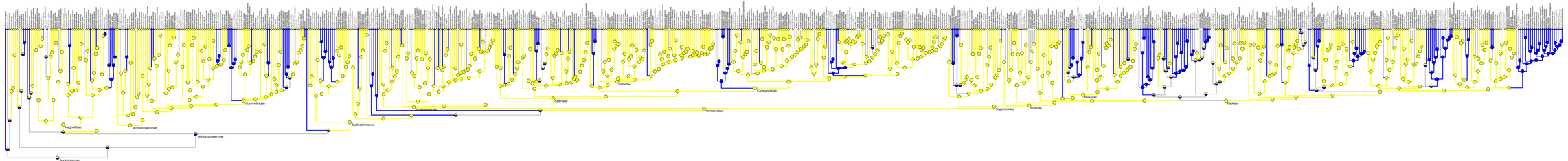
MP ancestral state reconstruction using ancestral pars
(R phangorn)
100_A_Functional sex of flowers (D2d), 98 steps

bisexual
unisexual

| Node | MP state(s) |
|---|---|
| Angiospermae | bisexual / unisexual |
| Mesangiospermae | bisexual |
| Magnoliidae | bisexual |
| Monocotyledonae | bisexual |
| Eudicotyledonae | bisexual |
| Commelinidae | bisexual |
| Ranunculidae | bisexual |
| Superasteridae | bisexual |
| Asteridae | bisexual |
| Lamiidae | bisexual |
| Campanulidae | bisexual |
| Superrosidae | bisexual |
| Rosidae | bisexual |
| Malvidae | bisexual |
| Fabidae | bisexual |

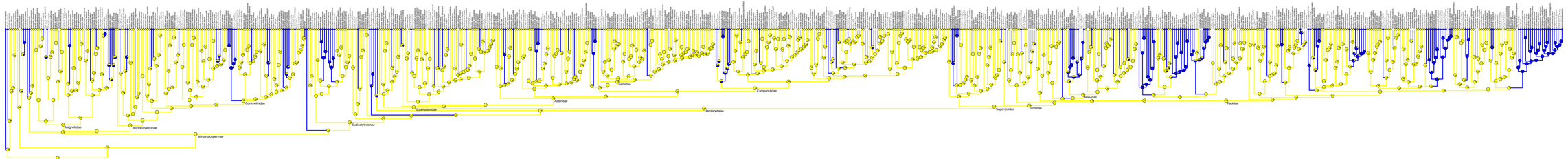


ML ancestral state reconstruction using rayDISC (R:corHMM) 100_A. Functional sex of flowers (02d), ARDeq model

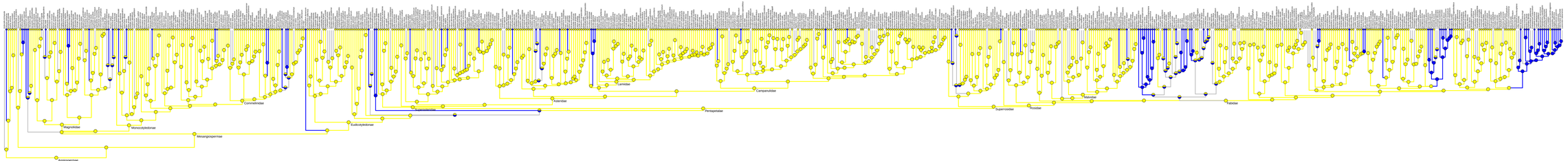
- bisexual
- unisexual

| Node | ML state | Prob |
|---|---|---|
| Angiospermae | bisexual | 1 |
| Mesangiospermae | bisexual | 1 |
| Magnoliidae | bisexual | 1 |
| Monocotyledonae | bisexual | 0.9999 |
| Eudicotyledonae | bisexual | 1 |
| Commelinidae | bisexual | 0.9996 |
| Ceratophyllidae | bisexual | 1 |
| Superasteridae | bisexual | 1 |
| Asteridae | bisexual | 1 |
| Lamiidae | bisexual | 1 |
| Campanulidae | bisexual | 0.9978 |
| Asterodiscidae | bisexual | 1 |
| Asterodiscus | bisexual | 0.9910 |
| Asterodiscus_hassleri | bisexual | 0.9910 |
| Pentapetalae | bisexual | 1 |
| Superrosidae | bisexual | 1 |
| Rosidae | bisexual | 1 |
| Malvidae | bisexual | 1 |
| Tabebuia | bisexual | 0.9911 |

| Model | Logl. | Npar | AIC | AICc | Weight | q01 | q10 |
|---|---|---|---|---|---|---|---|
| ARD | -313.91 | 2 | 631.81 | 631.97 | 0.7 | 0.0027 | 0.0001 |
| ARDeq | -313.24 | 2 | 630.48 | 630.64 | 0.3 | 0.0011 | 0.0011 |
| ER | -315.34 | 1 | 632.69 | 632.69 | 2.2 | 0.15 | 0.0027 |
| UNI01 | -315.41 | 1 | 632.82 | 632.82 | 2.33 | 0.14 | 0.0028 |
| UNI10 | -364.24 | 1 | 730.49 | 730.49 | 100 | 0 | 0.0108 |



MP ancestral state reconstruction using ancestral pars
(R phangorn)
100_8. Structural sex of flowers (D2d), 57 steps



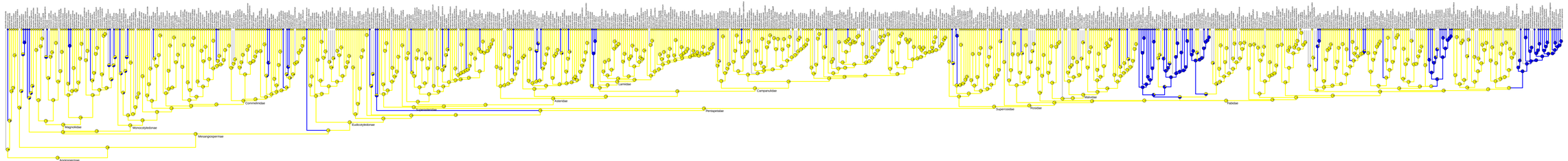

| Node | MP state(s) |
|---|---|
| Angiospermae | bisexual |
| Mesangiospermae | bisexual |
| Magnoliidae | bisexual |
| Monocotyledonae | bisexual |
| Eudicotyledonae | bisexual |
| Commelinidae | bisexual |
| Ceratophyllidae | bisexual |
| Superrosidae | bisexual |
| Lamiidae | bisexual |
| Lamiidae | bisexual |
| Campanulidae | bisexual |
| Superrosidae | bisexual |
| Rosidae | bisexual |
| Malvidae | bisexual |
| Fabidae | bisexual |

ML ancestral state reconstruction using rayDISC (R:corHMM) 100_B. Structural sex of flowers (D2d), ARDeq model

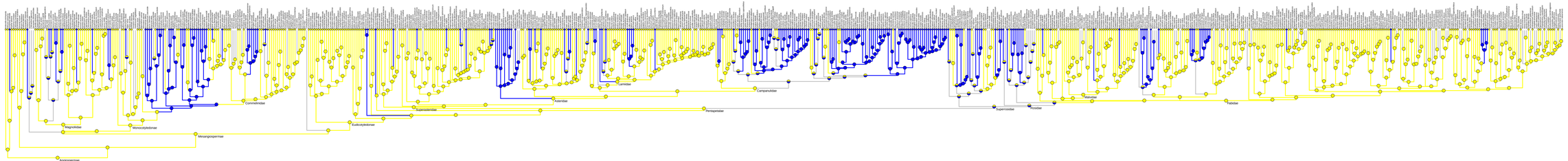
- bisexual
- unisexual

| Model | Logl. | Npar | AIC | AICc | AIC-AICc | Weight |
|---|---|---|---|---|---|---|
| ARD | −207.3 | 2 | 418.6 | 418.9 | 0.3 | 0.0042 |
| ARDeq** | −206.91 | 2 | 417.81 | 417.91 | 0 | 0.0064 |
| ER | −210.1 | 1 | 422.2 | 422.21 | 4.38 | 0.06 |
| UNI01 | −225.29 | 1 | 460.58 | 460.59 | 42.76 | 0 |
| UNI10 | −238.01 | 1 | 478.02 | 478.02 | 60.19 | 0 |

| Node | ML state | Prob |
|---|---|---|
| Angiospermae | bisexual | 0.9949 |
| Mesangiospermae | bisexual | 0.9995 |
| Magnoliidae | bisexual | 0.9995 |
| Monocotyledonae | bisexual | 0.9993 |
| Eudicotyledonae | bisexual | 0.999 |
| Commelinidae | bisexual | 0.9999 |
| Ranunculidae | bisexual | 0.9999 |
| Superasteridae | bisexual | 1 |
| Asteridae | bisexual | 1 |
| Lamiidae | bisexual | 0.9999 |
| Campanulidae | bisexual | 1 |
| Asterodae | bisexual | 1 |
| Pentapetalae | bisexual | 1 |
| Superrosidae | bisexual | 1 |
| Rosidae | bisexual | 1 |
| Malvidae | bisexual | 1 |
| Fabidae | bisexual | 1 |



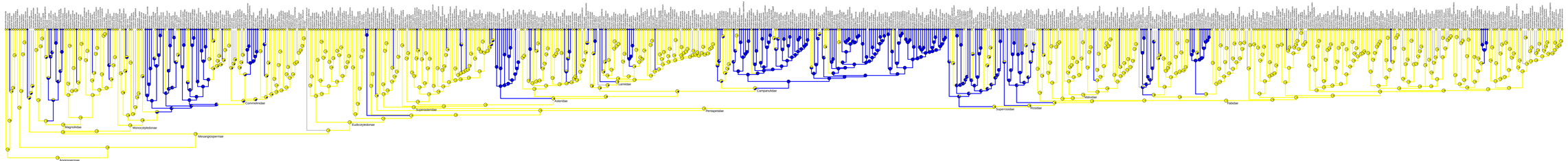
MP ancestral state reconstruction using ancestral pars
(R:phangorn)
102_B. Ovary position (binary) (D2d), 79 steps




superior
inferior

| Node | MP state(s) |
|---|---|
| Angiospermae | superior |
| Mesangiospermae | superior |
| Magnoliidae | superior |
| Monocotyledonae | superior |
| Eudicotyledonae | superior |
| Commelinidae | superior |
| Superasterids | superior |
| Superasteridae | superior |
| Asteridae | superior |
| Lamidae | superior |
| Campanulidae | superior |
| Superrosidae | superior / inferior |
| Rosidae | superior / inferior |
| Malvidae | superior |
| Fabidae | superior |

ML ancestral state reconstruction using rayDISC (R:corHMM)
102_B. Ovary position (binary) (D2d), ARDeq model

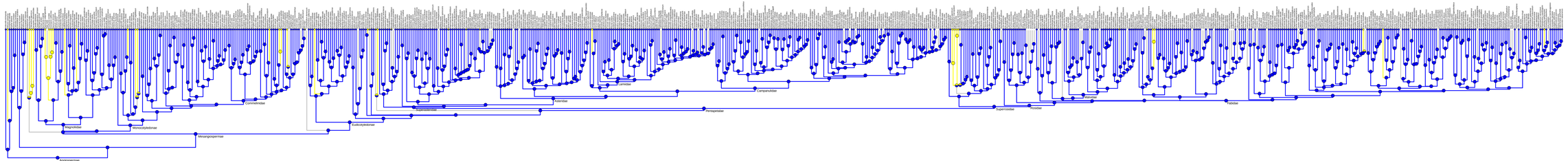



| Model | Logl. | Npar | AIC | AICc | AICc_wt | q01 | q10 | Node | ML state | Prob |
|---|---|---|---|---|---|---|---|---|---|---|
| ARD | −270.17 | 2 | 544.35 | 544.45 | 0.99 | 0.0038 | 0.0038 | Angiospermae | superior | 1 |
| ARDeq** | −269.55 | 2 | 543.09 | 543.19 | 1 | 0.0037 | 0.0037 | Magnoliidae | superior | 0.9881 |
| ER | −272.53 | 1 | 547.07 | 547.07 | 3.96 | 0.0022 | 0.0022 | Monocotyledonae | superior | 0.9939 |
| UN01 | −287.14 | 1 | 576.28 | 576.28 | 33.17 | 0 | 0.0026 | Eudicotyledonae | superior | 0.9811 |
| UN10 | −296.3 | 1 | 594.61 | 594.62 | 51.51 | 0 | 0.0092 | Mesangiospermae | superior | 0.9995 |
| | | | | | | | | Ceratophyllidae | superior | 0.6458 |
| | | | | | | | | Lamiidae | superior | 0.9996 |
| | | | | | | | | Superasteridae | superior | 0.9968 |
| | | | | | | | | Asteridae | superior | 0.9166 |
| | | | | | | | | Lamiidae | superior | 0.9266 |
| | | | | | | | | Campanulidae | superior | 0.6699 |
| | | | | | | | | Asteridae | superior | 0.9997 |
| | | | | | | | | Pentapetalae | superior | 0.9987 |
| | | | | | | | | Superrosidae | superior | 0.9999 |
| | | | | | | | | Rosidae | superior | 0.9999 |
| | | | | | | | | Malvidae | superior | 0.9999 |
| | | | | | | | | Fabidae | superior | 1 |

