

Supporting Information

Craft et al. 10.1073/pnas.0913084107

SI Materials and Methods

Study Area, Caterpillars, and Host Plants. We outlined an approximately equidistant grid of eight sites with an average distance of 160 km between neighboring sites and with pairwise distances ranging from 59 to 513 km. Sites were located at <500 m above sea level in vegetation classified as mixed evergreen hill forest (1). The area has a human population of <10 people per km² and has <1 km of roads per 100 km². The climate at these sites is humid, with a mean annual rainfall of 3,000–4,000 mm, a moderate dry season from July to September (monthly mean rainfall, <100 mm), and a mean monthly temperature of ~26 °C.

The study area is situated in a complex tectonic region at the convergence of two major plates, the Australian and Pacific, where ancient accretion of volcanic arc terranes to the central cordillera border the Sepik and Ramu river basins. Most of the study area was submerged from the Early Miocene until the Pliocene (2). Oceanic incursions across the northern lowlands during periods of elevated sea level continued until very recently, including a sea that stretched ~100 km inland and separated the Elem and Wamangu sites only 6,000 years ago (3). Climate and vegetation were very different during the last major glacial epoch than today, with a mosaic of open and closed-canopy forest covering the study area during a cooler and drier period about 17,000 years ago (4).

Caterpillars represent the most species-rich group of leaf-chewing insects in the study area (5). They were sampled from selected host plants during a single 3-month survey at each site between December 2001 and October 2005. Widespread and common caterpillar species, with numerous adults reared at each site, were the focus of intensive DNA barcoding, with approximately 10 individuals sequenced per site (Table S1). Herbivore diets ranged from monophagy to polyphagy (Table S1). Selected host plants are well represented in all stages of lowland rain forest succession (6) and together total at least 475 species in New Guinea (7). At each site, caterpillars were collected from 11 or 12 locally common plant species (4 or 5 *Ficus*, 3–5 *Macaranga*, 1 or 2 *Psychotria*, and 1 or 2 *Syzygium* species per site), except at Ohu and nearby Madang, where additional plant species were sampled as described previously (5). These species, composed of shrubs and small trees, represented <5% of the total basal area of the local woody vegetation (8). Geographic distributions of focal plant species ranged from widespread to narrowly endemic within the study area.

Phylogenetic Analysis. DNA barcodes were trimmed to 575 bp, the maximum contiguous sequence available for all taxa. A distribution of phylogenetic trees was obtained using MrBayes 3.1 (9, 10) to test monophyly of each species and to examine the extent of intraspecific variation. Modeltest 3.0 (11) was used to identify the most suitable model of nucleotide evolution. A model of molecular evolution, GTR + I + G, was selected on the basis of the Aikake information criterion and likelihood ratio tests. Two parallel analyses with six chains each were run for 5 × 10⁶ generations. Trees were sampled every 1,000 generations. The first 4 × 10⁶ generations were discarded as burn-in. The log-likelihood scores of sample points against generation time was plotted using Tracer 1.5 (<http://tree.bio.ed.ac.uk/software/tracer/>), to ensure that stationarity was achieved after the first 4 × 10⁶ generations by checking whether the log-likelihood values of the sample points reached stable equilibrium. A majority-rule consensus tree with average branch lengths was calculated with the “sumt” option of MrBayes, and posterior probabilities were obtained for each clade from the remaining 2,000 trees.

Phylogenetic analysis of mitochondrial COI haplotypes confirmed the reciprocal monophyly of species and species complexes (Fig. S1), but caution should be exercised when evaluating phylogenetic relationships among species in community samples because of incomplete taxon sampling. Although the monophyly of Tortricidae and Thyrididae was recovered, a number of erroneous groupings were evident; for example, Geometridae were nested within Crambidae, and Noctuidae were polyphyletic. Moreover, Gelechiidae relationships were unresolved, and the monophyly of three families represented by only single species could not be assessed. Evolutionary interpretation of phylogenetic trends in dietary specialization and geographic distribution must be based not on Fig. S1, but rather on the best available estimate of phylogeny, which necessarily is a synthesis of independent studies and expert knowledge for particular groups.

