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Proceedings of the Forum Herbulot 2006 Integration of molecular, ecological and morphological data: Recent progress towards the higher classification of the Geometridae (Hobart, 19-20 January 2006)

Axel Hausmann & Peter McQuillan (eds.)

Hausmann, A. & P. McQuillan (eds.) (2006): Proceedings of the Forum Herbulot 2006; Integration of molecular, ecological and morphological data: Recent progress towards the higher classification of the Geometridae (Hobart, 19-20 January 2006). – Spixiana **29/3:** 199-216

The Forum Herbulot 2006 in Hobart, Tasmania was focussed on the establishment of an integrated taxonomical approach in geometridology, including morphological and molecular techniques as well as data from biogeography and ecology. In fourteen lectures and five posters various studies and results on geometrid moths were presented using a wide range of different techniques. Extensive discussions helped to put these studies into a common context, and to plan integrative approaches and cooperations for the future.

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Short Report and Results

Axel Hausmann, Martin Krüger, Peter McQuillan, Manfred Sommerer & Cathy Young

Hausmann, A., Krüger, M., McQuillan, P., Sommerer, M. & C. Young (2006): Short report and results. In Hausmann, A. & McQuillan, P. (ed.): Proceedings of the Forum Herbulot 2006; Integration of molecular, ecological and morphological data: Recent progress towards the higher classification of the Geometridae (Hobart, 19-20 January 2006). – Spixiana **29/3:** 199-200

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1. The chairmen outlined once more the aims of the FORUM HERBULOT (see www.herbulot.de). After a brief inaugural address from Claude Herbulot, Paris (presented *in absentia* by Axel Hausmann), the participants welcomed the research initiative and stressed the need for, and advantages of, the opportunities offered for close scientific cooperation among geometrid experts.

2. The seminar session highlighted promising possibilities for systematic research. The first five talks (session on 'Biosystematics & Phylogeny': S.-W. Choi, J. Viidalepp, E. Õunap, C. Young, P. McQuillan) presented and summarised the actual stage of research concerning the phylogeny of Geometridae on the subfamily and tribal levels as resulting from different types of data sets, such as larval morphology (Viidalepp), adult morphology (all), host-plant relationships and zoogeographical patterns (McQuillan), and molecular analysis (Young, McQuillan, Õunap). The results focussed on Larentiinae (Choi, Viidalepp, McQuillan), but also offered deeper insights into the Geometrinae (Young) and the Sterrhinae (Õunap). Various different molecular data sets, derived from different nDNA and mtDNA genes, suggest a basal position of the Larentiinae within geometrid phylogeny (Õunap, Young). These results led to an extensive discussion of various possible scenarios in the evolution of this family.

In the session on 'Biogeography' distribution patterns were used to analyze refuges of Palaeogenic elements within the southern African geometrid fauna (M. Krüger), and to discuss taxonomy of great variation between island races (D. Stüning). In addition, diversity and phenology patterns in coastal Queensland were presented (P. Mackey).

The third session on 'Informatics and methodology' emphasized the importance of modern IT-based information systems to geometrid workers (African Geometridae: H. Staude; type specimens: A. Hausmann), of a new application of molecular techniques in ecosystem research (Hausmann) and of a new method for the study of egg morphology (Hausmann). Cooperation was agreed upon to collect and exchange digital images of, and information on, type specimens.

Refinement of molecular methods as valuable tools for evolutionary and systematic studies had been postulated by the previous Forum Herbulot 2001 and Forum Herbulot 2003 in order to supplement morphological and ecological data sets. Now, the first results of the four 'molecular' groups currently working on Geometridae, i.e. C. Young / P. McQuillan (Tasmania), E. Õunap / J. Viidalepp / U. Saarma (Estonia), A. Hausmann / S. Erlacher / M. Miller (Germany), T. Tammaru / N. Snäll (Estonia-Finland), offer a promising basis for future research. Closer cooperation in collecting and exchange of DNA samples was agreed upon, such as the coordinated use of techniques and target genes. Working plans were established in order to focus future common research on a better understanding of the basic phylogeny of Geometridae.

A statement of P. Sihvonen (Finland) with a number of theses for improvement of research coordination was distributed and welcomed. A common project could disclose and verify, in an integrated taxonomic approach, the relationships of the geometrids of Tasmania (C. Young / P. McQuillan), Chile (A. Hausmann), and South Africa (M. Krüger) ('southern clades').

Structure of, and access to, the Forum Herbulot webpage (www.herbulot.de) was discussed and open access to the 'scientific tools' emerged as the favoured option. The structure of the site will be changed in the course of 2006. The number of available type images of Geometridae will be restricted, but updated full versions of the type databases will be distributed to the active FH members in 2-year-intervals, at the FH meetings.

3. FORUM HERBULOT 2006 offered a very well organised post-conference tour in the South of the island. This tour and the collecting activities during the meeting brought very good results, and more than 130 of the 310 known Tasmanian geometrids could be recorded. Special tissue samples were collected for DNA analysis and common projects were planned. The results are presented and documented on the homepage (www.herbulot.de).

4. When receiving the sad message that Claude Herbulot passed away at the day of the opening of the Forum Herbulot 2006, the participants expressed their deep respect for the scientific achievements of the grandmaster of geometridology and patron of the Forum.

5. A proposal to have the next FORUM HERBULOT in Munich, Germany, in early 2008 (organisation: A. Hausmann) was discussed and welcomed. Future venues were proposed by the museums in Pretoria (South Africa) and Gainesville (Florida, U.S.A.). These offers were generally much appreciated by the participants.

6. Participants expressed their thanks to the organizers and sponsors of the FORUM HERBULOT 2006.

Hobart, 24.1.2006

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Cladistic analysis of the tribe Xanthorhoini in the Holarctic region (Lepidoptera, Geometridae)

Sei-Woong Choi

Choi, S.-W. (2006): Cladistic analysis of the tribe Xanthorhoini (Lepidoptera: Geometridae) in the Holarctic region. – Spixiana **29/3:** 201-202

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The tribe Xanthorhoini, a tribe of the Larentiinae, is a group of small to middle geometrid moths comprising more than 16 genera over the World. Previous studies indicated that this group is more or less a natural taxon, but the monophyly of the tribe is not clearly defined and this resulted in the ambiguity of the phylogenetic relationships. Two diagnostic characters for the tribe were recognized: a large pair of coremata just distal to the 8th segment in the male abdomen, and the presence of a 'calcar' in male genitalia.

