

# Supporting Information

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## SI Materials and Methods

**Taxon Sampling.** We analyzed up to 8 kb of DNA sequence data from a worldwide sample of 135 weevil genera representing all 7 weevil families, all 26 weevil subfamilies, and 97 genera representing most major tribes in the extraordinarily diverse family Curculionidae (supporting information (SI) Table S1 and Table S3). Outgroups included 7 subfamilies of basal Chrysomeloidea and *Ericmodes sylvaticus* (Protocucujidae), a member of the closely related superfamily Cucujoidea. Six genes (2 mitochondrial and 4 nuclear) were used in this study: *cytochrome oxidase I*, *18S rDNA*, *28S rDNA*, *16S rDNA*, *Elongation Factor-1 $\alpha$* , and *Arginine Kinase (AK)*. All *16S rDNA* (1), and select other sequences, were obtained from GenBank. For some genera, chimeras were constructed from sequences for different species to reduce the amount of missing data. All taxa except *Atractuchus* (18S), *Brachycerus* (28S, 18S), *Bruchela* (18S), *Caenominius* (28S, 18S), *Gonipterus* (18S, 28S), *Ithycerus* (18S, EF1 $\alpha$ ), *Microcerus* (18S), and *Nemonyx* (18S) were represented by DNA sequence data from at least 3 of the 6 genes targeted. We used a *16S rDNA* sequence of *Cheloderus* (Oxypeltidae) from GenBank in lieu of a comparable sequence for the closely related outgroup taxon *Oxypeltus* (Oxypeltidae). Overall, our supermatrix contained sequences for  $\approx 70\%$  of the 858 possible taxon-by-gene combinations (see Table S3). Voucher specimens are deposited at the Harvard University Museum of Comparative Zoology, and nucleotide sequences newly determined here have been deposited in GenBank.

**DNA Isolation and Amplification.** Protocols for DNA isolation and amplification are reported in refs. 2 and 3, with differences as follows: We amplified double-stranded DNA in 8- to 25- $\mu$ l reactions (depending on the gene amplified and other factors) using published or optimized primers (Table S5). All reactions were initially denatured at 94 °C, but the duration of denaturation, and the temperature, duration, and number of cycles of annealing and extension varied by gene. All reactions were performed on MJ Dyad, MJ PTC-200 (MJ Research), and MyCycler (Bio-Rad) thermal cyclers. Amplified *18S* PCR products were cleaned using an exonuclease and alkaline phosphatase protocol (3). Amplified fragments of all other genes were gel purified using a Qiagen QIAquick Gel Purification Kit (Qiagen) before sequencing.

**DNA Sequencing.** Amplified, cleaned PCR products were used in sequencing reactions employing BigDye Terminator chemistry [Applied Biosystems Inc.(ABI)]. Primers used for amplification served as sequencing primers, except when additional internal primers were designed to provide overlapping sequences for large fragments (see Table S5). Cycle sequencing reactions were mostly performed in 10- $\mu$ l reactions: 1.5  $\mu$ l ABI Prism BigDye Terminator 3.1, 1.0  $\mu$ l 5 $\times$  buffer, and 0.33  $\mu$ l each (10  $\mu$ M) primer. The remainder of the mixture was composed of water and template DNA (varied by gene and as needed to adjust DNA concentration). Cycle sequencing reactions consisted of an initial denaturation at 94 °C for 2 min, followed by 25 cycles of 10s at 94 °C denaturation, 5 s at 57 °C annealing and 4 min at 60 °C. Sequencing was performed on ABI 3100 and ABI 3730 DNA sequencers.

**Sequence Alignment.** DNA sequences were edited and preliminarily aligned using the program Sequencher 4.6 (Genecodes). Subsequent alignment was performed with the program Clust-

alX 1.831 (4) using the default settings. The resulting alignment for each gene was adjusted “by eye” in the program MacClade 4.06 (5). Regions of ambiguous alignment in *16S*, *18S*, and *28S*, and introns in *EF 1- $\alpha$*  and *AK* were removed. The individual alignments for each gene were then concatenated in MacClade, and the resulting aligned matrix (6 genes,  $\approx 8$  kb) used in subsequent analyses.