Median joining networks for each species were drawn in Network Publisher (Fluxus Technology) and Adobe Illustrator CS4. We calculated K2P pairwise distances among haplotypes in PAUP* (12). Divergence ≥2% is thought to reflect a degree of reproductive isolation in Lepidoptera (13, 14); however, because interspecific and intraspecific divergences of COI vary taxonomically (15, 16), we did not automatically conclude that lineages found to be ≥2% divergent are necessarily cryptic species without the presence of other corroborating evidence (e.g., morphology, diet). Pending thorough taxonomic reevaluation, we refer to cryptic lineages within species or species complexes as those separated by ≥2% divergence.

Population genetic analyses were performed using Arlequin version 3.11 (17) with the exception of haplotype number, which was determined using DnaSP version 4 (18). Nucleotide diversity (the average number of nucleotide differences among haplotypes) was calculated to estimate haplotype polymorphism within species.

Analysis of host-associated genetic differentiation involved the identification of host clades through molecular phylogenetic analyses of *ndhF* sequences for *Macaranga*, *rbcl* sequences for *Psychotria*, and ITS sequences for *Syzygium* and *Ficus*, as reported previously (19). Defining a host clade level in the Lepidoptera AMOVA is analogous to grouping sites within geographic regions; for example, in the case of the *Syzygium* specialist *Zeugma recusataria*, two host clades were defined in the AMOVA as *Syzygium malaccense* Merrill & Perry plus *Syzygium* sp. “SRB” and *Syzygium longipes* (Warb.) Merrill & Perry plus *Syzygium* cf. “stipulare.”

Moth Taxonomy. The taxonomic methods followed were as described by Miller et al. (20) and Holloway et al. (21), with initial sorting to morphospecies conducted by parataxonomists in the field. Species concepts following Miller (22) were based on male genitalia, and since 2003, on DNA barcodes as well. Comparisons of mitochondrial COI DNA sequence divergence with morphology were used to identify polymorphic species including cases of sexual dimorphism (13, 23). Lepidoptera species are illustrated at <http://www.entu.cas.cz/png/caterpillars>. Most species were identified with reference to type specimens in the Natural History Museum (London) and elsewhere. Pinned voucher specimens for DNA sequences are deposited in the Smithsonian Institution, Washington, DC, and additional voucher specimens of the same species are deposited in National Agriculture Research Institute, Port Moresby, Papua New Guinea. Notes on the a posteriori morphological evaluation of species complexes in light of mitochondrial evidence for cryptic diversity are included here to facilitate future taxonomic revision. Of the

four species complexes including cryptic taxa in need of description, *Arctornis* and *Meekiaria* were recognized in our earlier work, whereas *Jodis* and *Dichomeris* were discovered through the population genetic analysis described herein. We expect only a minimal impact of splitting these complexes on our previous ecological findings. Lepidoptera from Papua New Guinea, through Novotny et al. (8) were based on extensive use of genitalic morphology (22) and, since 2003, on DNA barcoding as well (23), to refine taxonomic species concepts.

Choreutidae. *Choreutis* cf. *anthorma* (Meyrick) is near but not *Choreutis anthorma*, as illustrated by Diakonoff (24) and Clarke (25).

Crambidae. “*Coelorhycidia*” *nitidalis* (Hampson) was matched to the type specimen, but the species does not belong in the genus *Coelorhycidia* and should be reassigned.

The *Meekiaria* species complex includes several species related to *M. purpurea* that have yet to be described. *M. purpurea* (Hampson) was recently matched to the type specimen by dissection of genitalia. This species was misplaced in the genus *Coelorhycidia* in earlier publications (19). This is a new generic combination with *Meekiaria* Munroe (26).

Glyphodes margaritaria (Clerck) is a widespread species reviewed by Sutrisno et al. (27).

Talanga deliciosa (Butler) is a widespread species placed in the genus *Agrioglypta* by Nielsen et al. (28), but because of problems in definition of *Agrioglypta* (27, 29), we retain it in *Talanga*.

Talanga excelsalis (Walker) is a widespread species (29). Placed in the genus *Agrioglypta* by Nielsen et al. (28), we retain it in *Talanga* due to problems with the definition of *Agrioglypta* (27, 29).

Talanga sexpunctalis is considered a widespread species (30) but appears to be a complex of species, including several in New Guinea. It remains unclear whether any of the New Guinea specimens are conspecific with *T. sexpunctalis* sensu stricto as described from the Andaman Islands. A specimen of *T. sexpunctalis* from Sulawesi (GenBank accession no. AB158250) also may represent a new species in the complex (27, 29).

