Supplementary Materials for
Fossil record of stem groups employed in evaluating the chronogram of insects (Arthropoda: Hexapoda)

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Supplementary material legends:

Table S1. Comparison between the prior and posterior marginal densities of calibrated points under various settings of the lower and upper bounds of 95% HPD in normal distribution. The blue indicates the prior distribution and the gray indicates the posterior distribution.

Table S2. Stem group fossils collected from the fossil insect database Paleobiology Database and EDNA.

Table S3. Taxon sampling of nuclear genes and mitochondrial genomes. The sequence indicated by asterisk was newly sequenced in this study.

Table S4. Fossil record and prior distributions for different analyses.

File S5. Detailed phylogenetic justification and age justification for each fossil item.

Fig. S1. Phylogenetic trees inferred from matrix 1, i.e., the combined dataset of rDNAs and protein-coding genes. A) ML topology with DNA model applied to the paired sites of rDNAs, B) MP topology, C) ML topology with Doublet model applied to the paired sites of rRNAs. Posterior probabilities and bootstrap values are shown at each node, respectively.

Fig. S2. Phylogenetic trees inferred from matrix 2, i.e., the combined dataset of nuclear genes and the first codon positions of mitochondrial PCGs. A) BI topology, B) ML topology, C) MP topology. Posterior probabilities and bootstrap values are shown at each node, respectively.

Fig. S3. Phylogenetic trees inferred from matrix 3, i.e., the combined dataset of nuclear genes and the second codon positions of Mitochondrial PCGs. A) BI topology, B) ML topology, C) MP topology. Posterior probabilities and bootstrap values are shown at each node, respectively.

Fig. S4. Phylogenetic trees inferred from matrix 4, i.e., the combined dataset of nuclear genes and the first two codon positions of mitochondrial PCGs. A) BI topology, B) ML topology, C) MP topology. Posterior probabilities and bootstrap values are shown at each node, respectively.

Fig. S5. Phylogenetic trees inferred from matrix 5, i.e., the combined dataset of nuclear genes and the amino acid sequences of mitochondrial PCGs. A) BI topology, B) ML topology, C) MP topology. Posterior probabilities and bootstrap values are shown at each node, respectively.

Table S1. Comparison between the prior and posterior marginal densities of calibrated points under various settings of the lower and upper bounds of 95% HPD in normal distribution. The blue indicates the prior distribution and the gray indicates the posterior distribution.

