Supplementary Information

The megaherbivore gap after the non-avian dinosaur extinctions modified trait evolution and diversification of tropical palms

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Supplementary methods

Scenario construction and simulations
One confounding issue is the simultaneous change in environmental conditions during the PMHG that may have affected ecological opportunities, and thus diversification and trait evolution. Ideally, a comparative framework would incorporate these additional variables and their effect on diversification, such as paleoclimate [2], species competition [3], and habitat or biome change [4]. However, an analytical framework that can address such complexity is currently not available. Instead, we tackled the potential effect of confounding diversification drivers by phylogenetic comparative ‘scenario-construction’. That is, we specifically assessed models that were able to test our hypotheses comparatively, i.e., comparing rates of lineages with megaherbivore traits to those without these traits (see Tables 1, S1-S4), rather than evaluating an unlimited number of possible diversification scenarios [5]. We thus addressed criticism on diversification inferences [5] by identifying the most likely diversification scenarios out of the set of suitable alternative scenarios. In addition, we performed phylogenetic simulations to further assess to what extent the inferred diversification estimates were associated with megaherbivore traits vs. neutral trait evolution.

Simulations for trait-dependent diversification
Criticism on trait-dependent diversification models has encouraged researchers to perform simulations to test for type I and type II error rates in the data. For example, the shape of the phylogenetic tree may affect the inference of trait-dependent diversification, even if the trait itself is not actually associated with diversification [1]. To explore this possibility, we randomly evolved a neutral binary trait (that does not affect speciation and extinction rates) on the 100 empirical palm phylogenetic trees under our observed transition rates from the empirical dataset (transition rates megafaunal to small = 0.014, and small to megafaunal = 0.006, transition rates no armature to armature = 0.011, and armature to no armature = 0.002 transitions/million years), as well as under an equal back- and forward transition rate (q = 0.01 transitions/million years). We then repeated the time- and trait-dependent diversification analyses under the best-fitting model from the empirical dataset, and visualised the 95% Bayesian credibility intervals of the inferred parameter estimates.
Supplementary results

Diversification rate and trait evolution simulations
When simulating neutral traits of fruit length under the observed, empirical transition rate parameters or under equal transition rates, we observed slightly higher speciation rates of lineages with small fruits during megaherbivore periods compared with speciation rates during the PMHG (Fig. S2). Similarly, we observed a slightly higher transition rate from small to megafaunal fruits during the PMHG compared with any of the other transition rates. This suggests that the phylogenetic tree shape rather than fruit size has influenced palm speciation and transition rates. However, the speciation and transition rate increase under neutral fruit size evolution was not as pronounced as observed in the empirical data, and the 95% Bayesian credibility intervals (i.e., showing confidence intervals on the estimation of the rates) overlapped in the simulations, suggesting that the effect of phylogenetic tree shape on fruit size-dependent speciation and transition rates is minimal. These 95% Bayesian credibility intervals between small vs. large fruit-dependent speciation and transition did not overlap in the empirical estimates, as would be expected if diversification rates are influenced by fruit size rather than phylogenetic tree shape.

Concerning armature, simulations under the observed transition rates did not show any effect of armature on speciation rates, as would be expected under neutral trait evolution (Fig. S3). However, for transition rates, the simulated results showed a similar pattern to those obtained from the empirical data, that is, increased evolution of armature during megaherbivore periods. This may be caused by simulating armature evolution under the observed, empirical transition rates. Indeed, when simulating the trait under equal transition rates (i.e., armature to no armature = no armature to armature = 0.01 transitions/million years), we did not detect such transition rate difference between time periods or trait states (armature or no armature), as should be expected. However, in this scenario, speciation rates of armature and no armature lineages during the PMHG were slightly lower than those during megaherbivore periods.