Gelechiidae. *Dichomeris ochreoviridella* represents a species complex. The traditional concept of *D. ochreoviridella* (24, 30) is clearly two species according to male genitalia and mitochondrial DNA sequence divergence. The Australian *D. euchroa* Lower has sometimes been placed as a synonym (28) but appears to be a distinct species based on male genitalia. New Guinea specimens are placed in *Dichomeris* following Hodges (31).

Dichomeris sp. [XXXX068] and *Dichomeris* sp. [XXXX120] are undescribed species near *Dichomeris resignata* Meyrick, as illustrated by Clarke (25).

Geometridae. “*Jodis*” *albifusa*, new combination, is a complex of at least three species in New Guinea and at least three more in

Australia according to mitochondrial DNA sequence divergence. These species have been placed in *Thalassodes*, *Gelasma*, and *Maxates*, but genitalia point to a closer relationship with *Jodis* and *Berta* (32). One of the New Guinea species in particular has been confirmed as *albifusa* through comparison with the genitalia of the male type. After Holloway (32), we refer to the species complex as “*Jodis*” *albifusa* until the generic classification can be reviewed.

Zeugma recusataria Walker is a widespread species (33).

Noctuidae. *Asota carica* (Fabricius) and *A. plana* (Walker) are widespread species (34).

Lycaenidae. *Philiris helena* (Snellen) and *P. moira* (Grose-Smith) are species endemic to New Guinea (35).

Lymantriidae. *Arctornis intacta* complex is widespread in New Guinea and includes at least four morphospecies closely allied to, but not conspecific with, *A. intacta* (Walker) based on examination of the holotype at the University of Oxford Museum. This is a new generic combination in *Arctornis* (36).

Pyralidae. *Paraphomia disjuncta* Whalley appears to be a species endemic to New Guinea (37).

Unadophanes trissomita (Turner) is a widespread species identified by Horak based on her knowledge of the Australian fauna.

Thyrididae. *Addaea pusilla* (Butler) is a widespread species (28, 38).

Mellea nitida (Pagenstecher) is a new generic combination necessitated by the resurrection of *Mellea* (28). *M. ordinaria* (Warren) is considered a widespread species complex with a highly variable in wing pattern (39), but male genitalia do not show distinguishing characteristics among members of the complex. Thus, which of the New Guinea specimens are conspecific with the *ordinaria* type specimen is not clear, and the name is applied provisionally. *Mellea* sp. [THYR012] is a segregate of the *M. ordinaria* complex based on mitochondrial DNA sequence divergence.

Rhodoneura aurata (Butler) is a widespread species (28).

Tortricidae. *Adoxophyes thoracica* Diakonoff was identified based on male genitalia of the lectotype. Novotny et al. (40) identified the species as matching Diakonoff's illustration of female *A. nebrodes*, but we have confirmed that Diakonoff (41) misidentified the illustrated specimen.

Adoxophyes sp. nr. *orana* is evidently an undescribed species in the *A. orana* complex distinct from *A. orana* and *A. honmai* according to genitalia and mitochondrial DNA sequence divergence (42).

Dudua new species near *aprobola* (Meyrick) is quite similar to the widespread and polyphagous *D. aprobola* (30) but differs consistently by a clear white forewing mark.

Ophiorrhabda deceptor (Diakonoff) is a widespread species (43).

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Table S1. New Guinea lowland rainforest Lepidoptera included in analyses of geographic and host-associated population genetic differentiation

