<u>**Eyespots originated multiple times independently across the Lepidoptera**</u>

Brian Hanotte[1],*, Beatriz Willink[1,2], and Antónia Monteiro[1],*

1) Department of Biological Sciences, National University of Singapore, Singapore

2) Department of Zoology, Stockholm University, Sweden

*Corresponding authors

Abstract

Eyespot color patterns often function as a defense against predators and in mate choice. In

Nymphalid butterflies, eyespots have a single evolutionary origin close to the base of this clade, but

eyespots are also present in many other lepidopteran lineages and may have multiple independent

origins. Here we use phylogenetic comparative methods to investigate the evolution of eyespots

across a multi-superfamily phylogeny of Lepidoptera, and to pinpoint lineages in which eyespots

likely originated independently. We find a total of 28 separate origins of *Discal* eyespots (in the discal

wing region) and 19 separate origins of *Marginal* eyespots (in the marginal wing region), including

four separate instances where eyespots were preserved in most extant representatives of a species

radiation. The first two eyespot radiations we observed are in the Nymphalidae, with a *Marginal*

eyespot radiation occurring before a *Discal* one. While the remaining two eyespot radiations were

observed in the Saturniidae, occurring in a reverse fashion, where a *Discal* eyespot radiation

preceded a *Marginal* eyespot radiation. Even though eyespots do not appear to be homologous

across Lepidoptera they may share a homologous gene-regulatory network. Our phylogenetic

inference provides a roadmap for future developmental and functional studies addressing this

hypothesis. This study therefore has implications for our understanding of the evolution of serial

homologues and of convergent evolution of visual signals in insects.

Introduction

Lepidopteran wing color patterns have been a source of fascination and human inspiration for

centuries (Hogue, 1987). While some of the classic early research focused on the adaptive role of

general wing coloration, such as "industrial melanism" in moths (Kettlewell, 1973), other research

focused on the role of localized color patterns, such as eyespots (Blest, 1957). Eyespots consist of

more than one concentric ring of contrasting colored scales, often mimicking a vertebrate eye (Oliver

et al., 2014; Labanderia et al., 2016). These visually striking color patterns play roles in predator

deterrence, predator deflection, and mate selection (Breuker & Brakefield 2002; Stevens, 2005;

Robertson and Monteiro 2005; Vallin et al. 2007; Kodandaramaiah, 2011; Merilaita et al., 2011;

Prudic et al. 2012; Kodandaramaiah et al., 2013; Prudic et al., 2015; Mukherjee & Kodandaramaiah,

2015; Huq et al., 2019; Halali et al., 2019). Eyespots are thus adaptive, having evolved in several

clades of Lepidoptera, but their evolutionary history remains poorly understood.

Research on eyespot evolution to date has focused on nymphalid butterflies. Here eyespots develop

in between veins at the wing margins (Fig. 1a-b). Such *Marginal* eyespots evolved once in

Nymphalidae, shortly after the origin of the clade (Oliver et al., 2012 & 2014), and are therefore

considered homologous. Several moth lineages (e.g., Semanturidae, Saturniidae, Cambridae) also

exhibit *Marginal* eyespots, but their evolutionary history has not been investigated. In contrast to

Marginal eyespots, *Discal* eyespots are centered on cross veins or placed within the discal cell region

(Otaki., 2020; Fig. 1c-d). Across Lepidoptera, species may have *Marginal* eyespots, *Discal* eyespots, or

eyespots located on both wing regions (Fig. 2). Because these distinct wing regions express different

genes during development (Banerjee et al., 2023), the evolution of *Marginal* and *Discal* eyespots

might have occurred independently in each region (Fig. 1E). Alternatively, eyespots might have first

evolved on one wing region, and later evolved on the other region, with the order of these regions

potentially varying if there are multiple independent eyespot origins (Fig. 1e-g). By investigating the

evolution of eyespots across the Lepidoptera we aim to discover whether *Marginal* and *Discal*

eyespots are homologous or convergently evolved across the Lepidoptera.

Here we used modern phylogenetic methods to investigate the evolutionary origins of *Discal* and

Marginal eyespot across Lepidoptera. We first inferred a species-level phylogeny for Lepidoptera,

sampling up to 27 (5-24 fragments per species) molecular sequences in over 715 species. Our

phylogeny covers 90% of Lepidoptera families, allowing comparative inferences of eyespot evolution

in moths and butterflies. We then modeled evolutionary origins and losses of eyespots and inferred

ancestral states across the phylogeny. For each possible subtree with an ancestral eyespot origin, we

implemented a model comparison approach, based on marginal likelihood estimation, to quantify

support for eyespot homology among extant taxa. These analyses suggested differently ordered

sequences of eyespot evolution in the two main eyes-spot bearing radiations, the silkmoths

(Saturniidae) and the brush-footed butterflies (Nymphalidae). Our results demonstrate that eyespots

in the Lepidoptera have evolved multiple times, and that *Discal* and *Marginal* eyespots have evolved

in different temporal sequences in the main clades where they radiated (Nymphalidae and

Saturniidae). We also find that eyespots have evolved in a further 10 superfamilies and numerous

families across the Lepidopteran family tree. Finally, we find that eyespots across the lepidoptera are

more commonly observed in the *Discal* region (28 occurrences) than the *Marginal* region (19

occurrences) which was unexpected as most eyespot research is focused on *Marginal* eyespots

found in the Nymphalidae.

Materials and methods

<u>Molecular data collection for phylogenetic tree construction</u>

DNA sequence data for 645 species of Lepidoptera (moths and butterflies) and seven species of

Trichoptera (caddisflies, outgroup) were kindly provided by Professor Emeritus Charles Mitter

(University of Maryland, Table S1 & S2). Additional sequences for 70 species of Saturniidae

(silkmoths) were downloaded from NCBI (GenBank). The full dataset was composed of 27 protein-

coding genes (Table S2), with 5-24 fragments available across all species. Our taxonomic sampling

includes ~68% (90/133, Van Nieukerken et al., 2011) of all families and ~65% (28/43, Van Nieukerken

et al., 2011) of all superfamilies in the order Lepidoptera. This study focuses on the suborder Ditrysia,

which comprises ~98% of currently described lepidopterans. Of these, ~90% of families (90/100,

Reiger et al., 2009) and ~93-96% (28/29-30) of superfamilies (Van Nieukerken et al., 2011; Heikkla et

al., 2015; Mitter et al., 2017) are represented. We chose the Trichoptera for our outgroup because

they are the closest extant relatives to the Lepidoptera (Mey et al., 2017), but distant enough to

provide ingroup monophyly.

<u>Sequence alignment and phylogenetic inference</u>

DNA sequences were aligned via MAFFT v 7.490 (Katoh & Standley, 2013). A global alignment

strategy with iterative refinement (G-INS-i) was employed to maximize alignment accuracy based on

weighted sum-of-pairs and a consistency scores. The length of the final alignment, consisting of all 27

concatenated gene fragments, was 22,643 bp.

IQ-TREE v 1.6.12 (Nguyen et al., 2015, Kalyaanamoorthy et al., 2017 & Hoang et al., 2018) was used

for phylogenetic inference under maximum likelihood. All genes were subject to a single substitution

process automatically set by IQ-TREE,using ModelFinder (Kalyaanamoorthy et al., 2017).

Substitutions followed a generalized time reversible (GTR) model, with estimated base frequencies.

Rate variation among sites followed a gamma distribution containing 10 categories. Node support

was estimated using ultra-fast bootstrap in UFBoot (Hoang et al., 2018) for 100,000 iterations.

UFBoot is an efficient approximation to the traditional bootstrap method that is particularly well-

suited for large datasets such as ours. After pruning the outgroup, our maximum likelihood tree was

transformed into an ultrametric tree, with branch lengths scaled to time, using the ape package v

5.7-1 (Paradis & Schliep, 2019) in R v 4.3.0 (R Core Team 2023). For branch scaling, we used an age of

~290 Ma for the most recent common ancestor of Ditrysia, following the most recent dated

phylogeny of Lepidoptera (Kawahara et al., 2019).