MP ancestral state reconstruction using ancestral pars (R:phangorn)
201_A. Perianth presence (D2c), 21 steps

absent
present

| Node | MP state(s) |
|---|---|
| Angiospermae | present |
| Mesangiospermae | present |
| Magnoliidae | present |
| Monocotyledonae | present |
| Eudicotyledonae | present |
| Commelinidae | present |
| Ranunculidae | present |
| Superasteridae | present |
| Asteridae | present |
| Lamiidae | present |
| Campanulidae | present |
| Superrosidae | present |
| Rosidae | present |
| Malvidae | present |
| Fabidae | present |

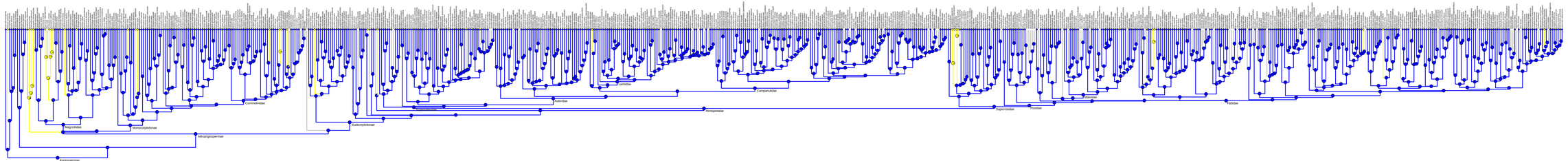


ML ancestral state reconstruction using rayDISC (R:corHMM) 201_A. Perianth presence (D2c), UNI10 model

absent
present

| Node | ML state | Prob |
|---|---|---|
| Angiosperm | present | 1 |
| Mesangiosperm | present | 1 |
| Magnoliidae | present | 1 |
| Monocotyledonae | present | 1 |
| Eudicotyledonae | present | 1 |
| Commelinidae | present | 1 |
| Ranunculidae | present | 1 |
| Superasterids | present | 1 |
| Asteridae | present | 1 |
| Lamiidae | present | 1 |
| Campanulidae | present | 1 |
| Caryophyllidae | present | 1 |
| Asteroids/Rosids/CC | present | 1 |
| Asterids/Rosids | present | 1 |
| Rosidae | present | 1 |
| Fabidae | present | 1 |
| Malvidae | present | 1 |
| Eudicots | present | 1 |
| Core Eudicots | present | 1 |
| Pentapetalae | present | 1 |
| Superrosidae | present | 1 |
| Rosids | present | 1 |
| Fabids | present | 1 |

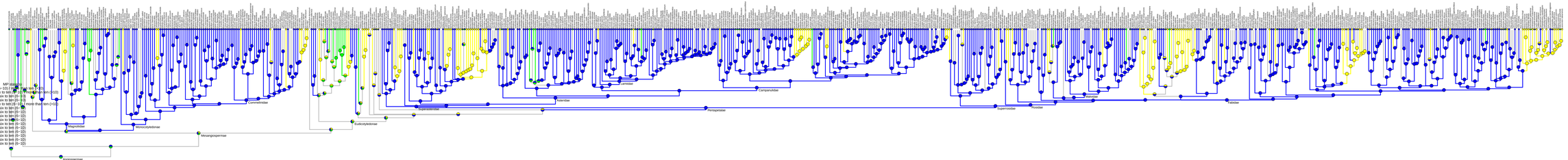
| Model | Logl. | Npar | AIC | AICc | ΔAICc | ΔAICc rel | w | w rel |
|---|---|---|---|---|---|---|---|---|
| ARD | −95.7 | 2 | 195.39 | 195.49 | 0.00 | 0 | 0.0e+00 | 0e+00 |
| ARDeq | −95 | 2 | 194 | 194.1 | 0.61 | 0.00 | 0.0e+00 | 0e+00 |
| ER | −95.83 | 1 | 193.66 | 193.67 | 0.27 | 0.29 | 5e-04 | 5e-04 |
| UNI01 | −117.13 | 1 | 236.26 | 236.27 | 42.87 | 0 | 0.0186 | |
| UNI10* | −95.7 | 1 | 193.39 | 193.4 | 0 | 0.34 | 5e-04 | |



MP ancestral state reconstruction using ancestral pars
(R:phangorn)
201_8. Number of perianth parts (3–state) (D2c), 86 steps

one to five (1–5)
six to ten (6–10)
more than ten (>10)

| Node | MP state |
|---|---|
| Angiospermae | six to ten (6–10) / more than ten (>10) |
| Mesangiospermae | one to five (1–5) / six to ten (6–10) |
| Magnoliidae | six to ten (6–10) |
| Monocotyledonae | six to ten (6–10) |
| Eudicotyledonae | one to five (1–5) / six to ten (6–10) |
| Commelinidae | six to ten (6–10) |
| Ranunculidae | six to ten (6–10) |
| Superasteridae | six to ten (6–10) |
| Asteridae | six to ten (6–10) |
| Lamiidae | six to ten (6–10) |
| Campanulidae | six to ten (6–10) |
| Superrosidae | six to ten (6–10) |
| Rosidae | six to ten (6–10) |
| Malvidae | six to ten (6–10) |
| Fabidae | six to ten (6–10) |



ML ancestral state reconstruction using rayDISC (R:corHMM)
201_B. Number of perianth parts (3–state) (D2c), ARDeq model

- one to five (1–5)
- six to ten (6–10)
- more than ten (>10)

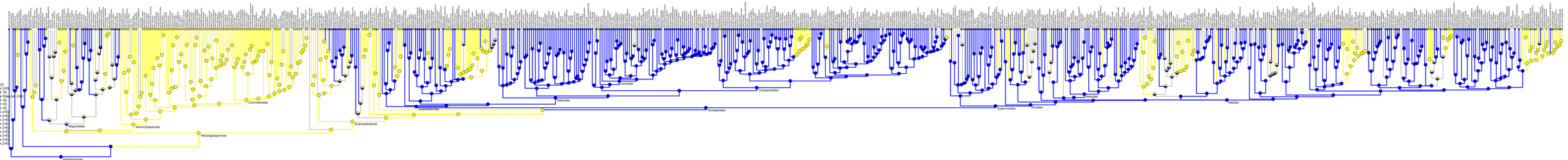
| Model | LogL | Npar | AIC | AICc | ΔAICc | AICcW |
|---|---|---|---|---|---|---|
| ARD | -326.29 | 6 | 664.57 | 664.96 | 0 | 0.9998 |
| ARDdep* | -325.2 | 6 | 662.4 | 662.79 | 2.18 | 0.3346 |
| ER | -351.28 | 1 | 704.56 | 704.59 | 40.06 | 0.0000 |
| SYM | -338.55 | 3 | 683.1 | 683.29 | 18.76 | 0.0000 |
| SYMeq | -339.55 | 3 | 685.09 | 685.29 | 20.76 | 0.0000 |
| ORD | -331.52 | 4 | 671.05 | 671.36 | 6.83 | 0.0298 |
| ORDeq | -330.43 | 4 | 668.87 | 669.18 | 6.42 | 0.0245 |
| ORDSYM | -343.51 | 2 | 691.02 | 691.03 | 28.53 | 0 |
| ORDSYMeq | -342.81 | 2 | 689.61 | 689.63 | 27.12 | 0 |
| ORDER | -352.85 | 1 | 707.7 | 707.71 | 45.2 | 0 |

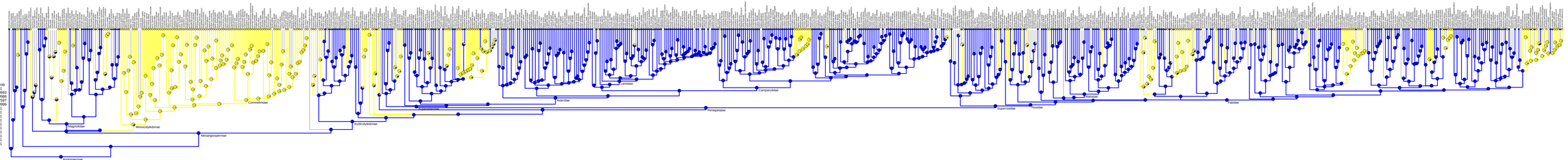
| Node | ML state | Prob |
|---|---|---|
| Angiospermae | more than ten (>10) | 1 |
| Mesangiospermae | more than ten (>10) | 0.9985 |
| Magnoliidae | more than ten (>10) | 0.9977 |
| Monocotyledonae | six to ten (6–10) | 0.5596 |
| Eudicotyledonae | more than ten (>10) | 0.9825 |
| Commelinidae | six to ten (6–10) | 0.9999 |
| Arecidae | six to ten (6–10) | 0.9999 |
| Alismatidae | six to ten (6–10) | 0.9976 |
| Zingiberidae | six to ten (6–10) | 0.9998 |
| Liliidae | six to ten (6–10) | 0.9999 |
| Commelinidae | six to ten (6–10) | 0.9999 |
| Ceratophyllidae | six to ten (6–10) | 0.9998 |
| Eudicotyledonae | six to ten (6–10) | 0.9998 |
| Gunneridae | six to ten (6–10) | 0.9999 |
| Pentapetalae | six to ten (6–10) | 0.9999 |
| Rosidae | six to ten (6–10) | 0.9998 |
| Fabidae | six to ten (6–10) | 0.9999 |
| Malvidae | six to ten (6–10) | 0.9999 |
| Brassicales | six to ten (6–10) | 0.9998 |
| Malvidae | six to ten (6–10) | 0.9999 |
| Asterids | six to ten (6–10) | 0.9999 |
| Lamiidae | six to ten (6–10) | 0.9999 |
| Asterids | six to ten (6–10) | 0.9999 |
| Campanulidae | six to ten (6–10) | 0.9999 |
| Asterids | six to ten (6–10) | 0.9999 |
| Asterids | six to ten (6–10) | 0.9999 |
| Asterids

MP ancestral state reconstruction using ancestral pars
(R:phangorn)
201_C. Number of perianth parts (binary) (D2c), 69 steps

one to six (1–6)
more than six (>6)

| Node | MP state(s) |
|---|---|
| Angiospermae | more than six (>6) |
| Mesangiospermae | more than six (>6) |
| Magnoliidae | one to six (1–6) / more than six (>6) |
| Monocotyledonae | one to six (1–6) |
| Eudicotyledonae | one to six (1–6) |
| Commelinidae | one to six (1–6) |
| Ceratophyllidae | more than six (>6) |
| Superasteridae | more than six (>6) |
| Asteridae | more than six (>6) |
| Lamiidae | more than six (>6) |
| Campanulidae | more than six (>6) |
| Superrosidae | more than six (>6) |
| Rosidae | more than six (>6) |
| Malvidae | more than six (>6) |
| Fabidae | more than six (>6) |

