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Temporal lags and overlap in the diversification of weevils and flowering plants

Duane D. McKenna, Andrea S. Sequeira, Adriana E. Marvaldi, and Brian D. Farrell

*Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA 02138; †Department of Biological Sciences, Wellesley College, Wellesley, MA 02481; and ‡Instituto Argentino de Investigaciones de Zonas Aridas, Consejo Nacional de Investigaciones Científicas y Técnicas, C.C. 507, 5500 Mendoza, Argentina

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The extraordinary diversity of herbivorous beetles is usually attributed to coevolution with angiosperms. However, the degree and nature of contemporaneity in beetle and angiosperm diversification remain unclear. Here we present a large-scale molecular phylogeny for weevils (herbivorous beetles in the superfamily Curculionoidea), one of the most diverse lineages of insects, based on ≈8 kilobases of DNA sequence data from a worldwide sample including all families and subfamilies. Estimated divergence times derived from the combined molecular and fossil data indicate diversification into most families occurred on gymnosperms in the Jurassic, beginning 166 Ma. Subsequent colonization of angiosperms occurred during the Early Cretaceous, but this alone evidently did not lead to an immediate and major diversification event in weevils. Comparative trends in weevil diversification and angiosperm dominance reveal that massive diversification began in the mid-Cretaceous (ca. 112.0 to 93.5 Ma), when angiosperms first rose to widespread floristic dominance. These and other evidence suggest a deep and complex history of coevolution between weevils and angiosperms, including cophylogeny, resource tracking, and sequential evolution.

Weevils [superfamily Curculionoidea; (Fig. 1)] are an extraordinarily diverse group of insects. They reach their greatest diversity in the humid tropics, but also occur in subaquatic, subterranean, desert, tundra, and other environments at nearly all latitudes and altitudes with vegetation. Weevils collectively feed on nearly all plant taxa and all kinds of living, dead, dying, and decaying plant parts. The ≈62,000 described species are classified into 7 families and ≈5,800 genera. [Recent authors recognize between 6 and 22 weevil families, and between 10 and 100 subfamilies (1). Here we follow the classification of ref. 2 (see supporting information (SI) Table S1).] The likely total number of species, including those awaiting discovery or description, is conservatively estimated at more than 220,000 (2). More than 80% of living weevil species belong to the family Curculionidae, the diversity of which exceeds that of any other known family of animals (3). Today, as more than a half century ago, “the classification of Curculionidae into natural subfamilies and tribes probably remains the largest outstanding problem in the higher classification of Coleoptera” (2, 4). Consequently, relationships within Curculionidae are both of greatest interest for reconstructing the evolutionary history of weevil associations with plants, and most critical for achieving stability in weevil classification.

Weevils first appear unequivocally in the Late Jurassic fossil record (Karatau, Oxfordian-Kimmeridgian, 161.2–150.8 Ma) (5). These early weevils belong to the family Nemonychidae (2) and most likely developed in the reproductive structures of conifers in a manner similar to living nemonychids (6, 7). While early weevils most likely fed on conifers, most living weevil species are specialist herbivores on flowering plants (angiosperms; >250,000 living species). Shifts to feeding on angiosperms are associated with enhanced taxonomic diversification in weevils (6), and weevils underwent considerable diversification during the Cretaceous (145.5–65.5 Ma) (2, 5, 6), a period when angiosperms also flourished (8–10). Consequently, the extraordinary taxonomic diversity of weevils is often attributed to coevolution with angiosperms (2, 6, 11). However, because of uncertainties about higher-level relationships and divergence times in weevils, the evolutionary history of weevil-angiosperm interactions remains unclear.

To gain insight into the degree and nature of contemporaneity in weevil and angiosperm diversification, we used a large-scale temporally calibrated phylogeny for weevils estimated from combined molecular and fossil data. Our molecular data set included up to 8 kilobases (kb) of DNA sequence data (4 nuclear and 2 mitochondrial genes) from a worldwide sample of 135 weevil genera representing all families and subfamilies and 8 outgroups.

