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**MOLECULAR SYSTEMATICS
OF NOCTUOIDEA (INSECTA, LEPIDOPTERA)**

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To Maryam, my mother and father

MOLECULAR SYSTEMATICS OF NOCTUOIDEA (INSECTA, LEPIDOPTERA)

Reza Zahiri

This thesis is based on the following original research contributions, which are referred to in the text by their Roman numerals:

- I Zahiri, R, Kitching, IJ, Lafontaine, JD, Mutanen, M, Kaila, L, Holloway, JD & Wahlberg, N (2011) A new molecular phylogeny offers hope for a stable family-level classification of the Noctuoidea (Lepidoptera). *Zoologica Scripta*, 40, 158–173
- II Zahiri, R, Holloway, JD, Kitching, IJ, Lafontaine, JD, Mutanen, M & Wahlberg, N (2012) Molecular phylogenetics of Erebidae (Lepidoptera, Noctuoidea). *Systematic Entomology*, 37,102–124
- III Zaspel, JM, Zahiri, R, Hoy, MA, Janzen, D, Weller, SJ & Wahlberg, N (2012) A molecular phylogenetic analysis of the vampire moths and their fruit-piercing relatives (Lepidoptera: Erebidae: Calpinae). *Submitted manuscript*
- IV Zahiri, R, Lafontaine, JD, Holloway, JD, Kitching, IJ, Schmidt, BC, Kaila, L, & Wahlberg, N. Major lineages of Nolidae (Lepidoptera, Noctuoidea) elucidated by molecular phylogenetics. *Submitted manuscript*
- V Zahiri, R, Lafontaine, JD, Kitching, IJ, Holloway, JD, Schmidt, BC, Mutanen, M & Wahlberg, N. Relationships of the early lineages of Noctuidae (Lepidoptera, Noctuoidea) based on eight gene regions. *Manuscript*

Abstract

In this thesis, I conduct a series of molecular systematic studies on the large phytophagous moth superfamily Noctuoidea (Insecta, Lepidoptera) to clarify deep divergences and evolutionary affinities of the group, based on material from every zoogeographic region of the globe. Noctuoidea are the most speciose radiations of butterflies and moths on earth, comprising about a quarter of all lepidopteran diversity. The general aim of these studies was to apply suitably conservative genetic markers (DNA sequences of mitochondrial—mtDNA—and nuclear gene—nDNA—regions) to reconstruct, as the initial step, a robust skeleton phylogenetic hypothesis for the superfamily, then build up robust phylogenetic frameworks for those circumscribed monophyletic entities (i.e., families), as well as clarifying the internal classification of monophyletic lineages (subfamilies and tribes), to develop an understanding of the major lineages at various taxonomic levels within the superfamily Noctuoidea, and their inter-relationships. The approaches applied included: i) stabilizing a robust family-level classification for the superfamily; ii) resolving the phylogeny of the most speciose radiation of Noctuoidea: the family Erebidae; iii) reconstruction of ancestral feeding behaviors and evolution of the vampire moths (Erebidae, Calpinae); iv) elucidating the evolutionary relationships within the family Nolidae and v) clarifying the basal lineages of Noctuidae *sensu stricto*. Thus, in this thesis I present a well-resolved molecular phylogenetic hypothesis for higher taxa of Noctuoidea consisting of six strongly supported families: Oenosandridae, Notodontidae, Euteliidae, Erebidae, Nolidae, and Noctuidae. The studies in my thesis highlight the importance of molecular data in systematic and phylogenetic studies, in particular DNA sequences of nuclear genes, and an extensive sampling strategy to include representatives of all known major lineages of entire world fauna of Noctuoidea from every biogeographic region. This is crucial, especially when the model organism is as species-rich, highly diverse, cosmopolitan and heterogeneous as the Noctuoidea, traits that represent obstacles to the use of morphology at this taxonomic level.

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“In scientific investigations, it is permitted to invent any hypothesis and, if it explains various large and independent classes of facts, it rises to the rank of a well-grounded theory”

Charles Darwin

1. INTRODUCTION

1.1 Why Noctuoidea?

I quote a magnificent passage from Charles Darwin who said “*all the organic beings which have ever lived on this earth have descended from some one primordial form.*” It can be obviously interpreted from this simple and meaningful passage that every characteristic of every species on Earth is the outcome of an evolutionary history (Futuyma, 2005). The evolutionary perspective and phylogenetic relationships have illuminated every subject in biology, from the molecular and morphology level to ecosystem and beyond. The geneticist Theodosius Dobzhansky (1973) famously argued that “*Nothing in biology makes sense, except in the light of evolution.*” Evolution governs diversity on Earth, and insects are the most diverse organisms in the whole history of life (Grimaldi & Engel, 2005). Consequently, insects should provide profound insights into evolution.

The Order Lepidoptera (moths and butterflies) is one of four super-radiations of insects (along with beetles, flies and wasps) that account for the majority of animal life on Earth. Noctuoidea are the largest superfamily within Lepidoptera—belonging to a large ditrysian clade that also includes e.g., geometroids and bombycoids (Regier *et al.*, 2009, Mutanen *et al.*, 2010)—with approximately 45,000 described (Nieuwerkerken *et al.*, 2011) and

many unknown as well as unnamed species, particularly from tropical regions.

To understand Noctuoidea evolution, their systems of evolutionary relationships—phylogenies based on extensive evidence from living lineages of noctuids—must be recognized. Fortunately, the monophyly of Noctuoidea is firmly established. It is based on the presence of a single apomorphic character, the metathoracic tympanal organ (Miller, 1991). This organ is a highly specialized hearing apparatus that detects the echolocation signals of bats (Kitching & Rawlins, 1998); however, there is increasing evidence that the tympanum may also be involved in reception of mating signals (Kitching & Rawlins, 1998).

Noctuoidea, like most lepidopterans, are plant feeding as caterpillars and nectar feeding as adults, and they are a prominent element of terrestrial ecosystems, functioning as herbivores, pollinators and prey, as well as being one of the most damaging groups of pests to agriculture (Regier *et al.*, 2009). Of the approximately 6,000 Lepidoptera species noted to be of economic importance by Zhang (1994), about one-quarter belong to Noctuoidea. Although a large number of these can be assigned to what Mitchell *et al.* (2006) termed the ‘pest clade’, many more are

distributed across the whole superfamily Noctuoidea in over 500 genera (Zhang, 1994). The caterpillars of many noctuid genera have massive economic impact annually (Kitching, 1984). In addition, the adults of some genera damage fruit crops by piercing the skins to suck juices (Baenziger, 1982).

The study of relationships among major lineages of organisms—phylogenetic analysis—has been closely associated with the classification and naming of the diversity of life on Earth (i.e., taxonomy), which both are a branch of the science of systematics. The classification of organisms has been one of the major ongoing accomplishments of human society (Wilson, 2000), but is still far from completion, both in terms of the inventory of species and of the classification of those species in a hierarchical system that has a phylogenetic basis. However, there has been a striking improvement in the theory and computational methodology for inferring phylogenies (Regier *et al.*, 1995). In particular, the use of molecular data, in particular DNA sequences, is becoming increasingly important for testing and improving classifications, especially for highly diverse groups of organisms such as insects.

The main theme of my thesis, as well as my ongoing research, is to improve our understanding of the reasons and causes behind the flourishing diversification of Noctuoidea on Earth. To address tens of such questions—diversity of their adaptations, biomass, species-richness, ecological and economical impacts, etc.—it is necessary, as a first step, to place Noctuoidea and its major lineages in a phylogenetic context, by reconstructing a

strong phylogenetic hypothesis. The resolution of a stable, extrapolative higher-level classificatory structure for the major lineages of Noctuoidea, and understanding their phylogenetic relationships, is also of importance for pest bionomic studies.

1.2 Status of Noctuoidea

Historically, the classification of noctuid moths has been highly unstable, with different classification systems being used by different authors. It seems that the fundamental distinction between the different systems is based on the use of unsatisfactory (occasionally plesiomorphic) characters in phylogenetic reconstruction. Various authors have recognized between five and thirteen families, and strikingly, no two publications have agreed on the same divisions of the superfamily into families (Kitching & Rawlins, 1998, Lafontaine & Fibiger, 2006). For instance, in Figure 1, I have summarized most recent Noctuoidea classifications and have compared them with the most recent one, which is presented in this thesis (I). Kitching (1984) published a historical review of noctuid subfamily relationships and showed that the higher classifications of Noctuidae used up to that time had been based upon superficial resemblance and vaguely defined characters, rather than on rigorous application of cladistic principles. Subsequently, Speidel and co-workers attempted to progress beyond the age of traditional morphological noctuid taxonomy by initiating investigations based mainly on the male genitalia and the tympanal region, which they considered particularly useful in elucidating the basic relationships of the noctuid subfamilies (Speidel & Naumann, 1995, Speidel *et al.*, 1996, Kühne & Speidel, 2004, 2005).







































































<i>classification system</i>	Kitching, 1984	Miller, 1991	Scoble, 1992	Speidel <i>et al.</i> , 1996	Kitching & Rawlins, 1998	Fibiger & Lafontaine, 2005	Mitchell <i>et al.</i> , 2006	Lafontaine & Fibiger, 2006	Zahiri <i>et al.</i> 2011
<i>Family-group name</i>									
Oenosandridae									
Notodontidae									
Doidae									
Strepsimanidae									
Micronoctuidae									
Arctiidae									
Lymantriidae									
Aganaiidae									
Hermiidae									
Erebidae									
Hypenidae									
Catocalidae									
Euteliidae									
Stictopteridae									
Noctuidae									
Pantheidae									
Nolidae									

Figure 1 Different classification systems of the superfamily Noctuoidea that have been used since Kitching (1984) to date (I). In every classification moths (except the one for Micronoctuidae for which the author's portrait—the late Michael Fibiger—is used) indicate family-group name being used in the system.

Their work set the stage for the study of the systematics of noctuids, and made it clear that increased character and taxon sampling were necessary to resolve the relationships of the diverse clades.

Recently, three landmark publications (Fibiger & Lafontaine, 2005, Lafontaine & Fibiger, 2006, Mitchell *et al.*, 2006) presented detailed phylogenetic hypotheses and revised the classification of Noctuoidea three times (Figure 1), each

classification having its own limitations and strengths (Roe *et al.*, 2010). Fibiger & Lafontaine (2005) proposed a rather new classification with ten families: Oenosandridae, Doidae, Notodontidae, Strepsimanidae, Nolidae, Lymantriidae, Arctiidae, Erebiidae, Micronoctuidae and Noctuidae (Figure 1). Later on, Lafontaine & Fibiger (2006) proposed a further revision to the classification of the families of Noctuoidea, in which Nolidae, Strepsimanidae, Arctiidae, Lymantriidae

and Erebidae sensu Fibiger & Lafontaine (2005) were downgraded to subfamily status within an expanded family concept of Noctuidae based on the quadrid venation of the forewing and the presence of a tympanal sclerite in the tympanal membrane. In their view, the superfamily should consist of five families: Oenosandridae, Doidae, Notodontidae, Micronoctuidae and Noctuidae (Figure 1).

To resolve the dominant complexity of relationships in higher systematics of Noctuoidea, it was crucial to understand their phylogenetic relationships by building a robust skeleton phylogenetic hypothesis, i.e., a phylogeny that was based on certain specialized features, and that had a common ancestor and unique evolutionary history. To achieve a more robust phylogenetic hypothesis, one strategy is to increase the number of characters to obtain a dataset with a strong phylogenetic signal. In molecular systematics, datasets with a weak phylogenetic ‘signal’ tend to be strongly influenced by the assumptions made by the analytical methods applied, whereas datasets with a strong phylogenetic signal are not influenced as much (Wahlberg & Wheat, 2008). One avenue for acquiring more characters is to use morphology. However, a species-rich, cosmopolitan and heterogeneous group such as the Noctuoidea (Speidel & Naumann, 1995) with a vast number of species presents obstacles to the use of morphology at this taxonomic level. The adults and larvae of species in Noctuoidea exhibit a bewildering diversity of size, coloration, adaptation, behaviour and ecology (Kitching & Rawlins, 1998). Morphological data are thus often difficult to homologize and code, require great experience to identify character states

correctly and can be subject to extensive homoplasy (character convergence and reversal). As a result, morphological analyses have often failed to determine relationships among most groups with confidence.

1.3 Initiation of molecular phylogenetic approaches

As noted above, until recently, the higher systematics of Noctuoidea had been based primarily on morphological characters with a predominantly phenetic approach, until the introduction and application of cladistic philosophy by Kitching (1984, 1987) and Miller (1991). More recently, molecular data, in particular DNA sequences of mitochondrial and nuclear genes (mtDNA and nDNA, respectively), have opened new and fruitful avenues for the study of phylogenetic relationships. Molecular studies have often been based on a small number of molecular markers, usually between one and three genes (Sperling, 2003, Wahlberg & Wheat, 2008). The utility of using many mitochondrial genes alone is certainly questionable, as they have a shared evolutionary history, and even entire mitochondrial genomes (15,000–20,000 bp in insects) fail to provide robust inferences at deep levels (Cameron *et al.*, 2004). However, they are useful in the recognition of cryptic species and sometimes resolve relationships among closely related species and genera (Lafontaine & Schmidt, 2010). They have proven most valuable for relatively recent divergences, especially those of mid-Tertiary and later age, although they have also been applied, albeit infrequently, at deeper levels (Wiegmann *et al.*, 2000). In contrast, protein-coding nuclear genes generally have slower mutation rates compared with mtDNA. They are most

frequently used to study older evolutionary divergences and are particularly good at resolving deeper nodes in phylogenetic hypotheses, where they have been important in establishing the family, subfamily and tribal classification of Lepidoptera (Regier *et al.*, 2009, Wahlberg *et al.*, 2009, Mutanen *et al.*, 2010). Over the past few years, a series of papers have been published with a shared objective: to contribute to the development of a more satisfactory classification of Noctuoidea at levels above that of the genus and particularly the ‘quadrifid’ part—those noctuoids with forewing vein M2 arises closer to the origin of M3 than M1, in the lower part of the discal cell—of the superfamily. It began with the exploration of molecular markers by Weller *et al.* (1994), who were then followed by Mitchell *et al.* (1997, 2000, 2006). The utility of DNA sequences was undeniable, and systematists were able to gain fascinating insights that were not obvious before, e.g., the polyphyly of the old concept of Noctuidae (Mitchell *et al.*, 1997). Mitchell *et al.* (2006) found a strongly supported clade of quadrifine noctuid moths that also included the families Lymantriidae and Arctiidae. They termed this the L.A.Q. clade (Lymantriidae, Arctiidae and Quadrifine Noctuidae).

Two recent molecular studies on ditrysian Lepidoptera sampled members of Noctuoidea and found that the enigmatic family Doidae did not group with the other noctuoids, but instead appeared to be related to Drepanoidea (Regier *et al.*, 2009, Mutanen *et al.*, 2010). Otherwise both studies found Noctuoidea to be monophyletic, with Oenosandridae being sister to the rest and Notodontidae the next lineage branching off.

However, all of these studies had very poor sampling of the higher taxa putatively belonging to the L.A.Q. clade, and critically they did not sample type genera of many higher taxa. Given that the monophyly of many named groups remains questionable, it is crucial to sample the type genera of each family, subfamily and tribe to assess the taxonomic limits of a given category. Furthermore, previous molecular studies have used only a small number of molecular markers, usually one to three gene regions (Wahlberg & Wheat, 2008).

1.4 Outline of the thesis

In this thesis, I employed the methods of molecular phylogenetics using eight markers for genomic DNA extractions of Lepidoptera to study the evolution of Noctuoidea and reconstruct a skeleton phylogenetic hypothesis for its major lineages. The first chapter gives a comprehensive overview of the higher-level phylogeny and evolutionary affinities of noctuid moths, in an extensive sampling strategy of the entire Noctuoidea (I). It reveals a new high-level phylogenetic hypothesis comprising six major, well-supported lineages that are interpreted as families (I). The second chapter aims to understand the higher-level phylogeny and elucidate the evolutionary history of the moth family Erebidae, the most controversial group among the newly circumscribed families (II). Erebidae is a massive clade and includes a diverse groups exhibiting a broad range of feeding behaviors, including those that can be considered ‘piercers’ of fruits or other hosts (skin-piercers: hematophagous) and ‘tear feeders’ (lachryphagous) (III). Within butterflies and moths, adult hematophagy is limited to species within the vampire moth genus *Calyptra*

Ochsenheimer, which are placed within the subfamily Calpinae, Erebidae. Paper **III** focused on the subfamily Calpinae using both morphological and molecular data to reconstruct ancestral feeding behaviors within Calpinae as well as whether fruit-piercing behavior and associated modifications of the tongue have evolved independently in different groups of Erebidae (**III**). The fourth chapter seeks to elucidate the deep divergences and evolutionary relationships of the major lineages within the moth family Nolidae (**IV**). As a result of expanded sampling, a new lineage (i.e., Diphtherinae) within Noctuoidea—which includes taxa of previously uncertain affinity—was recovered. Diphtherinae is considered to be the plesiomorphic sister lineage to the rest of Nolidae (**IV**), thus a new phylogenetic hypothesis for Nolidae is presented (**IV**). The fifth chapter elucidates the evolutionary relationships of the basal

lineages of the moth family Noctuidae (**V**). A summary flow chart is presented in Fig. 2, representing my thesis process with their main outputs.

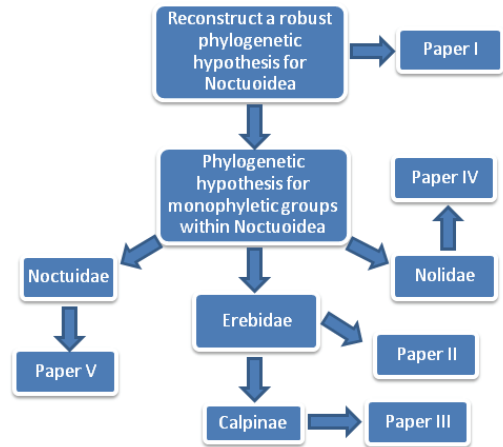


Figure 2 A flow chart summarizing five chapters included in this thesis.

