

Supporting Information

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Table S1. Primer sequences used in this study

No. fragment [*]	Primer ID	Nucleotide sequence (5'-3')	Reference
1	F-200	GTGCCTGATAAAAAGGATTATTTTG	Present study
	R-586	TCTTTCTGAGCTTAGAGAATTAGAA	Present study
2	N2-J586	CCATTCCATTTYTGATTTCC	Simon <i>et al.</i> , 2006
	C1-N1738	TTTATTCGTGGAAATGCTATGTC	Simon <i>et al.</i> , 2006
3	C1-J1709	AATTGGTGGTTTTGGAAATTG	Simon <i>et al.</i> , 2006
	C1-N2776	GGTAATCAGAGTATCGACG	Simon <i>et al.</i> , 2006
4	C1-J2756	ACATTTTTTCTCAACATTT	Simon <i>et al.</i> , 2006
	C2-N3665	CCACAAATTTCTGAACACTG	Simon <i>et al.</i> , 2006
5	C2-J3399	TCTATTGGTCATCAATGGTACTG	Simon <i>et al.</i> , 2006
	A8-N4061	GAAAATAAATTTGTTATCATTTTCA	Simon <i>et al.</i> , 2006
6	C3-J4792	GTAGATGCAAGCCCTTGACC	Simon <i>et al.</i> , 2006
	N3-N5731	ATTGGATCAAATCCACATTC	Simon <i>et al.</i> , 2006
7	F-5731	CAAATAATACCCCTCAATTG	Present study
	R-6172	ATTGAAGATGTTAGAGTGAT	Present study
8	TN-J6172	AGAGGCAATTTATTGTTAATAA	Simon <i>et al.</i> , 2006
	N5-N7211	TAAAGCCTTTATTATTTATATGTGC	Simon <i>et al.</i> , 2006
9	N5-J7077	TTAAATCCTTWGARTAAAAYCC	Simon <i>et al.</i> , 2006
	N5-N7793	TTAGGTTGRGATGGNYTAGG	Simon <i>et al.</i> , 2006
10	F-N7793	CTATCAAAATAGCTGCATCC	Present study
	R-J8641	TGGTATTATACGTGTGTTAG	Present study
11	N4-J8641	CCAGAAGAACACAAACCATG	Simon <i>et al.</i> , 2006
	N4L-N9629	GTTTGTGAGGGTGCAATAGG	Simon <i>et al.</i> , 2006
12	F-9629	TACTATATCGCACCCAAAAA	Present study
	R-9648	TGATTTACAAAATCAAGGTT	Present study
13	N4L-J9648	ACCTAAAGCTCCCTCACAWAC	Simon <i>et al.</i> , 2006
	CB-N11010	TATCTACAGCRAATCCYCCYCA	Simon <i>et al.</i> , 2006
14	F-J11010	ACCAACATGATTCGTAGGTA	Present study
	R-N11867	GAGGAGGGTTTGCTTTAATT	Present study
15	N1-J11876	CGAGGTAAAGTMCCWTTTGATTTTGC	Simon <i>et al.</i> , 2006
	N1-N12595	GTWGCTTTTTTAACTTTATTRGARCG	Simon <i>et al.</i> , 2006
16	N1-J12261	AACTTCATAAGAAATAGTYTGRGC	Simon <i>et al.</i> , 2006
	LR-N13000	TTACCTAGGATAACAGCGTAA	Simon <i>et al.</i> , 2006
17	LR-J12888	CCGGTCTGAACTCAGATCATGTA	Simon <i>et al.</i> , 2006
	LR-N13889	ATTTATTGTACCTTTTGTATCAG	Simon <i>et al.</i> , 2006
18	F-13889	GTTTTTGTAAACAAGCGAA	Present study
	R-14197	ATATCAAATCAAGATGCAGT	Present study
19	LR-J14197	GTAAAYCTACTTTGTTACGACTT	Simon <i>et al.</i> , 2006
	SR-N14745	GTGCCAGCAAYCGCGTTATAC	Simon <i>et al.</i> , 2006
20	SR-J14610	ATAATAGGGTATCTAATCCTAGT	Simon <i>et al.</i> , 2006
	TM-N200	ACCTTTATAAATGGGGTATGAACC	Simon <i>et al.</i> , 2006