Species	Family	Individuals reared	Individuals sequenced	Haplotypes	Sites	Host species	Host range
<i>Addaea pusilla</i> (Butler)	Thyrididae	910	61	9	8	8	<i>Macaranga</i>
<i>Adoxophyes</i> sp. nr. <i>orana</i> (Fischer von Roeslerstamm) [TORT94, TORT066]	Tortricidae	75	36	6	5	8	Generalist
<i>Adoxophyes thoracica</i> Diakonoff	Tortricidae	37	37	9	6	12	Generalist
<i>Arctornis intacta</i> Walker complex	Lymantriidae	203	53	11	7	7	Generalist
<i>Asota carica</i> (F.)	Noctuidae	301	48	2	5	2	<i>Ficus</i>
<i>Asota plana</i> Walker	Noctuidae	150	40	1	5	2	<i>Ficus</i>
<i>Choreutis</i> sp. nr. <i>anthorma</i> (Meyrick) [TORT005]	Choreutidae	736	47	25	7	7	<i>Ficus</i>
" <i>Coelorhycidia</i> " <i>nitidalis</i> Hampson	Crambidae	324	43	3	6	3	<i>Psychotria</i>
<i>Dichomeris ochreoviridella</i> (Pagenstecher) complex	Gelechiidae	1,069	60	22	8	8	<i>Macaranga</i>
<i>Dichomeris</i> sp. [XXXX068]	Gelechiidae	907	66	10	8	5	<i>Macaranga</i>
<i>Dichomeris</i> sp. [XXXX120]	Gelechiidae	77	37	8	6	9	<i>Macaranga</i>
<i>Dudua</i> sp. nov. nr. <i>aprobola</i> (Meyrick) [TORT143]	Tortricidae	160	30	7	5	2	<i>Syzygium</i>
<i>Glyphodes margaritaria</i> (Cramer)	Crambidae	225	50	2	8	7	<i>Ficus</i>
<i>Meekiaria purpurea</i> Hampson	Crambidae	1,178	41	12	7	4	<i>Psychotria</i>
<i>Meekiaria</i> sp. complex [CRAM041]	Crambidae	1,048	80	16	7	4	<i>Psychotria</i>
<i>Mellea nitida</i> (Pagenstecher)	Thyrididae	357	47	12	8	9	<i>Macaranga</i>
<i>Mellea ordinaria</i> (Warren)	Thyrididae	1,283	39	11	8	5	<i>Macaranga</i>
<i>Mellea</i> sp. [THYR012]	Thyrididae	101	35	12	5	2	<i>Macaranga</i>
<i>Ophiorrhabda deceptor</i> Diakonoff	Tortricidae	267	35	16	7	4	<i>Syzygium</i>
<i>Paraphomia disjuncta</i> Whalley	Noctuidae	394	39	19	6	1	<i>M. aleuritoides</i>
<i>Philiris helena</i> (Snellen)	Lycaenidae	189	41	20	6	6	<i>Macaranga</i>
<i>Philiris moira</i> Grose-Smith	Lycaenidae	85	29	5	4	6	<i>Ficus</i>
<i>Rhodoneura aurata</i> (Butler)	Thyrididae	484	47	19	7	3	<i>Macaranga</i>
<i>Talanga deliciosa</i> (Butler)	Crambidae	290	45	11	6	6	<i>Ficus</i>
<i>Talanga excelsalis</i> (Walker)	Crambidae	1,275	78	9	8	3	<i>Ficus</i>
<i>Talanga sexpunctalis</i> (Moore) complex	Crambidae	543	70	16	8	5	<i>Ficus</i>
" <i>Jodis</i> "(s.l.) <i>albifusa</i> (Warren) complex	Geometridae	247	41	14	6	3	Generalist
<i>Unadophanes trissomita</i> (Turner)	Pyralidae	482	37	15	6	6	<i>Macaranga</i>
<i>Zeugma recusataria</i> (Walker)	Geometridae	550	47	5	6	4	<i>Syzygium</i>

Species codes from Novotny et al. (8) are reported for new taxa and species complexes.

Table S2. AMOVA for geographic and host-associated population genetic structure in New Guinea lowland rainforest Lepidoptera