<u>Image data collection</u>

We scored images of each of the 715 species in our phylogeny for presence or absence of eyespot

patterns (in any wing surface or sex). An eyespot pattern was identified as present only if it met three

criteria: 1) it had at least two concentric rings of distinct colors, 2) the rings were circular or oblong in

shape, and 3) the color inside the internal ring differed from the color on the outside of both rings

(Fig. 3). To explore the sensitivity of our results to these conservative criteria, we repeated our main

comparative analyses under a more relaxed definition of eyespots, where criterion 2 was extended

to non-circular/oblong shapes (e.g., triangles, rectangles, teardrops, see Fig. S1 for examples).

Eyespots were further classified based on their locations on the wing surface. *Discal* eyespots

straddle the cross veins in the discal cell region or are found within and around the discal cell (Otaki

et al., 2020 & Figure 1), whereas *Marginal* eyespots are found in between longitudinal veins, at the

wing margins and within the discal cell of the wing (Fig. 1a-d).

We first queried a wide range of online databases for images of the type specimen of each of the

sampled species (Table S3, Supplementary data file 1). If not available, images of other (non-type)

specimens were collected from the same databases with a preference for museum specimens over

other specimens. In cases where sequence data was assigned to a particular subspecies, we

prioritized images of the same taxonomic rank when available. Ninety-six species included in our

data set lacked publicly available and reliably identified images. We photographed 81 of these

species at the Mcguire Center for Lepidoptera (MGCL, Florida Museum of Natural History, 3215 Hull

Rd, Gainesville, Fl 32611), using a Cannon D50 DSLR camera. We were unable to obtain images for 15

species (2%), which are treated as missing data in all comparative analyses.

<u>Modelling the origin and loss of eyespots in Lepidoptera</u>

RevBayes v 1.2.1 (Höhna et al., 2016) was used in this and subsequent analyses to model eyespot

evolution across Lepidoptera. RevBayes is an open-source software package designed for Bayesian

phylogenetic inference. It allows users to build probabilistic graphical models using an interactive

model-specification language.

Eyespots were modelled as a discrete trait with two states (presence/absence) with unequal

transition rates drawn from identical exponential priors. The rate parameters of these priors were set

to reflect an expectation of 10 events (10 eyespot gains and 10 eyespot losses) along the tree. Root

state frequencies were in turn drawn from a Dirichlet prior, assuming equal probability of presence

or absence of eyespots at the origin. Eyespot evolution was modelled separately using three

datasets: eyespot presence/absence irrespective of eyespot location on the wing, presence/absence

of *Marginal* eyespots, and presence/absence of *Discal* eyespots. For all three datasets, eyespots

could be located on any wing surface and either sex.

Each model was run for 100,000 iterations with an initial burn-in of 10,000, and tuning parameter

proposals every 1,000 iterations on two independent chains. Joint conditional ancestral states were

sampled every 100 iterations and plotted using RevGadgets v 1.1.1 (Tribble et al., 2023) in R. We

evaluated the convergence and stationarity of the MCMC chains for each model using the R package

Convenience v 1.0.0 (Fanreti et al., 2013)

<u>Testing eyespot homology in selected clades</u>

We next implemented a model testing approach to investigate eyespot homology among extant

species of Lepidoptera. We identified all subclades including three or more taxa bearing eyespots,

regardless of their location. If the most recent ancestor of these clades also displayed eyespots, it is

likely that eyespots in extant taxa are homologous. To test this hypothesis, we extracted all subclades

from the complete ultrametric phylogeny and applied in each case two alternative versions of the

discrete-trait model described above. In the first version (hereafter the multiple-origin model), we

set the root frequency of eyespot presence to zero, effectively constraining the common ancestor of

the subclade to lack eyespots. In the second version (the common-ancestor model), we instead

enforced a common ancestor with eyespots by setting the root frequency of eyespot presence to

one. We then compared the marginal likelihood (ML) of these alternative models using log 10 of the

raw Bayes factor using thresholds based on Jeffreys (1998). In our study, results above positive 0.1

were considered to show some support for an eyespot originating at a specific node. Results above

0.5 were considered to have strong support, results above 1.0 were considered to have very strong

support and results which were positive numbers but below 0.1 were considered to demonstrate

very weak support which wasn't worth mentioning. Finally negative results were considered to

represent no support for an eyespot origin at a given node. These thresholds for the support of

eyespots being present at a particular node were chosen due to the high number of negative values

we obtained in our study (values above -1.0) which is indicative of a lack of support for a single origin

of eyespots.

ML estimates gauge the fit of a model, including its priors, to the data, in this case, the phylogeny

and presence or absence of eyespots in extant taxa. Because the two models being compared differ

only in their prior assumptions about the character state at the root, their direct comparison serves

as a statistical test of the support for eyespot presence in the most recent common ancestor of the

clade. ML was estimated via the use of two sampling methods, steppingstone sampling (SS) and path

sampling (PS, Lartillot and Philippe, 2006, Fan et al., 2011 & Xie et al., 2011). For both methods the

power posterior analysis was split into 50 intervals between the prior and posterior and was run for

5,000 iterations with a burn-in of 5,000 generations. We repeated ML approximations for each

subclade and eyespot dataset and confirmed that both PS and SS estimates were stable (i.e. differing

by no more than 0.5 between independent runs of each set of power posteriors). The results of

these analyses were summarized and plotted onto the phylogeny using the R packages phytools v1.9-

16 (Revell, 2012), ggplot2 v3.4.3 (Wickham et al., 2016) and ggtree v3.9.0 (Yu et al., 2017 & 2018, Yu,

2020 & 2022 & Xu et al., 2022), followed by the online tool ITOL (2023).

Results

<u>Tree topology</u>

The phylogeny constructed for this study contains 28 superfamilies, each containing 1 – 128 species

in our samples (median = 14). The full list of superfamilies as well as the number of species

representatives for each superfamily are outlined in Table S1 (Supplementary tables and figures). The

topology of our tree is largely congruent with previous phylogenies (Heikkilä et al., 2015; Mitter et

al., 2017; Kawahara et al., 2019). Topological differences observed between this study and previous

ones involve species whose placement is phylogenetically uncertain (*incertae cedis*) or superfamilies

previously shown to require reclassification (Tineoidea or the Cossioidea-Sesioidea complex for

example; Mutanen et al., 2010; Bazinet et al., 2013; Reiger et al., 2013; Heikkilᵈ et al., 2015 Reiger et

al., 2015A; Mitter et al., 2017; Appendix 1). These differences in topology are unlikely to have a

significant impact on the main findings of this work, as they primarily nested within large clades

entirely lacking eyespots. A summary and discussion of novel species relationships identified in this

work can be found in the Supplementary Information (Appendix 1).

<u>Ancestral state reconstructions and evolutionary rates</u>

Our three ancestral state reconstructions (*Both*, *Marginal* and *Discal*) indicate that the common

ancestor, at the root of Lepidoptera did not have any eyespots (Fig. 4, Figs. S16 & S17). Eyespots thus

evolved multiple times in the history of Lepidoptera (Figs. 4 & 5). Nonetheless, eyespots may often

be evolutionarily short lived. Our results show a higher rate of eyespot losses than eyespot gains

regardless of eyespot type. The *Both* eyespot model (Fig. 4), *Marginal* eyespot model and *discal*

eyespot model all showing a higher rate of eyespot losses than gains (Fig. 4 & Fig. S16 & S17). To

explore the sensitivity of these results, we repeated all analyses under a more relaxed definition of

eyespots, where we also included non-circular/oblong shapes as eyespots. These results were

qualitatively similar to the results in our main analysis and are therefore presented in the

supplementary tables and figures section (Fig. S18).