2. MATERIAL AND METHODS

2.1 Sampling strategy

The sampling strategy that I adopted has treated the world fauna. I attempted to include representatives of all known major lineages of quadrifine Noctuoidea from every biogeographic region. This strategy is being used to establish priorities for ongoing studies, to test further the robustness of the major clades of Noctuoidea, both in relation to each other and internally.

Based on the results of recent publications (Fibiger & Hacker, 2005, Lafontaine & Fibiger, 2006, Mitchell *et al.*, 2006, Lafontaine & Schmidt, 2010), 152, 237, 35, 120 and 76 terminal taxa were sampled as representatives of the most recognized Noctuoidea lineages for papers I–V, respectively. Furthermore, there were numerous unplaced taxa of uncertain status that were included in each paper. Indeed, the allocation of the unplaced taxa into any higher taxa of Noctuoidea, however tentatively, could not be determined in previous classifications. I was unable to sample/amplify a few rare taxa with restricted distributions and/or low species richness (e.g., Strepsimaninae, Afridinae, Camptolominae). Where possible, a representative of the type genus of each lineage is included, but this was not possible for a few tribes/subtribes, in which case a closely related genus was selected.

Appendix 1 summarizes all 393 terminal taxa that are used in the five papers with their voucher codes and GenBank accession numbers.

To test the monophyly of the target taxon under study in the different papers, I included representatives from the most

closely related taxa of other families of Lepidoptera (papers I, II, IV, V) or subfamilies of Erebidae (III). I rooted the cladograms, in different papers, with different taxa, which represents what I consider to be the putative sister family to the remainder of the terminal taxa.

2.2 Molecular markers

The total genomic DNA from one or two legs, dried or freshly preserved in 96% ethanol, was extracted using the DNeasy tissue extraction kit (Qiagen, Hilden, Germany) following the manufacturer's instructions. For each specimen, I sequenced *cytochrome c oxidase subunit I* (COI) from the mitochondrial genome, and *elongation factor-1 α* (EF-1 α), *ribosomal protein S5* (RpS5), *carbamoylphosphate synthase domain protein* (CAD), *cytosolic malate dehydrogenase* (MDH), *glyceraldehyde-3-phosphate dehydrogenase* (GAPDH), *isocitrate dehydrogenase* (IDH) and *wingless* genes from the nuclear genome. For paper III, I sequenced an additional gene, the D2 region of the nuclear ribosomal RNA (rRNA) 28S region. All genes—except 28S, which is multiple-copy and encodes ribosomal RNA—are single-copy, protein-coding exons and have previously been found to be highly informative in phylogenetic analyses of Lepidoptera at higher taxonomic levels (Wahlberg *et al.*, 2009, Mutanen *et al.*, 2010, I, II).

DNA amplification (PCR) and sequencing protocols follow Wahlberg & Wheat (2008). Sequencing was performed mainly with an ABI 3730XL capillary sequencer (Macrogen, Seoul, Korea), and a smaller part with an ABI PRISM 3130XL capillary sequencer (Turku,

Finland). The resulting chromatograms were checked and DNA sequences aligned by eye using BioEdit v. 7.0.4.1 (Hall, 1999). Alignment was trivial and the few insertion/deletion events that were detected were of entire codons (in CAD, IDH and RpS5), and could be easily aligned. To minimize the risk of any kind of confusion during the sequencing protocol and errors in alignments, I constructed neighbor-joining and Maximum Likelihood trees separately for each gene region and checked them carefully for identical sequences and other doubtful patterns. In addition, to minimize the risk of misidentification, all the specimens were cross-checked with their DNA barcodes (COI) in BOLD (Barcode of Life Data System, <http://www.boldsystems.org/views/login.php>) (Ratnasingham & Hebert, 2007), where reference specimens were available for many of the species used in this study.

2.3 Phylogenetic analyses and character optimizations

The gene regions were analyzed using various phylogenetic approaches including model-based (Maximum Likelihood, ML; and Bayesian Inference, BI), and non model-based (i.e., parsimony) methods. Initially, the data matrices were analysed in various combinations using ML to explore their phylogenetic signal. Single genes were analyzed on their own, nuclear genes were combined, third codon positions were removed, data was partitioned into mtDNA and nDNA and finally the data was partitioned by gene regions (8 partitions). The effects of varying taxon and gene combinations were compared against the analyses of the full, combined and partitioned by gene data. Based on these data explorations, it was decided to include all genes and third

codon positions as well as to partition the data by genes (8 partitions) in the ML analyses, and by nDNA and mtDNA (two partitions) in the BI analyses.

Parsimony analyses (MP) were undertaken using New Technology heuristic searches implemented in the program, TNT v 1.1 (Goloboff *et al.*, 2003). New technology searches (Goloboff, 1999) consisted of Tree Fusion, Ratchet, Tree Drifting and Sectorial Searches performed, with default parameters applied, until the minimal tree was found 1000 times. All characters were treated as unordered and equally weighted, and robustness of the hypothesis was assessed through the bootstrap (BP) with 1000 pseudoreplicates (Felsenstein, 1985). In addition, in papers **I** and **II** clade support was estimated by Bremer support (BS) (Bremer, 1988, 1994) using a script (Peña *et al.*, 2006) in TNT. Model-based phylogenetic analyses were performed using ML and a GTR + Γ model was selected as the most appropriate model of sequence evolution for each gene partition based on the Akaike Information Criterion using FindModel (<http://www.hiv.lanl.gov/content/sequence/findmodel/findmodel.html>). ML analyses were conducted using the default settings on the web-server RAxML III BlackBox (Stamatakis *et al.*, 2008). ML bootstrap analysis with 1000 pseudoreplicates (Felsenstein, 1985) was also conducted with RAxML III.

BI was not used for papers **I** and **II**. In the other papers, BI analyses were carried out using the software MrBayes v3.1 (Ronquist *et al.*, 2005) on the freely available Bioportal server (<http://www.bioportal.uio.no>). The dataset was divided into two partitions: mtDNA and nDNA, as partitioning by gene resulted in poor

mixing of chains and problems with convergence of likelihoods. I modeled the evolution of sequences according to the GTR + Γ model independently for the two partitions using the “unlink” command in MrBayes. The Bayesian analyses were separately run two times for five, 23 and 20 million generations for papers **III–V**, respectively, with every 1000th generation sampled. Clade robustness was estimated by posterior probabilities (PP) in MrBayes. Convergence was determined when the standard deviation of split frequencies went below 0.05 and the PSRF (Potential Scale Reduction Factor) approached 1, and both runs had properly converged to a stationary distribution after the burn-in

stage (which was 1,000 sampled generations).

To understand character evolution in higher noctuoids, a character optimization analysis based on parsimony was undertaken in paper **IV** using the software Mesquite v2.75 (Maddison & Maddison, 2011). Ancestral state reconstructions and character transformations were optimized onto the topology resulting from the Bayesian analysis (**IV**).

All laboratory procedures and phylogenetic data analyses are detailed in the original papers.

3. RESULTS AND DISCUSSION

3.1 Phylogenetic hypothesis for Noctuoidea

In the initial study, I aimed, as a first step, to reconstruct a robust phylogenetic hypothesis for higher taxa of Noctuoidea. The results strongly supported the monophyly of Noctuoidea. The major groups within the Noctuoidea clade all shared a particular morphological synapomorphy—a metathoracic tympanal organ. I found six strongly supported major lineages within Noctuoidea that deserved family status. These are Oenosandridae, Notodontidae, Euteliidae, Erebidae, Nolidae and Noctuidae (Fig. 3). The first two major lineages are well-recognized taxa that have often been considered families within Noctuoidea. Oenosandridae are a small family, only known from Australia, comprising eight species in four genera (Nielsen *et al.*, 1996), which mainly feed on Myrtaceae (Miller, 1991). Notodontidae contain approximately 3,800 species (Nieukerken *et al.*, 2011) and occur worldwide. The other four lineages have been split into as many as 10 families, with arctiines, lymantriines and nolines frequently being considered to be sufficiently distinct from the rest to warrant full family status. My phylogenetic hypothesis (I) placed previously recognized families—arctiines, lymantriines, aganaines, herminiines and micronoctuines—into the strongly supported Erebidae clade. Within Erebidae, relationships of only a few lineages (e.g., Arctiinae, Aganainae and Herminiinae) were well supported (I). The low support for some nodes within

Erebidae and Noctuidae probably stems from high levels of homoplasy (particularly in the third codon position) and very sparse sampling.

At this stage, with well-supported monophyletic groups established within a phylogenetic framework, the question arose of how best to apply the Linnaean system of nomenclature to the structure of that framework, by making decisions on the content and arrangement of families, subfamilies, tribes and subtribes in a manner that was most likely to optimize the stability of that system and facilitate access to its information content (II). In particular, the establishment of a well-founded family-level noctuid classification is certainly an issue of considerable practical importance, because it affects the classification of about a quarter of the world's lepidopteran species, according to current estimates (Nieukerken *et al.*, 2011). In paper II, I discussed in detail reasons for applying the six family-group system to the higher systematics of Noctuoidea with their advantages and drawbacks.

One of the most striking features of the application of molecular data in my thesis was uncovering the phylogenetic relationships of many unplaced taxa of uncertain affinity. Molecular phylogenetic techniques allowed the easy allocation of these taxa, which had remained 'incertae sedis' or with uncertain limits for many years. For example, the position of a number of taxa characterized by the pseudoquadrifine hindwing venation had

been unstable for a long time (IV–V). Most of these groups (i.e., pseudoquadrifine Noctuidae) were previously assumed to be related to erebid subfamilies (Fibiger & Lafontaine, 2005, Lafontaine & Fibiger, 2006) (II) or even considered as distinct families (e.g., Pantheidae) (Kitching & Rawlins, 1998) (V). The results of papers IV–V placed them in a basal position within the family Noctuidae with strong support.

3.2 Pattern of relationships among major lineages of Noctuoidea

Notodontidae are found to be the sister group of all other Noctuoidea, with Oenosandridae branching off next (I). However, this pattern of relationships relative to the rest of Noctuoidea is not well supported in all papers. Both Oenosandridae and Notodontidae have a trifold forewing venation similar to that of Geometridae, a character state that appears to be plesiomorphic relative to the quadrifid forewing venation found in the other noctuid families. All these terms are discussed and defined in detail in paper II.

The results of paper I recovered the six recognized families within Noctuoidea and the monophyly of the quadrifid Noctuoidea (i.e., Euteliidae, Erebidae, Nolidae, and Noctuidae). Although, the relationships amongst the remaining four families are not clear, they formed a monophyletic group (i.e., quadrifid Noctuoidea clade) with very strong support (Fig. 3) and shared a synapomorphy (i.e., quadrifid forewing venation). The relationships of the four clades of quadrifid lineage remained somewhat ambiguous in papers I–II, although the results of papers IV–V suggested a basal position for Euteliidae in all three phylogenetic methods (MP, ML

and BI). In paper I, Euteliidae were sister to Noctuidae in ML analyses (Fig. 3), and sister to the other three families together in MP analyses. Similarly, in papers IV–V, Euteliidae were placed as sister to the rest of the quadrifid clade with moderately good support in MP, ML and BI analyses (Figs 4–5). In paper I, Nolidae were sister to Erebidae in ML analyses, but form a trichotomy with Erebidae and Noctuidae in MP analyses.

The short internal nodes, with little or no support for many basal divergences, in all quadrifid Noctuoidea lineages (I, II, IV, V), suggest that these groups diversified rapidly within a relatively short period of time (Whitfield & Kjer, 2008). Evolutionary rates in basal divergences appear punctuated and such explosive radiations are generally interpreted in two different ways: (i) there is an historical explanation (e.g., rapid radiation or the signature of a mass extinction event) or (ii) it is simply an artefact. Under the rapid radiation scenario, it is hypothesized that the lineages diverged so rapidly and within such a narrow time window that there was little opportunity for the ancestors of each monophyletic group to evolve distinctive apomorphies (Futuyma, 2005). However, such a pattern of short internal nodes and lineages with low support can be produced by other factors, such as inadequate data quality, poor and sparse sampling strategy, conflict within or among datasets (data inconsistency), incongruence between the real evolutionary process and the assumed models of sequence evolution, or even lack of phylogenetic signal due to accumulation of overlapping mutations (i.e., the probability of substitutional saturation at a given site).

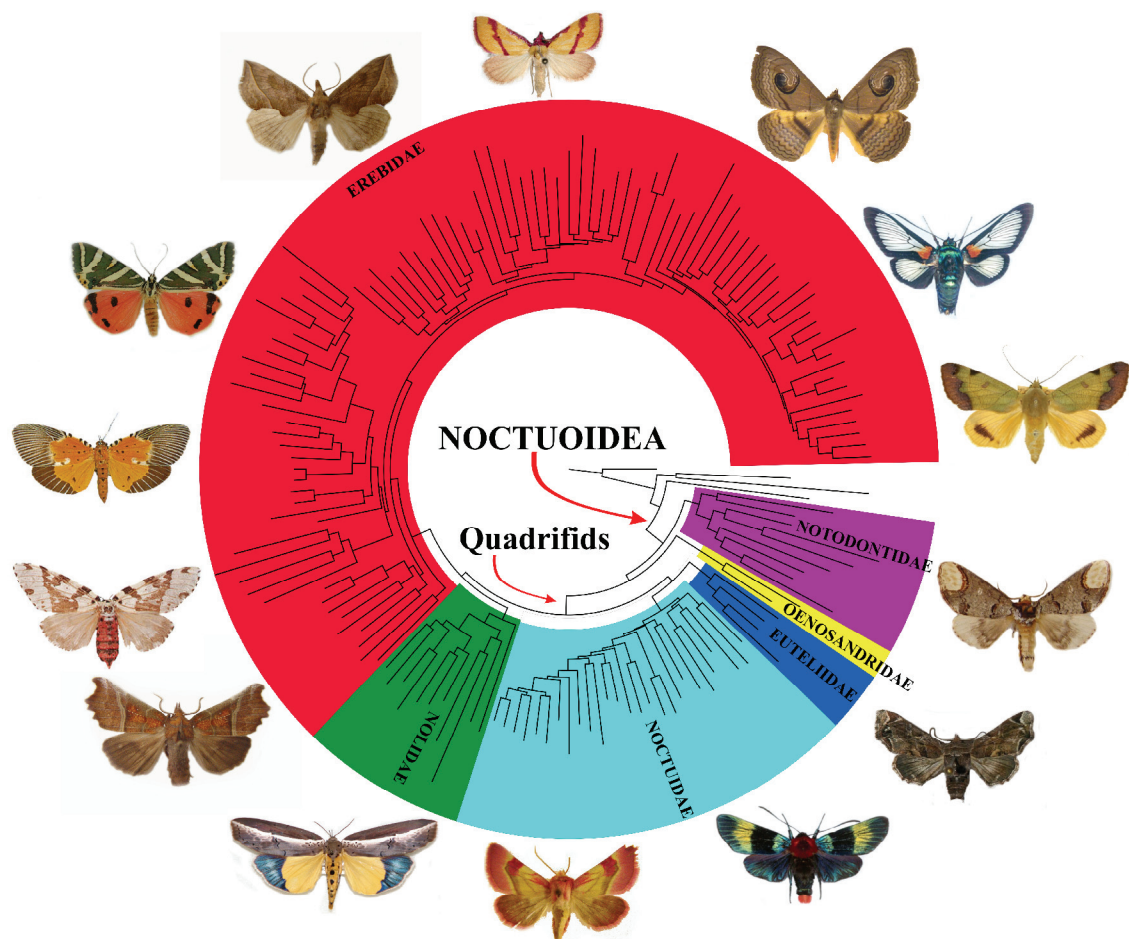


Figure 3 The phylogenetic hypothesis of the superfamily Noctuoidea based on a maximum likelihood analysis, along with outgroups. Clades representing families are coloured. The six families recognized here are indicated. Names of moths shown in figure clockwise are: Notodontidae: *Phalera* Hübner; Euteliidae: *Eutelia* Hübner, Noctuidae: *Eucoctyia* Rothschild & Jordan (Pantheinae), *Periphanes* Hübner (Heliiothinae); Nolidae: *Eligma* Hübner (Eligminae); Erebidae: *Scoliopteryx* Germar (Scoliopteryginae), *Lymantria* Hübner (Lymantriinae), *Peridrome* Walker (Aganainae), *Euplagia* Hübner (Arctiinae), *Calyptra* Ochseneimer (Calpinae), *Phytometra* Haworth (Boletobiinae), *Spirama* Guenée (Erebinae), *Cocytia* Boisduval (Erebinae), and *Ophiusa* Ochseneimer (Erebinae).

In addition, a recent study indicates that such phylogenetic patterns may well be signature of mass extinction events (Crisp & Cook, 2009), because mass extinction produces a sharp drop in the cumulative fossil diversity and is commonly thought to stimulate subsequent adaptive radiation,

creating a sharp increase in the rate of diversification (Benton & Emerson, 2007).

3.3 Phylogenetic hypothesis for quadrifid Noctuoidea

Paper I revealed an urgent need for a comprehensive series of revisions for the higher classifications of quadrifid Noctuoidea families used up to that time. My results in paper I almost failed to recover some previously recognized subfamilies within Erebidae as monophyletic groups. For instance, they suggested that some recent concepts of subfamilies Calpinae, Catocalinae, Erebiniae and Phytometrinae were polyphyletic (I). Consequently, the focus in paper II was designed to elucidate the higher-level phylogeny and evolutionary relationships of the massive Erebidae clade (II). I thus conducted a large-scale molecular phylogenetic analysis, which uncovered a well-resolved skeletal phylogenetic hypothesis. I thus presented a new phylogenetic hypothesis for Erebidae consisting of 18 moderate to strongly supported subfamilies (Fig. 4): Scoliopteryginae, Rivulinae, Anobinae, Hypeninae, Lymantriinae, Pangraptinae, Herminiinae, Aganainae, Arctiinae, Calpinae, Hypocalinae, Eulepidotinae, Toxocampinae, Tinoliinae, Scolecocampinae, Hypenodinae, Boletobiinae and Erebiniae (Fig. 4). Where possible, I diagnosed apomorphic morphological character states for each monophyletic lineage (II).