Species	Geography				Host association				
	% within sites	% among sites	Φ_{ST}	% significant F_{ST}	% within species	% among species	% among clades	Φ_{ST}	% significant F_{ST}
<i>Addaea pusilla</i>	96.95	3.05	0.031	3.6	56.22	36.12	7.66	0.438***	39.9
<i>Adoxophyes</i> sp. nr. <i>orana</i> [TORT94, TORT066]	77.75	22.25	0.222**	33.3	100.17	-0.17 [†]	NA	-0.02	0
<i>Adoxophyes thoracica</i>	58.26	41.74	0.417***	40	73.47	28.82	-2.29	0.265*	1.5
<i>Arctornis intacta</i> complex	73.05	26.95	0.269***	53.3	88.25	11.75	NA	0.117*	9.5
<i>Asota carica</i>	100.57	-0.57 [†]	-0.006	0	103.08	-3.08 [†]	NA	-0.031	0
<i>Choreutis</i> sp. nr. <i>anthorma</i> [TORT005]	96.59	3.41	0.034*	4.8	95.23	9	-4.23	0.048*	4.8
" <i>Coelorrhycidia</i> " <i>nitidalis</i>	13.01	86.99	0.870***	60	59.56	40.44	NA	0.404***	33.3
<i>Dichomeris ochreoviridella</i> complex	77.55	22.45	0.224***	60.7	87.77	13.79	-1.56	0.122***	35.7
<i>Dichomeris</i> sp. [XXXX068]	43.66	56.34	0.563**	64.3	79.49	29.67	-9.16	0.205***	40
<i>Dichomeris</i> sp. [XXXX120]	100.96	-0.96 [†]	-0.010	0	106.6	-8.33	1.73	-0.066	0
<i>Dudua</i> sp. nov. nr. <i>aprobola</i> [TORT143]	68.72	31.28	0.313**	20	NA	NA	NA	NA	NA
<i>Glyphodes margaritaria</i>	94.51	5.49	0.055	0	112.07	-12.07 [†]	NA	-0.121	0
<i>Meekiaria purpurea</i>	71.57	28.43	0.284***	47.6	90.08	9.92	NA	0.099**	16.7
<i>Meekiaria</i> sp. complex [CRAM041]	97.57	2.43	0.024	0	63.46	6.19	30.35	0.365**	33.3
<i>Mellea nitida</i>	89.69	10.31	0.103*	14.3	87.95	12.05	NA	0.120*	8.3
<i>Mellea ordinaria</i>	75.86	24.14	0.241***	33.3	71.48	28.52	NA	0.285***	20
<i>Mellea</i> sp. [THYR012]	49.13	50.87	0.509***	90	NA	NA	NA	NA	NA
<i>Ophiorrhabda deceptor</i>	87.06	12.94	0.129**	20	95.72	4.28	NA	0.043	33.3
<i>Paraphomia disjuncta</i>	56.12	43.88	0.439***	60	NA	NA	NA	NA	NA
<i>Philiris helena</i>	87.89	12.11	0.121***	50	100.15	-0.15 [†]	NA	-0.002	0
<i>Philiris moira</i>	25.58	74.42	0.744***	66.7	81.18	18.82	NA	0.188	0
<i>Rhodoneura aurata</i>	61.89	38.11	0.381***	81	84.92	15.08	NA	0.151***	33.3
<i>Talanga deliciosa</i>	80.34	19.66	0.197***	70	69.39	25.09	5.52	0.306***	53.3
<i>Talanga excelsalis</i>	92.88	7.12	0.071	7.1	114.46	-14.46 [†]	NA	-0.145	0
<i>Talanga sexpunctalis</i> complex	98.45	1.55	0.016	10.7	99.38	0.62	NA	0.006	0
" <i>Jodis</i> " (s.l.) <i>albifusa</i> complex	68.85	31.15	0.311***	80	90.77	9.23	NA	0.092**	66.7
<i>Unadophanes trissomita</i>	85.59	14.41	0.144**	20	93.03	6.97	NA	0.070	6.7
<i>Zeugma recusataria</i>	105.1	-5.1 [†]	-0.051	0	70.28	29.72	NA	0.297**	50

NA, not applicable.

Significance: * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.

[†]Negative AMOVA covariance estimates may arise when components are approximately 0.

Table S3. Qualitative descriptions of geographic and host-associated population genetic structure in New Guinea lowland rainforest Lepidoptera based on haplotype network analysis

