Supplementary Tables and Figures

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **A** |  | **DR+RR+** | | **DR+RR-** | | **DR-RR+** | | **DR-RR-** | | **Type 1** | | **tip ratio path** |
|  | **significant** | **focal** | **path** | **focal** | **path** | **focal** | **path** | **focal** | **path** | **focal** | **path** |
| **DR+RR+** | 92.437 | 84.454 | 3.361 | 0.420 | 1.261 | 0.840 | 2.101 | 0 | 0 | 0 | 3.361 | 0.826 |
| 87.815 | | 1.681 | | 2.941 | | 0 | | 3.361 | |
| **DR+RR-** | 95.299 | 0 | 0 | 91.026 | 0.427 | 0 | 0 | 1.282 | 2.564 | 0.427 | 2.137 | 0.619 |
| 0 | | 91.453 | | 0 | | 3.846 | | 2.564 | |
| **DR-RR+** | 72.556 | 2.632 | 1.88 | 0 | 0 | 56.391 | 11.278 | 0.376 | 0 | 0 | 1.88 | 1.326 |
| 4.512 | | 0 | | 67.669 | | 0.376 | | 1.88 | |
| **DR-RR-** | 83.206 | 0 | 0 | 2.290 | 0.382 | 0 | 0.382 | 69.466 | 10.687 | 1.145 | 4.58 | 0.766 |
| 0 | | 2.672 | | 0.382 | | 80.153 | | 5.725 | |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| **B** |  | **DR+BR+** | | **DR+BR-** | | **DR-BR+** | | **DR-BR-** | | **Type 1** | | **tip ratio path** |
|  | **significant** | **focal** | **path** | **focal** | **path** | **focal** | **path** | **focal** | **path** | **focal** | **path** |
| **DR+BR+** | 93.277 | 87.815 | 3.361 | 0 | 0 | 0.840 | 1.261 | 0 | 0 | 0.840 | 2.101 | 0.978 |
| 91.176 | | 0 | | 2.101 | | 0 | | 2.941 | |
| **DR+BR-** | 96.154 | 0 | 0 | 91.453 | 0 | 0 | 0 | 1.282 | 3.419 | 1.709 | 0.855 | 0.355 |
| 0 | | 91.453 | | 0 | | 4.701 | | 2.564 | |
| **DR-BR+** | 78.571 | 2.632 | 1.880 | 0 | 0 | 67.669 | 6.391 | 0 | 0 | 1.127 | 2.256 | 1.101 |
| 4.512 | | 0 | | 74.060 | | 0 | | 3.383 | |
| **DR-BR-** | 79.771 | 0 | 0 | 2.290 | 0 | 0 | 0 | 67.557 | 9.924 | 0.763 | 2.290 | 0.546 |
| 0 | | 2.290 | | 0 | | 77.481 | | 3.053 | |

Table S1. Results of clade-associated diversification simulations performed under the ‘node’ mode by using *RR*rates (A) and *BMrates* (B) as rates of phenotypic evolution. Simulations are classified in four models (rows) based on simulated DR and  (the Brownian rate for the clade under scrutiny): positive shift in both DR and phenotypic rate (DR+RR+ or DR+BR+), positive shift in DR and negative shift in phenotypic rate (DR+RR- or DR+BR-), negative shift in DR and positive shift in phenotypic rate (DR-RR+ or DR-BR+), and negative shift in both DR and phenotypic rate (DR-RR- or DR-BR-). For simulations producing no significant results for the focal clade, the clades along its path were inspected. significant = the percentage of simulations producing significant results for either the focal clade (focal) or at least one clade along its path (path); DR+RR+/DR+RR-/DR-RR+/DR-RR- or DR+BR+/DR+BR-/DR-BR+/DR-BR- = the percentage of significant simulations which classify in each category, computed for the focal clade (focal), the clades along its the path (path), and the sum of both; Type 1 = the incidence of Type 1 error rate for either the focal clade (focal) or the clades along its path (path); tip ratio path = the average ratio between the number of tips belonging to the shifting ‘path’ clade and the number of tips in the focal clade (for significant simulations producing significance on path nodes only).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **A.** |  |  |  |  |  |
| **Clade** | **DR difference** | **p-value DR** | **absolute RRrate difference** | **p-value RRrates** | **sigma ratio** |
| Dryomorpha | 0.056 | 0.985 | -0.023 | 0.001 | 3.208 |
| 0.059 | 0.991 | -0.022 | 0.004 | 3.403 |
| Dryomorpha + *Tenontosaurus* | 0.057 | 0.984 | -0.025 | 0.002 | 3.464 |
| 0.057 | 0.982 | -0.023 | 0.001 | 3.425 |
| 0.052 | 0.975 | -0.024 | 0.001 | 3.639 |
|  |  |  |  |  |  |
| **B.** |  |  |  |  |  |
| **Clade** | **DR difference** | **p-value DR** | **absolute RRrate difference** | **p-value RRrates** | **sigma ratio** |
| Hadrosauriphormes | 0.084 | 0.992 | -0.023 | 0.002 | 3.573 |
| Dryomorpha + *Tenontosaurus* | 0.056 | 0.985 | -0.023 | 0.002 | 3.759 |
| Iguanodontia excluding *Anabisetia saldiviai* | 0.077 | 0.983 | -0.026 | 0.001 | 4.080 |
| Iguanodontia + stem Iguanodontia | 0.110 | 0.999 | -0.023 | 0.001 | 3.493 |