Paper II provides strong support for subordinating five taxa where previously treated as families—Arctiidae, Lymantriidae, Micronoctuidae, Herminiidae and Aganaidae—within Erebidae. One of the most striking features, a strong association among three of them, was shown in papers I–II: Aganainae + Herminiinae + Arctiinae are

recovered as monophyletic clade (Fig. 4), in which Arctiinae have a sister relationship with a strongly supported pairing of Aganainae and Herminiinae. The clade also has a morphological synapomorphy in the prespiracular position of the counter-tympanal hood, which was until then thought to be plesiomorphic. Adults of many aganaines and arctiines are visually striking and aposematic, and aganaines and herminiines share long labial palps and a bare lower frons. Herminiinae are generally cryptic, feeding on vegetable detritus, and Aganainae are aposematic, feeding on the same suite of toxic cardenolide-synthesizing plant families (Apocynaceae and Moraceae) as the danaine Nymphalidae and other moth genera such as *Glyphodes* (Crambidae) and *Agathia* (Geometridae) (Holloway, 2008).

Another interesting result from paper II was the placement of the new established family Micronoctuidae. Hypenodinae are enlarged to incorporate Micronoctuini as a tribe, corroborating the findings of paper I. The subfamily Erebiniae, brings together the core catocalines (with the exceptions of Hypocalinae, Toxocampinae and Tinoliinae).

Calpinae *sensu* Lafontaine & Fibiger (2006) consisted of four tribes, Anomini, Scoliopterygini, Calpini and Phyllodini on the basis of the sharing of peculiar morphological adaptations. A robust, highly developed fruit-piercing (and in some cases skin-piercing and blood sucking) proboscis is found widely in Calpini and in some of the more robust scoliopterygines such as *Anomis* Hübner, with many similar features in the structure. However, my phylogenetic analysis

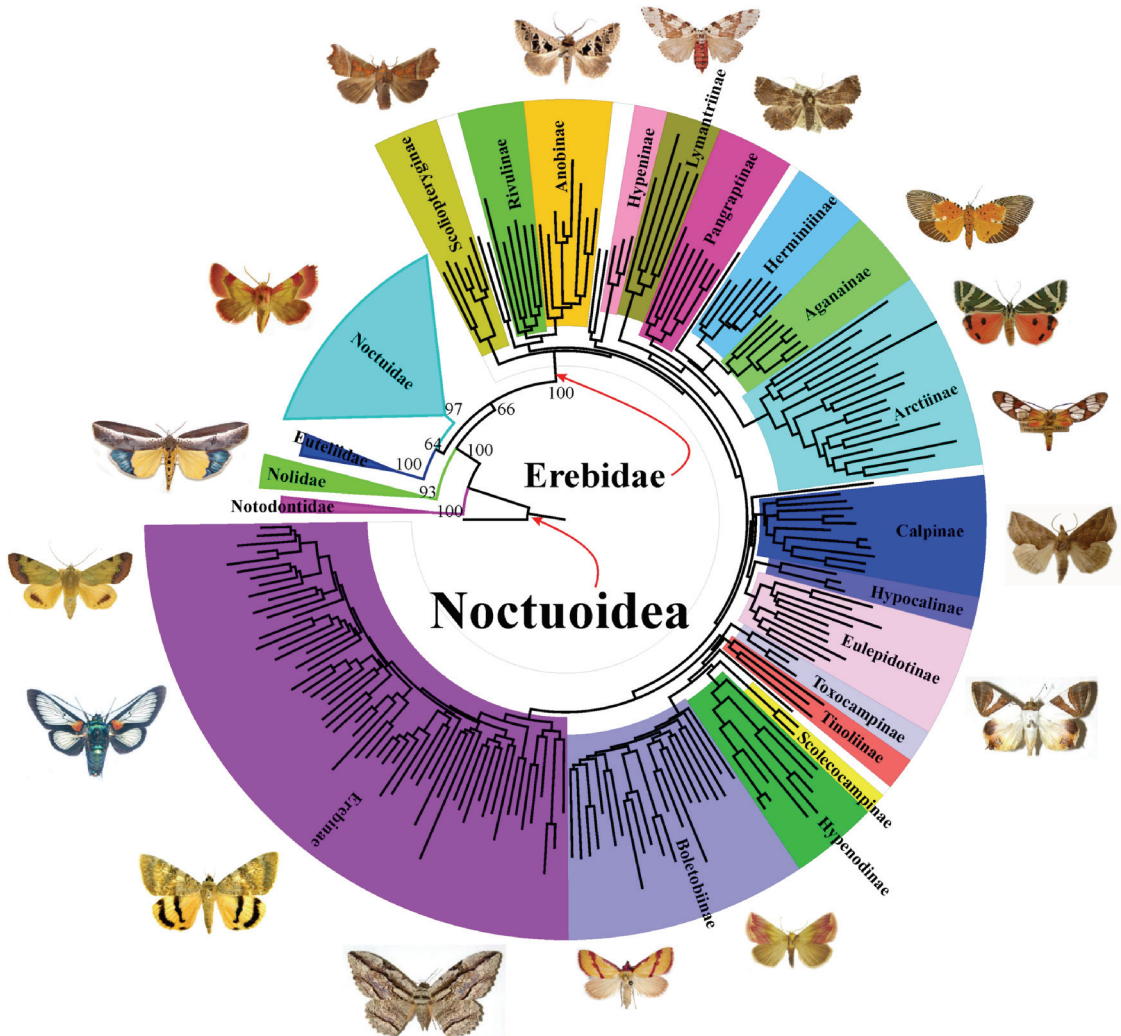


Figure 4 Phylogenetic hypothesis of the moths family Erebidae, based on ML analysis. Clades representing the major clades are coloured. Support values (bootstrap) are shown next to the branches. Names of moths shown in figure clockwise are: Nolidae: *Eligma* (Eligminae); Noctuidae: *Periphanes* (Heliiothinae); Erebidae: *Scoliopteryx* (Scoliopteryginae), *Anoba* Walker (Anobinae), *Lymantria* (Lymantriinae), *Pangrapta* Hübner (Pangraptinae), *Peridrome* (Aganainae), *Euplagia* Hübner (Arctiinae), *Syntomis* Ochseneheimer (Arctiinae), *Calyptra* (Calpinae), *Eulepidotis* Hübner (Eulepidotinae), *Eublemma* Hübner (Boletobiinae), *Phytometra* (Boletobiinae), *Thysania* Dalman (Erebinae), *Catocala* Schrank (Erebinae), *Cocytia* (Erebinae), and *Ophiusa* (Erebinae).

confirmed the polyphyly of the old concept of Calpinae, and supports a monophyletic Calpinae that places members of Anomini and Scoliopterygini in other noctuid subfamilies (II–III). These results

suggesting that the fruit-piercing behavior and the associated modifications of the tongue seen in moths of both groups have evolved independently (III). The phylogenetic hypothesis suggested three

subclades for the subfamily Calpinae that were treated as tribes: Phyllodini, Ophiderini and Calpini (II). The polyphyly of the former concept of Calpinae provides an object lesson in how the sharing of peculiar morphological adaptations may mislead classifications, and how shared features of a more subtle nature may be overlooked in an unchallenged traditional classification. Within the entire Lepidoptera, adult hematophagy—the ability to pierce mammalian tissue and extract a blood meal—is limited to species within the vampire moth genus *Calyptra* Ochseneimer, which belongs to the subfamily Calpinae. In paper III, we tested whether hematophagy in *Calyptra* arose from plant (e.g., fruit-piercing) or animal-related behaviors (e.g., tear feeding or lachryphagy). To do that, we subjected the resulting phylogenetic trees to a Bayesian method of ancestral state reconstruction to reconstruct ancestral feeding behaviors within Calpinae and test competing hypotheses regarding their evolution. The results supported the hypothesis that blood feeding in vampire moth evolved from the fruit-piercing habit as opposed to tear feeding or other animal-related feeding behaviors (e.g., dung feeding, urine feeding) (III).

In paper IV, I aimed to elucidate the higher-level phylogeny of Nolidae and to clarify relationships in basal lineages of Noctuidae (V). My phylogenetic hypothesis (I) had already recovered Nolidae and Noctuidae as well-supported monophyletic clades (Fig. 3). The results were fascinating and fairly robust. Many genera previously placed in Nolidae and the former subfamily Ophiderinae (Erebidae) were placed with strong support within Noctuidae, in the subfamily Bagisarinae, supporting an expanded

concept of the subfamily (V). In addition, by increasing taxon sampling of several unassigned Neotropical taxa, I uncovered a previously unknown lineage of Noctuoidea with Neotropical origins (*Diphthera* Hübner + *Lepidodes* Guenée) with strong support. This lineage appears to be the sister group to Nolidae, and it shares an unambiguous feature and the most characteristic Nolidae apomorphy yet proposed—the structure of the boat-shaped cocoon with a vertical, anterior exit slit—, suggesting that the clade could be included in the family Nolidae as the subfamily Diphtherinae (IV). Diphtherinae is considered to be the plesiomorphic sister lineage to the rest of Nolidae, characterized by the loss of the proximal pair of tibial spurs on the hindlegs of males, and the presence of a frontal tubercle or process, which is presumably associated with a derived strategy of emergence from the cocoon (IV). My analyses (IV) revealed a well-resolved phylogenetic hypothesis for Nolidae, allowing me to present a new classification for Nolidae consisting of eight strongly supported subfamilies: Diphtherinae, Risobinae, Collomeninae, Beaninae, Eligminae, Westermanniinae, Nolinae, and Chloephorinae. Among these, two groups are suggested as new subfamilies (i.e., Collomeninae and Beaninae). I also defined each monophyletic group by autapomorphic morphological character states.

3.4 Character optimizations

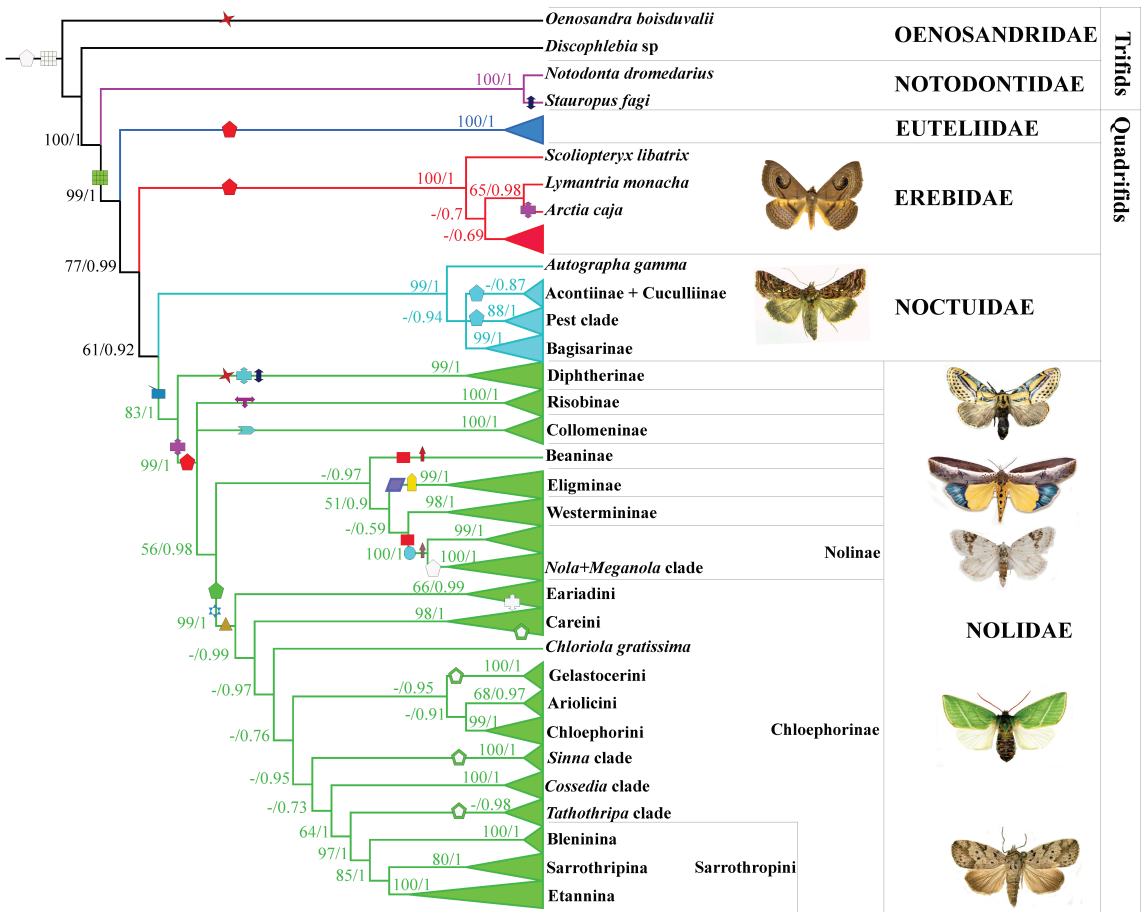
The higher systematics of the quadrifid Noctuoidea is often discussed in terms of whether the hindwings have a trifine or quadrifine venation. To understand character evolution in higher noctuoids and major nolds, I undertook a character optimization analysis based on parsimony

using the software Mesquite v2.75 (Maddison & Maddison, 2011). My results of ancestral-state reconstructions and character optimization (Fig. 5) showed that most traits—those characters that are considered to be of phylogenetic significance—are clearly synapomorphic for major lineages of quadrids, except the hindwing venation which was an ambiguous character state (IV). It is generally thought that the pseudoquadridine condition is the ancestral state for Noctuoidea. This condition concerns the position of three veins (M2, M3 and CuA1), in which M2 arises about one-third of the way up the discal cell, and M2 is strong and parallel to M3. My character examinations indicated that the pseudoquadridine condition is shared by the basal lineages of Noctuidae s.s. (i.e., Bagisarinae, Plusiinae, Dilobinae and Pantheinae) (V), and a few erebid subfamilies (Hypeninae, Herminiinae, Scoliopteryginae and Rivulinae) (II), as well as Diphtherinae (Nolidae) (IV). I evaluated the distribution patterns and evolutionary trends of this complex trait under the two most commonly used character optimization algorithms of parsimony analysis: ACCTRAN—accelerated transformation—and DELTRAN—delayed transformation—(Agnarsson & Miller, 2008). I finally favoured DELTRAN optimization (IV), which minimizes reversals and maximizes convergences and parallel evolution. This favours the acquisition of the derived quadridine state—base of M2 close to M3—independently in Erebidae, Nolidae (with Diphtherinae excluded), and Euteliidae (Fig. 5). In other words, the plesiomorphic condition of M2 in the hindwing of the four quadrid lineages is the form found in Diphtherinae and basal lineages of Noctuidae, and arguably some

basal lineages of Erebidae. This trend of character evolution can be traced by checking the position of the vein M2 in different groups of quadrids. For instance, the condition of M2 in Diphtherinae is exactly the same condition that occurs in Pantheinae, Plusiinae, Dilobinae and Bagisarinae (V), where M2 is very slightly reduced. In higher noctuids (i.e., Hadeninae) the vein is still visible in exactly the same position, but is even more reduced, and then entirely lost in Noctuidae (Fibiger & Lafontaine, 2005). In the Erebidae lineage, M2 is seen in this condition in some primitive lineages (e.g., Rivulinae, Hypeninae, and Herminiinae). As a consequence, the quadridine (M2 adjacent to M3) form of venation must have been independently gained several times within Erebidae, acquired once in Nolidae (after the Diphtherinae lineage branched off), and once in Euteliidae (Fig. 5). Thus, all these so-called primitive lineages have retained the ancestral (symplesiomorphic) hindwing venation trait with a pseudoquadridine condition (Fig. 5).

3.5 Evolution of host-plant associations in Noctuoidea

There have been few attempts to study the evolution of host-plant use in Noctuoidea. The results from the character optimizations (IV) drove me to learn more about the evolution of feeding habits in higher noctuids. One feature that has been suggested as the prime factor governing the evolution of butterfly-host plant associations, is host growth form, which appears, on the whole, to be more conserved phylogenetically than host-plant taxon affiliation (Janz & Nylin, 1998). Given its prevalence among the deeper lineages, woody-plant feeding can be



- Ocelli reduced or absent
- ★ Frontal process present
- ▤ Forewing elongation, in terms of depth from right-angle at costa to tornal angle as a proportion of costal length
- Quadrifid forewing
- ▤ Trifid forewing venation
- ⬠ Hindwing M2 strong (pseudoquadrifine condition)-base well separated from M3
- ⬠ Hindwing M2 reduced or absent: noctuid trifine condition
- ⬠ Hindwing CuA1+M3 stalked/fused
- ⬠ Reversal where M2, M3, CuA1 non-stalked/fused, all separate near lower margin of cell
- ⬠ Hindwing M2 strong base of M2 close to M3
- ▤ Retinaculum finger-like, projecting away from cost
- ⬠ Retinaculum with an elongated scroll parallel to costa (plesiomorphic condition)
- ⬠ Retinaculum is lost
- ▤ Proximal pair of tibial spurs lost in males
- ▤ Uncus sigmoid, ventrally deflexed, tegumen 'spanner'-like long subbasal process, laminate 'wrinkles' on valve
- ▤ Raised, lobed accessory tympanal membrane
- ⬠ Tymbal organ
- ▤ Larva with the first pair of prolegs lost
- ▤ Larva with the first pair of prolegs vestigial
- ▤ Larva with the first two pairs of prolegs vestigial
- ⬠ Woolly-bear caterpillars with secondary setae on verrucae
- ▤ Stridulatory ridges on the inside of cocoons
- ▤ Boat-shaped cocoon with vertical exit slit

Fig. 5 Summary of ancestral states reconstruction on Bayesian tree under DELTRAN optimization. Clades representing higher taxa (i.e., families) are coloured. Support values under the two support measures (bootstrap/posterior probabilities) shown next to the branches. Coloured characters on terminal branches and internal nodes indicate the presence of morphological traits as shown below the tree. Names of moths shown in figure from top to bottom are: *Spirama* (Erebidae, Erebiniae), *Autographa* Hübner (Noctuidae, Plusiinae), *Diphthera* (Nolidae: Diphtherinae), *Eligma* Hübner (Nolidae: Eligminae), *Nola* Leach (Nolidae, Nolinae), *Pseudoips* Hübner (Nolidae, Chloephorinae, Chloephorini), *Giaura* Walker (Nolidae, Chloephorinae, Sarrothropini).

reasonably inferred as ancestral for entire Noctuoidea (Holloway, 1989, Mitchell *et al.*, 2006), as it is, apparently, for most

other macrolepidopteran superfamilies (Powell *et al.*, 1998).

