22.8.132	21.8.134	22.12.134	27.9.141	28.13.132	24.10.124	19.14.148	21.14.144	19.14.145	26.9.144	22.10.137	22.10.137	22.10.130	25.8.139	23.8.131	24.11.127
97 Palaeephatoidea	36.14.139	35.13.149	36.12.143	39.12.144	40.14.149	36.13.140	36.12.128	40.11.138	42.17.143	42.17.143	45.16.145	40.13.138	39.13.137	36.11.147	32.13.121	34.16.137	33.13.129	35.13.129	33.12.133	39.12.136	42.16.130	39.11.131	34.13.145	36.13.139	34.13.145	38.13.142	42.15.142	42.15.143	35.12.125	37.12.149	34.14.137	34.11.133
98 Pantheinae	28.9.147	28.7.149	29.7.148	29.7.144	30.7.149	28.5.137	30.9.146	28.7.147	31.9.144	31.9.145	32.7.155	29.6.139	29.6.142	30.8.151	27.5.131	29.12.139	30.7.140	29.5.145	30.11.145	30.6.142	32.10.146	28.7.148	29.11.162	29.11.156	29.11.157	27.6.142	28.7.139	28.7.139	30.9.136	30.5.129	29.7.140	30.9.139
99 Papilionidae	4.1.41	2.0.47	1.0.51	2.0.49	4.1.44	5.0.48	5.0.49	2.0.46	1.0.46	1.0.46	5.1.50	3.0.47	3.0.48	4.0.44	1.0.40	3.1.48	4.0.50	3.0.42	3.0.45	4.0.43	4.0.50	3.0.41	3.0.43	4.0.41	3.0.41	2.0.44	2.1.47	2.1.43	5.0.43	4.0.46	4.0.52	4.0.49
100 Phalerinae	32.14.128	31.14.134	32.11.130	34.11.126	36.14.122	33.12.127	37.13.119	36.10.137	39.15.122	39.15.122	38.13.126	36.13.123	36.13.126	33.13.124	37.14.124	33.17.127	35.12.121	37.12.125	35.15.126	35.11.127	36.15.130	35.10.125	34.14.132	34.14.133	34.14.128	34.13.124	38.13.127	38.13.128	37.13.123	34.10.126	34.13.128	33.13.122
101 Prodoxinae	40.19.141	41.14.146	39.14.151	40.14.152	44.17.144	42.15.151	43.16.144	39.16.152	44.19.142	44.19.143	43.17.145	43.16.145	44.16.138	46.16.152	40.16.144	42.22.148	41.16.159	41.16.152	41.18.158	44.15.143	42.19.143	40.16.145	41.20.151	41.20.147	41.20.150	43.16.148	42.16.146	42.16.146	42.16.145	45.15.150	41.16.157	41.17.154
102 Psychidae	42.16.147	33.13.149	35.13.132	33.13.136	40.14.143	40.14.152	38.11.138	34.13.146	40.16.143	40.16.143	39.16.146	40.13.147	40.13.152	38.11.144	38.11.134	40.14.139	39.12.135	40.11.143	39.11.136	41.12.142	38.16.132	32.13.124	38.15.145	40.15.147	38.15.145	38.13.150	34.15.144	34.15.145	39.11.135	36.12.144	40.11.133	40.12.130
103 Stictopterinae	26.10.141	26.12.141	30.9.135	32.9.134	28.10.151	31.10.138	28.10.134	31.10.137	32.16.135	32.16.136	34.13.135	31.9.149	31.9.143	29.11.154	27.11.130	26.14.132	29.9.135	28.10.136	29.12.140	30.12.148	33.15.127	30.10.120	27.14.141	27.14.135	27.14.136	29.9.148	30.13.141	30.13.140	29.10.132	28.10.140	28.10.140	28.11.141
104 Tineidae	37.20.125	33.15.139	39.17.149	37.17.146	39.19.129	39.15.138	39.18.139	31.16.141	37.18.143	37.18.143	38.17.145	36.18.132	37.18.132	39.16.128	39.17.135	38.21.133	36.19.140	38.16.144	36.19.146	37.17.128	36.19.156	34.16.137	35.20.149	37.20.152	35.20.147	36.18.128	33.16.147	33.16.144	38.18.135	38.15.139	37.18.139	36.18.137
105 Tischerioidea	39.17.148	36.16.144	40.12.153	44.12.155	39.18.148	37.16.139	38.14.152	43.14.147	43.18.142	43.18.142	45.15.153	39.17.152	38.17.148	43.15.142	37.16.145	39.21.147	37.14.152	38.16.142	37.14.158	40.16.149	42.18.161	41.14.155	38.17.152	38.17.147	38.17.150	37.17.153	43.16.154	43.16.155	35.14.148	38.14.141	38.16.148	40.15.147

Table 18. (continued)