Species	Geography	Host association
<i>Addaea pusilla</i>	Two cryptic lineages, no structure	Two lineages with host-associated structure
<i>Adoxophyes</i> sp. nr. <i>orana</i> [TORT94, TORT066]	No structure	No structure
<i>Adoxophyes thoracica</i>	East-west structure	No structure
<i>Arctornis intacta</i> complex	Five cryptic lineages, some geographic structure	No structure
<i>Asota carica</i>	No structure	No structure
<i>Choreutis</i> sp. nr. <i>anthorma</i> [TORT005]	No structure, but extreme haplotype diversity	No structure
" <i>Coelorhycidia</i> " <i>nitidalis</i>	East-west structure, low diversity	Some host-associated structure
<i>Dichomeris ochreoviridella</i> complex	Two of five cryptic lineages with geographic structure	Four lineages with host-associated structure
<i>Dichomeris</i> sp. [XXXX068]	Two of three cryptic lineages with geographic structure	Two lineages with host-associated structure
<i>Dichomeris</i> sp. [XXXX120]	No structure	No structure
<i>Dudua</i> sp. nov. nr. <i>aprobola</i> [TORT143]	No structure	No structure
<i>Glyphodes margaritaria</i>	No structure	No structure
<i>Meekiaria purpurea</i>	Three cryptic lineages; east-west structure	One monophagous cryptic lineage
<i>Meekiaria</i> sp. complex [CRAM041]	Six cryptic lineages; endemic lineage in Utai	Two lineages with host-associated structure
<i>Mellea nitida</i>	No structure	No structure
<i>Mellea ordinaria</i>	Three cryptic lineages; east-west structure	Host-associated structure, but not partitioned among cryptic lineages
<i>Mellea</i> sp. [THYR012]	Private haplotypes	No structure
<i>Ophiorrhabda deceptor</i>	No structure	No structure
<i>Paraphomia disjuncta</i>	Three cryptic lineages, all haplotypes geographically structured	No structure
<i>Philiris helena</i>	Private haplotypes	No structure
<i>Philiris moira</i>	East-west structure	Some host-associated structure
<i>Rhodoneura aurata</i>	Four cryptic lineages; all haplotypes geographically structured	Three of four lineages with host-associated structure
<i>Talanga deliciosa</i>	Two cryptic lineages	Two lineages with host-associated structure
<i>Talanga excelsalis</i>	No structure	No structure
<i>Talanga sexpunctalis</i> complex	No structure	No structure
" <i>Jodis</i> " (s.l.) <i>albifusa</i> complex	Two cryptic lineages	No structure
<i>Unadophanes trissomita</i>	No structure	No structure
<i>Zeugma recusataria</i>	No structure	No structure

Table S4. Mean pairwise nucleotide differences among individuals at eight sites for 28 lowland rainforest moth species

Species	Ohu	Morox	Wanang	Yapsiei	Niksek	Elem	Utai	Wamangu
<i>Addaea pusilla</i>	4.68	7.17	0.40	5.78	6.33	0	6.50	6.17
<i>Adoxophyes</i> sp. nr. <i>orana</i>	0.81	0.76	NA	NA	NA	NA	0	0
<i>Adoxophyes thoracica</i>	0.79	0.44	NA	0	0	NA	0	NA
<i>Arctornis intacta</i> complex	0.44	5.51	NA	NA	13.28	10.80	4.06	16.20
<i>Asota carica</i>	0	NA	0	0	0.2	NA	NA	0
<i>Choreutis</i> sp. nr. <i>anthorma</i>	3.70	4.00	0	8.18	4.51	NA	3.40	2.00
" <i>Coelorhycidia</i> " <i>nitidalis</i>	0	0	0.39	0	NA	NA	0	0
<i>Dichomeris ochreoviridella</i> complex	13.78	21.00	0	20.94	15.94	14.13	0.91	16.78
<i>Dichomeris</i> sp. [XXXX068]	0.50	0	0.33	0.29	4.68	0.20	0	0.54
<i>Dichomeris</i> sp. [XXXX120]	0.68	0.50	NA	0	0.83	NA	0	0.67
<i>Dudua</i> sp. nov. nr. <i>aprobola</i>	0	1.00	NA	NA	0	NA	2.44	2.03
<i>Glyphodes margaritaria</i>	0	0	0.40	0	0	0	0	0
<i>Meekiaria purpurea</i>	13.17	0	NA	4.40	1.29	5.91	0.67	1.00
<i>Meekiaria</i> sp. complex	8.15	8.57	8.22	0.17	NA	0.50	19.16	14.28
<i>Mellea nitida</i>	5.14	NA	0	6.22	2.57	3.53	4.61	5.57
<i>Mellea ordinaria</i>	10.87	0.67	0	0.18	10.59	NA	8.20	NA
<i>Mellea</i> sp. [THYR012]	NA	0	NA	1.40	5.33	NA	0.44	5.43
<i>Ophiorrhabda deceptor</i>	0.33	2.57	NA	NA	3.43	3.00	3.16	0
<i>Paraphomia disjuncta</i>	NA	NA	1.25	0	2.07	0.40	6.80	4.67
<i>Philiris helena</i>	1.89	0	NA	11.19	NA	NA	4.46	4.29
<i>Philiris moira</i>	1.72	NA	NA	0	NA	NA	NA	0.20
<i>Rhodoneura aurata</i>	3.67	0.22	NA	0.68	7.17	0	4.14	8.20
<i>Talanga deliciosa</i>	0.25	NA	0.25	NA	4.26	NA	1.89	6.11
<i>Talanga excelsalis</i>	0.47	0.78	1.17	1.56	0	0.56	0.87	0.89
<i>Talanga sexpunctalis</i> complex	1.22	1.80	1.82	1.53	1.89	1.71	1.64	0.95
" <i>Jodis</i> " (s.l.) <i>albifusa</i> complex	9.86	NA	7.05	NA	NA	1.00	9.11	0.29
<i>Unadophanes trissomita</i>	NA	NA	NA	3.93	4.67	1.18	3.00	0.73
<i>Zeugma recusataria</i>	0.47	0.20	0	NA	NA	0	0.44	0

NA, not applicable.