Table S2. Clade-associated diversification shifts in ornithodirans phylogeny by using *RRrates* within the *FSO* routine. A) Shifting clades located by *search*.*shiftDR*. B) Shifting clades as located by *overfitDR*. DR difference = DR means difference between the clade and the rest of the tree; p-value DR = significance level for DR difference assessed by randomization; absolute RRrates difference = absolute *RRrates* means difference between the clade and the rest of the tree; p-value RRrates = significance level for *RRates* difference assessed by randomization; sigma ratio = maximum to minimum Brownian rate ratio computed by fitting a two-rates Brownian model on the clade and the rest of the tree; 2\*blim = twice the maximum 2 ratio of a Brownian phenotype generated on the tree, computed by fitting two-rates Brownian models on each candidate clade and the rest of the tree.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **A.** |  |  |  |  |  |  |  |
| **Clade** | **DR difference** | **p-value DR** | **sigma ratio** | **sigma clade** | **sigma back** | **p-value sigma** | **2\*blim** |
| Hadrosauriphormes | 0.061 | 0.981 | 4.159 | 0.053 | 0.220 | 0.001 | 4.136 |
| Dryomorpha | 0.059 | 0.979 | 3.403 | 0.065 | 0.222 | 0.001 | 3.135 |
|  |  |  |  |  |  |  |  |
| **B.** |  |  |  |  |  |  |  |
| **Clade** | **DR difference** | **p-value DR** | **sigma ratio** | **sigma clade** | **sigma back** | **p-value sigma** |  |
| Hadrosauroidea | 0.115 | 0.998 | 3.701 | 0.047 | 0.172 | 0.002 |  |
| 0.099 | 0.997 | 8.805 | 0.020 | 0.174 | 0.001 |  |
| 0.114 | 0.990 | 3.905 | 0.046 | 0.181 | 0.001 |  |
| 0.099 | 0.987 | 8.834 | 0.020 | 0.174 | 0.001 |  |
| Hadrosauriphormes | 0.074 | 0.983 | 3.769 | 0.046 | 0.175 | 0.001 |  |
| 0.122 | 0.997 | 4.616 | 0.040 | 0.184 | 0.001 |  |