33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68
21	27	13	32	13	13	19	20	13	24	23	34	29	23	25	13	34	30	20	14	15	25	9	11	16	15	23	31	31	29	26	33	34	52	36	22
18	13	19	35	18	19	24	21	15	18	24	32	29	14	16	17	32	12	21	20	8	16	11	22	22	21	22	38	33	37	29	37	40	53	39	22
10	33	38	21	38	37	39	37	24	37	41	10	15	35	36	37	12	43	35	37	17	34	21	39	41	36	12	28	26	22	15	26	28	44	40	23
5	13	21	14	19	20	21	19	18	20	23	3	4	13	14	19	5	19	20	21	15	14	19	21	22	19	13	19	14	14	16	17	18	34	17	23
19	21	8	28	7	7	14	14	10	20	17	32	28	19	21	7	32	24	17	10	11	19	5	7	10	9	21	33	30	29	24	32	34	51	31	23
20	18	20	28	19	18	22	20	10	10	23	32	26	15	18	17	32	18	23	17	9	16	10	19	20	19	19	33	29	29	23	29	33	53	40	26
17	39	36	18	37	36	36	36	25	33	39	26	19	31	33	35	28	38	39	35	22	35	22	35	36	33	13	8	18	11	6	8	9	47	40	24
3	27	32	21	31	30	33	31	20	29	36	9	5	24	25	30	13	34	30	30	14	25	17	33	35	30	12	21	18	22	16	22	24	44	34	23
20	39	40	31	40	39	41	41	31	44	45	29	28	39	40	39	32	45	32	36	21	40	24	37	40	38	21	34	29	35	23	35	37	48	46	26
20	39	40	31	40	39	41	41	31	44	45	29	28	39	40	39	32	45	32	36	21	40	24	37	40	38	21	34	29	35	23	35	37	48	46	26
22	34	41	32	40	39	41	40	28	38	41	27	28	32	33	39	24	40	35	37	18	33	22	40	42	41	21	39	31	37	30	39	41	50	46	27
19	21	8	29	7	5	12	10	15	18	19	36	28	20	24	5	35	23	22	12	15	24	4	9	8	7	25	33	33	29	25	31	32	53	36	27
18	19	7	28	5	5	11	9	13	18	17	33	28	17	21	3	33	20	20	10	15	20	4	6	7	6	25	30	30	27	24	29	31	53	33	27
21	24	18	28	15	17	21	21	18	22	10	36	33	18	20	16	36	21	30	21	15	20	13	17	17	18	21	28	30	32	23	32	32	55	38	26
20	26	28	9	28	27	29	30	22	32	30	28	25	27	28	27	28	33	29	27	19	27	21	27	29	26	13	23	24	18	13	22	24	48	37	26
21	38	36	13	35	34	38	37	30	35	37	28	24	38	39	34	31	42	36	38	25	37	26	37	39	34	18	20	20	21	16	20	22	41	35	29
16	39	34	14	33	32	32	32	23	34	33	27	22	32	34	30	29	39	34	31	22	35	22	33	34	31	13	8	16	5	3	5	2	41	37	25
16	22	26	7	23	24	25	24	25	24	25	17	14	22	21	23	19	26	23	23	20	23	23	24	25	24	12	10	14	9	9	8	9	30	25	24
17	40	35	15	34	33	34	36	27	36	35	29	23	33	35	33	31	41	37	33	26	37	26	32	36	33	17	4	17	13	8	12	11	41	34	26
17	25	16	31	15	11	11	11	17	22	23	34	29	22	24	13	36	26	29	16	19	26	12	16	15	14	24	30	32	29	22	29	31	51	35	27
20	35	39	24	38	37	37	37	27	35	36	28	26	32	33	37	27	40	37	38	16	31	24	38	40	38	14	23	16	27	17	24	26	41	39	25
5	28	35	27	35	34	35	33	20	33	38	19	12	30	31	32	19	35	36	34	15	31	20	36	38	33	14	27	25	24	18	24	27	42	38	26
18	32	35	19	34	33	32	34	25	30	32	23	21	25	26	33	23	36	31	35	16	26	23	34	36	35	12	18	9	23	18	20	22	42	35	25
16	16	24	14	22	23	20	22	20	21	21	12	14	14	13	22	12	21	19	24	15	14	22	22	23	24	11	15	7	16	17	14	15	32	20	24
17	30	33	17	32	31	30	32	24	28	30	21	19	25	26	31	21	35	29	33	15	26	22	32	34	33	11	18	7	21	17	18	22	40	35	24
17	18	6	30	4	6	14	12	13	20	15	33	29	16	20	5	34	19	21	12	12	20	3	7	7	6	22	34	33	31	24	33	35	53	36	24
14	23	32	21	31	30	33	31	20	31	34	21	20	24	25	30	18	33	27	28	12	24	18	31	33	32	14	29	21	27	23	29	31	47	33	23
14	12	20	15	18	19	20	18	17	19	20	9	12	12	13	18	7	17	16	18	12	11	18	18	19	20	14	23	14	17	23	20	21	35	19	23
19	41	38	19	38	37	35	35	27	36	39	31	24	36	38	35	33	41	39	36	24	40	26	37	38	35	15	12	21	11	6	8	10	42	43	28
16	17	14	31	11	11	15	11	13	13	16	33	26	15	19	10	33	17	26	15	12	19	9	15	15	14	22	33	30	31	24	31	35	51	36	29
17	37	30	13	30	29	30	29	23	31	32	28	22	31	33	28	30	37	36	28	22	33	21	29	30	27	15	8	17	5	4	4	3	41	35	27
17	37	33	13	33	32	32	32	24	31	35	25	19	31	33	31	27	37	33	31	21	35	21	32	33	30	13	10	14	7	6	5	7	41	40	24
-.-.-	14	20	17	17	18	20	18	19	19	23	7	4	14	15	17	9	20	20	19	15	17	18	20	21	18	15	18	15	16	17	17	18	32	20	23
18.4.159	-.-.-	21	33	18	19	24	20	11	18	24	29	27	7	8	18	27	15	26	19	3	8	10	21	22	21	17	40	31	38	25	38	41	53	40	24
23.7.157	18.5.182	-.-.-	31	5	7	16	14	14	20	18	35	30	19	23	7	35	22	23	12	15	23	5	5	8	5	25	35	34	31	26	33	35	52	35	24
17.5.142	30.9.187	35.8.199	-.-.-	30	29	31	32	25	32	30	22	19	31	34	29	23	37	31	31	19	31	21	30	32	29	13	15	16	11	13	15	17	43	33	26
21.7.164	17.5.165	11.0.90	32.8.204	-.-.-	4	13	11	12	19	15	34	29	16	20	4	34	17	22	11	13	20	3	6	7	6	23	34	33	31	24	33	35	54	36	25
21.8.161	16.6.166	10.1.82	31.9.204	1.1.35	-.-.-	11	9	13	18	17	35	28	17	21	4	35	20	21	11	14	21	5	8	7	8	24	33	32	30	25	32	34	53	35	26
24.4.157	18.4.177	14.3.96	34.5.205	9.3.64	8.4.66	-.-.-	4	17	22	21	35	31	19	23	11	35	25	27	16	15	22	10	15	12	15	23	34	33	30	23	32	34	53	40	30
22.3.157	16.3.177	12.4.95	33.6.204	5.4.73	4.5.70	4.1.43	-.-.-	16	18	21	35	29	18	22	9	35	22	27	14	13	20	8	15	12	13	23	36	33	30	23	32	34	51	40	30
23.5.164	13.3.109	17.4.156	25.8.151	16.4.145	16.5.149	18.5.145	19.4.144	-.-.-	14	19	21	19	9	10	13	21	15	17	13	8	10	13	12	14	15	19	28	23	22	24	24	25	41	24	26
20.4.157	13.4.112	19.5.183	28.9.190	18.5.168	17.6.166	21.4.170	17.3.173	13.4.110	-.-.-	23	34	27	17	18	17	34	18	26	19	10	18	11	21	22	19	22	36	28	34	26	32	36	52	40	27
21.6.168	19.6.183	17.4.139	36.6.198	16.4.140	15.5.139	21.3.141	17.4.146	22.7.151	20.7.178	-.-.-	35	36	21	23	15	35	25	27	19	16	22	14	17	17	18	20	35	31	33	27	35	36	53	40	28
6.4.124	26.11.199	30.14.206	22.8.168	29.14.212	28.15.212	31.11.216	30.10.222	21.7.167	29.13.211	31.12.201	-.-.-	11	27	28	35	4	38	32	31	13	26	19	34	36	33	11	27	20	24	16	26	30	46	38	22
9.1.115	23.7.172	25.10.196	21.6.151	24.10.206	23.11.200	26.7.202	25.6.203	24.4.151	24.9.187	28.10.192	13.4.136	-.-.-	26	27	28	13	33	31	28	15	27	16	31	33	28	13	21	18	20	15	20	24	43	36	24
20.3.160	5.3.71	15.4.183	30.8.194	14.4.170	13.5.170	15.3.169	13.2.175	15.2.111	12.3.126	16.6.186	25.10.204	22.6.180	-.-.-	3	17	27	13	22	17	3	5	11	18	18	19	15	32	26	32	22	32	34	52	36	21
20.3.163	5.2.65	15.5.190	30.9.187	14.5.175	13.6.173	15.4.180	13.3.181	15.2.121	10.4.124	14.7.190	25.9.197	22.5.174	2.1.52	-.-.-	21	28	17	24	19	4	6	13	22	22	23	14	34	27	36	22	34	36	54	39	21
20.6.161	14.4.169	8.2.82	31.8.198	5.2.72	4.3.68	8.3.81	6.4.76	15.5.144	17.5.171	15.2.140	28.14.209	23.10.195	11.4.168	11.5.171	-.-.-	35	18	20	11	13	21	2	8	7	6	23	33	32	29	23	31	32	53	35	25
6.5.122	22.12.192	26.15.194	23.9.175	29.15.198	28.16.197	31.12.200	30.11.205	21.8.160	27.14.200	31.13.197	6.1.81	15.5.125	23.11.198	23.10.190	26.15.197	-.-.-	38	33	31	13	26	19	34	36	35	11	29	20	26	18	28	32	48	40	24
25.6.164	22.4.162	26.6.201	35.10.187	21.6.194	22.5.187	24.5.192	22.4.194	18.5.147	21.5.151	23.6.203	34.14.203	31.10.193	19.4.160	19.5.167	20.4.195	34.15.203	-.-.-	26	23	9	17	11	23	23	22	23	38	37	39	28	39	41	59	43	25
26.7.166	21.9.152	26.10.205	34.14.209	27.10.198	26.11.196	28.11.193	26.10.192	21.8.123	22.11.153	29.11.197	30.14.202	30.10.195	18.8.146	18.7.151	24.9.193	29.15.206	22.9.184	-.-.-	22	13	24	14	22	24	23	20	37	29	33	27	36	37	53	40	21
19.5.164	19.2.179	11.5.145	36.9.211	12.5.136	11.4.135	15.4.140	13.3.140	18.4.156	20.4.180	18.7.158	27.11.211	24.7.203	14.3.186	16.2.183	9.5.126	27.12.203	27.3.203	27.9.211	-.-.-	13	19	9	9	12	11	21	33	32	29	23	31	33	53	37	28
18.5.109	1.1.35	12.4.108	20.6.98	11.4.97	11.5.100	10.3.104	10.2.107	8.3.84	7.2.58	13.5.99	16.5.105	15.4.90	2.2.27	3.2.27	9.3.100	16.6.110	11.3.88	11.8.78	12.2.110	-.-.-	1	13	13	14	15	16	26	16	21	26	23	24	37	15	23
21.4.163	7.1.72	17.4.192	32.8.192	16.4.177	15.5.178	15.3.190	13.2.191	14.3.120	14.3.128	16.6.199	25.10.196	24.6.180	4.2.61	4.1.54	13.4.181	25.11.193	21.4.171	18.8.161	16.1.201	1.1.11	-.-.-	12	22	22	23	15	36	27	35	25	36	38	52	37	22
19.6.113	8.2.92	5.1.22	21.5.116	4.1.46	4.2.46	5.2.41	5.3.39	11.5.105	10.3.90	12.2.72	17.6.117	14.5.102	7.3.98	8.3.100	2.0.39	17.7.111	10.4.107	15.7.111	5.3.65	9.3.103	8.2.106	-.-.-	5	5	4	23	25	23	21	25	22	23	42	21	25
20.7.161	16.5.179	4.0.41	33.8.210	9.0.79	8.1.76	12.3.86	10.4.88	14.4.151	17.5.173	15.4.137	28.14.206	23.10.197	13.4.180	13.5.183	6.2.72	26.15.194	24.6.194	24.10.196	9.5.132	9.4.107	15.4.188	2.1.11	-.-.-	7	6	23	32	33	30	24	32	34	55	36	25
22.7.155	16.6.169	6.3.49	33.9.198	7.3.73	6.4.70	8.4.84	8.5.84	14.6.144	19.6.166	15.5.132	28.15.202	23.11.190	13.5.174	13.6.174	6.3.67	28.16.190	22.7.192	26.11.191	11.6.129	10.4.102	15.5.181	3.1.22	4.3.30	-.-.-	7	24	36	35	31	24	33	35	57	38	26
20.6.156	15.4.177	3.1.46	32.7.200	7.1.77	6.2.75	10.2.79	8.3.82	14.5.148	16.4.173	14.3.138	27.13.205	22.9.199	12.3.174	12.4.178	4.1.73	25.14.197	23.5.188	23.9.197	8.4.140	9.3.103	14.3.184	2.0.16	1.1.29	3.2.34	-.-.-	25	33	34	28	21	30	32	52	35	23
17.1.109	20.3.96	23.6.111	13.4.94	20.6.108	20.7.109	20.3.110	21.2.117	15.4.109	18.4.100	22.5.105	11.1.94	16.0.78	21.2.94	20.2.95	20.5.112	13.2.94	24.5.105	22.6.116	23.4.119	19.4.99	20.3.99	20.5.116	20.6.115	19.6.109	20.5.118	-.-.-	17	10	14	17	14	15	33	20	24
20.7.132	34.13.195	32.12.208	17.6.145	31.12.217	30.11.211	29.9.212	32.10.211	23.10.149	30.13.191	31.12.227	24.12.169	24.8.151	33.10.194	31.11.194	28.12.207	28.13.178	35.10.201	35.14.210	31.11.219	21.10.97	33.12.188	18.9.113	30.12.212	28.13.197	29.11.203	12.6.91	-.-.-	17	12	8	9	10	45	35	25
15.3.133	24.11.183	28.12.222	15.6.171	27.12.216	26.13.215	29.9.208	28.8.214	23.8.146	23.10.200	27.12.216	15.10.166	14.6.144	23.8.185	21.9.185	26.12.215	17.11.165	34.12.209	27.14.200	29.11.225	15.8.95	23.10.184	18.9.118	26.12.220	26.13.213	25.11.219	8.4.77	18.6.171	-.-.-	18	14	15	19	39	36	24
18.5.131	35.11.190	29.13.195	18.5.125	30.13.198	29.14.196	30.10.199	31.9.201	20.8.153	29.12.194	34.10.204	25.9.153	25.7.139	34.9.182	34.10.183	27.12.195	29.10.159	38.12.191	36.14.207	30.12.204	19.7.105	34.11.185	14.8.110	27.13.201	27.14.188	26.12.195	10.3.84	9.7.91	21.7.173	-.-.-	6	6	6	40	37	26
19.4.93	20.6.103	17.9.109	11.5.69	14.9.120	14.10.117	14.6.115	15.5.117	17.7.111	16.7.106	18.8.112	17.4.77	16.3.74	21.5.101	20.5.102	14.8.116	19.5.88	22.8.110	23.9.116	17.7.116	21.7.101	22.6.103	16.8.114	14.9.116	13.9.106	14.8.111	10.3.86	4.3.42	10.3.81	2.2.28	-.-.-	3	4	35	24	27
19.4.131	36.11.186	30.12.204	19.6.129	31.12.210	30.13.205	31.9.203	32.8.208	21.7.155	30.11.195	33.12.213	24.10.159	26.6.147	35.8.184	33.9.186	28.12.205	28.11.166	39.12.199	37.14.212	31.11.209	22.7.99	35.10.187	17.8.114	28.12.210	28.13.199	27.11.205	9.3.83	8.4.87	20.4.160	5.5.50	3.0.15	-.-.-	6	41	40	26
19.6.133	36.12.197	30.13.199	19.7.133	31.13.209	30.14.204	31.10.201	32.9.206	21.9.155	28.12.195	33.13.217	26.11.158	26.7.155	35.9.183	33.10.184	28.13.200	30.12.168	39.13.195	37.15.212	31.12.208	20.8.100	35.11.191	15.9.111	28.13.203	28.14.193	27.12.199	9.4.85	8.5.95	20.5.178	1.4.63	1.1.27	4.3.55	-.-.-	43	40	27
33.14.130	42.22.193	45.23.187	43.19.189	42.23.180	41.24.184	42.20.189	41.19.185	33.17.124	43.21.202	46.23.191	46.23.198	46.21.196	42.21.198	41.22.195	42.23.175	46.24.192	51.23.205	46.29.187	45.22.194	31.15.136	42.21.195	36.16.124	43.23.185	43.24.187	43.22.184	35.15.140	41.22.192	39.19.195	46.20.190	31.15.139	43.19.187	45.20.196	-.-.-	47	36
28.12.188	42.16.252	45.15.260	46.15.251	49.15.255	48.14.251	48.14.250	48.15.259	23.10.168	45.14.246	47.17.245	42.21.245	49.17.253	43.15.255	43.16.247	46.15.260	44.22.243	48.15.254	47.21.244	45.14.249	18.7.136	41.15.255	23.8.140	43.15.257	44.16.254	43.14.258	19.11.140	44.16.247	42.19.256	47.19.251	21.13.131	48.18.254	48.19.248	46.23.201	-.-.-	21
24.11.121	23.10.128	27.11.130	26.15.124	25.11.134	25.10.132	28.12.131	26.11.136	22.11.128	23.9.126	27.12.122	24.12.121	27.11.131	24.9.134	23.9.138	25.10.136	24.13.126	25.8.136	24.11.137	24.9.138	22.11.127	23.10.127	25.10.133	25.11.133	26.11.127	25.10.133	23.11.123	25.12.126	23.14.127	25.13.131	25.13.127	26.13.128	24.14.131	27.18.128	19.12.148	-.-.-
32.15.129	40.24.190	47.25.199	44.21.184	44.25.207	43.24.208	44.22.204	43.21.205	25.18.130	41.23.195	46.25.198	45.25.198	49.23.189	40.23.192	39.24.189	46.25.202	45.26.190	49.23.200	47.31.185	49.22.210	25.16.134	40.23.191	34.17.141	46.25.208	45.26.209	45.24.204	29.16.130	47.23.204	42.21.192	50.23.188	31.17.134	49.21.188	49.23.191	25.9.138	42.25.210	23.19.138
20.18.85	20.18.82	23.18.75	21.17.89	20.18.84	20.19.87	21.16.84	19.17.86	19.20.86	19.18.81	24.18.75	19.20.83	22.19.79	21.19.81	21.19.78	22.18.81	20.21.89	24.20.91	23.24.86	22.19.88	19.19.78	20.18.81	23.18.80	22.18.80	21.19.84	22.18.82	22.19.76	21.20.84	18.18.81	19.19.81	20.19.87	21.19.86	19.20.79	11.5.69	18.19.91	15.21.79
24.14.91	19.14.87	22.16.90	23.15.86	21.16.93	21.17.93	22.14.90	20.13.92	20.16.89	19.14.89	20.16.85	25.16.90	22.15.87	20.15.89	20.15.81	21.16.93	24.17.90	21.16.93	24.21.81	23.15.91	18.15.85	19.14.83	22.16.92	21.16.93	22.17.96	21.16.94	24.15.81	25.17.90	22.14.82	23.14.87	24.14.90	25.14.86	23.15.92	18.5.72	16.19.93	20.18.90
28.13.139	26.13.129	30.16.124	30.14.122	26.16.132	26.17.137	27.13.135	25.12.139	27.16.128	28.13.133	30.15.133	26.15.136	29.14.132	27.14.132	26.14.128	28.15.134	28.16.135	30.15.130	30.20.143	31.14.139	25.14.129	26.13.131	30.15.135	28.16.134	27.16.131	28.15.129	27.14.129	29.16.132	24.14.127	29.13.133	29.13.132	30.13.132	28.14.131	18.3.106	24.18.134	24.18.134
36.15.192	42.23.253	46.24.230	50.20.224	43.24.245	42.25.250	45.21.243	44.20.245	32.18.180	45.22.256	49.24.236	46.26.244	47.22.233	43.22.252	41.23.240	46.24.231	46.27.250	51.24.256	49.30.230	49.23.240	26.14.136	43.22.247	31.15.136	45.24.230	44.25.236	44.23.234	28.14.132	48.23.246	41.20.247	51.22.228	28.14.136	50.20.233	50.22.240	23.3.113	48.23.255	24.17.132
45.19.149	42.18.154	41.21.151	41.16.138	43.21.149	43.20.154	42.18.153	42.17.155	43.21.144	43.19.156	46.18.150	43.17.152	44.18.145	42.19.157	43.19.151	41.20.159	41.18.149	41.16.161	41.21.152	40.17.150	43.19.154	43.18.149	39.20.150	41.21.151	42.21.156	41.20.158	46.18.152	46.17.148	47.20.154	42.16.142	44.18.139	45.18.141	43.18.140	55.24.151	41.20.142	40.20.151
20.12.143	20.10.133	22.11.141	26.12.135	22.11.139	22.10.136	19.12.135	21.11.141	24.11.136	24.11.132	20.11.132	20.11.141	21.11.135	19.9.125	20.9.134	20.10.134	20.12.147	24.10.130	25.13.139	23.9.139	20.11.126	19.10.130	22.10.143	20.11.140	21.11.140	20.10.135	22.11.135	23.12.130	22.13.129	21.10.141	23.11.137	22.11.137	22.12.142	36.18.137	19.11.119	28.10.140
23.10.128	24.8.131	29.11.131	25.10.132	27.11.134	27.10.131	28.10.130	26.9.136	30.9.133	26.9.120	24.11.123	23.9.131	24.9.130	23.7.122	24.7.126	27.10.130	23.10.130	24.8.122	30.13.136	30.7.119	24.9.127	23.8.129	27.10.133	27.11.129	28.11.129	27.10.130	27.9.129	32.9.128	24.11.133	30.7.136	32.8.132	31.8.130	31.9.134	38.17.129	26.9.130	28.11.125
27.9.139	23.7.144	28.10.142	24.9.128	27.10.140	27.11.137	28.9.139	26.8.145	25.8.144	21.8.140	23.10.132	27.8.135	28.8.135	24.6.147	23.6.139	27.9.137	27.9.137	27.9.142	28.12.140	30.8.132	23.8.145	24.7.144	29.9.140	27.10.138	28.10.134	27.9.144	24.8.133	25.12.135	22.10.136	25.8.134	25.9.132	26.9.130	24.10.140	31.17.149	20.12.132	21.13.129
44.22.140	41.23.153	44.22.151	39.21.157	43.22.151	43.21.162	41.21.148	42.22.153	42.24.143	44.24.155	44.19.150	40.20.147	39.21.147	42.22.152	43.22.156	43.21.158	41.21.148	42.21.159	39.21.167	42.22.145	40.24.151	41.23.153	41.21.152	43.22.153	42.22.156	43.21.159	43.21.157	42.20.152	39.25.151	40.21.146	42.23.146	41.23.147	41.23.151	46.31.148	37.21.151	39.21.140
28.12.134	23.10.136	30.11.150	30.13.127	27.11.142	27.10.144	28.12.146	26.11.144	23.11.144	25.11.145	27.10.147	28.10.132	31.11.127	24.9.138	25.9.142	27.10.141	28.11.132	23.10.151	28.13.144	30.9.137	23.11.138	24.10.137	27.10.152	27.11.151	28.11.145	27.10.147	30.11.134	31.14.130	32.15.127	29.11.123	31.13.125	30.13.120	30.14.130	36.18.143	28.12.137	23.9.144
52.23.152	51.24.153	55.27.145	44.22.138	55.27.151	55.26.160	55.24.151	56.23.153	50.24.147	54.25.153	54.24.147	50.21.145	53.22.152	51.23.155	52.23.151	53.26.155	49.22.143	53.23.156	46.24.158	52.23.149	50.23.147	50.24.153	51.26.148	53.27.149	54.27.152	53.26.145	49.22.161	50.23.148	46.24.150	48.21.148	50.23.145	51.23.147	49.23.150	54.32.147	42.26.144	43.25.134
43.22.142	47.24.140	50.27.147	47.26.142	51.27.145	51.27.148	51.26.147	50.25.150	51.25.137	48.24.137	48.27.140	44.23.140	47.23.145	47.23.143	46.23.139	50.26.155	44.24.145	44.23.154	42.23.147	49.24.142	47.25.143	47.24.142	50.26.147	50.27.146	51.27.147	50.26.146	47.23.151	50.23.146	47.23.144	50.24.146	50.23.147	49.23.147	49.24.149	50.29.140	48.27.143	45.22.141
28.12.130	26.10.142	31.13.139	27.13.135	29.13.151	29.12.152	30.12.144	28.11.146	28.11.131	28.11.141	29.12.133	30.10.132	33.11.140	27.9.140	28.9.136	29.12.142	30.11.133	31.8.133	32.13.138	30.9.145	26.11.138	27.10.137	29.12.144	29.13.145	30.13.142	29.12.139	33.11.144	31.11.121	29.15.127	29.10.129	31.12.125	32.12.124	30.13.132	30.21.130	22.12.119	22.11.130
52.24.145	47.24.151	51.25.158	47.22.149	52.25.156	52.24.158	51.22.161	51.23.159	50.26.152	50.25.153	50.22.153	50.22.153	51.23.153	47.24.154	46.24.151	50.24.163	49.23.154	48.22.160	42.25.156	51.23.154	46.25.151	46.24.151	48.24.157	50.25.159	51.25.157	50.24.161	49.23.151	49.20.139	47.25.154	49.23.147	49.23.142	50.23.140	48.24.138	54.32.148	47.24.151	45.25.148
36.13.134	33.11.130	35.12.141	26.11.114	35.12.139	35.13.144	32.11.137	34.12.139	31.12.132	33.12.127	35.12.134	34.12.134	35.12.128	34.10.131	35.10.134	33.11.142	34.13.129	33.11.125	32.12.138	36.12.142	33.12.131	34.11.132	35.11.142	33.12.139	34.12.141	33.11.144	32.12.132	27.11.114	29.14.123	25.11.118	27.12.120	28.12.120	26.13.127	37.19.138	28.12.125	32.13.129
29.8.137	23.8.130	29.11.134	24.9.133	29.11.130	29.12.128	28.8.129	28.7.130	26.9.136	23.9.131	25.10.121	25.8.131	26.7.143	24.7.132	23.7.126	27.10.126	25.9.134	25.10.133	29.13.142	28.9.122	24.9.132	25.8.135	27.10.126	27.11.126	28.11.123	27.10.128	27.7.146	27.9.139	25.9.139	27.6.134	27.6.134	28.6.137	26.7.132	35.15.130	22.11.135	24.13.125
46.22.143	43.23.145	45.22.155	38.21.145	46.22.150	46.21.155	45.21.156	45.22.155	46.23.140	47.24.148	48.19.159	46.20.138	43.21.151	43.22.146	44.22.144	44.21.153	45.21.150	45.21.153	41.21.152	45.22.152	42.22.144	42.23.147	42.21.149	44.22.151	45.22.155	44.21.153	46.21.159	44.20.150	42.25.148	42.21.145	44.23.147	45.23.148	43.23.146	50.31.138	40.21.153	39.21.151
38.14.145	37.15.147	42.18.150	38.15.144	41.18.150	41.17.152	40.15.155	40.14.152	40.15.145	43.16.152	41.15.151	36.12.149	39.13.145	38.14.149	39.14.149	41.17.153	37.13.143	40.13.141	36.16.147	40.14.155	36.14.148	37.15.148	39.17.149	41.18.145	40.18.156	41.17.155	40.13.153	38.14.151	38.17.151	38.13.152	38.15.155	39.15.150	39.15.155	42.23.144	39.15.145	34.15.143
28.12.150	26.12.131	28.13.147	26.14.142	26.13.154	26.12.157	27.14.150	25.13.154	26.13.149	26.12.137	22.13.135	28.13.143	29.13.141	25.11.132	26.11.138	26.12.147	28.14.144	24.12.141	26.15.139	29.11.143	26.13.134	25.12.134	28.12.148	26.13.146	27.13.150	26.12.145	28.13.137	29.13.134	27.13.146	29.11.130	31.12.135	30.12.134	30.13.137	29.19.130	28.11.140	27.12.140
21.10.132	25.8.129	27.11.143	27.10.128	25.11.143	25.10.149	25.10.147	24.9.154	29.9.141	27.9.129	23.11.141	23.9.137	24.9.137	24.7.127	25.7.132	25.10.149	23.10.138	27.8.127	30.13.131	28.7.136	25.9.124	24.8.121	27.10.145	25.11.142	26.11.144	25.10.142	27.9.132	30.10.136	24.11.130	28.8.133	30.9.130	29.9.131	29.10.133	38.16.133	27.9.144	32.10.132
60.35.141	58.36.151	60.37.150	59.35.141	61.37.151	61.37.156	61.36.156	60.35.154	62.37.143	60.37.155	62.35.157	63.34.147	63.34.142	58.35.155	57.35.155	60.36.146	62.35.146	61.35.162	56.32.155	60.36.144	57.37.149	57.36.149	59.36.150	60.37.144	61.35.146	60.36.151	63.34.149	60.33.146	60.36.146	62.32.149	60.33.144	61.33.140	61.34.144	64.43.147	61.37.144	54.34.138
35.12.134	33.10.153	35.13.154	30.13.139	35.13.155	35.12.159	36.12.160	34.11.160	35.11.140	33.11.145	33.12.144	37.10.141	38.11.151	32.9.150	33.9.151	35.12.143	37.11.144	31.10.138	31.13.145	38.9.149	33.11.147	32.10.144	35.12.152	35.13.148	36.13.147	35.12.148	36.11.149	35.14.147	34.15.138	33.11.140	35.13.141	34.13.139	34.14.143	40.19.142	33.11.131	26.11.139
33.13.125	25.12.136	31.13.134	29.12.128	31.13.135	31.13.141	28.12.139	30.11.138	30.14.136	29.13.146	27.11.130	29.12.136	30.12.129	26.12.133	27.12.133	29.12.135	29.13.136	27.13.145	26.16.134	32.12.140	24.13.130	25.12.131	29.12.134	29.13.133	30.13.133	29.12.133	28.12.136	31.14.126	28.14.128	30.11.124	32.12.122	33.12.122	31.13.117	34.17.144	28.15.142	25.12.135
31.10.128	27.10.129	30.13.142	26.10.123	30.13.140	30.13.140	31.10.142	29.9.141	30.11.121	29.11.134	30.11.137	29.9.133	34.9.131	27.9.123	28.9.124	30.12.139	29.10.131	26.11.125	23.15.141	31.10.138	26.11.122	26.10.124	30.12.140	30.13.143	31.11.137	30.12.138	31.9.132	31.12.123	29.11.135	29.9.122	31.10.126	32.10.129	30.11.126	30.18.131	25.14.120	22.15.151
25.11.71	18.12.85	21.15.93	24.13.96	24.15.96	24.14.99	23.13.98	23.12.99	23.13.83	21.13.91	22.14.91	21.10.89	22.10.91	19.11.86	20.11.87	22.14.99	20.11.90	20.12.88	21.15.88	24.11.96	18.13.83	19.12.84	21.14.94	22.15.95	23.15.98	22.14.99	25.10.84	28.12.96	23.14.85	26.10.94	28.11.93	28.11.93	27.12.90	30.19.86	22.15.93	23.13.94
35.10.127	29.10.135	31.13.150	30.13.139	35.13.135	35.14.142	34.12.141	34.11.150	32.11.121	33.10.136	33.14.136	33.12.135	38.11.136	30.9.137	29.9.133	33.12.142	31.13.131	33.12.141	32.15.142	34.11.140	28.11.131	29.10.130	33.12.142	33.13.143	34.11.138	33.12.144	33.11.144	33.13.139	29.11.134	33.10.138	33.10.130	34.10.133	32.11.134	38.17.137	26.14.146	26.14.129
26.11.129	22.7.133	29.10.145	21.8.125	27.10.143	27.11.147	28.9.141	26.8.144	23.10.119	20.8.143	23.9.142	25.9.134	28.10.137	23.8.131	22.8.131	27.9.144	25.10.143	24.9.138	25.14.136	30.8.134	22.8.129	23.7.128	28.9.148	27.10.148	28.10.144	27.9.144	21.10.145	23.12.130	21.12.130	23.7.130	23.9.127	24.9.130	22.10.134	30.16.136	18.10.132	16.14.131
43.12.141	35.13.136	41.14.148	32.13.132	41.14.142	41.15.145	40.11.150	40.12.149	34.13.133	33.14.135	37.13.145	39.12.149	41.11.137	36.12.136	35.12.137	39.13.140	39.13.150	34.13.150	36.13.134	41.14.133	34.12.138	35.13.134	39.13.143	39.14.142	40.14.140	39.13.148	36.11.142	34.12.135	34.15.144	34.13.132	34.13.130	35.13.130	33.14.131	39.21.143	34.12.139	34.15.132
28.8.141	24.4.144	30.7.146	27.5.137	28.7.138	28.7.143	29.6.141	27.5.147	29.7.140	26.5.139	30.6.147	29.6.144	30.7.146	24.5.150	25.5.144	28.6.144	29.7.146	29.5.138	28.11.146	29.4.131	24.5.146	24.4.148	27.6.145	28.7.145	29.7.140	28.6.144	31.7.146	31.10.143	29.9.136	29.6.143	31.8.140	32.8.140	30.9.144	34.14.140	21.9.131	22.11.131
2.0.43	1.0.45	4.1.46	1.0.43	3.1.44	3.1.45	3.0.43	3.0.45	3.1.40	4.0.46	4.0.47	2.0.50	3.0.43	1.0.45	2.0.42	3.0.45	3.0.47	3.0.49	0.0.45	4.0.42	1.0.41	1.0.41	4.0.44	3.1.44	3.0.45	3.0.45	3.0.44	3.0.46	2.1.44	3.0.47	4.0.49	4.0.51	4.0.50	2.0.50	1.0.39	2.1.48
38.11.124	31.11.126	37.14.127	37.14.128	37.14.124	37.15.128	36.11.123	36.10.127	33.12.112	31.12.123	32.13.117	35.11.134	38.10.123	32.10.125	31.10.129	35.13.126	35.12.126	31.13.129	33.15.135	36.12.129	30.12.125	31.11.123	36.13.126	35.14.129	36.12.129	35.13.128	35.10.118	35.15.127	33.14.118	36.12.127	36.12.128	37.12.127	35.13.122	35.19.134	28.15.126	29.16.123
44.17.153	39.14.143	45.17.137	40.16.155	44.17.148	44.16.145	43.16.149	43.15.153	40.16.144	43.15.142	43.16.145	40.15.153	44.16.153	40.15.142	41.15.143	44.16.147	41.16.151	42.12.150	38.17.143	43.13.150	39.13.141	40.14.142	42.16.145	44.17.141	43.17.145	44.16.143	41.16.150	42.16.158	41.20.145	40.15.155	42.17.155	41.17.156	41.17.164	46.25.138	37.15.156	35.17.140
33.14.137	35.13.142	41.14.156	39.11.138	39.14.148	39.15.152	38.11.151	38.12.153	38.15.132	38.14.150	37.13.142	31.14.128	37.13.138	36.14.144	37.14.142	39.13.151	31.15.135	35.13.152	40.16.144	41.14.145	36.12.141	37.13.144	37.13.149	39.14.149	40.14.149	39.13.149	36.13.138	38.11.133	38.15.135	38.12.134	40.12.133	37.12.133	39.13.137	46.20.135	31.14.148	39.18.140
32.11.132	28.9.141	32.10.147	27.11.138	30.10.150	30.11.149	31.11.149	29.10.147	30.10.134	26.10.136	26.10.145	32.10.136	33.10.135	27.8.142	26.8.136	30.9.154	32.11.136	26.11.144	26.10.136	31.10.152	28.10.137	27.9.134	30.9.151	30.10.153	31.10.144	30.9.153	27.10.145	30.12.134	29.12.132	30.8.140	30.9.138	29.9.139	29.10.137	37.16.141	28.14.131	19.12.127
36.16.134	33.16.123	38.19.121	40.17.138	37.19.128	37.19.134	34.16.134	36.15.138	35.19.138	36.15.128	38.17.127	34.16.142	35.16.134	34.17.126	35.17.129	37.18.135	36.17.148	38.15.142	39.18.139	38.16.129	33.17.122	34.16.125	37.18.125	37.19.126	36.19.126	37.18.124	38.16.150	35.19.141	34.19.138	35.18.145	37.19.138	36.19.141	36.20.141	40.25.141	36.21.139	36.21.143
40.13.149	38.15.134	36.18.152	37.16.152	38.18.144	38.19.144	39.15.155	37.14.159	35.16.137	38.15.138	44.15.146	42.13.155	45.14.155	39.14.134	40.14.135	38.17.158	40.14.151	37.15.142	36.15.142	39.16.151	37.16.132	38.15.134	38.17.152	38.18.154	39.18.153	38.17.154	42.14.154	38.16.152	40.16.153	36.13.157	38.15.151	39.15.153	37.16.154	41.21.145	32.19.145	32.14.137