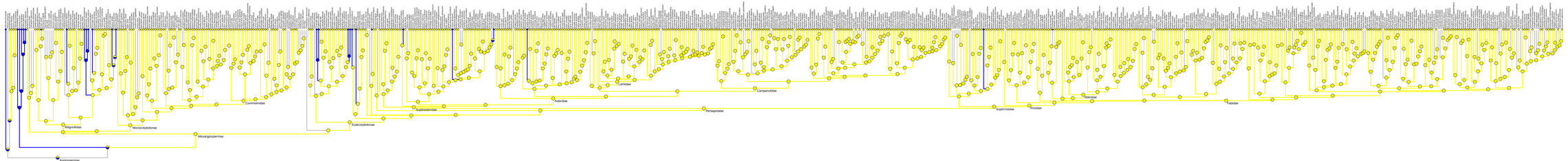



ML ancestral state reconstruction using rayDISC (R:corHMM)
201_C. Number of perianth parts (binary) (D2c), ARDeq model
one to six (1–6)
more than six (>6)
Node ML state Prob
Angiospermae more than six (>6) 1
Mesangiospermae more than six (>6) 0.9892
Magnoliidae more than six (>6) 0.9986
Monocotyledonae one to six (1–6) 0.7587
Eudicotyledonae more than six (>6) 0.9956
Commelinidae one to six (1–6) 1
Ceratophyllidae more than six (>6) 1
Superasterridae more than six (>6) 1
Asteridae more than six (>6) 1
Lamiidae more than six (>6) 1
Campanulidae more than six (>6) 1
Asterids more than six (>6) 1
Rosidae more than six (>6) 1
Fabidae more than six (>6) 1
Model Logl. Npar AIC AICc ΔAICc ΔAICc_rel w
ARD −247.5 2 499 499.08 0.00 0.9999 1
ARDeq** −246.81 2 497.61 497.69 −1.39 0.0001 1
ER −252.73 1 507.45 507.46 9.83 0 0.002
UN01 −330.51 1 663.03 663.03 165.4 0 0.0074
UN10 −253.47 1 508.94 508.94 11.32 0 0.0028
Angiospermae
Magnoliidae
Monocotyledonae
Mesangiospermae
Commelinidae
Ceratophyllidae
Eudicotyledonae
Asteridae
Lamiidae
Campanulidae
Asterids
Superasteridae
Rosidae
Fabidae
Fagales
Rosales
Fabales

MP ancestral state reconstruction using ancestral.pars
(R phangorn)
230_A_Perianth phyllotaxy (binary) (D2d), 16 steps

whorled
spiral

| Node | MP state(s) |
|---|---|
| Angiospermae | whorled / spiral |
| Mesangiospermae | whorled |
| Magnoliidae | whorled |
| Monocotyledonae | whorled |
| Eudicotyledonae | whorled |
| Commelinidae | whorled |
| Ranunculidae | whorled |
| Superasteridae | whorled |
| Asteridae | whorled |
| Lamiidae | whorled |
| Campanulidae | whorled |
| Superrosidae | whorled |
| Rosidae | whorled |
| Malvidae | whorled |
| Fabidae | whorled |

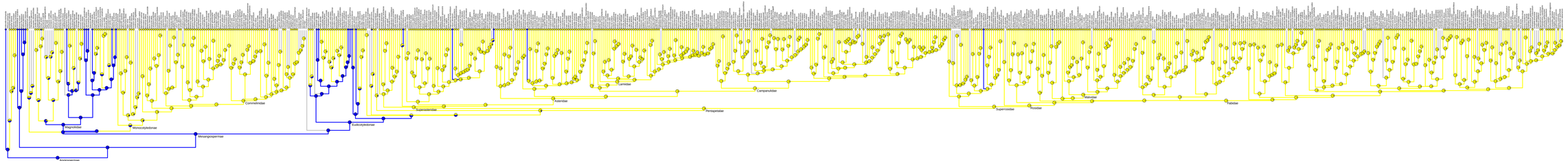


ML ancestral state reconstruction using rayDISC (R:corHMM)
230_A. Perianth phylotaxy (binary) (D2d), ARD model

whorled
spiral

| Model | Logl. | Npar | AIC | AICc |
|---|---|---|---|---|
| ARD*** | -70.11 | 2 | 144.22 | 144.3 |
| ARDeq | -76.18 | 2 | 156.35 | 156.43 |
| ER | -76.64 | 1 | 155.29 | 155.29 |
| UNI01 | -78.9 | 1 | 155.8 | 155.81 |
| UNI10 | -80.35 | 1 | 162.69 | 162.7 |

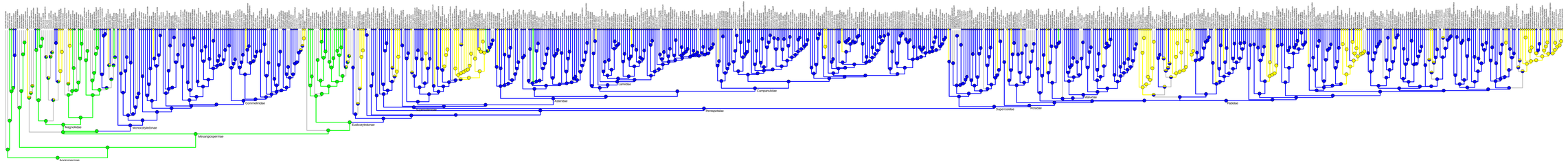
| Node | ML state | Prob |
|---|---|---|
| Angiospermae | spiral | 0.9994 |
| Mesangiospermae | spiral | 0.9993 |
| Magnoliidae | spiral | 0.9911 |
| Monocotyledonae | whorled | 0.5314 |
| Eudicotyledonae | spiral | 0.9977 |
| Commelinidae | whorled | 0.9999 |
| Superasteridae | whorled | 0.9838 |
| Superrosidae | whorled | 0.9997 |
| Asteridae | whorled | 0.9997 |
| Lamiidae | whorled | 1 |
| Campanulidae | whorled | 1 |
| Superlamiidae | whorled | 0.9547 |
| Asterales | whorled | 0.9992 |
| Campanulales | whorled | 0.9997 |
| Pentapetalae | whorled | 0.9997 |
| Rosidae | whorled | 1e+04 |
| Malvidae | whorled | 1e+04 |
| Fabidae | whorled | 4e-04 |
| Fabiae | whorled | 4e-04 |
| | | 0.0148 |



MP ancestral state reconstruction using ancestral pars
(R:phangorn)
231_A, Number of perianth whorls (D2c), 73 steps

one (1)
two (2)
more than two (>2)

| Node | MP state(s) |
|---|---|
| Angiospermae | more than two (>2) |
| Mesangiospermae | more than two (>2) |
| Magnoliidae | more than two (>2) |
| Monocotyledonae | two (2) |
| Eudicotyledonae | more than two (>2) |
| Commelinidae | two (2) |
| Arecidae | two (2) |
| Superasteridae | two (2) |
| Asteridae | two (2) |
| Lamiidae | two (2) |
| Campanulidae | two (2) |
| Superrosidae | two (2) |
| Rosidae | two (2) |
| Malvidae | two (2) |
| Fabidae | two (2) |

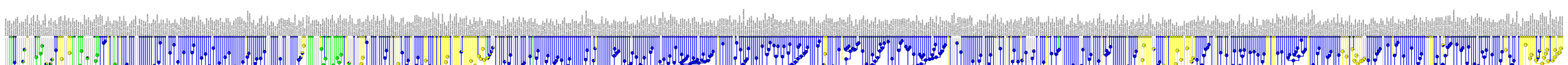


ML ancestral state reconstruction using rayDISC (R:corHMM)
231_A. Number of perianth whorls (D2c), ARDeq model

- one (1)
- two (2)
- more than two (>2)

| Model | Logl. | Npar | AIC | AICc | Weight |
|---|---|---|---|---|---|
| ARD | -266.49 | 6 | 544.97 | 545.38 | 0.2667 |
| ARDeq* | -266.39 | 6 | 542.79 | 543.20 | 0.7333 |
| ER | -308.73 | 1 | 619.46 | 619.56 | 0.0001 |
| SYM | -286.54 | 3 | 579.08 | 579.29 | 0.0000 |
| SYMeq | -286.54 | 3 | 566.08 | 566.29 | 0.0000 |
| ORD | -273.44 | 4 | 554.88 | 554.98 | 0.0000 |
| ORDeq | -272.34 | 4 | 552.68 | 552.78 | 0.0000 |
| ORDSYM | -296.72 | 2 | 597.44 | 597.46 | 0.0000 |
| ORDSYMeq | -295.37 | 2 | 595.93 | 595.95 | 0.0000 |
| ORDER | -311.99 | 1 | 625.97 | 625.98 | 0.0000 |

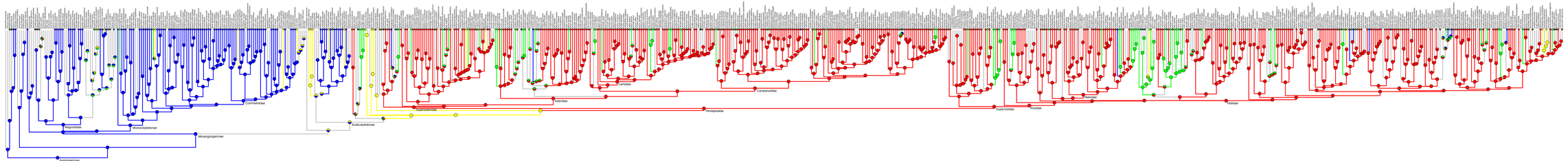
| Node | ML state | Prob |
|---|---|---|
| Angiospermae | more than two (>2) | 1 |
| Mesangiospermae | more than two (>2) | 0.8596 |
| Magnoliidae | more than two (>2) | 1 |
| Monocotyledonae | two (2) | 0.6631 |
| Eudicotyledonae | more than two (>2) | 0.9892 |
| Commelinidae | two (2) | 0.9999 |
| Zingiberidae | two (2) | 0.9999 |
| Arecidae | two (2) | 0.9997 |
| Liliidae | two (2) | 0.9997 |
| Alismatidae | two (2) | 0.9999 |
| Dasypogonidae | two (2) | 0.9999 |
| Pandanidae | two (2) | 0.9999 |
| Cyclanthidae | two (2) | 0.9999 |
| Pinidae | two (2) | 0.9999 |
| Gnetidae | two (2) | 0.9999 |
| Cycadidae | two (2) | 0.9999 |
| Ginkgoidae | two (2) | 0.9999 |
| Lycopodiidae | two (2) | 0.9999 |
| Polypodiidae | two (2) | 0.9999 |
| Campanulidae | two (2) | 0.9999 |
| Lamiidae | two (2) | 0.9999 |
| Caryophyllidae | two (2) | 0.9999 |
| Dilleniidae | two (2) | 0.9999 |
| Rosidae | two (2) | 0.9999 |
| Asteridae | two (2) | 0.9999 |
| Ranunculidae | two (2) | 0.9999 |
| Magnoliidae | two (2) | 0.9999 |
| Chloranthidae | two (2) | 0.9999 |
| Piperidae | two (2) | 0.9999 |
| Saururidae | two (2) | 0.9999 |
| Nymphaeidae | two (2) | 0.9999 |
| Ceratophyllidae | two (2) | 0.9999 |
| Amborellidae | two (2) | 0.9999 |



MP ancestral state reconstruction using ancestral pars
(R:phangorn)
232_A. Perianth merism (4–state) (D2c), 84 steps

- dimerous
- trimerous
- tetramerous
- pentamerous

| Node | MP state(s) |
|---|---|
| Angiospermae | trimerous |
| Mesangiospermae | trimerous |
| Magnoliidae | trimerous |
| Monocotyledonae | trimerous |
| Eudicotyledonae | dimerous / trimerous |
| Commelinidae | trimerous |
| Ranunculidae | pentamerous |
| Superasteridae | pentamerous |
| Asteridae | pentamerous |
| Lamiidae | pentamerous |
| Campanulidae | pentamerous |
| Superrosidae | pentamerous |
| Rosidae | pentamerous |
| Malvidae | pentamerous |
| Fabidae | pentamerous |

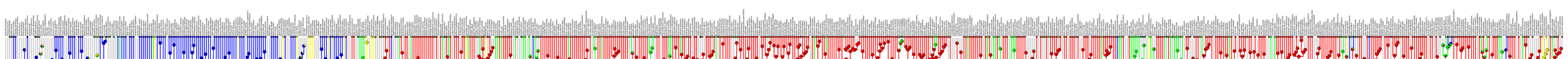


ML ancestral state reconstruction using rayDISC (Ronquist et al. 2012) on
232_A. Perianth merism (4-state) (D2c), SYMeq model