Table S3. Clade-associated diversification shifts in ornithodirans phylogeny by using *BMrates* within the *FSO* routine. A) Shifting clades located by *search*.*shiftDR*. B) Shifting clades as located by *overfitDR*. DR difference = DR means difference between the clade and the rest of the tree; p-value DR = significance level for DR difference assessed by randomization; sigma ratio = maximum to minimum Brownian rate ratio computed by fitting a two-rates Brownian model on the clade and the rest of the tree; sigma clade = Brownian rate for the clade; sigma clade = Brownian rate for the rest of the tree; p-value sigma = significance level for 2 ratio; 2\*blim = twice the maximum 2 ratio of a random Brownian phenotype generated on the tree, computed by fitting two-rates Brownian models on each candidate clade and the rest of the tree.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **A.** |  |  |  |  |  |  |
|  | **DR difference** | **p-value DR** | **absolute RRrate difference** | **p-value RRrates** | **sigma ratio** | **2\*blim** |
| - | - | - | - | - | - | - |
|  |  |  |  |  |  |  |
| **B.** |  |  |  |  |  |  |
| **Clade** | **DR difference** | **p-value DR** | **absolute RRrate difference** | **p-value RRrates** | **sigma ratio** |  |
| Hadrosauroidea | 0.069 | 0.984 | -0.027 | 0.001 | 8.553 |  |
| 0.064 | 0.976 | -0.030 | 0.001 | 8.814 |  |
| 0.138 | 1.000 | -0.033 | 0.001 | 9.149 |  |
| Hadrosauriphormes | 0.070 | 0.980 | -0.021 | 0.001 | 3.179 |  |

Table S4. Clade-associated diversification shifts in Ornithodirans phylogeny obtained by using *RRrates* within *search.shiftDR* and *overfitDR* performed on the original tree dichotomized by means of ape’s function *multi2di*. A) Shifting clades located by *search*.*shiftDR*. The row is empty because no significant shift was found. B) Shifting clades as located by *overfitDR*. DR difference = DR means difference between the clade and the rest of the tree; p-value DR = significance level for DR difference assessed by randomization; absolute RRrates difference = absolute *RRrates* means difference between the clade and the rest of the tree; p-value RRrates = significance level for *RRates* difference assessed by randomization; sigma ratio = maximum to minimum Brownian rate ratio computed by fitting a two-rates Brownian model on the clade and the rest of the tree; 2\*blim = twice the maximum 2 ratio of a random Brownian phenotype generated on the tree, computed by fitting two-rates Brownian models on each candidate clade and the rest of the tree.

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| --- | --- | --- | --- | --- | --- | --- | --- |
| **A.** |  |  |  |  |  |  |  |
| **Clade** | **DR difference** | **p-value DR** | **sigma ratio** | **sigma clade** | **sigma back** | **p-value sigma** | **2\*blim** |
| Dryomorpha + *Tenontosaurus* | 0.048 | 0.989 | 3.024 | 0.072 | 0.217 | 0.001 | 2.918 |
|  |  |  |  |  |  |  |  |
| **B.** |  |  |  |  |  |  |  |
| **Clade** | **DR difference** | **p-value DR** | **sigma ratio** | **sigma clade** | **sigma back** | **p-value sigma** | **ssdr tips** |
| Hadrosauroidea | 0.148 | 1.000 | 3.972 | 0.045 | 0.178 | 0.001 | 0.594 |
| 0.143 | 1.000 | 4.519 | 0.040 | 0.181 | 0.001 | 0.594 |
| 0.083 | 0.995 | 3.657 | 0.048 | 0.177 | 0.001 | 0.594 |
| 0.107 | 0.999 | 3.643 | 0.048 | 0.176 | 0.002 | 0.594 |
| Hadrosauriphormes | 0.073 | 0.994 | 3.437 | 0.051 | 0.175 | 0.001 | 0.625 |