Within Noctuoidea, arboreal feeding is predominant among the oldest and basal lineages in trifid families—Oenosandridae and Notodontidae—and, within quadrifids, in diverse lineages of Erebidae (e.g., many Erebinae, Aganainae, Lymantriinae, etc.) as well as Euteliidae (Table 1). My results corroborate those of previous results (Forbes, 1923, Holloway, 1987, Weller, 1989, Miller, 1991, Richards, (1933) 1932) in accepting that trifids are the plesiomorphic sister lineage to the rest of Noctuoidea (i.e. quadrifid Noctuoidea) (**I**, **II**, **IV**, **V**). For example, the family Oenosandridae—only known from Australia—mainly feeds on the woody plant family Myrtaceae (Miller, 1991). In Notodontidae—with a worldwide distribution but more diverse in tropics and especially the Neotropics (Weller, 1989, Miller, 1991)—almost all species feed on trees, and only a few are found on herbaceous plants (Miller, 1991). Within Euteliidae, Euteliinae most commonly feed on Anacardiaceae (Powell *et al.*, 1998), a plant family that contains trees and shrubs with highly poisonous flowers. Among their other prominent hosts are Burseraceae (includes both shrubs and trees), Dipterocarpaceae (mainly tropical lowland rainforest trees), Moraceae and Hamamelidaceae (which consists of small trees and shrubs) (Holloway, 1985, Powell *et al.*, 1998). Stictopterinae, the sister group of Euteliinae, is associated primarily with Dipterocarpaceae and Clusiaceae (Table 1). Within quadrifids, where tree feeding is probably also ancestral, it seems clear that there have been many independent colonizations and subsequent radiations on herbaceous plants, most spectacularly in Arctiinae (Erebidae) and derived trifine lineages (e.g., the pest clade). Although, the great majority of quadrifids feed on living higher plants,

consumption of lower plants and detritus has arisen in several groups, most notably Erebidae (**II**). For example, lichen-feeding is predominant among lithosiines (Arctiinae) and a number of Aventiini (Boletobiinae) species (Wagner *et al.*, 2008), while detritivory, mycophagy and algivory is dominant in Herminiinae and Boletobiinae (**II**) and recurs sporadically in other noctuid subfamilies (e.g., some Bryophilinae, see Table 1) (**V**).

The results in paper **V** also suggested that Noctuidae included a number of lineages that are exclusively arboreal feeders, such as Dilobinae (Rosaceae), Raphiinae (Salicaceae), Pantheinae (Pinaceae) and Acronictinae (polyphagous but mostly on trees) (Table 1). The first three of these groups are associated with basal Noctuidae lineages in my phylogenetic hypothesis (Fig. 6)—those characterized by the plesiomorphic pseudoquadrifine condition of the hindwing venation. There are also a few groups among the derived noctuid lineages that generally feed on trees and shrubs, such as some Xylenini, Psaphidini (Mitchell *et al.*, 2006), and Orthosiini. Some other subfamilies are more specialized; for example, Agaristinae, often show a strong preference for Vitaceae (Holloway, 1989). My review of major trends in feeding habits in the subfamily Dyopsinae (Table 1) indicates that most of them feed on the plant family Urticaceae, a flowering plant family of mostly trees and shrubs. In contrast, herbaceous-feeding larvae are predominant in the higher trifines (i.e., the ‘pest clade’, Amphipyrinae, Metoponiinae, etc.).

Table 1 Larval host-plant families for Noctuidae study taxa. Zoogeographic regions are abbreviated as follows: P = Palearctic; O = Oriental; Au = Australasia; Nea = Nearctic; Neo = Neotropical; Af = Afrotropical.

Family	Subfamily	Tribe	Species	Main host-plant family	Main Host-plants	Host growth form	Typical distribution
			Outgroup				
Notodontidae	Notodontinae		<i>Notodonta dromedaris</i>	Betulaceae	<i>Betula</i>	Trees	P
Notodontidae	Thaumetopoeinae		<i>Thaumetopoea solitaria</i>	Pinaceae/Anacardiaceae	<i>Pistacia</i>	Trees	P/O/Af
Euteliidae	Euteliinae		<i>Eutelia adalatrix</i>	Anacardiaceae/Famamelidaceae	<i>Rhus/Liquidambar/Altingia</i>	Trees	P
Euteliidae	Euteliinae		<i>Targatila subocellata</i>	Myrtaceae	<i>Engenia</i> spp	Trees	O/Au
Euteliidae	Suctopterinae		<i>Lophoptera squamigera</i>	Dipterocarpaceae/Euphorbiaceae/Malvaceae	<i>Shorea/Grewia</i>	Herbs/Trees	O
Euteliidae	Suctopterinae		<i>Stictoptera columba</i>	Clusiaceae (=Guttiferae)	<i>Calophyllum/Garcinia/Mesua</i>	Trees	O
Erebidae	Erebinae	Catocalini	<i>Catocala sponsa</i>	Fagaceae	<i>Quercus</i>	Trees	P
Erebidae	Lymaenirinae	Lymaenirini	<i>Lymaeniria monacha</i>	Polyphagous	Polyphagous	Trees	P
Erebidae	Arctiinae	Arctiini	<i>Arctia caja</i>	Polyphagous	Polyphagous	Herbs/Trees	P/Nea
Erebidae	Calpinae	Calpini	<i>Calyptra thalictri</i>	Ranunculaceae/Menispermaceae	<i>Thalictrum/</i> vines	Herbs	P
Nolidae	Collomeninae		<i>Neostictoptera nigropuncta</i>	-	-	-	Nco
Nolidae	Collomeninae		<i>Callomena siopera</i>	Combretaceae	<i>Terminalia</i>	Trees	Nco
Nolidae	Eligminae		<i>Eligma naricissus</i>	Simaroubaceae	<i>Ailanthus</i>	Trees	O
Nolidae	Chloephorinae	Chloephorini	<i>Pseudopsis prasimana</i>	Fagaceae/Salicaceae	<i>Fagus/Quercus/Populus</i>	Trees	P
			Ingroup				
Noctuidae	Dyopsinae	Dyopsini	<i>Dyops chromatophila</i>	Urticaceae	<i>Cecropia</i>	Trees	Nco
Noctuidae	Dyopsinae	Arctiini	<i>Pseudaerete melanis</i>	-	-	-	Af
Noctuidae	Dyopsinae	Arctiini	<i>Arcte modesta</i>	Urticaceae/Ulmaceae	<i>Boehmeria/Dehraquasta/Trema</i>	Shrubs/small trees	O
Noctuidae	Dyopsinae	Arctiini	<i>Pararcte schneideriana</i>	Urticaceae	<i>Cecropia</i>	Trees	Nco
Noctuidae	Dyopsinae	Ceroctenini	<i>Belciana kala</i>	Malvaceae	<i>Grewia Heritiera</i>	Trees	O
Noctuidae	Dyopsinae	Ceroctenini	<i>Belciana biformis</i>	Malvaceae	<i>Grewia Heritiera</i>	Trees	O
Noctuidae	Dyopsinae	Ceroctenini	<i>Cyelodes omma</i>	Arecaceae	palm trees	Trees	O
Noctuidae	Dyopsinae	Ceroctenini	<i>Ceroctena amyta</i>	Meliaceae	<i>Trichilia</i>	Shrubs/trees	Nco
Noctuidae	Dyopsinae	Ceroctenini	<i>Sosxena grata</i>	Meliaceae	<i>Trichilia</i>	Shrubs/trees	Nco
Noctuidae	Plusinae	Plusini	<i>Autographa gamma</i>	Polyphagous	Polyphagous	Herbs/Shrubs	P/Nea
Noctuidae	Plusinae	Abrostolini	<i>Abrostola tripartita</i>	Urticaceae	<i>Urtica dioica</i>	Herbs	P
Noctuidae	Eustrotiinae		<i>Deltote uncala</i>	Cyperaceae	<i>Carex</i>	Herbs	P
Noctuidae	Cucullinae		<i>Cucullia umbratica</i>	Asteraceae	Oligophagous	Herbs	P
Noctuidae	Dilobinae		<i>Diloba caeruleocephala</i>	Rosaceae	<i>Malus/Prunus/Pyrus/Sorbus</i>	Trees	P
Noctuidae	Raphinae		<i>Raphia abrupta</i>	Salicaceae/Betulaceae	<i>Populus/Betula</i>	Trees	Nco
Noctuidae	Pantheinae	Eucocytiini	<i>Eucocytiia meeki</i>	-	-	-	Au
Noctuidae	Pantheinae	Pantheini	<i>Thiacidas</i> sp.	Rhamnaceae/Fabaceae	<i>Ziziphus/Azacia</i>	Shrubs/Trees	O
Noctuidae	Pantheinae	Pantheini	<i>Antirrhinoides catocalina</i>	-	-	-	O
Noctuidae	Pantheinae	Pantheini	<i>Panthea coenobita</i>	Pnaeaceae	<i>Pinus</i>	Trees	P
Noctuidae	Acontinae		<i>Emmella trabecalis</i>	Convolvulaceae	<i>Convolvulus</i>	Herbs	P
Noctuidae	Acontinae		<i>Acontia lucida</i>	Convolvulaceae	<i>Convolvulus</i>	Herbs	P
Noctuidae	Bagisarinae		<i>Amyra octo</i>	Polyphagous	Polyphagous	Herbs	Nco/Nea/O/Au/Af

Continuation of Table 1.

Noctuidae	Bagisariinae	<i>Xanthodes albago</i>	Malvaceae	Oligophagous	Herbs	O/A/I//Au
Noctuidae	Bagisariinae	<i>Ramadasa pavo</i>	–	–	–	O
Noctuidae	Bagisariinae	<i>Dyzela plogiata</i>	Malvaceae	<i>Grewia</i>	Trees	O
Noctuidae	Bagisariinae	<i>Enicniphon leena</i>	Malvaceae	<i>Luehea</i>	Trees	Neo
Noctuidae	Bagisariinae	<i>Vespolia caeruleifera</i>	Malvaceae	<i>Ceiba pentandra</i>	Trees	Neo
Noctuidae	Bagisariinae	<i>Parangitia temperata</i>	Moraceae	<i>Machira</i>	Trees	Neo
Noctuidae	Bagisariinae	<i>Parangitia mosata</i>	Malvaceae/Moraceae	–	Trees	Neo
Noctuidae	Bagisariinae	<i>Diopa corone</i>	Ochnaceae/Malvaceae	<i>Cespedesia Pachira</i>	Shrubs/Trees	Neo
Noctuidae	Bagisariinae	<i>Concana mimidissima</i>	Malpighiaceae	<i>Heteropterys/Byrsomima</i>	Shrubs/Trees	Neo
Noctuidae	Bagisariinae	<i>Concana lecta</i>	Malpighiaceae	<i>Banisteriopsis</i>	Trees	Neo
Noctuidae	Bagisariinae	<i>Concana permixta</i>	Malpighiaceae	–	–	Neo
Noctuidae	Amplipyriini	<i>Amplipyria perfusa</i>	Polyphagous	Polyphagous	Shrubs	P
Noctuidae	Amplipyriinae	<i>Brachionycha mibesculosa</i>	Polyphagous	Polyphagous	Shrubs/Trees	P
Noctuidae	Metoponiinae	<i>Flammia quadrfasciata</i>	Orchidaceae	orchids	Epiphytes	O
Noctuidae	Metoponiinae	<i>Panameria tenebrata</i>	Caryophyllaceae	<i>Cerastium</i>	Herbs	P
Noctuidae	Acronictinae	<i>Craniochora ligustri</i>	Betulaceae/Oleaceae	<i>Alnus/Fraxinus</i>	Trees	P
Noctuidae	Acronictinae	<i>Acronicta americana</i>	Polyphagous	Polyphagous	Trees	Nea
Noctuidae	Acronictinae	<i>Acronicta ruminis</i>	Polyphagous	Polyphagous	Trees	P
Noctuidae	Acronictinae	<i>Cerna cerintha</i>	Rosaceae	<i>Prunus/Alnus</i>	Trees	Nea
Noctuidae	Acronictinae	<i>Comachara cadburyi</i>	Cornaceae	<i>Nyssa sylvatica</i>	Trees	Nea
Noctuidae	Acronictinae	<i>Harrisimemna trisignata</i>	Polyphagous	<i>Nyssa sylvatica</i>	Trees	Nea
Noctuidae	Acronictinae	<i>Polygrammate hebraeicum</i>	Cornaceae	<i>Nyssa sylvatica</i>	Trees	Nea
Noctuidae	Acronictinae	<i>Agriopodes fallax</i>	Adoxaceae	<i>Viburnum</i>	Shrubs	Nea
Noctuidae	Agaristinae	<i>Perisepta polysticta</i>	Dilleniaceae	<i>Hibbertia</i>	Shrubs	Au
Noctuidae	Aedinae	<i>Aedia leucomelas</i>	Convolvulaceae	<i>Ipomoea/Convolvulus</i>	Herbs	Au/O
Noctuidae	Condicinae	<i>Condica illecta</i>	Asteraceae	<i>Carthamus/Coreopsis</i>	Herbs	O
Noctuidae	Condicinae	<i>Hemicephalis atlesa</i>	Boraginaceae	<i>Cortia panamensis</i>	Shrubs	Nea
Noctuidae	Heliothinae	<i>Pyrrhia umbra</i>	Polyphagous	Polyphagous	Shrubs	P
Noctuidae	unassigned	<i>Chytonix diehli</i>	–	–	–	O
Noctuidae	Bryophilinae	<i>Cryphia repticala</i>	Lichenes	Lichenes	Lichenes	P
Noctuidae	Bryophilinae	<i>Stenoloba futii</i>	Lichenes	Lichenes	Lichenes	O
Noctuidae	unassigned	<i>Ecpatia</i> sp.	Phyllanthaceae	–	shrubby	O
Noctuidae	unassigned	<i>Ecpatia longinquua</i>	Phyllanthaceae	<i>Antidesma</i>	shrubby	O
Noctuidae	Noctuiniae	<i>Tracola aureata</i>	Polyphagous	Polyphagous	Herbs	O
Noctuidae	Noctuiniae	<i>Actinoita polyodon</i>	Hypericaceae	<i>Hypericum</i>	Herbs	P
Noctuidae	Noctuiniae	<i>Hoplodrina octogemaria</i>	Polyphagous	Polyphagous	Herbs	P
Noctuidae	Noctuiniae	<i>Diaphone</i> sp.	Polyphagous	Polyphagous	Herbs	Af
Noctuidae	Noctuiniae	<i>Apamea crenata</i>	Poaceae	Oligophagous	Grass	P
Noctuidae	Noctuiniae	<i>Ujeus fannas</i>	Salicaceae	<i>Salix/Populus</i>	Trees	Nea
Noctuidae	Noctuiniae	<i>Noctua fimbriata</i>	Polyphagous	Polyphagous	Herbs	P

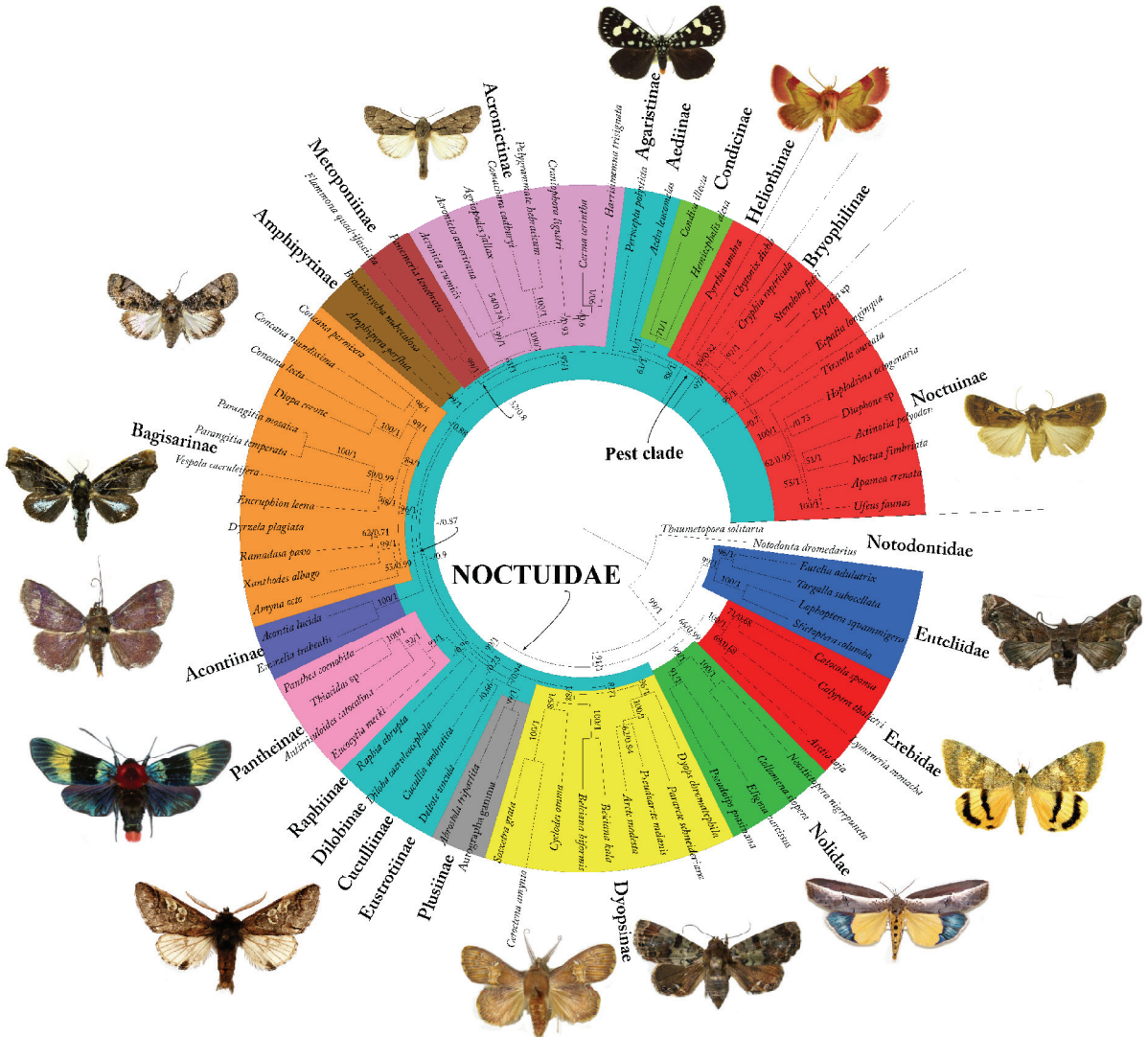
These results are also widely corroborated by the study of Mitchell *et al.* (2006), who studied the role of ecological and geographical factors in the diversification of Noctuoidea. They presented a provisional synopsis of species diversity, latitudinal distribution, and host-plant use for major noctuid groups sampled in their study, superimposed onto the phylogeny. It is revealed that the growth form (i.e., woody-plant feeding vs. herb-feeding) of the host-plant appears on the whole more conserved phylogenetically than host-plant taxon affiliation, where woody-plant feeding can be reasonably inferred as ancestral for Noctuoidea, as it is, apparently, for most other macrolepidopteran superfamilies.