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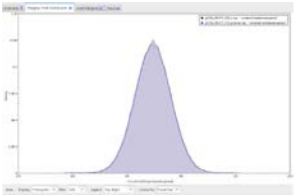
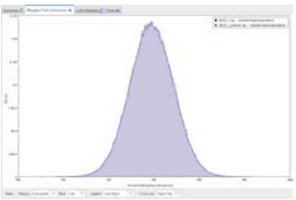
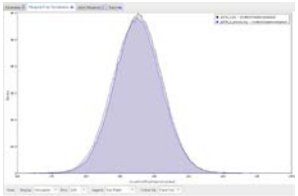
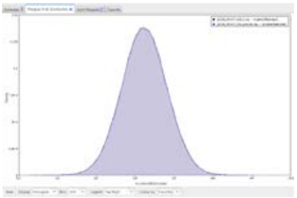
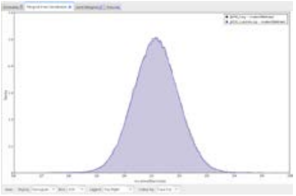
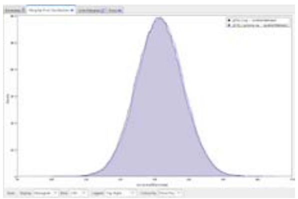
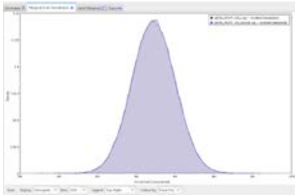
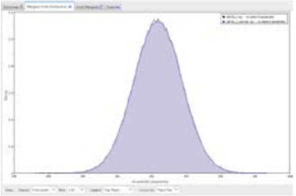
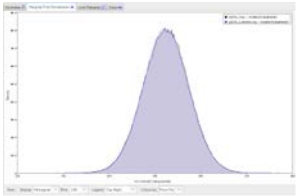
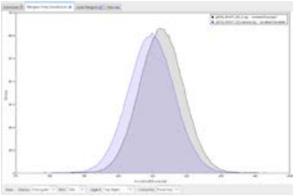
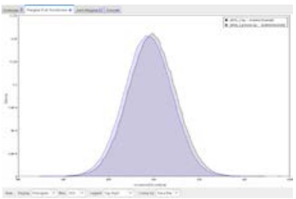
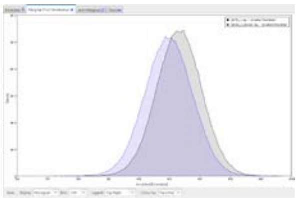
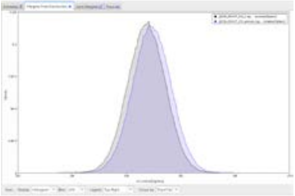
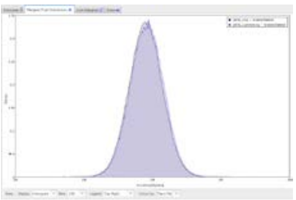
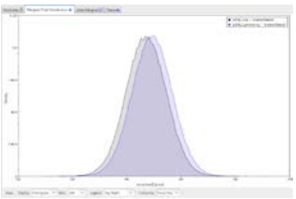
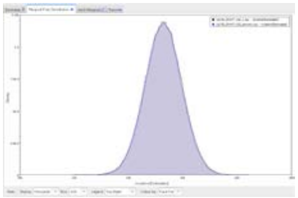
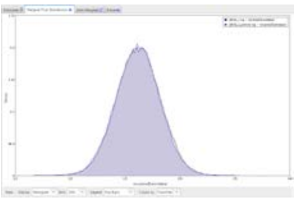
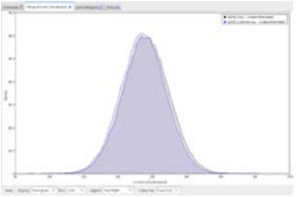
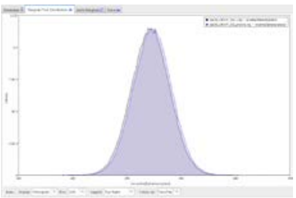
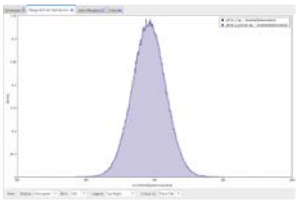
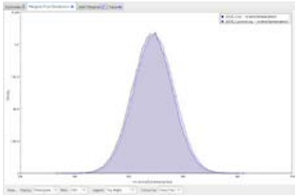
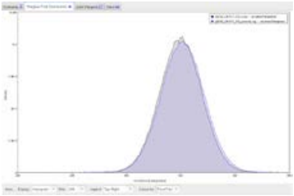
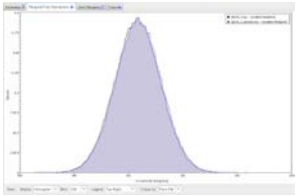
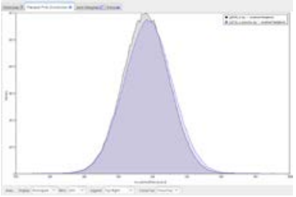
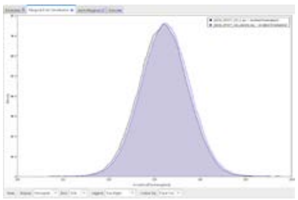
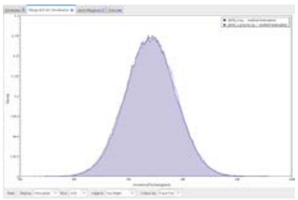
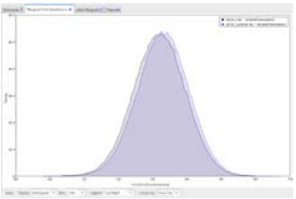
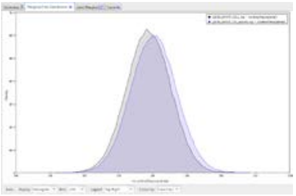
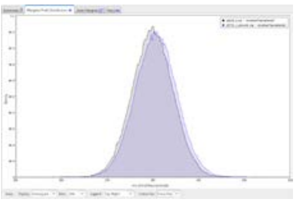
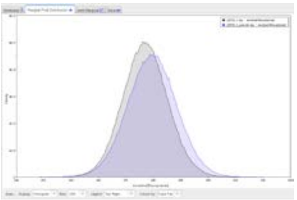
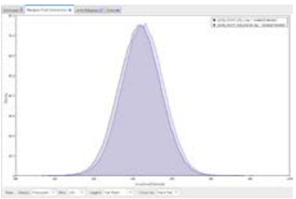
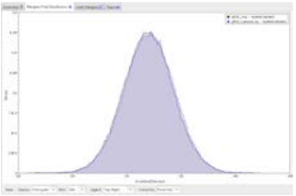
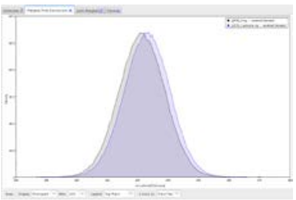
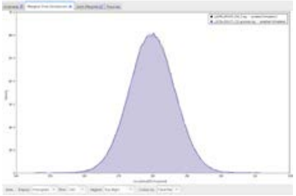
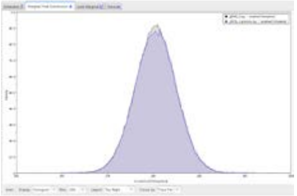
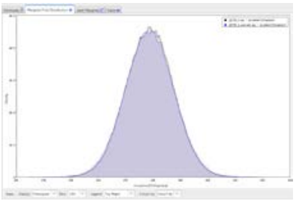
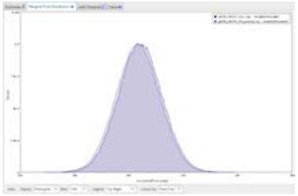
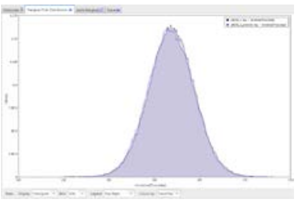
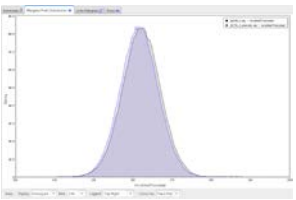
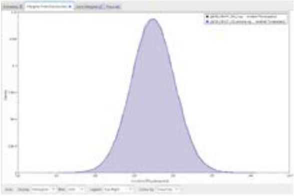
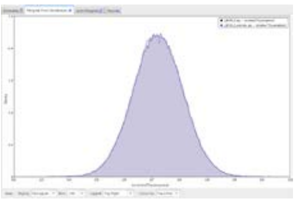
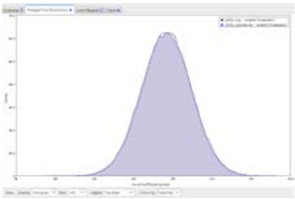
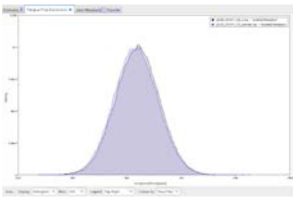
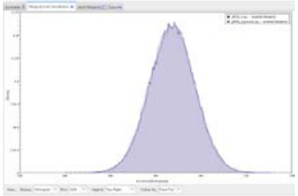
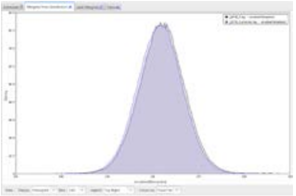
Amphiesmenoptera			
Blattodea			
Coleopterida			
Dicondylia			
Diptera			
Eukinolabia			
Ephemeroptera			

Hemiptera			
Hymenoptera			
Neuropterida			
Odonata			
Orthoptera			
Psocodea			
Thysanoptera			
Notoptera			

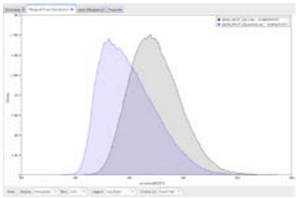
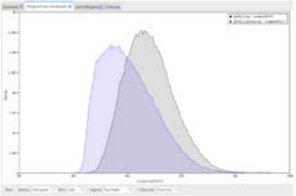
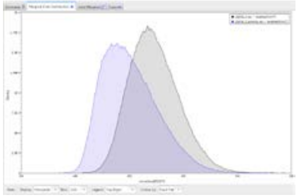
Root			

Table S2. Stem group fossils collected from the fossil insect database Paleobiology Database and EDNA.