Table S5. Nucleotide diversity per site for 28 lowland rainforest moth species and species complexes

Species	Ohu	Morox	Wanang	Yapsiei	Niksek	Elem	Utai	Wamangu
<i>Addaea pusilla</i>	0.011	0.017	0.001	0.014	0.015	0	0.015	0.015
<i>Adoxophyes</i> sp. nr. <i>orana</i>	0.001	0.001	NA	NA	NA	NA	0	0
<i>Adoxophyes thoracica</i>	0.001	0.0008	NA	0	0	NA	0	NA
<i>Arctornis intacta</i> complex	0.0008	0.010	NA	NA	0.024	0.020	0.007	0.030
<i>Asota carica</i>	0	NA	0	0	0.0004	NA	NA	0
<i>Choreutis</i> sp. nr. <i>anthorma</i>	0.007	0.008	0	0.016	0.009	NA	0.007	0.004
" <i>Coelorhycidia</i> " <i>nitidalis</i>	0	0	0.0007	0	NA	NA	0	0
<i>Dichomeris ochreoviridella</i> complex	0.026	0.040	0	0.039	0.030	0.027	0.002	0.032
<i>Dichomeris</i> sp. [XXXX068]	0.001	0	0.0006	0.0005	0.009	0.0004	0	0.001
<i>Dichomeris</i> sp. [XXXX120]	0.001	0.0009	NA	0	0.001	NA	0	0.001
<i>Dudua</i> sp. nov. nr. <i>aprobola</i>	0	0.002	NA	NA	0	NA	0.004	0.004
<i>Glyphodes margaritaria</i>	0	0	0.0007	0	0	0	0	0
<i>Meekiaria purpurea</i>	0.027	0	NA	0.009	0.003	0.012	0.001	0.002
<i>Meekiaria</i> sp. complex	0.1087	0.1143	0.1096	0.0022	NA	0.0067	0.2555	0.1905
<i>Mellea nitida</i>	0.010	NA	0	0.012	0.005	0.007	0.009	0.010
<i>Mellea ordinaria</i>	0.022	0.001	0	0.0004	0.022	NA	0.017	NA
<i>Mellea</i> sp. [THYR012]	NA	0	NA	0.003	0.010	NA	0.0008	0.010
<i>Ophiorrhabda deceptor</i>	0.0006	0.005	NA	NA	0.007	0.006	0.006	0
<i>Paraphomia disjuncta</i>	NA	NA	0.002	0	0.004	0.0007	0.013	0.009
<i>Philiris helena</i>	0.003	0	NA	0.020	NA	NA	0.008	0.008
<i>Philiris moira</i>	0.003	NA	NA	0	NA	NA	NA	0.0004
<i>Rhodoneura aurata</i>	0.007	0.0004	NA	0.001	0.014	0	0.008	0.016
<i>Talanga deliciosa</i>	0.0005	NA	0.0005	NA	0.009	NA	0.004	0.013
<i>Talanga excelsalis</i>	0.0009	0.002	0.002	0.003	0	0.001	0.002	0.002
<i>Talanga sexpunctalis</i> complex	0.002	0.004	0.004	0.003	0.004	0.003	0.003	0.002
" <i>Jodis</i> " (s.l.) <i>albifusa</i> complex	0.022	NA	0.015	NA	NA	0.002	0.020	0.0006
<i>Unadophanes trissomita</i>	NA	NA	NA	0.007	0.009	0.002	0.006	0.001
<i>Zeugma recusataria</i>	0.001	0.0005	0	NA	NA	0	0.001	0

NA, not applicable.