- dimerous
- trimerous
- tetramerous
- pentamerous

| Node | ML state | Prob |
|---|---|---|
| Angiospermae | trimerous | 1 |
| Mesangiospermae | trimerous | 0.9975 |
| Magnoliidae | trimerous | 1 |
| Monocotyledonae | trimerous | 1 |
| Eudicotyledonae | trimerous | 0.7223 |
| Commelinidae | trimerous | 1 |
| Ceratophyllidae | trimerous | 0.9991 |
| Eudicotyledonae | trimerous | 0.9997 |
| Ranunculidae | trimerous | 1 |
| Proteiniae | trimerous | 1 |
| Superasteridae | trimerous | 1 |
| Asterales | trimerous | 1 |
| Campanulidae | trimerous | 1 |
| Lamiidae | trimerous | 1 |
| Asterids | trimerous | 1 |
| Dipsacomorphae | trimerous | 1 |
| Rosidae | trimerous | 1 |
| Malvaceae | trimerous | 1 |
| Fabidae | trimerous | 1 |

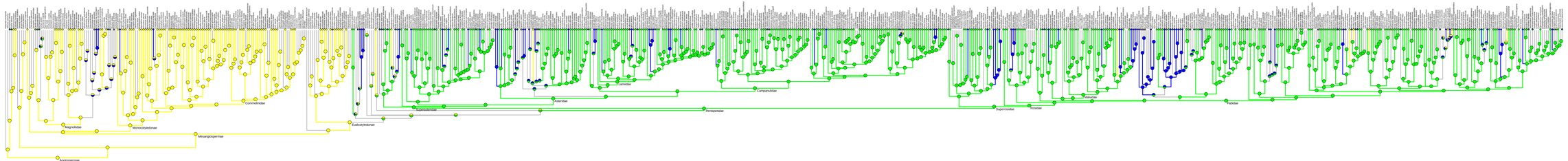
| Model | Logl. | Npar | AIC | AICc | ΔAICc | AICw | ΔAICc rel. | AICw rel. |
|---|---|---|---|---|---|---|---|---|
| ARD | −320.52 | 12 | 665.03 | 665.24 | 0 | 0.9997 | 0 | 0.9997 |
| ARDeq | −319.49 | 12 | 662.98 | 663.19 | 2.25 | 0.3258 | 0.3258 | 0.3258 |
| ER | −361.07 | 1 | 724.14 | 724.20 | 59.01 | 0 | 59.01 | 0 |
| SYM | −324.51 | 3 | 655.02 | 655.14 | 0.95 | 0.5000 | 0.5000 | 1 |
| SYMeq** | −324.51 | 6 | 661.03 | 661.29 | 7.09 | 0.0250 | 0.0250 | 1 |
| ORD | −336.08 | 6 | 684.16 | 684.42 | 30.22 | 0 | 0 | 1 |
| ORDeq | −335.41 | 6 | 682.82 | 683.08 | 28.88 | 0 | 0 | 1 |
| ORDSYM | −345.1 | 3 | 696.2 | 696.23 | 35.11 | 0 | 0.0018 | 1 |
| ORDSYMeq | −343.87 | 3 | 693.75 | 693.78 | 32.66 | 0 | 0.0018 | 1 |
| ORDER | −347.12 | 1 | 696.24 | 696.25 | 35.13 | 0 | 0.0023 | 1 |



MP ancestral state reconstruction using ancestral pars (R:phangorn)
232_8. Perianth merism (3–state) (D2c), 70 steps

- trimerous
- tetramerous
- pentamerous

| Node | MP state(s) |
|---|---|
| Angiospermae | trimerous |
| Mesangiospermae | trimerous |
| Magnoliidae | trimerous |
| Monocotyledonae | trimerous |
| Eudicotyledonae | trimerous |
| Commelinidae | trimerous |
| Ceratophyllidae | pentamerous |
| Superasteridae | pentamerous |
| Asteridae | pentamerous |
| Lamiidae | pentamerous |
| Campanulidae | pentamerous |
| Superrosidae | pentamerous |
| Rosidae | pentamerous |
| Malvidae | pentamerous |
| Fabidae | pentamerous |

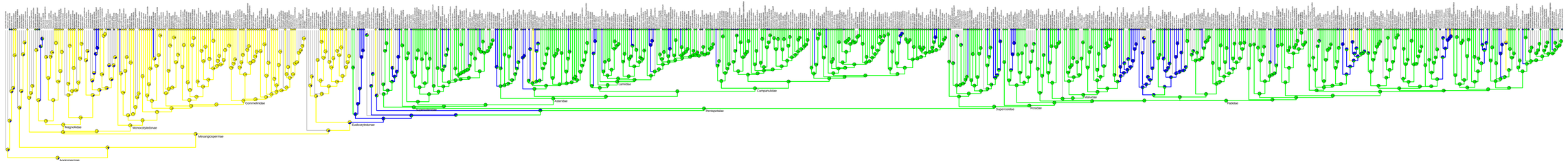


ML ancestral state reconstruction using rayDISC (R:corHMM) 232_8. Perianth merism (3–state) (D2c), ORD model

- trimerous
- tetramerous
- pentamerous

| Model | Logl. | Npar | AIC | AICw |
|---|---|---|---|---|
| ARD | −253.8 | 6 | 519.6 | 0.66 |
| ARDeq | −253.04 | 6 | 518.08 | 0.31 |
| ER | −280.95 | 1 | 563.9 | 0.00 |
| ERmix | −280.95 | 3 | 569.9 | 0.00 |
| SYMeq | −254.91 | 3 | 515.82 | 0.02 |
| ORD* | −253.8 | 4 | 515.6 | 0.02 |
| ORDeq | −254.1 | 4 | 516.2 | 0.01 |
| ORDSYM | −257.57 | 2 | 519.14 | 0.00 |
| ORDSYMeq | −256.57 | 2 | 517.14 | 0.00 |
| ORDER | −260.29 | 1 | 522.58 | 0.00 |

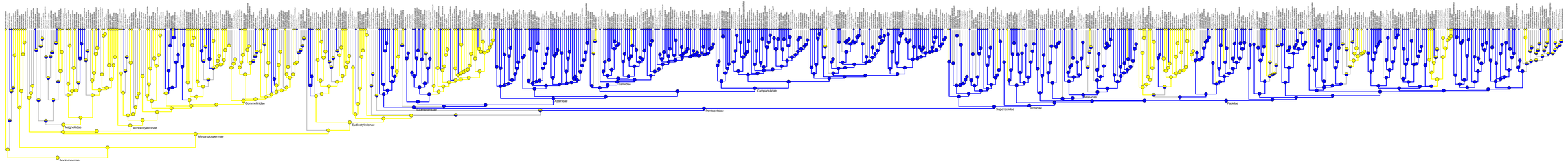
| Node | ML state | Prob. |
|---|---|---|
| Angiospermae | trimerous | 0.8059 |
| Magnoliophytina | trimerous | 0.9952 |
| Magnoliidae | trimerous | 0.9852 |
| Monocotyledonae | trimerous | 0.9968 |
| Eudicotyledonae | trimerous | 0.6132 |
| Commelinidae | trimerous | 0.9 |
| Commelinales | trimerous | 0.3857 |
| Arecidae | trimerous | 0.9903 |
| Alismatidae | trimerous | 0.9977 |
| Zingiberidae | trimerous | 0.9956 |
| Liliidae | trimerous | 0.9998 |
| Dasypogonidae | trimerous | 0.9981 |
| Arecales | trimerous | 0.9999 |
| Dasypogonales | trimerous | 0.9998 |
| Poales | trimerous | 1 |
| Ceratophyllidae | trimerous | 0.0014 |
| Ceratophyllales | trimerous | 0.0022 |



MP ancestral state reconstruction using ancestral pars
(R:phangorn)
234_A_Perianth differentiation (binary) (D2d), 64 steps

undifferentiated
differentiated

| Node | MP state(s) |
|---|---|
| Angiospermae | undifferentiated |
| Mesangiospermae | undifferentiated |
| Magnoliidae | undifferentiated |
| Monocotyledonae | undifferentiated |
| Eudicotyledonae | undifferentiated |
| Commelinidae | undifferentiated |
| Zingiberales | differentiated |
| Superasteridae | differentiated |
| Asteridae | differentiated |
| Lamiidae | differentiated |
| Campanulidae | differentiated |
| Superrosidae | differentiated |
| Rosidae | differentiated |
| Malvidae | differentiated |
| Fabidae | differentiated |

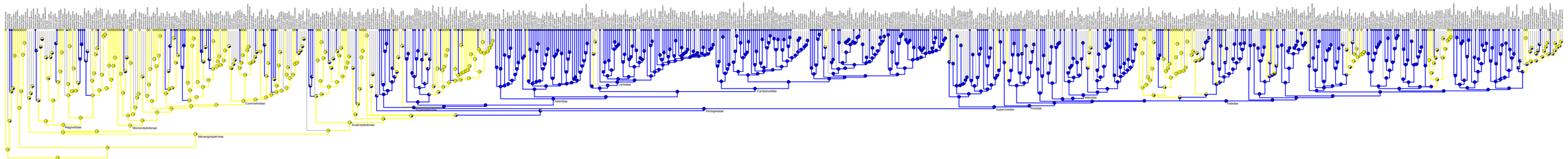


ML ancestral state reconstruction using rayDISC (R:corHMM)
234_A. Perianth differentiation (binary) (D2d), ARDeq model

- undifferentiated
- differentiated

| Node | ML state | Prob |
|---|---|---|
| Angiospermae | undifferentiated | |
| Mesangiospermae | undifferentiated | 0.9994 |
| Magnoliidae | undifferentiated | 0.999 |
| Monocotyledonae | undifferentiated | 0.9998 |
| Eudicotyledonae | undifferentiated | 0.9541 |
| Commelinidae | undifferentiated | 0.9998 |
| Arecidae | differentiated | 0.9999 |
| Superasteridae | differentiated | 0.949 |
| Asteridae | differentiated | 0.9983 |
| Lamidae | differentiated | 0.9998 |
| Campanulidae | differentiated | 1 |
| Rosidae | differentiated | 0.9999 |
| Fabidae | differentiated | 0.9999 |
| Malvidae | differentiated | 0.9999 |
| Sapindidae | differentiated | 0.9999 |
| Dipsacidae | differentiated | 0.9999 |
| Caprifoliidae | differentiated | 0.9999 |
| Asterales | differentiated | 0.9999 |
| Campanulales | differentiated | 0.9999 |
| Ericales | differentiated | 0.9999 |
| Lamiales | differentiated | 0.9999 |
| Solanales | differentiated | 0.9999 |
| Gentianales | differentiated | 0.9999 |
| Rubiales | differentiated | 0.9999 |
| Dipsacales | differentiated | 0.9999 |
| Malpighiales | differentiated | 0.9999 |
| Oxalidales | differentiated | 0.9999 |
| Fabales | differentiated | 0.9999 |
| Rosales | differentiated | 0.9999 |
| Cucurbitales | differentiated | 0.9999 |
| Fagales | differentiated | 0.9999 |
| Malvales | differentiated | 0.9999 |
| Sapindales | differentiated | 0.9999 |
| Brassicales | differentiated | 0.9999 |
| Myrtales | differentiated | 0.9999 |
| Geraniales | differentiated | 0.9999 |
| Saxifragales | differentiated | 0.9999 |
| Vitales | differentiated | 0.9999 |
| Gunnerales | differentiated | 0.9999 |
| Pinophyta | undifferentiated | 0.9999 |
| Gnetophyta | undifferentiated | 0.9999 |
| Ginkgoophyta | undifferentiated | 0.9999 |
| Lycopodiophyta | undifferentiated | 0.9999 |
| Polypodiophyta | undifferentiated | 0.9999 |
| Bryophyta | undifferentiated | 0.9999 |
| Marchantiophyta | undifferentiated | 0.9999 |
| Anthocerotophyta | undifferentiated | 0.9999 |