In general, herbaceous-feeding larvae are predominant in the higher trifines (i.e., the ‘pest clade’, Amphipyrae, Metoponiinae, etc.), whereas in the basal noctuid and basal trifines lineages arboreal feeding is predominant. This evolutionary pattern of feeding habits, postulating a general evolutionary trend from a tree feeding to a herb feeding habit, has also been shown for butterflies (Janz & Nylin, 1998). Thus it can be suggested that the host-growth form in Noctuoidea is more

evolutionarily conservative than host affiliation (Mitchell *et al.*, 2006). However, my preliminary study of host-plant associations showed that in a few Noctuidae subfamilies a strong preference toward feeding on a specific plant family can be seen, such as Bagisarinae which feed mainly on Malvaceae.

One of the fundamental reasons for studying the evolutionary history of noctuid moths is to determine the main driving forces behind the diversification of this species-rich group. It has become apparent that the evolution of host-plant use has likely been a key ecological mechanism behind the rapid diversification and evolutionary divergence in the butterfly families (Janz & Nylin, 1998, Janz *et al.*, 2006). Noctuoidea are about three times more diverse than the butterflies, and the role of host plant specialization in the diversification of the moths has yet to be studied in detail. With the phylogenetic relationships of the major lineages of Noctuoidea becoming clearer (**I**, **II**, **IV**, **V**), questions about host plant associations and diversification can now be addressed for this megadiverse clade.

Fig. 6 Phylogenetic hypothesis of the basal Noctuidae subfamilies, based on a Bayesian inference analysis. Clades representing major lineages are coloured. Support values under the two support measures (Bootstrap/posterior probabilities) shown next to the branches. Names of moths shown in figure clockwise are: *Eutelia* (Euteliidae); *Catocala* (Erebidae); *Eligma* (Nolidae); *Dyops* (Noctuidae Dyopsinae, Dyopsini), *Sosxetra* Walker (Dyopsinae, *Ceroctena* clade), *Diloba* Boisduval (Dilobinae), *Eucoctyia* (Pantheinae), *Amyna* Guenée (Bagisarinae), *Vespola* Walker (Bagisarinae), *Concana* Walker (Bagisarinae), *Acronicta* Ochseneimer (Acronictinae), *Periphanes* (Heliiothinae), *Euxoa* Hübner (Noctuinae).



4. CONCLUSIONS AND FUTURE DIRECTIONS

4.1 Conclusions

To conclude my Ph.D. thesis, I have summarized a number of distinctive issues and strategies that I have employed in this thesis that are different from those in previous works.

First of all and probably the most important scheme was the taxon sampling strategy. Elucidating the evolutionary history of the massive superfamily Noctuoidea clade (potentially including 45,000 species) required extensive taxon sampling. A deliberate and carefully considered sampling strategy could only be accomplished by selecting exemplars from significant groupings of genera and morphologically well-supported concepts of higher taxa. In my five projects, I chose up to 393 taxa (Appendix 1) of 45,000 noctuoids that have been formally described, covering almost all recognized major clades of Noctuoidea, as representatives for major lineages of Noctuoidea. This extensive taxon sampling was made possible through the extensive network that I built up during my studies. One of the main causes for the previous low support of phylogenetic relationships for some massive clades probably stems from very sparse sampling.

The second feature was the obstacles that are met in applying morphological traits, in particular, in a species-rich, cosmopolitan and heterogeneous taxon such as Noctuoidea. The high number of species presents complications to the use of morphology and any other kinds of phenotypic traits at this taxonomic level. Morphological data are thus often difficult to homologize and code, require great experience to identify character states

correctly and can be subject to extensive homoplasy (character convergence and reversal). Consequently, despite their major role in inferring phylogenies, morphological analyses have often failed to determine relationships among most groups with confidence. On the other hand, phenotypic traits (e.g., morphological, ecological, host-plant associations, behavioural characters, etc.) and synapomorphies can be properly recognized from molecular phylogeny-based systems. In the context of such a robust evolutionary hypothesis, morphological, ecological and behavioural characters can be better understood. For example, I demonstrated that the prespiracular counter-tympanal hood of Aganainae, Herminiinae and Arctiinae is not the result of convergent (independent) evolutionary events, as previously thought (I–II). I proved that this is the result of a common ancestry of these groups within the family Erebidae (II). Polyphyly of the old concept of Calpinae was another clear case (II–III). My results recovered a monophyletic subfamily Calpinae that was restricted to three monophyletic tribes (i.e., Phyllochini, Ophiderini and Calpini) (III), and placed all other groups that had previously been placed as tribes within Calpinae (e.g., Anobini, Anomini and Scoliopterygini), as independent and distant well-defined lineages (i.e., Scoliopteryginae and Anobinae) within Erebidae (II). Calpinae sensu lato was traditionally restricted to the fruit-piercing (and in some cases skin piercing and blood sucking) moths (Kitching & Rawlins, 1998). However, my molecular phylogeny revealed that this feeding behavior, as well as its associated modifications of the proboscis and adaptations (III), have

evolved independently in Calpinae, Scoliopteryginae (including Anomini), Anobinae and some Erebiinae (II). This provides again an object lesson on how the sharing of peculiar morphological adaptations may mislead in classification, and how shared features of a more subtle nature may be overlooked in an unchallenged traditional classification (I). Other examples of discovering morphological apomorphies based on my molecular phylogeny results were in Diphtherinae—characterized by the loss of the proximal pair of tibial spurs on the hindlegs of males and the presence of a frontal tubercle—(IV), Nolidae—construction of a boat-shaped cocoon with a vertical exit slit, and finger-like retinaculum on the forewings of the males—(IV), trifold and quadrifold lineages—condition of vein M2 in forewing—(I, II, IV, V), host-plant associations—e.g., detritivory, lichen-feeding, mycophagy and algivory—in Boletobiinae (Erebidae) (II) and finally speculation for a potential broad evolutionary feeding habit trend in Noctuoidea from tree feeding in trifold lineages toward herb feeding in more derived lineages (i.e., pest clade in Noctuidae), similar to the pattern that has been suggested for butterflies (Janz & Nylin, 1998).

A third issue was related to determining the evolutionary relationships of noctuid taxa of uncertain systematic position using molecular data. In particular, those taxa characterized by the pseudoquadrifine hindwing venation, which have been previously assigned to various noctuid groups (IV–V). Molecular phylogenetics methods illustrate how easy is it can be to pinpoint their certain phylogenetic position.

To conclude, I had been able to address a massive and long-recalcitrant phylogenetic problem, that of the relationships among and within major lineages of the largest superfamily of Lepidoptera, Noctuoidea. The phylogenetic analyses that I employed were well designed, and many relatively deep nodes are strongly resolved and substantial progress has been made on the backbone phylogeny of Noctuoidea. This group of insects is of major economic and ecological importance. It constitutes an exemplar case in which molecular methods, which seem to be highly informative at this level, have been of enormous help, in part because the sheer size of the group has greatly impeded progress via the morphological approach.

4.2 Future directions

This Ph.D. thesis addressed several phylogenetic problems concerning the evolution of Noctuoidea, but there are still many unanswered questions. For example, it is crucial to determine where, when and how the major groups of noctuoids diverged and evolved. The common factors that influence the speciation process and identifying possible reasons for this remarkable and extraordinary diversity of species among other herbivorous insects are not yet understood. Likewise, the patterns of diversification, the main driving forces behind the diversification of this species-rich group, and plausible explanations for the differences in diversity among the various groups within Noctuoidea have yet to be determined—for instance, why does a family such as Euteliidae contain about 500 species, but another like Erebidae contains 25,000 species? It would be of great interest to know whether major climatic changes and mass extinction events over geological

time scales have had a major impact on the diversification of Noctuoidea. And it would be most interested to infer a scenario of the evolutionary history and biogeography of noctuoids, based on all available data (i.e., morphology, DNA sequences, ecological data, geographical distributions, and geological and paleontological information).

Further studies are also needed to identify the reasons and causes for the short basal branches, i.e., whether there is a historical explanation behind them (e.g., rapid radiation), or whether it is simply an artefact of insufficient data.

The use of novel tools in DNA sequencing technologies, such as Next-Generation Sequencing (NGS) methods and relatively new field of phylogenomics, might be able to address the state of uncertainty in Noctuoidea diversification and their rapid radiations. Phylogenomics is useful for evolutionary studies, in particular resolving ambiguous phylogenies and for verifying relationships created on the basis of a few gene regions (Hackett *et al.*, 2008). Since the cost of whole genome sequencing is decreasing, anticipation of total genome sequences from the major lineages of interest, is no longer a distant dream (Murphy *et al.*, 2004).

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APPENDIX

Family	Subfamily	Species	Paper	Specimen ID	COLLCT	COL-lety	EPI	EP1	Wings	GAPDH	RpSS	MDB	CAD	MDH	Type status	Locality
		Ooutgroup														
Drepanidae	Thyatridae	<i>Thyatira basus</i>	I	MM00027	GU828580	GU828380	GU828919	GU829212	GU829481	GU829743	GU830597	GU830293	GU828083	GU829969	TG/TS	FINLAND
Sphingidae	Sphinginae	<i>Sphinx ligasari</i>	I	NW141-12	EU141358	EU141358	EU136665	EU136665	EU141239	EU141494	EU141391	EU141615	EU141313	EU141550	TG/TS	FINLAND
Bombycidae	Bombycinae	<i>Bombyx mori</i>	I	NW149-1	EU141360	EU141360	EU136667	EU141241	EU141495	EU141493	EU141617	EU141315	EU141552	TG/TS	USA	
Geometridae	Archaeirinae	<i>Archaearis parthianus</i>	I	NW107-1	DQ018928	DQ018928	DQ018899	DQ018899	DQ018869	EU141485	EU141381	EU141604	EU141303	EU141539	TG/TS	SWEDEN
		I n g r o u p														
Oenosiandridae		<i>Oenosiandra boisduvali</i>	I,II,IV	MM07590	GU828791	GU929762	GU829098	GU829377	GU829651	GU829871	GU830751	GU830492	GU828266	GU830173	TG/TS	AUSTRALIA
Oenosiandridae		<i>Discophlebia</i> sp.	IV	RZ403	HQ006217	HQ006513	HQ006404	HQ006480	HQ006525	HQ006480	HQ006729	HQ006638	-	HQ006551	-	AUSTRALIA
Notodontidae	Phalerinae	<i>Phalera bucephala</i>	I,II	MM00122	GU828607	GU828405	GU828941	GU829235	GU829502	-	GU830617	GU830108	GU828108	GU829995	TG/TS	FINLAND
Notodontidae	Heterocampinae	<i>Stauropus fagi</i>	I,II,IV	MM00981	GU828651	GU828449	GU828983	GU829266	GU829539	GU829780	GU830650	GU830357	GU828148	GU830038	TS	FINLAND
Notodontidae	Notodontinae	<i>Noiodonta dromedarius</i>	I,II,IV,V	MM000998	GU828653	GU828451	GU828984	GU829268	GU829540	GU829781	GU830652	GU830359	GU828150	GU830040	TG/TS	FINLAND
Notodontidae	Pygmaeinae	<i>Clostera nigra</i>	I	MM01005	GU828654	GU828452	GU828985	GU829269	GU829541	GU829782	GU830653	GU830360	GU828151	GU830041	-	FINLAND
Notodontidae	Thaumetopocinae	<i>Epixoma melanosticta</i>	I	MM07592	GU828792	GU929763	GU829099	GU829378	GU829652	GU829872	GU830752	GU830493	GU828267	GU830174	-	AUSTRALIA
Notodontidae	Thaumetopocinae	<i>Thaumetoposa solitaria</i>	I,V	MM09888	GU828843	GU929807	GU829144	-	GU828692	GU829904	GU830791	GU830534	GU828307	GU830223	TG	GREECE
Notodontidae	Dulsiinae	<i>Crimodes besckei</i>	I	05-SKNP-57213	GU828527	-	GU828873	GU829175	GU829434	-	GU830563	GU830251	GU828039	GU829918	-	COSTA RICA
Notodontidae	Nysaliniinae	<i>Nysalea striata</i>	I	05-SKNP-4443	GU828525	-	GU828871	GU829173	GU829432	GU829717	GU830561	GU830249	GU828037	GU829916	TG	COSTA RICA
Notodontidae	Dopinae	<i>Scouta leucophleps</i>	I	06-SRNP-22781	GU828532	GU828334	GU828878	GU829179	GU829439	GU829721	GU830568	GU830256	GU828044	GU829923	-	COSTA RICA
Euteliidae	Eutelinae	<i>Eutelia adultatrix</i>	I,II,IV	MM00160	GU828621	GU828419	GU828956	GU829246	GU829516	GU829764	GU830629	GU830330	GU828122	GU830010	TG/TS	GREECE
Euteliidae	Eutelinae	<i>Eutelia geyeri</i>	IV	RZ508	X	X	X	X	X	X	X	X	-	X	TG	HONG KONG
Euteliidae	Eutelinae	<i>Marathyssa basalis</i>	I	RZ23	HQ006183	HQ006887	HQ006279	HQ006374	HQ006791	HQ006455	HQ006698	HQ006606	HQ006979	HQ006528	TS	USA
Euteliidae	Eutelinae	<i>Targalla subcellata</i>	I,II,IV,V	RZ35	HQ006210	HQ006914	HQ006306	HQ006397	HQ006818	HQ006473	HQ006722	HQ006631	HQ007000	-	-	HONG KONG
Euteliidae	Stictopterninae	<i>Aegilia desarbens</i>	II	RZ287	JN401234	JN401118	JN401352	-	JN400927	JN401566	JN401873	JN401772	JN401036	-	TS	INDONESIA
Euteliidae	Stictopterninae	<i>Lophoptera hemithyris</i>	I,II	MM07614	GU828802	GU929772	GU829307	GU829385	GU829661	GU829879	GU830759	GU830601	GU828274	GU830183	-	AUSTRALIA
Euteliidae	Stictopterninae	<i>Lophoptera squamifigera</i>	IV,V	RZ120	X	X	X	X	X	X	X	X	-	X	TG	HONG KONG
Euteliidae	Stictopterninae	<i>Stictoptera columba</i>	IV,V	RZ541	X	X	X	X	X	X	X	X	-	X	TG	MALAYSIA
Erebidae	Scoliopteryginae	<i>Scoliopteryx libarix</i>	I,II,IV	MM000407	GU828641	GU828439	GU828975	GU829260	GU829532	-	GU830643	GU830348	GU828140	GU830028	TG/TS	FINLAND
Erebidae	Scoliopteryginae	<i>Oxonoba torpida</i>	II	RZ411	JN401252	JN401134	JN401369	JN401480	JN401093	JN401582	JN401893	-	JN401050	-	TS	MALAYSIA
Erebidae	Scoliopteryginae	<i>Rusicada fulvata</i>	II	RZ101	JN401253	JN401135	JN401370	JN401481	JN401093	JN401583	JN401790	JN401051	JN401683	-	TS	HONG KONG
Erebidae	Scoliopteryginae	<i>Rusicada metaxantha</i>	II	RZ55	HQ006237	HQ006930	HQ006315	HQ006414	HQ006835	-	HQ006739	HQ006647	HQ007016	HQ006560	TG	TAIWAN
Erebidae	Scoliopteryginae	<i>Gontis imvolua</i>	I,II	RZ13	HQ006166	HQ006963	HQ006263	HQ006357	HQ006775	-	HQ006682	HQ006592	HQ006963	-	TG	TANZANIA
Erebidae	Scoliopteryginae	<i>Anomis flava</i>	II	RZ100	JN401254	JN401136	JN401137	JN401482	JN401093	JN401584	-	-	JN401052	JN401684	-	HONG KONG
Erebidae	unassigned	<i>Rhesata imparata</i>	II	RZ265	JN401255	JN401137	JN401137	JN401483	JN400940	JN401585	-	JN401791	JN401053	JN401685	TS	HONG KONG
Erebidae	unassigned	<i>Nychoptera noctuidalis</i>	II	RZ283	JN401256	JN401138	JN401137	-	JN400941	-	-	JN401792	-	-	TS	USA
Erebidae	Rivulinae	<i>Rivula sericealis</i>	I,II	MM01404	GU828664	GU828462	GU828995	GU829278	-	GU829791	-	GU830370	GU828161	GU830051	TG/TS	FINLAND