Table S2. Summary of taxonomic groups used in this study

Order	exemplar	Collection data or reference
Outgroup		
Hemiptera	<i>Hydrometra</i> sp.	NC_012842
Thysanoptera	<i>Thrips imaginis</i>	NC_004371
Ingroup		
Coleoptera	<i>Cyphon</i> sp.	NC_011320
	<i>Hydroscapha granulum</i>	NC_012144
	<i>Tetraphalerus bruchi</i>	NC_011328
Diptera	<i>Aedes aegypti</i>	NC_010241
	<i>Ceratitis capitata</i>	NC_000857
	<i>Cydistomyia duplonotata</i>	NC_008756
Hymenoptera	<i>Abispa ephippium</i>	NC_011520
	<i>Apis cerana</i>	NC_014295
	<i>Cephus cinctus</i>	NC_012688
Lepidoptera	<i>Acraea issoria</i>	NC_013604
	<i>Actias selene</i>	NC_018133
	<i>Adoxophyes honmai</i>	NC_008141
	<i>Ahamus yunnanensis</i>	NC_018095
Mecoptera	<i>Bittacus pilicornis</i>	NC_015118
	<i>Boreus elegans</i>	NC_015119
	<i>Neopanorpa pulchra</i>	NC_013180
Megaloptera	<i>Corydalus cornutus</i>	NC_011276
	<i>Neochauliodes punctatolosus</i>	NC_018772
	<i>Sialis hamata</i>	NC_013256
Neuroptera	<i>Chrysoperla nipponensis</i>	NC_015093
	<i>Libelloides macaronius</i>	NC_015609
	<i>Thyridosmylus langii</i>	NC_021415
Trichoptera	<i>Eubasilissa regina</i>	Present study
	<i>Apatanla</i> sp.	Present study

Table S3. Organization of *Eubasilissa regina* mt genome

Gene	Direction	Location (bp)	Size (bp)	Anticodon	Start Codon	Stop Codon	Intergenic Nucleotide*
<i>tRNA^{Ile}</i>	J	1-65	65	31-33 GAT			0
<i>tRNA^{Gln}</i>	N	63-131	69	99-101 TTG			-3
<i>tRNA^{Met}</i>	J	142-209	68	172-174 CAT			10
<i>nad2</i>	J	210-1227	1018		ATT	T-tRNA	0
<i>tRNA^{Trp}</i>	J	1228-1294	67	1258-1260 TCA			0
<i>tRNA^{Cys}</i>	N	1287-1350	64	1318-1320 GCA			-8
<i>tRNA^{Tyr}</i>	N	1352-1418	67	1385-1387 GTA			1
<i>cox1</i>	J	1420-2950	1531		CGA	T-tRNA	1
<i>tRNA^{Leu(UUR)}</i>	J	2951-3015	65	2980-2982 TAA			0
<i>cox2</i>	J	3016-3695	680		ATC	TA-tRNA	0
<i>tRNA^{Lys}</i>	J	3696-3761	66	3724-3726 CTT			0
<i>tRNA^{Asp}</i>	J	3775-3839	65	3804-3806 GTC			13
<i>atp8</i>	J	3840-3995	156		ATC	TAA	0
<i>atp6</i>	J	3989-4666	678		ATG	TAA	-7
<i>cox3</i>	J	4670-5458	789		ATG	TAA	3
<i>tRNA^{Gly}</i>	J	5461-5525	65	5491-5493 TCC			2
<i>nad3</i>	J	5526-5877	352		ATC	T-tRNA	0
<i>tRNA^{Ala}</i>	J	5878-5941	64	5908-5910 TGC			0
<i>tRNA^{Arg}</i>	J	5948-6011	64	5974-5976 TCG			6
<i>tRNA^{Asn}</i>	J	6011-6075	65	6041-6043 GTT			-1
<i>tRNA^{Ser(AGN)}</i>	J	6076-6131	56	6094-6096 GCT			0
<i>tRNA^{Glu}</i>	J	6132-6193	62	6162-6164 TTC			0
<i>tRNA^{Phe}</i>	N	6193-6257	65	6225-6227 GAA			-1
<i>nad5</i>	N	6258-7983	1726		ATA	T-tRNA	0
<i>tRNA^{His}</i>	N	7984-8048	65	8015-8017 GTG			0
<i>nad4</i>	N	8051-9391	1341		ATG	TAA	2
<i>nad4l</i>	N	9391-9681	291		ATG	TAA	-1
<i>tRNA^{Thr}</i>	J	9684-9747	64	9714-9716 TGT			2
<i>tRNA^{Pro}</i>	N	9748-9812	65	9780-9782 TGG			0
<i>nad6</i>	J	9815-10321	507		ATT	TAA	2
<i>cytb</i>	J	10321-11464	1144		ATG	T-tRNA	-1
<i>tRNA^{Ser(UCN)}</i>	J	11465-11530	66	11494-11496 TGA			0
<i>nad1</i>	N	11531-12491	961		ATT	T-tRNA	0
<i>tRNA^{Leu(CUN)}</i>	N	12492-12558	67	12527-12529 TAG			0
<i>rrnL</i>	N	12559-13902	1344				0
<i>tRNA^{Val}</i>	N	13903-13972	70	13938-13940 TAC			0
<i>rrnS</i>	N	13973-14751	779				0
CR		14752-15021	270				0