Table S5. Clade-associated diversification shifts in ornithodirans phylogeny obtained by using *BMrates* within *search.shiftDR* and *overfitDR* performed on the original tree dichotomized by means of ape’s function *multi2di*. A) Shifting clades located by *search.shiftDR*. B) Shifting clades as located by *overfitDR*. DR difference = DR means difference between the clade and the rest of the tree; p-value DR = significance level for DR difference assessed by randomization; sigma ratio = maximum to minimum Brownian rate ratio computed by fitting a two-rates Brownian model on the clade and the rest of the tree; sigma clade = Brownian rate for the clade; sigma clade = Brownian rate for the rest of the tree; p-value sigma = significance level for 2 ratio; 2\*blim = twice the maximum 2 ratio of a random Brownian phenotype generated on the tree, computed by fitting two-rates Brownian models on each candidate clade and the rest of the tree; ssdr tips = proportion of tips occurring in the shifting clade corresponding to the tips belonging to the shift located by *search.shiftDR*.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **A.** |  |  |  |  |  |  |  |
| **search.shiftDR** | | | **overfitDR** | | | **ES-sim** | |
| **slope** | **p-value** | **p random** | **slope** | **p-value** | **p random** | **rho** | **p-rho** |
| -0.003 | 0.849 | 0.417 | -0.006 | 0.451 | 0.318 | 0.006 | 0.874 |
| -0.003 | 0.820 | 0.400 | -0.009 | 0.436 | 0.165 | -0.011 | 0.945 |
| -0.002 | 0.889 | 0.454 | -0.002 | 0.875 | 0.435 | -0.007 | 0.889 |
| -0.002 | 0.864 | 0.433 | 0.009 | 0.464 | 0.755 | -0.008 | 0.935 |
| -0.003 | 0.842 | 0.422 | -0.007 | 0.547 | 0.283 | -0.010 | 0.823 |
| -0.004 | 0.780 | 0.385 | -0.015 | 0.230 | 0.109 | -0.014 | 0.869 |
| -0.001 | 0.937 | 0.475 | 0.006 | 0.620 | 0.703 | -0.004 | 0.969 |
| -0.003 | 0.851 | 0.398 | -0.015 | 0.212 | 0.095 | -0.009 | 0.939 |
| -0.003 | 0.822 | 0.379 | -0.012 | 0.327 | 0.144 | -0.011 | 0.849 |
| -0.003 | 0.839 | 0.411 | -0.011 | 0.345 | 0.172 | -0.010 | 0.901 |
|  |  |  |  |  |  |  |  |
| **B.** |  |  |  |  |  |  |  |
| **search.shiftDR** | | | **overfitDR** | | | **ES-sim** | |
| **slope** | **p-value** | **p random** | **slope** | **p-value** | **p random** | **rho** | **p-rho** |
| -0.004 | 0.773 | 0.362 | -0.008 | 0.519 | 0.240 | -0.014 | 0.875 |
| -0.010 | 0.417 | 0.169 |
| -0.006 | 0.641 | 0.364 |
| -0.018 | 0.126 | 0.056 |
| 0.001 | 0.962 | 0.519 |
| -0.009 | 0.461 | 0.212 |
| -0.008 | 0.521 | 0.268 |
| 0.001 | 0.959 | 0.522 |
| -0.008 | 0.513 | 0.229 |
| -0.004 | 0.764 | 0.369 |

Table S6. Character-associated diversification test in ornithodirans. A) Results of *search.shiftDR*, *overfitDR*, and *ES-sim* performed on the tree dichotomized by means of *fix.poly* within 10 *FSO* replications. B) Results of *search.shiftDR*, *overfitDR*, and *ES-sim* performed on the tree dichotomized by means of ape’s function *multi2di*. slope = slope of log body size (rescaled in the 0-1 range) versus log DRs regression; p-value = p-value for the regression slope; p-random = p-value for the regression slope compared to a random distribution of Brownian Motion slopes; rho = Pearson’s correlation coefficient; p-rho = p-value for the Pearson’s correlation coefficient.

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| --- | --- | --- | --- | --- | --- | --- |
| **A.** |  |  |  |  |  |  |
| **Clade** | **DR difference** | **p-value DR** | **absolute *RRrates* difference** | **p-value *RRrates*** | **sigma ratio** | **2\*blim** |
| Suidae | -0.121 | 0.002 | -0.037 | 0.001 | 3.050 | 3.616 |
| Rhinocerotidae (partim) | -0.099 | 0.010 | -0.030 | 0.001 | 3.326 | 3.368 |
|  |  |  |  |  |  |  |
| **B.** |  |  |  |  |  |  |
| **Clade** | **DR difference** | **p-value DR** | **absolute *RRrates* difference** | **p-value *RRrates*** | **sigma ratio** |  |
| Suidae | -0.149 | 0.001 | -0.030 | 0.001 | 2.984 |  |
| Borophaginae | 0.150 | 0.991 | -0.022 | 0.006 | 4.603 |  |