Table S6. Numbers of Lepidoptera mtDNA haplotypes (and individuals) sampled from eight lowland rainforests in New Guinea

Species	Ohu	Morox	Wanang	Yapsiei	Niksek	Elem	Utai	Wamangu
<i>Addaea pusilla</i>	4 (14)	3 (4)	2 (5)	3 (9)	3 (9)	NA	3 (8)	4 (9)
<i>Adoxophyes cf orana</i>	4 (19)	3 (10)	NA	NA	NA	NA	1 (1)	1 (6)
<i>Adoxophyes thoracica</i>	6 (20)	3 (9)	NA	1 (1)	1 (4)	NA	1 (3)	NA
<i>Arctornis intacta</i> complex	3 (9)	3 (10)	NA	NA	4 (10)	2 (5)	5 (9)	3 (5)
<i>Asota carica</i>	1 (10)	NA	1 (9)	1 (10)	2 (10)	NA	NA	1 (9)
<i>Asota plana</i>	1 (10)	NA	1 (9)	1 (10)	1 (2)	NA	NA	1 (10)
<i>Choreutis</i> sp. nr. <i>Anthorma</i>	8 (12)	6 (6)	1 (1)	7 (10)	8 (10)	NA	4 (5)	2 (3)
" <i>Coelorhycidia</i> " <i>nitidalis</i>	1 (9)	1 (3)	2 (9)	1 (8)	NA	NA	1 (5)	1 (9)
<i>Meekiaria purpurea</i>	3 (4)	1 (2)	NA	2 (5)	3 (10)	5 (10)	3 (6)	2 (4)
<i>Meekiaria</i> sp. Complex	6 (20)	2 (7)	3 (11)	2 (12)	NA	2 (4)	6 (11)	2 (15)
<i>Dichomeris ochreoviridella</i> complex	3 (9)	2 (2)	1 (2)	7 (9)	4 (9)	5 (10)	3 (10)	7 (9)
<i>Dichomeris</i> sp. [XXXX068]	2 (9)	1 (8)	2 (6)	2 (7)	3 (8)	2 (10)	1 (10)	2 (8)
<i>Dichomeris</i> sp. [XXXX120]	3 (8)	2 (4)	NA	1 (1)	4 (9)	NA	1 (9)	3 (6)
<i>Dudua</i> sp. nov. nr. <i>Aprobola</i>	1 (9)	2 (2)	NA	NA	1 (1)	NA	5 (9)	4 (9)
<i>Glyphodes margaritaria</i>	1 (9)	1 (1)	2 (5)	1 (10)	1 (3)	1 (5)	1 (7)	1 (10)
<i>Mellea nitida</i>	2 (7)	NA	1 (1)	4 (9)	2 (7)	3 (6)	4 (9)	6 (8)
<i>Mellea ordinaria</i>	5 (6)	2 (3)	1 (2)	2 (11)	4 (12)	NA	3 (5)	NA
<i>Mellea</i> sp.	NA	1 (5)	NA	3 (10)	2 (4)	NA	3 (9)	5 (7)
<i>Ophiorrhabda deceptor</i>	2 (6)	6 (7)	NA	NA	6 (8)	2 (2)	6 (10)	1 (2)
<i>Paraphomia disjuncta</i>	NA	NA	4 (8)	1 (10)	5 (8)	2 (5)	5 (5)	3 (3)
<i>Philiris helena</i>	6 (10)	1 (1)	NA	5 (7)	NA	NA	10 (18)	3 (7)
<i>Philiris moira</i>	3 (9)	NA	NA	1 (10)	NA	NA	NA	2 (10)
<i>Rhodoneura aurata</i>	3 (4)	2 (9)	NA	3 (8)	6 (9)	1 (4)	5 (8)	3 (5)
<i>Talanga deliciosa</i>	2 (8)	NA	2 (8)	NA	3 (10)	NA	7 (9)	2 (10)
<i>Talanga excelsalis</i>	3 (12)	3 (9)	4 (9)	4 (10)	1 (9)	3 (10)	3 (10)	4 (9)
<i>Talanga sexpunctalis</i> complex	5 (10)	4 (5)	4 (10)	7 (10)	6 (9)	6 (8)	6 (10)	3 (7)
" <i>Jodis</i> " (s.l.) <i>albifusa</i> complex	4 (8)	NA	5 (7)	NA	NA	2 (9)	5 (10)	2 (7)
<i>Unadophanes trissomita</i>	NA	NA	NA	4 (6)	3 (4)	4 (8)	5 (9)	3 (10)
<i>Zeugma recusataria</i>	3 (12)	2 (10)	1 (1)	NA	NA	1 (6)	3 (9)	1 (7)

NA, not applicable.