“*”: Negative numbers indicate that adjacent genes overlap.

Table S4. The Size of PCGs, tRNAs, *rrnL*, *rrnS*, and CR, respectively, among Holometabola mt genomes used in this study

Order	Species	PCGs	tRNAs	<i>rrnL</i>	<i>rrnS</i>	CR	Whole
Hemiptera	<i>Hydrometra</i> sp.	11003	1431	1258	786	694	15416
Thysanoptera	<i>Thrips imaginis</i>	10922	1463	1142	734	945	15407
Coleoptera	<i>Cyphon</i> sp.	11158	1459	1297	781	1043	15919
	<i>Hydroscapha granulum</i>	10457	1398	1339	789	1144	15975
	<i>Tetraphalerus bruchi</i>	11144	1449	1322	791	1000	15689
Diptera	<i>Aedes aegypti</i>	11191	1488	1335	790	1709	16655
	<i>Ceratitis capitata</i>	11183	1472	1335	788	1004	15980
	<i>Cydistomyia duplonotata</i>	11192	1471	1337	793	1376	16247
Hymenoptera	<i>Abispa ephippium</i>	11305	1787	1368	812	308	16953
	<i>Apis cerana</i>	11050	1486	1328	786	562	15895
	<i>Cephus cinctus</i>	11291	1489	1386	1011	3873	19339
Lepidoptera	<i>Acraea issoria</i>	11186	1537	1331	788	430	15245
	<i>Actias selene</i>	11217	1460	1364	762	339	15236
	<i>Adoxophyes honmai</i>	11252	1478	1387	779	489	15680
	<i>Ahamus yunnanensis</i>	11191	1495	1329	777	852	15816
Mecoptera	<i>Bittacus pilicornis</i>	11190	1466	1320	803	1059	15842
	<i>Boreus elegans</i>	11209	1475	1352	787	1970	16803
	<i>Neopanorpa pulchra</i>	11200	1460	1317	817	718	15531
Megaloptera	<i>Corydalis cornutus</i>	11175	1504	1311	786	967	15687
	<i>Neochauliodes punctatolus</i>	11166	1449	1318	789	1006	15734
	<i>Sialis hamata</i>	11192	1515	1321	784	814	15608
Neuroptera	<i>Chrysoperla nipponensis</i>	11155	1497	1307	776	1244	16057
	<i>Libelloides macaronius</i>	11177	1470	1313	782	1049	15890
	<i>Thyridosmylus langii</i>	11172	1469	1325	798	1365	16221
Trichoptera	<i>Eubasilissa regina</i>	11174	1434	1344	779	270	15021