Table S7. Clade-associated diversification shifts in mammalian phylogeny by using *RRrates* within the *FSO* routine. A) Shifting clades located by *search.shiftDR*. B) Shifting clades as located by *overfitDR*. DR difference = DR means difference between the clade and the rest of the tree; p-value DR = significance level for DR difference assessed by randomization; absolute RRrates difference = absolute *RRrates* means difference between the clade and the rest of the tree; p-value RRrates = significance level for *RRates* difference assessed by randomization; sigma ratio = maximum to minimum Brownian rate ratio computed by fitting a two-rates Brownian model on the clade and the rest of the tree; 2\*blim = twice the maximum 2 ratio of a random Brownian phenotype generated on the tree, computed by fitting two-rates Brownian models on each candidate clade and the rest of the tree.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **A.** |  |  |  |  |  |  |  |
| **Clade** | **DR difference** | **p-value DR** | **sigma ratio** | **sigma clade** | **sigma back** | **p-value sigma** | **2\*blim** |
| Suidae | -0.121 | 0.001 | 3.050 | 0.010 | 0.031 | 0.001 | 2.605 |
| -0.122 | 0.001 | 2.626 | 0.010 | 0.027 | 0.001 | 4.224 |
| Aceratheriini + Teleoceratini | -0.100 | 0.018 | 3.406 | 0.008 | 0.027 | 0.001 | 4.224 |
| Rhinocerotidae | -0.093 | 0.010 | 3.354 | 0.008 | 0.027 | 0.001 | 3.290 |
|  |  |  |  |  |  |  |  |
| **B.** |  |  |  |  |  |  |  |
| **Clade** | **DR difference** | **p-value DR** | **sigma ratio** | **sigma clade** | **sigma back** | **p-value sigma** |  |
| Aceratheriini + Teleoceratini | -0.121 | 0.018 | 4.014 | 0.006 | 0.025 | 0.001 |  |
| Borophaginae excluding *Oxetocyon* and *Archaeocyon* | 0.120 | 0.976 | 4.601 | 0.005 | 0.025 | 0.001 |  |
| Camelidae | -0.166 | 0.001 | 2.849 | 0.009 | 0.024 | 0.001 |  |
| Suidae | -0.179 | 0.001 | 2.690 | 0.009 | 0.024 | 0.001 |  |
| Hipparionini | 0.587 | 1.000 | 5.670 | 0.004 | 0.024 | 0.001 |  |

Table S8. Clade-associated diversification shifts in mammalian phylogeny by using *BMrates* within the *FSO* routine. A) Shifting clades located by *search.shiftDR*. B) Shifting clades as located by *overfitDR*. DR difference = DR means difference between the clade and the rest of the tree; p-value DR = significance level for DR difference assessed by randomization; sigma ratio = maximum to minimum Brownian rate ratio computed by fitting a two-rates Brownian model on the clade and the rest of the tree; sigma clade = Brownian rate for the clade; sigma clade = Brownian rate for the rest of the tree; p-value sigma = significance level for 2 ratio; 2\*blim = twice the maximum 2 ratio of a random Brownian phenotype generated on the tree, computed by fitting two-rates Brownian models on each candidate clade and the rest of the tree.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **A.** |  |  |  |  |  |  |
| **Clade** | **DR difference** | **p-value DR** | **absolute *RRrates* difference** | **p-value *RRrates*** | **sigma ratio** | **2\*blim** |
| - | - | - | - | - | - | - |
|  |  |  |  |  |  |  |
| **B.** |  |  |  |  |  |  |
| **Clade** | **DR difference** | **p-value DR** | **absolute *RRrates* difference** | **p-value *RRrates*** | **sigma ratio** |  |
| Giraffidae | -0.075 | 0.016 | -0.021 | 0.001 | 4.562 |  |
| -0.068 | 0.008 | -0.022 | 0.001 | 4.562 |  |