Nodes	**Period**	**Age**	**Genus-species**	**References**
Stem Palaeoptera	Carboniferous	Bashkirian 323.2-315.2	*Delitzschala bitterfeldensis*	Brauckmann and Schneider 1996
Stem Orthoptera	Carboniferous	Bashkirian 323.2-315.2	Archaeorthoptera	Béthoux and Nel, 2002
Stem Dictyoptera	Carboniferous	Bashkirian 323.2-315.2	*Qilianiblatta namurensis*	Zhang et al. 2013
Stem Notoptera	Carboniferous	Bashkirian 323.2-315.2	*Sinonamuropteris ningxiaensis*	Peng et al. 2005
Condylognatha - Thripida	Carboniferous	Moscovian 315.2-307	*Westphalothripides oudardi*	Nel et al. 2012
Stem Hymenoptera	Carboniferous	Moscovian 315.2-307	*Avioxyela gallica*	Nel et al. 2013
Stem Coleopterida	Carboniferous	Gzhelia 303.7-298.9	*Stephanastus polinae*	Nel et al. 2013
Mecopterida	Carboniferous	Bashkirian 323.2-315.2	*Westphalomerope maryvonneae*	Nel et al. 2007

Table S3. Taxon sampling of nuclear genes and mitochondrial genomes. The sequence indicated by asterisk was newly sequenced in this study.

		Taxon of 28S rDNA	Acc. No. of 28S rDNA	Taxon of 18S rDNA	Acc. No. of 18S rDNA	Taxon of DPD, RPB1 & RPB2	Acc. No. of DPD1	Acc. No. of RPB1	Acc. No. of RPB2	Taxon of Mt-genomes	Acc. No. of Mt-genomes
Diplura	Campodeidae1	*Lepidocampa weberi*	EU376050	*Lepidocampa weberi*	AY037167	*Lepidocampa weberi*	AB598693	AB596892	AB597583	*Lepidocampa weberi*	NC_022675
	Campodeidae2	*Campodea augens*	EF199977	*Campodea tillyardi*	AF173234	*Metriocampa* sp.	AB598692	AB596891	AB597582	*Campodea lubbocki*	NC_008234
Archaeognatha	Petrobiinae1	*Pedetontus okajimae*	EU376055	*Pedetontus okajimae*	EU368614	*Pedetontus unimaculatus*	AB598694	AB596893	AB597584	*Pedetontus silvestrii*	NC_011717
	Petrobiinae2	Petrobiinae sp. NKU-010	JQ309935	Petrobiinae sp. NKU-010	JQ309931	*Petrobiellus takunagae*	AB598695	AB596894	AB597585	*Petrobiellus sp.*	KJ754503
Zygentoma	Lepismatidae	Lepismatidae sp. NKU-008	JQ309933	Lepismatidae sp. NKU-008	JQ309928	*Nipponatelura* sp.	AB598696	AB596895	AB597586	*Atelura formicaria*	NC_011197
Odonata	Anisozygoptera	*Epiophlebia superstes*	EU424328	*Epiophlebia superstes*	AF461247	*Epiophlebia superstes*	AB598699	AB596898	AB597589	*Epiophlebia superstes*	JX050223
	Zygoptera	*Rimanella arcana*	FJ009944	*Devadatta podolestoides*	FN356078	*Mnais pruinosa pruinosa*	AB598700	AB596899	AB597590	*Vestalis melania*	NC_023233
Ephemeroptera	Setisura	*Epeorus sylvicola*	EU414715	*Macdunnoa hipawinia*	AY749874	*Isonychia japonica*	AB598702	AB596901	AB597592	*Isonychia ignota*	HM143892
	Pisciforma	*Siphlonurus aestivalis*	EU414716	*Edmundsius agilis*	AY749877	*Ephemera japonica*	AB598701	AB596900	AB597591	*Ephemera orientalis*	NC_012645
Phasmatodea	Anareolatae	*Carausius morosus*	EU426878	*Phobaeticus heusii*	AY121184	*Phraortes illepidus*	AB598703	AB596902	AB597593	*Phraortes illepidus*	NC_014695
Embiodea	Oligotomidae	*Oligotoma* sp. NKU-001	HQ857603	*Oligotoma nigra*	Z97593	*Aposthonia japonica*	AB598704	AB596903	AB597594	*Aposthonia japonica*	AB639034
Grylloblattodea	Grylloblattidae	*Galloisiana nipponensis*	DQ457320	*Grylloblatta* sp.	AY521850	*Galloisiana yuasai*	AB598705	AB596904	AB597595	*Grylloblatta sculleni*	DQ241796
Mantophasmatodea	Mantophasmatodea	*Tyrannophasma gladiator*	EU426875	*Tyrannophasma gladiator*	AY521863	*Karoophasma biedouwensis*	AB598706	AB596905	AB597596	*Sclerophasma paresisense*	NC_007701
Orthoptera	Caelifera	*Gomphocerinae* sp. JM-2004	AY859546	*Romalea* sp.	AY521868	*Patanga japonica*	AB598707	AB596906	AB597597	*Gomphocerus sibiricus*	NC_021103
	Ensifera	*Leptophyes punctatissima*	EU414721	*Pterophylla camellifolia*	AY121147	*Euconocephalus varius*	AB598708	AB596907	AB597598	*Conocephalus maculatus*	NC_016696
Plecoptera	Perloidea	*Isoperla* sp. Plec1	EU414717	*Mesoperlina pecircai*	U68400	*Oyamia lugubris*	AB598710	AB596909	AB597600	*Kamimuria wangi*	NC_024033
Dermaptera	Forficuloidea	*Forficula auricularia*	EU426876	*Forficula* sp. NC-1995	X89490	*Forficula hiromasai*	AB598712	AB596911	AB597602	*Challia fletcheri*	NC_018538
Zoraptera	Zorotypidae	*Zorotypus weidneri*	JN192452	*Zorotypus weidneri*	JQ259056	*Zorotypus* sp.	AB598713	AB596912	AB597603	*Zorotypus medoensis*	NC_026077