Table 18. (continued)

69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
51	34	29	34	52	40	21	23	25	42	25	53	53	24	52	28	25	45	44	26	22	60	31	28	29	27	32	27	39	28	2	33	46	40	22	35	36
50	31	27	29	53	38	23	20	20	42	24	51	46	23	48	25	20	44	40	27	21	61	29	26	24	21	29	20	37	24	1	28	39	30	19	30	35
50	30	27	27	50	37	25	25	24	40	28	47	51	27	46	29	26	38	38	30	24	62	30	29	29	23	34	25	37	24	0	31	39	34	24	37	34
33	29	26	26	28	37	23	23	22	40	26	47	51	25	47	30	24	38	36	30	22	60	29	27	27	21	32	23	37	23	0	29	40	32	23	35	34
50	32	27	32	50	39	22	24	24	43	25	52	54	25	51	26	23	45	45	26	22	60	32	28	27	26	31	24	38	27	2	32	46	38	21	36	36
50	33	28	32	52	38	24	19	21	46	30	49	52	29	52	25	18	48	45	28	20	62	30	27	25	26	31	21	37	26	4	30	44	35	23	34	38
55	32	27	29	49	34	26	26	24	42	33	49	53	31	46	26	21	42	42	31	26	62	36	29	32	30	32	24	36	26	3	35	43	35	23	43	35
49	27	25	25	48	38	23	23	22	40	26	47	50	25	47	29	23	38	38	31	21	62	29	27	27	22	32	23	37	23	0	29	39	31	23	34	34
52	28	28	30	50	41	30	29	32	43	28	48	48	28	44	33	30	41	37	37	30	64	33	28	30	28	39	29	40	26	0	39	41	37	31	35	38
52	28	28	30	50	41	30	29	32	43	28	48	48	28	44	33	30	41	37	37	30	64	33	28	30	28	39	29	40	26	0	39	41	37	31	35	38
50	31	29	30	50	35	30	25	26	46	32	46	55	31	45	31	25	44	40	30	26	61	31	27	25	23	37	25	40	27	3	27	40	37	26	36	38
52	34	31	34	53	40	25	27	27	43	28	54	55	28	54	29	25	45	47	29	25	62	35	31	30	28	35	27	42	29	2	34	46	40	22	37	38
53	33	31	34	51	40	23	25	27	41	26	53	52	26	52	28	25	44	45	29	24	61	33	29	29	28	34	27	41	28	2	34	44	40	22	34	38
54	32	29	32	55	37	24	25	24	41	30	50	55	31	48	26	20	44	44	25	24	59	36	26	29	29	34	23	34	29	3	31	46	34	20	37	38
54	28	25	28	47	33	26	25	25	40	32	44	54	30	44	22	22	38	41	30	26	62	35	28	29	28	31	24	33	23	1	37	43	36	26	39	35
50	26	25	27	47	42	32	32	31	45	38	53	51	37	46	29	27	41	44	37	33	67	41	34	37	33	37	29	35	31	3	36	46	42	27	42	41
52	29	25	27	46	36	25	26	23	43	31	48	52	29	45	23	22	42	42	28	25	62	35	28	30	30	30	24	35	26	3	33	43	38	22	41	33
34	26	24	23	31	36	25	26	21	42	31	45	54	29	45	22	21	41	41	28	25	60	34	27	28	29	32	21	36	21	2	35	42	37	23	39	35
51	29	27	29	44	38	26	28	26	41	32	50	51	30	45	24	24	41	41	31	27	62	35	31	35	34	33	26	36	27	2	38	44	38	27	42	33
52	32	29	31	48	38	27	28	28	42	27	53	51	26	49	31	24	45	44	33	26	63	33	29	30	27	36	28	38	29	3	32	44	39	25	36	37
48	26	23	25	45	41	25	26	23	43	27	49	49	28	45	26	23	44	41	31	24	63	33	30	29	30	29	22	37	27	1	32	44	34	26	38	35
47	25	22	23	48	38	19	21	18	39	25	49	46	22	46	26	21	39	35	26	17	63	26	27	26	22	30	20	38	20	1	28	38	28	21	37	33
48	26	24	27	44	40	25	24	23	42	29	48	49	28	43	26	22	41	40	32	24	63	34	29	28	27	29	23	34	28	2	31	43	33	24	38	36
34	26	24	26	27	39	24	23	22	41	28	47	48	27	42	25	21	40	39	31	23	62	33	28	27	27	28	22	33	27	1	30	42	32	23	37	35
46	26	24	26	42	39	24	23	22	41	28	47	48	27	42	25	21	40	39	31	23	62	33	28	27	27	28	22	33	27	1	30	42	32	23	37	35
52	32	29	31	54	40	22	24	24	41	25	52	52	25	51	26	22	43	45	26	22	60	32	28	27	25	32	24	39	27	1	31	44	37	19	34	36
48	28	25	25	45	35	25	22	23	45	29	46	54	26	45	28	24	43	41	29	25	61	31	27	24	23	34	21	39	23	1	30	41	34	23	32	36
34	28	25	25	28	35	25	22	23	45	29	46	54	26	45	28	24	43	41	29	25	61	31	27	24	23	34	21	39	23	1	30	41	34	23	32	36
52	29	25	27	48	36	24	26	22	43	33	51	51	29	46	22	21	42	40	29	24	64	34	31	31	31	30	23	37	25	3	36	42	35	23	45	33
48	30	27	29	52	40	23	22	23	43	28	51	54	27	52	27	20	44	45	27	21	61	32	27	24	24	33	24	38	28	2	27	44	34	21	30	36
52	29	25	27	44	37	27	28	25	45	32	49	53	31	46	24	22	44	44	30	27	63	37	29	31	31	31	24	37	26	3	35	44	38	24	41	35
52	30	27	29	46	35	27	26	25	42	34	48	50	31	44	23	22	41	41	31	26	62	37	29	31	30	32	26	34	27	3	35	43	36	24	40	35
31	27	25	25	34	39	22	24	21	41	25	48	49	24	48	29	24	41	39	29	20	61	28	28	28	23	32	23	38	23	0	29	42	32	24	34	31
48	30	26	26	51	38	22	19	21	43	25	49	48	24	48	27	20	45	41	26	20	62	30	25	24	20	29	20	37	22	1	27	38	30	18	30	35
51	32	29	33	53	41	23	25	24	43	27	53	51	26	53	27	23	45	47	27	23	61	31	29	26	24	31	25	41	28	2	32	46	38	20	35	37
51	28	25	28	46	33	26	25	25	40	32	44	54	30	44	22	22	38	41	30	26	62	35	28	29	28	31	24	33	23	1	37	43	36	26	39	35
53	32	29	32	55	40	23	25	25	42	26	53	53	26	52	27	23	44	46	27	23	61	33	29	28	26	33	25	40	28	2	32	45	38	20	35	37
52	33	30	33	54	41	23	26	26	43	27	54	54	27	53	28	24	45	47	28	23	62	34	30	29	27	34	26	41	29	2	33	46	39	22	36	38
52	34	28	34	53	38	24	25	26	44	28	53	55	27	51	26	21	47	45	30	23	63	34	28	26	26	33	27	40	30	3	32	47	33	25	38	36
50	32	27	30	53	38	25	24	25	44	29	53	54	27	52	29	22	46	45	29	23	63	34	29	26	24	33	26	41	28	3	29	45	35	22	35	36
35	32	26	32	37	41	23	22	22	46	28	51	55	26	54	28	23	48	45	29	21	62	32	31	29	25	32	25	36	28	4	30	44	36	25	35	35
50	32	28	30	53	40	25	22	22	46	31	53	50	30	50	29	19	48	45	30	23	63	32	30	28	27	31	22	36	29	4	29	42	35	21	31	38
54	32	28	32	54	41	22	25	24	44	29	52	53	27	50	30	23	47	42	26	24	60	34	25	29	26	33	24	35	31	3	29	46	38	21	37	42
51	28	24	26	50	36	22	22	21	41	25	46	51	24	46	28	23	39	37	30	20	61	28	26	26	22	31	22	36	22	0	30	40	31	24	35	33
49	27	25	26	48	37	24	24	23	39	27	48	51	26	48	28	22	37	39	32	22	63	30	28	28	23	33	24	36	24	1	30	40	32	24	35	33
48	32	26	28	50	36	20	17	19	42	23	47	48	21	46	25	19	44	38	23	18	60	28	23	22	18	27	20	34	22	1	26	38	28	17	31	32
49	32	26	27	51	37	21	18	18	44	25	49	48	23	45	27	18	45	40	25	19	59	29	25	24	20	27	19	34	23	2	26	40	30	17	33	34
52	32	29	32	54	39	23	25	25	42	26	53	53	26	52	27	23	44	46	27	23	61	33	29	28	26	33	25	40	28	2	32	45	38	20	35	37
51	30	26	28	52	38	22	22	21	43	27	46	53	26	48	28	23	41	39	30	20	61	30	28	26	24	31	22	38	24	0	29	42	31	24	35	35
55	33	30	32	59	36	25	21	25	41	27	51	48	27	48	26	21	43	40	27	23	64	28	27	25	24	34	23	36	27	2	28	39	32	20	32	34
54	34	32	33	54	40	25	25	25	41	28	47	50	26	48	27	26	42	38	28	25	59	29	29	26	26	31	25	36	29	0	31	43	38	20	35	33
53	33	27	32	52	39	20	23	25	46	25	52	53	23	53	29	24	49	43	29	21	62	32	29	28	24	33	26	40	26	3	33	45	39	25	35	38
31	31	25	27	30	38	22	19	21	44	25	47	50	24	48	27	21	45	39	26	20	61	30	25	24	21	28	20	34	22	1	27	38	29	20	31	34
49	30	24	26	52	37	21	18	20	44	24	48	49	23	47	26	20	46	40	25	19	61	29	24	23	20	27	19	35	21	1	27	39	30	19	31	34
39	33	30	34	39	37	25	25	27	40	26	51	53	26	50	29	23	42	44	29	25	60	33	29	28	25	33	26	40	27	3	33	43	36	20	35	37
54	34	29	34	54	39	21	23	25	42	24	52	53	24	51	27	23	45	44	27	22	60	31	27	28	27	33	25	40	26	2	34	45	38	22	35	37
56	35	30	35	56	40	24	26	26	45	27	54	56	27	53	28	24	47	47	28	24	60	34	30	27	28	32	26	41	29	2	33	48	39	23	38	38
53	32	29	32	53	39	25	27	27	41	26	55	53	26	52	29	25	44	46	27	25	63	33	29	30	26	33	27	40	28	2	34	45	40	22	37	37
32	29	23	23	27	41	20	21	19	45	32	47	52	25	49	27	20	45	39	29	22	62	32	29	26	25	29	21	35	24	1	29	42	33	20	39	39
53	31	29	31	49	37	25	27	26	39	30	49	51	28	44	24	24	40	40	32	26	62	34	30	34	32	34	26	36	26	2	38	43	38	26	42	34
45	26	23	24	41	41	23	22	21	46	33	47	50	30	47	26	21	45	43	28	22	61	36	28	28	29	27	22	37	25	2	31	45	35	22	36	38
51	29	25	28	45	34	24	25	24	42	30	47	55	28	48	22	23	41	41	27	24	63	34	27	29	28	31	25	36	25	2	34	42	37	23	40	32
42	32	29	31	31	38	28	30	25	44	33	50	56	33	49	27	25	43	42	30	27	63	37	32	34	33	30	26	39	28	3	37	47	39	26	45	35
52	30	26	28	46	37	26	27	24	44	32	49	53	30	46	24	22	43	43	29	26	63	36	29	31	30	31	25	36	27	3	34	44	38	23	42	34
54	31	27	29	48	37	27	28	25	44	33	49	54	31	47	25	23	43	43	30	27	63	37	30	32	31	32	26	37	27	3	35	44	39	24	43	34
24	14	16	12	16	54	38	37	34	58	45	62	55	37	56	36	36	52	50	33	38	76	45	37	36	32	39	34	46	35	2	37	51	47	33	50	49
46	28	24	27	45	38	20	21	20	40	24	47	55	22	49	27	24	40	38	26	21	63	26	28	30	25	31	19	36	19	0	31	43	31	25	38	34
35	34	30	30	31	39	28	25	25	42	27	49	49	25	45	31	29	44	40	25	30	58	27	27	30	24	32	25	37	26	3	36	45	38	24	39	36
-.-.-	19	18	14	23	53	33	31	28	57	40	58	55	33	60	40	30	56	52	32	32	74	42	36	32	27	37	31	47	33	3	33	52	43	29	46	50
9.10.55	-.-.-	14	10	14	41	30	32	29	46	36	50	44	31	44	30	30	41	41	35	31	63	37	33	35	32	34	28	37	29	0	38	44	35	29	39	41
14.10.63	13.10.75	-.-.-	9	11	38	26	27	25	44	31	50	40	24	42	27	24	42	38	32	27	58	32	29	31	30	29	24	35	25	0	33	43	30	29	38	37
10.6.91	7.7.57	12.4.76	-.-.-	8	46	29	28	25	51	38	57	53	30	54	33	27	48	46	30	30	71	36	31	33	26	35	24	42	26	2	33	47	41	26	44	43
21.10.118	7.6.59	12.4.53	8.2.80	-.-.-	47	32	31	28	55	39	57	58	32	56	36	30	50	48	33	33	70	39	32	35	29	37	28	43	30	2	36	51	41	31	48	44
53.25.160	35.25.100	35.22.99	48.24.151	52.23.154	-.-.-	41	37	41	34	40	41	63	39	29	43	38	27	32	43	40	57	40	38	42	34	47	38	36	35	8	50	37	39	38	46	33
30.17.136	20.18.85	18.19.86	27.18.137	27.17.129	45.19.155	-.-.-	12	12	44	25	51	53	18	54	23	18	45	40	19	10	63	24	23	24	25	27	18	43	20	0	30	45	34	17	40	41
34.15.138	23.19.92	21.16.90	30.15.137	32.16.134	42.16.144	12.4.96	-.-.-	12	42	28	46	47	20	47	23	15	45	39	18	12	63	22	22	22	25	25	16	40	18	1	29	41	31	16	34	40
23.16.137	18.19.96	16.17.90	23.16.134	25.16.145	45.20.140	14.5.121	18.4.106	-.-.-	47	29	47	52	22	53	21	14	47	43	18	9	63	23	27	20	24	21	11	43	17	2	26	46	33	16	42	39
49.32.143	32.31.96	31.30.98	45.31.145	47.30.140	33.21.133	45.21.144	44.21.142	46.24.142	-.-.-	43	44	63	41	48	47	44	26	31	45	44	60	45	44	43	40	50	46	40	42	6	50	35	45	42	48	32
32.17.135	23.20.94	20.18.88	34.18.138	34.17.136	42.20.133	23.7.124	24.8.126	24.10.131	46.21.143	-.-.-	49	53	22	49	34	32	44	40	34	29	60	25	29	31	26	36	28	44	26	3	40	45	35	29	40	37
52.30.148	36.33.106	39.30.106	53.31.145	52.31.153	36.22.125	52.24.145	50.22.148	50.23.143	39.24.142	49.24.138	-.-.-	67	53	48	52	49	38	40	52	48	56	49	50	44	43	51	49	46	45	8	56	42	42	49	51	40
48.31.148	35.31.98	33.28.92	51.29.153	51.28.154	55.30.131	48.25.152	43.22.146	46.25.145	60.32.145	49.23.145	61.34.140	-.-.-	49	58	52	51	63	56	58	52	77	48	51	49	43	50	52	54	51	12	57	53	58	48	54	55
27.19.123	18.23.93	19.19.88	27.19.125	29.20.130	42.18.139	22.8.122	24.6.119	20.7.118	39.21.142	23.7.110	48.24.119	49.25.134	-.-.-	48	28	26	45	34	28	23	63	17	30	26	20	32	23	41	21	2	35	39	34	26	40	35
53.33.148	35.26.100	36.25.103	51.32.158	52.31.154	24.15.105	51.26.160	49.21.143	48.27.146	43.24.136	48.25.139	40.28.112	54.32.134	50.22.134	-.-.-	53	52	38	38	53	55	61	48	49	50	38	58	51	40	50	12	54	45	46	49	50	43
37.22.132	23.21.93	22.18.88	35.19.136	37.18.139	45.19.137	27.9.114	29.9.114	24.7.104	43.21.134	29.13.128	48.25.123	48.23.139	26.8.120	51.23.137	-.-.-	19	46	46	26	20	68	29	31	27	33	29	20	43	25	3	37	46	37	25	44	40
32.15.137	22.17.90	19.14.98	31.13.135	31.14.137	35.19.132	26.8.133	26.4.120	21.6.124	33.22.130	31.9.137	44.22.134	47.25.136	28.9.121	46.26.121	25.11.121	-.-.-	48	44	22	13	63	31	25	18	26	17	14	38	24	4	26	46	32	18	40	39
51.32.139	33.30.95	32.29.102	47.31.144	48.30.147	25.15.125	46.22.156	41.22.156	49.25.150	29.16.136	43.21.141	34.22.115	58.31.124	41.21.132	27.22.99	46.22.137	42.24.116	-.-.-	29	50	48	59	45	47	48	40	54	46	32	43	6	50	31	41	44	51	32
45.24.138	29.26.95	32.23.93	42.23.145	43.22.146	32.14.142	39.16.148	39.15.134	45.17.137	29.12.144	36.15.147	44.16.147	51.26.147	36.14.136	35.20.135	45.16.124	37.16.147	25.15.140	-.-.-	46	42	58	35	40	42	34	49	42	34	37	5	47	26	39	40	45	33
32.17.141	24.21.86	20.18.85	31.17.140	33.18.129	44.22.156	19.6.114	16.4.91	17.8.130	40.23.146	23.10.124	51.26.148	45.26.148	25.10.130	48.29.149	25.13.125	23.8.131	46.25.146	39.19.151	-.-.-	18	66	32	26	22	24	26	22	47	24	1	32	47	41	17	45	44
33.15.124	21.18.88	19.17.84	28.16.132	30.15.126	48.17.155	10.2.114	12.2.105	15.3.109	48.21.151	29.7.119	55.22.140	47.23.146	27.6.124	56.24.155	28.7.111	26.6.137	49.22.154	44.14.140	16.6.115	-.-.-	65	25	25	21	25	21	16	45	19	2	28	45	34	18	39	40
66.44.148	44.44.97	46.40.97	60.41.141	64.42.149	54.34.135	62.36.160	59.35.155	62.37.138	57.38.136	56.35.146	58.33.137	69.36.153	57.37.142	54.36.142	65.36.135	62.33.134	51.39.132	50.33.133	62.35.150	66.36.151	-.-.-	67	65	57	54	63	62	64	62	10	68	68	62	62	61	57
36.20.136	23.23.103	24.19.98	36.19.145	38.18.147	49.19.150	25.9.135	23.9.129	22.9.119	45.21.141	25.7.116	54.24.139	49.23.143	13.5.91	53.23.139	28.7.127	33.12.116	45.22.136	42.14.150	25.13.133	28.7.120	60.37.138	-.-.-	31	30	28	38	24	42	23	3	39	41	36	30	40	32
29.19.131	23.20.97	20.17.90	30.17.135	29.16.141	41.19.132	22.11.123	26.11.132	24.13.116	40.24.133	29.12.121	48.27.133	46.25.147	30.16.113	46.26.134	30.15.119	25.12.124	41.23.127	36.18.142	21.14.130	26.11.125	63.32.138	33.14.115	-.-.-	25	24	34	26	42	24	4	32	42	39	22	38	45
31.16.141	22.20.96	26.18.97	30.17.134	32.17.140	38.19.139	27.9.130	25.7.115	23.7.139	34.22.133	28.10.124	40.21.129	40.27.141	22.11.113	44.26.143	24.13.129	19.5.96	41.24.136	36.17.145	20.11.132	28.7.141	55.33.143	25.13.115	25.13.125	-.-.-	22	21	23	44	26	1	28	44	35	22	37	41
25.17.86	23.21.71	24.18.74	24.17.91	24.18.84	32.19.86	21.12.90	23.9.85	20.12.97	34.23.91	25.11.88	40.25.90	36.21.89	23.11.83	33.20.73	27.17.74	22.11.79	33.24.83	31.16.82	19.13.89	21.10.85	50.34.91	26.13.89	16.14.83	20.13.86	-.-.-	27	27	35	24	0	27	35	33	21	31	35
37.17.135	23.18.90	23.15.99	36.15.138	36.16.144	38.23.127	33.10.142	33.6.130	27.8.125	37.27.135	34.11.121	43.26.126	44.25.126	30.10.109	44.30.109	28.13.131	14.4.102	41.28.112	36.20.144	30.8.132	33.8.137	57.35.136	36.14.117	29.15.124	19.6.120	20.13.69	-.-.-	24	45	30	5	31	52	41	26	47	44
24.18.129	18.20.98	17.14.93	25.14.130	25.15.134	40.18.145	20.10.117	21.6.116	12.8.116	39.23.146	22.10.107	45.25.127	47.25.144	19.8.97	45.26.146	23.10.126	16.7.118	41.25.137	38.17.148	17.10.133	23.8.117	57.35.157	22.9.100	21.13.113	19.11.114	19.14.84	21.10.108	-.-.-	43	14	2	28	43	32	17	39	40
36.24.134	27.20.96	26.21.96	39.21.142	38.20.144	34.17.110	41.17.148	40.16.143	37.16.141	33.16.142	38.17.130	40.20.118	52.24.129	37.16.117	37.20.99	37.13.122	28.14.127	24.14.108	32.10.135	39.20.145	46.15.150	61.33.123	43.16.130	33.18.129	32.17.122	28.17.75	31.18.118	31.17.132	-.-.-	47	6	40	41	37	41	41	30
30.14.145	19.18.81	16.14.92	31.13.135	31.13.139	41.15.132	21.8.136	24.6.113	21.6.120	42.22.146	25.9.116	47.21.137	45.23.148	20.9.110	52.23.156	35.10.136	27.8.124	43.22.145	39.14.143	24.10.134	25.6.131	55.34.149	26.9.110	29.9.134	29.9.113	24.12.94	32.10.124	18.5.110	43.15.132	-.-.-	3	35	38	33	23	40	37
3.0.50	0.0.0	0.0.0	3.0.42	4.0.44	8.2.39	3.0.46	4.0.39	3.0.44	6.2.44	4.0.43	9.2.43	10.2.25	3.0.33	12.6.39	5.0.37	6.0.39	7.2.41	7.1.41	2.0.44	5.0.44	9.2.37	5.0.40	4.1.42	1.0.37	0.0.14	8.0.38	3.0.41	7.1.36	4.0.41	-.-.-	2	6	7	1	5	4
30.19.131	25.21.92	21.17.105	34.18.132	33.18.132	48.22.133	32.13.122	35.11.119	26.11.129	42.24.144	35.13.127	52.26.131	46.28.144	30.12.109	50.26.141	33.14.120	24.9.108	46.24.147	42.19.144	27.15.130	33.11.128	67.39.136	34.14.114	28.16.129	29.9.97	19.14.79	26.9.107	23.13.110	31.17.132	30.13.135	4.0.28	-.-.-	51	41	27	41	45
43.25.135	31.28.91	32.23.92	43.23.148	44.24.140	31.16.143	41.18.147	44.15.135	41.18.143	30.15.142	37.17.142	36.19.128	51.25.133	36.14.132	36.23.130	45.18.126	38.18.128	26.15.131	18.9.115	39.19.145	46.16.144	56.39.140	44.16.143	36.21.142	38.19.135	28.18.96	38.20.134	36.15.133	29.14.128	37.13.141	6.1.44	41.22.144	-.-.-	42	38	49	40
46.22.139	30.20.87	29.17.89	45.18.139	41.19.139	47.19.135	34.18.146	36.15.129	41.16.141	42.22.145	36.18.126	49.22.125	55.29.129	41.17.133	47.23.122	48.15.136	39.11.116	42.19.118	39.16.150	39.19.137	39.16.142	66.34.145	46.20.135	40.18.129	41.15.137	28.19.86	44.15.119	38.14.139	39.12.131	39.13.136	9.2.39	45.17.136	42.16.142	-.-.-	36	39	33
30.16.134	22.18.87	21.15.93	31.14.133	31.15.139	39.20.131	22.6.129	21.5.120	19.6.124	38.23.132	23.9.135	44.23.133	43.22.133	27.10.120	42.26.123	28.9.108	23.7.115	39.23.125	35.17.136	17.7.137	24.6.136	55.33.137	25.11.131	22.12.126	23.10.117	21.11.76	28.9.114	18.9.122	32.16.119	27.8.134	3.0.39	26.13.122	30.17.128	42.16.132	-.-.-	37	40
38.25.143	25.25.84	30.21.95	38.24.132	39.24.133	47.21.156	31.24.133	36.20.122	40.21.144	43.30.141	37.22.139	53.31.143	56.25.142	37.18.135	53.27.156	40.21.144	43.22.146	48.27.156	36.24.147	40.25.138	37.22.128	63.35.159	46.20.138	38.22.148	39.20.140	26.21.98	45.25.141	39.18.132	39.20.153	42.17.125	6.3.41	41.22.128	41.24.142	37.21.140	37.22.156	-.-.-	42
41.23.157	28.24.92	31.19.102	38.19.146	42.20.160	36.20.140	40.17.152	41.15.138	35.15.142	36.19.143	36.17.168	44.19.149	52.24.137	33.13.148	43.24.149	39.14.158	39.14.147	35.20.150	34.16.152	39.17.154	43.15.153	57.32.159	36.12.144	43.19.148	30.17.144	33.17.93	35.16.147	38.15.153	32.12.145	39.15.146	6.1.47	47.16.145	34.18.156	42.16.156	39.15.137	44.23.151	-.-.-