**Phylogenetic Analyses.** Phylogenetic analyses were conducted on the 8-kb molecular supermatrix using Bayesian and ML inference. A partitioned ML BS analysis (1,000 inferences, 12 partitions, CAT substitution model, individual per partition branch-length optimization) was implemented in the program RAXML version 7.04 (6) using the CIPRES cluster at the San Diego Supercomputing Center. Partitions were: *28S*, *18S*, *16S*, *COI* (separate partitions for first, second, and third positions), *EF1- $\alpha$*  (separate partitions for first, second, and third positions), and *AK* (separate partitions for first, second, and third positions). Partitioned BI analyses (12 partitions, GTR+I+ $\Gamma$ , estimated base frequencies, four  $\Gamma$  categories) were implemented in the program BEAST 1.4.7 (7). Analyses employing an unweighted-pair group method with arithmetic mean or random starting tree failed to execute (returning the “initial model is invalid” error), so we obtained a more optimal starting tree by executing a preliminary run of  $10^6$  generations with monophyly constraints on the ingroup, outgroup, all weevil families, and select subfamilies of Curculionidae (Dryophthorinae, Platypodinae, and Scolytinae). We used the last tree (with branch lengths) obtained from this analysis as a starting tree for subsequent more thorough analyses. We ran 2 separate BEAST analyses on the maximum- and minimum-age constrained data sets, each with a constraint on the monophyly of the ingroup (but no other monophyly constraints). We ran two BEAST analyses on the maximum- and minimum-age data sets (65–75 million generations, preburnin  $10^6$  generations, sampling every 1,000 generations), for a total of 4 separate analyses. All trees were rooted with *Ericmodes sylvaticus* based on refs. 8 and 9. Graphical and statistical analyses implemented in the program Tracer 1.4 (10) were used to assess convergence and otherwise check performance and accuracy of the BEAST analyses. Specifically with regard to convergence, a trace plot of log-likelihoods from the BEAST output (ultimately, the last 5 million generations from each run) showed no obvious trends or large-scale fluctuations. This suggested that the Markov Chain Monte Carlo had converged and that mixing was adequate. We also used Tracer to assess effective sample size and to analyze/evaluate the marginal posterior probability distribution of select parameters (e.g., mutation rate and tree height) from the BEAST analyses. Based on these analyses, we imposed a very conservative burn-in on each tree file, then combined the last 5,000 trees from each of the paired minimum- and maximum-age analyses (for a total of 10,000 trees), and used these to estimate PPs, to obtain maximum clade-credibility trees, and to estimate divergence times (see below) and associated 95% confidence intervals for the minimum- and maximum-age analyses [using the programs LogCombiner 1.4.7, PAUP\* 4.03b10 (11), and TreeAnnotator 1.4.7]. BS values  $\geq 90\%$  (under ML) or posterior probability values  $\geq 0.95$  (under BI) were considered to constitute strong internodal support, while BS values  $\geq 75\%$  (and  $< 90\%$ ) or posterior probability values  $\geq 0.80$  (and  $< 0.95$ ) were considered to constitute moderate internodal support.

**Testing Alternative Phylogenetic Hypotheses.** We investigated the degree to which select alternative phylogenetic hypotheses were supported by our data by estimating the posterior probabilities of alternative topologies (under BI), and by comparing the ML trees obtained with and without monophyly constraints on each group of interest using the KH test (12), as implemented in PAUP. The KH test is in principle not appropriate in this situation; that is, it is insufficiently conservative because the individual topologies compared were chosen in advance. However, because we recovered no significant *P*-values, more appropriate tests, such as the Shimodaira-Hasegawa test (13) and the Approximately Unbiased test (14), which are more conservative, also will not recover significant *P*-values. For the KH test, constraint trees were prepared in MacClade, and a thorough ML search was performed on each in RAxML using the CIPRES cluster (12 partitions, GTR+I+G substitution model, individual per partition branch-length optimization). The significance of differences between trees was determined with a BS test (1,000 replicates, resampling estimated log likelihoods approximation) imposing the parameter estimates and base frequencies estimated from the ML tree without partitions.