The purpose of the present study is to define the monophyly of the tribe and certain subgroups and to reveal the phylogenetic relationships among genera in the Holarctic region. Fifty-nine morphological characters from head, body, wing and male and female genitalia were analysed. Thirty-eight ingroup taxa were selected – 28 species from the Palearctic, 6 species from the Nearctic and 4 species common in both Palearctic and Nearctic regions. A parsimony software package 'Winclada' (ver. 1.00.08; K. Nixon, 1999) was implemented for finding

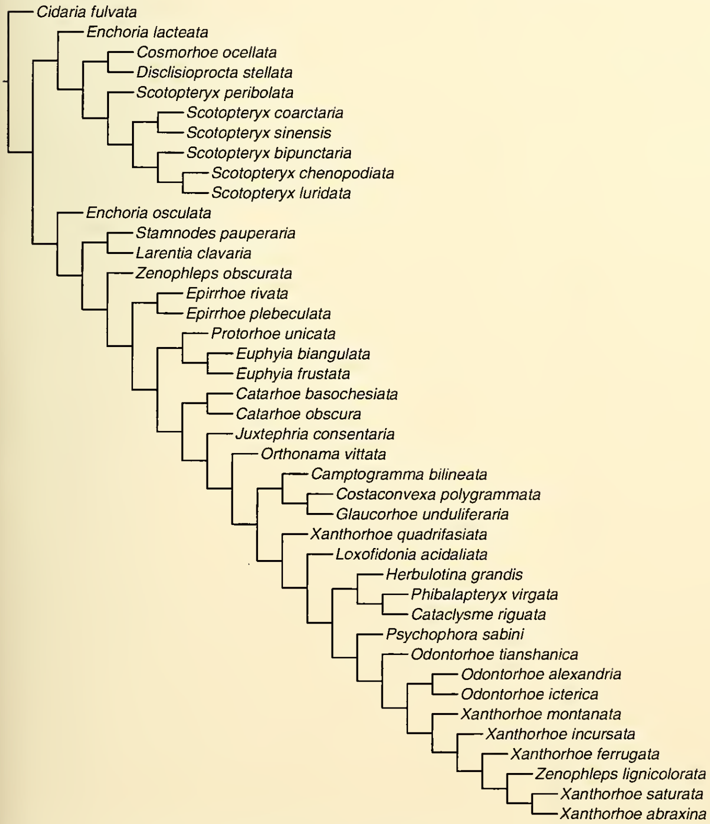

Fig. 1. Most parsimonious cladogram of 38 putative Xanthorhoini species and 3 outgroup taxa (see text).

the most parsimonious cladogram. Three outgroup taxa, *Cidaria fulvata*, *Stamnodes pauperaria*, and *Larentia clavaria* were chosen for rooting the cladograms.

One most parsimonious cladogram was found (L=452, ci=0.21, ri=0.47). However, the resulting cladogram (Fig. 1) is divided into two clades and does not support the monophyly of the Xanthorhoini. In the cladogram, *Scotopteryx*, *Epirrhoe*, and *Euphyia* were monophyletic, while *Enchoria*, *Zenophleps*, *Odontorhoe*, and *Xanthorhoe* were not monophyletic. Overlapping the character 'presence and length of coremata' with the most parsimonious cladogram showed that two states, long and short coremata, occurred independently in different clades and the state, long coremata, occurred three times independently in the cladogram. The overlap of the character 'presence of calcar' with the cladogram showed that the transition from the large, expanded shape of calcar to the digitate and relatively short calcar occurred three times independently. The future study including taxon sampling from the Nearctic region and character analysis from immature stages will reveal the monophyly of the Xanthorhoini and provide refined information on relationships among ingroup taxa.

Cladistic analysis of the subfamily Larentiinae

Jaan Viidalepp

Viidalepp, J. (2006): Cladistic analysis of the subfamily Larentiinae. – Spixiana **29/3:** 202-203

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Altogether about 230 species from 125 mostly Holarctic larentiine genera were studied preliminarily, checking the relations between traditionally recognized tribes. Synapomorphies of main generic clades are coded in the final matrix. Forty-six ingroup taxa and *Idaea aversata* (Linnaeus, 1758) as an outgroup species were included, 129 characters coded as unordered by convenience. The parsimony analysis using the application of Hennig86 yielded one weighted tree of 795 steps length, with consistency index, ci=0,72 and rescaled consistency index, ri=0,89. 17 suprageneric groups are supported by synapomorphic characters.

Synthesis. The monophyly of generic groups is analyzed using cladistic methodology, the sequence of resulting clades is defined by other means.

Larval chaetotaxy is studied fragmentarily. However, the Eudulini, Operophterini, Asthenini, Rheumapterini a.s.o. to the Eupitheciini, Chesiadini and Trichopterygini (cf. Table 1) bear four secondary setae laterally on the prolegs. The Lythriini, Xanthorhoini, Stamnodini, Larentiini and Hydriomenini have eight or more, the Euphyiini and Cidariini five or six secondary setae (according to literature, and original data). It is merely to decide which state of this character is primitive, and which is derived.

Males in three tribes, the Xanthorhoini, Cataclysmini and Euphyiini, have large coremata associated with membranization of last but one and last abdominal segments. In the Eupitheciini, the coremata are attached to the ninth segment and the male eighth sternite is specialized to open the female colliculum during the early phase of copulation (Mikkola 1994). The structures are not homologous, as well as the presence of two pairs of coremata on the male eighth abdominal segment in some Rheumapterini, and their sporadical occurrence in scattered cidariine and asthenine genera, judged by the differences in sclerotization of last abdominal segments.

The labides are present in several clades. The valvae often are ornamented and projecting distally at dorsal or ventral margin, or on both; only in the Chesiadini, the presence of a harpe is more or less constant.

A peculiar, *Eupithecia*-type of ornamentation of female bursa copulatrix with numerous spines having star-shaped or petaloid bases, is observed within Geometridae only in some tribes of Larentiinae and in some species-groups of the sterrhine genus *Idaea*. If the groups with the *Eupithecia*-type of bursa ornamentation are relatively derived, the groups with four secondary setae laterally on the larval prolegs are to be grouped with Eupitheciini, and the larger number of setae on the prolegs results to be less derived. An early analysis of Kuznetsov (1969), based on food-plant associations of tortricids, has shown the leading evolutionary trend from detritophagy to leaf-eating and further to antho- and carpophagy. The Perizomini are anthophagous, the Eupitheciini are antho- and carpophagous.

The same way, labides, branching from base of costa towards juxta and tegumen, more often occur in groups with four secondary setae on the larval prolegs. Labides are not derived in Chesiadini, and Trichopterygini, which have four secondary setae on the larval prolegs. However, a long dorsal projection from the valve costa base is present in both mentioned tribes: a precursor of labides? Labides as dorsal appendages of juxta characterize tribes with relatively more setose larvae.

The deduction of listed morphological peculiarities justifies the presented model of the arrangement and order of tribes within the subfamily Larentiinae, from the Lythriini, Cataclysmini and Xanthorhoini to the Eupitheciini and Trichopterygini (Tab. 1). The results also indicate directions for further study.

How to check the results of cladistic analysis of morphological datasets?

Molecular systematics up to now have provided much smaller data-sets than classical morphology, but it will allow to infer a large quantity of data which, analyzed by means of comparable methods, will conquer with, or complement the results obtained by morphological analyses in future.