Table 19. Preliminary maximum parsimony (MP) heuristic searches. A range of MP heuristic search strategies across various taxon sets was conducted for (a) EF, (b) DDC and (c) combined EF&DDC data matrices. Identical heuristic searches for smaller taxon sets were repeated four times under 10, 100, 1,000 or 10,000 random sequence addition replicates to illustrate the efficiency of treespace exploration by a TBR-based search algorithm. Parsimony-based tree statistics (length, CI, RI) are reported for each set of found trees, along with the number of islands across which those trees are distributed. Filtering saved trees for optimal parsimony score significantly reduced the size of MP tree sets required for further evaluation. Three analyses conducted for the Sphingidae&2OG taxon set and reported in Figures 6, 7 & 8 are shaded. Third codon position was excluded from analyses only in the combined EF&DDC data matrix, as the low number of parsimony informative characters precluded analysis for each gene separately. '-dups' indicates taxon set was trimmed of samples containing identical EF amino acid haplotypes, in an effort to reduce computation time by eliminating minimally informative taxa.

(a) EF Data Matrix

Log	Taxon Set	ntax	Data Partition	nchar	Reps	Random Seed	Rearrangements	Time	Length	CI	RI	Trees	Islands	*Filtered Trees*	Filtered Islands	Bootstrap Replicates
5	Lepidoptera	**118**	EF ntall	**452**	200	1607577416	237,160,000,000	45h5m58s	4,932	0.156	0.470	680	1	***680***	na	116
6	Bombycoidea	**82**	EF ntall	**398**	1,000	1139344340	36,127,000,000	4h49m35s	2,695	0.241	0.520	7,316	406	***280***	2	81
12A	Sphingidae	**64**	EF ntall	**336**	10	2063643223	125,356,440	0h1m0s	1,494	0.315	0.574	630	8	***243***	3	2315
12B	Sphingidae	**64**	EF ntall	**336**	100	2063643223	1,232,234,304	0h9m55s	1,494	0.315	0.574	2,605	74	***243***	3	
12C	Sphingidae	**64**	EF ntall	**336**	1,000	2063643223	9,682,800,000	1h32m0s	1,494	0.315	0.574	5,862	383	***243***	3	
11D	Sphingidae	**64**	EF ntall	**336**	10,000	2063643223	86,192,000,000	13h18m6s	1,494	0.315	0.574	9,871	1,188	***243***	3	
25A	Sphingidae	**67**	EF ntall	**338**	10	1074512411	134,174,600	0h1m14s	1,525	0.311	0.590	357	8	***184***	2	1160
25B	Sphingidae	**67**	EF ntall	**338**	100	1074512411	1,099,848,504	0h10m15s	1,525	0.311	0.590	2,407	74	***244***	3	
25C	Sphingidae	**67**	EF ntall	**338**	1,000	1074512411	9,353,000,000	1h28m6s	1,525	0.311	0.590	6,216	470	***244***	3	
25D	Sphingidae	**67**	EF ntall	**338**	10,000	1074512411	89,681,000,000	14h22m28s	1,525	0.311	0.590	11,584	1,293	***244***	3	
18A	Sphingidae&2OG	**66**	EF ntall	**357**	10	52841009	255,317,280	0h1m0s	1,705	0.300	0.549	652	10	***161***	3	1145
18B	Sphingidae&2OG	**66**	EF ntall	**357**	100	52841009	1,390,727,616	0h9m55s	1,705	0.300	0.549	2,544	65	***161***	3	
18C	Sphingidae&2OG	**66**	EF ntall	**357**	1,000	52841009	12,085,000,000	1h32m0s	1,705	0.300	0.549	7,363	349	***161***	3	
18D	Sphingidae&2OG	**66**	EF ntall	**357**	10,000	52841009	110,270,000,000	13h18m6s	1,705	0.300	0.549	12,709	937	***161***	3	
26A	Sphingidae&2OG	**69**	EF ntall	**358**	10	654765370	252,768,884	0h1m53s	1,736	0.297	0.565	1,632	9	***560***	3	1200
26B	Sphingidae&2OG	**69**	EF ntall	**358**	100	654765370	2,294,900,000	0h17m3s	1,736	0.297	0.565	6,151	81	***580***	4	
26C	Sphingidae&2OG	**69**	EF ntall	**358**	1,000	654765370	17,051,000,000	2h9m15s	1,736	0.297	0.565	15,184	525	***580***	4	
26D	Sphingidae&2OG	**69**	EF ntall	**358**	10,000	654765370	156,710,000,000	20h40m27s	1,736	0.297	0.565	28,971	1,945	***580***	4	

(b) DDC Data Matrix

Log	Taxon Set	ntax	Data Partition	nchar	Reps	Random Seed	Rearrangements	Time	Length	CI	RI	Trees	Islands	*Filtered Trees*	Filtered Islands	Bootstrap Replicates
2	Bombycoidea	**73**	DDC ntall	**636**	10,000	1636539794	52,303,000,000	17h18m23s	5059(5062)	0.232	0.604	2,210	376	***20***	1	700
4	Lepidoptera	**105**	DDC ntall	**730**	1,000	1636539794	61,444,000,000	22h44m49s	8318(8320)	0.170	0.543	707	32	***240***	2	100
13A	Sphingidae	**64**	DDC ntall	**591**	10	65489846	19,519,816	0h0m21s	4,035	0.262	0.634	66	9	***20***	1	2584
13B	Sphingidae	**64**	DDC ntall	**591**	100	65489846	236,273,898	0h4m37s	4,035	0.262	0.634	204	34	***20***	1	
13C	Sphingidae	**64**	DDC ntall	**591**	1,000	65489846	19,519,816	0h39m12s	4,035	0.262	0.634	608	116	***20***	1	
13D	Sphingidae	**64**	DDC ntall	**591**	10,000	65489846	19,519,816	6h53m21s	4,035	0.262	0.634	1,372	297	***20***	1	
27A	Sphingidae	**65**	DDC ntall	**593**	10	1641822553	36,696,460	0h0m36s	4,117	0.259	0.633	117	7	***20***	1	5000
27B	Sphingidae	**65**	DDC ntall	**593**	100	1641822553	235,332,752	0h4m2s	4,117	0.259	0.633	282	38	***20***	1	
27C	Sphingidae	**65**	DDC ntall	**593**	1,000	1641822553	2,283,800,000	0h40m54s	4,117	0.259	0.633	591	99	***20***	1	
27D	Sphingidae	**65**	DDC ntall	**593**	10,000	1641822553	23,298,000,000	7h36m36s	4,117	0.259	0.633	1,259	237	***20***	1	
15A	Sphingidae&2OG	**66**	DDC ntall	**618**	10	315856485	56,764,988	0h1m14s	4,484	0.249	0.611	54	7	***10***	1	1248
15B	Sphingidae&2OG	**66**	DDC ntall	**618**	100	315856485	361,051,904	0h7m53s	4,484	0.249	0.611	167	30	***10***	1	
15C	Sphingidae&2OG	**66**	DDC ntall	**618**	1,000	315856485	3,245,700,000	1h11m0s	4,484	0.249	0.611	353	70	***10***	1	
15D	Sphingidae&2OG	**66**	DDC ntall	**618**	10,000	315856485	33,006,000,000	12h3m14s	4,484	0.249	0.611	800	173	***10***	1	