Erebidae	Rivulinae	<i>Rivula ochrea</i>	RZ159	JN401257	JN401339	JN401374	JN401484	JN400979	JN401586	JN401793	JN401054	—	TG	GHANA
Erebidae	Rivulinae	<i>Oxyella ando</i>	RZ24	HQ006184	HQ006888	HQ006280	HQ006792	HQ006456	—	HQ006607	HQ006529	—	—	USA
Erebidae	Rivulinae	<i>Bocula bifaria</i>	RZ413	JN401258	JN401140	JN401375	JN401485	JN400942	JN401587	—	JN401055	JN401686	—	MALAYSIA
Erebidae	Rivulinae	<i>Ogasa ansorgeri</i>	RZ167	JN401259	JN401141	JN401376	JN401486	JN400986	JN401588	—	JN401056	JN401687	—	GHANA
Erebidae	Rivulinae	<i>Alesia etialis</i>	RZ94	JN401260	JN401142	JN401377	JN401487	JN400943	JN401589	—	JN401794	—	JN401688	TS
Erebidae	Anobinae	<i>Anoba anguliplaga</i>	RZ332	HQ006206	HQ006910	HQ006302	HQ006395	HQ006814	HQ006469	—	HQ006627	—	HQ006544	TG
Erebidae	Anobinae	<i>Marcipa</i> sp.	RZ177	HQ006177	HQ006881	—	HQ006368	HQ006785	HQ006450	—	HQ006601	HQ006973	HQ006522	GHANA
Erebidae	Anobinae	<i>Marcipa</i> sp.	RZ200	JN401261	JN401143	JN401378	JN401488	JN400944	JN401591	—	JN401795	—	JN401689	GHANA
Erebidae	Anobinae	<i>Plecoptera major</i>	RZ183	JN401262	JN401144	—	JN401489	JN400945	JN401591	—	JN401796	—	JN401690	GHANA
Erebidae	Anobinae	<i>Cribote prominens</i>	RZ109	JN401263	JN401145	JN401379	JN401490	JN400946	JN401592	—	JN401797	JN401057	JN401691	HONG KONG
Erebidae	Anobinae	<i>Rema costimaculata</i>	RZ103	JN401264	JN401146	JN401380	JN401491	JN400947	JN401593	—	JN401798	JN401058	JN401692	TS
Erebidae	Anobinae	<i>Baniana strigata</i>	RZ92	JN401265	JN401147	JN401381	JN401492	JN400948	JN401594	—	JN401799	JN401059	JN401693	COSTA RICA
Erebidae	Anobinae	<i>Deinopa signiplena</i>	RZ311	JN401266	JN401148	JN401382	JN401493	JN400949	JN401595	—	JN401800	JN401060	JN401694	COSTA RICA
Erebidae	Hypeninae	<i>Hypena proboscoidalis</i>	MM101545	GJ828668	GJ828466	GJ828999	GJ829282	GJ829553	GJ829794	GJ828165	GJ828055	GJ828055	TG/TS	FINLAND
Erebidae	Hypeninae	<i>Hypena balimorialis</i>	RZ367	JN401267	JN401149	JN401383	JN401494	JN400953	JN401596	JN401801	JN401061	JN401695	—	USA
Erebidae	Hypeninae	<i>Hypena lacertalis</i>	RZ368	JN401268	JN401150	JN401384	JN401495	JN400950	—	JN401806	—	JN401696	—	HONG KONG
Erebidae	unassigned	<i>Cultripalpa</i> sp.	RZ394	JN401269	JN401151	JN401385	JN401496	JN400951	JN401597	JN401802	—	JN401697	—	MALAYSIA
Erebidae	unassigned	<i>Cobocochyla salicis</i>	RZ4	HQ006215	HQ006919	HQ006311	HQ006402	HQ006823	HQ006478	HQ006727	HQ006636	HQ007005	—	TS
Erebidae	Lymantirinae	<i>Lymantiria monacha</i>	LI,LI,IV,V	GJ828655	GJ828453	GJ828986	GJ829270	GJ829542	—	GJ830654	GJ830361	GJ828152	GJ830042	TG
Erebidae	Lymantirinae	<i>Lacomas salicis</i>	LI	GJ828748	GJ829722	GJ829962	GJ829247	GJ829611	—	GJ830719	GJ830449	GJ828232	GJ830132	TG/TS
Erebidae	Lymantirinae	<i>Nygnia plana</i>	RZ34	HQ006209	HQ006913	HQ006305	HQ006396	HQ006817	HQ006472	HQ006620	HQ006999	HQ006546	—	TG
Erebidae	Lymantirinae	<i>Orygia antiopa</i>	RZ130	HQ006167	HQ006964	HQ006264	HQ006358	HQ006776	HQ006443	HQ006683	HQ006593	HQ006964	HQ006513	TG/TS
Erebidae	Lymantirinae	<i>Arctornis</i> sp.	RZ89	HQ006241	HQ006943	HQ006335	HQ006428	HQ006849	HQ006752	HQ006659	HQ007024	HQ006572	—	JAPAN
Erebidae	Pangrapinae	<i>Pangrapa bicornuta</i>	RZ40	HQ006216	HQ006920	HQ006312	HQ006403	HQ006824	HQ006479	HQ006628	HQ006637	HQ007006	HQ006550	TG
Erebidae	Pangrapinae	<i>Pangrapa decoralis</i>	RZ66	HQ006236	HQ006939	HQ006331	HQ006423	HQ006844	—	HQ006747	—	HQ007022	HQ006568	TG/TS
Erebidae	Pangrapinae	<i>Chrysograpta igneola</i>	RZ408	JN401270	JN401152	JN401386	JN401497	JN400952	JN401598	JN401808	JN401803	—	—	TS
Erebidae	Pangrapinae	<i>Hyposemansis singha</i>	RZ279	JN401271	JN401153	JN401387	JN401498	JN400953	JN401599	JN401804	JN401804	JN401063	JN401698	TS
Erebidae	Pangrapinae	<i>Cracilodes caffra</i>	RZ292	JN401272	JN401154	JN401388	JN401499	JN400954	JN401600	JN401900	JN401805	JN401064	JN401699	TS
Erebidae	Pangrapinae	<i>Episyaris costariga</i>	RZ319	JN401273	JN401155	JN401389	JN401500	JN400955	JN401601	JN401901	—	—	JN401700	TS
Erebidae	Pangrapinae	<i>Masca abacalis</i>	RZ18	HQ006178	HQ006882	HQ006274	HQ006369	HQ006786	HQ006451	HQ006693	—	HQ006974	HQ006523	TS
Erebidae	unassigned	<i>Schistophya argemistriga</i>	RZ119	JN401274	JN401156	JN401390	JN401501	JN400956	JN401602	JN401902	JN401806	JN401065	JN401701	TS
Erebidae	Hermiinae	<i>Polygona strigilata</i>	MM101286	GJ828663	GJ828461	GJ828994	GJ829277	GJ829549	GJ829790	GJ828160	GJ828050	GJ828050	TG/TS	FINLAND
Erebidae	Hermiinae	<i>Paracelax trisialis</i>	RZ5	HQ006224	HQ006927	HQ006319	HQ006411	HQ006832	—	HQ006736	—	HQ007013	—	HUNGARY
Erebidae	Hermiinae	<i>Hermia tarsterialis</i>	RZ6	HQ006232	HQ006935	HQ006327	HQ006419	HQ006840	HQ006489	—	—	—	—	TG
Erebidae	Hermiinae	<i>Stimplicia</i> sp.	RZ166	HQ006175	HQ006879	HQ006272	HQ006366	—	HQ006448	HQ006691	HQ006599	HQ006971	HQ006520	GHANA
Erebidae	Hermiinae	<i>Idia aemula</i>	RZ271	JN401275	JN401157	JN401391	JN401502	JN400957	—	—	JN401807	JN401066	JN401702	TS
Erebidae	Hermiinae	<i>Lysimelia nelensis</i>	RZ260	JN401276	JN401158	—	JN401303	JN400958	JN401603	—	JN401808	JN401067	JN401703	TS
Erebidae	Hermiinae	<i>Nodaria verticalis</i>	RZ180	JN401277	JN401159	JN401392	JN401504	JN400959	JN401604	—	—	JN401704	—	GHANA

Erebidae	Agmatinae	<i>Asota caricae</i>	GIJ	MM00145	GIJ28615	GIJ28413	GIJ28949	GIJ29240	GIJ29509	—	GIJ30624	GIJ30325	GIJ28115	GIJ30060	TG/TS	TAIHLAND
Erebidae	Agmatinae	<i>Asota heliconia</i>	LIJ	RZ44	HQ00620	HQ00624	HQ006316	HQ006407	HQ006828	HQ006483	HQ006732	HQ006641	HQ007009	HQ006554	TG	HONG KONG
Erebidae	Agmatinae	<i>Neochera itrops</i>	II	RZ346	JN401278	JN401160	JN401393	—	JN400960	JN401605	—	JN401809	JN401068	JN401705	—	JAPAN
Erebidae	Agmatinae	<i>Euplocia memblaria</i>	II	RZ345	JN401279	JN401161	JN401394	JN401505	JN400961	JN401606	—	JN401810	—	JN401706	TS	MALAYSIA
Erebidae	Agmatinae	<i>Peridroma orbicularis</i>	II	RZ280	JN401280	JN401162	JN401395	JN401506	JN400962	JN401607	JN401903	JN401811	—	JN401707	TS	MALAYSIA
Erebidae	Agmatinae	<i>Mecodina praecipua</i>	II	RZ268	JN401281	JN401163	JN401396	JN401507	JN400963	JN401608	—	JN401812	JN401069	JN401708	—	HONG KONG
Erebidae	Agmatinae	<i>Psimada quadrigenis</i>	II	RZ27	JN401282	JN401164	JN401397	JN401508	JN400964	—	JN401904	JN401813	JN401070	JN401709	TG/TS	HONG KONG
Erebidae	Aectinae	<i>Brimia antica</i>	LIJ	RZ248	HQ006193	HQ006897	HQ006289	HQ006353	HQ006801	HQ006462	HQ006706	HQ006614	—	HQ006534	TS	HONG KONG
Erebidae	Aectinae	<i>Garudinia simulana</i>	II	RZ199	JN401283	JN401165	JN401398	JN401509	JN400965	JN401609	JN401905	JN401814	JN401071	JN401710	—	MALAYSIA
Erebidae	Aectinae	<i>Eugoa bipunctata</i>	II	RZ400	JN401284	JN401166	JN401399	JN401510	JN400966	—	JN401906	JN401815	JN401072	JN401711	—	MALAYSIA
Erebidae	Aectinae	<i>Cyna</i> sp	II	RZ398	JN401285	JN401167	JN401400	JN401511	JN400967	JN401610	JN401876	JN401816	JN401073	JN401712	—	MALAYSIA
Erebidae	Aectinae	<i>Barstae</i> sp	II	RZ397	JN401286	JN401168	JN401401	JN401512	JN400968	—	JN401878	JN401817	JN401074	JN401713	—	MALAYSIA
Erebidae	Aectinae	<i>Apisa canescens</i>	LIJ	MM05843	HQ006146	HQ006853	—	HQ006339	HQ006765	—	HQ006663	—	—	—	TS	OMAN
Erebidae	Aectinae	<i>Synonimis phlegae</i>	LIJ	RZ8	HQ006238	HQ006941	—	HQ006425	HQ006846	HQ006492	HQ006656	—	—	—	TG/TS	HUNGARY
Erebidae	Aectinae	<i>Dysnaxos fumida</i>	LIJ	MM00154	GIJ28619	GIJ28417	GIJ28954	GIJ29244	GIJ29514	—	—	GIJ30328	GIJ28120	GIJ30068	—	GREECE
Erebidae	Aectinae	<i>Anichloris viridis</i>	LIJ	MM05380	HQ006151	HQ006858	HQ006249	HQ006344	HQ006740	HQ006433	HQ006668	HQ006579	HQ006951	HQ006501	—	EQUADOR
Erebidae	Aectinae	<i>Ctenocha virgatica</i>	LIJ	AM-94-0396	GIJ28235	GIJ28337	GIJ28381	GIJ29181	GIJ29442	GIJ29722	GIJ30570	—	—	—	TG	USA
Erebidae	Aectinae	<i>Coscinea eribarria</i>	LIJ	MM05671	HQ006149	HQ006856	HQ006247	HQ006342	HQ006758	—	HQ006666	—	HQ006949	HQ006499	—	FINLAND
Erebidae	Aectinae	<i>Pseudophaloe troescchi</i>	LIJ	06-SRNP-35191	GIJ28234	GIJ28336	GIJ28380	GIJ29180	GIJ29441	—	GIJ30569	GIJ30258	GIJ28046	GIJ29925	—	COSTA RICA
Erebidae	Aectinae	<i>Dysychemia leucophaea</i>	LIJ	RZ88	HQ006240	—	HQ006334	HQ006427	HQ006848	HQ006493	HQ006751	HQ006658	—	HQ006571	—	COSTA RICA
Erebidae	Aectinae	<i>Nyctemera banalis</i>	II	RZ387	JN401287	JN401169	JN401402	JN401513	JN400969	JN401611	JN401909	JN401818	—	JN401714	—	MALAYSIA
Erebidae	Aectinae	<i>Callimorpha dominula</i>	LIJ	MM06169	HQ006169	HQ006873	HQ006266	HQ006360	HQ006778	HQ006444	HQ006685	HQ006594	HQ006965	HQ006514	TG/TS	RUSSIA
Erebidae	Aectinae	<i>Creatonotos transiens</i>	LIJ	RZ30	HQ006198	HQ006902	HQ006294	HQ006387	HQ006806	—	HQ006711	HQ006619	HQ006991	HQ006537	—	HONG KONG
Erebidae	Aectinae	<i>Arctia caja</i>	LIJ,IV,V	MM03713	GIJ28609	GIJ28489	—	GIJ29305	GIJ29573	GIJ29813	—	GIJ30398	GIJ28185	GIJ30080	TG/TS	FINLAND
Erebidae	Aectinae	<i>Amerita astraea</i>	II	RZ404	JN401288	JN401170	JN401403	JN401514	—	JN401612	JN401910	—	—	JN401715	TS	MALAYSIA
Erebidae	Unassigned	<i>Epitarsia dilina</i>	II	RZ93	JN401289	JN401171	JN401404	JN401515	JN400970	JN401613	JN401911	JN401819	—	JN401716	—	COSTA RICA
Erebidae	Calpinae	<i>Phyllodes eynahovii</i>	LIJ,III	RZ56	HQ006228	HQ006931	HQ006323	HQ006415	HQ006836	—	HQ006740	HQ006648	—	HQ006561	TG	TAIWAN
Erebidae	Calpinae	<i>Phyllodes imperialis</i>	LIJ,III	RZ546	JN674869	JN674851	JN674886	JN674902	JN674968	JN674919	JN674950	JN674934	—	JN674991	TG	AUSTRALIA
Erebidae	Calpinae	<i>Minodes pharosoma</i>	LIJ,III	RZ153	HQ006173	HQ006877	HQ006270	HQ006364	HQ006762	HQ006446	HQ006689	HQ006597	HQ006969	HQ006517	—	GHANA
Erebidae	Calpinae	<i>Hemicserotoides sitacea</i>	LIJ,II	RZ155	JN401290	JN401172	JN401405	JN401516	JN400971	JN401614	JN401912	JN401820	—	JN401717	—	GHANA
Erebidae	Calpinae	<i>Eudocima salamina</i>	LIJ,II	RZ338	JN401291	JN401173	JN401406	JN401517	JN400990	JN401615	JN401913	JN401821	—	JN401740	TG/TS	HONG KONG
Erebidae	Calpinae	<i>Eudocima fallonia</i>	LIJ,III	RZ16	HQ006174	HQ006878	HQ006271	HQ006365	HQ006783	HQ006447	HQ006690	HQ006598	HQ006970	HQ006519	TG	MALAYSIA
Erebidae	Calpinae	<i>Eudocima divitiosa</i>	III	RZ210	JN674870	JN674852	JN674887	JN674903	JN674969	JN674920	JN674951	—	—	JN674992	TG	GHANA
Erebidae	Calpinae	<i>Eudocima tyrannus</i>	III	RZ430	JN674871	JN674853	JN674888	JN674904	JN674970	JN674921	JN674952	JN674935	—	JN674993	TG	RUSSIA
Erebidae	Calpinae	<i>Gonodonta azor</i>	LIJ,III	RZ335	HQ006208	HQ006912	HQ006304	—	—	HQ006816	HQ006720	HQ006629	—	HQ006545	—	COSTA RICA
Erebidae	Calpinae	<i>Gonodonta lineus</i>	III	RZ417	JN674872	JN674854	JN674889	JN674905	JN674971	JN674922	JN674953	JN674936	—	JN674994	—	BRAZIL
Erebidae	Calpinae	<i>Gonodonta milia</i>	III	RZ421	JN674873	JN674855	JN674890	JN674906	JN674972	JN674923	JN674954	JN674937	—	JN674995	—	BRAZIL
Erebidae	Calpinae	<i>Gonodonta styra</i>	III	RZ420	JN674874	JN674856	JN674891	JN674907	JN674973	JN674924	JN674955	JN674938	—	JN674996	—	BRAZIL