**Divergence-Time Estimates.** Divergence times were coestimated with phylogeny using the Bayesian relaxed molecular clock method (15) in the program BEAST (7). We assumed the uncorrelated lognormal prior model of rate change, a Yule prior process to model speciation, and used automatic tuning of operators. We conservatively selected and applied fossil age

constraints from 2 recent reviews (16, 17), using only the oldest fossils that could be unequivocally assigned (based on character evidence) to extant weevil subfamilies or families (Table S4). Consequently, several fossils were excluded from use as constraints because their age or identity was uncertain, or their placement was rendered equivocal by paraphyly or polyphyly in preliminary analyses. The stage boundaries and terminology we used follow ref. 18. Prior estimates for the divergence dates for selected nodes were specified using uniform distributions, except for the ingroup root node, for which we had sufficient information to specify a transformed lognormal distribution with a “hard” minimum bound based on the minimum age of the oldest unequivocal fossil weevil (150.8 Ma; with 0% probability of the divergence being younger than this date) (see Table S4), a mean estimate of 171.5 Ma based on a mean estimate for the age of Curculionoidea from ref. 8, and a “soft” maximum bound based on the maximum age reported in ref. 8 for the series Cucujiformia (236.2 Ma, with 5% probability of the divergence being older than this date). The minimum bounds placed on uniform distributions were based on the minimum age of the oldest unequivocal fossil for a given taxon. The maximum bounds represent the oldest age plausible for a given taxon based on palaeontological or other evidence. When the stratigraphic position of a fossil was not well resolved, or the age was reported with stage-level (or similar) resolution, or was otherwise uncertain, we used the accepted absolute age of the upper and lower boundary of the reported formation or stage interval as constraints in separate minimum- and maximum-age analyses.

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**Table S1. Extant families and subfamilies of Curculionoidea recognized in this study, following Oberprieler, Marvaldi, and Anderson (1)**

Family	Subfamily
Anthribidae	Anthribinae, Choraginae, Urodontinae
Attelabidae	Attelabinae, Rhynchitinae
Belidae	Belinae, Oxycoryninae
Brentidae	Apioninae, Brentinae, Eurhynchinae, Ithycerinae, Microcerinae, Nanophyinae
Caridae	
Curculionidae	Baridinae, Brachycerinae (including Eirrhinae), Cossoninae, Curculioninae, Cyclominae, Dryophthorinae, Entiminae, Molytinae, Platypodinae, Scolytinae
Nemonychidae	Kimberidinae, Nemonychinae, Rhinorhynchinae

1. Oberprieler RG, Marvaldi AE, Anderson RS (2007) Weevils, weevils, weevils everywhere. *Zootaxa* 1668:491–520.

**Table S2. Molecular divergence dates (point estimates based on the minimum-age and maximum-age maximum-clade credibility trees) and 95% confidence intervals (CI) calculated for the ages of family-level nodes and monophyletic (or near) subfamilies of Curculionidae**

	Node age (Ma) / 95% CI (Ma)	
	Minimum ages	Maximum ages
Ingroup	165.48 (154.23–181.56)	172.95 (174.88–206.99)
Anthribidae (excl. Urodontinae)	62.01 (33.15–101.64)	55.75 (46.54–113.83)
Attelabidae	133.91 (89.38–144.4)	132.62 (99.04–165.93)
Belidae	114.70 (63.99–132.34)	139.06 (91.38–168.10)
Brentidae	120.53 (80.34–129.69)	114.17 (112.49–141.48)
Caridae	130.4 (130.0–137.8)	137.44 (136.0–144.36)
Curculionidae	130.18 (109.71–137.51)	138.69 (123.08–144.16)
Dryophthorinae	74.5 (60.33–111.0)	95.62 (89.97–128.46)
Entiminae + Cyclominae	77.97 (40.64–87.29)	97.17 (63.58–99.81)
Platypodinae	92.32 (50.41–104.24)	114.16 (80.28–114.19)
Scolytinae	86.0 (56.69–104.06)	99.66 (92.24–120.66)
Nemonychidae + Anthribidae	156.47 (136.8–179.02)	162.56 (159.11–196.77)

**Table S3. Weevil genera sampled and the geographic distribution of each as reported in Alonso-Zarazaga and Lyal, except for Platypodinae and Scolytinae which are not included in this reference, and for which we have listed the geographic region from which the specimen was collected (not the entire known distribution)**