28A	Sphingidae&2OG	**67**	DDC ntall	**620**	10	1953784988	40,715,536	0h0m43s	4,566	0.246	0.610	47	5	***20***	1	5000
28B	Sphingidae&2OG	**67**	DDC ntall	**620**	100	1953784988	337,945,312	0h5m56s	4,566	0.246	0.610	228	41	***20***	1	
28C	Sphingidae&2OG	**67**	DDC ntall	**620**	1,000	1953784988	2,885,300,000	0h53m7s	4,566	0.246	0.610	511	136	***20***	1	
28D	Sphingidae&2OG	**67**	DDC ntall	**620**	10,000	1953784988	29,322,000,000	9h25m29s	4,566	0.246	0.610	1,047	278	***20***	1	

(c) EF&DDC Data Matrix

Log	**Taxon Set**	**ntax**	**Data Partition**	**nchar**	**Reps**	**Random Seed**	**Rearrangements**	**Time**	**Length**	**CI**	**RI**	**Trees**	**Islands**	***Filtered Trees***	**Filtered Islands**	**Bootstrap Replicates**
7	Lepidoptera	**91**	EF&DDC ntall	**1,108**	1,000	370101926	6,466,100,000	2h27m21s	10,119	0.196	0.538	35	19	***2***	1	1000
8	Bombycoidea	**72**	EF&DDC ntall	**1,011**	1,000	1636539794	1,750,946,322	0h52m20s	7,243	0.242	0.577	43	32	***1***	1	1000
10A	Sphingidae	**64**	EF&DDC ntall	**927**	10	984651357	14,471,140	0h0m22s	5,612	0.272	0.613	19	7	***3***	1	2520
10B	Sphingidae	**64**	EF&DDC ntall	**927**	100	984651357	114,652,264	0h2m59s	5,612	0.272	0.613	57	26	***3***	1	
10C	Sphingidae	**64**	EF&DDC ntall	**927**	1,000	984651357	1,089,478,592	0h28m34s	5,612	0.272	0.613	111	57	***3***	1	
10D	Sphingidae	**64**	EF&DDC ntall	**927**	10,000	984651357	10,649,000,000	4h37m6s	5,612	0.272	0.613	237	1335	***3***	1	
16A	Sphingidae&2OG	**66**	EF&DDC ntall	**975**	10	644781007	12,183,998	0h0m15s	6,280	0.259	0.588	18	8	***3***	1	2160
16B	Sphingidae&2OG	**66**	EF&DDC ntall	**975**	100	644781007	136,286,734	0h2m43s	6,280	0.259	0.588	39	20	***3***	1	
16C	Sphingidae&2OG	**66**	EF&DDC ntall	**975**	1,000	644781007	1,296,544,020	0h26m3s	6,280	0.259	0.588	82	44	***3***	1	
16D	Sphingidae&2OG	**66**	EF&DDC ntall	**975**	10,000	644781007	12,742,000,000	4h17m3s	6,280	0.259	0.588	216	125	***3***	1	
22	Lepidoptera-dups	**77**	EF&DDC nt1&2	**322**	421	281468754	116,140,000,000	42h47m5s	1,209	0.343	0.629	6369	112	***243***	43	2435
9	Bombycoidea	**72**	EF&DDC nt1&2	**247**	337	436992825	81,847,000,000	26h21m53s	814	0.365	0.715	36177	200	***1296***	2	2000
20A	Sph+Bomby-dups	**58**	EF&DDC nt1&2	**247**	10	137523599	95,099,680	0h0m32s	779	0.379	0.671	295	5	***234***	3	821
20B	Sph+Bomby-dups	**58**	EF&DDC nt1&2	**247**	100	137523599	1,346,074,986	0h7m34s	779	0.379	0.671	1494	55	***234***	3	
20C	Sph+Bomby-dups	**58**	EF&DDC nt1&2	**247**	1,000	137523599	10,309,000,000	0h58m12s	779	0.379	0.671	5942	431	***234***	3	
20D	Sph+Bomby-dups	**58**	EF&DDC nt1&2	**247**	10,000	137523599	100,430,000,000	9h44m56s	779	0.379	0.671	13777	1697	***234***	3	
21A	Sph&2OG-dups	**52**	EF&DDC nt1&2	**226**	10	870775331	61,188,966	0h0m29s	667	0.385	0.660	583	9	***223***	4	885
21B	Sph&2OG-dups	**52**	EF&DDC nt1&2	**226**	100	870775331	495,436,250	0h3m30s	667	0.385	0.660	1684	79	***235***	6	
21C	Sph&2OG-dups	**52**	EF&DDC nt1&2	**226**	1,000	870775331	3,781,100,000	0h31m0s	667	0.385	0.660	6131	545	***235***	6	
21D	Sph&2OG-dups	**52**	EF&DDC nt1&2	**226**	10,000	870775331	35,156,000,000	4h44m29s	667	0.385	0.660	16593	2127	***235***	6	
19A	Sphingidae-dups	**50**	EF&DDC nt1&2	**195**	10	80275767	79,361,196	0h0m32s	559	0.392	0.693	1731	8	***994***	1	35
19B	Sphingidae-dups	**50**	EF&DDC nt1&2	**195**	100	80275767	446,032,648	0h3m1s	559	0.392	0.693	3867	72	***994***	1	
19C	Sphingidae-dups	**50**	EF&DDC nt1&2	**195**	1,000	80275767	3,546,100,000	0h28m38s	559	0.392	0.693	12034	490	***994***	1	
19D	Sphingidae-dups	**50**	EF&DDC nt1&2	**195**	10,000	80275767	25,879,000,000	3h10m15s	559	0.392	0.693	29375	2468	***994***	1	

Table 20. Performance of data on alternative topologies, evaluated under the criterion of maximum parsimony (MP). Variable (i.e., autapomorphic and parsimony-informative) characters from EF, DDC and combined EF&DDC data matrices were mapped onto the sets of MP topologies derived from independent analyses on the Sphingidae&2OG taxon set from each data matrix. Each row in the data table indicates a unique topology: for EF, 2 of 161MP trees filtered for compatibility with the 50% majority rule consensus tree; for DDC, all 10MP trees; for combined EF&DDC, all 3MP trees. Data from the three matrices was optimized onto each topology, and four parsimony-based performance measures were recorded: 'length' indicates total of all inferred character state changes across a topology, and is minimized when the original data set is mapped onto its own tree (see shaded cells); '%diff' indicates the percentage increase in tree length incurred for a given data set relative to the minimal observed length (shaded cells); 'ci' and 'ri' are the consensus and retention indices, respectively. Mean values for all four measures were calculated across the three data matrices for each tree, as a measure of overall parsimony penalty imposed by mapping one data set on another's topology. That topology with lowest mean 'length' and '%diff' and highest 'ci' and 'ri' was selected as the optimal MP tree for a given data set. These trees are indicated by an asterisk and were used as seed topologies for maximum likelihood parameter estimation and heuristic searches. The procedure was repeated for (a) all nt and (b) nt1 & nt2 only within each data set.

(a) all nt positions

		Data Partition															
		EF				DDC				ED				Mean Values			
	Trees	length	*%diff*	ci	ri	length	*%diff*	ci	ri	length	*%diff*	ci	ri	length	*%diff*	ci	ri
EF	**i**	1705	*0.00*	0.300	0.549	4785	*6.71*	0.233	0.576	6490	*3.34*	0.251	0.570	4327	***3.35***	**0.261**	**0.565**
	***ii**	1705	*0.00*	0.300	0.549	4782	*6.65*	0.233	0.577	6487	*3.30*	0.251	0.570	4325	***3.31***	**0.261**	**0.565**
DDC	**i**	1802	*5.69*	0.284	0.512	4484	*0.00*	0.249	0.611	6286	*0.10*	0.259	0.588	4191	***1.93***	**0.264**	**0.570**
	ii	1808	*6.04*	0.283	0.510	4484	*0.00*	0.249	0.611	6292	*0.19*	0.259	0.587	4195	***2.08***	**0.264**	**0.569**
	iii	1800	*5.57*	0.284	0.513	4484	*0.00*	0.249	0.611	6284	*0.06*	0.259	0.588	4189	***1.88***	**0.264**	**0.571**
	iv	1807	*5.98*	0.283	0.510	4484	*0.00*	0.249	0.611	6291	*0.18*	0.259	0.588	4194	***2.05***	**0.264**	**0.570**
	***v**	1798	*5.45*	0.284	0.514	4484	*0.00*	0.249	0.611	6282	*0.03*	0.259	0.588	4188	***1.83***	**0.264**	**0.571**
	vi	1800	*5.57*	0.284	0.513	4484	*0.00*	0.249	0.611	6284	*0.06*	0.259	0.588	4189	***1.88***	**0.264**	**0.571**
	vii	1805	*5.87*	0.283	0.511	4484	*0.00*	0.249	0.611	6289	*0.14*	0.259	0.588	4193	***2.00***	**0.264**	**0.570**
	viii	1806	*5.92*	0.283	0.511	4484	*0.00*	0.249	0.611	6290	*0.16*	0.259	0.588	4193	***2.03***	**0.264**	**0.570**
	ix	1800	*5.57*	0.284	0.513	4484	*0.00*	0.249	0.611	6284	*0.06*	0.259	0.588	4189	***1.88***	**0.264**	**0.571**
	x	1806	*5.92*	0.283	0.511	4484	*0.00*	0.249	0.611	6290	*0.16*	0.259	0.588	4193	***2.03***	**0.264**	**0.570**
E+Dntall	***i**	1787	*4.81*	0.286	0.518	4493	*0.20*	0.248	0.610	6280	*0.00*	0.259	0.588	4187	***1.67***	**0.264**	**0.572**
	ii	1786	*4.75*	0.286	0.518	4494	*0.22*	0.248	0.610	6280	*0.00*	0.259	0.588	4187	***1.66***	**0.264**	**0.572**
	iii	1787	*4.81*	0.286	0.518	4493	*0.20*	0.248	0.610	6280	*0.00*	0.259	0.588	4187	***1.67***	**0.264**	**0.572**

(b) nt1 & nt2 positions only (nt3 excluded)

		Data Partition, excluding nt3															
		EFnt12				DDCnt12				EDnt12				Mean Values			
Trees		length	*%diff*	ci	ri	length	*%diff*	ci	ri	length	*%diff*	ci	ri	length	*%diff*	ci	ri
EF	**i**	135	*0.00*	0.267	0.610	643	*9.17*	0.350	0.678	778	*6.87*	0.335	0.667	519	***5.35***	**0.317**	**0.652**
	ii	135	*0.00*	0.267	0.610	643	*9.17*	0.350	0.678	778	*6.87*	0.335	0.667	519	***5.35***	**0.317**	**0.652**
DDC	**i**	139	*2.96*	0.259	0.594	590	*0.17*	0.381	0.719	729	*0.14*	0.358	0.699	486	***1.09***	**0.333**	**0.671**
	ii	139	*2.96*	0.259	0.594	591	*0.34*	0.381	0.718	730	*0.27*	0.358	0.698	487	***1.19***	**0.333**	**0.670**
	iii	139	*2.96*	0.259	0.594	590	*0.17*	0.381	0.719	729	*0.14*	0.358	0.699	486	***1.09***	**0.333**	**0.671**
	iv	139	*2.96*	0.259	0.594	591	*0.34*	0.381	0.718	730	*0.27*	0.358	0.698	487	***1.19***	**0.333**	**0.670**
	***v**	138	*2.22*	0.261	0.598	589	*0.00*	0.382	0.720	727	*-0.14*	0.359	0.700	485	***0.69***	**0.334**	**0.673**
	vi	138	*2.22*	0.261	0.598	589	*0.00*	0.382	0.720	727	*-0.14*	0.359	0.700	485	***0.69***	**0.334**	**0.673**
	vii	138	*2.22*	0.261	0.598	590	*0.17*	0.381	0.719	728	*0.00*	0.359	0.699	485	***0.80***	**0.334**	**0.672**
	viii	138	*2.22*	0.261	0.598	590	*0.17*	0.381	0.719	728	*0.00*	0.359	0.699	485	***0.80***	**0.334**	**0.672**
	ix	138	*2.22*	0.261	0.598	589	*0.00*	0.382	0.720	727	*-0.14*	0.359	0.700	485	***0.69***	**0.334**	**0.673**
	x	138	*2.22*	0.261	0.598	590	*0.17*	0.381	0.719	728	*0.00*	0.359	0.699	485	***0.80***	**0.334**	**0.672**
E+Dntall	***i**	140	*3.70*	0.257	0.591	588	*-0.17*	0.383	0.721	728	*0.00*	0.359	0.699	485	***1.18***	**0.333**	**0.670**
	ii	140	*3.70*	0.257	0.591	588	*-0.17*	0.383	0.721	728	*0.00*	0.359	0.699	485	***1.18***	**0.333**	**0.670**
	iii	140	*3.70*	0.257	0.591	588	*-0.17*	0.383	0.721	728	*0.00*	0.359	0.699	485	***1.18***	**0.333**	**0.670**

Table 21. Iterative maximum liklihood (ML) model parameter estimation and heuristic searches. For each data matrix, ten parameters in the GTR+I+G nucleotide substitution model were estimated from the data based on all three starting topologies derived from MP analyses of EF, DDC and combined EF&DDC data (see Figures 6, 7 & 8, and Table 20). Parameter values from this first stage (estimate i) were then fixed in the GTR+I+G model, and TBR branch swapping was conducted on the original MP starting topology until a maximum likelihood heuristic search located a globally optimal topology (tree A). That tree was in turn used as input for parameter re-estimation (estimate ii), and those parameters fixed for a random addition sequence heuristic search using SPR branch swapping to locate the ML topology (tree B). This cycle was repeated two more times for each data set, and the estimate at which parameter values first converged is indicated in boldface. Topologies generated after each iteration were compared across starting trees, and identical topologies are indicated by shared symbols: 'e' for EF data, 'd' for DDC data and 'c' for combined data. Notes about the heuristic search itself are presented in italics, including ranges of likelihood scores for suboptimal trees encountered on different islands. All characters, including invariant and autapomorphic sites, were included in these analyses. This procedure was repeated for each of three MP starting topologies within a given data set, and all three convergent parameter estimates from each data set (boldface) are presented in the summary table. The two topologies generated by ML analayis of combined EF&DDC data differ only in relative placement of Pachysphinx and Paonis. Note, cases in which -lnL scores differ between the tree and the previous estimate (iv) are attributable to use of different numbers of discrete rate categories (4 vs. 8) to approximate the gamma distribution.

Start				Equilibrium Base Frequencies				Relative Rate Parameters							Gamma
Tree	Iteration	-lnL	Tree	A	C	G	T	AC	AG	AT	CG	CT	GT	pInv	Shape
EF	estimate i	9866.40890		0.270037	0.264224	0.224773	0.240966	2.083831	13.309599	5.201402	2.215088	22.999231	1.0	0.624215	0.724428
	tree A	9848.71090	e	*95,173 rearrangements*											
	estimate ii	**9836.20528**		**0.271855**	**0.260711**	**0.224495**	**0.242939**	**2.261761**	**13.998292**	**5.385792**	**2.310256**	**25.061543**	**1.0**	**0.616341**	**0.679515**
	tree B	9849.20925	e	*84,390 rearrangements; 6 other islands [9849.30124...9874.18398]*											
	estimate iii	9836.20528		0.271855	0.260711	0.224495	0.242939	2.261761	13.998292	5.385792	2.310256	25.061543	1.0	0.616341	0.679515
	tree C	9849.20925	e	*100,170 rearrangements; 2 identical ML trees (including two trichotomies) from two separate islands; 5 other islands [9849.30124...9875.47942]*											
	estimate iv	9836.20528		0.271855	0.260711	0.224495	0.242939	2.261761	13.998292	5.385792	2.310256	25.061543	1.0	0.616341	0.679515
	tree D	9849.20925	e	*300,393 rearrangements; 13 other islands [9849.30124...9889.82807]*											
DDC	estimate i	10013.46872		0.268910	0.259672	0.224306	0.247112	2.208843	13.597483	4.878705	2.189306	23.425677	1.0	0.623982	0.693267
	tree A	9836.54721		*72,110 rearrangements*											
	estimate ii	9836.26202		0.272504	0.260927	0.223731	0.242837	2.290440	14.341559	5.432694	2.354036	25.382307	1.0	0.615662	0.675366
	tree B	9849.33662		*68,598 rearrangements; 2 different ML trees from same island; 4 other islands [9853.83292...9871.80406]*											
	estimate iii	9836.26202		0.272504	0.260927	0.223731	0.242837	2.290440	14.341559	5.432694	2.354036	25.382307	1.0	0.615662	0.675366
	tree C	9849.28293	e	*131,160 rearrangements; 7 other islands [9849.33661...9893.33645]*											
	estimate iv	**9836.20528**		**0.271855**	**0.260711**	**0.224495**	**0.242939**	**2.261761**	**13.998292**	**5.385792**	**2.310256**	**25.061543**	**1.0**	**0.616341**	**0.679515**
	tree D	9836.20528	e	*79,726 rearrangements; 7 other islands [9836.28013...9866.91601]*											
EF&DDC	estimate i	10009.72970		0.267098	0.262628	0.224041	0.246232	2.211722	13.461395	4.920453	2.166527	22.954691	1.0	0.624388	0.702701
	tree A	9836.56188		*76,198 rearrangements*											
	estimate ii	9836.26202		0.272504	0.260927	0.223731	0.242837	2.290440	14.341559	5.432694	2.354036	25.382307	1.0	0.615662	0.675366
	tree B	9836.22323	e	*30,139 rearrangements; 8 other islands [9840.1406...9853.41955]*											
	estimate iii	**9836.20528**		**0.271855**	**0.260711**	**0.224495**	**0.242939**	**2.261761**	**13.998292**	**5.385792**	**2.310256**	**25.061543**	**1.0**	**0.616341**	**0.679515**
	tree C	9836.20528	e	*84,440 rearrangements; 4 other islands [9836.28013...9868.09629]*											
	estimate iv	9836.20528		0.271855	0.260711	0.224495	0.242939	2.261761	13.998292	5.385792	2.310256	25.061543	1.0	0.616341	0.679515
	tree D	9836.20528	e	*110,395 rearrangements; 7 other islands [9836.28013...9875.26308]*											