Table S5. Nucleotide composition of the *Eubasilissa regina* mt genome

Feature	Proportion of nucleotides						No. of nucleotides
	%T(U)	%C	%A	%G	A+T%	AT Skew	
Whole genome	38.25	14.23	39.86	7.66	78.10	0.02	15021
Protein-coding genes	42.99	12.51	32.94	11.55	75.93	-0.13	11148
First codon position	34.58	12.16	36.98	16.28	71.56	0.03	3716
Second codon position	49.46	16.58	20.78	13.19	70.24	-0.41	3716
Third codon position	44.94	8.80	41.07	5.19	86.01	-0.05	3716
Protein-coding genes J-strand	40.24	16.32	33.85	9.59	74.08	-0.09	6837
First codon position	31.24	15.58	38.31	14.87	69.55	0.10	2279
Second codon position	47.17	19.66	21.15	12.02	68.32	-0.38	2279
Third codon position	42.30	13.73	42.08	1.89	84.38	0.00	2279
Protein-coding genes N-strand	47.37	6.47	31.50	14.66	78.87	-0.20	4311
First codon position	39.87	6.75	34.86	18.51	74.74	-0.07	1437
Second codon position	53.10	11.69	20.18	15.03	73.28	-0.45	1437
Third codon position	49.13	0.97	39.46	10.44	88.59	-0.11	1437
tRNA genes	41.35	9.83	41.84	6.97	83.19	0.01	1434
tRNA genes J-strand	39.80	9.53	42.24	8.43	82.04	0.03	902
tRNA genes N-strand	43.98	10.34	41.17	4.51	85.15	-0.03	532
rRNA genes	41.83	10.83	42.44	4.90	84.27	0.01	2123
Control region	50.74	5.19	39.26	4.81	90.00	-0.13	270

Table S6. Base composition and strand bias in PCGs of *Eubasilissa regina*.

Protein	A%	T%	A+T%	AT-skew	C%	G%	C+G%	GC-skew
<i>atp6</i>	33.63	39.09	72.71	-0.08	16.67	10.62	27.29	-0.22
<i>atp8</i>	32.08	47.17	79.25	-0.19	17.61	3.14	20.75	-0.70
<i>cox1</i>	28.42	38.42	66.84	-0.15	18.04	15.12	33.16	-0.09
<i>cox2</i>	33.48	38.03	71.51	-0.06	16.89	11.60	28.49	-0.19
<i>cox3</i>	30.16	39.16	69.33	-0.13	16.73	13.94	30.67	-0.09
<i>cytb</i>	30.96	40.19	71.15	-0.13	17.59	11.26	28.85	-0.22
<i>nad1</i>	28.69	47.05	75.74	-0.24	7.49	16.77	24.26	0.38
<i>nad2</i>	34.81	43.26	78.07	-0.11	13.96	7.96	21.93	-0.27
<i>nad3</i>	32.20	42.66	74.86	-0.14	15.25	9.89	25.14	-0.21
<i>nad4</i>	31.06	46.41	77.47	-0.20	7.26	15.27	22.53	0.36
<i>nad4l</i>	27.84	49.83	77.66	-0.28	5.15	17.18	22.34	0.54
<i>nad5</i>	31.69	45.42	77.11	-0.18	7.88	15.01	22.89	0.31
<i>nad6</i>	38.43	42.55	80.98	-0.05	13.33	5.69	19.02	-0.40
Avg.	31.80	43.02	74.82	-0.15	13.37	11.80	25.18	-0.06

Table S7. Codon usage of protein-coding genes in the *Eubasilissa regina* mt genome.