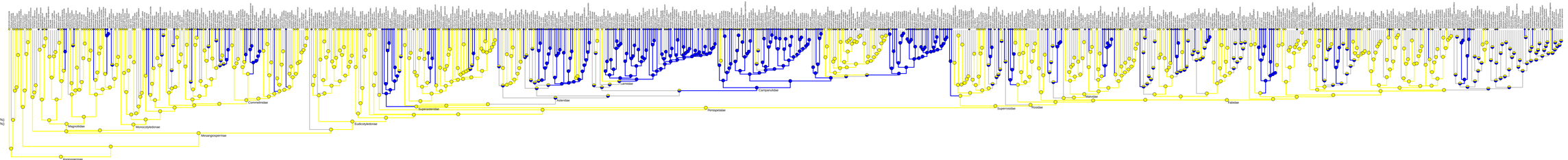
| Model | Logl. | Npar | AIC | AICc | ΔAICc | AICc wt | Pseudo-R² |
|---|---|---|---|---|---|---|---|
| ARD | −199.18 | 2 | 402.36 | 402.36 | 0.00 | 0.9999 | 0.0000 |
| ARDeq** | −198.51 | 2 | 401.02 | 401.02 | −1.34 | 0.5122 | 0.0034 |
| ER | −206.88 | 1 | 415.76 | 415.76 | 14.72 | 0 | 0.0024 |
| UN01 | −230.87 | 1 | 463.74 | 463.75 | 62.71 | 0 | 0.0078 |
| UN10 | −232.79 | 1 | 467.58 | 467.58 | 66.54 | 0 | 0.0032 |



MP ancestral state reconstruction using ancestral pars
(R:phangorn)
204_A. Fusion of perianth (D2c), 77 steps

tree (<5%)
fused (>5%)

| Node | MP state(s) |
|---|---|
| Angiospermae | tree (<5%) |
| Mesangiospermae | tree (<5%) |
| Magnoliidae | tree (<5%) |
| Monocotyledonae | tree (<5%) |
| Eudicotyledonae | tree (<5%) |
| Commelinidae | tree (<5%) |
| Ceratophyllidae | tree (<5%) |
| Superasteridae | tree (<5%) |
| Asteridae | tree (<5%) / fused (>5%) |
| Lamiidae | tree (<5%) / fused (>5%) |
| Campanulidae | fused (>5%) |
| Superosidae | tree (<5%) |
| Rosidae | tree (<5%) |
| Malvidae | tree (<5%) |
| Fabidae | tree (<5%) |

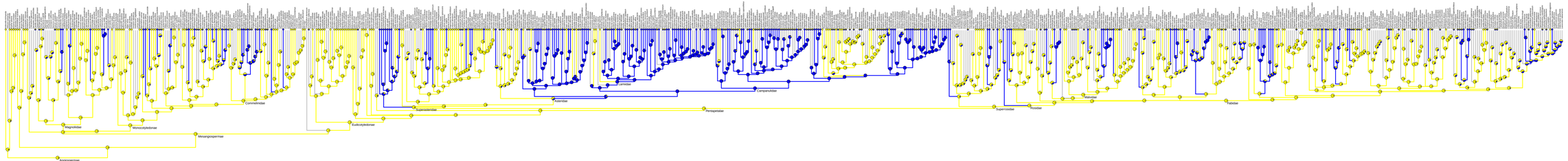


ML ancestral state reconstruction using rayDISC (R:corHMM)
204_A. Fusion of perianth (D2c), ER model

free (<5%)
fused (>5%)

| Node | ML state | Prob |
|---|---|---|
| Angiospermae | free (<5%) | 0.9586 |
| Mesangiospermae | free (<5%) | 0.9586 |
| Magnoliidae | free (<5%) | 0.9975 |
| Monocotyledonae | free (<5%) | 0.9987 |
| Eudicotyledonae | free (<5%) | 0.9992 |
| Commelinidae | free (<5%) | 0.9955 |
| Superasteridae | free (<5%) | 0.9936 |
| Superrosteridae | free (<5%) | 0.9836 |
| Asteridae | free (<5%) | 0.6657 |
| Lamiidae | fused (>5%) | 0.9781 |
| Campanulidae | fused (>5%) | 0.9789 |
| Pentapetalae | fused (>5%) | 0.9986 |
| Superrosidae | fused (>5%) | 0.9986 |
| Rosidae | fused (>5%) | 0.9986 |
| Malvidae | fused (>5%) | 0.9986 |
| Fabidae | fused (>5%) | 0.9986 |

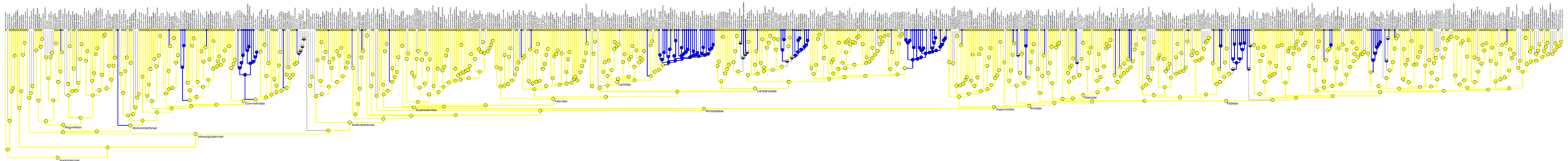
| Model | LogL | Npar | AIC | AICc | ΔAICc | AICc wt | Q | ER |
|---|---|---|---|---|---|---|---|---|
| ARD | −226.07 | 2 | 456.15 | 456.30 | 0.00 | 0.99 | 0.00 | 0.0067 |
| ARDeq | −225.46 | 2 | 454.92 | 454.78 | 0.48 | 0.01 | 0.00 | 0.0066 |
| ER* | −228.08 | 1 | 454.15 | 454.16 | 0 | 0.49 | 0.004 | 0.004 |
| UN01 | −243.31 | 1 | 488.63 | 488.63 | 34.48 | 0 | 0.0045 | |
| UN10 | −234.89 | 1 | 471.78 | 471.79 | 17.63 | 0 | | 0.0075 |



MP ancestral state reconstruction using ancestral pars
(R phangorn)
207_A. Symmetry of perianth (binary) (D2d), 55 steps

actinomorphic
zygomorphic

| Node | MP state(s) |
|---|---|
| Angiospermae | actinomorphic |
| Mesangiospermae | actinomorphic |
| Magnoliidae | actinomorphic |
| Monocotyledonae | actinomorphic |
| Eudicotyledonae | actinomorphic |
| Commelinidae | actinomorphic |
| Pentapetalae | actinomorphic |
| Superasterids | actinomorphic |
| Asteridae | actinomorphic |
| Lamidae | actinomorphic |
| Campanulidae | actinomorphic |
| Superosidae | actinomorphic |
| Rosidae | actinomorphic |
| Malvidae | actinomorphic |
| Fabidae | actinomorphic |

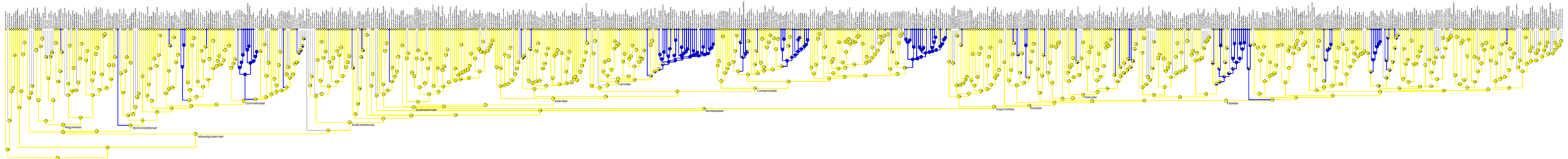


ML ancestral state reconstruction using rayDISC (R:corHMM) 207_A. Symmetry of perianth (binary) (D2d), ARDeq model

- actinomorphic
- zygomorphic

| Model | Logl. | Npar | AIC | AICc | ΔAICc | ΔAICc rel. | AICc wt |
|---|---|---|---|---|---|---|---|
| ARD | −209.71 | 2 | 423.41 | 423.54 | 0 | 0 | 0.9999 |
| ARDeq** | −209.18 | 2 | 422.37 | 422.50 | −1.04 | 0.0015 | 0.0015 |
| ER | −219.05 | 1 | 440.1 | 440.13 | 17.73 | 0 | 0.0015 |
| UN01 | −263.15 | 1 | 528.3 | 528.3 | 105.02 | 0 | 0.0017 |
| UN10 | −217.79 | 1 | 437.58 | 437.59 | 15.2 | 0 | 0.0151 |

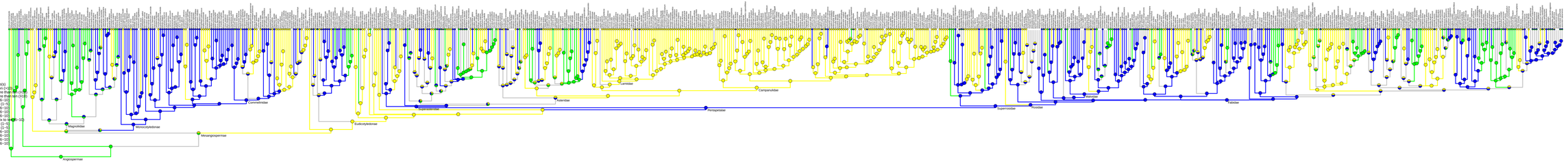
| Node | ML state | Prob. |
|---|---|---|
| Angiospermae | actinomorphic | 0.9992 |
| Mesangiospermae | actinomorphic | 0.9991 |
| Magnoliidae | actinomorphic | 0.9991 |
| Monocotyledonae | actinomorphic | 0.9964 |
| Eudicotyledonae | actinomorphic | 0.9988 |
| Commelinidae | actinomorphic | 0.9948 |
| Superasteridae | actinomorphic | 1 |
| Superrosteridae | actinomorphic | 1 |
| Asteridae | actinomorphic | 0.9999 |
| Lamiidae | actinomorphic | 0.9976 |
| Campanulidae | actinomorphic | 0.9999 |
| Pentapetalae | actinomorphic | 1 |
| Rosidae | actinomorphic | 1 |
| Superrosidae | actinomorphic | 1 |
| Malvidae | actinomorphic | 0.9999 |
| Fabidae | actinomorphic | 0.9999 |



MP ancestral state reconstruction using ancestral pars
(R:phangorn)
301_8. Number of fertile stamens (3–state) (D2c). 155 steps

one to five (1–5)
six to ten (6–10)
more than ten (>10)

| Node | MP state(s) |
|---|---|
| Angiospermae | more than ten (>10) |
| Mesangiospermae | one to five (1–5) / more than ten (>10) |
| Magnoliidae | six to ten (6–10) / more than ten (>10) |
| Monocotyledonae | six to ten (6–10) |
| Eudicotyledonae | one to five (1–5) |
| Commelinidae | six to ten (6–10) |
| Arecidae | six to ten (6–10) |
| Superasteridae | six to ten (6–10) |
| Asteridae | one to five (1–5) / six to ten (6–10) |
| Lamiidae | one to five (1–5) |
| Campanulidae | one to five (1–5) |
| Superrosidae | six to ten (6–10) |
| Rosidae | six to ten (6–10) |
| Malvidae | six to ten (6–10) |
| Fabidae | six to ten (6–10) |

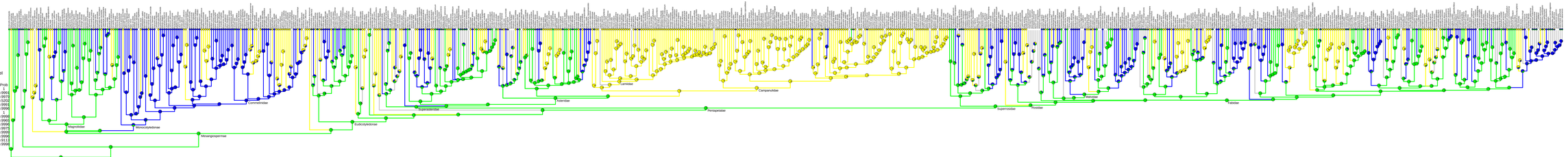


ML ancestral state reconstruction using rayDISC (R:corHMM)
301_B. Number of fertile stamens (3–state) (D2c), ARDeq model