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Tab. 1. Estimating the sequence of tribes within the subfamily Larentiinae. Characters: 1, Star-shaped or petaloid signa in female bursa: present or absent; 2, Number of secondary setae on ventral proleg of mature larva; 3, The presence of hairy "labides" in the anellus region of male genital armature; 4, "Labides" arising from dorsal or lateral margin of juxta; 5, "labides" arising from the base of valve costa; 6, The base of valve costa with a long, simple projection bent dorsad

Tribes/characters	1	2	3	4	5	6
Lythriini		13-14				
Cataclysmini		?				
Xanthorhoini		8-10	labides	from juxta		
Larentiini		8-14				
Euphyiini		5-6				
Hydriomenini		12-18	labides	from juxta		
Stamnodini		11-18				
Cidariini		5-6	labides	from juxta		
Eudulini		4				
Operophterini		4	labides	from juxta		
Rheumapterini		4	labides		from valva	
Triphosini		4	labides		from valva	
Phileremini		4	labides		from valva	
Melanthiini	present +/–	4	labides	from juxta	from valva	
Asthenini	present –/+	4-5	labides	from juxta	from valva	simple
Perizomini		?	labides		from valva	
Eupitheciini	present	4	labides		from valva	
Chesiadini	present	4				simple
Trichopterygini	present	4				simple

Preliminary insight into the molecular phylogeny of Sterrhinae

Erki Õunap, Jaan Viidalepp & Urmas Saarma

Õunap, E., J. Viidalepp & U. Saarma (2006): Preliminary insight into the molecular phylogeny of Sterrhinae. – Spixiana **29/3:** 204

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Phylogeny of Geometridae in general and Sterrhinae in particular has significantly improved during the last two decades (e.g. Holloway 1994, 1996, 1997, Abraham et al. 2001, Sihvonen & Kaila 2004, Sihvonen 2005). Most of the recent studies on the phylogeny of Geometridae have been conducted primarily on the basis of morphological characters, and only few studies based on the molecular data are available (Abraham et al. 2001, Snäll et al. in press). As several recent findings are in conflict, further research in this area is highly recommended.

We have focussed on resolving the molecular phylogeny of geometrid subfamily Sterrhinae, which comprises more than 110 genera in at least seven tribes. 1530 bp fragment of the mitochondrial cytochrome oxidase gene subunit I was obtained for 28 sterrhine species belonging to nine genera and five tribes. In addition, the same gene fragment was sequenced from six other geometrids belonging to subfamilies Archiearinae, Geometrinae and Larentiinae, and one drepanid and one noctuid species, which were used as outgroups in phylogenetic analysis. Bayesian phylogenetic analysis of nucleotide data revealed that Sterrhinae is a monophyletic entity, but its exact position in the family Geometridae as well as relationships with other geometrid subfamilies remained unresolved. Two earlier expected evolutionary lineages, "Timandrini lineage" and "Scopulini lineage" within Sterrhinae were approved, as well as the monophyly of most tribes. Since nucleotide variation was too high for MP analysis, amino acid data of COI gene were used for phylogenetic inference instead. MP analysis revealed a phylogenetic tree almost identical to the one obtained by Bayesian analysis, but with poor support in several critical nodes. The results are therefore considered preliminary and final conclusions on the phylogeny of Sterrhinae require additional research.

Evolutionary Relationships of the Emerald Moths of Australia

Catherine J. Young & Peter B. McQuillan

Young, C. J. & P. B. McQuillan (2006): Evolutionary Relationships of the Emerald Moths of Australia. – Spixiana **29/3:** 204-205

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The emerald moths, or Geometrinae, comprise one of the six sub-families of the Geometridae (Lepidoptera) and, worldwide, include around 2300 species in 250 genera. They are well-known and recognised by their beautiful green wing colour and slender bodies. The Australian fauna is estimated at 350 species and is diverse in forests and myrtaceous heathlands, but with some unusual arid zone endemics as well.

Australia, with Africa, is the only continent lacking a modern treatment of the Geometrinae and A. J. Turner last reviewed the fauna in 1922. Australia is the centre of diversity for an interesting sub-set of the emeralds, the so-called 'greys', recogniseable by their mostly dull colouration and robust bodies. This tribe of the Geometrinae, the Pseudoterpnini, may be pivotal in understanding the evolutionary relationships of the sub-family.

This study builds on a recent large systematic study of the Australian Geometridae. We explore relationships suggested by the latter study between the 'greys' and the 'greens' and also the Geometrinae and other geometrid sub-families.

Fragments of the nuclear genes 28S D2 and LW Rhodopsin were used to construct a phylogeny for the sub-family. To date approximately 50 taxa have been sequenced for 28S D2, including 15 outgroup and sister group taxa, and a smaller subset of 22 taxa with 4 outgroups, has been sequenced for the LW Rhodopsin fragment. Both trees were well resolved and many clades well supported. Some of the supported relationships obtained, so far, from this molecular analysis are as follows:

1. The Geometrinae is monophyletic apart from *Anomogenes*, a 'grey' geometrine (Pseudopterpnini), which forms a clade with the Boarmiini using 28S D2 data;
2. The Pseudopterpnini, apart from *Anomogenes*, forms a clade within the Geometrinae;
3. *Oenochlora imperialis*, a large emerald, that occurs in sub-tropical Australia is well supported as having basally derived characters in the Geometrinae;
4. '*Chlorocoma*' *cadmaria* is distinct genetically from *Chlorocoma* s. str. This species is the only *Chlorocoma* that feeds on *Leptospermum*;
5. '*Prasinocyma*' *semicrocea* is genetically and morphologically very close to *Chlorocoma*.
6. The Dysphanini, represented by *Dysphania numana*, forms a distinct sister group to the Geometrinae (LW Rhodopsin data only).

This study is not complete. More taxa are yet to be included in the molecular analysis and relationships will be further explored in the context of morphological structures.

Recent developments in our understanding of the southern Australian Larentiinae

Peter B. McQuillan & Catherine J. Young

McQuillan, P. B. & C. J. Young (2006): Recent developments in our understanding of the southern Australian Larentiinae. – Spixiana **29/3:** 205-206

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There is renewed interest in the Larentiinae since their basal position in the family was inferred from molecular data (Abraham et al. 2001, Young 2004).

Southern Australia, defined as the Bassian biogeographical region, has a moderately diverse fauna of larentiines of perhaps 200 species. Several major tribes (e.g. Xanthorhoini, Eupitheciini, Trichopterygiini) are represented although Australian "Hydriomenini" need further study to clarify their tribal relationships (Schmidt 2001) and enigmatic taxa such as *Chaetolopha*, associated with ferns, currently defy tribal placement (Schmidt 2002).

Larentiine diversity in Australia is greatest in regions of higher rainfall. The Xanthorhoini are strongly concentrated in the moister parts of southern Australia and there is considerable local endemism at higher elevations. The genus *Chrysolarentia* is available for many of the Australian members of this tribe.

There are several genera shared with New Zealand, including *Austrocidaria* (Tasmania), *Epyaxa* and "*Anzarhoe*". The phenotypically variable and multivoltine *E. subidaria* is one the most familiar urban moths in southern Australia, thriving in lawns and gardens on *Plantago* and other weeds.