FAMILY/Subfamily	Tribe/Subtribe	Genus	Origin	16S	18S	28S	AK	COI	EF1a	
<b>ANTHRIBIDAE</b>										
Anthribinae	Anthribini	<i>Trigonorhinus</i>	NA, NT, WP		X	X		X		
	Platystomini	<i>Toxonotus</i>	NA		X		X	X		
	Ptychoderini	<i>Ptychoderes</i>	NT		X		X		X	
Choraginae	Choragini	<i>Choragus</i>	NA, PA, AT		X					
Urodontinae		<i>Bruchela</i>	PA, OL		X					
		<i>Urodontus</i>	AT		X	X		X	X	
<b>ATTELABIDAE</b>										
Attelabinae	Attelabini	<i>Attelabus</i>	HA		X	X	X	X	X	
Rhynchitinae	Rhynchitini	<i>Eugnamptus</i>	Nearly cosmopolitan			X		X	X	
	Rhynchitini	Gen.	NT	X	X	X				
	Rhynchitini	<i>Merhynchites</i>	NA		X	X		X	X	
<b>BELIDAE</b>										
Belinae	Agnesiotidini	<i>Atractuchus</i>	NT		X					
	Pachyurini	<i>Basiliobelus</i>	AU		X	X	X	X	X	
	Belini	<i>Isacantha</i>	AU		X	X	X	X	X	
	Belini	<i>Rhinotia</i>	AU	X	X	X	X	X	X	
Oxycoryninae	Aglycyderini	<i>Aralius</i>	AU		X		X		X	
	Oxycorynini	<i>Oxycraspedus</i>	NT		X	X	X	X	X	
	Oxycorynini	<i>Rhopalotria</i>	NA, NT	X	X	X	X		X	
<b>BRENTIDAE</b>										
Apioninae	Antliarhinini	<i>Antliarhis</i>	AT		X	X		X	X	
	Apionini	<i>Apion</i>	PA	X	X	X		X	X	
	Exapiiini	<i>Exapion</i>	PA	X	X			X	X	
	Oxystomatini	<i>Holotrichapion</i>	PA	X	X			X		
	Oxystomatini	<i>Ischnopterapion</i>	PA	X	X			X		
	Rhadinocybini	<i>Pterapion</i>	AU		X	X	X	X	X	
	Rhinorhynchidiini	<i>Rhinorhynchidius</i>	AU		X	X		X		
Brentinae	Arrhenodini	<i>Arrhenodes</i>	NA	X	X		X			
	Cyladini	<i>Cylas</i>	AT, NA, NT		X	X	X	X	X	
Eurhynchinae		<i>Aporhina</i>	AU		X	X	X	X		
		<i>Eurhynchus</i>	AU		X	X	X	X		
		<i>Ithycerus</i>	NA		X				X	
Microcerinae	Microcerini	<i>Microcerus</i>	AT		X					
Nanophyinae	Nanophyini	<i>Nanophyes</i>	AT, OL, PA	X	X			X		
<b>CARIDAE</b>										
Carinae		<i>Caenominurus</i>	NT		X	X				
		<i>Car</i>	AU	X	X	X	X		X	
<b>CURCULIONIDAE</b>										
Brachycerinae	Bagoiini <sup>1</sup>	<i>Bagous</i>	Cosmopolitan	X	X	X	X			
	Bagoiini	Gen.	AT		X	X	X			
	Brachycerini	<i>Brachycerus</i>	AT, PA	X	X					
	Erirehiniini/ Erirehinina	<i>Echinocnemus</i>	AT, AU, PA		X	X	X		X	
	Erirehiniini/ Stenopelmina	<i>Lissorhoptrus</i>	NA, NT		X	X	X	X	X	
	Erirehiniini/ Stenopelmina	<i>Penestes</i>	NT		X	X		X	X	
	Erirehiniini/ Stenopelmina	<i>Stenopelmus</i>	NA, NT, WP		X	X	X		X	
	Erirehiniini/ Tanysphyrina	<i>Tanysphyrus</i>	HA, OL	X	X	X	X	X	X	
	Ocladiiini	<i>Ocladius</i>	AT, WP	X	X	X		X	X	
	Raymondionymini	<i>Schizomicrus</i>	NA		X	X		X	X	
	Cyclominae	Amycterini	<i>Acantholophus</i>	AU	X	X		X		
		Aterpini	<i>Aesiotes</i>	AU		X	X	X	X	X
		Aterpini	<i>Chrysolopus</i>	AU	X	X		X		
Hipporhinini		<i>Bronchus</i>	AT		X	X	X	X		
Baridinae	Rhithirrinini/Listroderina	<i>Listronotus</i>	Nearly cosmopolitan		X	X		X		
	Baridini	<i>Baris</i>	Cosmopolitan	X	X	X				
Cossoninae	Ceutorhynchini	<i>Ceutorhynchus</i>	Nearly cosmopolitan	X		X	X	X	X	
	Ceutorhynchini	<i>Nedyus</i>	HA	X	X			X	X	
	Phytobiini	<i>Phytobius</i>	AT, HA, OR		X	X	X			
	Zygopini	<i>Cylindrocopturus</i>	NA, NT		X	X	X			
	Araucariini	<i>Araucarius</i>	NT		X	X	X	X	X	
Cossoninae	Cossonini	<i>Cossonus</i>	Cosmopolitan	X	X	X				
	Pentarthriini	<i>Tychiodes</i>	AU, OR		X	X	X			