Our ancestral state reconstructions are consistent with 28 independent Discal eyespot gains, and 19

independent Marginal eyespot gains across 12 superfamilies of Lepidoptera represented in this tree

(Figs. 4, 5, S16 & S17). In contrast, we did not find any eyespots in specimens sampled from 16

superfamilies: Cimelioidea, Thyridoidea, Copromorphoidea, Hyblaeoidea, Sesioidea, Gelechioidea,

Epermenioidea, Tortricoidea, Galacticoidea, Immoidea, Choreutoidea, Urodoidea, Pterophoroidea,

Gracillarioidea, Yponomeutoidea and Tineoidea). Most of the eyespots found in the remaining 12

superfamilies occur in the single species/genera sampled and are not present in sister lineages on

the tree. There are, however, two major independent radiations of Both Marginal and Discal

eyespots found in the families Nymphalidae and Saturniidae, where Both eyespot types were

retained in multiple members of these families after they originated (Fig. 5, Figs. S10 & S15).

<u>Homology of eyespot radiations</u>

To further investigate the ancestral nodes of independent eyespot origins, as suggested by our

ancestral state reconstructions above, we contrasted the fit of a common-ancestor model *vs* a

multiple-origin model, for the ancestor of each putative eyespot radiation. Our results using the

combined eyespot data (i.e. all eyespots regardless of location), supported our earlier findings of

eyespot bearing ancestors in Nymphalidae and Saturniidae (Table 1). By contrasting the results of

analyses on the *Marginal* data and the *Discal* data, we inferred which eyespot location likely evolved

first in each radiation (Fig. 1e-g). We were surprised to find that the area of the wing where eyespots

first appeared was reversed between these two main clades. In nymphalids, the first eyespots

appeared along the margin and were followed by *Discal* eyespots (Figs. 5, S10 & S15). The opposite

was observed in saturniids, where *Discal* eyespots originated first followed by *Marginal* eyespots

(Fig. 5. Figs. S10 & S15). *Discal* eyespots likely originated in the most recent common ancestor of all

saturniids, while *Marginal* eyespots evolved within the Attacini tribe of the subfamily Saturniinae. In

nymphalids, *Marginal* eyespots first evolved at the base of the sister lineage to the Libytheinae, and

Discal eyespots followed in ancestors of Heliconiine and Nymphaline. We found that the Bayes Factor

(BF) between our two sapling methods (PS & SS) was largely consistent between runs for the same

taxa (Table 1). When the circular criteria for eyespot shape was relaxed (Fig. S18), we found some

evidence for a more ancestral origin of Discal eyespots in the Saturniidae. The BF for this more

relaxed model is available in the supplementary information (Fig. S18).

Table 1. Log 10 of the raw Bayes factor for each of our eyespot radiations identified in our tree. Values for both PS and SS sampling methods are provided.						
Taxa (Family)	*Discal* PS	*Discal* SS	*Marginal* PS	*Marginal* SS	*Both* PS	*Both* SS
Saturniidae	0.146	0.145	0.110	0.104	0.247	0.253
Nymphalidae	0.127	0.126	0.131	0.126	0.150	0.132

To investigate the 27 other Discal and 18 other Marginal eyespot occurrences which were not part of

any eyespot radiation (Fig. 5), we investigated the occurrence of eyespots in up to 3 closely related

species. These closely related species did not feature on our tree and were limited from the genus to

the family level (Fig. S19). We found that many clades with eyespots that were represented by a

single species on our tree (Fig. 5) had several closely related species also baring eyespots (Fig. S19).

This suggests that these multiple clades represent separate, independent eyespot radiations (Fig. 5 &

Fig. S19).

Discussion

Our results show that eyespot evolution in Lepidoptera is diverse and complex. The majority of

eyespot research, up to now, has been conducted in a single clade (Nymphalidae), but here we

demonstrate that eyespots have evolved multiple times independently across the Lepidoptera,

including in many poorly known moth clades (Fig. 4 & Fig. 5). In our phylogeny, these clades are often

represented by a single species. However, we documented eyespots in close relatives to each of

these lineages (Fig. S19), suggesting eyespots have been preserved across additional radiations.

Future phylogenetic studies, with a denser taxonomic sampling, will be required to characterize the

evolutionary history of eyespots in these lesser-known clades. Nonetheless, our study strongly

suggests that eyespots are not homologous across the entire Lepidoptera.

The evolution of Marginal eyespots in the Nymphalidae has been studied before and we report

similar findings to these previous studies. Our findings align more closely with the 'early' model of

eyespot evolution first proposed by Oliver et al. (2012 & 2014), as opposed to the 'late' model that

became the preferred model (Oliver et al. 2014). In Both our analysis, and in the 'early' model,

eyespots were coded as being present or absent anywhere on the wing, whereas the 'late' model

preferred by Oliver et al., (2014) had increased resolution by scoring the presence of eyespots in

specific wing sectors. This late model brought the origin of eyespots to a node above the one

discovered here, to the base of the lineage that is sister to the Danainae. Despite minor conflict as to

when exactly *Marginal* eyespots first evolved, this and previous studies agree on a single and

relatively early origin of Marginalthese eyespots in Nymphalidae.

Nymphalid *Discal* eyespots and their evolutionary history have not been investigated before. Here

we presented a first estimate of *Discal* eyespot evolution in the nymphalidae, as Oliver et al., (2012 &

2014) did not study these *Discal* eyespots. *Discal* nymphalid eyespots appear to have evolved in two

separate clades and are not homologous across all species in the family Nymphalidae. Firstly, in the

closely related Nymphalidae subclades Heliconiine (Limenitidinae- *Limenitis arthemis*) and

Nymphaline (Apaturinae-*Asterocampa celtis*, Biblidinae-*Hamadryas arinome*, Melitaeini-P*hyciodes*

phaon & Nymphalini-*Vanessa carye*), we find that the *Discal* eyespot evolved once and then radiated

across several groups, making discal eyespots homologus across the Heliconiine and Nymphalini (Fig.

5 & Fig S10). The second instance of discal eyespot evolution which is not homologus to the other

Nymphalidae is *Neope goschkevitschii* (Satryinae, Nymphalidae. Figs. 2 & 5 & Figs. S10 & S19). *Neope*

sp. and closely related species within the Satryinae were found to have *Discal* eyespot patterns (Fig.

S19), upon our investigation of closely related species not featured on the tree and may represent a

unique *Discal* eyespot radiation within the Satyrinae (Fig. S19).

We provided the first examination of the evolution of eyespots (*Discal* and *Marginal*) in the

Saturniidae and demonstrate that *Discal* eyespots in the Saturniidae are homologus while *Marginal*

eyespots are not. We found that *Discal* eyespots likely originated in the most recent common

ancestor of all Saturniids, with *Discal* eyespots being present in 62% of the represented clades within

the family. Making discal eyespots homologus across the family Saturniidae. *Marginal* eyespots, on

the other hand, have evolved and radiated within the Attacini tribe of the subfamily Saturniinae. The

Marginal eyespot radiation observed within the Attacini includes species of the genus *Samia*,

Callosamia, Epiphora & Hyalophora. We also observed independent origins of *Marginal* eyespots

within the Saturniidae in three additional taxonomic groups, meaning that marginal eyespots in the

Saturniidae are not homologus. Two of the three representatives of these groups in our phylogeny

(*Copaxa multifenestrata*-tribe Saturniinae & subfamily Saturniinae and *Asthenidia transversaria*-

subfamily Oxytenninae) were found to have close relatives with Marginal eyespots suggesting

individual eyespot radiations within these taxa (Fig. 5 & Figs. S15A, S15C & S19). One species,

Eupackardia calleta (tribe Attacini, subfamily Saturniinae) is monotypic at the genus level and its

closest relatives are other Saturniidae of the tribe Attacini. Despite being in the Attacini, this species

is not picked up in our analysis as being part of the *Marginal* eyespot radiation associated with the

other Attacini in our study SS Log10 of BF = -0.123, PS Log 10 of BF = -0.130) (Fig. 5, Fig. S15A &

S15C). We therefore conclude that the marginal eyespot in this species likely evolved independently

to its congeners in the Attacini.