Mantodea	Mantidae	*Mantis religiosa*	AY859585	*Tenodera aridifolia*	AF423805	*Tenodera aridifolia*	AB598714	AB596913	AB597604	*Tamolanica tamolana*	NC_007702
Blattaria	Ectobiidae	*Ectobius lapponicus*	EU426877	*Blattella germanica*	AF005243	*Blattella nipponica*	AB598715	AB596914	AB597605	*Blattella germanica*	NC_012901
Isoptera	Termopsidae	*Zootermopsis angusticollis*	AY859614	*Hodotermopsis japonica*	AY521856	*Reticulitermes speratus*	AB598716	AB596915	AB597606	*Zootermopsis angusticollis*	NC_018123
Thysanoptera	Terebrantia	*Frankliniella intonsa*	JQ259051	*Frankliniella intonsa*	JQ259051	*Thrips palmi*	AB598717	AB596916	AB597607	*Frankliniella intonsa*	JQ917403
	Tubulifera	*Haplothrips chinensis*	JQ259052	*Haplothrips chinensis*	JQ259052	*Gynaikothrips ficorum*	AB598718	AB596917	AB597608	*Haplothrips aculeatus*	NC_027488
Hemiptera	Aphididae	*Aphis glycines*	JQ259057	*Acyrthosiphon pisum*	U27819	*Uroleucon nigrotuberculatum*	AB598722	AB596921	AB597612	*Acyrthosiphon pisum*	NC_011594
	Cicadidae	Cicadidae sp. NKU-013	JQ309936	*Okanagana utahensis*	U06478	*Cryptotympana facialis*	AB598719	AB596918	AB597609	*Gaeana maculata*	KM244671
	Heteroptera	*Rhaphigaster nebulosa*	EU426880	*Rhaphigaster nebulosa*	X89495	*Anacanthocoris striicornis*	AB598720	AB596919	AB597610	*Hydaropsis longirostris*	NC_012456
Psocoptera	Psocidae	Cerastipsocinae sp. NKU-002	JQ259058	Cerastipsocinae sp.	JQ259054	*Metylophorus* sp.	AB598723	AB596922	AB597613	*Psococerastis albimaculata*	NC_021400
Phthiraptera	Anoplura	*Haematopinus* sp. NKU-011	JQ309932	*Haematopinus* sp.	JQ309927	*Pediculus humanus*	XM_002429812	XM_002426633	XM_002425468	*Ibidoecus bisignatus*	NC_015999
Hymenoptera	Apocrita	*Vespula pensylvanica*	AY859612	*Vespula pensylvanica*	AY859613	*Vespa analis insularis*	AB598725	AB596924	AB597615	*Vespa mandarinia*	NC_027172
	Symphyta	*Tenthredinidae gen.* sp.	EU414729	*Notofenusa surosa*	GQ410584	*Neocolochelyna itoi*	AB598724	AB596923	AB597614	*Tenthredo tienmushana*	KR703581
Megaloptera	Corydalidae	*Acanthacorydalis* sp.	JQ259049	*Archichauliodes* sp.	EU815228	*Protohermes grandis*	AB598726	AB596925	AB597616	*Protohermes concolorus*	NC_011524
Raphidioptera	Raphidiidae	*Raphidiidae sp. Sus1d*	GU169693	*Mongoloraphidia martynovae*	EU815252	*Inocellia japonica*	AB598727	AB596926	AB597617	*Mongoloraphidia harmandi*	NC_013251
Neuroptera	Mantispoidea	Mantispidae sp. NKU-006	JQ259053	*Zeugomantispa minuta*	EU815253	*Chrysoperla nipponensis*	AB598728	AB596927	AB597618	*Chrysoperla nipponensis*	NC_015093
Strepsiptera	Mengenillidae	*Mengenilla sp. BMW-2012*	KC177631	*Caenocholax fenyesi texensis*	DQ026302	*Stichotrema asahinai*	AB598729	AB596928	AB597619	*Mengenilla moldrzyki*	NC_018545
Coleoptera	Polyphaga	*Tenebrio* sp. JMM-2003	AY210843	*Bolitophagus reticulatus*	EF362998	*Tribolium castaneum*	XM_962197	XM_968377	XM_969560	*Tribolium castaneum*	KM009121
	Adephaga	Cicindelidae sp.	KJ825855*	*Cicindela aurulenta*	DQ337114	*Eretes sticticus*	AB598730	AB596929	AB597620	*Aspidytes niobe*	NC_012139
Lepidoptera	Glossata	*Pieris napi*	EU414731	*Anthocharis sara*	AF423785	*Papilio polytes*	AB598732	AB596931	AB597622	*Papilio polytes*	NC_024742
Trichoptera	Integripalpia	Phryganeidae sp. NKU-007	JQ259059	*Pycnopsyche lepida*	AF286292	*Stenopsyche marmorata*	AB598733	AB596932	AB597623	*Eubasilissa regina*	NC_023374
Diptera	Brachycera	*Drosophila melanogaster*	M21017	*Drosophila melanogaster*	M21017	*Drosophila melanogaster*	X88928	NM_078569	BT003265	*Drosophila melanogaster*	NC_024511
	Nematocera	*Anopheles albimanus*	L78065	*Anopheles punctulatus*	AF121062	*Anopheles gambiae*	XM_320778	XM_317690	XM_313416	*Anopheles gambiae*	NC_002084
Mecoptera	Boreidae	*Boreus hyemalis*	EU426882	*Boreus* sp. NC-1995	X89487	*Panorpa takenouchii*	AB598734	AB596933	AB597624	*Neopanorpa pulchra*	NC_013180
Siphonaptera	Pulicidae	*Ctenocephalides felis*	FJ040538	*Archaeopsylla erinacei*	X89486	*Ctenocephalides felis*	AB598735	AB596934	AB597625	*Jellisonia amadoi*	NC_022710