Overall, our simulation study shows that most of the empirical diversification rate inferences (Figs. 3 and S1) did not result from methodological artefacts related to the palm phylogenetic tree shape (distribution of branch lengths) (i.e., compare Figs. 3 and S1 to Figs. S2 and S3).
**Table S1**: Time-dependent and trait-dependent binary state speciation and extinction (BiSSE) model selection for **fruit size** in palms (Arecaceae) in relation to their co-occurrence with or without megaherbivores. Models assess whether lineages with small (smaller than 4 cm in length) or large, megafaunal (equal to or larger than 4 cm in length) fruits differ in their speciation, extinction and transition rates, in three different time periods. Period 1 (> 66 Ma) refers to the megaherbivorous dinosaur period, period 2 (66-40 Ma) refers to the megaherbivore gap, and period 3 (40 Ma until present) refers to the megaherbivorous mammal period. The best model, with the lowest Akaike information criterion (AIC), is indicated in bold, and was used in the Bayesian Markov chain Monte Carlo (mcmc) analysis. Model details of each model (Df, Ln.Lik, ChiSq, Pr) are provided in comparison to the full model, but model selection was performed using a likelihood-ratio test with the best fitting model so far, which would be the ‘supported’ model in the nearest proximity in the table above the respective model. Df = degrees of freedom, ln.Lik = log likelihood, ChiSq = Chi square, Pr = p-value.

| Rationale                                                                 | Model                                                      | Df | ln.Lik    | AIC    | ChiSq  | Pr(>|Chi|) | Step-wise selection conclusion |
|--------------------------------------------------------------------------|-------------------------------------------------------------|----|-----------|--------|--------|-----------|-----------------------------|
| No constraints on speciation, extinction and transition rates through time | full                                                        | 18 | -7836.20  | 15708.39 |        |           |                            |
| Period 1 & 3 have a similar response in terms of speciation, extinction and transition rates of large vs. small fruits*     | Equal period 1 & 3                                          | 12 | -7839.14  | 15702.28 | 5.89   | 0.44      | Supported                   |
| In addition, are lineages with small or large fruits similar in their speciation and extinction rates in period 2?         | Equal lambda and mu trait period 2                          | 10 | -7840.02  | 15700.04 | 7.65   | 0.47      | Supported                   |
| In addition, are speciation, extinction and transition rates from small to large fruits, and vice versa, also similar in periods 1 & 3? | Equal lambda, mu and q trait periods 1 & 3                  | 7  | -7904.11  | 15822.22 | 135.83 | 0.00      | Not supported               |
| Or only for speciation rates?                                            | Equal lambda trait periods 1 & 3                            | 9  | -7852.02  | 15722.04 | 31.65  | 0.00      | Not supported               |
| Or only for extinction rates?                                            | Equal mu trait periods 1 & 3                                | 9  | -7840.03  | 15698.06 | 7.67   | 0.57      | Supported                   |
| Or only for transition rates?                                            | Equal q trait periods 1 & 3                                 | 9  | -7848.17  | 15714.34 | 23.95  | 0.00      | Not supported               |
| In addition to a similar response in periods 1 & 3, constrained speciation and extinction rates of lineages with small or large fruits in period 2, and constrained extinction rates of lineages with small or large fruits in periods 1 & 3, are transition rates from large to small fruits and vice versa also similar in period 2? ** | Equal q trait period 2                                      | 8  | -7842.26  | 15700.51 | 12.12  | 0.28      | Not supported               |
| In addition, are speciation rates in period 2 similar to those of lineages with small fruits in periods 1 & 3?             | Additional constraints period 2 (lambda 0)                   | 8  | -7845.20  | 15706.41 | 18.02  | 0.05      | Not supported               |
| Or are speciation rates in period 2 similar to those of lineages with large fruits in periods 1 & 3?                      | Additional constraints period 2 (lambda 1)                   | 8  | -7840.50  | 15696.99 | 8.60   | 0.57      | Supported                   |
| Or are extinction rates in period 2 similar to those in periods 1 & 3?                                                  | Additional constraints period 2 (mu)                        | 8  | -7840.51  | 15697.01 | 8.62   | 0.57      | Supported                   |
| Or are backward and forward transition rates in period 2 similar to those in periods 1 & 3?                            | Additional constraints period 2 (q)                         | 7  | -7844.42  | 15702.84 | 16.45  | 0.13      | Not supported               |
| Or are forward transition rates in period 2 similar to those in periods 1 & 3?                                         | Additional constraints period 2 (q 01 - 1)                   | 8  | -7842.80  | 15701.59 | 13.20  | 0.21      | Not supported               |
| Question                                                                 | Additional constraints period 2 | $\Delta$AIC | $\Delta$A | $p$-value | Result          |
|-------------------------------------------------------------------------|---------------------------------|--------------|-----------|------------|----------------|
| Or are forward transition rates in period 2 similar to backward transition rates in periods 1 & 3? | $q_{01-2}$                       | -7842.37     | 15700.75  | 12.36      | Not supported  |
| Or are backward transition rates in period 2 similar to those in periods 1 & 3? | $q_{10-1}$                       | -7839.74     | 15695.48  | 7.09       | Supported      |
| Or are backward transition rates in period 2 similar to forward transition rates in periods 1 & 3? | $q_{10-2}$                       | -7839.68     | 15695.36  | 6.97       | Supported      |
| And in combination, speciation, extinction and backward transition rates in period 2 are similar to those in periods 1 & 3 | $\lambda, 1, \mu, q_{10-1}$     | -7840.53     | 15693.05  | 8.66       | Supported      |
| And the alternative combination, speciation, extinction and backward transition rates in period 2 are similar to speciation, extinction and forward transition rates in periods 1 & 3 | $\lambda, 1, \mu, q_{10-2}$     | -7840.53     | 15693.06  | 8.67       | Supported      |