Table S9. Clade-associated diversification shifts in mammalian phylogeny obtained by using *RRrates* within *search.shiftDR* and *overfitDR* performed on the original tree dichotomized by means of ape’s function *multi2di*. A) Shifting clades located by *search.shiftDR*. It is empty because no significant shift was found. B) Shifting clades as located by *overfitDR*. DR difference = DR means difference between the clade and the rest of the tree; p-value DR = significance level for DR difference assessed by randomization; absolute RRrates difference = absolute *RRrates* means difference between the clade and the rest of the tree; p-value RRrates = significance level for *RRates* difference assessed by randomization; sigma ratio = maximum to minimum Brownian rate ratio computed by fitting a two-rates Brownian model on the clade and the rest of the tree; 2\*blim = twice the maximum 2 ratio of a random Brownian phenotype generated on the tree, computed by fitting two-rates Brownian models on each candidate clade and the rest of the tree.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **A.** |  |  |  |  |  |  |  |
| **Clade** | **DR difference** | **p-value DR** | **sigma ratio** | **sigma clade** | **sigma back** | **p-value sigma** | **2\*blim** |
| Borophagini | 0.115 | 0.985 | 3.328 | 0.006 | 0.019 | 0.002 | 3.080 |
|  |  |  |  |  |  |  |  |
| **B.** |  |  |  |  |  |  |  |
| **Clade** | **DR difference** | **p-value DR** | **sigma ratio** | **sigma clade** | **sigma back** | **p-value sigma** | **ssdr tips** |
| Giraffidae | -0.070 | 0.023 | 4.705 | 0.003 | 0.016 | 0.001 | 0 |
| Borophagini | 0.191 | 1.000 | 3.572 | 0.005 | 0.016 | 0.001 | 1.000 |
| 0.154 | 0.996 | 3.434 | 0.005 | 0.016 | 0.001 | 1.000 |
| 0.142 | 0.999 | 3.536 | 0.005 | 0.016 | 0.001 | 1.000 |
| 0.136 | 0.993 | 3.209 | 0.005 | 0.016 | 0.001 | 1.000 |
| Borophagini + Phlaocyonini | 0.100 | 0.976 | 3.269 | 0.005 | 0.016 | 0.001 | 1.273 |
| Borophagini + Phlaocyonini + *Rhizocyon* | 0.141 | 1.000 | 3.175 | 0.005 | 0.016 | 0.001 | 1.303 |

Table S10. Clade-associated diversification shifts in mammalian phylogeny by using *BMrates* within *search.shiftDR* and *overfitDR* performed on the original tree dichotomized by means of ape’s function *multi2di*. A) Shifting clades located by *search.shiftDR*. B) Shifting clades as located by *overfitDR*. DR difference = DR means difference between the clade and the rest of the tree; p-value DR = significance level for DR difference assessed by randomization; sigma ratio = maximum to minimum Brownian rate ratio computed by fitting a two-rates Brownian model on the clade and the rest of the tree; sigma clade = Brownian rate for the clade; sigma clade = Brownian rate for the rest of the tree; p-value sigma = significance level for 2 ratio; 2\*blim = twice the maximum 2 ratio of a random Brownian phenotype generated on the tree, computed by fitting two-rates Brownian models on each candidate clade and the rest of the tree; ssdr tips = proportion of tips occurring in the shifting clade corresponding to the tips beloning to the shift located by *search*.*shiftDR*.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **A.** |  |  |  |  |  |  |  |
| **search.shiftDR** | | | **overfitDR** | | | **ES-sim** | |
| **slope** | **p-value** | **p random** | **slope** | **p-value** | **p random** | **rho** | **p-rho** |
| -0.027 | 0 | 0.081 | -0.025 | 0 | 0.078 | -0.132 | 0.096 |
| -0.025 | 0 | 0.063 | -0.021 | 0 | 0.088 | -0.130 | 0.084 |
| -0.026 | 0 | 0.049 | -0.024 | 0 | 0.062 | -0.133 | 0.122 |
| -0.029 | 0 | 0.063 | -0.024 | 0 | 0.067 | -0.147 | 0.106 |
| -0.028 | 0 | 0.046 | -0.028 | 0 | 0.042 | -0.146 | 0.086 |
| -0.026 | 0 | 0.055 | -0.020 | 0 | 0.101 | -0.134 | 0.116 |
| -0.025 | 0 | 0.068 | -0.018 | 0 | 0.101 | -0.129 | 0.122 |
| -0.025 | 0 | 0.071 | -0.028 | 0 | 0.029 | -0.130 | 0.132 |
| -0.024 | 0 | 0.069 | -0.019 | 0 | 0.111 | -0.125 | 0.126 |
| -0.026 | 0 | 0.059 | -0.024 | 0 | 0.065 | -0.134 | 0.086 |
|  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |
| **B.** |  |  |  |  |  |  |  |
| **search.shiftDR** | | | **overfitDR** | | | **ES-sim** | |
| **slope** | **p-value** | **p random** | **slope** | **p-value** | **p random** | **rho** | **p-rho** |
| -0.037 | 0 | 0.033 | -0.031 | 0 | 0.031 | -0.159 | 0.062 |
| -0.038 | 0 | 0.031 |
| -0.036 | 0 | 0.026 |
| -0.034 | 0 | 0.027 |
| -0.033 | 0 | 0.032 |
| -0.034 | 0 | 0.020 |
| -0.035 | 0 | 0.024 |
| -0.036 | 0 | 0.024 |
| -0.030 | 0 | 0.038 |
| -0.033 | 0 | 0.038 |