Table S4. Fossil record and prior distributions for different analyses.

Calibration Nodes	Fossils	Age (Ma)	BEAST analyses			Bayesian analysis	References
			±one Stage/Age	**Within certain Stage/Age**	**±two Stage/Age**		
Root	*Rhyniognatha hirsti*	Pragian (410.8±2.8 - 407.6±2.6)	Normal Mean=465.15, SD=28.3	Normal Mean=465.15, SD=28.3	Normal Mean=465.15, SD=28.3	--	Engel and Grimaldi, 2004
Amphiesmenoptera	*Archaeolepis mane*	Sinemurian (199.3±0.3 - 190.8±1.0)	Normal mean=194.7, SD=3.3	Normal mean=194.7, SD=2.4	Normal mean=194.7, SD=6.8	Min=189.8, Max=411	Whalley, 1985, 1986
Blattodea	*Valditermes brenanae*	Hauterivian (132.9-129.4)	Normal Mean=131.15, SD=2.9	Normal Mean=131.15, SD=0.8	Normal Mean=131.15, SD=6.9	Min=129.4, Max=411	Jarzembowski, 1981; Engel et al., 2009
Coleopterida = (Strepsiptera+Coleoptera)	*Triaplus sibiricus*	Changhsingian-Induan (254.14±0.07 - 251.2)	Normal Mean=252.71 SD=2.8	Normal Mean=252.71, SD=0.7	Normal Mean=252.71, SD=5.0	Min=251.2, Max=411	Volkov, 2013
Dicondylia	*Rhyniognatha hirsti*	Pragian (410.8±2.8 - 407.6±2.6)	Normal Mean=409.3, SD=6.7	Normal Mean=409.3, SD=2.6	Normal Mean=409.3, SD=7.8	Min=405, Max=521	Engel and Grimaldi, 2004
Diptera	*Archilimonia vogesiana*	Anisian (247.2 - 242.0)	Normal Mean=244.6, SD=3.5	Normal Mean=244.6, SD=1.2	Normal Mean=244.6, SD=3.7	Min=242.0, Max=411	Krzemiński and Krzemińska, 2003; Zhang, 2011
Eukinolabia = (Embiodea+Phasmatodea)	*Cretophasmomima melanogramma*	Barremian-Early Aptian (129.7 ± 0.5 - 122.1 ± 0.3)	Normal Mean=126, SD=3.4	Normal Mean=126 SD=2.0	Normal Mean=126, SD=6.8	Min=121.8, Max=411	Wang et al., 2014
Ephemeroptera	*Triassonurus doliiformis*	Anisian (247.2 - 242.0)	Normal Mean=244.6, SD=3.5	Normal Mean=244.6, SD=1.2	Normal Mean=244.6, SD=3.7	Min=242.0, Max=521	Sinitshenkova and Marchal-Papier, 2005
Hemiptera	*Aviorrhyncha magnifica*	Moscovian (315.2±0.2-307.0±0.1)	Normal Mean=311.15, SD=3.9	Normal Mean=311.15, SD=2.1	Normal Mean=311.15, SD=6.9	Min=306.9, Max=411	Nel et al., 2013
Hymenoptera	*Triassoxyela foveolata*	Carnian (237.0 – 227.0)	Normal Mean=232.0, SD=5.3	Normal Mean=232.0, SD=2.3	Normal Mean=232.0, SD=7.5	Min=227.0, Max=411	Rasnitsyn, 1964; Ronquist et al., 2012
Neuropterida	*Elmothone martynovae*	Artinskian – Kungurian (290.1±0.26 - 272.3±0.5)	Normal Mean=281.08, SD=6.6	Normal Mean=281.08, SD=4.5	Normal Mean=281.08, SD=8.8	Min=271.8, Max=411	Carpenter, 1976
Odonata	*Triassothemis mendozensis*	Carnian (237.0 - 227.0)	Normal Mean=232, SD=5.3	Normal Mean=232, SD=2.3	Normal Mean=232, SD=7.5	Min=227.0, Max=521	Carpenter, 1960
Orthoptera	*Raphogla rubra*	Artinskian- Kungurian (290.1±0.26 - 272.3±0.5)	Normal Mean=281.08, SD=6.6	Normal Mean=281.08, SD=4.5	Normal Mean=281.08, SD=8.8	Min=271.8, Max=411	Béthoux et al., 2002
Psocodea	*Paramesopsocus adibi*	Callovian-Oxfordian (166.1±1.2 - 157.3±1.0)	Normal Mean=161.8, SD=4.0	Normal Mean=161.8, SD=2.5	Normal Mean=161.8, SD=4.8	Min=156.3, Max=411	Azar et al., 2008; Mockford et al., 2013
Thysanoptera	*Tethysthrips libanicus*	Barremian (129.4 - 125.0)	Normal Mean=127.2, SD=2.8	Normal Mean=127.2, SD=0.9	Normal Mean=127.2, SD=6.5	Min=125.0, Max=411	Nel et al., 2010
Notoptera	*Juramantophasma sinica*	Callovian – Oxfordian (166.1±1.2 - 157.3±1.0)	Normal Mean=161.8, SD=4.0	Normal Mean=161.8, SD=2.5	Normal Mean=161.8, SD=4.8	Min=156.3, Max=411	Huang et al., 2008

File S5. Detailed phylogenetic justification and age justification for each fossil item.

i) Fossil specimen: *Rhyniognatha hirsti* Tillyard, 1928

Phylogenetic justification:

The anterior mandibular articulation of *R. hirsti* forms an acetabulum (socket) on the inner angle of the appendage. This trait demonstrates that they are dicondylic, a mandibular form known only within the insects and corresponding to a monophyletic lineage comprising the Zygentoma and Pterygota. The mandibles of *Rhyniognatha* also are of the cutting form found only in metapterygotes (= Odonatoptera + Neoptera), a result of the close position of the posterior condyle to the anterior acetabulum and restructuring of the mandible into a more triangular form, demonstrating that *Rhyniognatha* possessed wings (Engel and Grimaldi 2004). Thus, characters of its mandibular form implies “metapterygote” affinities and accordingly crown-group membership within Insecta (and even within Pterygota).

Age justification:

Rhyniognatha hirsti is found in the Rhynie Chert of Aberdeenshire, Scotland. Spore assemblages that stratigraphically underly the Rhynie Chert are dated to the early Pragian to early Emsian (Wellman 2004, 2006; Parry et al., 2011; Wolfe et al., 2016). Based on this evidence a minimum age constraint may be defined at 405.0 Ma for the Rhynie Chert, using the Pragian-Emsian boundary (407.6 Ma ± 2.6 Myr) as a reference.

ii) **Fossil specimen:** *Triassonurus doliiformis* Sinitshenkova et al., 2005

Phylogenetic justification:

Triassonurus doliiformis has morphological features suggesting an affinity with the modern family Siphlonuridae, specifically large, non-flattened nymphs with a head longer than the prothorax, a massive mesothorax and considerably reduced metathorax, broad forewing pads that nearly completely cover the hind pads, abdominal segments lacking sharp denticles, large and rounded tergaliae, and elongate cerci and paracercus (Sinitshenkova et al., 2005; Wolfe et al., 2016). Siphlonuridae are within crown-group Ephemeroptera (Ogden et al., 2009).

Age justification:

Triassonurus doliiformis was found in the Grès-a-Voltzia Formation, Vosges, northeastern France (Gall and Grauvogel-Stamm, 1993). Sequence stratigraphy correlates the Grès-a-Voltzia Formation to the middle Anisian stage (Bourquin et al., 2006, 2007), the upper boundary of which is ca. 242 Ma (Cohen et al., 2013), and which may be used as a minimum age (Wolfe et al., 2016).

iii) Fossil specimen: *Triassothemis mendozensis* Carpenter, 1960.

Phylogenetic justification:

Triassothemis mendozensis is the earliest species of the extinct family Triassolestidae (Nicholson et al., 2015). Davis et al. (2011) support the placement of Triassolestidae within crown-group Epiprocta (= Anisozygoptera + Anisoptera) based on combination of molecular data and morphological characters.