*Direct evaluation whether diversification response in presence of megaherbivores (periods 1 & 3) is similar (in contrast to diversification during the megaherbivore gap - period 2). If true, this model should be 'supported'.

**Direct evaluation whether transition rates (to evolving or losing the megaherbivore trait) are equal during the megaherbivore gap, and thus not dependent on megaherbivores (in contrast to transition rates in presence of megaherbivores - periods 1 & 3). If true, this model should be 'supported'.

| Question                                                                 | Additional constraints period 2 | $\Delta$AIC | $\Delta$A | $p$-value | Result          |
|-------------------------------------------------------------------------|---------------------------------|--------------|-----------|------------|----------------|
| Or are forward transition rates in period 2 similar to backward transition rates in periods 1 & 3? | $q_{01-2}$                       | -7842.37     | 15700.75  | 12.36      | Not supported  |
| Or are backward transition rates in period 2 similar to those in periods 1 & 3? | $q_{10-1}$                       | -7839.74     | 15695.48  | 7.09       | Supported      |
| Or are backward transition rates in period 2 similar to forward transition rates in periods 1 & 3? | $q_{10-2}$                       | -7839.68     | 15695.36  | 6.97       | Supported      |
| And in combination, speciation, extinction and backward transition rates in period 2 are similar to those in periods 1 & 3 | $\lambda, 1, \mu, q_{10-1}$     | -7840.53     | 15693.05  | 8.66       | Supported      |
| And the alternative combination, speciation, extinction and backward transition rates in period 2 are similar to speciation, extinction and forward transition rates in periods 1 & 3 | $\lambda, 1, \mu, q_{10-2}$     | -7840.53     | 15693.06  | 8.67       | Supported      |
Table S2: Time-dependent and trait-dependent binary state speciation and extinction (BiSSE) model selection for armature in palms (Arecaceae) in relation to their co-occurrence with or without megaherbivores. Models assess whether lineages with or without armature (spines, thorns, prickles on leaves and/or stems) differ in their speciation, extinction and transition rates, in three different time periods. Period 1 (> 66 Ma) refers to the megaherbivorous dinosaur period, period 2 (66-40 Ma) refers to the megaherbivore gap, and period 3 (40 Ma until present) refers to the megaherbivorous mammal period. The best model, with the lowest Akaike information criterion (AIC), is indicated in bold, and was used in the Bayesian Markov chain Monte Carlo (MCMC) analysis. Model details of each model (Df, Ln.Lik, ChiSq, Pr) are provided in comparison to the full model, but model selection was performed using a likelihood-ratio test with the best fitting model so far, which would be the ‘supported’ model in the nearest proximity in the table above the respective model. Df = degrees of freedom, ln.Lik = log likelihood, ChiSq = Chi square, Pr = p-value. For model selection for leaf armature and stem armature separately, see Tables S3 and S4.