Erebidae	Calpineae	<i>Gomodontia fulvanguis</i>	III	RZ423	JN674875	JN674882	JN674908	JN674974	—	JN674957	JN674940	—	JN674997	BRAZIL	
Erebidae	Calpineae	<i>Gomodontia natrix</i>	III	RZ432	JN674876	JN674893	JN674909	JN674975	—	JN674956	JN674939	—	JN674998	USA	
Erebidae	Calpineae	<i>Gomodontia sitchensis</i>	III	RZ419	JN674877	JN674894	JN674910	JN674976	JN674925	JN674959	JN674941	—	JN674999	Ecuador	
Erebidae	Calpineae	<i>Calyptra thalictri</i>	I,II,III,IV,V	MM400963	HQ006156	HQ006252	HQ006348	HQ006673	HQ006435	HQ006671	HQ006532	HQ006955	HQ006504	TG TS FINLAND	
Erebidae	Calpineae	<i>Calyptra hobkaidi</i>	II,III	RZ336	JN401292	JN401174	JN401407	JN401518	JN400972	JN401616	JN401823	JN401075	JN401718	TG JAPAN	
Erebidae	Calpineae	<i>Calyptra lata</i>	III	RZ431	JN674884	JN674900	JN674917	JN674982	JN674931	JN674965	JN674947	JN674988	—	TG RUSSIA	
Erebidae	Calpineae	<i>Calyptra comadenis</i>	III	CTW2	—	JN674887	—	JN674983	JN674933	JN674967	JN674989	JN674989	JN674906	TG USA	
Erebidae	Calpineae	<i>Calyptra minuticornis</i>	III	RZ314	JN674885	JN674901	JN674918	JN674984	JN674932	JN674966	JN674948	JN674990	JN674906	TG MALAYSIA	
Erebidae	Calpineae	<i>Platodonta nitissima</i>	I,II,III	RZ333	HQ006307	HQ006911	HQ006303	—	HQ006815	HQ006470	HQ006719	HQ006628	—	COSTA RICA	
Erebidae	Calpineae	<i>Platodonta coriolota</i>	III	RZ106	JN674878	JN674895	JN674911	JN674977	JN674926	JN674960	JN674942	—	JN674900	HONG KONG	
Erebidae	Calpineae	<i>Platodonta casta</i>	III	RZ429	JN674879	JN674861	JN674912	JN674978	JN674927	JN674961	JN674943	—	JN674901	RUSSIA	
Erebidae	Calpineae	<i>Oreastia emarginata</i>	I,II,III	RZ102	HQ006159	HQ006864	HQ006256	HQ006351	HQ006768	HQ006439	HQ006675	HQ006586	HQ006958	TS HONG KONG	
Erebidae	Calpineae	<i>Oreastia excavata</i>	II,III	RZ337	JN401293	JN401175	JN401408	JN401519	JN400987	JN401617	JN401915	JN401824	JN401076	JN401719	HONG KONG
Erebidae	Calpineae	<i>Oreastia excavata</i>	III	RZ434	JN674880	JN674862	—	JN674913	—	JN674958	—	JN674986	—	USA	
Erebidae	Calpineae	<i>Oreastia nobilis</i>	III	RZ422	JN674881	JN674897	JN674914	JN674979	JN674928	JN674962	JN674944	—	JN674902	BRAZIL	
Erebidae	Calpineae	<i>Oreastia nobilis</i>	III	RZ418	JN674882	JN674864	JN674898	JN674915	JN674980	JN674929	JN674963	JN674945	JN674987	JN674903	BRAZIL
Erebidae	Calpineae	<i>Oreastia recetraria</i>	III	RZ433	JN674883	JN674865	JN674899	JN674916	JN674981	JN674930	JN674964	JN674946	—	JN674904	NEPAL
Erebidae	Hypocalinae	<i>Hypocrita hormos</i>	I,II,III	RZ17	HQ006176	HQ006880	HQ006273	HQ006367	HQ006784	HQ006449	HQ006692	HQ006600	HQ006972	HQ006521	USA
Erebidae	Hypocalinae	<i>Hypocrita deflorata</i>	II	RZ105	JN401294	JN401176	JN401409	JN401520	JN400985	JN401618	JN401916	JN401825	JN401077	JN401720	TG TS HONG KONG
Erebidae	Hypocalinae	<i>Hypocrita andromena</i>	II,III	RZ40	JN401295	JN401177	JN401410	JN401521	JN400980	JN401619	JN401917	JN401826	JN401078	JN401721	TG COSTA RICA
Erebidae	Eulepidoinae	<i>Tanopoda glaucopsis</i>	II	RZ354	JN401296	JN401178	—	JN400977	—	JN401827	—	JN401827	—	COSTA RICA	
Erebidae	Eulepidoinae	<i>Tanopoda rufinargo</i>	I,II,III	RZ359	HQ006231	HQ006934	HQ006326	HQ006418	HQ006839	HQ006488	HQ006743	HQ006651	HQ007018	HQ006564	TG USA
Erebidae	Eulepidoinae	<i>Aniblemma fasciata</i>	I,II,III	RZ334	JN401297	JN401179	JN401411	—	JN400975	JN401620	JN401918	JN401828	—	COSTA RICA	
Erebidae	Eulepidoinae	<i>Sanyx irroxa</i>	II	RZ443	JN401298	JN401180	JN401412	—	JN400973	JN401621	JN401919	JN401829	JN401079	JN401722	COSTA RICA
Erebidae	Eulepidoinae	<i>Eulepidotis recinargo</i>	I,II,III	RZ12	HQ006162	HQ006960	HQ006259	HQ006354	HQ006771	—	HQ006678	HQ006588	HQ006960	HQ006511	TG COSTA RICA
Erebidae	Eulepidoinae	<i>Anticarsia gemmadis</i>	II	RZ467	JN401299	JN401181	JN401413	JN401522	JN400974	JN401622	JN401920	JN401830	—	JN401723	TS USA
Erebidae	Eulepidoinae	<i>Anticarsia irroata</i>	II	RZ370	JN401300	JN401182	JN401414	JN401523	JN400995	JN401623	JN401921	JN401831	JN401080	JN401724	HONG KONG
Erebidae	Eulepidoinae	<i>Hemeroplanis finitima</i>	II	RZ298	JN401301	JN401183	JN401415	JN401524	JN401004	JN401624	JN401922	JN401832	—	JN401725	USA
Erebidae	Eulepidoinae	<i>Oxidercia toxea</i>	I,II	RZ295	HQ006196	HQ006900	HQ006292	—	HQ006604	—	HQ006709	HQ006617	HQ006989	—	TS COSTA RICA
Erebidae	Eulepidoinae	<i>Azeta ceramina</i>	I,II,III	RZ22	HQ006182	HQ006886	HQ006278	HQ006373	HQ006790	—	HQ006697	HQ006605	HQ006978	HQ006527	COSTA RICA
Erebidae	Toxocampinae	<i>Autophila chamaeplanax</i>	II	RZ276	JN401302	JN401184	JN401416	JN401525	JN401006	JN401625	JN401923	JN401833	JN401081	JN401726	COSTA RICA
Erebidae	Toxocampinae	<i>Lysiphila pastinum</i>	I,II	MM405092	—	—	—	—	—	—	—	—	—	—	FINLAND
Erebidae	Toxocampinae	<i>Lysiphila maxima</i>	I,II	RZ57	HQ006229	HQ006932	HQ006324	HQ006416	HQ006837	HQ006487	HQ006649	—	HQ006562	TG JAPAN	
Erebidae	Tinodinae	<i>Tinodis eburnigata</i>	II	RZ331	JN401303	JN401185	JN401417	—	—	—	JN401924	JN401834	JN401082	—	TG TS THAILAND
Erebidae	Tinodinae	<i>Poeta denotata</i>	II	RZ445	JN401304	JN401186	JN401418	JN401526	JN401006	JN401626	JN401925	—	JN401727	TS MALAYSIA	
Erebidae	Tinodinae	<i>Tamsia hieroglyphica</i>	II	RZ389	JN401305	JN401187	JN401419	JN401527	JN401007	JN401627	JN401926	JN401835	JN401083	JN401728	TS MALAYSIA
Erebidae	Unassigned	<i>Ptilyntonia maltonifa</i>	II	RZ111	JN401306	JN401188	JN401420	JN401528	JN400991	JN401628	JN401926	—	JN401084	JN401729	HONG KONG
Erebidae	Scoteceampinae	<i>Scoteceampa liburna</i>	I,II	RZ9	HQ006242	HQ006944	HQ006336	HQ006429	HQ006850	HQ006495	HQ006753	HQ006660	HQ007025	HQ006573	TG USA

Erebidae	Scotobocampinae		RZ297	JN401307	JN401189	JN401421	JN401529	-	JN401629	JN401927	JN401836	JN401085	JN401730	USA
Erebidae	Hypenodinae	<i>Hypenodes humidalis</i>	MM101780	GU828671	GU828469	-	GU829285	GU829556	-	GU830666	-	GU828168	GU830058	TG TS FINLAND
Erebidae	Hypenodinae	<i>Schrankia costaevirgatis</i>	RZ27	HQ006192	HQ006896	HQ006288	HQ006382	HQ006800	HQ006461	HQ006705	HQ006613	HQ006987	-	HONG KONG
Erebidae	Hypenodinae	<i>Luceria striata</i>	RZ42	JN401308	JN401190	JN401422	JN401530	JN401008	-	JN401928	-	-	-	HONG KONG
Erebidae	Hypenodinae	<i>Luceria oculalis</i>	RZ369	JN401309	JN401191	JN401423	JN401531	JN401009	-	JN401929	-	JN401086	JN401731	HONG KONG
Erebidae	Hypenodinae	<i>Anachroasis</i> sp.	RZ288	JN401310	JN401192	JN401424	-	-	-	JN401930	JN401837	JN401087	-	INDONESIA
Erebidae	Hypenodinae	<i>Micronoctua</i> sp.	RZ138	HQ006671	HQ006875	HQ006268	HQ006362	HQ006780	HQ006445	HQ006687	HQ006595	HQ006947	HQ006516	TG INDONESIA
Erebidae	Hypenodinae	<i>Biancus</i> sp. 1	RZ475	-	JN401193	JN401425	JN401532	JN400992	JN401630	JN401931	JN401838	JN401088	JN401732	GHANA
Erebidae	Hypenodinae	<i>Biancus</i> sp. 2	RZ476	JN401311	JN401194	JN401426	-	JN400994	JN401631	JN401930	JN401839	JN401089	JN401733	GHANA
Erebidae	Bolotobiinae	<i>Saroba pusillifera</i>	RZ104	HQ006160	HQ006865	HQ006257	HQ006352	HQ006769	-	HQ006676	-	-	HQ006509	TS HONG KONG
Erebidae	Bolotobiinae	<i>Comdote</i> sp.	RZ393	JN401312	JN401195	JN401427	JN401533	JN401010	JN401632	JN401932	JN401840	JN401090	JN401734	MALAYSIA
Erebidae	Bolotobiinae	<i>Corgatha nitens</i>	RZ36	HQ006211	HQ006915	HQ006307	HQ006398	HQ006819	HQ006474	HQ006723	HQ006632	HQ007001	HQ006547	HONG KONG
Erebidae	Bolotobiinae	<i>Phytometra viridaria</i>	RZ129	HQ006165	HQ006962	HQ006262	HQ006356	HQ006774	HQ006442	HQ006681	HQ006591	HQ006962	HQ006512	TG FINLAND
Erebidae	Bolotobiinae	<i>Laspeyria flexula</i>	RZ3	HQ006197	HQ006991	HQ006293	HQ006386	HQ006805	HQ006463	HQ006710	HQ006618	HQ006990	HQ006536	TG TS HUNGARY
Erebidae	Bolotobiinae	<i>Zurobata rostrata</i>	RZ385	JN401313	JN401196	JN401428	JN401534	JN400996	-	JN401933	JN401841	JN401091	JN401735	TS MALAYSIA
Erebidae	Bolotobiinae	<i>Homodes crocea</i>	RZ412	JN401314	JN401197	JN401429	JN401535	JN401011	-	JN401934	JN401842	JN401092	JN401736	TS MALAYSIA
Erebidae	Bolotobiinae	<i>Enispedes purpurea</i>	RZ390	JN401315	JN401198	JN401430	-	JN401012	JN401633	JN401935	JN401843	JN401093	JN401737	TS MALAYSIA
Erebidae	Bolotobiinae	<i>Tamba misonomera</i>	RZ415	JN401316	JN401199	JN401431	JN401536	-	JN401634	JN401936	JN401844	-	JN401738	MALAYSIA
Erebidae	Bolotobiinae	<i>Paradals abstimilis</i>	RZ392	JN401317	JN401200	JN401432	JN401537	-	JN401635	JN401937	JN401845	-	JN401739	MALAYSIA
Erebidae	Bolotobiinae	<i>Araopipteron</i> sp.	RZ137	HQ006170	HQ006874	HQ006267	HQ006361	HQ006779	-	HQ006686	-	HQ006966	HQ006515	TG INDONESIA
Erebidae	Bolotobiinae	<i>Araopipteron</i> sp.	RZ410	JN401318	JN401201	JN401433	JN401538	JN401013	JN401636	JN401938	JN401846	JN401094	-	TG MALAYSIA
Erebidae	Bolotobiinae	<i>Eublemma purpurina</i>	RZ7	HQ006237	HQ006940	HQ006332	HQ006424	HQ006845	HQ006491	HQ006748	HQ006655	-	HQ006569	TG HUNGARY
Erebidae	Bolotobiinae	<i>Eublemma anachoreis</i>	RZ98	JN401319	JN401202	JN401434	JN401539	JN400989	JN401637	JN401939	JN401847	-	JN401741	TG HONG KONG
Erebidae	Bolotobiinae	<i>Eublemma albifascia</i>	RZ220	JN401320	JN401203	JN401435	JN401540	JN401014	JN401638	JN401940	-	-	JN401742	TG GHANA
Erebidae	Bolotobiinae	<i>Parascotia fuliginaria</i>	MM100340	HQ006154	HQ006862	HQ006253	HQ006347	HQ006764	HQ006436	HQ006672	HQ006583	HQ006954	HQ006505	TG TS FINLAND
Erebidae	Bolotobiinae	<i>Metaterra edilis</i>	RZ72	JN401321	JN401204	JN401436	JN401541	JN401015	JN401639	JN401941	JN401848	-	JN401744	FINLAND
Erebidae	Bolotobiinae	<i>Trisades emortialis</i>	MM04877	GU828707	GU828502	GU829030	GU829319	GU829583	GU829821	GU830695	GU830411	GU828195	GU830093	TG TS FINLAND
Erebidae	Bolotobiinae	<i>Protophota trigonifera</i>	RZ37	HQ006212	HQ006916	HQ006308	HQ006399	HQ006820	HQ006475	HQ006724	HQ006633	HQ007002	-	TS HONG KONG
Erebidae	Bolotobiinae	<i>Hypenogonia ?brachypalpia</i>	RZ409	JN401322	-	JN401437	JN401542	JN401016	JN401640	JN401942	JN401849	-	-	MALAYSIA
Erebidae	Bolotobiinae	<i>Metamele ariginta</i>	RZ41	HQ006218	HQ006922	HQ006314	HQ006405	HQ006826	HQ006481	HQ006730	HQ006629	HQ007007	HQ006552	HONG KONG
Erebidae	Bolotobiinae	<i>Atacamera semiloba</i>	RZ107	JN401323	JN401205	JN401438	-	-	JN401641	-	JN401850	JN401095	JN401746	HONG KONG
Erebidae	Erebinae	<i>Evaonia semirufa</i>	RZ385	JN401324	JN401206	JN401439	JN401543	JN401017	JN401642	JN401943	-	JN401096	JN401746	TS USA
Erebidae	Erebinae	<i>Acantholipes circumdata</i>	RZ248	HQ006189	HQ006893	HQ006285	HQ006379	HQ006797	-	HQ006702	-	HQ006984	HQ006531	TG UAE
Erebidae	Erebinae	<i>Acantholipes regularis</i>	RZ135	HQ006168	HQ006872	HQ006265	HQ006359	HQ006777	-	HQ006684	-	-	-	TG TS RUSSIA
Erebidae	Erebinae	<i>Hypopygia balmodes</i>	RZ116	JN401325	JN401207	JN401440	JN401544	JN400997	JN401643	JN401944	JN401851	-	JN401748	TS HONG KONG
Erebidae	Erebinae	<i>Ugia insuspecta</i>	RZ45	HQ006221	HQ006925	-	HQ006408	HQ006829	HQ006484	HQ006733	HQ006642	HQ007010	HQ006555	HONG KONG
Erebidae	Erebinae	<i>Ugodes cinerea</i>	RZ226	JN401326	JN401208	-	-	-	JN401644	JN401945	-	JN401097	-	TS GHANA