(b) DDC data

Start				Equilibrium Base Frequencies				Relative Rate Parameters							Gamma
Tree	Iteration	-lnL	Tree	A	C	G	T	AC	AG	AT	CG	CT	GT	pInv	Shape
EF	estimate i	21315.34521		0.265803	0.218021	0.216613	0.298963	1.548052	5.708376	1.352207	1.136922	6.707771	1.0	0.513455	1.415038
	tree A	20776.05376	d	*84,875 rearrangements*											
	estimate ii	**20771.82306**		**0.274066**	**0.219258**	**0.215995**	**0.290681**	**1.502608**	**5.571131**	**1.333153**	**1.150866**	**6.838060**	**1.0**	**0.510070**	**1.399595**
	tree B	20775.55706	d	*51,995 rearrangements; 1 other island [20781.32586]*											
	estimate iii	20771.82306		0.274066	0.219258	0.215995	0.290681	1.502608	5.571131	1.333153	1.150866	6.838060	1.0	0.510070	1.399595
	tree C	20775.55706	d	*69,039 rearrangements; 1 other island [20781.32586]*											
	estimate iv	20771.82306		0.274066	0.219258	0.215995	0.290681	1.502608	5.571131	1.333153	1.150866	6.838060	1.0	0.510070	1.399595
	tree D	20775.55706	?	*output lost, tree not saved*											
DDC	estimate i	20809.12010		0.275327	0.220694	0.217132	0.286847	1.446916	5.408308	1.341116	1.129692	6.707951	1.0	0.511308	1.440494
	tree A	20776.21237	d	*77,580 rearrangements*											
	estimate ii	**20771.82036**		**0.274066**	**0.219258**	**0.215995**	**0.290681**	**1.502608**	**5.571131**	**1.333513**	**1.150866**	**6.838060**	**1.0**	**0.510070**	**1.399595**
	tree B	20775.55706	d	*55,811 rearrangements; 1 other island [20781.32586]*											

Table 21. (continued)

	estimate iii	20771.82036		0.274066	0.219258	0.215995	0.290681	1.502608	5.571131	1.333513	1.150866	6.838060	1.0	0.510070	1.399595
	tree C	20775.55706	d	*70,081 rearrangements; 1 other island [20781.32586]*											
	estimate iv	20771.82036		0.274066	0.219258	0.215995	0.290681	1.502608	5.571131	1.333513	1.150866	6.838060	1.0	0.510070	1.399595
	tree D	20775.55706	d	*173,018 rearrangements; 1 other island [20781.32586]*											
EF&DDC	estimate i	20807.90239		0.274008	0.220909	0.216143	0.288940	1.450891	5.456497	1.338920	1.112771	6.649230	1.0	0.511846	1.458255
	tree A	20772.05824	d	*81,920 rearrangements*											
	estimate ii	**20771.82036**		**0.274066**	**0.219258**	**0.215995**	**0.290681**	**1.502608**	**5.571131**	**1.333153**	**1.150866**	**6.838060**	**1.0**	**0.510070**	**1.399595**
	tree B	20771.82036	d	*105,992 rearrangements; 1 other island [20777.34186]*											
	estimate iii	20771.82036		0.274066	0.219258	0.215995	0.290681	1.502608	5.571131	1.333153	1.150866	6.838060	1.0	0.510070	1.399595
	tree C	20771.82036	d	*103,945 rearrangements; 1 other island [20777.34186]*											
	estimate iv	20771.82036		0.274066	0.219258	0.215995	0.290681	1.502608	5.571131	1.333153	1.150866	6.838060	1.0	0.510070	1.399595
	tree D	20771.82036	d	*72,624 rearrangements; 1 other island [20777.34186]*											

(c) combined EF&DDC EF&DDC data

Start				Equilibrium Base Frequencies				Relative Rate Parameters							Gamma
Tree	**Iteration**	**-lnL**	**Tree**	**A**	**C**	**G**	**T**	**AC**	**AG**	**AT**	**CG**	**CT**	**GT**	**pInv**	**Shape**
EF	estimate i	31641.43966		0.261769	0.241367	0.222335	0.274529	1.428825	6.378758	1.823303	1.097377	7.833578	1.0	0.574423	1.020463
	tree A	31249.93690		*79,521 rearrangements*											
	estimate ii	31241.97825		0.266192	0.241775	0.218030	0.274002	1.423766	6.397491	1.809089	1.115201	8.133311	1.0	0.573487	1.043336
	tree B	31230.35368	c1	*24,369 rearrangements; 2 other islands [31240.66054...31290.45183]*											
	estimate iii	**31221.47311**		**0.268178**	**0.240423**	**0.220771**	**0.270628**	**1.413892**	**6.385676**	**1.835360**	**1.105062**	**8.201244**	**1.0**	**0.573686**	**1.039287**
	tree C	31230.19768	c1	*45,127 rearrangements; 3 other islands [31231.03992...31277.35428]*											
	estimate iv	31221.47311		0.268178	0.240423	0.220771	0.270628	1.413892	6.385676	1.835360	1.105062	8.201244	1.0	0.573686	1.039287
	tree D	31230.19768	c1	*48,987 rearrangements; 8 other islands [31231.67144...31289.87335]*											
DDC	estimate i	31265.28480		0.267618	0.241289	0.221067	0.270025	1.386938	6.299045	1.819246	1.096481	8.030910	1.0	0.575522	1.062515
	tree A	31230.09800	c1	*74,134 rearrangements*											
	estimate ii	**31221.47311**		**0.268178**	**0.240423**	**0.220771**	**0.270628**	**1.413892**	**6.385676**	**1.835360**	**1.105062**	**8.201244**	**1.0**	**0.573686**	**1.039287**
	tree B	31230.19768	c1	*64,591 rearrangements; 3 other islands [31238.09553...31260.53561]*											
	estimate iii	31221.47311		0.268178	0.240423	0.220771	0.270628	1.413892	6.385676	1.835360	1.105062	8.201244	1.0	0.573686	1.039287
	tree C	31230.19768	c1	*50,298 rearrangements; 4 other islands [31233.92265...31281.97766]*											
	estimate iv	31221.47311		0.268178	0.240423	0.220771	0.270628	1.413892	6.385676	1.835360	1.105062	8.201244	1.0	0.573686	1.039287
	tree D	31230.19768	c1	*69,814 rearrangements; 5 other islands [31250.22379...31285.65724]*											
EF&DDC	estimate i	31263.23365		0.265896	0.242508	0.220701	0.270894	1.399164	6.336312	1.831596	1.087868	7.967988	1.0	0.575700	1.070484
	tree A	31221.48129	c2	*81,979 rearrangements*											
	estimate ii	**31221.29642**		**0.268032**	**0.240620**	**0.220863**	**0.270486**	**1.411799**	**6.379233**	**1.834034**	**1.101840**	**8.187761**	**1.0**	**0.574004**	**1.043732**
	tree B	31221.29642	c2	*32,506 rearrangements; 2 other islands [31271.57985...31274.37460]*											
	estimate iii	31221.29642		0.268032	0.240620	0.220863	0.270486	1.411799	6.379233	1.834034	1.101840	8.187761	1.0	0.574004	1.043732
	tree C	31221.29642	c2	*23,503 rearrangements; 3 other islands [31254.30769...31271.14336]*											
	estimate iv	31221.29642		0.268032	0.240620	0.220863	0.270486	1.411799	6.379233	1.834034	1.101840	8.187761	1.0	0.574004	1.043732
	tree D	31221.29642	?	*17,046 rearrangements; output lost, tree not saved*											

(d) Summary

	Starting				Equilibrium Base Frequencies				Relative Rate Parameters							Gamma
Data	**MP Tree**	**Iteration**	**-lnL**	**Tree**	**A**	**C**	**G**	**T**	**AC**	**AG**	**AT**	**CG**	**CT**	**GT**	**pInv**	**Shape**
	EF	estimate ii	9836.20528	e	0.271855	0.260711	0.224495	0.242939	2.261761	13.998292	5.385792	2.310256	25.061543	1.0	0.616341	0.679515
EF	DDC	estimate iv	9836.20528	e	0.271855	0.260711	0.224495	0.242939	2.261761	13.998292	5.385792	2.310256	25.061543	1.0	0.616341	0.679515
	EF&DDC	estimate iii	9836.20528	e	0.271855	0.260711	0.224495	0.242939	2.261761	13.998292	5.385792	2.310256	25.061543	1.0	0.616341	0.679515
	EF	estimate ii	20771.82306	d	0.274066	0.219258	0.215995	0.290681	1.502608	5.571131	1.333153	1.150866	6.838060	1.0	0.510070	1.399595
DDC	DDC	estimate ii	20771.82036	d	0.274066	0.219258	0.215995	0.290681	1.502608	5.571131	1.333513	1.150866	6.838060	1.0	0.510070	1.399595
	EF&DDC	estimate ii	20771.82036	d	0.274066	0.219258	0.215995	0.290681	1.502608	5.571131	1.333153	1.150866	6.838060	1.0	0.510070	1.399595
	EF	estimate iii	31221.47311	c1	0.268178	0.240423	0.220771	0.270628	1.413892	6.385676	1.835360	1.105062	8.201244	1.0	0.573686	1.039287
EF&DDC	DDC	estimate ii	31221.47311	c1	0.268178	0.240423	0.220771	0.270628	1.413892	6.385676	1.835360	1.105062	8.201244	1.0	0.573686	1.039287
	EF&DDC	estimate ii	31221.29642	c2	0.268032	0.240620	0.220863	0.270486	1.411799	6.379233	1.834034	1.101840	8.187761	1.0	0.574004	1.043732

Table 22. Performance of data on alternative topologies, evaluated under the criterion of maximum likelihood (ML). Parameters of the GTR+I+G model specific to each data matrix were fixed (see Table 21d) and used to calculate likelihood scores by fitting the EF, DDC and combined EF&DDC data to the sets of (a) four ML topologies (Table 21) and (b) fifteen MP topologies (Table 20) derived from separate analyses on the Sphingidae&2OG taxon set. Each row in the data table indicates a unique topology, and the columns correspond to the single models optimized for EF and DDC, and the two models optimized for the combined EF&DDC data. Values in bold indicate topologies with maximum likelihood, which best explain the observed distribution of character states given the specified model of nucleotide substitution.

(a) Maximum Likelihood topologies

		Model			
Topology		**EF**	**DDC**	**EF&DDCi**	**EF&DDCii**
EF		**9831.17404**	21287.25301	31582.35831	31582.35202
DDC		10028.65251	**20772.01394**	31238.01742	31238.00865
EF&DDC	i	9986.24572	20784.15003	31221.28558	31221.27737
EF&DDC	ii	9989.40732	20782.12303	**31221.11648**	**31221.11370**

(b) Maximum Parsimony topologies

		Model			
Topology		**EF**	**DDC**	**EF&DDCi**	**EF&DDCii**
EF	i	**9855.42474**	21315.95287	31639.78980	31639.79569
	ii	9857.96464	21310.96800	31637.28333	31637.28812
DDC	i	10010.20405	20811.23203	31267.72705	31267.71504
	ii	10016.50019	20811.86241	31275.90706	31275.89242
	iii	10008.63221	20811.54285	31265.84700	31265.83585
	iv	10014.91693	20812.17336	31274.03314	31274.01942
	v	10008.63221	20809.34130	31264.49019	31264.47856
	vi	10010.20405	20809.34130	31265.77540	31265.76321
	vii	10014.91693	20809.97158	31272.67753	31272.66333
	viii	10016.50020	20809.97158	31273.95927	31273.94445
	ix	10010.20405	20809.34130	31265.77540	31265.76321
	x	10016.50020	20809.97158	31273.95927	31273.94445
EF&DDC	i	10004.78418	20808.06890	31262.74412	31262.72189
	ii	10001.32864	**20805.01000**	**31257.69963**	**31257.68088**
	iii	10003.75880	20809.61940	31264.33443	31264.31172

Figure 1. Phylogenetic relatedness among fourteen genera of Sphingidae (Lepidoptera: Bombycoidea) presented in the pilot study of Regier, *et al.* (2001). Topology derived from phylogenetic analysis under the criterion of maximum parsimony for combined EF&DDC nucleotide data (1,240bp EF; 709bp DDC), excluding third codon positions (nt3). Number of parsimony-informative characters was 502 for all nucleotides, and 84 when nt3 were excluded. Bootstrap proportions and decay indices compiled from analyses on all data and excluding nt3 are presented above each internal branch. Number of synapomorphies and percentage average pairwise difference are mapped below each branch, calculated separately for each codon position within EF and DDC partitions. Outgroups consisted of two genera each from two other bombycoid families, Brahmaeidae and Saturniidae. Monophyletic recognized higher taxonomic groups and selected life history traits of special interest are mapped onto the topology. Copied from Figure 1 of Regier, *et al.* 2001.

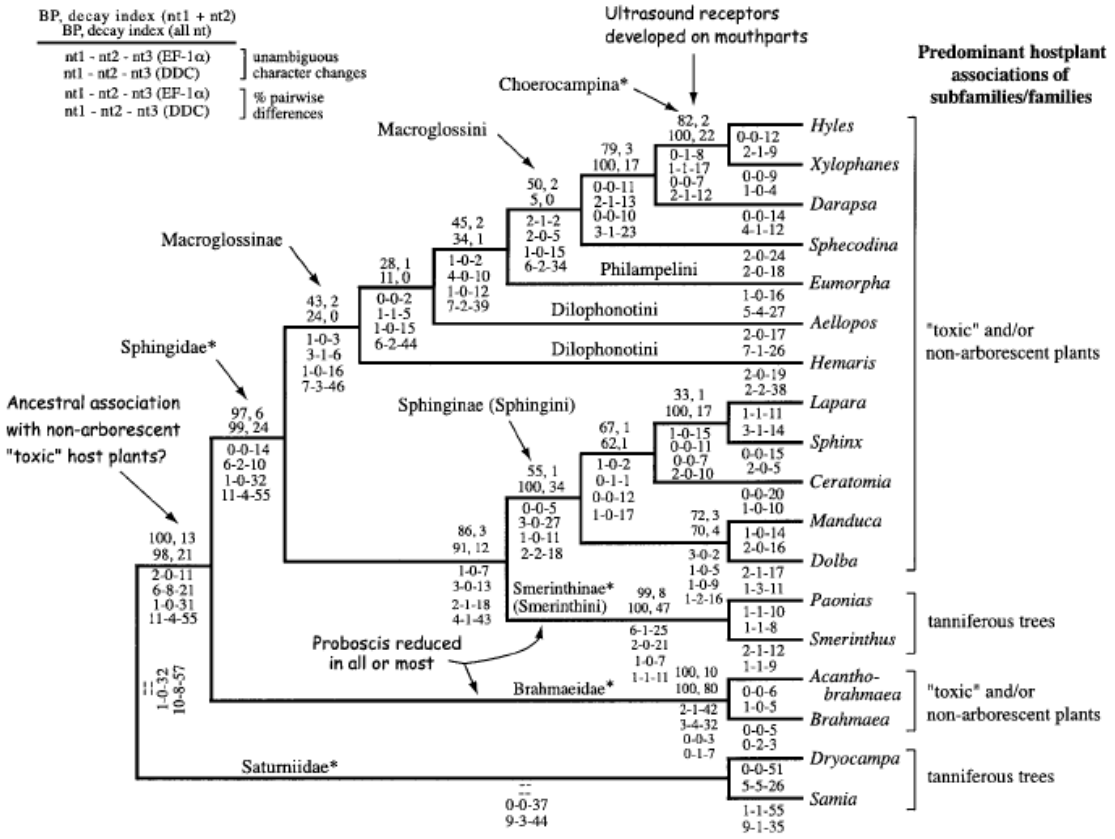

Figure 2. Instructions distributed to sphingid collectors. The following one-page instruction sheet was distributed to participating collectors in Fall 2002 and Spring 2003 as part of a Sphingidae collection kit containing labeled vials filled with 100% ethanol, glassine envelopes, blank data sheets and return postage. Special emphasis was placed on conveying the importance of complete immersion in 100% ethanol immediately after death to ensure viable tissue for nucleic acid extraction (see guideline #2).

Collecting Adult Sphingidae for DNA Analysis

UNIVERSITY OF MARYLAND
Department of Entomology (MCSE)
Plant Sciences Building, room 4138
College Park, MD 20742 USA

ANDRÉ MIGNAULT
tel: **301-405-2089**
fax: **301-314-9290**
email: **mignault@wam.umd.edu**

Project Description:

In conjunction with my advisors, Drs. Charlie Mitter and Jerry Regier, I am pursuing a **molecular phylogeny of the Sphingidae** (Lepidoptera: Bombycoidea) to provide a foundation for understanding life history evolution in this spectacular group. I am collecting adult moths from every sphingid genus worldwide, as delineated in Kitching & Cadiou's (2000) comprehensive taxonomic revision, with special emphasis on obtaining all North American species because of their notably diverse life history strategies.

Collection Guidelines:

1. Only **one to three specimens of each taxon** freshly collected into 100% ethanol are required for this project. I would gladly accept surplus specimens collected in glassine envelopes in the traditional manner for pinning and incorporation into the collection as voucher specimens.
2. As soon as a moth dies, its nucleic acids (DNA and RNA) begin to break down. This process is rapid and irreversible, and jeopardizes our ability to obtain useful molecular data from a specimen. It is critical that **as soon as possible after death the moth be processed into 100% ethanol**, a non-toxic preservative which desiccates the specimen and retards processes of cellular degradation. Obtaining viable molecular data from a freshly processed specimen is nearly foolproof. Specimens long-dead or preserved in a medium containing any water may still be useful, but chances for success are diminished.
3. After capturing a moth, store it in a cool place to keep it alive until processing. Immediately after killing the moth, carefully **remove the wings from the body*** (e.g., via forceps or surgical scissors) and place them into a glassine envelope labeled in pencil or waterproof pen. **Insert the wingless body into a numbered vial of 100% ethanol** provided for you. The body of an extremely large specimen may be cut into smaller fragments and placed into several vials. Also, multiple smaller specimens (e.g., of the same genus or species) may be safely fit into a single vial to save space.