| Rationale | Model | Df | lnLik | AIC | ChiSq | Pr(>|Chi|) | Step-wise selection conclusion |
|-----------|-------|----|-------|-----|-------|----------|-------------------------------|
| No constraints on speciation, extinction and transition rates through time | full | 18 | -8005.59 | 16047.19 |       |          |                               |
| Period 1 & 3 have a similar response in terms of speciation, extinction and transition rates of armature vs. no armature. | Equal period 1 & 3 | 12 | -8009.62 | 16043.23 | 8.05 | 0.23 | Supported |
| In addition, are lineages with armature or no armature similar in their speciation and extinction rates in period 2? | Equal lambda and mu trait period 2 | 10 | -8012.72 | 16045.45 | 14.26 | 0.08 | Not supported |
| Or only for speciation rates? | Equal lambda trait period 2 | 11 | -8012.10 | 16046.20 | 13.01 | 0.07 | Not supported |
| Or only for extinction rates? | Equal mu trait period 2 | 11 | -8010.63 | 16043.26 | 10.07 | 0.18 | Supported |
| In addition, are speciation, extinction and transition rates from armature to no armature, and vice versa, also similar in periods 1 & 3? | Equal lambda, mu and q trait periods 1 & 3 | 8 | -8026.74 | 16069.47 | 42.28 | 0.00 | Not supported |
| Or only for speciation rates? | Equal lambda trait periods 1 & 3 | 10 | -8011.55 | 16043.09 | 11.90 | 0.16 | Supported |
| Or only for extinction rates? | Equal mu trait periods 1 & 3 | 10 | -8015.59 | 16051.18 | 19.99 | 0.01 | Not supported |
| Or only for transition rates? | Equal q trait periods 1 & 3 | 10 | -8025.16 | 16070.31 | 39.12 | 0.00 | Not supported |
| In addition to a similar response in periods 1 & 3, constrained extinction rates of lineages with armature or no armature in period 2, and constrained speciation rates of lineages with armature or no armature in periods 1 & 3, are transition rates from armature to no armature and vice versa also similar in period 2? | Equal q trait period 2 | 9 | -8011.99 | 16041.98 | 12.79 | 0.17 | Supported |
| In addition, are speciation rates of the no armature state in period 2 similar to speciation rates in periods 1 & 3? | Additional constraints period 2 (lambda 0) | 8 | -8017.95 | 16051.90 | 24.71 | 0.01 | Not supported |
| Or are speciation rates of the armature state in period 2 similar to speciation rates in periods 1 & 3? | Additional constraints period 2 (lambda 1) | 8 | -8014.59 | 16045.17 | 17.99 | 0.06 | Not supported |
| Or are extinction rates in period 2 similar to extinction rates of the no armature state in periods 1 & 3? | Additional constraints period 2 (\(\mu_0\)) | 8 | -8012.86 | 16041.72 | 14.54 | 0.15 | Supported |
|---|---|---|---|---|---|---|---|
| Or are extinction rates in period 2 similar to extinction rates of the armature state in periods 1 & 3? | Additional constraints period 2 (\(\mu_1\)) | 8 | -8014.60 | 16045.20 | 18.01 | 0.05 | Not supported |
| Or are transition rates in period 2 similar to transition rates from no armature to armature in periods 1 & 3? | Additional constraints period 2 (\(q_{01}\)) | 8 | -8014.57 | 16045.13 | 17.94 | 0.06 | Not supported |
| Or are transition rates in period 2 similar to transition rates from armature to no armature in periods 1 & 3? | Additional constraints period 2 (\(q_{10}\)) | 8 | -8011.99 | 16039.99 | 12.80 | 0.24 | Supported |
| And in combination, extinction rates in period 2 similar to extinction rates of the no armature state in periods 1 & 3, and transition rates in period 2 similar to transition rates from armature to no armature in periods 1 & 3 | Additional constraints period 2 (\(\mu_0\) and \(q_{10}\)) | 7 | -8012.86 | 16039.73 | 14.54 | 0.20 | Supported |