Age justification:

Triassothemis mendozensis was recovered from the Potrerillos Formation of Mendoza, Argentina (Martins-Neto et al., 2008). U-Pb dating of zircons from the uppermost tuff layer of the formation provides an age of 230.3 Ma ± 2.3 Myr, or Carnian (Spalletti et al., 2009), and allowing for a minimum age of 228.0 Ma for *T. mendozensis* (Wolfe et al., 2016).

iv) Fossil specimen: *Raphogla rubra* Béthoux et al., 2002

Phylogenetic justification:

Raphogla rubra likely belongs to the stem of Gryllidea + Tettigoniidea, as evidenced by the broad area between Sc and the anterior wing margin; the moderately long Rs basal to the fusion with MA1a; and MP + CuA1 with merely one simple, anterior branch (Béthoux et al., 2002). Both Gryllidea and Tettigoniidea belong to the crown-group of Ensifera and accordingly *R. rubra* belongs to crown-group Orthoptera.

Age justification:

Raphogla rubra was uncovered from site F21D of the Salagou Formation in Hérault, France (Béthoux et al., 2002). U-Pb dating of zircons from tuff beds near the lower two-thirds of formation, corresponding to the Octon Member, recovered an age in the Artinskian (Michel et al., 2015). Based on this dating, the overlying Mérifrons Member has been inferred to start in the Artinskian and continuing into the Kungurian (Michel et al., 2015). Unfortunately, the precise layer of F21D within the Mérifrons Member is not known (Michel et al., 2015). Accordingly, we have followed Wolfe et al. (2016) and conservatively employed the upper boundary of the Kungurian (272.3 Ma ± 0.5 Myr) as a minimum age.

v) Fossil specimen: *Juramantophasma sinica* D. Huang et al., 2008

Phylogenetic justification:

Juramantophasma sinica shares traits with crown-group Mantophasmatodea, a suborder within Notoptera. Of particular importance is the presence of an elongate, dorsal process on the third tarsomere, the orthogonal orientation of the distal tarsomere relative to the preceding tarsomeres, the presence of enlarged and fan-shaped pretarsal arolia, and short, claw-like gonoplacs (Huang et al., 2008). The unsegmented cerci excludes the species from crown-group Grylloblattodea and a conservative placement for *J. sinica* is in the stem-group to Mantophasmatodea. Thus, the species at least belongs to Notoptera (=Grylloblattodea + Mantophasmatodea) (Wolfe et al., 2016).

Age justification:

Juramantophasma sinica is from the Jiulongshan Formation of the famous Daohugou Beds in Inner Mongolia, China (Huang et al., 2008). 40Ar/39Ar and U-Pb radiometric dating of ignimbrites has recovered dates from 165 Ma ± 2.5 Myr to 158.7 Ma ± 0.6 Myr (e.g., Chang et al., 2009a; Peng et al., 2012). Given that the fossiliferous shales overlay the volcanic deposits (Gao and Ren, 2006), they are correspondingly younger in age. The fossil beds correlate with Oxfordian sediments in Kazakhstan and China

(Zhang, 2015). Wolfe et al. (2016) have provided a conservative minimum age based on the radiometric evidence at 158.1 Ma (Oxfordian).

vi) Fossil specimen: *Cretophasmomima melanogramma* Wang et al., 2014

Phylogenetic justification:

Cretophasmomima melanogramma shares a strong twig-like appearance resulting from an elongation of the meso- and metathoracic segments with Phasmatodea (Wang et al., 2014). However, the lack of synapomorphies with crown-Phasmatodea such as the vomer and forceps-like extensions of the 10th abdominal tergum, indicate that it is likely part of stem-group Phasmatodea (Wang et al., 2014), and certainly within crown-Eukinolabia.

Age justification:

This fossil was discovered in the Yixian Formation, Liutiaogou Village, Ningcheng Country, Inner Mongolia, China (Wang et al., 2014). The Yixian Formation sits beneath the Jiufotang Formation and overlays the Tuchengzi Formation (Chang et al., 2009b; Zhou, 2006). 40Ar/39Ar radiometric dating has given ages of 129.7 Ma ± 0.5 Myr for basalts from Yixian Formation's bottom, and 122.1 Ma ± 0.3 Myr for tuff layers at the bottom of the Jiufotang Formation (Chang et al., 2009b: see also Zhou, 2006). A conservative minimum age of 121.8 Ma is appropriate for fossils from the Yixian Formation (Wolfe et al., 2016).

vii) Fossil specimen: *Valditermes brenanae* Jarzembowski, 1981

Phylogenetic justification:

Valditermes brenanae has been included in cladistic studies of morphological data and a placement in the stem of Mastotermitidae was recovered (Engel et al., 2009, 2016). Given that Mastotermitidae is the surviving sister group to all other Isoptera (Krishna et al., 2013; Djernæs et al., 2015), the species may be considered as part of the crown-group to Dictyoptera, and more precisely as crown-group Isoptera.

Age justification:

The holotype of *V. brenanae* originated from the Clockhouse Brickworks, Surrey, England (Jarzembowski, 1981), and from fossiliferous concretions of the Weald Clay Formation (Anderson, 1985). Wolfe et al. (2016) have summarized that among included ostracods the species *Cytheridea tuberculata* indicates placement in the Lower Weald Clay, at BGS Bed 3a (Anderson, 1985; Ross and Cook, 1995), and that based on palynomorphs the boundary between the Lower and Upper Weald Clay corresponds to the Hauterivian-Barremian boundary (Ross and Cook, 1995). The upper boundary of the Hauterivian (~129.4 Ma: Cohen et al., 2013), may therefore serve as a minimum age.

viii) Fossil specimen: *Tethysthrips libanicus* Nel et al. 2010

Phylogenetic justification:

Tethysthrips libanicus can be placed among the 'higher' Thripidae owing to the presence of forked and long 'trichomes' on the third and fourth antennomeres (Mound et al. 1980; Nel et al., 2010). *Tethysthrips* also share a narrowed forewing, the absence of a pretarsal hamus, well-defined abdominal pleurites, and a well-developed, down-curved ovipositor (Nel et al., 2010).

Age justification:

Tethysthrips libanicus is represented by an amber inclusion from the Mdeyrij-Hammana outcrop, Baabda District, Lebanon (Nel et al., 2010). Maksoud et al. (in press) demonstrate an early Barremian age for the amber-bearing sediments, and, like Wolfe et al. (2016), we use a minimum age of 125.0 Ma.

ix) Fossil specimen: *Aviorrhyncha magnifica* Nel et al., 2013

Phylogenetic justification:

Aviorrhyncha magnifica has two synapomorphies of Euhemiptera (i.e., the group sister to Sternorrhyncha and containing all remaining extant Hemiptera): presence of an ambient vein and a well-developed concave CP (Nel et al., 2013). In contrast to most extant Euhemiptera, cua-cup is not zigzagged, and accordingly Nel et al. (2013) considered *A. magnifica* as stem-group Euhemiptera.