Our analyses revealed that eyespots appeared after each other (and in a different order in butterflies

and silk-moths). *Marginal* eyespots in Nymphalidae are considered serially homologous (Monteiro et

al., 2007 & Hombría 2011) but they appeared in a particular sequence on the wings. They first

originated in ventral hindwings, and millions of years later they appeared in forewings and dorsal

surfaces (Oliver 2014; Schachat et al 2015). *Discal* eyespots may be yet another instance of a serial

homolog, with a more distinct and central location on the wing. By statistically demonstrating that

eyespots, as a complex derived trait, can evolve in different locations on the wing in a different

sequence, we open the door to more in-depth developmental level studies that investigate how each

type of eyespot differentiates on the wing.

Although we demonstrate that nymphalid and saturniid eyespots evolved in lineages which are

currently understood to be ~110 million years apart (Kawahara et al., 2019) and are not

evolutionarily homologous, it is still possible that eyespots in these two superfamilies share the same

gene regulatory network (GRN). Previous research by Murugesan et al. (2022) found that an

appendage gene regulatory network was co-opted to build *Marginal* eyespots in *Bicyclus anynana*, a

nymphalid butterfly. We suggest that the co-option of the same GRN could have happened more

than once across the Lepidoptera. To test this, it will be important to characterize the *Marginal* and

298 *Discal* eyespot GRN in moth lineages and/or the *Discal* eyespot GRN in butterfly lineages, at the level

299 of gene expression. Early immunochemistry work in two saturniid species detected the presence of

300 two (nymphalid) eyespot marker proteins, Distal-less and Engrailed, in the moth *Discal* eyespots

301 (Monteiro et al. 2006). Stronger evidence for the use of the same appendage GRN in these Discal

302 moth eyespots may need to come from CRISPR knockouts of cis-regulatory elements belonging to

303 common eyespot and appendage genes, showing that Both appendages and eyespots are affected

304 (Murugesan et al. 2022).

305 Finally, while the focus of this work is on eyespot evolution, this phylogeny also provides evidence

306 supporting Both new and already established relationships among Lepidopteran lineages, including

307 at the superfamily level (Appendix 1). These insights can fuel future systematic research and further

308 comparative work on how wing color patterns, and other adaptive traits, evolve in the Lepidoptera.

309 **Acknowledgements:** We thank Dr Mark Willmott and Prof Akito Kawahara (MGCL) for hosting B.H. at
310 the MGCL and facilitating access to the collections; Prof emeritus Charles Mitter (University of
311 Maryland) for graciously sending us molecular sequence data for most specimens reanalyzed here;
312 Monteiro lab members for lively discussion, and Mr David Teo Yan Hua for expertise in PC
313 engineering and technological assistance. B.H was supported by a National Research Foundation
314 (NRF) Graduate Fellowship; B.W. was funded by an International Postdoc Grant from the Swedish
315 Research Council (VR; grant no. 2019-06444); and research was supported by a NRF Investigatorship
316 award (NRF-NRFI05-2019-0006) to A.M.

317 **Conflict of interest:** The authors declare no conflict of interests.

318 **References:**

319 Aarvik & Karisch in Aarvik L, Karisch T, plazi (2009). Revision of Multiquaestia, Karisch (Lepidoptera:
320 Tortricidae: Grapholitini). Plazi.org taxonomic treatments database. Checklist dataset
321 https://doi.org/10.5281/zenodo.274748 accessed via GBIF.org on 2023-02-22.

322 Arias, M., Mappes, J., Desbois, C., Gordon, S., McClure, M., Elias, M., . . . Gomez, D. (2019).
323 Transparency reduces predator detection in mimetic clearwing butterflies. Functional Ecology, 33(6),
324 1110-1119.

325 Auguie B (2017). _gridExtra: Miscellaneous Functions for "Grid" Graphics_. R package version 2.3,
326 <https://CRAN.R-project.org/package=gridExtra>.

327 Banerjee, T. D., Murugesan, S. N., Connahs, H., & Monteiro, A. (2023). Spatial and temporal
328 regulation of Wnt signaling pathway members in the development of butterfly wing patterns. Science
329 Advances, 9(30), eadg3877.

330 Bazinet, A. L., Cummings, M. P., Mitter, K. T., & Mitter, C. W. (2013). Can RNA-Seq resolve the rapid
331 radiation of advanced moths and butterflies (Hexapoda: Lepidoptera: Apoditrysia)? An exploratory
332 study. PloS one, 8(12), e82615.

Bhardwaj, S., Jolander, L. S.-H., Wenk, M. R., Oliver, J. C., Nijhout, H. F., & Monteiro, A. (2020). Origin
of the mechanism of phenotypic plasticity in satyrid butterfly eyespots. Elife, 9, e49544.

Blest, A. D. (1957). The function of eyespot patterns in the Lepidoptera. Behaviour, 209-256.

Brakefield, P. M. (2003). The power of evo-devo to explore evolutionary constraints: experiments
with butterfly eyespots. Zoology, 106(4), 283-290.

Breuker, C. J., & Brakefield, P. M. (2002). Female choice depends on size but not symmetry of dorsal
eyespots in the butterfly Bicyclus anynana. Proceedings of the Royal Society of London. Series B:
Biological Sciences, 269(1497), 1233-1239.

Carter, D. J., & Hargreaves, B. (1986). A field guide to caterpillars of butterflies and moths in Britain
and Europe: Collins.

Connahs, H., Rhen, T., & Simmons, R. B. (2016). Physiological perturbation reveals modularity of
eyespot development in the painted lady butterfly, Vanessa cardui. PloS one, 11(8), e0161745.

D'Abrera, B. (1995). Saturniidae Mundi, Saturniid moths of the world part I. Keltern, Germany:
Automeris press in association with Victoria Australia Melborne & London: Hill house.

D'Abrera, B. (2012). Saturniidae Mundi, Saturniid moths of the world part II. Victoria Australia,
Melborne & London: Hill house.

D'Abrera, B. (1998). Saturniidae Mundi, Saturniid moths of the world part III. Keltern, Germany:
Goecke & Evers in association with Victoria Australia Melborne & London: Hill house.

De Prins, J., & Kawahara, A. Y. (2012). Systematics, revisionary taxonomy, and biodiversity of
Afrotropical Lithocolletinae (Lepidoptera: Gracillariidae). Zootaxa, 3594(1), 1–283-281–283.

De Prins W. & Steeman C. 2003–2023. *Catalogue of the Lepidoptera of Belgium*. Last accessed on
the 22/02/2023. Available online at https://projects.biodiversity.be/lepidoptera

Epstein, M. E. (1996). Revision and phylogeny of the limacodid-group families, with evolutionary
studies on slug caterpillars (Lepidoptera: Zygaenoidea).

Fabreti, L. Hoehna, S & Magee, A. (2023). _convenience: Convergence assessment for phylogenetic
inference_. R package version 1.0.0.

Fan, Y., Wu, R., Chen, M.-H., Kuo, L., & Lewis, P. O. (2011). Choosing among partition models in
Bayesian phylogenetics. Molecular biology and evolution, 28(1), 523-532.

Halali, D., Krishna, A., Kodandaramaiah, U., & Molleman, F. (2019). Lizards as predators of butterflies:
shape of wing damage and effects of eyespots. The Journal of the Lepidopterists' Society, 73(2), 78-
86.