Results

Weevil Relationships. Overall, we recovered moderate to strong bootstrap (BS) or posterior probability (PP) support for ≈53%
(71 out of 134) of ingroup internodes (Fig. 2).* Family-level relationships were mostly compatible with recent concepts (2, 11, 14–16); however, several new and intriguing relationships were recovered at the subfamily level. A clade including Nemonychidae and Anthribidae (<50% ML BS; 0.82 Bayesian PP) was sister to all other weevils. Nemonychidae was rendered paraphyletic by the family Anthribidae (minus Urodontinae) (<50% BS; 1.0 PP), consistent with other authors who have noted this possibility based on similarities in hind wings and other adult and larval features. Most Anthribidae use angiosperm-dependent fungi as hosts, consistent with their first appearance in the fossil record coeval with a rapidly diversifying angiosperm flora in the late Early Cretaceous (2), and much later than the largely conifer-associated Nemonychidae. Placement of the subfamily Urodontinae separate from other Anthribidae (and Nemonychidae) was unexpected, and conflicts with morphology. The hypothesis of monophyly for Anthribidae plus Urodontinae was rejected under BI (PP = 0), but not under ML inference (Kishino-Hasegawa test or KH, P = 0.47). The belid subfamilies Oxycryoninae (including Aglycyderini) and Belinae were recovered as sister groups within a monophyletic family Belidae (78% BS; 1.0 PP), consistent with recent analyses of morphological characters (11, 14, 16–18). We recovered moderate-to-strong support for monophyly of the families Attelabidae (<50% BS; 1.0 PP) and Caridae (100% BS; 1.0 PP) under ML and/or BI. The placement of Caridae as sister group of the megaclade Brentidae plus Curculionidae received strong support under BI (54% BS; 1.0 PP), in agreement with morphology (11). The subfamilies Apioninae, Brentinae, Euryhynchinae, and Nanophyinae (but not the enigmatic Ithycerinae and Microcerinae) together comprised a monophyletic but poorly supported family Brentidae (<50% BS; 0.60 PP). The hypothesis of monophyly for Brentidae, including Microcerinae and Ithycerinae, was rejected under BI (PP = 0), but not under ML (KH, P = 0.22).

We recovered a monophyletic family Curculionidae (<50% BS; 0.61 PP; including Ithycerinae and Microcerinae). Basal positions in Curculionidae were occupied by weevils with the ancestral “pedotectal” (19) type of male genitalia: Brachycerini, Microcerinae, Platypodinae, Dryophthorinae, and Ithycerinae, followed by “higher” Curculionidae (<50% BS; 0.99 PP), comprised of groups with the derived “pedal” type of male genitalia. Brachycerinae (which in the concept adopted here also includes the Erirhininae of authors) occupied basal positions in Curculionidae, forming a paraphyletic grade that also included the subfamilies Dryophthorinae and Platypodinae. Ithycerinae and Microcerinae were intermingled among these “basal” curculionids in our analyses, in contrast with morphological studies, which increasingly favor their placement in the family Brentidae (2). The enigmatic subfamily Platypodinae (ambrosia beetles) was recovered in a position sister to Dryophthorinae (<50% BS; 0.93 PP), a relationship first proposed and supported by larval morphology (15), but not previously recovered in molecular phylogenetic studies, which mostly recover Platypodinae as apomorphic derivatives of Scolytinae. While the hypothesis of monophyly for Platypodinae plus Scolytinae was rejected under BI (PP = 0), it could not be rejected under ML (KH, P = 0.49). Dryophthorinae was monophyletic (<50% BS; 0.79 PP) minus Stroboscerini.

We recovered several groups among higher Curculionidae with moderate-to-strong internodal support (under ML or BI), comprising what are usually treated as subfamilies or tribes, [e.g., Baridinae: Ceutorhynchini (97% BS, 1.0 PP), Molytinae: Lixini (100% BS, 1.0 PP), and Scolytinae (<50% BS, 0.84 PP)]. However, a more thorough understanding of relationships and timing and patterns of diversification in Curculionidae will apparently require additional sampling. The limited resolution obtained herein reinforces the idea that clarifying curculionid relationships is a difficult task (2, 4, 11). Nevertheless, several groups emerge from our analyses that were suspected on the basis of similar morphological features, life histories, or habits, but whose relationships had otherwise been obscured by homoplasy.