* Direct evaluation whether diversification response in presence of megaherbivores (periods 1 & 3) is similar (in contrast to diversification during the megaherbivore gap - period 2). If true, this model should be 'supported'.

** Direct evaluation whether transition rates (to evolving or losing the megaherbivore trait) are equal during the megaherbivore gap, and thus not dependent on megaherbivores (in contrast to transition rates in presence of megaherbivores - periods 1 & 3). If true, this model should be 'supported'.
Table S3: Time-dependent and trait-dependent binary state speciation and extinction (BiSSE) model selection for stem armature in palms (Arecaceae) in relation to their co-occurrence with or without megaherbivores. Models assess whether lineages with or without stem armature differ in their speciation, extinction and transition rates, in three different time periods. Period 1 (> 66 Ma) refers to the megaherbivorous dinosaur period, period 2 (66-40 Ma) refers to the megaherbivore gap, and period 3 (40 Ma until present) refers to the megaherbivorous mammal period. The best model, with the lowest Akaike information criterion (AIC), is indicated in bold, and was used in the Bayesian Markov chain Monte Carlo (MCMC) analysis. Model details of each model (Df, Ln.Lik, ChiSq, Pr) are provided in comparison to the full model, but model selection was performed using a likelihood-ratio test with the best fitting model so far, which would be the ‘supported’ model in the nearest proximity in the table above the respective model. Df = degrees of freedom, ln.Lik = log likelihood, ChiSq = Chi square, Pr = p-value.