Heikkilä, M., Kaila, L., Mutanen, M., Peña, C., & Wahlberg, N. (2012). Cretaceous origin and repeated
tertiary diversification of the redefined butterflies. Proceedings of the Royal Society B: Biological
Sciences, 279(1731), 1093-1099.

Heikkilä, M., Mutanen, M., Kekkonen, M., & Kaila, L. (2014). Morphology reinforces proposed
molecular phylogenetic affinities: a revised classification for Gelechioidea (Lepidoptera). Cladistics,
30(6), 563-589.

Heikkilä, M., Mutanen, M., Wahlberg, N., Sihvonen, P., & Kaila, L. (2015). Elusive ditrysian phylogeny:
an account of combining systematized morphology with molecular data (Lepidoptera). BMC
Evolutionary Biology, 15(1), 1-27.

Hoang, D, T. Chernomor, O. Von Haeseler, A. Minh, B, Q & Vinh, L, S. (2018). UFBoot2: Improving the
ultrafast bootstrap approximation. Mol. Biol. Evol., 35:518–522.

Hogue, C. L. (1987). Cultural entomology. Annual Review of Entomology, 32(1), 181-199.

Höhna, Landis, Heath, Boussau, Lartillot, Moore, Huelsenbeck, Ronquist. (2016). RevBayes: Bayesian
phylogenetic inference using graphical models and an interactive model-specification language.
Systematic Biology, 65:726-736.

Hombría, J. C.-G. (2011). Butterfly eyespot serial homology: enter the Hox genes. BMC biology, 9(1),
1-3.

Hsu Y-F, Powell JA (2005) Phylogenetic relationships within Heliodinidae and systematics of moths
formerly assigned to Heliodines Stainton (Lepidoptera: Yponomeutoidea). University California
Publications Entomology 124: 1–158.

Huq, M., Bhardwaj, S., & Monteiro, A. (2019). Male *Bicyclus anynana* butterflies choose females on
the basis of their ventral UV-reflective eyespot centers. Journal of insect science, 19(1), 25.

Jeffreys, H. (1998). The theory of probability: OuP Oxford.

Kalyaanamoorthy, S. Minh, B, Q. Wong, T, K, F. Von Haeseler, A. & Jermiin, L, S. (2017). ModelFinder:
Fast Model Selection for Accurate Phylogenetic Estimates, Nature Methods, 14:587–589.

Katoh, K. & Standley, D. M. (2013). MAFFT Multiple Sequence Alignment Software Version 7:
Improvements in Performance and Usability. Molecular Biology and Evolution, 30(4), 772–780.

Kawahara, A., Ohshima, I., Kawakita, A., Regier, J., Mitter, C., Cummings, M., . . . Lopez-Vaamonde, C.
(2011). Increased gene sampling provides stronger support for higher-level groups within gracillariid
leaf mining moths and relatives (Lepidoptera: Gracillariidae). BMC Evol. Biol, 11, 182.

Kawahara, A. Y., & Rubinoff, D. (2012). Three new species of Fancy Case caterpillars from threatened
forests of Hawaii (Lepidoptera, Cosmopterigidae, Hyposmocoma). ZooKeys(170), 1.

Kawahara, A. Y., & Breinholt, J. W. (2014). Phylogenomics provides strong evidence for relationships
of butterflies and moths. Proceedings of the Royal Society B: Biological Sciences, 281(1788),
20140970.

Kawahara, A. Y., Plotkin, D., Espeland, M., Meusemann, K., Toussaint, E. F., Donath, A., . . . Dos Reis,
M. (2019). Phylogenomics reveals the evolutionary timing and pattern of butterflies and moths.
Proceedings of the National Academy of Sciences, 116(45), 22657-22663.

Kawahara, A. Y., Plotkin, D., Ohshima, I., LOPEZ-VAAMONDE, C., Houlihan, P. R., Breinholt, J. W., . . .
Davis, D. R. (2017). A molecular phylogeny and revised higher-level classification for the leaf-mining
moth family Gracillariidae and its implications for larval host-use evolution. Systematic Entomology,
42(1), 60-81.

Kawahara, A. Y., Storer, C., Carvalho, A. P. S., Plotkin, D. M., Condamine, F. L., Braga, M. P., . . .
Lohman, D. J. (2023). A global phylogeny of butterflies reveals their evolutionary history, ancestral
hosts and biogeographic origins. Nature Ecology & Evolution. doi:10.1038/s41559-023-02041-9

Kettlewell, H. (1973). The Evolution of Melanism: The Study of Recurring Necessity; with Special
Reference to Industrial Melanism in the Lepidoptera. Clarendon Press, Oxford.

Kristensen, N. P., & Schmidt-Rhaesa, A. (1998). Volume 1: Evolution, Systematics, and Biogeography
(Vol. 1): Walter de Gruyter.

Kodandaramaiah, U. (2011). The evolutionary significance of butterfly eyespots. Behavioral Ecology,
22(6), 1264-1271.

Kodandaramaiah, U., Lindenfors, P., & Tullberg, B. S. (2013). Deflective and intimidating eyespots: a
comparative study of eyespot size and position in Junonia butterflies. Ecology and evolution, 3(13),
4518-4524.

Labandeira, C. C., Yang, Q., Santiago-Blay, J. A., Hotton, C. L., Monteiro, A., Wang, Y.-J., . . . Rose, T. R.
(2016). The evolutionary convergence of mid-Mesozoic lacewings and Cenozoic butterflies.
Proceedings of the Royal Society B: Biological Sciences, 283(1824), 20152893.
421
Lartillot, N., & Philippe, H. (2006). Computing Bayes factors using thermodynamic integration.
Systematic biology, 55(2), 195-207.Miller, J. Y. (2008). Studies in the Castniidae. V. Description of a
New Species of Zegara: Florida Museum of Natural History, University of Florida.

Merilaita, S., Vallin, A., Kodandaramaiah, U., Dimitrova, M., Ruuskanen, S., & Laaksonen, T. (2011).
Number of eyespots and their intimidating effect on naive predators in the peacock butterfly.
Behavioral Ecology, 22(6), 1326-1331.

Mey, W., Wichard, W., Müller, P., & Wang, B. (2017). The blueprint of the Amphiesmenoptera–
Tarachoptera, a new order of insects from Burmese amber (Insecta, Amphiesmenoptera). Fossil
Record, 20(2), 129-145.

Mitter, C., Davis, D. R., & Cummings, M. P. (2017). Phylogeny and evolution of Lepidoptera. Annual
review of entomology.

Monteiro, A., Glaser, G., Stockslager, S., Glansdorp, N., & Ramos, D. (2006). Comparative insights into
questions of Lepidopteran wing pattern homology. BMC Developmental Biology, 6(1), 1-13.

Monteiro, A., Chen, B., Scott, L. C., Vedder, L., Prijs, H. J., Belicha-Villanueva, A., & Brakefield, P. M.
(2007). The combined effect of two mutations that alter serially homologous color pattern elements
on the fore and hindwings of a butterfly. BMC genetics, 8, 1-10.

Monteiro, A. (2015). Origin, development, and evolution of butterfly eyespots. Annual review of
entomology, 60, 253-271.

Mukherjee, R., & Kodandaramaiah, U. (2015). What makes eyespots intimidating–the importance of
pairedness. BMC Evolutionary Biology, 15(1), 1-10.

Murugesan, S. N., Connahs, H., Matsuoka, Y., Das Gupta, M., Tiong, G. J., Huq, M., . . . Werner, T.
(2022). Butterfly eyespots evolved via cooption of an ancestral gene-regulatory network that also
patterns antennae, legs, and wings. Proceedings of the National Academy of Sciences, 119(8),
e2108661119.

Mutanen, M., Wahlberg, N., & Kaila, L. (2010). Comprehensive gene and taxon coverage elucidates
radiation patterns in moths and butterflies. Proceedings of the Royal Society B: Biological Sciences,
277(1695), 2839-2848.