Age justification:

The species was discovered at the Terril No. 7 locality of the Avion outcrop, in Pas-de-Calais, France (Nel et al., 2013). This outcrop has been dated to Westphalian C/D (Bolsovian/Asturian), equivalent to the uppermost Moscovian of the Pennsylvanian (Nel et al., 2013; Richards, 2013). This allows for a minimum age of 306.9 Ma, using the upper boundary of the Moscovian (307.0 ± 0.1 Ma: Cohen et al., 2013).

x) Fossil specimen: *Paramesopsocus adibi* Azar et al. 2008

Phylogenetic justification:

Paramesopsocus adibi has the typically sclerotized and thickened pterostigma of the family Paramesopsocidae (Azar et al., 2008). The presence in the wing of well-developed veins Sc and A2 demonstrate that *Paramesopsocus* do not belong to Psocomorpha (Azar et al., 2008), and Mockford et al. (2013) have assigned the species to Electrentomidae.

Age justification:

This fossil was found at Karatau in southern Kazakhstan, and in the lacustrine-siltstones of the Karabastau Formation (Callovian/Oxfordian). The upper boundary of the Oxfordian is 157.3±1.0 Ma (Cohen et al., 2013), and provides a minimum age at 156.3 Ma.

xi) Fossil specimen: *Triassoxyela foveolata* Rasnitsyn, 1964

Phylogenetic justification:

Triassoxyela foveolata was recovered as stem-group Xyelidae in the cladistic analysis of Ronquist et al. (2012), but overall the wing venation is plesiomorphic for Xyelomorpha (Rasnitsyn, 1964, 1980), particularly in the retention of all primary veins. Nonetheless, the venation is overall characteristic for Hymenopterida (Rasnitsyn, 1964).

Age justification:

As elaborated by Wolfe et al. (2016), *T. foveolata* was found in the Madygen Formation, near the Fergana Valley, Kyrgyzstan. Paleobotanical evidence correlates the Madygen to the upper Keuper lithographic unit (Ladinian-Carnian: Dobruskina, 1995), and with the Cortaderitian Stage of Gondwana owing to the abundance of *Scytophyllum* (Morel et al., 2003). Wolfe et al. (2016) summarize the radiometric evidence that supports a minimum age of 227 Ma (Carnian upper boundary).

xii) Fossil specimen: *Elmothone martynovae* Carpenter, 1976

Phylogenetic justification:

Elmothone martynovae belongs to the extinct family Permithonidae. Morphological characters demonstrate placement of Permithonidae (=Protoneuroptera of Grimaldi and Engel, 2005), as the sister group to Neuroptera (Ren et al., 2009). Although permithonid monophyly is inconclusive and placement of other permithonids is obscure (Prokop et al., 2015), the presence of a straight apex to vein RA vein at the minimum establishes the species as part of this group (see also Wolfe et al., 2016).

Age justification:

This fossil was found at Elmo, Dickinson County, Kansas and in the Carlton Limestone Member of the Wellington Formation (Zambito et al., 2012; Prokop et al., 2015). Wolfe et al. (2016) note that the insect-bearing layer is correlated with the Leonardian regional Stage (Zambito et al., 2012), and on the basis of conchostracan biostratigraphy (Tasch, 1962). Given that the Leonardian spans the Artinskian and Kungurian Stages (Henderson et al., 2012), and that the upper boundary of the latter is at 272.3 Ma ± 0.5 Myr, a conservative minimum age of 271.8 Ma is employed (Wolfe et al., 2016).

xiii) Fossil specimen: *Triaplus sibiricus* Volkov, 2013

Phylogenetic justification:

Triaplus sibiricus belongs to the extinct family Triaplidae owing to the following traits: elongate beetle with comparatively smooth elytra, lacking punctate grooves; procoxae contiguous, without intercoxal process; metacoxae completely separating metaventrite from abdomen, long, with large metafemoral plates covering basal abdominal sterna; length of metacoxa subequal to its width (Volkov, 2013). Putative apomorphies of Adephaga, but excluding Triaplidae and Gyrinidae, are the presence of a ventral procoxal joint and a posteriorly elongate prosternal process (Beutel et al., 2013), and their absence are presumably plesiomorphies for Triaplidae.

Age justification:

The fossil was discovered in the Mal’tseva Formation, Babii Kamen, Novokuznetsk District, Kemerovo Region, Russia (Volkov, 2013). The Babii Kamen locality sits slightly above the Permian-Triassic boundary and the boundary of the Induan, at ~251.2 Ma (Cohen et al., 2013), is used as a minimum age.

xiv) Fossil specimen: *Archaeolepis mane* Whalley, 1985

Phylogenetic justification:

The holotype specimen of *A. mane* is an isolated hind wing, preserving some venation but more importantly bearing scales, the latter of which excludes the species from crown-group Trichoptera (Whalley, 1985, 1986). The scales demonstrate placement in Amphiesmenoptera and the presence of a single Sc branch in the venation of *A. mane* excludes the species from the groundplan of Lepidoptera (Kukalová-Peck and Willmann, 1990; Minet et al., 2010; Sukatsheva and Vassilenko, 2011). Placement as crown-Lepidoptera cannot be determined (Schachat and Brown, 2015), but placement among the stem-group is likely based on the hind wing scales (Whalley, 1986).

Age justification:

Archaeolepis mane was found in the 'Shales with Beef' (Lang et al., 1923), and specifically a calcareous flatstone layer of the *Caenisites turneri* ammonoid Zone (Sohn et al., 2012). Chemostratigraphic evidence places this zone within the middle Sinemurian (Jenkyns et al., 2002), and the upper boundary provides a minimum age of 195.3 Ma (Wolfe et al., 2016).

xv) Fossil specimen: *Archilimonia vogesiana* Krzemiński and Krzemińska, 2003

Phylogenetic justification:

Although originally placed in an extinct family as Archilominiidae (Krzemiński and Krzemińska, 2003), the species has been supported within Pediciidae, a family placed by Petersen et al. (2010) as sister to all other Tipuloidea. Pediciidae have many morphological features considered similar to the tipuloid groundplan: a large, well-sclerotized larval head capsule, presence of ommatrichia, and a Sc2 vein proximal to Rs in the wing (Oosterbroek & Theowald, 1991; Starý, 1992; Petersen et al., 2010).