AA	Codon*	n	%	RSCU	AA	Codon	n	%	RSCU
Phe	UUU(F)	331	8.89	1.73	Ser2	UCU(S)	91	2.44	2.21
	UUC(F)	51	1.37	0.27		UCC(S)	19	0.51	0.46
Leu1	UUA(L)	389	10.45	4.15	Ser1	UCA(S)	80	2.15	1.94
	UUG(L)	30	0.81	0.32		UCG(S)	9	0.24	0.22
Leu2	CUU(L)	66	1.77	0.70	Thr	AGU(S)	56	1.50	1.82
	CUC(L)	16	0.43	0.17		AGC(S)	20	0.54	0.65
	CUA(L)	60	1.61	0.64		AGA(S)	45	1.21	1.46
	CUG(L)	2	0.05	0.02		AGG(S)	2	0.05	0.07
Ile	AUU(I)	373	10.02	1.75	Ala	ACU(T)	76	2.04	1.82
	AUC(I)	54	1.45	0.25		ACC(T)	21	0.56	0.50
Met	AUA(M)	281	7.55	1.81	Cys	ACA(T)	64	1.72	1.53
	AUG(M)	30	0.81	0.19		ACG(T)	6	0.16	0.14
Val	GUU(V)	61	1.64	1.57	Trp	GCU(A)	79	2.12	2.49
	GUC(V)	10	0.27	0.26		GCC(A)	13	0.35	0.41
	GUA(V)	65	1.75	1.68		GCA(A)	31	0.83	0.98
	GUG(V)	19	0.51	0.49		GCG(A)	4	0.11	0.13
Tyr	UAU(Y)	132	3.55	1.58	Arg	UGU(C)	19	0.51	1.58
	UAC(Y)	35	0.94	0.42		UGC(C)	5	0.13	0.42
	UAA(*)	6	0.16	2.00		UGA(W)	86	2.31	1.83
	UAG(*)	0	0.00	0.00		UGG(W)	8	0.21	0.17
His	CAU(H)	48	1.29	1.35	Pro	CGU(R)	17	0.46	1.33
	CAC(H)	23	0.62	0.65		CGC(R)	1	0.03	0.08
Gln	CAA(Q)	57	1.53	1.81	Gly	CGA(R)	30	0.81	2.35
	CAG(Q)	6	0.16	0.19		CGG(R)	3	0.08	0.24
Asn	AAU(N)	198	5.32	1.72	Lys	CCU(P)	45	1.21	1.09
	AAC(N)	32	0.86	0.28		CCC(P)	4	0.11	0.10
Asp	AAA(K)	89	2.39	1.65	Glu	CCA(P)	82	2.20	1.99
	AAG(K)	19	0.51	0.35		CCG(P)	0	0.00	0.00
Glu	GAU(D)	44	1.18	1.42	Gly	GGU(G)	34	0.91	0.72
	GAC(D)	18	0.48	0.58		GGC(G)	5	0.13	0.11
Glu	GAA(E)	63	1.69	1.77	Gly	GGA(G)	104	2.79	2.19
	GAG(E)	8	0.21	0.23		GGG(G)	47	1.26	0.99

“*”: A total of 3711 codons from *Eubasilissa regina* are analyzed, excluding the start and stop codons.

AA, amino acid; RSCU, Relative synonymous codon usage; n = frequency of each codon. % = n/3711.