The Eupitheciini is poorly studied though relatively diverse with a number of undescribed species. Many are associated with the reproductive parts of plants as they are elsewhere in the world. Some are highly vagile, including *Phrissogonus laticostatus*, which is a member of a suite of (often) polyphagous moths which experience breeding peaks is wet years in the semi-arid parts of Australia and then disperse widely to coastal areas and off-shore islands. A few eupitheciines (e.g. *Chloroclystis approximata*) and xanthorhoines (e.g. *Epyaxa* spp.) have adapted to agricultural crops and orchards. Alpine adaptation is apparent in several lineages: *Aponotoreas*, *Melitulias*, "*Hydriomena*" and several xanthorhoine genera.

Foodplant associations remain poorly known. As elsewhere, most xanthorhoines are herb-feeders although *Austrocidaria* on *Coprosma* (as in New Zealand). *Tympanota* on *Podocarpus* is the only larentiine associated with Australian conifers (Dugdale 1980). Sclerophyllous understorey shrubs are important hosts of many "Hydriomenini": *Hibbertia* (Dilleniaceae) supports *Anachloris* (Schmidt 2001) and Fabaceae shrubs support several other taxa. Epacridaceae is eaten by some *Poecilasthena*. It is noteworthy that almost no larentiines feed on *Eucalyptus*, but the reasons for this are unclear. Although Schmidt (2005, 2006a,b) has subjected some tropical taxa to recent review, much remains to be done.

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Filling in the gaps: South-Eastern Mountain Grassland as an important corridor and refuge for Montane Palaeogenic Elements within the southern African geometrid fauna (Lepidoptera, Geometridae)

Martin Krüger

Krüger, M. (2006): Filling in the gaps: South-Eastern Mountain Grassland as an important corridor and refuge for Montane Palaeogenic Elements within the southern African geometrid fauna (Lepidoptera, Geometridae). – Spixiana **29/3:** 206-207

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Revisionary work on various groups of moths, with a focus on Geometridae, since the late 1990's has provided substantial evidence for the existence of a Montane Palaeogenic Element as defined by Stuckenberg (1962) within the southern African geometrid fauna. However, although distribution patterns for several taxa are now well documented for the Western Cape, the Maloti Mountains of Lesotho and mountainous areas of the escarpment further north, virtually no data from suitable high-lying areas that may support this relictual fauna have been available for the vast area between the Western Cape and the foothills of the Malotis, representing a gap of more than 500 km.

A recent sample comprising 141 species of Geometridae collected in the Sneeuberge (approx. 32°10'S 24°55'E), situated in the western part of Eastern Cape Province, South Africa at altitudes between 993 and 1618 m, was analyzed for trends in composition according to altitude and/or vegetation type. (The highest peak in the area reaches 2122 m but areas above 1618 m could not be sampled due to difficulty of access.) Above 1600 m, the area is occupied by a southerly extension of South-Eastern Mountain Grassland (grassland biome), whereas the lower-lying areas fall into the semiarid Eastern Mixed Nama Karoo (Nama Karoo biome), a semiarid veld type ecotonal to grassland.

No trends were observed regarding altitudinal distribution at subfamily level, and representation of Geometrinae, Sterrhinae and Ennominae as a percentage of the species total for southern Africa was similar (9.94 to 12.96 %), although Larentiinae were more strongly represented (34 species or 21.94 % of the total for the subregion). When viewed in isolation, the fauna of South-Eastern Mountain Grassland is characterized by a marked reduction in Geometrinae and Sterrhinae, with a concomitant increase in Larentiinae. Within Ennominae, however, samples from Eastern Mixed Nama Karoo were dominated by Macariini, whereas the diversity of Ennomini, Gnophini and especially Nacophorini increased in South-Eastern Mountain Grassland. Nacophorini have only recently been recorded from southern Africa; the tribe remains unsatisfactorily defined but is probably basal within Ennominae and almost entirely limited in its distribution to the former Gondwanan continents Australia, South America and southern Africa.

As would be expected from its being contiguous to Alti-Mountain Grassland, one of the two dominant high-altitude veld types in Lesotho, in the eastern part of its range, the montane moth community dependent on South-Eastern Mountain Grassland is overall more similar to that of the Maloti range and adjacent montane areas than to that of the Western

Cape. However, a number of species are continuously distributed, suggesting that South-Eastern Mountain Grassland plays an important role as a corridor. Conversely, the comparative isolation of the Sneeuberge was sufficient to allow the development of at least nine local endemics.

The genus *Bracca* Hübner in the Oriental and Australian tropics: Distribution patterns and the phenomenon of strikingly different island-races (Geometridae, Ennominae)

Dieter Stüning

Stüning, D. (2006): The genus *Bracca* Hübner in the Oriental and Australian tropics: Distribution patterns and the phenomenon of strikingly different island-races (Geometridae, Ennominae). – Spixiana **29/3:** 207-208

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Species in the genus *Bracca* Hübner [1820] are distributed in the Oriental and Australian tropics; the geographic range extends from the extreme south of Thailand to tropical Australia. 26 species are recorded for the genus (Parsons et al., 1999), the majority (14 species) inhabit New Guinea and the surrounding islands, 4 species are found in Northern Australia (2 endemic). A further species has been described from Sulawesi recently (Stüning, 2005), but several undescribed species are still known to occurs (Sulawesi, Luzon, Mindanao). A striking feature of the species now included in Bracca is the diversity of wing pattern. Until Holloway (1991) united them in the present genus, they have been scattered over at least fifteen genera. Five of them, *Arycanda* Walker, 1856, *Cosmethis* Hübner [1820], *Duga* Walker [1865], *Panaethia* Guenée [1858] and *Tigridoptera* Herrich-Schäffer, 1855, Holloway (l.c.) proved to be junior subjective synonyms of *Bracca*, the other names were just applied erroneously to certain species, belonging even to different families like Arctiidae and Noctuidae.

Besides the variety of wing pattern on species level, some widespread species show a similar feature on subspecies level: this phenomenon of largely different island races has been found so explicit only in the genus *Bracca*. Four examples are discussed in detail:

B. maculosa Warren: the nominate subspecies, occurring in Sumatra, Borneo and Peninsular Malaysia has black pattern elements on a blue-grey ground colour, its subspecies *radiolata* Warren from Palawan has several dull orange, longitudinal streaks in addition and the black pattern elements are of different shape and arrangement (Fig. 1).