Age justification:

The fossil was found at Bust, Vosges, France, and in an Aegean delta plain claystone/siltstone of the Gres-a-Voltzia Formation. Bourquin et al. (2006, 2007) correlate the Grès-a-Voltzia Formation to the middle Anisian based on sequence stratigraphy. We therefore use the upper boundary of the Anisian at ~242 Ma (Cohen et al., 2013) as a minimum age.

xvi) Fossil specimen: *Yicaris dianensis* Zhang et al., 2007

Phylogenetic justification:

Phylogenetic morphological analyses as well as simultaneous analyses with DNA sequence data place *Y. dianensis* within crown-group Pancrustacea (Edgecombe, 2010; Legg et al., 2013; Oakley et al., 2013; Wolfe and Hegna, 2014). Of particular importance are the presence of epipodites on the thoracic appendages; paddle-shaped mandibular and maxillary exopods; and the protopodite of post-mandibular appendages formed as soft, setiferous endites (Wolfe et al., 2016).

Age justification:

Yicaris dianensis was recovered from the Yu'anshan Formation in Yunnan Province, China and has been attributed to the *Eoredlichia-Wutingaspis* Biozone (Zhang et al., 2007), although this biozone is no longer recognized (Peng, 2003, 2009). *Eoredlichia* are known to co-occur with *Hupeidiscus*, and this is diagnostic of the

Hupeidiscus-Sinodiscus Biozone — a formally recognized biozone of the Nangaoan Stage in China (Peng and Babcock, 2008). The Nangaoan Stage is the third stage of the Cambrian System (Peng et al., 2012), therefore a maximum constraint can be placed for its lower boundary at 521 Ma (Peng et al., 2012; Peng and Babcock, 2008; Wolfe et al., 2016).

Fig. S1. Phylogenetic trees inferred from matrix 1, i.e., the combined dataset of rDNAs and protein-coding genes. A) ML topology with DNA model applied to the paired sites of rDNAs, B) MP topology, C) ML topology with Doublet model applied to the paired sites of rRNAs. Posterior probabilities and bootstrap values are shown at each node, respectively.

Fig. S2. Phylogenetic trees inferred from matrix 2, i.e., the combined dataset of nuclear genes and the first codon positions of mitochondrial PCGs. A) BI topology, B) ML topology, C) MP topology. Posterior probabilities and bootstrap values are shown at each node, respectively.

Fig. S3. Phylogenetic trees inferred from matrix 3, i.e., the combined dataset of nuclear genes and the second codon positions of Mitochondrial PCGs. A) BI topology, B) ML topology, C) MP topology. Posterior probabilities and bootstrap values are shown at each node, respectively.

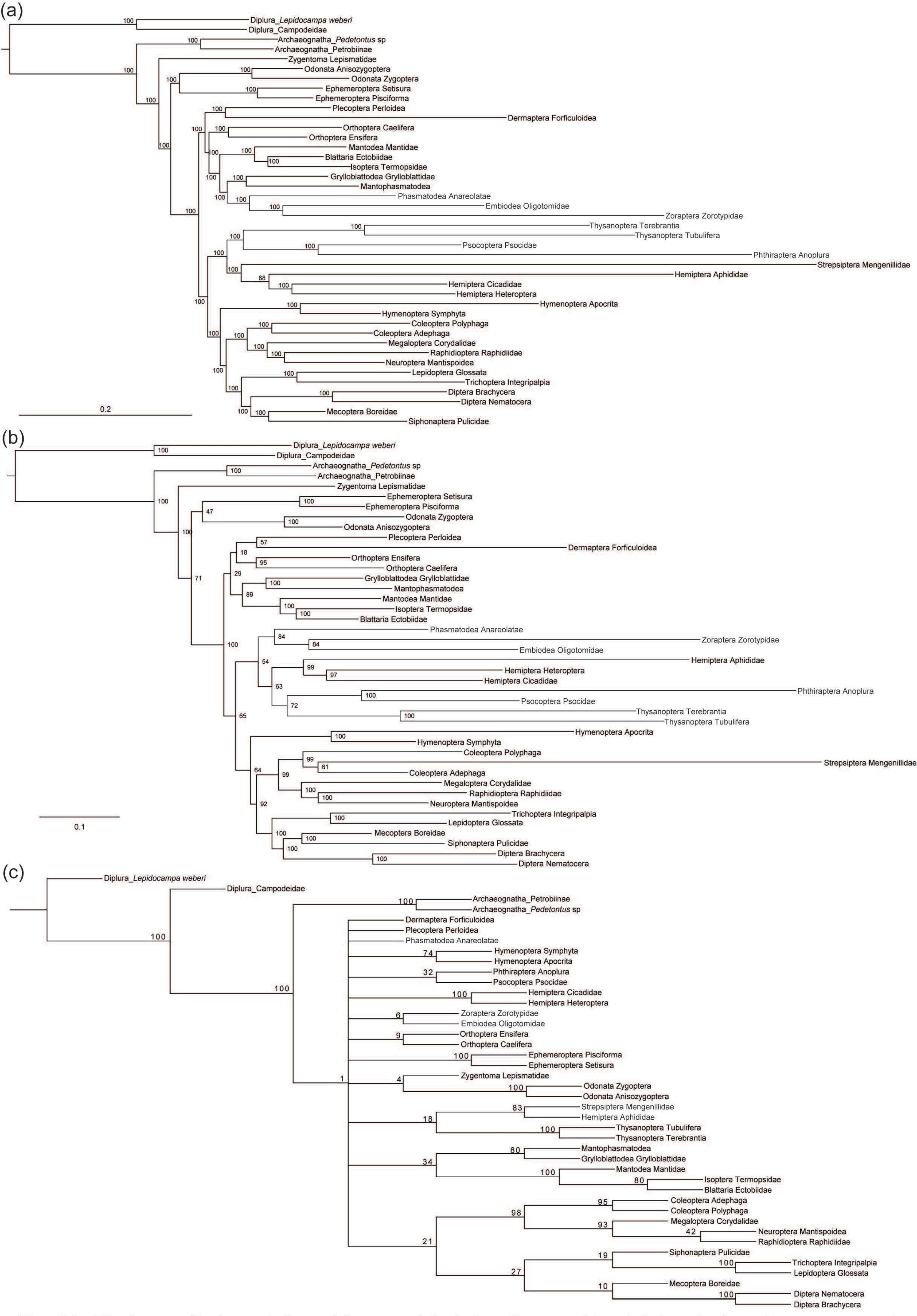


Fig. S4. Phylogenetic trees inferred from matrix 4, i.e., the combined dataset of nuclear genes and the first two codon positions of mitochondrial PCGs. A) BI topology, B) ML topology, C) MP topology. Posterior probabilities and bootstrap values are shown at each node, respectively.

Fig. S5. Phylogenetic trees inferred from matrix 5, i.e., the combined dataset of nuclear genes and the amino acid sequences of mitochondrial PCGs. A) BI topology, B) ML topology, C) MP topology. Posterior probabilities and bootstrap values are shown at each node, respectively.

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