Cyclophini, Entimini, Gonipterini, and Hyperini together comprised a single clade (56% BS, 1.0 PP) in a position between Brachycerinae: Erirhinini (minus Stenotelmus) and the remaining higher weevils. The phylogenetic position of Scolytinae was particularly notable. Scolytinae are usually considered close relatives of Platypodinae and Cossoninae (14, 20). However, there is little support for a close relationship between Scolytinae and Platypodinae under BI (see above), and a sister-group relationship between Scolytinae and all or a subset of cossonine genera, including Araucarini, the ostensibly link between Cossoninae and Scolytinae (21), also appears unlikely, implying multiple origins of the gallery-forming habit, but the alternative scenario of a single origin cannot be ruled out under ML (Scolytinae + Cossoninae PP = 0, KH P = 0.49; Scolytinae + Araucarini PP = 0, KH P = 0.34). Sister to Scolytinae we recovered a poorly supported clade comprised of most other higher Curculionidae, including taxa classified in the subfamilies Baridinae, Cossoninae, Curculioninae, and Molytinae. Many workers have noted the difficulty of separating Molytinae from the traditional “Cryptorhynchini,” Cossoninae, and “Lixini,” using morphological characters (2, 22), an observation consistent with our results. All subfamilies of higher Curculionidae, except Scolytinae, were poly- or paraphyletic in our analyses, but Scolytinae were relatively well sampled, and we expect that including more taxa or characters from other curculionid subfamilies will contribute additional well-supported resolution.

Weevils on Plants in Evolutionary Time. We recover an Early to early Middle Jurassic origin of modern weevils (ca. Aalenian-Bathonian, 175.6–164.7 Ma), with all families and most subfamilies arising by the end of the Cretaceous (Figs. 2 and 3; Table S2). The ancestrally angiosperm-associated sister groups Brentidae and Curculionidae diverged during the earlier Early Cretaceous (ca. Valanginian–Hauterivian, 140.2–130 Ma). Crown diversification of both families appears to have commenced by the late Early Cretaceous (Aptian, 125.0–112.0 Ma), and all subfamilies appeared by the early Late Cretaceous (Turonian, 93.5–89.3 Ma). The family Curculionidae shows sustained higher-level diversification throughout the Late Cretaceous (99.6 Ma to 65.5 Ma) and Paleogene (particularly Paleocene–Eocene, 65.5–33.9 Ma) (see Fig. 2). Superimposed plots of stem-group divergence times for major weevil clad and for angiosperm dominance over the course of the Cretaceous (see Fig. 3), reveal evidence for a major increase in diversity of angiosperm-associated weevils approximately concurrent with the mid-Cretaceous rise of angiosperms to widespread floristic dominance (ca. Albian–Cenomanian, 112.0 to 93.5 Ma) (8, 9).

Discussion
The larvae and adults of most extant Nemonychidae feed on conifers, and primarily on pollen. Most Anthribidae feed on ascomycete fungi growing on or in angiosperm wood, a habit proposed to have evolved from phytophagy in decaying cones of conifers or possibly cycads (23). This scenario is compatible with our results, which support a Late Cretaceous origin of Anthribidae (excluding Urodontinae) from within the largely conifer-associated Nemonychidae. Conifers are abundantly represented in the Mesozoic fossil record (8, 9), and are also thought to be the ancestral hosts of weevils in the families Attelabidae (2),

*Computer simulations have shown that Bayesian PP associated with short branch lengths and low values for nonparametric BS support (or other non-Bayesian measures of support) may be particularly as the size of the data set increases (12, 13). Therefore, relationships for which PP support is elevated as compared to maximum likelihood (ML) BS, should be interpreted cautiously.
Fig. 2. Maximum clade credibility tree for weevils based on the minimum age Bayesian analysis. Bayesian PP ≥ 0.50 and maximum likelihood BS values ≥ 50% are shown on the tree (PP/BS). Ninety-five percent confidence intervals for the ages of family- and subfamily-level clades, and for the ingroup, are indicated with blue bars. Letters correspond to fossil calibration points used in the molecular dating analysis. Numbers of described species are from ref. 2. Images of weevil exemplars are not shown on the tree (PP/BS).
Belidae (18), and Caridae (2), consistent with estimated divergence times for stem-group representatives of these families (ca. 150–170 Ma) (see Fig. 3), which predate most estimates for the first appearance of crown-group angiosperms [fossils ~132–141 Ma (24), molecules ~140–180 Ma (25)]. Conifers are also thought to be the ancestral hosts of the weevil sister group, superfamily Chrysomeloidea (long-horned beetles, leaf-beetles, and allies) (6, 26, 27).