| Rationale | Model | Df | ln.Lik | AIC | ChiSq | Pr(>|Chi Sq|) | Step-wise selection conclusion |
|-----------|-------|----|--------|-----|-------|-----------|-------------------------------|
| No constraints on speciation, extinction and transition rates through time | full | 18 | -7738.18 | 15512.36 | NA | NA | |
| Period 1 & 3 have a similar response in terms of speciation, extinction and transition rates of armature vs. no armature. * | Equal period 1 & 3 | 12 | -7740.50 | 15505.00 | 4.64 | 0.59 | Supported |
| In addition, are lineages with armature or no armature similar in their speciation and extinction rates in period 2? | Equal lambda and mu trait period 2 | 10 | -7740.88 | 15501.76 | 5.40 | 0.71 | Supported |
| In addition, are speciation, extinction and transition rates from armature to no armature, and vice versa, also similar in periods 1 & 3? | Equal lambda, mu and q trait periods 1 & 3 | 7 | -7818.80 | 15651.59 | 161.23 | 0.00 | Not supported |
| Or only for speciation rates? | Equal lambda trait periods 1 & 3 | 9 | -7748.21 | 15514.42 | 20.06 | 0.02 | Not supported |
| Or only for extinction rates? | Equal mu trait periods 1 & 3 | 9 | -7746.78 | 15511.56 | 17.20 | 0.05 | Not supported |
| Or only for transition rates? | Equal q trait periods 1 & 3 | 9 | -7808.48 | 15634.95 | 140.59 | 0.00 | Not supported |
| In addition to a similar response in periods 1 & 3 and constrained extinction rates of lineages with armature or no armature in period 2, are transition rates from armature to no armature and vice versa also similar in period 2? ** | Equal q trait period 2 | 9 | -7740.90 | 15499.80 | 5.43 | 0.79 | Supported |
| In addition, are speciation rates of the no armature state in period 2 similar to speciation rates in periods 1 & 3? | Additional constraints period 2 (lambda 0) | 8 | -7744.60 | 15508.79 | 16.43 | 0.09 | Not supported |
| Or are speciation rates of the armature state in period 2 similar to speciation rates in periods 1 & 3? | Additional constraints period 2 (lambda 1) | 8 | -7741.80 | 15499.60 | 7.24 | 0.70 | Supported |
| Or are extinction rates in period 2 similar to extinction rates of the no armature state in periods 1 & 3? | Additional constraints period 2 (mu 0) | 8 | -7742.84 | 15501.69 | 9.33 | 0.50 | Not supported |
| Or are extinction rates in period 2 similar to extinction rates of the armature state in periods 1 & 3? | Additional constraints period 2 (mu 1) | 8 | -7741.33 | 15498.66 | 6.30 | 0.79 | Supported |
| Or are transition rates in period 2 similar to transition rates from no armature to armature | Additional constraints | 8 | -7743.25 | 15502.49 | 10.13 | 0.43 | Not supported |

8
| armature to armature in periods 1 & 3? | period 2 \((q_{01})\) |  |  |  |  |
|----------------------------------------|----------------|---|---|---|---|
| Or are transition rates in period 2 similar to transition rates from armature to no armature in periods 1 & 3? | Additional constraints period 2 \((q_{10})\) | 8 | -7745.96 | 15507.92 | 15.56 | 0.11 | Not supported |
| And in combination, are speciation rates in period 2 similar to speciation rate of armature state in periods 1 & 3, and are extinction rates in period 2 similar to extinction rates of the armature state in periods 1 & 3? | Additional constraints period 2 \((\lambda_1\ and\ \mu_1)\) | 7 | -7750.10 | 15514.20 | 23.84 | 0.01 | Supported |

* Direct evaluation whether diversification response in presence of megaherbivores (periods 1 & 3) is similar (in contrast to diversification during the megaherbivore gap - period 2). If true, this model should be 'supported'.

** Direct evaluation whether transition rates (to evolving or losing the megaherbivore trait) are equal during the megaherbivore gap, and thus not dependent on megaherbivores (in contrast to transition rates in presence of megaherbivores - periods 1 & 3). If true, this model should be 'supported'.

Table S4: Time-dependent and trait-dependent binary state speciation and extinction (BiSSE) model selection for leaf armature in palms (Arecaceae) in relation to their co-occurrence with or without megaherbivores. Models assess whether lineages with or without leaf armature differ in their speciation, extinction and transition rates, in three different time periods. Period 1 (> 66 Ma) refers to the megaherbivorous dinosaur period, period 2 (66-40 Ma) refers to the megaherbivore gap, and period 3 (40 Ma until present) refers to the megaherbivorous mammal period. The best model, with the lowest Akaike information criterion (AIC), is indicated in bold. Model details of each model (Df, ln.Lik, AIC, ChiSq, Pr) are provided in comparison to the full model, but model selection was performed using a likelihood-ratio test with the best fitting model so far, which would be the ‘supported’ model in the nearest proximity in the table above the respective model. Df = degrees of freedom, ln.Lik = log likelihood, ChiSq = Chi square, Pr = p-value.