FAMILY/Subfamily	Tribe/Subtribe	Genus	Origin	16S	18S	28S	AK	COI	EF1a	
Molytinae	Rhyncolini	<i>Stenancylus</i>	NT		X	X			X	
	Amorphocerini	<i>Portheles</i>	AT		X			X	X	
	Conotrachelini	<i>Conotrachelus</i>	NA, NT		X	X		X		
	Cryptorhynchini	<i>Acalles</i>	Cosmopolitan	X	X					
	Cryptorhynchini	<i>Bepharus</i>	AU		X	X	X			
	Hylobiini	<i>Heilipodus</i>	NT			X		X	X	
	incertae sedis	<i>Tranes</i>	AU		X	X	X	X	X	
	Lixini	<i>Larinus</i>	Nearly cosmopolitan	X	X		X			
	Lixini	<i>Microlarinus</i>	AT, WP		X		X		X	
	Magdolidini	<i>Magdalis</i>	HA	X	X	X	X		X	
	Pissodini	<i>Pissodes</i>	AT, NT, HA	X	X			X		
	Psepholacini	<i>Sympiezoscelus</i>	AU		X	X	X	X		
	Trypetidini	<i>Araucarietius</i>	NT			X	X	X		
	Trypetidini	<i>Eisingius</i>	NT			X	X		X	
	Curculioninae	Camarotini	<i>Camarotus</i>	NT		X	X		X	
		Cionini	<i>Cionus</i>	AT, HA, OL	X	X			X	
Cryptoplini		<i>Haplonyx</i>	AU	X	X	X	X	X		
Curculionini		<i>Curculio</i>	Cosmopolitan	X	X	X	X	X	X	
Derelomini		<i>Perelleschus</i>	NT		X	X		X	X	
Ellescini		<i>Dorytomus</i>	HA	X	X			X		
Eugnomini		<i>Meriphys</i>	AU		X	X	X			
Gonipterini		<i>Gonipterus</i>	AU (widely introduced)		X	X				
Gonipterini		<i>Oxyops</i>	AU	X	X		X		X	
Hyperini		<i>Hypera</i>	HA	X	X		X	X		
Mecinini		<i>Gymnetron</i>	PA	X	X	X	X			
Otidocephalini		<i>Myrmex</i>	USA		X	X	X	X		
Rhamphini		<i>Tachygonus</i>	NA, NT		X		X	X		
Smicronychini		<i>Smicronyx</i>	AT, AU, HA	X	X	X	X	X	X	
Storeini		<i>Melanterius</i>	AU		X	X	X		X	
Dryophthorinae		Litosomini (= Sitophilini)	<i>Sitophilus</i>	Cosmopolitan	X	X	X	X	X	X
	Orthognathini	<i>Mesocordylus</i>	NT		X	X	X	X	X	
	Orthognathini	<i>Rhinostomus</i>	AT, AU, NT		X	X		X	X	
	Rhynchophorini	<i>Rhynchophorus</i>	AT, AU, NT		X	X		X	X	
	Sphenophorini	<i>Metamasius</i>	NT		X	X		X	X	
	Sphenophorini	<i>Rhabdoscelus</i>	AU, OR			X		X	X	
	Sphenophorini	<i>Rhodoabaenus</i>	NA, NT			X		X	X	
	Sphenophorini	<i>Sphenophorus</i>	Nearly cosmopolitan		X	X	X	X	X	
	Stromboscerini	Gen	AT		X	X		X		
	Tanymecini	<i>Tanymecus</i>	AT, HA, NT	X	X	X	X	X		
	Eupholini	<i>Gymnopholus</i>	AU		X	X			X	
	Entiminae	Naupactini	<i>Naupactus</i>	NT (widely introduced)		X	X	X	X	X
Otiorhynchini		<i>Otiorhynchus</i>	PA	X	X			X	X	
Phyllobiini		<i>Phyllobius</i>	AT, PA	X	X			X		
Polydrusini		<i>Polydrusus</i>	AT, HA, NT	X	X			X		
Sciaphilini		<i>Barypeithes</i>	HA	X	X			X		
Sitonini		<i>Sitona</i>	HA	X	X	X		X	X	
Tropiphorini		<i>Catasarcus</i>	AU	X	X	X	X	X		
Tropiphorini		<i>Spartecerus</i>	AT		X	X		X	X	
Platypodinae		Platypodini	<i>Austroplatypus</i>	AU		X	X	X	X	X
		Platypodini	<i>Dinoplatypus</i>	AU		X	X			X
		Platypodini	<i>Platypus</i>	NA		X	X		X	X
		Tesserocerini	<i>Chaetastus</i>	AT		X	X			X
Scolytinae	Tesserocerini	<i>Notoplatypus</i>	AU		X		X	X	X	
	Bothrosterini	<i>Cnesinus</i>	NT		X	X			X	
	Corthylini	<i>Araptus</i>	NT		X	X		X	X	
	Cryphalini	<i>Cryphalus</i>	WP		X	X		X	X	
	Cryphalini	<i>Hypothenemus</i>	AT	X	X	X		X	X	
	Ctenophorini	<i>Scolytodes</i>	NT		X	X		X	X	
	Drycoetini	<i>Dryocoetes</i>	WP		X			X	X	
	Hylastini	<i>Hylurgops</i>	NA	X	X	X		X	X	
	Hylesinini	<i>Alniphagus</i>	NA		X	X		X	X	
	Hylesinini	<i>Hylesinopsis</i>	AT		X	X			X	
	Hylesinini	<i>Hylesinus</i>	WP		X	X			X	