The ancestrally angiosperm-associated sister groups Brentidae and Curculionidae (2) diverged during the earlier Early Cretaceous (ca. Berriasian–Valanginian, 145.5–130 Ma). Brentidae noticeably lack associations with monocots; however, many basal Curculionidae, particularly Brachycerinae and Dryophthorinae, are associated primarily or solely with them. Monocots were among the most abundant and ecologically successful early angiosperms. Indeed, most early angiosperm fossils, for example Barremian–Aptian, are from Magnoliales or monocots (28–30), not eudicots. Most other Curculionidae, and most extant species of Anthribidae, Attelabidae, and Brentidae, feed on the living, dead, dying, or fungus-infested tissues of core eudicots, the most diverse group of living angiosperms. The large number of monocot-associated taxa near the base of the family Curculionidae is consistent with a common origin of monocot feeding. Some curculionid tribes are intimately associated with gymnosperms; however, they are all nested within clades of angiosperm-feeders. Thus, while some primitive weevils may be primary associates of gymnosperms (e.g., certain Nemonychidae, Belidae, Attelabidae, and Caridae), others, such as gymnosperm-associated Curculionidae and Brentidae, are most likely secondary colonists, an interpretation consistent with other authors (2, 11, 18, 31, 32).†

†Supported by their comparatively early appearance in the fossil record (when known), Gondwanan distributions (at least of the oldest, and often conifer-associated lineages), and phylogenetic position, generally at the base of their respective groups (6).

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The larvae of Platypodinae feed on ambrosia fungi cultivated by adults in galleries in wood.

All living weevil families are known from the fossil record, and all weevil families in the fossil record are extant. [Julyanidae] is most likely associated with Nemonychidae (2), consistent with the contention that reduced extinction has played an important role in the extraordinary diversity of modern insects (36).
Materials and Methods
See the SI Materials and Methods for more details.

Taxon Sampling and DNA Sequencing. 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 family Curculionidae (2) (see Tables S1 and S3). Outgroups included 7 subfamilies of basal Chrysomeloidea, the weevil sister group (6, 26), and Eriomorphae sylvestricus (Cucujoidea: Protococcidae). Six genes (2 mitochondrial and 4 nuclear) were used in this study: cytochrome oxidase I (cox I) and elongation factor 1-α (EF 1-α), and arginine kinase (AK). For primers used, see Table S4.

Phylogenetic Analyses. We ran two partitioned BI phylogenetic analyses in the program BEAST 1.4.7 (65–75 million generations, 12 partitions, GTR+I+I substitution model, estimated base frequencies) on the maximum- and minimum-age data sets, for a total of 4 analyses. All trees were rooted with Eriomorphae sylvestricus (50, 51). Graphical and statistical analyses implemented in the program Tracer 1.4 were used to assess convergence and otherwise check performance and accuracy of the BEAST analyses. Based on these results, we combined the last 5,000 trees from each of the paired minimum- and maximum-age analyses and used them to estimate PPs, to obtain maximum-age analyses and used them to estimate divergence times and corresponding 95% confidence intervals (LogCombiner 1.4.7, PAUP* 4.03b10, TreeAnnotator 1.4.7). We implemented a partitioned ML BS analysis (1,000 inferences, 12 partitions, CAT substitution model, individual per partition branch-length optimization) using the program RAxML 7.0.4 on the CIPRES Supercomputing Center.

Hypothesis Testing. 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 HK test (52) as implemented in PAUP* 4.0310.

Divergence-Time Estimates. Divergence times were coestimated with phylogeny using the Bayesian relaxed molecular clock method (53) (BEAST 1.4.7). 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 (2, 5), using only the oldest fossils that could be unequivocally assigned (based on character evidence) to extant weevil subfamilies or families in our analyses (Table S5).

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