Table S8. Base composition and strand bias in Amphipsectera insect mt genomes

Order	Species	Total	A	T	A+T	AT-skew	C	G	C+G	GC-skew
Lepidoptera										
	<i>Acraea issoria</i>	15245	38.94	40.81	79.76	-0.02	7.74	12.50	20.24	-0.24
	<i>Adoxophyes honmai</i>	15679	40.16	40.24	80.39	0.00	7.88	11.73	19.61	-0.20
	<i>Adoxophyes orana</i>	15343	39.94	40.02	79.96	0.00	7.91	12.14	20.04	-0.21
	<i>Agrotis ipsilon</i>	15377	40.38	40.87	81.25	-0.01	7.71	11.04	18.75	-0.18
	<i>Ahamus yunnanensis</i>	15816	40.93	41.41	82.34	-0.01	7.30	10.36	17.66	-0.17
	<i>Antheraea pernyi</i>	15566	39.22	40.94	80.16	-0.02	7.77	12.06	19.84	-0.22
	<i>Apatura metis</i>	15236	39.75	40.69	80.44	-0.01	7.71	11.85	19.56	-0.21
	<i>Aporia crataegi</i>	15140	39.65	41.61	81.25	-0.02	7.32	11.43	18.75	-0.22
	<i>Argynnis hyperbius</i>	15156	39.40	41.42	80.81	-0.02	7.53	11.65	19.19	-0.21
	<i>Artogeia melete</i>	15140	40.38	39.41	79.78	0.01	7.87	12.35	20.22	-0.22
	<i>Athyma sulphitia</i>	15268	39.04	42.91	81.95	-0.05	7.43	10.62	18.05	-0.18
	<i>Biston panterinaria</i>	15516	42.32	37.23	79.56	0.06	7.56	12.88	20.44	-0.26
	<i>Bombyx mandarina</i>	15928	43.08	38.60	81.68	0.05	7.21	11.11	18.32	-0.21
	<i>Bombyx mori</i>	15635	43.05	38.26	81.31	0.06	7.34	11.35	18.69	-0.21
	<i>Bombyx mori strain Xiafang</i>	15664	43.05	38.30	81.35	0.06	7.32	11.33	18.65	-0.21
	<i>Calinaga davidis</i>	15267	38.45	42.01	80.45	-0.04	7.81	11.74	19.55	-0.20
	<i>Catopsilia pomona</i>	15142	39.45	41.84	81.29	-0.03	7.64	11.07	18.71	-0.18
	<i>Chilo suppressalis</i>	15395	40.64	40.03	80.67	0.01	7.39	11.94	19.33	-0.24
	<i>Choristoneura longicellana</i>	15759	40.96	40.18	81.14	0.01	7.61	11.25	18.86	-0.19
	<i>Cnaphalocrocis medinalis</i>	15388	40.36	41.58	81.94	-0.01	7.45	10.61	18.06	-0.18
	<i>Corecyra cephalonica</i>	15273	38.76	41.67	80.43	-0.04	7.65	11.92	19.57	-0.22
	<i>Coreana raphaelis</i>	15314	39.37	43.29	82.66	-0.05	7.30	10.04	17.34	-0.16
	<i>Ctenoptilum vasava</i>	15468	39.09	41.45	80.54	-0.03	7.73	11.73	19.46	-0.21
	<i>Cupido argiades</i>	15330	40.44	41.36	81.81	-0.01	7.58	10.61	18.19	-0.17
	<i>Cydia pomonella</i>	15253	39.92	40.21	80.13	0.00	7.88	11.99	19.87	-0.21
	<i>Danaus plexippus</i>	15314	38.75	42.61	81.36	-0.05	7.41	11.23	18.64	-0.20
	<i>Diatraea saccharalis</i>	15490	40.87	39.15	80.02	0.02	7.42	12.56	19.98	-0.26
	<i>Dichocrocis punctiferalis</i>	15355	39.30	41.30	80.60	-0.02	7.69	11.71	19.40	-0.21
	<i>Elophila interruptalis</i>	15351	39.73	40.59	80.32	-0.01	7.59	12.09	19.68	-0.23
	<i>Eriogyna pyretorum</i>	15327	39.17	41.65	80.82	-0.03	7.63	11.55	19.18	-0.20
	<i>Erynnis montanus</i>	15530	40.83	40.93	81.76	0.00	7.48	10.77	18.24	-0.18
	<i>Eurema hecabe</i>	15160	39.60	41.05	80.65	-0.02	7.63	11.72	19.35	-0.21
	<i>Fabriciana nerippe</i>	15140	39.36	41.55	80.90	-0.03	7.54	11.55	19.10	-0.21
	<i>Glyphodes quadrimaculalis</i>	15255	40.10	40.70	80.80	-0.01	7.75	11.45	19.20	-0.19
	<i>Grapholita molesta</i>	15716	40.26	40.61	80.87	0.00	7.88	11.24	19.13	-0.18
	<i>Gynaephora menyanensis</i>	15770	40.88	40.60	81.48	0.00	6.77	11.75	18.52	-0.27
	<i>Hebomoia glaucippe</i>	15701	38.53	41.39	79.92	-0.04	7.85	12.22	20.08	-0.22
	<i>Helicoverpa armigera</i>	15347	40.54	40.43	80.97	0.00	7.69	11.34	19.03	-0.19
	<i>Hyphantria cunea</i>	15481	40.58	39.81	80.39	0.01	7.55	12.06	19.61	-0.23
	<i>Issoria lathonia</i>	15171	39.34	41.83	81.17	-0.03	7.64	11.19	18.83	-0.19
	<i>Junonia orithya</i>	15214	39.53	40.85	80.38	-0.02	8.05	11.57	19.62	-0.18