** I realize this unconventional collecting method requires more time and effort than you may be able to invest. If the entire moth can be inserted into the ethanol vial without destroying its wings then I can process the wings after receiving it. Again, it is most critical that the **body (with or without wings) be submerged into the ethanol as soon as possible after death**.*

4. Record specimen collection information as specifically as possible. **Location, date and time** of collection are crucial. Moth identification, sex, method of collection, time since death or other notes of interest (e.g., weather, elevation) are also most welcome if you have the occasion to record them.
5. These vials hold liquid quite well if the caps are screwed on snugly (paraffin is included to wrap the caps if any doubt). Once the specimen has been sealed in the vial and its wings stored in a labeled envelope, it requires no further processing. Preservation is enhanced by keeping specimens **cold and dark**, but storage at room temperature is fine if refrigeration/freezing is not possible.
6. Return the **vials** containing moth bodies preserved in 100% ethanol, the corresponding **envelopes** containing wings and/or voucher specimens and **field collection data** for each specimen.

Please contact me if you have any questions or comments regarding the procedures described above, or details of the project as a whole. Your participation and input is greatly appreciated, and I look forward to continued correspondence with you. Many thanks for your invaluable aid in this project!

Figure 3. Data entry page of the University of Maryland Lepidoptera Collections Database. One of several screens available for viewing records in the UMD Lepidoptera Collections, the main data entry page displays fields in seven modules for all critical information about every specimen available for collection of molecular sequence data. Codes in the 'Identification' module provide unique serial identifiers for every specimen in the collections. Higher taxonomic information in the 'Taxonomy' module is autopopulated upon entry of a valid genus name, via relational lookup to a companion database of all valid genus names in Lepidoptera compiled from varied sources. Detailed collections information is compiled in the 'Specimen Profile' module, including a notes text field to accommodate special information. All specimens are stored at –80C, indexed by coordinates in the 'Specimen Location' module. Individual buttons for each gene in the 'Sequences' module lead to a separate screen detailing information about collected nucleotide sequence, including amplicon primers and GenBank numbers. Function buttons at the top of the screen perform customized scripts, including generation of reports sorted by taxonomy or accession number, and printing of preformatted labels for vials and wing vouchers. The database was created in FileMaker Pro version 3.1, customized for management of the UMD Lepidoptera Collections, and is presently available in FileMaker Pro version 6.0.

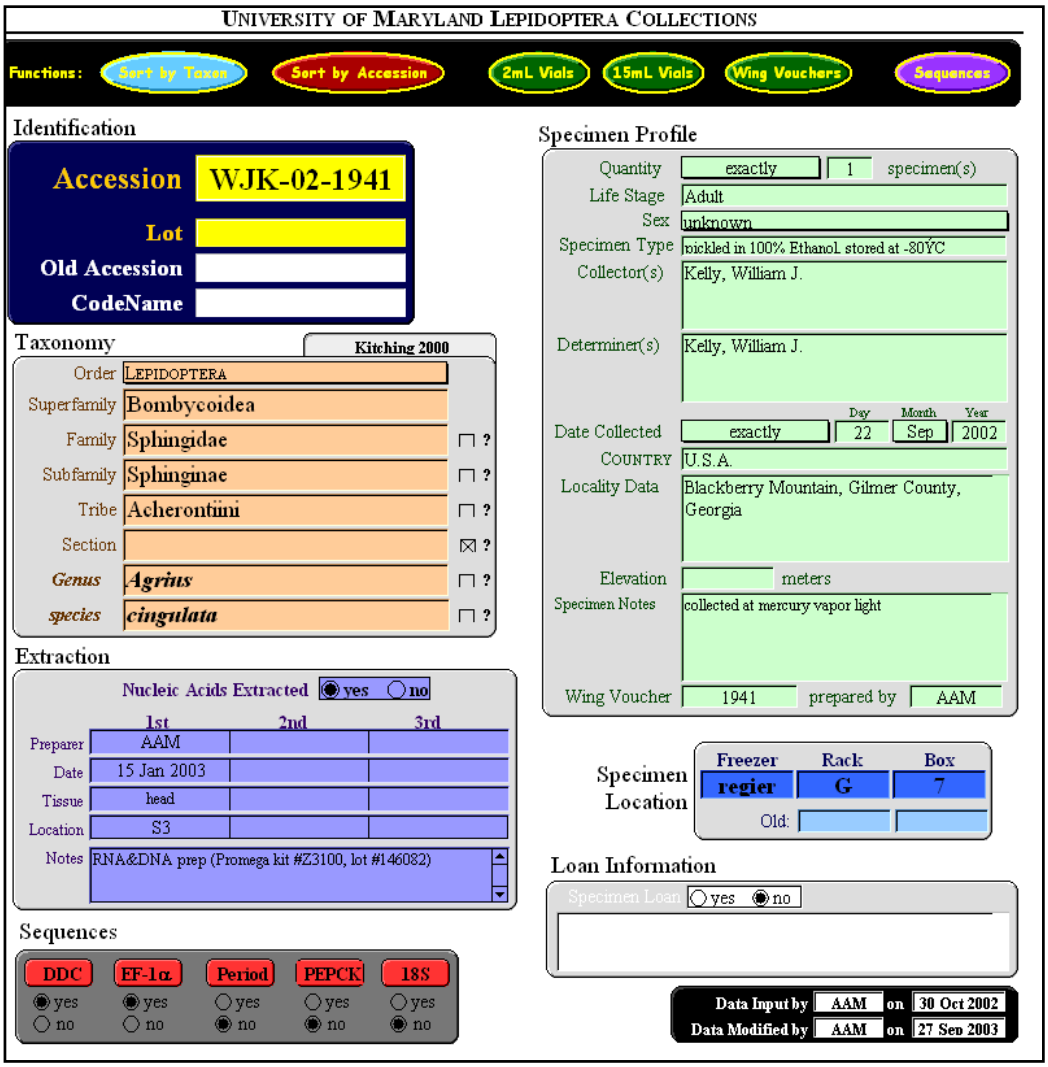

Figure 4. Reference sequence for Elongation Factor 1-alpha. Top row: *Bombyx mori* (Bombycoidea: Bombycidae) mRNA reference sequence used to standardize alignments in this study. Sequence provided by Kamiie, *et al.* (1993), Genbank accession number D13338. Base composition of 1,687 bp fragment: 500nt (29.6%) A; 396nt (23.5%) C; 375nt (22.2%) G; 416nt (24.7%) T. Bottom row: *Acherontia styx medusa* (Sphingidae) exemplar mRNA sphingid sequence. Sequenced *de novo* in this study, UMD Lepidoptera Collections accession number IJK-02-5989. Base composition of 1,274 bp fragment: 317nt (24.9%) A; 366nt (28.7%) C; 322nt (25.3%) G; 262nt (20.6%) T. '.' marks bases identical to the *Bombyx* reference sequence. Terminal primer sequences (30f and m41.21rc) were eliminated from all phylogenetic analyses. Gray boxes denote untranscribed regions, 47bp upstream of the start ATG and 1bp downstream of the stop TAG codon [note: an additional 247 bp of downstream sequence from the original Genbank accession is omitted here]. Sequences of primers used in this study contained within arrows, indicating the direction of amplification. Primer names are inserted at the primer 5' end: forward primer names above the sequence, reverse primer names below (note overlap between some primer versions). Primer sequences from Regier & Shultz (1997) are **boldface**; primers from Cho, *et al.* (1995) are *italicized*. Numbers at the ends of each line denote position relative to the fragment sequenced for this study; for example, position '1' is the 5'-most base of the terminal primer 30f and position '1,274' is the 3'-most base of the terminal primer m41.21rc.

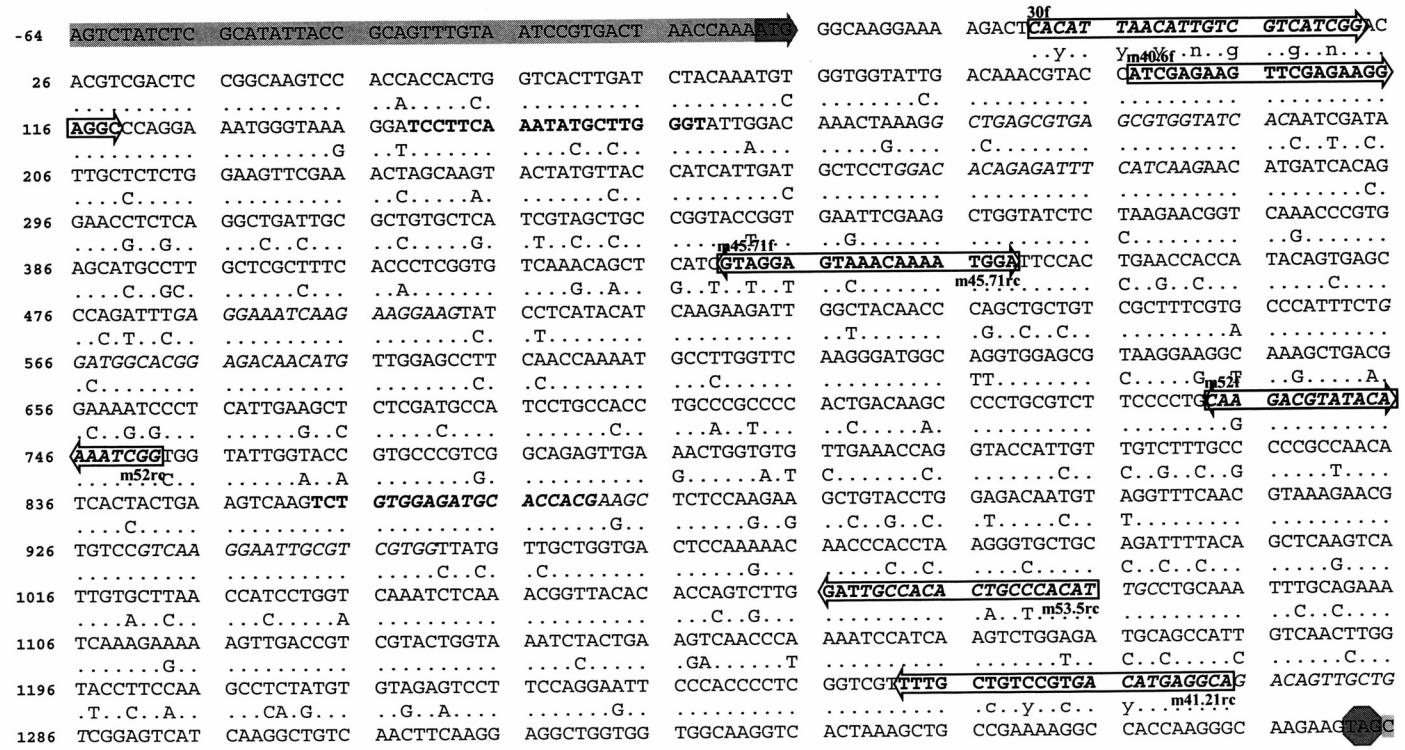

Figure 5. Reference sequence for Dopa Decarboxylase. Top row: *Manduca sexta* (Bombycoidea: Sphingidae) mRNA reference sequence used to standardize alignments in this study. Sequence provided by Hiruma, *et al.* (1995), Genbank accession number U03909. Base composition of 3,063bp fragment: 922 (30.1%) A ; 542 (17.7%) C ; 618 (20.2%) G ; 981 (32.0%) T. Bottom row: *Acherontia styx medusa* (Sphingidae) exemplar mRNA sphingid sequence. Sequenced *de novo* in this study, UMD Lepidoptera Collections accession number IJK-02-5989. Base composition of 1,373 bp fragment: 354nt (25.8%) A; 306nt (22.3%) C; 343nt (25.0%) G; 358nt (26.1%) T. '.' marks bases identical to the *Manduca* reference sequence. Terminal primer sequences (1.0F and 7.5sR) were eliminated from all phylogenetic analyses. Gray boxes denote untranscribed regions, 86bp upstream of the start ATG and 7bp downstream of the stop TAG codon [note: an additional 90bp upstream and 1,353 bp downstream sequence from the original Genbank accession is omitted here]. Sequences of primers used in this study are contained within arrows, indicating the direction of amplification. Primer names are inserted at the primer 5' end: forward primer names above the sequence, reverse primer names below (note overlap between some primer versions). Primers developed and used in the Regier Lab are **boldface** (see Tables 4 & 5). Numbers at the ends of each line denote position relative to the fragment sequenced for this study; for example, position '1' is the 5'-most base of the terminal primer 1.0F and position '1,373' is the 3'-most base of the terminal primer 7.5sR.

```
-100 TATACTTGCG CTAATTACCG AAACGCTGTG ATTAATTTGC AACAGAAAGG TCTTGCATTA GCTGATTGAA CAAAAACTTT GAAGTCATGA  -11
                1.0F
 -10 ATCCCGGAGA GTTTAAAGAC TTCGCGAAAG CGATGACTGA CTACATCACA GAGTATCTGG AAAACATTAG AGATAGACAA GTAGTGCCGT   79
                .....r..t ..t..w..rr .r...... .......... .....C.... .......... ...C...... ..........
  80 CAGTGAAGCC AGGCTACCTA CGTCCCCTAG TCCCAGAGCA GGCGCCCCAG CAAGCTGAGC CCTGGACAGC AGTGATGGCG GATATCGAAA  169
     .G........ C........G .......... ....G..T.. ......A... .......... .A........ ...A...... ..C.......
 170 GGGTGGTCAT GTCTGGCGTC ACCCACTGGC AATCACCTCG TTTCCACGCC TATTTCCCGA CGGCCAACTC TTACCCTTCT ATTGTGGCGG  259
     .......T.. ....1.7FT... ..T..T.... ....C..... G......... .........A. ....G..... A..T...G.. ........A.
 260 ATATGTTGAG CGGCGCTATT GCTTGTATCG GTTTCACCTG GATTGCAAGC CCAGCATGTA CGGAACTTGA AGTTGTTATG TTAGACTGGC  349
     .C...C.... T......... ..C..C..T. ....T..... ......G... .......... .......... .....T....
 350 TCGGTCAAAT GTTGGGTCTT CCGGACCAGT TCTTAGCACG TTCTGGCGGA GAAGGTGGCG GTGTCATCCA AGGCACTGCA AGTGAAGCCA  439
     ....C....1.9d/sR....C... .....AG... ..C....T.. ...C.....T ....C...T. ....A..... G..T...... ..........
 440 CGTTTGTAGC TCTCCTTGGT GCCAAATCTC GTATGATGCA CAGAGTCAAA GAACAACACC CCGAGTGGAC TGAGACAGAC ATTCTCGGCA  529
     ..C....... C......... .......... .C.C...... .C....T... .......... .G......T. .........T ..C..T.A..
 530 AGCTTGTAGG CTACTGCAAT CAACAGGCCC ATTCGTCAGT AGAGCGGGCT GGACTTCTTG GTGGGGTAAA ACTTAGATCA TTGAAACCGG  619
     .......... ...T..T... .....A.... ....A..... ...A..A... ..T..G.... .A..T..G.. ...G.....G ..........
 620 ATTCTAAGAG ACGCCTTCGC GGGGACACTT TGCGTGAAGC AATCGACGAG GACATTCGCA ATGGACTTAT TCCCTTCTAT GTGGTCGCCA  709
     .......... ...T.....T ..A....... .A........ ...A..A... .......... .......A.. ....3.2d/sFT.. .CT.....
 710 CATTAGGTAC CACTTCTTCG TGTGCCTTTG ACGCATTAGA TGAAATTGGA GATGTTTGCA ATGCAAGCGA TATATGGTTG CATGTGGACG  799
     ..C....C.. A.....C... .....T.... ...T.C.G.. ......A... .......... .C.......G C.......... ..........
 800 CGGCCTATGC TGGCTCTGCG TTTATTTGTC CCGAATACCG TCACTTTATG AAAGGGGTTG AAAAGGCTGA TTCTTTCAAT TTCAACCCAC  889
     .C..T..C.. C..G.....A .......... ....G..... ...T.A.... .....C.... .......... .......... ........C.
 890 ATAAATGGAT GCTTGTCAAT TTCGACTGCT CAGCTATGTG GTTGAAACAA CCGCGATGGA TTGTTGACGC GTTCAATGTG GACCCTCTGT  979
     .C..3.3R/sR..  ......T..C ..T....... .T..C..... ...A...... ..A..C.... .C........ .........A ........C.
 980 ACTTGAAGCA CGAACAGCAG GGATCGGCAC CAGACTACCG TCACTGGCAA ATTCCTTTAG GACGACGATT CAGGTCACTT AAACTGTGGT 1069
     ..C....... T..C.....A .......... .......... .......... 4dd/dn/sR..... ....T..C.. .......... ..........
1070 TCGTTTTGAG GCTGTATGGC GTAGAAAATC TTCAAAAATA CATTAGAAAA CAAATTGGAT TTGCTCACCT GTTCGAAAGG CTTTTAACTT 1159
     .T..C...C. .........A ..T.....Y. ........C. T......... .....C.... .G..G..T.K ...T...C.. ..G..GG...
1160 CGGATGAAAG ATTTGAGCTA TTTGAAGAGG TGACTATGGG GCTTGTATGT TTTAGGCTCA AAGGATCTAA TGAAATCAAT GAAGAATTAT 1249
     .A........ .........G .AC....... ....C..... ...C...... .....A..T. .......... .......... .....G....
1250 TGAGACGCAT AAATGGCCGC GGAAAAATCC ATTTAGTGCC CTCTAAAGTC GATGACGTAT ACTTCCTTAG ATTAGCAATC TGTTCACGGT 1339
     .......... T....T.... .......... .......... 7.5R/sR G..T.. A..C...A.. .......... .......... ...G..G... ........A.
1340 TCACTGAAGA AAGTGACATG CATGTATCTT GGGAAGAAAT AAAAGATCGG CTGATGATGT TCTTAAAAAG TAAGGGAGCG GTGTTGATCA 1429
     .......... ......y..y ..y..n..y. ....
1430 AAATAATCTG TTCAACAACG CGTAGGACCA AAAATATACT AACCTATATT AAACAAAATA TATTCCGTGA TGTAGGCCTT TAGATCTTAT 1519
```

Figure 6. Exemplar most parsimonious phylogram reconstructed from phylogenetic inference on EF ntall data for the Sphingidae&2OG taxon set. Single topology was one of two selected from 161 equally MP trees by filtering for consistency with the 50% majority rule consensus tree. Gray branches denote regions of conflict between the 161 alternative EF MP trees, and these collapse in the strict consensus. Number of inferred synapomorphies is plotted above each branch. Bootstrap proportions (1,145 pseudoreplicates) are italicized and plotted below each branch. Monophyletic recognized higher taxonomic groups are boxed and shaded; outlier taxa deviating from their traditional taxonomic placement are left unshaded. Paraphyletic Smerinthinae is indicated by a dashed bar.