B. exul Herrich-Schäffer: the nominate subspecies, distributed in Java, also has black pattern elements on a blue-grey ground, several dull orange, longitudinal streaks and a broad distal area without any markings on both wings. Its subspecies *actinoides*

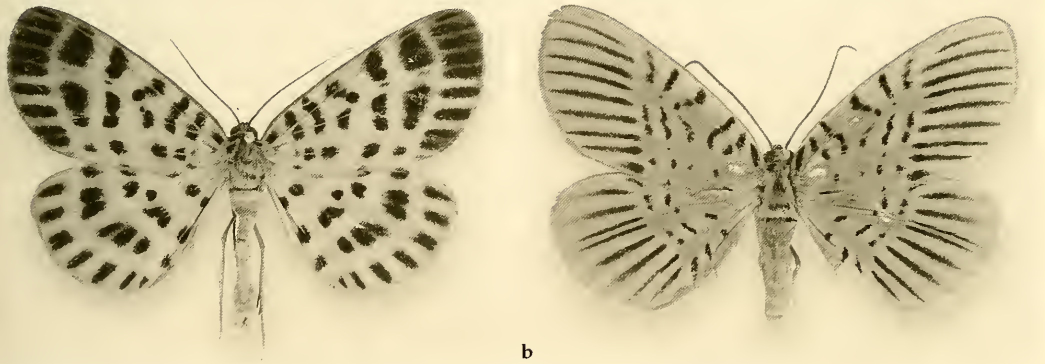

Fig. 1. *Bracca maculosa maculosa* Warren (**a**) and its subspecies *B. m. radiolata* Warren (**b**).

Sommerer & Stüning from Sumatra has this area extensively marked with longitudinal, black stripes and the number of dull orange stripes is reduced.

B. monochrias Meyrick, described from Sangihe Island, and its subspecies *cuneiplena* Swinhoe (Mindanao) and *benguetana* Schultze (Luzon) exhibit comparatively strong differences.

B. georgiata Guenée, with the nominate subspecies, found in Sumatra, Borneo, Peninsular Malaysia and Sulawesi, similar in pattern and coloration to *B. maculosa*, its race *pervasata* Walker from Java also with additional, dull orange streaks. The name *pervasata* is applied to several more or less different island races (Buru, Seram, several Philippine islands) at present which may deserve subspecies-rank as well. In Sulawesi, the nominate *georgiata* seems to occur sympatrically with its race *pervasata*, but studies of the genitalia structures have revealed that the *pervasata*-like form is specifically different. This phenomenon may be explained by subsequent arrival (of *georgiata*) after initial vicariance, as observed also in other groups of moths and butterflies.

The conspicuous pattern of adult *Bracca* moths and their larvae – the latter are strikingly coloured with red, black and white elements – may indicate that they are distasteful or toxic for predators. Consequently, mimicry phenomena are a possible explanation for the development of those strongly different island races, encountered in the genus *Bracca* so explicitely.

Diversity and Phenology of Geometridae in coastal Central Queensland

Peter Mackey

Mackey, P. (2006): Diversity and Phenology of Geometridae in coastal Central Queensland. – Spixiana **29/3:** 208-209

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Light trapping was carried out on 5 nights per week over 7 years at Rockhampton in Central Queensland, circa 40 km inland. Rockhampton lies close to the Tropic of Capricorn in an arid corridor between wetter regions, north to Mackay, and south-east Queensland. The December mean maximum temperature is 31.4 °C and the mean minimum for July is 22.9 °C. The mean number of rain days per year is 92. Good rain events are often associated with cyclones during the wet (hot or summer) season.

Most collecting was carried out during low to average rainfall periods, with 1983 having the highest rainfall and 1982 the lowest. The trap was a Robinson style trap located in the University grounds and was surrounded by Eucalyptus 'scrub' which is regrowth, possibly 40 years old at the time of trapping. The daily catch was identified and recorded using 'Rothampstead Weeks'. Seasons were allocated as follows: Summer, weeks 49-9; Autumn, weeks 9-21; Winter, weeks 22-34; Spring, weeks 35-48.

Trapping yielded 13,324 individuals and 123 species of Geometridae. Between 53 and 84 species were recorded each year. Ennominae accounted for 38 species; Sterrhinae, 23 species; Geometrinae, 35 species; Larentiinae, 10 species; Oenochrominae 17 species. Of the 10 most abundant species 2 were Ennominae, 4 Oenochrominae, 1 Geometrinae and 3 Sterrhinae. A species accumulation curve calculated using EstimateS (Colwell 2005) predicted a total fauna 136 geometrid species. There is a relationship between annual rainfall and the number of geometrid species present each year. However, using Ecosim (Gotelli and Entsminger 2001) to standardise the annual community to 1000 individuals shows there to be few significant differences between years. In wet years more species were collected because many species become more abundant and are therefore more likely to be collected.

Phenology of the species was assessed by pooling the annual counts on a weekly basis and some illustrative examples are presented. *Arhodia lasiocamparia* (Oenochrominae) is present throughout the year. *Oenochroma pallida* (Oenochrominae) is another relatively common species with probably 3 discreet generations in summer, autumn and spring but which is not present in winter (the dry season). *Cleora decisaria* (Ennominae) is present all year, but with ~85 % of occurrences in autumn and spring. *C. acaciaria* (?*illustraria*) also appears to be an autumn and spring species. *Pachyplocia griseata* (Ennominae) appears to be a summer, autumn, winter species. *Psilalcis isombra* (Ennominae) occurs predominantly in winter and spring. *Scopula innocens* (Sterrhinae) is a spring-summer-autumn species. *S. rubraria* is an autumn-winter-spring species with only 1 occurrence in 7 years in late summer. This species was first found in 1985 and then in subsequent years in increasing abundance as was the spring time species *Zermizinga sinuata* (Ennominae). *Mixocera latilineata*

(Geometrinae) is found in late spring but is predominantly a summer and autumn species. *Prasinocyma rhodocosma* (Geometrinae) is a common species which can be found throughout the year, but given its abundance, it has very few occurrences (7 %) in spring. There also seems to be some indication of several distinct generations throughout the year.

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Towards a global online information system Geometridae (GlobInG)

Axel Hausmann & Sven Erlacher

Hausmann, A. & S. Erlacher (2006): GBIF/GlobInG: Towards a global online information system Geometridae (GlobInG). – Spixiana **29/3:** 209-210

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Supported by the GBIF programme of the German Federal Ministry of Education and Research, umbrella project ID: 01 LI 02043, Oct. 2002 – Dec. 2005, lead: Dr. Ch. Häuser, Stuttgart

The GlobInG project aims to improve access to

- collections by providing digital photographs of the ca. 5000 primary type specimens of Geometridae stored in German museums and by inventorying accompanying scientific data (examined primary data)
- relevant literature data with scientific control of taxonomic status and nomenclatural availability; as far as possible with digital facsimile of original description

Until today 1500 primary types are photo-documentarily recorded, including more than 4000 picture data of dorsal and ventral view of the specimens and the labels. To date, about 800 object data sets (including all primary types of the Herbulot collection at the ZSM) are processed in detail and are integrated into the existing database according to the standards of the GART/GloBIS project on the butterflies of the world. For this the respective original descriptions were evaluated and all relevant taxonomic information was included into the database. These data sets contain the citation of the original description, information about the locus typicus, a listing of the type material, and, additionally, the digital photographs of each specimen mentioned above. So far the database contains 2000 image data sets of these completely processed primary types, 300 accompanying literature data sets, 400 image data sets of the facsimile of the original descriptions and 150 images of genitalia slides. The data are accessible through the internet-based SYSTAX database system at Ulm University (SYSTAX; GBIF-D). Sustainability is guaranteed by continuous maintenance through ZSM. Similarly, Geometridae types from other collections in Germany and other countries have been inventoried within the framework of the FORUM HERBULOT initiative, thus great international impact is expected from both of these activities, and Geometridae as model group will get established further for various kinds of research.