<i>Kallima inachus</i>	15183	39.64	40.66	80.30	-0.01	7.77	11.93	19.70	-0.21
<i>Leptidea morsei</i>	15122	38.51	41.73	80.24	-0.04	7.93	11.83	19.76	-0.20
<i>Leucoptera malifoliella</i>	15646	41.93	40.63	82.56	0.02	6.99	10.45	17.44	-0.20
<i>Lymantria dispar</i>	15569	40.58	39.30	79.88	0.02	7.57	12.55	20.12	-0.25
<i>Manduca sexta</i>	15516	40.67	41.11	81.79	-0.01	7.46	10.76	18.21	-0.18
<i>Melanitis leda</i>	15122	38.41	41.40	79.80	-0.04	7.68	12.52	20.20	-0.24
<i>Melitaea cinxia</i>	15170	40.27	39.74	80.01	0.01	7.55	12.44	19.99	-0.24
<i>Ochlodes venata</i>	15622	40.58	41.42	81.99	-0.01	7.36	10.65	18.01	-0.18
<i>Ochrogaster lunifer</i>	15593	40.09	37.75	77.84	0.03	7.56	14.60	22.16	-0.32
<i>Ostrinia furnacalis</i>	14535	41.46	38.92	80.38	0.03	7.91	11.71	19.62	-0.19
<i>Ostrinia nubilalis</i>	14535	41.36	38.81	80.17	0.03	8.02	11.82	19.83	-0.19
<i>Papilio bianor</i>	15332	39.78	40.87	80.65	-0.01	7.61	11.74	19.35	-0.21
<i>Papilio maackii</i>	15357	39.77	40.93	80.69	-0.01	7.59	11.72	19.31	-0.21
<i>Papilio machaon</i>	15185	38.94	41.40	80.34	-0.03	7.87	11.79	19.66	-0.20
<i>Papilio maraho</i>	16082	40.52	40.03	80.56	0.01	7.18	12.27	19.44	-0.26
<i>Paracymoriza prodigalis</i>	15326	40.84	40.70	81.53	0.00	7.54	10.92	18.47	-0.18
<i>Parnassius bremeri</i>	15390	39.76	41.29	81.05	-0.02	7.63	11.32	18.95	-0.19
<i>Phalera flavescens</i>	15659	40.07	40.80	80.87	-0.01	7.87	11.26	19.13	-0.18
<i>Phthonandria atrilineata</i>	15499	40.78	40.24	81.02	0.01	7.67	11.31	18.98	-0.19
<i>Pieris rapae</i>	15157	40.41	39.33	79.74	0.01	7.79	12.48	20.26	-0.23
<i>Protantigius superans</i>	15248	39.36	42.32	81.68	-0.04	7.57	10.75	18.32	-0.17
<i>Rhyacionia leptotubula</i>	15876	40.10	40.19	80.28	0.00	7.61	12.11	19.72	-0.23
<i>Rondotia menciana</i>	15301	41.42	37.45	78.86	0.05	7.82	13.31	21.14	-0.26
<i>Samia cynthia ricini</i>	15384	39.65	40.13	79.78	-0.01	7.81	12.41	20.22	-0.23
<i>Sasakia charonda</i>	15233	39.68	40.22	79.91	-0.01	7.85	12.24	20.09	-0.22
<i>Sasakia funebris</i>	15233	39.91	41.32	81.23	-0.02	7.58	11.19	18.77	-0.19
<i>Sesamia inferens</i>	15413	40.06	40.17	80.24	0.00	7.61	12.15	19.76	-0.23
<i>Sphinx morio</i>	15299	40.64	40.53	81.17	0.00	7.58	11.26	18.83	-0.20
<i>Spilonota lechriaspis</i>	15368	39.86	41.34	81.19	-0.02	7.63	11.17	18.81	-0.19
<i>Spindasis takanonis</i>	15349	41.34	41.01	82.35	0.00	6.93	10.72	17.65	-0.21
<i>Spodoptera exigua</i>	15365	40.87	40.06	80.93	0.01	7.68	11.39	19.07	-0.19
<i>Spodoptera litura</i>	15388	41.02	39.96	80.98	0.01	7.66	11.37	19.02	-0.20
<i>Teinopalpus aureus</i>	15242	39.72	40.09	79.81	0.00	7.69	12.50	20.19	-0.24
<i>Thitarodes renzhiensis</i>	16173	41.09	40.20	81.28	0.01	7.54	11.17	18.72	-0.19
<i>Timelaea maculata</i>	15178	39.06	41.97	81.03	-0.04	7.63	11.34	18.97	-0.20
<i>Troides aeacus</i>	15263	38.52	41.72	80.24	-0.04	7.61	12.15	19.76	-0.23
<i>Sericinus montela</i>	15242	40.14	40.81	80.95	-0.01	7.40	11.65	19.05	-0.22
<i>Actias selene</i>	15236	38.54	40.37	78.91	-0.02	8.05	13.03	21.09	-0.24
<i>Antheraea yamamai</i>	15338	39.26	41.04	80.29	-0.02	7.69	12.02	19.71	-0.22
<i>Apatura ilia</i>	15242	39.77	40.68	80.45	-0.01	7.75	11.80	19.55	-0.21
<i>Euploea mulciber</i>	15166	39.17	42.25	81.43	-0.04	7.35	11.23	18.57	-0.21
<i>Hipparchia autonoe</i>	15489	38.92	40.17	79.09	-0.02	7.92	13.00	20.91	-0.24
<i>Libythea celtis</i>	15164	39.92	41.28	81.21	-0.02	7.67	11.13	18.79	-0.18
<i>Pieris melete</i>	15140	40.38	39.41	79.78	0.01	7.87	12.35	20.22	-0.22