Erebidae	Erebinae		RZ113	HQ006201	HQ006905	HQ006297	HQ006300	HQ006809	HQ006466	HQ006714	HQ006622	HQ006894	HQ006539	JAPAN
Erebidae	Erebinae	<i>Symoides fumosa</i>	RZ120	JN401327	JN401209	JN401441	JN401545	JN400998	JN401645	JN401946	JN401852	JN401098	JN401747	JAPAN
Erebidae	Erebinae	<i>Daidala lucilla</i>	RZ127	HQ006164	HQ006961	HQ006261	HQ006355	HQ006773	HQ006441	HQ006680	HQ006590	HQ006961	—	TG TS GERMANY
Erebidae	Erebinae	<i>Caeptia alchymista</i>	RZ350	JN401328	JN401210	JN401442	JN401546	JN401002	JN401646	JN401947	JN401860	—	JN401748	USA
Erebidae	Erebinae	<i>Heteranassa</i> sp.	RZ270	JN401329	JN401211	JN401443	JN401547	JN401018	JN401647	JN401948	JN401853	—	JN401749	USA
Erebidae	Erebinae	<i>Thysanota zenobia</i>	RZ53	HQ006225	HQ006928	HQ006320	HQ006412	HQ006833	HQ006486	HQ006737	HQ006645	HQ007014	HQ006558	TG COSTA RICA
Erebidae	Erebinae	<i>Toconoprucha</i> sp.	RZ307	JN401330	JN401212	JN401444	JN401548	—	JN401648	JN401949	JN401854	—	JN401750	USA
Erebidae	Erebinae	<i>Pseudobarydia cressida</i>	RZ91	JN401331	JN401213	JN401445	JN401549	JN401019	JN401649	JN401950	JN401855	JN401099	JN401751	COSTA RICA
Erebidae	Erebinae	<i>Pandema robusta</i>	RZ321	HQ006204	HQ006908	HQ006300	HQ006393	HQ006812	—	HQ006717	HQ006625	HQ006997	HQ006542	TG TS SPAIN
Erebidae	Erebinae	<i>Heteropalpa acrosticta</i>	RZ243	HQ006186	HQ006890	HQ006282	HQ006376	HQ006794	—	HQ006700	—	HQ006981	—	UAE
Erebidae	Erebinae	<i>Springemorphia chlorata</i>	RZ291	HQ006195	HQ006899	HQ006291	HQ006385	HQ006803	—	HQ006708	HQ006616	—	—	TS TANZANIA
Erebidae	Erebinae	<i>Percyma cruegeri</i>	RZ99	HQ006244	HQ006946	HQ006338	HQ006431	HQ006852	HQ006497	HQ006755	HQ006662	HQ007027	HQ006575	TG HONG KONG
Erebidae	Erebinae	<i>Sympis rifibasis</i>	RZ48	HQ006223	—	HQ006318	HQ006410	HQ006831	HQ006485	HQ006735	HQ006644	HQ007012	HQ006557	TS HONG KONG
Erebidae	Erebinae	<i>Erebna ephesperis</i>	RZ11	HQ006161	HQ006886	HQ006258	HQ006353	HQ006770	HQ006440	HQ006677	HQ006687	HQ006959	HQ006510	TG TAIWAN
Erebidae	Erebinae	<i>Erycia apicalis</i>	RZ29	HQ006194	HQ006898	HQ006290	HQ006384	HQ006802	—	HQ006707	HQ006615	HQ006988	HQ006535	TS HONG KONG
Erebidae	Erebinae	<i>Bulia dedicata</i>	RZ314	JN401332	JN401214	JN401446	JN401550	JN401020	JN401650	JN401951	JN401856	JN401100	JN401752	USA
Erebidae	Erebinae	<i>Forschia perlacta</i>	RZ284	JN401333	JN401215	JN401447	JN401551	JN401021	JN401651	JN401952	JN401857	JN401101	JN401753	TS USA
Erebidae	Erebinae	<i>Melipotis punctiflavis</i>	RZ242	JN401334	JN401216	JN401448	JN401552	JN401022	JN401652	JN401953	JN401858	JN401102	JN401754	TG COSTA RICA
Erebidae	Erebinae	<i>Melipotis jucunda</i>	RZ58	HQ006230	HQ006933	HQ006325	HQ006417	HQ006838	—	HQ006742	HQ006650	HQ007017	HQ006563	TG TS USA
Erebidae	Erebinae	<i>Phoberia atomaris</i>	RZ286	JN401335	JN401217	JN401449	—	JN401023	—	JN401954	JN401859	JN401103	JN401755	TS USA
Erebidae	Erebinae	<i>Audea bipunctata</i>	RZ60	HQ006233	HQ006936	HQ006328	HQ006420	HQ006841	—	HQ006744	HQ006652	HQ007019	HQ006566	TG TS CONGO
Erebidae	Erebinae	<i>Audea humeralis</i>	RZ90	JN401336	JN401218	JN401450	JN401553	JN401024	JN401653	JN401955	—	JN401104	JN401756	TG TANZANIA
Erebidae	Erebinae	<i>Hypoacha braundbergensis</i>	RZ75	JN401337	JN401219	JN401451	JN401554	JN400999	JN401654	JN401956	—	JN401105	JN401757	NAMIBIA
Erebidae	Erebinae	<i>Cancelata sponsa</i>	LI,LI,IV,V	MM04358	GU828700	GU828495	GU829023	GU829576	GU829816	GU830088	GU830404	GU828189	GU830086	TG FINLAND
Erebidae	Erebinae	<i>Ularichopus macida</i>	RZ241	HQ006185	HQ006889	HQ006281	—	HQ006793	HQ006457	HQ006699	HQ006608	—	HQ006530	TAIWAN
Erebidae	Erebinae	<i>Hypopyra capensis</i>	RZ149	HQ006172	HQ006876	HQ006269	HQ006363	HQ006781	—	HQ006688	HQ006596	HQ006968	HQ006517	TG GHANA
Erebidae	Erebinae	<i>Syrama reorta</i>	RZ359	JN401338	JN401220	JN401452	—	JN401025	JN401655	JN401957	—	JN401106	JN401758	TAIWAN
Erebidae	Erebinae	<i>Calyptis idonea</i>	RZ473	JN401339	JN401221	JN401453	—	JN401000	JN401656	JN401958	JN401861	JN401107	JN401759	ECUADOR
Erebidae	Erebinae	<i>Ommatophora luminosa</i>	RZ407	JN401340	JN401222	JN401454	JN401555	JN401026	JN401657	JN401959	JN401862	JN401108	JN401760	TG TS MALAYSIA
Erebidae	Erebinae	<i>Pantylia diemeni</i>	RZ309	HQ006199	HQ006903	HQ006295	HQ006388	HQ006807	HQ006464	HQ006712	HQ006620	HQ006992	HQ006538	AUSTRALIA
Erebidae	Erebinae	<i>Mocis latipes</i>	RZ20	HQ006180	HQ006884	HQ006276	HQ006371	HQ006788	HQ006453	HQ006619	HQ006603	HQ006976	HQ006525	COSTA RICA
Erebidae	Erebinae	<i>Callisagea mi</i>	MM05469	HQ006150	HQ006857	HQ006248	HQ006343	HQ006759	—	HQ006667	HQ006578	HQ006950	HQ006500	TS FINLAND
Erebidae	Erebinae	<i>Eucledia glyptica</i>	RZ82	HQ006239	HQ006942	HQ006333	HQ006426	HQ006847	—	HQ006750	HQ006657	HQ007023	HQ006570	TG FINLAND
Erebidae	Erebinae	<i>Erecha cyllaria</i>	RZ33	HQ006205	HQ006909	HQ006301	HQ006394	HQ006813	—	HQ006718	HQ006626	HQ006998	HQ006543	TG HONG KONG
Erebidae	Erebinae	<i>Hilodes caransea</i>	RZ126	HQ006163	—	HQ006260	—	HQ006772	—	HQ006679	HQ006659	—	—	TG MALAYSIA
Erebidae	Erebinae	<i>Erieta subinerea</i>	RZ39	HQ006214	HQ006918	HQ006310	HQ006401	HQ006826	HQ006477	HQ006635	HQ007004	HQ006549	—	HONG KONG
Erebidae	Erebinae	<i>Platyga umminea</i>	RZ261	JN401341	JN401223	JN401455	JN401556	JN401027	JN401658	JN401960	JN401863	—	JN401761	TS HONG KONG
Erebidae	Erebinae	<i>Anisomeneta salebrosa</i>	RZ38	HQ006213	HQ006917	HQ006309	HQ006400	HQ006821	HQ006476	HQ006725	—	HQ007003	HQ006548	TS HONG KONG

Noctuidae	Dyopsinae	<i>Betisiana bifornis</i>	II,V	RZ384	JN401237	JN401121	JN401355	JN401467	JN400929	JN401569	JN400877	JN401775	JN401039	JN401671	TS	MALAYSIA
Noctuidae	Dyopsinae	<i>Cyclodes omnia</i>	V	RZ636	X	X	X	X	X	X	X	X	X	X	TS	THAILAND
Noctuidae	Dyopsinae	<i>Ceroena amynta</i>	V	RZ552	X	X	X	X	X	X	X	X	X	X	TS	ECUADOR
Noctuidae	Dyopsinae	<i>Sioxera grata</i>	II,V	RZ281	JN401236	JN401120	JN401354	JN401466	JN400988	JN401568	JN401875	JN401774	JN401038	JN401670	TS	COSTA RICA
Noctuidae	Plusinae	<i>Auargrapha gamma</i>	II,II,V,V	MM100328	GIJ828636	GIJ82844	GIJ82870	GIJ829256	GIJ829528	-	GIJ830640	GIJ830344	GIJ828135	GIJ830023	TG,TS	FINLAND
Noctuidae	Plusinae	<i>Abroxola tripartita</i>	I,V	MM05132	HQ006152	HQ006859	HQ006250	HQ006345	HQ006761	-	HQ006669	HQ006580	HQ006952	HQ006502	TG	FINLAND
Noctuidae	Eustroniinae	<i>Deiotle uncula</i>	I,V	MM04601	GIJ828705	GIJ828498	GIJ829026	GIJ829315	GIJ829579	GIJ829818	GIJ830691	GIJ830407	GIJ828192	GIJ830089	FINLAND	FINLAND
Noctuidae	Ceculiinae	<i>Creatilia umbratica</i>	II,V,V	MM04543	GIJ828701	GIJ828496	GIJ829024	GIJ829313	GIJ829577	GIJ829817	GIJ830689	GIJ830405	GIJ828190	GIJ830087	TG,TS	FINLAND
Noctuidae	Dilobinae	<i>Diloba caeruleocephala</i>	II,V	MM09267	JN401246	JN401128	JN401364	JN401475	JN400982	-	JN401887	JN401784	-	JN401678	TG,TS	FINLAND
Noctuidae	Raphinae	<i>Raphia abrupta</i>	II,I,V	CWM-94-0372	GIJ828348	GIJ828350	GIJ828893	GIJ829193	GIJ829455	GIJ829728	GIJ830579	GIJ830270	GIJ828059	GIJ829939	TG	USA
Noctuidae	Pantheinae	<i>Eteocystia meeki</i>	II,V	RZ87	JN401247	JN401129	-	-	-	-	JN401888	JN401785	JN401047	-	TG,TS	INDONESIA
Noctuidae	Pantheinae	<i>Thauides</i> sp.	II,V	RZ459	JN401249	JN401131	JN401366	JN401477	JN400937	JN401579	JN401888	JN401787	-	JN401680	TG	INDIA
Noctuidae	Pantheinae	<i>Anitrisuloides catocalina</i>	II,V	RZ388	JN401248	JN401130	JN401365	JN401476	JN400936	JN401578	JN401889	JN401786	JN401048	JN401679	TG	MALAYSIA
Noctuidae	Pantheinae	<i>Panthea coenobia</i>	II,I,V	MM04583	GIJ828702	GIJ828497	GIJ829025	GIJ829314	GIJ829578	-	GIJ830690	GIJ830406	GIJ828191	GIJ830088	TG,TS	FINLAND
Noctuidae	Acontinae	<i>Emmelia trabealis</i>	I,V	MM09893	HQ006147	HQ006854	HQ006245	HQ006340	HQ006756	-	HQ006664	HQ006576	HQ006947	-	SARDINIA	
Noctuidae	Acontinae	<i>Acontia lucida</i>	II,V,V	MM00152	GIJ828617	GIJ828415	GIJ828952	GIJ829243	GIJ829512	GIJ829763	GIJ830627	GIJ830327	GIJ828118	GIJ830086	TG	GREECE
Noctuidae	Bagisarinae	<i>Amynta octo</i>	II,V	RZ50	JN401242	JN401125	JN401360	JN401471	JN400984	JN401574	JN401883	JN401780	JN401043	JN401675	TS	MALAYSIA
Noctuidae	Bagisarinae	<i>Xanthodes alboago</i>	II,I,V	MM09894	GIJ828844	GIJ828808	GIJ829145	GIJ829412	GIJ829693	-	GIJ830792	GIJ830535	GIJ828308	GIJ830224	SARDINIA	
Noctuidae	Bagisarinae	<i>Ramadasa parvo</i>	II,V	RZ382	JN401241	JN401124	JN401359	JN401470	JN400978	JN401573	JN401882	JN401779	-	JN401674	TS	MALAYSIA
Noctuidae	Bagisarinae	<i>Dyzeta plagiata</i>	II,V	RZ395	JN401240	JN401123	JN401358	JN401469	JN400932	JN401572	JN401881	JN401778	JN401042	JN401673	TS	MALAYSIA
Noctuidae	Bagisarinae	<i>Eneriphon leena</i>	II,V	RZ351	JN401243	JN401126	JN401361	JN401472	JN400933	JN401575	JN401884	JN401781	JN401044	JN401676	COSTA RICA	
Noctuidae	Bagisarinae	<i>Vespolia caeruleifera</i>	V	RZ595	X	X	X	X	X	X	X	X	X	X	TS	COSTA RICA
Noctuidae	Bagisarinae	<i>Parangitia temperata</i>	II,I,V,V	RZ463	JN401244	JN401127	JN401362	JN401473	JN400934	JN401576	JN401885	JN401782	JN401045	-	COSTA RICA	
Noctuidae	Bagisarinae	<i>Parangitia mosaica</i>	II,I,V,V	RZ464	JN401245	-	JN401363	JN401474	JN400935	JN401577	JN401886	JN401783	JN401046	JN401677	COSTA RICA	
Noctuidae	Bagisarinae	<i>Diapa corone</i>	II,I,V,V	RZ472	JN401239	JN401122	JN401357	-	JN400931	JN401571	JN401880	JN401777	JN401041	-	FRENCH GUIANA	
Noctuidae	Bagisarinae	<i>Concana mundissima</i>	IV,V	RZ621	X	X	X	X	X	X	X	X	X	X	TS	USA
Noctuidae	Bagisarinae	<i>Concana lecta</i>	IV,V	RZ474	X	-	-	X	X	-	X	X	-	-	COSTA RICA	
Noctuidae	Bagisarinae	<i>Concana permixta</i>	IV,V	RZ482	X	-	-	X	X	-	X	X	-	-	COSTA RICA	
Noctuidae	Amphipyriinae	<i>Amphipyra perflua</i>	II,II,I,V	MM01162	GIJ828660	GIJ828458	GIJ828991	GIJ829275	GIJ829546	GIJ829787	GIJ830657	GIJ830566	GIJ828157	GIJ830047	TG	GUATEMALA
Noctuidae	Amphipyriinae	<i>Brachionycha subcinctosa</i>	I,V	MM01542	GIJ828667	GIJ828465	GIJ828998	GIJ829281	GIJ829552	GIJ829793	GIJ830663	GIJ830573	GIJ828164	GIJ830054	TS	FINLAND
Noctuidae	Melipotiniinae	<i>Flammonea quadrifasciata</i>	V	RZ596	X	X	X	X	X	X	X	X	X	X	TS	MALAYSIA
Noctuidae	Melipotiniinae	<i>Panemeria tenebrosa</i>	I,V	MM00005	HQ006157	HQ006863	HQ006254	HQ006349	HQ006766	HQ006437	HQ006673	HQ006584	HQ006956	HQ006506	FINLAND	
Noctuidae	Acronictinae	<i>Cranophora ligustri</i>	I,V	MM06745	HQ006148	HQ006855	HQ006246	HQ006341	HQ006757	HQ006432	HQ006665	HQ006577	HQ006948	HQ006498	TS	FINLAND
Noctuidae	Acronictinae	<i>Acronicta americana</i>	V	RZ597	X	X	X	X	X	X	X	X	X	X	TG	USA
Noctuidae	Acronictinae	<i>Acronicta ramicis</i>	I,V	MM01529	GIJ828666	GIJ828464	GIJ828997	GIJ829280	GIJ829551	GIJ829792	GIJ830662	GIJ830572	GIJ828163	GIJ830053	TG	FINLAND
Noctuidae	Acronictinae	<i>Cerna ceratula</i>	V	RZ617	X	X	X	X	X	X	X	X	-	-	X	USA
Noctuidae	Acronictinae	<i>Comachara cadburyi</i>	V	RZ618	X	X	X	X	X	X	X	X	X	X	TS	USA

Noctuidae	Acronictinae	<i>Harrisianema frisingata</i>	V	RZ619	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	USA
Noctuidae	Acronictinae	<i>Polygrammate hebraeicum</i>	V	RZ620	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	USA
Noctuidae	Acronictinae	<i>Agriopodes fallax</i>	V	RZ616	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	USA
Noctuidae	Agrotinae	<i>Periscepta polysciata</i>	LI,IV	MM07669	GIJ28820	GIJ29788	GIJ29125	GIJ29400	GIJ29674	GIJ29892	GIJ30773	GIJ30619	GIJ28289	GIJ30201	GIJ30201	GIJ30201	GIJ30201	GIJ30201	GIJ30201	AUSTRALIA
Noctuidae	Aedinae	<i>Aedia leucomedas</i>	II,V	RZ277	JN401250	JN401132	JN401367	JN401478	JN400976	JN401580	JN401891	JN401788	-	JN401681	TIJ	JAPAN				
Noctuidae	Condinae	<i>Condica illaeta</i>	V	RZ511	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	MALAYSIA
Noctuidae	Condinae	<i>Condica vectors</i>	LIJ	CWM-95-0471	GIJ28530	GIJ28352	GIJ28895	GIJ29194	GIJ29457	-	GIJ30581	-	GIJ28061	GIJ29941	TIJ	USA				
Noctuidae	Condinae	<i>Hemicaphalis alesia</i>	II,V	RZ341	JN401251	JN401133	JN401368	JN401479	JN400938	JN401381	JN401892	JN401789	JN401049	JN401682	TIJ	COSTA RICA				
Noctuidae	Heliothinae	<i>Pyrrhia umbra</i>	I,V	MM05114	GIJ28712	GIJ28507	GIJ29034	GIJ29324	GIJ29588	GIJ29825	GIJ30700	GIJ30416	GIJ28200	GIJ30098	FINLAND					
Noctuidae	unassigned	<i>Chytonix diehli</i>	V	RZ517	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	MALAYSIA
Noctuidae	Bryophilinae	<i>Cryphia raptricula</i>	I,V	MM04919	GIJ28708	GIJ28503	GIJ29031	GIJ29320	GIJ29584	GIJ29822	GIJ30696	GIJ30412	GIJ28196	GIJ30094	FINLAND					
Noctuidae	Bryophilinae	<i>Stenoloba fitti</i>	V	RZ523	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	MALAYSIA
Noctuidae	unassigned	<i>Ecpatia</i> sp.	V	RZ545	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	MALAYSIA
Noctuidae	unassigned	<i>Ecpatia longiqua</i>	LI,IV	RZ25	HQ006190	HQ006894	HQ006286	HQ006380	HQ006798	-	HQ006703	HQ006611	HQ006985	HQ006532	HONG KONG					
Noctuidae	Noctuidae	<i>Tracota aureata</i>	V	RZ14	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	INDONESIA
Noctuidae	Noctuidae	<i>Actinotia polyodon</i>	I,V	MM05153	GIJ28714	GIJ28509	-	GIJ29326	GIJ29590	GIJ29827	GIJ30702	GIJ30418	GIJ28202	GIJ30100	TIJ	FINLAND				
Noctuidae	Noctuidae	<i>Hoplodrina octogenaria</i>	I,V	MM01651	HQ006153	HQ006860	HQ006251	HQ006346	HQ006762	HQ006434	HQ006670	HQ006581	HQ006953	HQ006503	FINLAND					
Noctuidae	Noctuidae	<i>Diaphone</i> sp.	LI,IV	MF-05-0053	GIJ28571	GIJ28372	GIJ28913	GIJ29206	GIJ29475	GIJ29738	GIJ30591	GIJ30285	GIJ28076	GIJ29960	TANZANIA					
Noctuidae	Noctuidae	<i>Apania areolata</i>	LI,IV,V	MM01170	GIJ28661	GIJ28459	GIJ28992	GIJ29276	GIJ29547	GIJ29788	GIJ30658	GIJ30567	GIJ28158	GIJ30048	TIJ	FINLAND				
Noctuidae	Noctuidae	<i>Ufens faunus</i>	I,V	RR-98-0914	GIJ28860	GIJ29822	GIJ29163	GIJ29425	GIJ29709	GIJ29911	GIJ30807	GIJ30552	GIJ28320	GIJ30238	TIJ	USA				
Noctuidae	Noctuidae	<i>Noctua fimbriata</i>	LI,IV,V	MM04752	GIJ28705	GIJ28500	GIJ29028	GIJ29317	GIJ29581	GIJ29820	GIJ30693	GIJ30409	GIJ28194	GIJ30091	TIJ	FINLAND				