At the Forum Herbulot 2006, two strategies are proposed for the future and disposed to discussion, in order to integrate other existing data sets worldwide into the 'Global Information System Geometridae' ('GlobInG-Input-Light' and 'GlobInG-Input-Full').

SYSTAX:
http://www.biologie.uni-ulm.de/systax/daten/index_e.html

SYSTAX: Geometridae (List of Taxa):
http://www.biologie.uni-ulm.de/cgi-bin/portal/portal.pl?tquery=geometridae&cquery=&locquery=&longfrom=&longto=&latfrom=&latto=&labquery=&iquery=&query=&wrapper=0&data=all&typus=yes&sort=tax&displ=s&lang=e&sid=T&expert=yes&acro=ZSM

GBIF-D:
http://www.biologie.uni-ulm.de/cgi-bin/query_all/query_all.pl?lang=d&pr=gbif-e1

GBIF-D: Geometridae:
http://www.biologie.uni-ulm.de/cgi-bin/system/zoosys.pl?pr=gbif-e1&id=1029&stufe=5&typ=ZOO&sid=T&only=no&syno=n&valid=n&lang=d

FORUM HERBULOT:
http://www.herbulot.de

The Lepiafrica Living Books Project

Hermann S. Staude, Andre Coetzer, Bennie Coetzer, Douglas M. Kroon, John Joannou & Martin Krüger

Staude, H. S., A. Coetzer, B. Coetzer, D. M. Kroon, J. Joannou & M. Krüger (2006): The Lepiafrica Living Books Project. – Spixiana **29/3:** 210

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Objective: The objective of this project is to accumulate and to ultimately offer known baseline information and images of as many as possible Afrotropical Lepidoptera in an easy to use structured electronic format to interested parties.

The project team: Members of the project team consist of editors and compilers. Each compiler carries the responsibility of a taxonomically defined part of the project, while editors have specific functions covering the whole project.

Contributors: Contributors are individuals and/or institutions who contribute information or images to the project. There are two categories of contributors. Primary contributors contribute bulk information or images. Secondary contributors contribute bits of information or images on an ad hoc basis. Contributors grant permission to the project to use their data but ownership of data remains with the contributor.

Distribution medium: The LepiAfrica Living Books Project is structured to work in conjunction with the Lepidops© database program already in use by members of The Lepidopterists' Society of Africa. Lepidops© is economical, effective and easy to use.

Duration of the project & publication units: The project team is aware that it is unlikely that the above objective will be met within the foreseeable future and therefore treats this as an ongoing project. Copies of various sections of the project are offered separately and are made available from time to time, when the project team considers a section to be ready for release. Updates will thereafter be made available periodically.

Structure & funding: The LepiAfrica Living Books Project is a Section 21 Company not for gain. The project is currently privately funded by its members. Income derived from the sale of LepiAfrica units will go towards funding the project in the future.

Molecular barcoding and larval gut content analysis in insects (Geometridae, Lepidoptera)

Axel Hausmann, Michael A. Miller & Günter C. Müller

Hausmann, A., M. A. Miller & G. C. Müller (2006): Molecular barcoding and larval gut content analysis in insects (Geometridae, Lepidoptera). – Spixiana **29/3:** 210-211

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On the background of the enormous species numbers in insects, the innovative technique of molecular barcoding will more and more play a major role in entomological research by facilitating identification of all stages, and thus for assessment of biodiversity. It may, however, also gain a certain importance for ecosystem research, and systematics.

In the year of 2005 the ZSM has got offered access to several thousands of neotropical Geometridae larvae collected in 1800 fogging samples of Terry

Erwin (Lucky et al. 2002; Erwin et al. 2006), who monitored the fauna of 200 trees in 9 replicates from 1994-1996 in north-eastern Ecuador. Identity of all the fogged trees, and their neighbours is known. In two pilot studies we could prove, that larvae can be identified to species by their 'barcode sequences' (mtDNA), and that sequencing of gut content is possible too, in order identify the larval plant meal and to prove feeding on the fogged host-tree, rather than on epiphytes or on the neighbouring tree (Miller et al. 2006; Matheson et al. 2006). Identification of the larvae was performed by analysis of the complete sequence of the mitochondrial gene cytochrome c oxidase I (COI) and comparison with sequences of collection specimens. The effectiveness of the 'barcoding' tool for species identification had already been shown in many other studies (cf e.g. Hebert & Mitchell 2006). Gut contents were successfully identified by comparing sequence of a 157 bp long fragment of the chloroplast gene *rbcL* with that of of the pre-identified host-plant and a wide set of other plants of the study area. Plant meals could be detected, when the insects were killed and preserved in Ethanol up to 12 hours after the last feeding (Matheson et al. submitted). For large sets of possible host-plants and for discrimination of closely related plant species, e.g. in tropical countries, additional markers (fragments/genes) may be necessary.

Results from the planned research project will provide, for the first time, comprehensive information on host-plant relationships and host specifity for a large group of phytophagous insects in the neotropical rain forest canopy. With these data the estimations of total species numbers in Geometridae and insects may be extrapolated and refined. Similar projects are planned for geometrid moth larvae in Israel.

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DNA barcoding of Australian Lepidoptera

Paul Hebert & Andrew Mitchell

Hebert, P. & A. Mitchell (2006): DNA barcoding of Australian Lepidoptera. – Spixiana **29/3:** 211-212

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DNA barcodes are short (658 bp) sequences from a standardized region of the mitochondrial gene cytochrome c oxidase I (COI or cox1). Past work has revealed that sequence diversity in this gene region is an effective tool for species identification and discovery. As a result, large-scale DNA barcoding programs are now underway, including efforts to assemble barcodes for all fish and all bird species. We intend to develop a comprehensive barcode library for Australian lepidopterans as a complement to a similar project underway in North America.

We now present results of a pilot study that has barcoded 3500 specimens representing over 800 species collected from sites in north-eastern Queensland and the Central West of New South Wales. All specimens were databased and photographed before DNA was extracted from a single leg. DNA barcodes were subsequently gathered from the specimens and analysed using the Barcode of Life Data System (www.barcodinglife.org) .

Levels of intra-specific variation at COI averaged just 0.2 %, while congeneric species showed sequence divergences that were, on average, 20 times higher. As with studies in other geographic regions, more than 95 % of the species that we examined possessed unique DNA barcodes, allowing their easy identification. Although there was little overlap in species coverage between our two sampling regions, our results suggest that geographic variation in barcode sequences will not be an important complication in species recognition.