Table S11. Character-associated diversification test in mammals. A) Results of *search.shiftDR*, *overfitDR*, and *ES-sim* performed on the tree dichotomized by means of *fix.poly* within 10 *FSO* replications. B) Results of *search.shiftDR*, *overfitDR*, and *ES-sim* performed on the tree dichotomized by means of ape’s function *multi2di*. slope = slope of log body size (rescaled in the 0-1 range) versus log DRs regression; p-value = p-value for the regression slope; p-random = p-value for the regression slope compared to a random distribution of Brownian Motion slopes; rho = Pearson’s correlation coefficient; p-rho = p-value for the Pearson’s correlation coefficient.

Figure S1. Sensitivity analysis of clade-associated diversification test to the combination of *RRrates* and DR values. a) DR+RR+ = positive shift in both DR and phenotypic rate; b) DR+RR- = positive shift in DR and negative shift in phenotypic rate; c) DR-RR+ = negative shift in DR and positive shift in phenotypic rate; d) DR-RR- = negative shift in both DR and phenotypic rate. *DRratio* = the ratio between the mean DR of the shifting clade before it is modified to simulate the shift and the mean DR of the rest of the tree, divided by the same figure computed after modification. At *DRratio* > 1 the focal clade gained in terms of DR, and *vice-versa*. sigma = the Brownian rate used to simulate the phenotypic values at the shifting clade. Sigma (=2) values < / > 1 indicate a slowdown/acceleration in phenotypic evolution simulated for the clade as compared to the rest of the tree. The color gradient represents non-significant (red) to significant (blue) results. The green solid lines represent the 95% significance isoline.

Figure S2. Sensitivity analysis of clade-associated diversification test to the combination of *BMrates* and DR values. a) DR+BM+ = positive shift in both DR and phenotypic rate; b) DR+BM- = positive shift in DR and negative shift in phenotypic rate; c) DR-BM+ = negative shift in DR and positive shift in phenotypic rate; d) DR-BM- = negative shift in both DR and phenotypic rate. *DRratio* = the ratio between the mean DR of the shifting clade before it is modified to simulate the shift and the mean DR of the rest of the tree, divided by the same figure computed after modification. At *DRratio* > 1 the focal clade gained in terms of DR, and *vice-versa*. sigma = the Brownian rate used to simulate the phenotypic values at the shifting clade. Sigma (=2) values < / > 1 indicate a slowdown/acceleration in phenotypic evolution simulated for the clade as compared to the rest of the tree. The color gradient represents non-significant (red) to significant (blue) results. The green solid lines represent the 95% significance isoline.

Figure S3. Sensitivity analysis of character-associated diversification testto variable intensity patterns. a) results of simulations with positive relationship between phenotypic values and DR values; b) results of simulations with negative relationship between phenotypic values and DR values. tree ratio = the ratio between the number of species of the final tree (i.e. with the additional tips to simulate the character-associated diversification pattern) with respect to the original tree. mean shift = a metric quantifying the position, in terms of percentile, of the mean of the phenotypic vector obtained after including the additional tips depending on the starting phenotypic value, relative to the original phenotype. The color gradient indicates the shift from non-significant (red) to significant (blue) results. The green solid lines represent the 95% significance isoline.