| Rationale                                                                 | Model                                                                 | Df | ln.Lik    | AIC         | ChiSq | Pr(>|Chi|) | Step-wise selection conclusion |
|--------------------------------------------------------------------------|-----------------------------------------------------------------------|----|-----------|-------------|-------|-----------|--------------------------------|
| No constraints on speciation, extinction and transition rates through time | Full                                                                  | 18 | -7801.45  | 15638.91    |       |           |                                |
| Period 1 & 3 have a similar response in terms of speciation, extinction and transition rates of armature vs. no armature * | Equal period 1 & 3                                                   | 12 | -7804.03  | 15632.07    | 5.16  | 0.52      | Supported                      |
| In addition, are lineages with armature or no armature similar in their speciation and extinction rates in period 2? | Equal lambda and mu trait period 2                                     | 10 | -7805.31  | 15630.61    | 7.71  | 0.46      | Supported                      |
| In addition, are speciation, extinction and transition rates from armature to no armature, and vice versa, also similar in periods 1 & 3? | Equal lambda, mu and q trait periods 1 & 3                             | 7  | -7806.34  | 15626.68    | 9.77  | 0.55      | Supported                      |
| In addition to a similar response in periods 1 & 3, constrained speciation and extinction rates of lineages with armature or no armature in period 2, and constrained speciation, extinction and transition rates of lineages with armature or no armature in periods 1 & 3, are transition rates from armature to no armature and vice versa also similar in period 2? ** | Equal q trait period 2                                                | 6  | -7806.82  | 15625.64    | 10.73 | 0.55      | Supported                      |
| In addition, are speciation, extinction and transition rates in period 2 similar to those in periods 1 & 3? | Additional constraints period 2 (lambda, mu and q)                     | 4  | -7817.72  | 15643.44    | 32.53 | 0.00      | Not supported                  |
| Or only for speciation rates?                                            | Additional constraints period 2 (lambda)                               | 5  | -7811.62  | 15633.24    | 20.34 | 0.09      | Supported                      |
| Or only for extinction rates?                                            | Additional constraints period 2 (mu)                                   | 5  | -7808.22  | 15626.44    | 13.53 | 0.41      | Supported                      |
| Or only for speciation and extinction rates?                             | Additional constraints period 2 (lambda and mu)                       | 4  | -7808.34  | 15624.68    | 13.77 | 0.47      | Supported                      |

* Direct evaluation whether diversification response in presence of megaherbivores (periods 1 & 3) is similar (in contrast to diversification during the megaherbivore gap - period 2). If true, this model should be ‘supported’.

** Direct evaluation whether transition rates (to evolving or losing the megaherbivore trait) are equal during the megaherbivore gap, and thus not dependent on megaherbivores (in contrast to transition rates in presence of megaherbivores - periods 1 & 3). If true, this model should be ‘supported’.
Figure S1: Speciation and transition rates of palm (Arecaceae) lineages lacking megaherbivore traits (i.e., small fruits and no armature) during the megaherbivore gap. a, b and c evaluate whether speciation rates increased or remained constant in the PMHG (H2, Table 1), whereas d, e and f evaluate whether trait change increased or remained constant in the PMHG (H3, Table 1). Small fruits were defined as <4 cm in length. Rates were inferred by fitting time-dependent binary state speciation and extinction (BiSSE) models to the phylogenetic data. Rates are given in lineages per million years. BiSSE models were selected using maximum likelihood optimisation, and box-and-whiskers show 95% posterior densities of the rates resulting from Bayesian Markov chain Monte Carlo (MCMC) analyses over 100 phylogenetic trees from the posterior distribution based on the diversification model with the best fit (see Tables S1–S3). For comparison, rates of palm lineages with megafaunal fruits or armature are illustrated in Fig. 3.
**Figure S2:** Simulation results for palm (Arecaceae) lineages based on neutral evolution of a binary trait (i.e., megafaunal fruits - state 1; small fruits - state 0) through geological time. The neutral trait was evolved under the observed transition rates from the empirical data for fruit size (top row), as well as under equal forward and backward transition rates (q = 0.01, bottom row). After evolving the neutral trait, the empirical time-dependent binary state speciation and extinction (BiSSE) model for fruit size was run over the data, to evaluate whether neutral traits would affect speciation, extinction and transition rates in a similar manner as observed in the empirical data. This was repeated over 100 palm phylogenetic trees. The expectation is that neutral traits should not affect speciation, extinction or transition rates of the binary states of the trait, and not be affected by the different time bins. Rates are given in lineages per million years, in the three time periods: megaherbivorous dinosaur period >66 Ma (period 1), megaherbivore gap 66-40 Ma (period 2), megaherbivorous mammal period 40 Ma until present (period 3). Box-and-whiskers show 95% posterior densities of the rates resulting from Bayesian Markov chain Monte Carlo (MCMC) analyses over 100 phylogenetic trees from the posterior distribution. The first number refers to the trait, the second to the time period. For example: lambda 0.1 refers to speciation of small fruits in period 1; q10.2 refers to transition rate from large to small fruits in period 2.
Simulation under observed transition rate $q$ for fruit size model