We expect to obtain barcode coverage for all common species of Australian Lepidoptera through intensive collecting at a few well-chosen sites. However, we also hope to broaden our network of collaborators so that more extensive sampling coverage is possible. As well, we expect that advances in sequencing technology will soon permit the analysis of museum collections, allowing rapid growth in sequence coverage for uncommon taxa.

Successful extraction of eggs from dry geometrid moth collection specimens

Axel Hausmann, Sławomir Kuczkowski & Marius Junker

Hausmann, A., S. Kuczkowski & M. Junker (2006): Successful extraction of eggs from dry geometrid moth collection specimens. – Spixiana **29/3:** 212

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Though modern techniques (scanning electron microscopy, SEM) offer very promising perspectives for the study of egg morphology, this kind of research has not achieved much attention in geometrid moth systematics, apart from a few publications (cf. Salkeld 1983; Young 2006).

SEM studies of egg morphology are generally thought to require fresh material. Very often, however, living females are unavailable due to rareness or restricted distribution areas in tropical countries, they may be hardly stimulated to egg deposition or their life cycles may not coincide with the study period.

In this contribution we present a way to get access to suitable egg material from dry female collection specimens. The method is based on enzymatic digestion of the abdomens and it is the same, which was recently proposed (Knölke et al. 2005) as a combined procedure for obtaining both DNA for sequence analysis and mazerated tissues for the preparation of the genitalia. Hence, this the new method can provide, simultaneously, three completely different data sets for taxonomic and phylogenetic research.

We analysed the influence of various parameters on the quality of the results, e.g. protease concentration, duration of digestion, humidity, and age of voucher (collection date).

In most cases the results are highly satisfying and provide clear SEM photographs of the chorionic sculpturing, which are very similar to those from fresh egg material of the same species. We got good results also from old collection specimens (up to >100 years). A number of examples was shown in the presentation, detailed results are published in Junker et al. (2006). The method is applied in a research program on Sterrhinae phylogeny, which was shortly presented, too.

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The Australasian genus *Scotocyma* Turner (Lepidoptera, Geometridae, Larentiinae)

Olga Schmidt

Schmidt, O. (2006): The Australasian genus *Scotocyma* Turner (Lepidoptera, Geometridae, Larentiinae). – Spixiana **29/3:** 213

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Larentiinae occur worldwide, are diverse and usually mesophilous, preferring temperate abiotic conditions. The Australasian genus *Scotocyma* is rather atypical for the subfamily because it occurs mainly in the tropics and subtropics. The genus comprises 11 species: *S. albinotata* (Walker), *S. legalis* (Warren), *S. mimula* (Warren), *S. miscix* Prout, *S. manusensis* Prout, *S. scotopepla* Prout, *S. asiatica* Holloway and the recently described species *S. samoensis* Schmidt, *S. rutilimixta* Schmidt, *S. sumatrensis* Schmidt, and *S. longiuncus* Schmidt. The main results of the revision of the genus *Scotocyma* are as follows: (1) keys to species and distribution maps are provided; (2) a phylogenetic analysis is performed to test the monophyly of the genus; (3) the distribution patterns of the species are examined; (4) a biogeographic discussion is included; (5) the tribal position of the genus is clarified and the relationships to closely related genera are discussed.

The following characters are diagnostic for the genus *Scotocyma*. Labial palpus is thick, short, curved, with the terminal segment small, blunt. Antenna is simple in both sexes. The seventh abdominal segment in males bears coremata, consisting of eversible hair tufts in a long, broad pocket bearing a narrow, finger-shaped appendix. A thin, weakly sclerotised ring between the seventh and the eighth segments is present, with a small medial sclerite attached. The ansa of a tympanal organ has a small, simple scoloparium. In the male genitalia uncus is sclerotised, with its base modified; tegumen is usually with short, sclerotised, sometimes serrated, arms; valva is narrowed medially, comb-like structures set on the valval sacculi; vinculum has no distinct saccus; calcar is present, with broad hood-shaped membrane connected to its basis; aedeagus is thick, short, with its coecum oblique-rounded. In the female genitalia antrum is large, sclerotised, somewhat funnel-shaped, longitudinally folded; ductus bursae is shortened, membranous; corpus bursae has patches of sclerotisation on its dorsal side, with a large diverticulum; signum is large, usually a patch of inwardly directed spicules on ventral side.

The new phylogenetic analysis confirmed the monophyly of the genus *Scotocyma*. According to the analysis, the species *(S. albinotata + S. legalis)* + *S. samoensis* are grouped in one clade. The defining characters are: teeth on lateral tegminal arms strongly developed; folds in antrum rather broad, two or three on each side. The second clade comprises the species *S. asiatica* + *S. sumatrensis*. The characters defining the second clade are: brownish median band in the forewing underneath with medial projection outwards narrowly rounded; medial spot at the termen in forewing underneath large, higher than wide, marginally speckled with darker scales. The third clade is not resolved and comprises the species *S. rutilimixta* + *S. scotopepla* + *S. longiuncus*. The defining character is: teeth on lateral tegminal arms in males moderately developed. The sister-clade is *(S. manusensis + S. mimula)*. The defining characters are: medial spot at the termen in the forewing underneath medium-sized, square, with distinct edges, signum in the corpus bursae of females shifted to the side.

The Indo-Australian genus *Visiana* Swinhoe and the identity of the supraspecific taxa of *V. sordidata* (Lepidoptera, Geometridae, Larentiinae)

Olga Schmidt

Schmidt, O. (2006): The Indo-Australian genus *Visiana* Swinhoe and the identity of the supraspecific taxa of *V. sordidata* (Lepidoptera, Geometridae, Larentiinae). – Spixiana **29/3:** 214

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The genus *Visiana* Swinhoe belongs to the geometrid moth subfamily Larentiinae which occurs worldwide. The genus contains medium- to relatively large-sized moths of which the dark-brownish colouration resembles that of several other genera (e.g. *Disclisioprocta* Wallengren from South Africa, Madeira (Portugal) and South America, "*Horisme*" from Papua New Guinea, and *Scotocyma* Turner from the Australasian region). *Visiana* is widely distributed within the Indo-Australian region, from north-eastern Himalaya through the Indonesia and Malaysia to Papua New Guinea and eastern Australia.

According to the present knowledge, the genus *Visiana* currently comprises the following species: *V. brujata* (Guenée) from eastern Australia, *V. excentrata* (Guenée) from the south-east of Australia, *V. hyperctenista* (Prout) from Bismarck Archipelago, *V. sordidata* (Moore) from the Indo-Australian region, and *V. vinosa* (Warren) from Papua New Guinea. *Visiana sordidata* comprises the following subspecies: *V. s. inimica* (Prout), *V. s. robinsoni* (Prout), *V. s. tamborica* (Prout) (Scoble, 1999). The species of the genus are difficult to tell apart using the characters of the wing colouration and pattern. The information about genitalic characters which would help distinguishing the species was still mostly lacking. Examination of phylogenetic relationships of *Visiana* and related larentiine genera suggested *Visiana* was not monophyletic.