<i>Samia cynthia ricini</i>	15384	39.65	40.13	79.78	-0.01	7.81	12.41	20.22	-0.23
<i>Sasakia charonda kuriyamaensis</i>	15222	39.68	40.21	79.89	-0.01	7.86	12.25	20.11	-0.22
<i>Saturnia boisduvalii</i>	15360	39.34	41.28	80.63	-0.02	7.58	11.79	19.38	-0.22
Average	15369.50	40.06	40.62	80.68	-0.01	7.62	11.70	19.32	-0.21
Trichoptera									
<i>Eubasilissa regina</i>	15021	39.86	38.25	78.10	0.02	7.66	14.23	21.90	-0.30

Table S9. Bayesian posterior probabilities and bootstrap values of ML recovered by various phylogenetic approaches.

Relationship	PCG12		PCG12R	
	BI	ML	BI	ML
1	1.00	100	1.00	100
2	1.00	100	1.00	100
3	1.00	97	1.00	93
4	1.00	100	1.00	100
5	1.00	100	1.00	100
6	1.00	100	1.00	100
7	1.00	-	1.00	89
8	1.00	100	1.00	100
9	1.00	100	1.00	100
10	1.00	57	1.00	99
11	1.00	94	1.00	100
12	0.75	87	1.00	96
13	1.00	100	1.00	100
14	1.00	100	1.00	100
15	0.89	69	0.95	72
16	1.00	100	1.00	100
17	1.00	100	1.00	100
18	1.00	100	1.00	100
19	0.59	88	1.00	60
20	1.00	100	1.00	100
21	1.00	100	1.00	100
22	1.00	88	1.00	100
23	0.72	-	-	-

Relationships 1-23 refer to the nodes 1-23 in Figure 11.