Nguyen, L, T. Schmidt, Heiko A. Haeseler, A & Minh, B, Q. (2015). IQ-TREE: A fast and effective
stochastic algorithm for estimating maximum likelihood phylogenies.

Oliver, J. C., Tong, X.-L., Gall, L. F., Piel, W. H., & Monteiro, A. (2012). A single origin for nymphalid
butterfly eyespots followed by widespread loss of associated gene expression.

Oliver, J. C., Beaulieu, J. M., Gall, L. F., Piel, W. H., & Monteiro, A. (2014). Nymphalid eyespot serial
homologues originate as a few individualized modules. Proceedings of the Royal Society B: Biological
Sciences, 281(1787), 20133262.

Otaki, J. M. (2020). Morphological and spatial diversity of the discal spot on the hindwings of
nymphalid butterflies: Revision of the nymphalid groundplan. Insects, 11(10), 654.

Paradis, E. & Schliep, K. (2019). ape 5.0: an environment for modern phylogenetics and evolutionary
analyses in R. Bioinformatics 35: 526-528.

Plummer, M. Best, N. Cowles, K. & Vines, K. (2006). CODA: Convergence Diagnosis and Output
Analysis for MCMC, R News, vol 6, 7-11

R Core Team (2023). R: A language and environment for statistical computing. R Foundation for
Statistical Computing, Vienna, Austria. URL https://www.R-project.org/.

Regier, J. C., Zwick, A., Cummings, M. P., Kawahara, A. Y., Cho, S., Weller, S., . . . Parr, C. (2009). Toward
reconstructing the evolution of advanced moths and butterflies (Lepidoptera: Ditrysia): an initial
molecular study. BMC Evolutionary Biology, 9(1), 1-21.

Regier, J. C., Brown, J. W., Mitter, C., Baixeras, J., Cho, S., Cummings, M. P., & Zwick, A. (2012). A
molecular phylogeny for the leaf-roller moths (Lepidoptera: Tortricidae) and its implications for
classification and life history evolution. PLoS ONE, 7(4), e35574. (2012A)

Regier, J. C., Mitter, C., Mitter, K., Cummings, M. P., Bazinet, A. L., Hallwachs, W., . . . Zwick, A. (2017).
Further progress on the phylogeny of Noctuoidea (Insecta: Lepidoptera) using an expanded gene
sample. Systematic Entomology, 42(1), 82-93.

Regier, J. C., Mitter, C., Solis, M. A., Hayden, J. E., Landry, B., Nuss, M., . . . Cummings, M. P. (2012). A
molecular phylogeny for the pyraloid moths (Lepidoptera: Pyraloidea) and its implications for
higher-level classification. Systematic Entomology, 37(4), 635-656. (2012B)

Regier, J. C., Mitter, C., Zwick, A., Bazinet, A. L., Cummings, M. P., Kawahara, A. Y., . . . Davis, D. R.
(2013). A large-scale, higher-level, molecular phylogenetic study of the insect order Lepidoptera
(moths and butterflies). PLoS ONE, 8(3), e58568.

Regier, J. C., Mitter, C., Davis, D. R., Harrison, T. L., SOHN, J. C., Cummings, M. P., . . . Mitter, K. T.
(2015). A molecular phylogeny and revised classification for the oldest ditrysian moth lineages (L
epidoptera: T ineoidea), with implications for ancestral feeding habits of the mega-diverse D itrysia.
Systematic Entomology, 40(2), 409-432.

Regier, J. C., Mitter, C., Solis, M. A., Hayden, J. E., Landry, B., Nuss, M., . . . Cummings, M. P. (2012). A
molecular phylogeny for the pyraloid moths (Lepidoptera: Pyraloidea) and its implications for
higher-level classification. *Systematic Entomology, 37*(4), 635-656.

Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things).
Methods in Ecology and Evolution, 3, 217-223.

Schachat, S. R., Oliver, J. C., & Monteiro, A. (2015). Nymphalid eyespots are co-opted to novel wing
locations following a similar pattern in independent lineages. BMC evolutionary biology, 15(1), 1-9.

Sohn, J.-C., Regier, J. C., Mitter, C., Davis, D., Landry, J.-F., Zwick, A., & Cummings, M. P. (2013). A
molecular phylogeny for Yponomeutoidea (Insecta, Lepidoptera, Ditrysia) and its implications for
classification, biogeography and the evolution of host plant use. PLoS ONE, 8(1), e55066.

Sohn, J. C., Regier, J. C., Mitter, C., Adamski, D., LANDRY, J. F., Heikkilä, M., . . . Zwick, A. (2016).
Phylogeny and feeding trait evolution of the mega-diverse Gelechioidea (Lepidoptera: Obtectomera):
new insight from 19 nuclear genes. Systematic Entomology, 41(1), 112-132.

Sohn, J.-C., & Choi, S.-W. (2016). First report of Saridoscelinae (Lepidoptera, Yponomeutidae) in
Korea with new records of Saridoscelis kodamai Moriuti from Korea and China. Korean journal of
applied entomology, 55(4), 347-350.

Sondhi, S., Karmakar, T., Sondhi, Y., & Kunte, K. (2021). Moths of Tale Wildlife Sanctuary, Arunachal
Pradesh, India with seventeen additions to the moth fauna of India (Lepidoptera: Heterocera).
Tropical Lepidoptera Research, 1-53.

Stevens, M. (2005). The role of eyespots as anti-predator mechanisms, principally demonstrated in
the Lepidoptera. Biological Reviews, 80(4), 573-588.

Tribble, C. May, M. Freyman, W. Landis, M. Ying, L. Barido-Sottani, J. Magee, A. Kopperud, B & Hohna,
S. (2023). _RevGadgets: Visualization and Post-Processing of 'RevBayes' Analyses

Van Nieukerken, E., Kaila, L., Kitching, I., Kristensen, N., Lees, D., Minet, J., . . . Simonsen, T. (2011).
Animal Biodiversity: an Outline of Higher-level Classification and Survey of Taxonomic Richness.
Zootaxa (3148). In.Wickham, H. (2016). ggplot2: Elegant Graphics for Data Analysis. Springer-Verlag
New York.

Wickham, H. Hester, J. Chang, W & Bryan J (2022). _devtools: Tools to Make Developing R Packages
Easier_. R package version 2.4.5, <https://CRAN.R-project.org/package=devtools>.

Wickham, H. Vaughan, D & Girlich M. (2023). _tidyr: Tidy Messy Data_. R package version 1.3.0,
<https://CRAN.R-project.org/package=tidyr>.

Xie, W., Lewis, P. O., Fan, Y., Kuo, L., & Chen, M.-H. (2011). Improving marginal likelihood estimation
for Bayesian phylogenetic model selection. Systematic biology, 60(2), 150-160.

Xu, S. Lin, L. Luo, X. Chen, M. Tang, W. Zhan, L. Dai, Z. Lam, T. Guan, Y. & Yu, G. (2022). Ggtree: A
serialized data object for visualization of a phylogenetic tree and annotation data. iMeta 2022,
4(1):e56. doi:10.1002/imt2.56

Yu, G. (2020). Using ggtree to visualize data on tree-like structures. Current Protocols in
Bioinformatics, 2020, 69:e96. doi: 10.1002/cpbi.96

Yu, G. (2022). Data Integration, Manipulation and Visualization of Phylogenetic Trees (1st edition).
Chapman and Hall/CRC. doi:10.1201/9781003279242

Yu, G. Lam, T. Zhu, H. & Guan, Y. (2018). Two methods for mapping and visualizing associated data on
phylogeny using ggtree. Molecular Biology and Evolution 2018, 35(2):3041-3043. doi:
10.1093/molbev/msy194

Yu, G. Smith, D. Zhu, H. Guan, & Y. Lam, T. (2017). ggtree: an R package for visualization and
annotation of phylogenetic trees with their covariates and other associated data. Methods in Ecology
and Evolution 2017, 8(1):28-36. doi:10.1111/2041-210X.12628

Zahiri, R., Kitching, I. J., Lafontaine, J. D., Mutanen, M., Kaila, L., Holloway, J. D., & Wahlberg, N.
(2011). A new molecular phylogeny offers hope for a stable family level classification of the
Noctuoidea (Lepidoptera). Zoologica Scripta, 40(2), 158-173.