The current studies of the external characters and the genitalia revealed that all supraspecific taxa within the species *V. sordidata* should be regarded as distinct species, *V. robinsoni*, *V. inimica*, and *V. tamborica*. The main distinguishing characters are: the shape and length of the uncus, saccus, lateral papillae of juxta, and the aedeagus in the male genitalia and the shape of the ductus and corpus bursae, and of signum in the female genitalia. Furthermore, the specimens from Borneo (Malaysia) are to be assigned to a new species, *V. hollowayi*.
The species of the genus *Visiana* occur in the forest zone. All known specimens were attracted to light at night. All attempts to collect the Australian *Visiana* s.str. species during the day time failed which suggests that the species of the genus are nocturnal.

The present study also revealed that *Visiana* species feed on species of the plant genus *Urtica* (Urticaceae) that is very common around the globe in the Holarctic region and occurs in the Indo-Australian region and in South Africa. This is the first record of feeding on the species of the plant family Urticaceae for the Australian larentiine moths. The biology and larvae of the *Visiana* species are awaiting description.

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A morphological approach to the Ennominae phylogeny (Lepidoptera, Geometridae)

Eugene A. Beljaev

Beljaev, E. A. (2006): A morphological approach to the Ennominae phylogeny (Lepidoptera, Geometridae). – Spixiana **29/3**: 215-216

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The Ennominae is the largest and, morphologically, most diversified subfamily in the Geometridae and the tribal composition and phylogeny of the subfamily are still far from being resolved. However modern molecular-phylogenetic investigations of the subfamily promise substantial breakthroughs in the construction of a meaningful phylogeny of the Ennominae (as well as of the Geometridae and other organisms). Nevertheless, in spite of the present predominant position of molecular-phylogenetic research in modern systematics, morphological analysis of organisms continues to be indispensable for the comprehension of taxonomy and evolution. Also, morphological analysis is irreplaceable for the definition of monophyletic groups, and even for the representational selection of specimens (samples) for molecular-phylogenetic analysis. A modern morphological tribal system and phylogeny for the Ennominae were proposed independently by Holloway (1994, 1997) and by Beljaev (1994). Here I propose a new hypothesis on basal branching in the Geometridae and Ennominae and tribal composition of the subfamily arising from the cladogram illustrated in Fig. 1.

In this analysis I applied direct weighting of characters based on comparative and functional-morphological analyses using outgroup comparison for the polarization of morphoclines. Structures of the anellar area of the male genitalia are mainly utilised in this investigation because they demon-

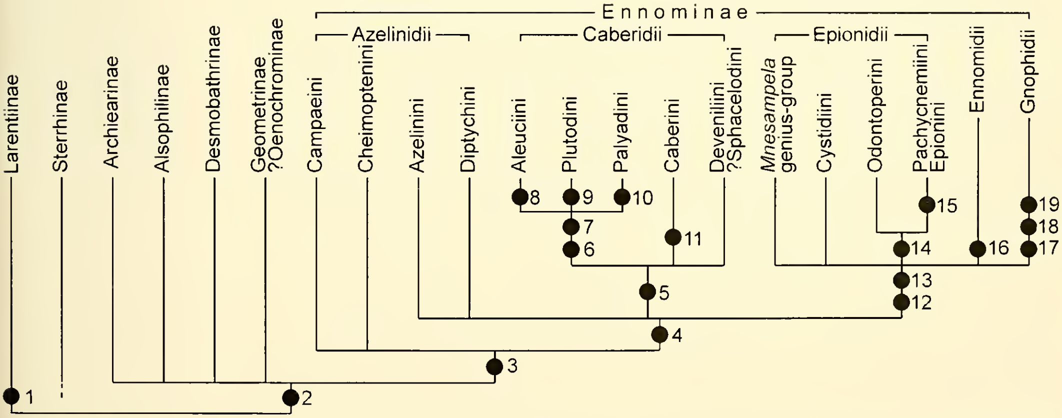

Fig. 1. Phylogenetic cladogram of basally derived branches in the Geometridae and Ennominae based on selected apomorpies. Apomorphies: **1,** labides which trend to medial shifting dorsad of aedeagus; **2,** labides removed from the bases of the valvae ventro-medially and which have approximately sagittal orientation of their bases; **3,** vein M_2 on hindwing lacking; **4,** signum deeply invaginated, toothed, sclerotized, hollow (mushroom-like); **5,** labides with bases orientated in frontal plane; **6,** cristae strongly developed; **7,** juxta broad, laterally almost reach base of transtilla; **8,** cristae integrated into juxta; **9,** sacculi with pointed and curved distal process; **10,** socii enlarged; **11,** sacculi articulated to each other directly, often connected to each other with traverse sclerotized bar; juxta placed posterior of sacculi; **12,** transtilla shaped as flat sclerite smoothly proceeds into costa of valva and possessing ventral process; **13,** muscle m_4 attached to transtilla mediad of $m2$, $m2$ and $m4$ crossed; **14,** labides flattening, horn-like, intromitted into ductus bursae at the copulation; **15,** labides with dorsal end of basis far from base of transtilla; **16,** labides shaped as narrow sclerotized 'bridges' between juxta and base of transtilla; **17,** labides absent; **18,** waist between tegument and vinculum absent; **19,** muscle $m4$ arising from tegumen.

strate high diversity in combination with nonrandom distribution of types in taxa. Among them, labides had been explored as the most phylogenetically informative anellar structure in Geometridae (i.e. applicable for the supporting of many basal nodes in the family). My understanding of the term 'labides' needs to be commented. Because of their high morphological diversity these structures have been named differently in literature (here, only the author is mentioned, who introduced the term, in the historical order): F. Pierce: labides, anellus lobes, furca (part); Th. Albers: Führungsarme; F. Rindge: lateral fold, postero-lateral structures, processes of the anellus, postero-lateral pair of sclerotized areas in manica, lateral ridges; R. Orfila & S. Schajovskoy: canaliculi (incorrect treatment of Pierce's term); J. Holloway: arms of juxta, haired processes from base of valva; W. McGuffin: lobes of juxta; J. Viidalepp: dorsal processes/appendages of juxta; P. McQuillan: lateral/dorsal processes of juxta; A. Hausmann: posterior processes of juxta; L. Pitkin: anellar sclerites. Based on the classic criteria of homology I consider all these structures as homologous and propose the term 'labides' (Pierce 1914) as the senior and most convenient name for them.

The transtilla also provides important apomorphies for basal branching in the Ennominae, but the phylogenetic significance of the transtilla characters can only be realised relative to the attached muscles: dorsal abductor and adductor valvae (*m2* and *m4*, following Kuznetzov & Stekolnikov).

A tentative tribal system of the Ennominae corresponding to the proposed phylogenetic cladogram is represented on the Forum Herbulot website (http://www.zsm.mwn.de/external/herbulot/famgroup2.htm; http://www.herbulot.de).

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