- one to five (1–5)
- six to ten (6–10)
- more than ten (>10)

| Node | ML state | Prob |
|---|---|---|
| Angiospermae | more than ten (>10) | 0.9999 |
| Mesangiospermae | more than ten (>10) | 0.9999 |
| Magnoliidae | more than ten (>10) | 0.9976 |
| Monocotyledonae | six to ten (6–10) | 0.5202 |
| Eudicotyledonae | more than ten (>10) | 0.9999 |
| Commelinidae | six to ten (6–10) | 0.9996 |
| Superasteridae | more than ten (>10) | 1 |
| Asteridae | more than ten (>10) | 0.9998 |
| Lamiidae | more than ten (>10) | 0.9960 |
| Campanulidae | more than ten (>10) | 1 |
| Rosidae | more than ten (>10) | 0.9978 |
| Superrosidae | more than ten (>10) | 0.9999 |
| Malvidae | more than ten (>10) | 0.9998 |
| Fabidae | more than ten (>10) | 0.9999 |

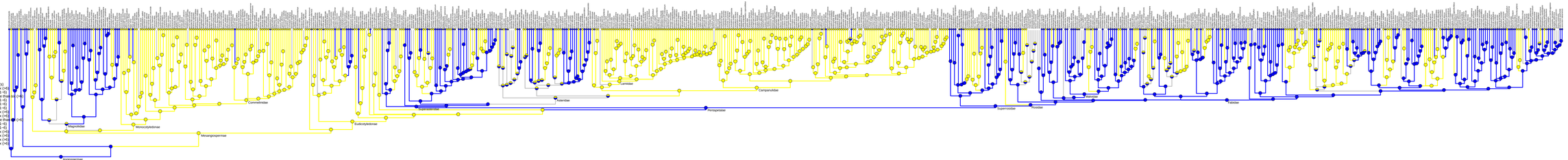
| Model | Logl. | Npar | AIC | AICc | ΔAICc | ΔAICc rel. | AICc wt |
|---|---|---|---|---|---|---|---|
| ARD | −497.08 | 6 | 1006.16 | 1006.37 | 2.18 | 0.0218 | 0.0960 |
| ARDeq* | −499.99 | 6 | 1003.98 | 1004.19 | 0 | one best fit | 0.2880 |
| ER | −532.45 | 1 | 1066.91 | 1066.94 | 62.75 | one worse fit | 0.0000 |
| SYM | −526.43 | 3 | 1058.86 | 1059.03 | 54.84 | more than twice as bad | 0.0000 |
| SYMeq | −526.43 | 3 | 1058.86 | 1059.03 | 54.84 | more than twice as bad | 0.0000 |
| ORD | −510.96 | 4 | 1029.92 | 1030.07 | 25.88 | more than twice as bad | 0.0000 |
| ORDeq | −510.4 | 4 | 1028.81 | 1028.95 | 24.76 | more than twice as bad | 0.0000 |
| ORDSYM | −532.42 | 2 | 1068.84 | 1068.85 | 64.77 | 0 | 0.0041 |
| ORDSYMeq | −532.02 | 2 | 1068.04 | 1068.05 | 63.97 | 0 | 0.0041 |
| ORDER | −532.43 | 1 | 1066.87 | 1066.87 | 62.79 | 0 | 0.0041 |

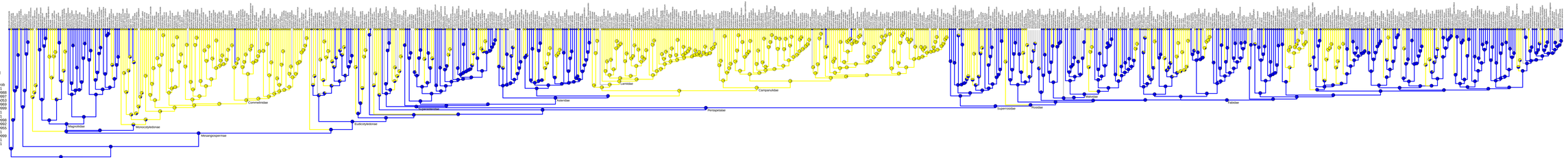


MP ancestral state reconstruction using ancestral pars
(R:phangorn)
301_C. Number of fertile stamens (binary) (D2c), 92 steps

one to six (1–6)
more than six (>6)

| Node | MP state(s) |
|---|---|
| Angiospermae | more than six (>6) |
| Mesangiospermae | more than six (>6) |
| Magnoliidae | one to six (1–6) / more than six (>6) |
| Monocotyledonae | one to six (1–6) |
| Eudicotyledonae | one to six (1–6) |
| Commelinidae | one to six (1–6) |
| Ranunculidae | one to six (1–6) |
| Superasteridae | more than six (>6) |
| Asteridae | one to six (1–6) / more than six (>6) |
| Lamiidae | one to six (1–6) |
| Campanulidae | one to six (1–6) |
| Superrosidae | more than six (>6) |
| Rosidae | more than six (>6) |
| Malvidae | more than six (>6) |
| Fabidae | more than six (>6) |






ML ancestral state reconstruction using rayDISC (Rcor:HMM)
301_C. Number of fertile stamens (binary) (D2c), ARDeq model

one to six (1–6)
more than six (>6)

| Node | ML state | Prob |
|---|---|---|
| Angiospermae | more than six (>6) | 1 |
| Mesangiospermae | more than six (>6) | 0.9868 |
| Magnoliidae | more than six (>6) | 0.9997 |
| Monocotyledonae | more than six (>6) | 0.5063 |
| Eudicotyledonae | more than six (>6) | 0.9969 |
| Cerinnetidae | one to six (1–6) | 0.9999 |
| Eudicotyledonae | more than six (>6) | 1 |
| Superasterids | more than six (>6) | 1 |
| Asterididae | more than six (>6) | 0.9986 |
| Lamiidae | one to six (1–6) | 0.9950 |
| Campanulidae | one to six (1–6) | 0.9955 |
| Dipsacoidae | more than six (>6) | 1 |
| Dipsacidae | more than six (>6) | 0.9999 |
| Rosidae | more than six (>6) | 1 |
| Malvidae | more than six (>6) | 1 |
| Fabidae | more than six (>6) | 1 |

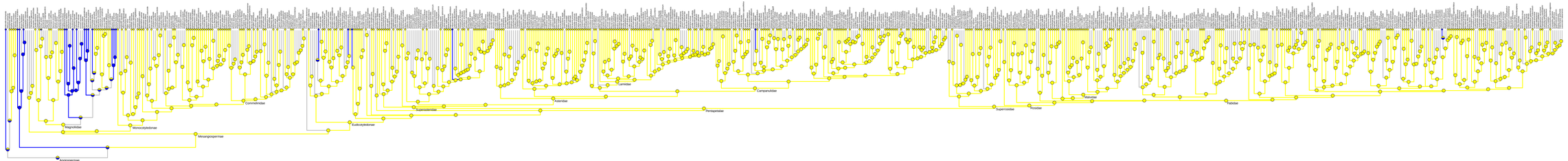
| Model | Logl. | Npar | AIC | AICc | ΔAICc | AICw |
|---|---|---|---|---|---|---|
| ARD | −290.01 | 2 | 584.02 | 584.08 | 0 | 0.9999 |
| ARDeq** | −289.32 | 2 | 582.63 | 582.69 | 0.61 | 0.7406 |
| ER | −319.76 | 1 | 641.51 | 641.52 | 59.87 | 0 |
| UN01 | −368.16 | 1 | 738.31 | 738.32 | 156.07 | 0 |
| UN10 | −327.03 | 1 | 656.07 | 656.07 | 73.43 | 0 |

| | | |
|---|---|---|
| 0.0029 | 0.0029 | 0 |
| 0.0043 | 0.0043 | 0 |
| 0.0067 | 0.0067 | 0 |

MP ancestral state reconstruction using ancestral pars
(R:phangorn)
330_A_Androecium structural phylotaxy (binary) (D2d), 12 steps

whorled
spiral

| Node | MP state(s) |
|---|---|
| Angiospermae | whorled \| spiral |
| Mesangiospermae | whorled |
| Magnoliidae | whorled |
| Monocotyledonae | whorled |
| Eudicotyledonae | whorled |
| Commelinidae | whorled |
| Ranunculidae | whorled |
| Superasteridae | whorled |
| Asteridae | whorled |
| Lamiidae | whorled |
| Campanulidae | whorled |
| Superrosidae | whorled |
| Rosidae | whorled |
| Malvidae | whorled |
| Fabidae | whorled |

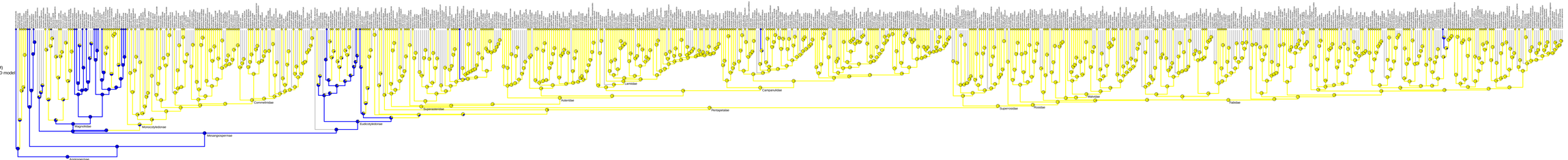


ML ancestral state reconstruction using rayDISC (R:corHMM)
330_A. Androecium structural phylotaxy (binary) (D2d), ARD model

whorled
spiral

| Model | Logl. | Npar | AIC | AICc | ΔAICc | ΔAICc rel. | w |
|---|---|---|---|---|---|---|---|
| ARD** | -53.79 | 2 | 111.58 | 111.58 | 0.00 | 1.00e+00 | 0.96 |
| ARDeq | -57.31 | 2 | 118.63 | 118.64 | 7.06 | 3.00e-02 | 0.04 |
| ER | -58.1 | 1 | 118.19 | 118.2 | 6.6 | 0.03 4e-04 | 4e-04 |
| UNI01 | -58.01 | 1 | 118.01 | 118.02 | 6.43 | 0.04 4e-04 | |
| UNI10 | -80.52 | 1 | 163.03 | 163.04 | 51.45 | 0 | 0.0168 |

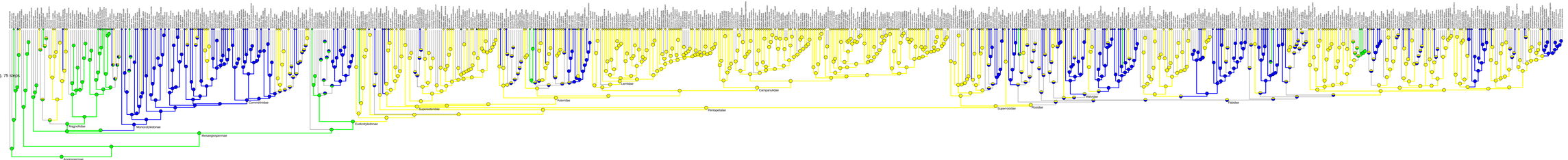
| Node | ML state | Prob |
|---|---|---|
| Angiospermae | spiral | 0.9993 |
| Mesangiospermae | whorled | 0.9999 |
| Magnoliidae | spiral | 0.9793 |
| Monocotyledonae | whorled | 0.5878 |
| Eudicotyledonae | spiral | 0.8702 |
| Commelinidae | whorled | 0.9999 |
| Arecanomorphae | whorled | 0.999 |
| Superasteridae | whorled | 0.9997 |
| Asteridae | whorled | 1 |
| Lamiidae | whorled | 1 |
| Campanulidae | whorled | 1 |
| Superrosidae | whorled | 0.9998 |
| Rosidae | whorled | 0.9999 |
| Malvidae | whorled | 0.9999 |
| Fabidae | whorled | 1 |
| Pentapetalae | whorled | 1 |



MP ancestral state reconstruction using ancestral pars
(R:phangorn)
331_A, Number of androecium structural whorls (3–state) (D2c), 75 taxa

one (1)
two (2)
more than two (>2)

| Node | MP state(s) |
|---|---|
| Angiospermae | more than two (>2) |
| Mesangiospermae | more than two (>2) |
| Magnoliidae | more than two (>2) |
| Monocotyledonae | two (2) |
| Eudicotyledonae | more than two (>2) |
| Commelinidae | two (2) |
| Arecidae | one (1) |
| Superasteridae | one (1) |
| Asteridae | one (1) |
| Lamiidae | one (1) |
| Campanulidae | one (1) |
| Superrosidae | one (1) |
| Rosidae | one (1) |
| Malvidae | one (1) / two (2) |
| Fabidae | one (1) / two (2) |