FAMILY/Subfamily	Tribe/Subtribe	Genus	Origin	16S	18S	28S	AK	COI	EF1a
	Hypoborini	<i>Liparthrum</i>	AT		X	X		X	X
	Ipini	<i>Ips</i>	NA		X	X		X	X
	Phloeotribini	<i>Phloeotribus</i>	NA		X	X		X	X
	Scolytini	<i>Ambrosiodmus</i>	NA		X	X		X	X
	Scolytoplatypodini	<i>Scolytoplatypus</i>	OR		X	X		X	
	Tomicini	<i>Dendroctonus</i>	NA		X	X	X	X	X
	Tomicini	<i>Hylurgonotus</i>	NT		X	X		X	X
	Tomicini	<i>Tomicus</i>	PA		X	X	X	X	X
	Tomicini	<i>Xylechinossomus</i>	NT		X	X		X	X
	Xyleborini	<i>Xyleborus</i>	WP	X	X			X	X
	Xyloctonini	<i>Ctonoxylon</i>	AT		X	X		X	X
	Xylosterini	<i>Xylosterinus</i>	NA		X	X			X
<b>NEMONYCHIDAE</b>									
	Cimberidinae								
	Cimberidini	<i>Cimberis</i>	HA	X	X	X	X	X	X
	Doydirhynchini	<i>Doydirhynchus</i>	NA, WP	X	X		X		X
	Nemonychinae	<i>Nemonyx</i>	PA		X				
	Rhinorhynchinae								
	Mecomacerini	<i>Rhynchitomacerinus</i>	NT		X	X	X	X	X
<b>OUTGROUPS</b>									
	Cerambycidae								
	Parandrinae	<i>Parandra</i>	Cosmopolitan		X	X	X		X
	Prioninae	<i>Prionoplus</i>	AU		X	X	X	X	X
	Chrysomelidae								
	Aulacoscelidinae	<i>Aulacoscelis</i>	NA, NT	X	X	X		X	
	Chrysomelidae	<i>Donacia</i>	Holarctic	X	X	X		X	
	Chrysomelidae	<i>Orsodacne</i>	Nearly cosmopolitan	X	X	X		X	
	Megalopodidae								
	Palophaginae	<i>Palophagoides</i>	NT		X	X		X	X
	Oxypeltidae	<i>Oxypeltus</i>	NT	X	X	X	X	X	X
	Protocucujidae	<i>Ericmodes</i>	NT	X	X	X	X	X	X

Abbreviations: Afrotropical (AT), Australasian (AU), Eastern Palearctic (EP), Holarctic (HA), Nearctic (NA), Neotropical (NT), Oriental (OL), Palearctic (PA), and Western Palearctic (WP). Detailed collection data is available from D.D.M.