Zhang, L., & Reed, R. D. (2016). Genome editing in butterflies reveals that spalt promotes and Distal-
less represses eyespot colour patterns. Nature communications, 7(1), 11769.

Websites:

Afro-Moths:

De Prins J. & De Prins W. 2011–2021. Afromoths, online database of Afrotropical moth species
(Lepidoptera). World Wide Web electronic publication (http://www.afromoths.net) [last accessed on
the 8/10/2022].

Bold V3 & V4:

Ratnasingham, S. & Hebert, P. D. N. (2007). BOLD: The Barcode of Life Data System
(www.barcodinglife.org). Molecular Ecology Notes 7, 355-364. DOI: 10.1111/j.1471-
8286.2006.01678.x

Ratnasingham S, Hebert P.D.N (2013). A DNA-Based Registry for All Animal Species: The Barcode
Index Number (BIN) System. PLoS ONE 8(8): e66213. DOI:10.1371/journal.pone.0066213

Butterflies of America:

Warren, A. D., K. J. Davis, E. M. Stangeland, J. P. Pelham, K. R. Willmott & N. V. Grishin. (2023).
Illustrated Lists of American Butterflies. Website version: [14-II-2023] last accessed on the 22/02/
2023. Available at: http://www.butterfliesofamerica.com

Cornell university insect collection:

Cornell University insect collection (2023). A database of insect images and collections made
available online by Cornell university. Last accessed on the 22/02/2023 and available at:
https://cuic.entomology.cornell.edu/

CSIRO:

Australian moths online (CSIRO project, 2022). Online database of the Australian national museum,
last accessed on the 16/11/2022 at: Australian Moths Online (csiro.au)

GBIF:

GBIF: The Global Biodiversity Information Facility (2022) What is GBIF? Available from
https://www.gbif.org/what-is-gbif

Gracillariidae database:

De Prins J. & De Prins W. 2006–2022. Global Taxonomic Database of Gracillariidae (Lepidoptera).
World Wide Web electronic publication (http://www.gracillariidae.net) [last accessed on the
22/02/2023].

Insecta Pro:

Insecta Pro (2022). A website which has a data base of many different species of Lepidoptera and
other insects. Last accessed on the 18/08/2022 at: http://insecta.pro/

ITOL

iTOL(2023). Interactive Tree Of Life. Available at: https://itol.embl.de (Accessed: 6th January 2024)

Japanese moths:

Japanese moths.org (2023). A large website containing many Japanese moth species. Last accessed
on the 22/02/2023. Available at: http://www.jpmoth.org

Lepi forum:

Lepi forum, a German Lepidopteran data base of online photos and other useful information about
Lepidoptera. Last accessed on the 19/07/2022 and available at: https://lepiforum.org/

Moths Photographers group:

The website for the North American Moth photographers group based at the Mississippi
entomological museum, part of Mississippi state university. Website was last accessed on the
16/08/2022 and is available at: Moth Photographers Group -- Main Menu (msstate.edu)

Moths of India:

Moths of India. (2023). An online database which holds the collection of many moths found in India.
Last accessed on the 22/02/2023 and available at: Welcome to the Moths of India website! | Moths

Scan Bugs:

SCAN bugs. (2022). A image archive of insects from various institutions. Available at: http//:scan-
bugs.org/portal/index.php. Last accessed on 02/08/2022.

Swedish museum of natural history:

Swedish museum of natural history. (2023). Available at Index of /en (nrm.se) Last accessed on
23/02/2023.

The museum of Shimane database:

The museum of Shimane database (2022). Database of Japanese Lepidoptera accessed on the
16/08/2022, last accessed at: http://museum-database.shimane-
u.ac.jp/specimen/detail/50242018033112216

The Smithsonian Tropical Research Institute:

The Smithsonian Tropical Research Institute database. Last accessed on the 19/08/2022. Available at:
Smithsonian Tropical Research Institute | (si.edu)

Taiwan encyclopedia of life:

Taiwan encyclopedia of life (2023). An online database of Taiwanese flora and fauna. Last accessed
on the 22/02/2022 and available at: https://taieol.tw/

Places/Physical collections:

The Maguire Center for Lepidoptera (MGCL, 2022). Collections accessed in person 14.05.2022 to
04.06.2022. Hosted by Dr Keith Willmott (Director and curator) and Professor Akito Kawahara
(Principal investigator and curator).

Discal

Pantoctenia prasina
Pterodecta felderi
Helicomitra pulchra
Morvina fissmacula
Cyclosemia subcaerulea
Colias eurytheme
Mesosemia carissima

Porita erycinoides
Neope goschkevitschii
Limenitis arthemis*
Phaedropsis alitemeralis
Cacographis osteolalis
Midila daphne
Cyclophora nanaria

Orthonoma obstipata
Zale lunifera
Raphia abrupta
Trichosea champa
Amphiria pyramioides
Xylena exoleta
Mimallo amilia

Habrosyne pyritoides
Tridepana unispina
Genduara acedesta
Lasiocampa quercus
Carthaea saturnioides
Hopilocnema branchycera
Antherina suraka*

Marginal

Cossula coerulescens
Paysandia archon
Pantoctenia prasina
Isochaetes beutenmuelleri
Helicomitra pluchra
Parnasius apollo
Morvina fissmacula

Strymon eurytulus
Caligo telamonius*
Cacographis osteolalis
Semantura luna
Thyatira batis
Tridepana unispina
Dactyloceras widenmani

Paonias myops
Asthenidia transversaria
Eupackardia calleta
Copaxa multifenestrata
Hyalophora gloveri*

Key

Cossoidea
Zygaenoidea
Calliduloidea
Papilionoidea
Pyraloidea
Geometroidea
Noctuoidea
Mimallonoidea
Drepanoidea
Lasiocampoidea
Bombycoidea