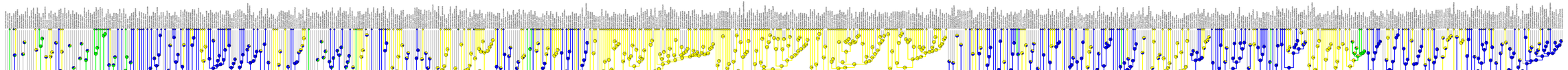
ML ancestral state reconstruction using rayDISC (R:corHMM)
331_A. Number of androecium structural whorls (3–state) (D2c), ARDeq model

one (1)
two (2)
more than two (>2)

| Node | ML state | Prob |
|---|---|---|
| Angiospermae | more than two (>2) | 1 |
| Mesangiospermae | more than two (>2) | 0.9919 |
| Magnoliidae | more than two (>2) | 0.9933 |
| Monocotyledonae | more than two (>2) | 0.9343 |
| Eudicotyledonae | more than two (>2) | 0.8191 |
| Commelinidae | two (2) | 0.9835 |
| Arecidae | more than two (>2) | 0.999 |
| Alismatidae | more than two (>2) | 0.999 |
| Zingiberidae | more than two (>2) | 0.9999 |
| Liliidae | more than two (>2) | 0.999 |
| Dilleniidae | more than two (>2) | 0.9943 |
| Rosidae | more than two (>2) | 0.9952 |
| Asteridae | more than two (>2) | 0.9995 |
| Lamiidae | more than two (>2) | 0.9999 |
| Campanulidae | more than two (>2) | 1 |
| Asterales | more than two (>2) | 1 |
| Dipsacidae | more than two (>2) | 1 |
| Apiales | more than two (>2) | 1 |
| Dipsacales | more than two (>2) | 1 |
| Rosidae | more than two (>2) | 1 |
| Fabidae | more than two (>2) | 1 |
| Malvidae | more than two (>2) | 1 |
| Fabidae | more than two (>2) | 1 |
| Malvidae | more than two (>2) | 1 |
| Fabidae | more than two (>2) | 1 |

| Model | Logl. | Npar | AIC | AICc | Weight |
|---|---|---|---|---|---|
| ARD | −230.1 | 6 | 472.2 | 472.4 | 0.999 |
| ARDeq* | −229.02 | 6 | 470.04 | 470.26 | 0.999 |
| ER | −277.21 | 1 | 556.42 | 556.42 | 0.9943 |
| ERdep | −252.29 | 2 | 508.58 | 508.59 | 0.9952 |
| SYMeq | −251.14 | 3 | 508.28 | 508.32 | 0.9995 |
| ORD | −232.46 | 4 | 472.93 | 473.04 | 0.9999 |
| ORDeq | −231.39 | 4 | 470.77 | 470.88 | 1 |
| ORDSYM | −253.43 | 2 | 510.87 | 510.88 | 0.0034 |
| ORDSYMeq | −252.69 | 2 | 509.38 | 509.39 | 0.0034 |
| ORDER | −259.05 | 1 | 520.1 | 520.1 | 0.0027 |

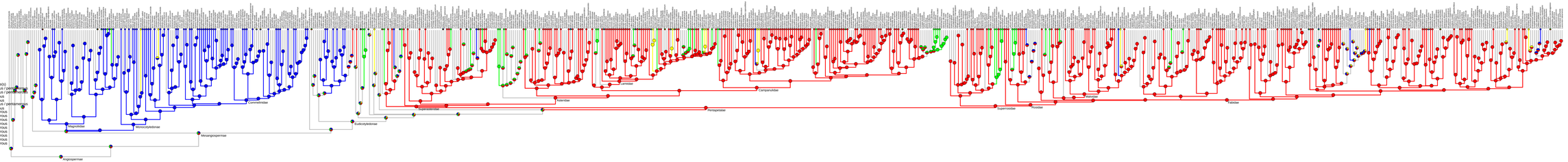
| Model | lnL | df | AIC | AICc | Weight |
|---|---|---|---|---|---|
| ARD | −2.16 | 6 | 16.32 | 16.32 | 0.4 |
| ARDeq | 0 | 5 | 10 | 10 | 0.4 |
| ER | −29.29 | 1 | 60.58 | 60.58 | 0.0016 |
| ERdep | −14.64 | 2 | 33.28 | 33.28 | 0.0008 |
| SYMeq | −13.82 | 3 | 33.64 | 33.64 | 0.0006 |
| ORD | −29.29 | 2 | 62.58 | 62.58 | 0.0016 |
| ORDeq | −29.29 | 2 | 62.58 | 62.58 | 0.0016 |
| ORDSYM | −13.82 | 3 | 33.64 | 33.64 | 0.0006 |
| ORDSYMeq | −13.82 | 3 | 33.64 | 33.64 | 0.0006 |
| ORDER | −29.29 | 2 | 62.58 | 62.58 | 0.0016 |



MP ancestral state reconstruction using ancestral pars
(R:phangorn)
332_A_Androecium structural merism (4–state) (D2c), 58 steps

- dimerous
- trimerous
- tetramerous
- pentamerous

| Node | MP state(s) |
|---|---|
| Angiospermae | trimerous / tetramerous / pentamerous |
| Mesangiospermae | trimerous / tetramerous / pentamerous |
| Magnoliidae | trimerous |
| Monocotyledonae | trimerous |
| Eudicotyledonae | trimerous / tetramerous / pentamerous |
| Commelinidae | trimerous |
| Ceratophyllidae | pentamerous |
| Superasteridae | pentamerous |
| Asteridae | pentamerous |
| Lamiidae | pentamerous |
| Campanulidae | pentamerous |
| Superrosidae | pentamerous |
| Rosidae | pentamerous |
| Malvidae | pentamerous |
| Fabidae | pentamerous |

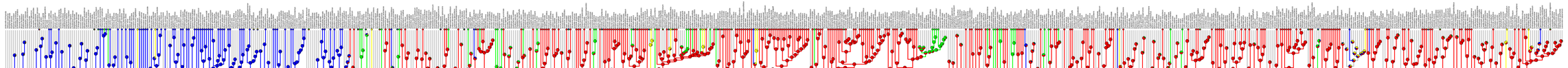


ML ancestral state reconstruction using rayDISC (R:corHMM)
332_A. Androecium structural merism (4–state) (D2c), SYMeq model

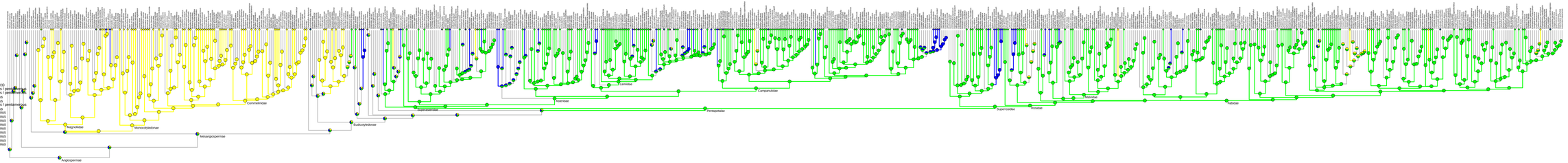
- dimerous
- trimerous
- tetramerous
- pentamerous

| Node | ML state | Prob. |
|---|---|---|
| Angiospermae | trimerous | 0.9997 |
| Mesangiospermae | trimerous | 0.9958 |
| Magnoliidae | trimerous | 1 |
| Monocotyledonae | trimerous | 1 |
| Eudicotyledonae | trimerous | 0.7926 |
| Commelinidae | trimerous | 1 |
| Ceratophyllidae | trimerous | 0.5999 |
| Eudicotyledonae | trimerous | 0.9999 |
| Gunneridae | trimerous | 0.9999 |
| Pentapetalae | trimerous | 0.9999 |
| Asterids | trimerous | 0.9999 |
| Lamiidae | trimerous | 1 |
| Campanulidae | trimerous | 1 |
| Asterales | trimerous | 1 |
| Rosidae | trimerous | 1 |
| Fabidae | trimerous | 1 |
| Superrosidae | trimerous | 1 |

| Model | Logl. | Npar | AIC | AICc | ΔAICc | ΔAICc rel. | Prob. | |
|---|---|---|---|---|---|---|---|---|
| ARD | −222.22 | 12 | 468.43 | 468.43 | 0.00 | 0.0000 | 0.9999 | 1 |
| ARDeq | −231.44 | 12 | 466.88 | 466.88 | 7.13 | 0.0000 | 0.0000 | 1 |
| ER | −238.12 | 1 | 478.25 | 478.25 | 11.82 | 0.0000 | 0.0000 | 1 |
| ERdep | −234.16 | 2 | 480.32 | 480.32 | 13.89 | 0.0000 | 0.0000 | 1 |
| SYMeq* | −229.99 | 6 | 468.38 | 468.38 | 1.95 | 0.0000 | 0.0004 | 1 |
| ORD | −235.11 | 6 | 482.22 | 482.22 | 15.79 | 0.0000 | 0.0000 | 1 |
| ORDeq | −235.28 | 6 | 482.57 | 482.57 | 16.14 | 0.0000 | 0.0000 | 1 |
| ORDSYM | −258.34 | 3 | 522.68 | 522.71 | 62.62 | 0 | 0.0019 | --- |
| ORDSYMeq | −257.5 | 3 | 520.99 | 521.02 | 60.93 | 0 | 0.0019 | --- |
| ORDER | −259.3 | 1 | 520.59 | 520.6 | 60.51 | 0 | 0.0029 | --- |



MP ancestral state reconstruction using ancestral pars
(R:phangorn)
332_8_Androecium structural merism (3–state) (D2c), 49 steps




| Node | MP state(s) |
|---|---|
| Angiospermae | trimerous / tetramerous / pentamerous |
| Mesangiospermae | trimerous / tetramerous / pentamerous |
| Magnoliidae | trimerous |
| Monocotyledonae | trimerous |
| Eudicotyledonae | trimerous / tetramerous / pentamerous |
| Commelinidae | trimerous |
| Eudicotyledonae | pentamerous |
| Superasteridae | pentamerous |
| Asteridae | pentamerous |
| Lamiidae | pentamerous |
| Campanulidae | pentamerous |
| Superrosidae | pentamerous |
| Rosidae | pentamerous |
| Malvidae | pentamerous |
| Fabidae | pentamerous |

ML ancestral state reconstruction using rayDISC (R:corHMM)
332_B. Androecium structural merism (3–state) (D2c), ARDeq model

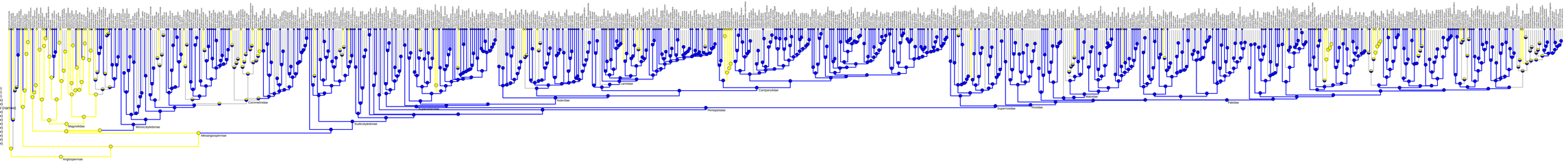
- trimerous
- tetramerous
- pentamerous

| Node | ML state | Prob |
|---|---|---|
| Angiospermae | trimerous | 1 |
| Mesangiospermae | trimerous | 0.9998 |
| Magnoliidae | trimerous | 1 |
| Monocotyledonae | trimerous | 1 |
| Eudicotyledonae | trimerous | 0.8221 |
| Commelinidae | trimerous | 1 |
| Ceratophyllidae | trimerous | 0.999 |
| [illegible] | trimerous | 1 |
| [illegible] | trimerous | 1 |
| [illegible] | trimerous | 1