<sup>1</sup>The placement of Bagoiini is tentative, based on morphology, but it has formerly been assigned to Curculioninae, Molytinae, and so forth. [Alonso-Zarazaga MA, Lyal CHC (1999) *A World Catalogue of Families and Genera of Curculionoidea (Insecta: Coleoptera) (excepting Scolytidae & Platypodidae)* (Entomopraxis SCP, Barcelona)].

**Table S4. Primers used for amplification and sequencing**

Locus	Name	Use	Sequence (5' >3')	Citation
18S	18e-s	Amp/Seq	CTGGTTGATCCTGCCAGT	1
18S	18p-c	Amp/Seq	TAATGATCCTTCCGAGGTTACCT	1
18S	18S1.2f	Seq	TGCTTGCTCAAAGATTAAGC	2
18S	r1138	Amp/Seq	GTTAGAGGTTGGAAGGCG	3
18S	f1094	Amp/Seq	GGATCGTCGCAAGACGGACAGAAG	3
28S	rD42b	Amp/Seq	CCTTGGTCCGTGTTCAAGACGG	2
28S	rD5b	Amp/Seq	CCACAGCGCCAGTTCTGCTTAC	2
28S	ZX1	Amp/Seq	ACCCGCTGAATTTAAGCATAT	4
28S	OP2	Amp/Seq	CAGACTAGAGTCAAGCTCAACAGG	5
28S	ZR1	Seq	GTCTTGA AACACGGACCAAGGAGTCT	5
28S	AS3/5	Seq	TGCGGGATGAACCGAACG	5
28S	AS7	Seq	GGTCAGTCGGTCTAAGA	5
28S	AS8	Seq	TTCACCTGGAGACCTGCTGCGG	5
EF 1- $\alpha$	Cho10(mod)	Amp	ACRGCVACKGTGTGHCKCATGC	6
EF 1- $\alpha$	Cho10rev1	Amp/Seq	AGCATDCCAGAYTTGATRGC	Present study
EF 1- $\alpha$	efa747	Amp/Seq	CCACCAATTTTGTAGACATC	7
EF 1- $\alpha$	efs149	Amp/Seq	ATCGAGAAGTTCGAGAAGGAGGCYCARGAAATGGG	7
EF 1- $\alpha$	efs372	Amp/Seq	CTGGTGAATTTGAAGCYGGTA	8
EF 1- $\alpha$	for1deg	Amp/Seq	GYATCGACAARCGTACSATYG	6
AK	ArgKforB2	Amp	GAYTCCGGWATYGGWATCTAYGCTCC	9
AK	ArgKforB4	Amp/Seq	GAYCCATCATCGARGATACC	10
AK	ArgKrevB1	Amp/Seq	TCNGTRAGRCCCATWCGTCTC	9
CoxI	A3014	Amp/Seq	TCCAATGCACTAATCTGCCATATTA	11
CoxI	LCO	Amp/Seq	GGTCAACAAATCATAAAGATATTGG	12
CoxI	HCO	Amp/Seq	TAAACTCAGGGTGACCAAAAATCA	12

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**Table S5. Fossil ages applied as constraints**

Taxon	Fossil min/max (Ma)	Fossil source	Citations
Attelabidae ( <i>Sayrevilleus</i> )	89.3/93.5*	New Jersey Amber, USA	(1–3)
Brentidae: Eurhynchinae ( <i>Axelrodiellus</i> )	99.6/112*	Santana, Brazil	(1, 4, 5)
Caridae ( <i>Baissorhynchus</i> )	130/136*	Baissa, Russia	(1, 2, 6)
Curculionidae: Dryophthorinae	34/34	Florissant, USA	(2, 7)
Curculionidae: Platypodinae	25/33*	Apenninian Amber, Italy	(2, 8, 9)
Curculionidae: Scolytinae	55/55	London Clay, UK	(2, 10)
Curculionidae (undescribed)	89.3/93.5*	Orapa, Botswana	(1, 11)
Nemonychidae (multiple)	150.8/161.2*	Karatau, Russia	(1, 6, 12)

Asterisks indicate that analyses were done with both minimum and maximum ages to account for uncertainty. Character evidence in support of the placements of these fossils in established groups can be found in the references cited.

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