Discal eyespots in the Saturniidae

Actias
isis

Actias
luna

Aguila
tau

Actias
selene

Anisota
stigma

Gonimbrasia
macrothyris

Erythromeris
flexilineata

Saturnia
walteorium

Graellsia
isabellae

Polythysana
apollina

Opodiphthera
eucalypti

Pseudimbrasia
deyrollei

Saturnia
galbania

Loepa
sikkima

Gonimbrasia
tyrrhea

Hemileuca
nevadensis

Saturnia
albofasciata

Saturnia
nassegi

Rhodina
fugnax

Eacles
imperialis

Orthorene
verana

Epiphora
mythimnia

Vegetia
ducalis

Eubergia
caisa

Antheraea
youngi

Copaxa
multifenestrata

Ceranchia
apollina

Antheraea
raffrayi

Antheraea
pakustadorum

Antheraea
pernyi

Antheraea
larissa

Antheraea
polyphemus

Antheraea
rosemariae

Antheraea
paphia

Saturnia
caecigena

Antherina
suraka

Antheraea
yamamaii

Antheraea
helferi

Antheraea
roylii

Heniocha
apollina

Argema
mimosae

Saturnia
mendocino

Antheraea
lampei

Cricula
elaezia

Antheraea
jana

Antheraea
godmani

Bunaea
alcinoe

Antheraea
kelimutuensis

Titaea
tamerlan

Marginal eyespots in the Saturniidae

Epiphora mythimnia

Samia cynthia

Samia luzonica

Samia ricini

Callosamia angulifera

Callosamia prometha

callosamia securifera

Hyalophora cecropia

Hyalophora euryalus

Hyalophora gloveri

Marginal eyespots in the Nymphalidae

caligo telamonius

Asterocampa celtis

Hamadryas arinome

Hypanartia godmani

Lethe sicelis

Marpesia petreus

Archeoprepona demophon

Manataria hercyna

Mycalesis gotama

Neope goschkevitschii

Phyciodes phaon

Pierella luna

Vanessa carye

Taygetis andromeda

Discal eyespots in the Nymphalidae

Limenitis arthemis

Vanessa carye

Phyciodes phaon

Hamadryas arinome

Asterocampa celtis

Eyespot like patterns in the Saturniidae

To Geometroidea

Oenosandra boisduvalii
Epanaphe carteri
Gluphisia septentrionis
Crinodes besckei
Furcula cinerea
Cerura rarata
Datana drexelii
Thaumetopoea pityocampa
Ochrogaster lunifer
Spatalia doerriesi
Rosema epigena
Hemiceras nigrescens
Ptilophora plumigera
Lirimiris guatemalensis
Cnethodonta grisescens
Hapigia nodicornis
Nystalea striata
Scotura leucophleps
Symmerista albifrons
Rhuda difficilis
Heterocampa obliqua
Schizura unicornis
Dicentria violacens
Hypena scabra
Anomis metaxantha
Eudocima salaminia
Gonodonta fulvangula
Pangrapta decoralis
Palthis asopialis
Asota egens
Hypoprepia miniata
Cisseps fulvicollis
Balacra pulchra
Amata fortunei
Rivula propinqualis
Lymantria dispar
Orgyia leucostigma
Mycterophora rubricans
Phobolosia anfracta
Micronoctua karsholti
Diascia hayesi
Zale lunifera
Catocala ultronia
Erebus ephesperis
Earias roseifera
Blenina senex
Meganola phylla
Iscadia producta
Negeta contrariata
Acontia aprica
Trichoplusia ni
Sphragifera sigillata
Raphia abrupta
Trichosea champa
Cucullia convexipennis
Stiria rugifrons
Psaphida resumens
Amphipyra pyramidoides
Eudryas grata
Acronicta lobeliae
Condica vecors
Pseudeustrotia carneola
Spodoptera frugiperda
Pyrrhia adela
Helicoverpa zea
Adisura bella
Cryphia cuerva
Caradrina meralis
Xylena exsoleta
Mythimna unipuncta
Agrotis ipsilon

More basal Ditrysia

To Pyraloidea

Oenosandridae + Notodontidae

Erebidae+Micronoctuidae

Nolidae

Noctuidae

To other Macroheterocerna

To Lasiocampoidea

Bombycidae
- 100 — *Zanola fieldi*
- 100 — *Olceclostera seraphica*
- — *Apatelodes torrefacta*

- 100 — *Malagasanja palliatella*
- 100 — *Cotana serranotata*
- 100 — *Ganisa plana*
- 100 — *Apha aequalis*

Brahmaeidae
- 100 — *Brahmaea tancrei*
- 100 — *Acanthobrahmaea europaea*
- 100 — *Dactyloceras widenmani*

Lemoniidae
- 100 — *Lemonia dumi*
- — *Sabalia picarina*

Endromidae+Mirinidae
- 100
  - 80 — *Phiditia cuprea*
  - — *Prismosticta fenestrata*
  - 100 — *Endromis versicolora*
  - 100 — *Obertheuria formosibia*
  - 63 / 81 — *Mirina christophi*

Bombycidae+Phiditiidae+

- 63 — *Carthaea saturnioides*
Carthaeidae Anthelidae
  - 100 — *Tededwardsius ravicardinalis*
  - 100 — *Munychryia senicula*
  - 100 — *Chelepteryx collesi*
  - 100 — *Nataxa flavescens*
  - 100 — *Anthela varia*

Sphingidae
- 100
  - 100 — *Hyles lineata*
  - 100 — *Euchloron megaera*
  - — *Cechenena subangustata*
  - 100 — *Hemaris diffinis*
  - 100 — *Erinnyis ello*
  - 100 — *Pachylia ficus*

- 100 — *Leptoclanis pulchra*
  - 100 — *Paonias myops*
  - 88 — *Falcatula falcatus*
  - 68 / 74 — *Coequosa triangularis*
  - 100 — *Batocnema africanus*

- 100 — *Synoecha marmorata*
  - 100 — *Hopliocnema brachycera*
  - 100 — *Hoplistopus penricei*
  - 100 — *Praedora marshalli*
  - 100 — *Manduca sexta*
  - 100 — *Sagenosoma elsa*
  - 100 — *Lapara coniferarum*

Bombycidae
- 100 — *Colla glaucescens*
  - 100 — *Quentalia crenulosa*
  - 100 — *Quentalia chromana*
- 100 — *Gastridiota adoxima*
- 50
  - 100 — *Bombyx mori*
  - 100 — *Bombyx mandarina*
  - 100 — *Ernolatia moorei*
  - 100 — *Triuncina brunnea*

To Saturniidae

To other Bombycoidea

- Asthenidia transversaria
- Oxytenis albilunulata — 100
- Oxytenis modestia — 100
- Janiodes laverna
- Polythysana apollina
- Hemileuca nevadensis — 100
- Eubergia caisa — 100
- Erythromeris flexilineata — 100
- Aglia tau
- Arsenura armida
- Rhescyntis hippodamia — 80
- Copiopteryx semiramis — 85
- Citheronia sepulcralis
- Eacles imperialis — 100
- Othorene verana — 100
- Anisota stigma — 100
- Titaea tamerlan
- Dysdaemonia boreas — 100
- Bunaea alcinoe
- Holocerina smilax — 100
- Vegetia ducalis — 100
- Heniocha apollonia
- Lonomia achelous — 100
- Cirina forda — 100
- Pseudimbrasia deyrollei — 100
- Gonimbrasia macrothyris — 100
- Gonimbrasia tyrrhea — 100
- Eupackardia calleta
- Rothschildia orizaba — 100
- Rothschildia forbesi — 100
- Archaeoattacus edwardsii
- Epiphora mythimnia
- Coscinocera hercules — 51
- Attacus lorquinii — 99
- Attacus caesar — 100
- Attacus atlas — 100
- Samia ricini — 96
- Samia cynthia — 100
- Samia luzonica — 100
- Callosamia angulifera — 100
- Callosamia promethea — 100
- Callosamia securifera — 100
- Hyalophora cecropia — 83
- Hyalophora euryalus — 100
- Hyalophora gloveri — 100
- Rhodinia fugax
- Loepa sikkima — 84
- Antherina suraka — 95
- Ceranchia apollina — 100
- Cricula elaezia
- Opodiphthera eucalypti
- Argema mimosae — 98
- Graellsia isabellae — 100
- Actias luna — 100
- Actias selene — 100
- Actias isis — 100
- Saturnia naessigi
- Copaxa multifenestrata — 100
- Saturnia galbina — 100
- Saturnia anona — 100
- Saturnia caecigena — 100
- Saturnia albofasciata — 79
- Saturnia walterorum — 100
- Saturnia mendocino — 100
- Antheraea godmani — 100
- Antheraea polyphemus
- Antheraea youngi — 100
- Antheraea rosemariae — 99
- Antheraea helferi — 98
- Antheraea yamamai
- Antheraea roylii — 99
- Antheraea lampei — 100
- Antheraea pernyi — 99
- Antheraea larissa — 76
- Antheraea jana — 98
- Antheraea raffrayi — 100
- Antheraea kelimutuensis — 96
- Antheraea paphia — 68
- Antheraea paukstadtorum — 70

No eyespots

Eyespots

Further evidence for possible eyespot radiations