Figure S4. Results of 10 *overfitDR* replications performed on the ornithodirans tree and log body size after tree dichotomization by means of ape’s function *multi2di* (i.e. keeping zero-length branches within the phylogeny). The shaded rectangles overlaying the clades indicate the direction of the shift in both DR and RR/BM rate. The percentages specify the proportion of *overfitDR* runsproducing significant result for each clade. The shaded circle indicate the location of the shift possibly found by *search.shiftDR*. a) *search.shiftDR* and *overfitDR* performed by using *RRrates.* 40% significant results pertain to Hadrosauroidea, 10% regard Hadrosauriformes. No shift was located by *search.shiftDR*. b) *search.shiftDR* and *overfitDR* performed by using *BMrates.* 40% significant results pertain to Hadrosauroidea, 10% regard Hadrosauriformes. The shift returned by *search.shiftDR* pertains the clade including Dryomorpha + the sister genus *Tenontosaurus*. *Parasaurolophus* silhouette was available for reuse under Creative Commons Attribution-NonCommercial-ShareAlike 3.0 Unported license (https://creativecommons.org/licenses/by-nc-sa/3.0/) at phylopic (<http://phylopic.org/>). The image was created by Matt Martyniuk.

Figure S5. Results of character-associated diversification test on ornithodirans. The solid line represents the slope of log body size (rescaled in a 0-1 range) versus log DRs regression as returned by *search.shiftDR* performed on the tree dichotomized by means of ape’s function *multi2di* (i.e. keeping zero-length branches within the phylogeny). The grey area marks the range of Brownian Motion slopes simulated within the function to assess significance. The dashed lines represent the maximum and minimum slopes derived by *search.shiftDR* performedwithin *FSO*.

Figure S6. Results of 10 *FSO* replicationsperformed on the mammalian tree and log body size data. The shaded rectangles overlaying the clades indicate the direction of the shift in both DR and RR/BM rate. The percentages specify the proportion of *overfitDR* runs within *FSO* producing significant result for each clade. a) *FSO* performed by using *RRrates.* From top to bottom: 10% significant results pertain to Borophaginae, 10% regard Suidae. b) *FSO* performed by using *BMrates.* From top to bottom: 10% significant results pertain to Borophaginae excluding the genera *Oxetocyon* and *Archaeocyon*, 10% regard Hipparionini, 10% pertain to the clade including Aceratheriini and Teleoceratini within Rhinocerotinae rhinoceros, 10% regard Suidae, 10% pertain to Camelidae. Animals silhouettes (excluding *Borophagus* which is our own) were available for reuse under Creative Commons Attribution-NonCommercial-ShareAlike 3.0 Unported license (https://creativecommons.org/licenses/by-nc-sa/3.0/) at phylopic (<http://phylopic.org/>). *Platygonus* (Suidae) created by Scott Harman; *Hipparion* (Hipparionini) created by Zimices; *Teleoceras* (Aceratheriini and Teleoceratini within Rhinocerotinae rhinoceros) created by Zimices; *Camelops* (Camelidae) created by Zimices.

Figure S7. Results of 10 *overfitDR* replications as performed on the mammalian tree and log body size data after tree dichotomization by means of ape’s function *multi2di* (i.e. keeping zero-length branches within the phylogeny). The shaded rectangles overlaying the clades indicate the direction of the shift in both DR and RR/BM rate. The percentages specify the proportion of *overfitDR* runsproducing significant result for each clade. The shaded circle indicate the location of the shift possibly found by *search.shiftDR*. a) *search.shiftDR* and *overfitDR* performed by using *RRrates.* 20% significant results pertain to Giraffidae. No shift was located by *search.shiftDR*. b) *search.shiftDR* and *overfitDR* performed by using *BMrates.* 60% significant results pertain to Borophagini, 10% regard Giraffidae. Additionally, in 20% of cases the shift pertaining Borophagini also includes Phlaocyonini, extending to the sister genus *Rhizocyon* in 10%. Such percentages are not printed on the figure for graphical reasons. The shift returned by *search.shiftDR* pertains Borophagini as well. *Samotherium* (Giraffidae) silhouette was available for reuse under Creative Commons Attribution-NonCommercial-ShareAlike 3.0 Unported license (https://creativecommons.org/licenses/by-nc-sa/3.0/) at phylopic (<http://phylopic.org/>). The image was created by Zimices.