Simulation under transition rate $q = 0.01$ for fruit size model
**Figure S3**: Simulation results armature. Speciation (\(\lambda\)), extinction (\(\mu\)) and transition (\(q\)) rates of palm (Arecaceae) lineages based on neutral evolution of a binary trait (i.e., armature - state 1; no armature - state 0) through geological time. The neutral trait was evolved under the observed transition rates from the empirical data for armature (top row), as well as under equal forward and backward transition rates (\(q = 0.01\), bottom row). After evolving the neutral trait, the empirical time-dependent binary state speciation and extinction (BiSSE) model for armature was run over the data, to evaluate whether neutral traits would affect speciation, extinction and transition rates in a similar manner as observed in the empirical data. This was repeated over 100 palm phylogenetic trees. The expectation is that neutral traits should not affect speciation, extinction or transition rates of the binary states of the trait, and not be affected by the different time bins. Rates are given in lineages per million years, in the three time periods: megaherbivorous dinosaur period >66 Ma (period 1), megaherbivore gap 66–40 Ma (period 2), megaherbivorous mammal period 40 Ma until present (period 3). Box-and-whiskers show 95% posterior densities of the rates resulting from Bayesian Markov chain Monte Carlo (MCMC) analyses over 100 phylogenetic trees from the posterior distribution. The first number refers to the trait, the second to the time period. For example: \(\lambda 0.1\) refers to speciation of no armature in period 1; \(q_{1.2}\) refers to transition rate from armature to no armature in period 2.
Simulation under observed transition rate $q$ for armature model

Simulation under transition rate $q = 0.01$ for armature model
**Figure S4:** Evolution of armature (stem and leaf combined) in palms (Arecales). Ancestral state reconstructions were performed using stochastic character mapping. The posterior probability of ancestral lineages possessing armature is indicated with the yellow colour. Armature evolved at least eight times independently in palms. Subfamilies are indicated at the tips of the phylogenetic tree.
**Figure S5**: Net diversification and extinction rates of palm (Arecaceae) lineages with (in yellow) and without (in grey) megaherbivore traits (large/small fruits; armature/no armature) during the megaherbivore gap (40-66 Ma), and the preceding (> 66 Ma) and following (> 40 Ma) periods. Small fruits were defined as < 4 cm in length. Rates were inferred by fitting time-dependent binary state speciation and extinction (BiSSE) models to the phylogenetic data. Rates are given in lineages per million years. BiSSE models were selected using maximum likelihood optimisation, and box-and-whiskers show 95% posterior densities of the rates resulting from Bayesian Markov chain Monte Carlo (MCMC) analyses over 100 phylogenetic trees from the posterior distribution based on the diversification model with the best fit (see Tables S1–S3).
Supplementary references

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