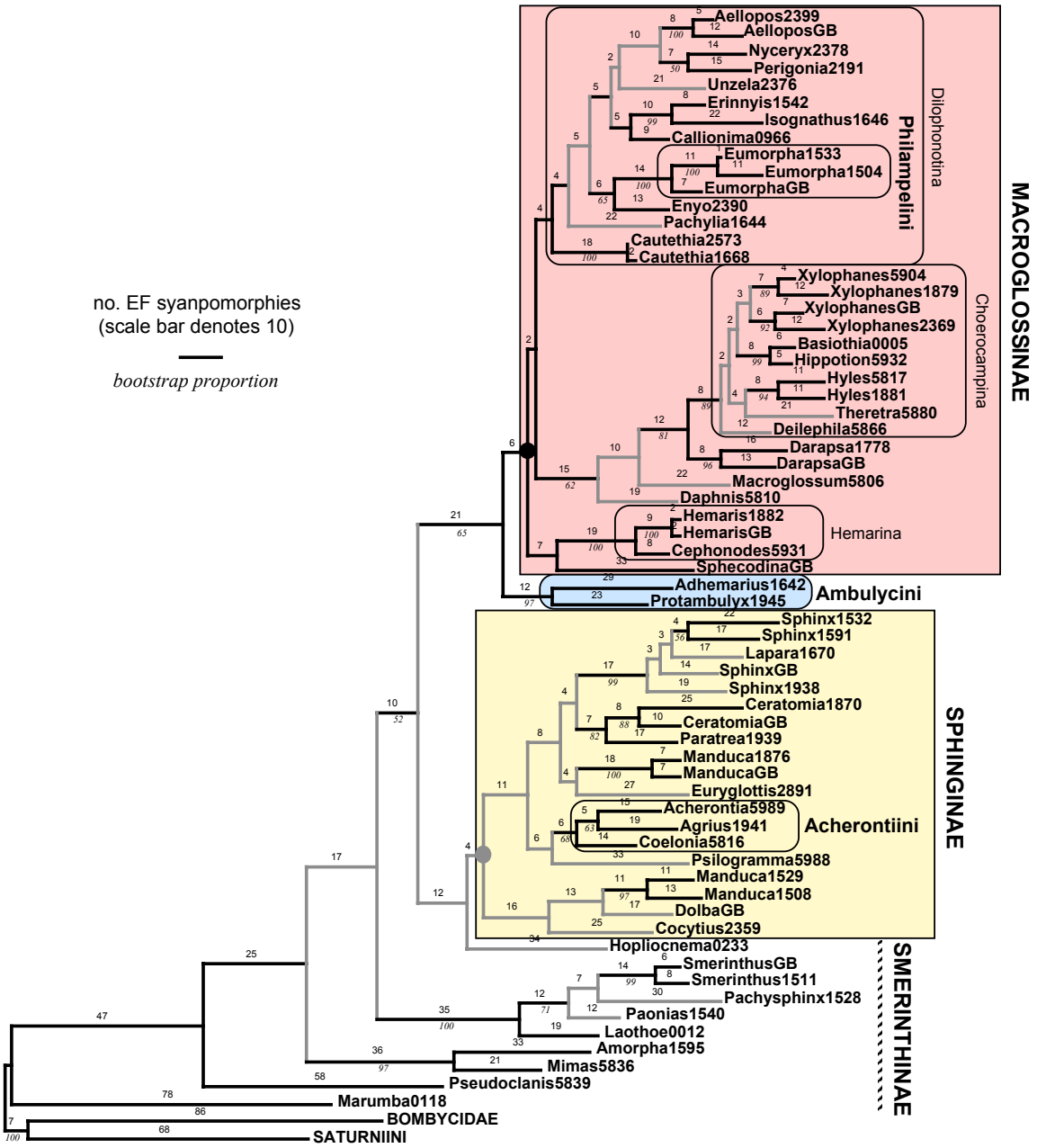

Figure 7. Exemplar most parsimonious phylogram reconstructed from phylogenetic inference on DDC ntall data for the Sphingidae&2OG taxon set. Single topology was selected from among 10 equally MP trees on the basis of parsimony mapping criteria (see asterisk in Table 20) . Gray branches denote regions of conflict between the 10 alternative DDC MP trees, and these collapse in the strict consensus. Number of inferred synapomorphies is plotted above each branch. Bootstrap proportions (1,248 pseudoreplicates) are italicized and plotted below each branch. Monophyletic recognized higher taxonomic groups are boxed and shaded; outlier taxa deviating from their traditional taxonomic placement are left unshaded. Paraphyletic Macroglossinae is indicated by a dashed bar.

Figure 8. Exemplar most parsimonious phylogram reconstructed from phylogenetic inference on combined EF&DDC ntall data for the Sphingidae&2OG taxon set. Single topology was selected randomly from among 3 equally MP trees, as parsimony mapping criteria were equivocal (see Table 20) . Gray branches denote regions of conflict between the 3 alternative EF&DDC MP trees, and these collapse in the strict consensus. Number of inferred synapomorphies is plotted above each branch. Bootstrap proportions (2,160 pseudoreplicates) are italicized and plotted below each branch. Monophyletic recognized higher taxonomic groups are boxed and shaded; outlier taxa deviating from their traditional taxonomic placement are left unshaded. Paraphyletic Smerinthinae is indicated by a dashed bar.

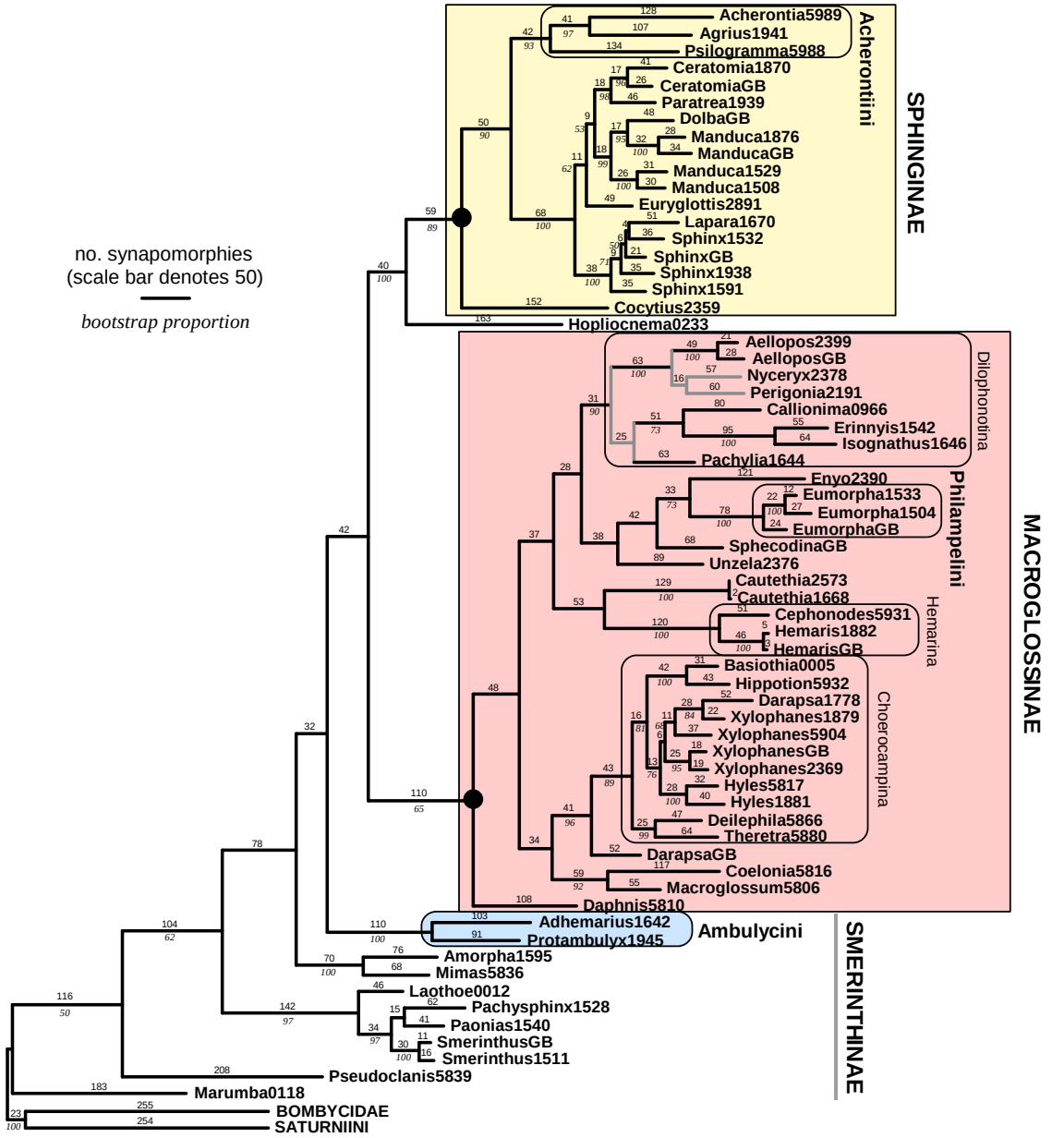

Figure 9. Maximum likelihood phylogram from phylogenetic inference on EF ntall data for the Sphingidae&2OG taxon set. Single globally convergent topology (Tree 'e' in Table 21) derived from four cycles of iterative parameter estimation / heuristic searches, using each of the MP trees in Figures 6, 7 and 8 as starting topologies. Branch length values, expressed as 1,000X number of substitutions per site along EF, are indicated above branches. Monophyletic recognized higher taxonomic groups are boxed and shaded; outlier taxa deviating from their traditional taxonomic placement are left unshaded. Paraphyletic Sphinginae and Smerinthinae are indicated by dashed bars. Inset contains maximum likelihood score of this topology and optimized parameters of the underlying GTR+I+G substitution model.

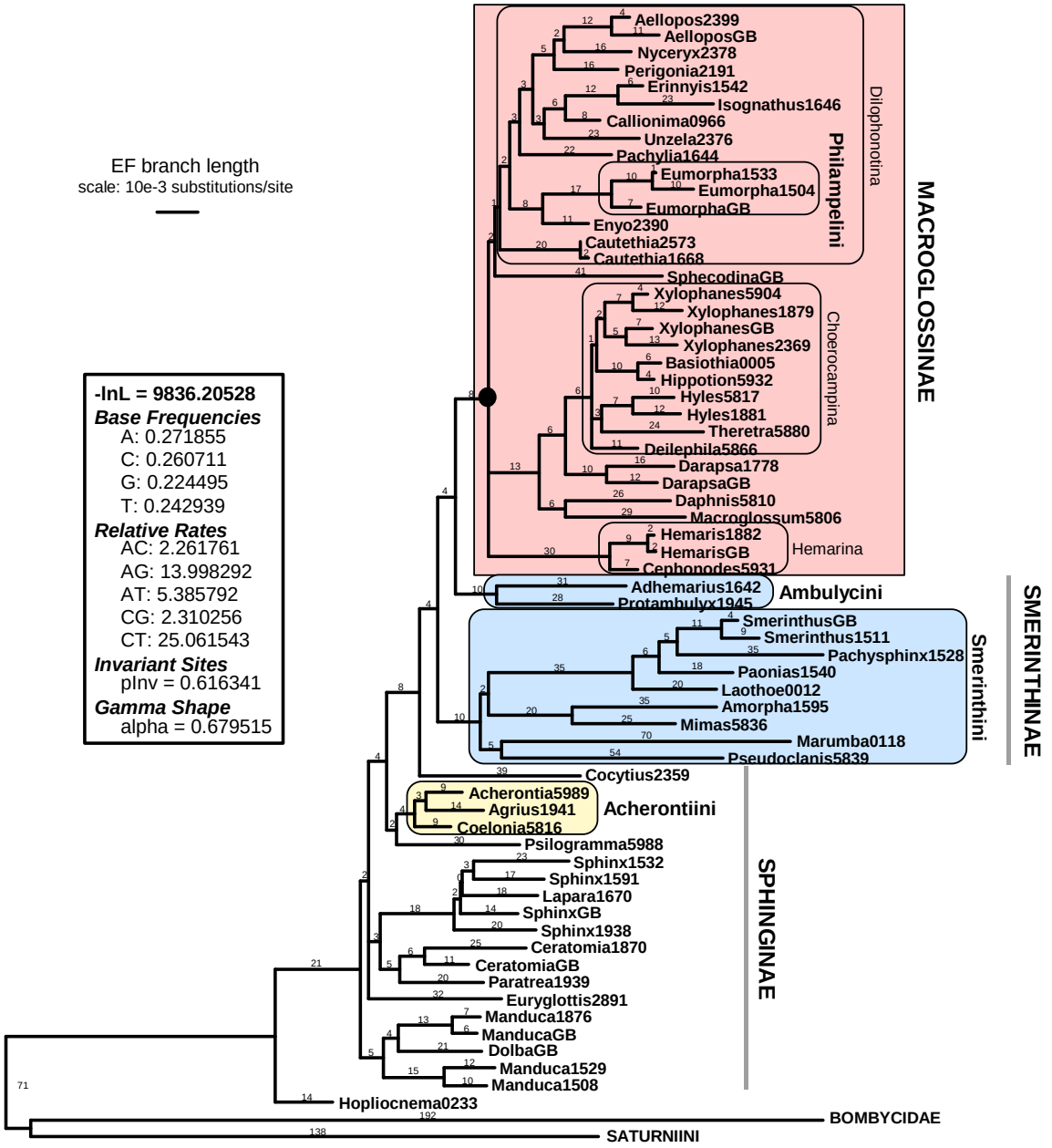

Figure 10. Maximum likelihood phylogram from phylogenetic inference on DDC ntall data for the Sphingidae&2OG taxon set. Single globally convergent topology (Tree 'd' in Table 21) derived from four cycles of iterative parameter estimation / heuristic searches, using each of the MP trees in Figures 6, 7 and 8 as starting topologies. Branch length values, expressed as 1,000X number of substitutions per site along EF, are indicated above branches. Monophyletic recognized higher taxonomic groups are boxed and shaded. Inset contains maximum likelihood score of this topology and optimized parameters of the underlying GTR+I+G substitution model.

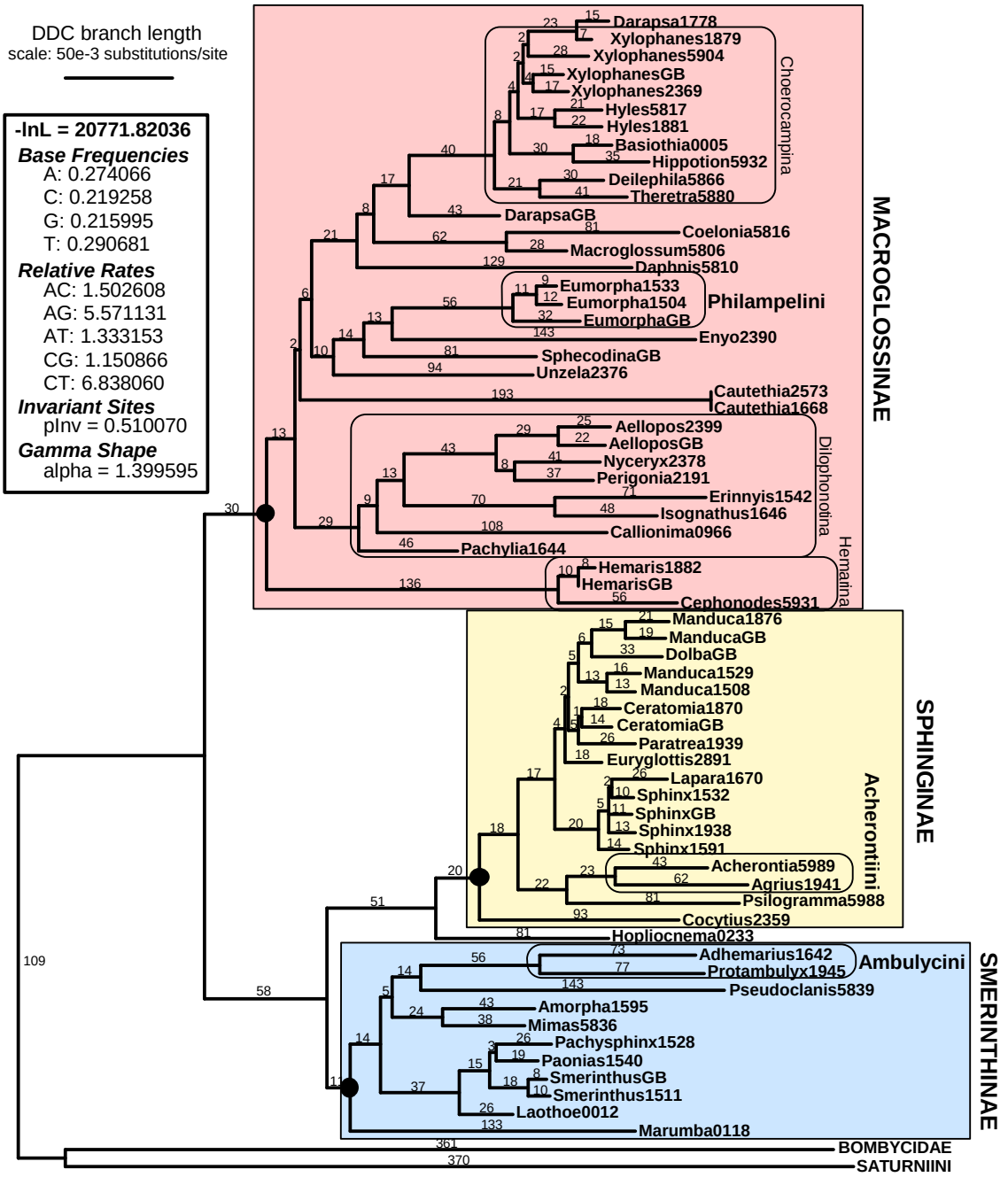

Figure 11. Exemplar maximum likelihood phylogram from phylogenetic inference on combined EF&DDC ntall data for the Sphingidae&2OG taxon set. One of two globally convergent topologies (Tree 'c2' in Table 21) derived from four cycles of iterative parameter estimation / heuristic searches, using the combined EF&DDC MP tree in Figure 8 as a starting topology. This ML topology differs from Tree 'c1' only in the relative placement of *Pachysphinx* and *Paonias*. Branch length values, expressed as 1,000X number of substitutions per site along EF, are indicated above branches. Monophyletic recognized higher taxonomic groups are boxed and shaded. Inset contains maximum likelihood score of this topology and optimized parameters of the underlying GTR+I+G substitution model.