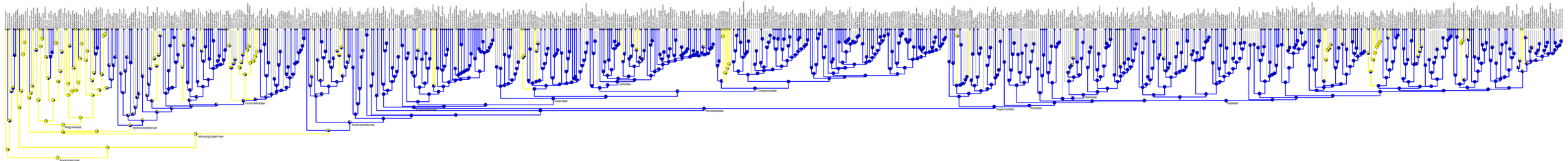
MP ancestral state reconstruction using ancestral pars
(R:phangorn)
305_A_Filament (binary) (D2d), 55 steps

laminar (wide)
typical (narrow)

| Node | MP state(s) |
|---|---|
| Angiospermae | laminar (wide) |
| Mesangiospermae | laminar (wide) |
| Magnoliidae | laminar (wide) |
| Monocotyledonae | typical (narrow) |
| Eudicotyledonae | typical (narrow) |
| Commelinidae | laminar (wide) / typical (narrow) |
| Gunneridae | typical (narrow) |
| Superasterridae | typical (narrow) |
| Asteridae | typical (narrow) |
| Lamiidae | typical (narrow) |
| Campanulidae | typical (narrow) |
| Superrosidae | typical (narrow) |
| Rosidae | typical (narrow) |
| Malvidae | typical (narrow) |
| Fabidae | typical (narrow) |



ML ancestral state reconstruction using rayDISC (R:corHMM) 305_A. Filament (binary) (D2d), ARDeq model



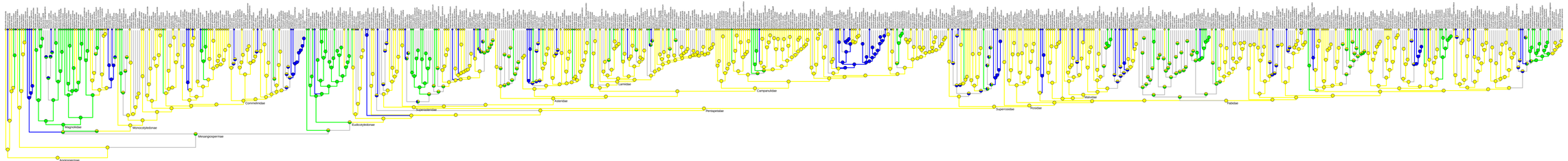

| Node | ML state | Prob |
|---|---|---|
| Angiospermae | laminar (wide) | 0.9968 |
| Mesangiospermae | laminar (wide) | 0.9968 |
| Magnoliidae | laminar (wide) | 0.9588 |
| Monocotyledonae | laminar (wide) | 0.6033 |
| Eudicotyledonae | typical (narrow) | 0.7663 |
| Commelinidae | typical (narrow) | 0.7267 |
| Ceratophyllidae | typical (narrow) | 0.9997 |
| Superasterids | typical (narrow) | 0.9997 |
| Asteridae | typical (narrow) | 0.9994 |
| Lamiidae | typical (narrow) | 0.9985 |
| Campanulidae | typical (narrow) | 0.9932 |
| Asterales | typical (narrow) | 0.9997 |
| Apiomorphae | typical (narrow) | 0.9997 |
| Rosidae | typical (narrow) | 0.9997 |
| Fabidae | typical (narrow) | 0.9997 |
| Fabiidae | typical (narrow) | 0.9997 |

| Model | Logl. | Nparam | AIC | AICc | ΔAICc | ΔAICc_wt | q01 | q10 |
|---|---|---|---|---|---|---|---|---|
| ARD | −172.1 | 2 | 348.2 | 348.3 | 0.00 | 0.9997 | 0.0003 | 0.0003 |
| ARDeq** | −171.68 | 2 | 347.35 | 347.45 | 0.12 | 0.0003 | 0.0003 | 0.0003 |
| ER | −177.95 | 1 | 357.9 | 357.91 | 10.54 | 0 | 0.0023 | 0.0023 |
| UNI01 | −192.39 | 1 | 386.79 | 386.79 | 39.43 | 0 | 0.0131 | 0 |
| UNI10 | −190.85 | 1 | 383.7 | 383.71 | 36.34 | 0 | 0 | 0.0022 |

MP ancestral state reconstruction using ancestral pars
(R:phangorn)
311_A_Anther orientation (D2d), 107 steps

- introrse
- latrorse
- extrorse

| Node | MP state(s) |
|---|---|
| Angiospermae | introrse |
| Mesangiospermae | introrse / extrorse |
| Magnoliidae | extrorse |
| Monocotyledonae | introrse |
| Eudicotyledonae | introrse / extrorse |
| Commelinidae | introrse |
| Ranunculidae | introrse |
| Superasteridae | introrse |
| Asteridae | introrse |
| Lamidae | introrse |
| Campanulidae | introrse |
| Superrosidae | introrse |
| Rosidae | introrse |
| Malvidae | introrse |
| Fabidae | introrse |

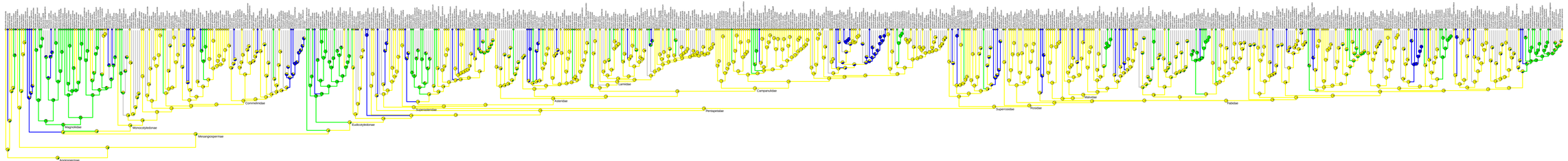


ML ancestral state reconstruction using rayDISC (R:corHMM)
311_A. Anther orientation (D2d), ER model

- introrse
- latrorse
- extrorse

| Node | ML state | Prob |
|---|---|---|
| Angiospermae | introrse | 0.8131 |
| Mesangiospermae | introrse | 0.8131 |
| Magnoliidae | extrorse | 0.8201 |
| Monocotyledonae | introrse | 0.8789 |
| Eudicotyledonae | introrse | 0.855 |
| Commelinidae | introrse | 0.9932 |
| Superasteridae | introrse | 0.9999 |
| Santalanae | introrse | 0.9999 |
| Asteridae | introrse | 0.9992 |
| Lamidae | introrse | 0.9998 |
| Campanulidae | introrse | 1 |
| Asterodae | introrse | 1 |
| Pentapetalae | introrse | 0.9999 |
| Superrosidae | introrse | 0.9999 |
| Rosidae | introrse | 0.9999 |
| Malvidae | introrse | 1 |
| Fabidae | introrse | 1 |

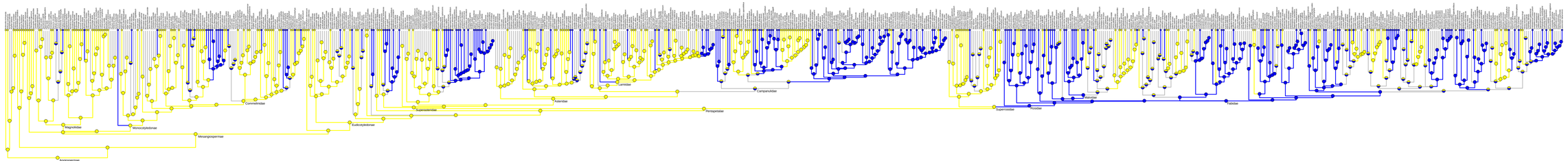
| Model | LogL | Npar | AIC | AICc | delAIC | delAICc | AICw | AICcw |
|---|---|---|---|---|---|---|---|---|
| ARD | −341.43 | 6 | 694.86 | 694.90 | 0.77 | 0.90 | 0.4064 | 0.4999 |
| ARDeq | −341.03 | 6 | 694.06 | 694.11 | 0 | 0 | 0.6064 | 0.7499 |
| ER* | −344.84 | 1 | 691.69 | 691.69 | 0 | 0.38 | 0.0025 | – |
| SYM | −343.81 | 3 | 693.63 | 693.66 | 1.96 | 0.14 | 0.0028 | – |
| SYMeq | −343.06 | 3 | 692.12 | 692.15 | 0.45 | 0.3 | 0.0028 | – |



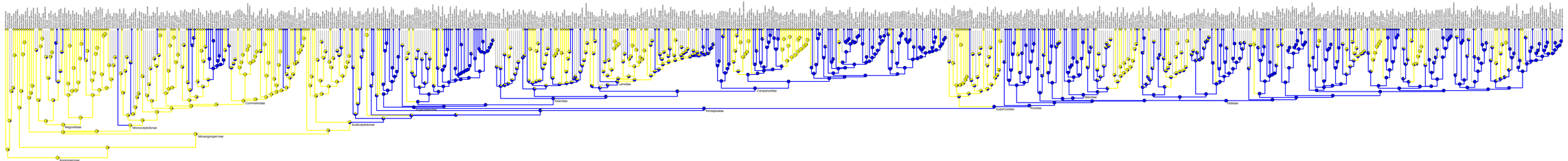
MP ancestral state reconstruction using ancestral pars
(R:phangorn)
312_A_Anther attachment (binary) (D2d), 97 steps

basifixed
dorsifixed

| Node | MP state(s) |
|---|---|
| Angiospermae | basifixed |
| Mesangiospermae | basifixed |
| Magnoliidae | basifixed |
| Monocotyledonae | basifixed |
| Eudicotyledonae | basifixed |
| Commelinidae | basifixed |
| Ranunculidae | basifixed |
| Superasteridae | basifixed |
| Asteridae | basifixed |
| Lamiidae | basifixed |
| Campanulidae | basifixed / dorsifixed |
| Superrosidae | basifixed |
| Rosidae | dorsifixed |
| Malvidae | dorsifixed |
| Fabidae | dorsifixed |



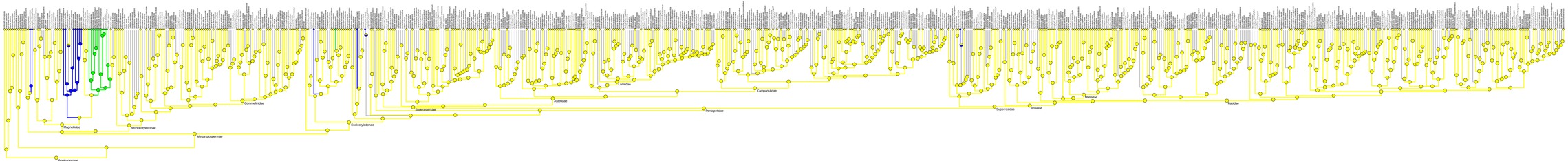
ML ancestral state reconstruction using rayDISC (Ree+Hill+Ronquist 2005) on
312_A. Anther attachment (binary) (D2d), ARDeq model




| Node | ML state | Prob |
|---|---|---|
| Angiospermae | basifixed | 0.98 |
| Mesangiospermae | basifixed | 0.9999 |
| Magnoliidae | basifixed | 0.958 |
| Monocotyledonae | basifixed | 0.9354 |
| Eudicotyledonae | basifixed | 0.6534 |
| Commelinidae | basifixed | 0.9446 |
| Caryophyllidae | dorsifixed | 0.9433 |
| Superasteridae | dorsifixed | 0.9419 |
| Asteridae | dorsifixed | 0.8678 |
| Lamiidae | dorsifixed | 0.5937 |
| Campanulidae | dorsifixed | 0.9739 |
| Dilleniidae | dorsifixed | 0.9459 |
| Rosidae | dorsifixed | 0.9459 |
| Fabidae | dorsifixed | 0.9459 |
| Malvidae | dorsifixed | 0.9459 |
| Campanulidae | dorsifixed | 0.9739 |
| Dipsacidae | dorsifixed | 0.9739 |
| Asteridae | dorsifixed | 0.8678 |
| Euphorbiales | dorsifixed | 0.9459 |
| Rosidae | dorsifixed | 0.9459 |
| Fabidae | dorsifixed | 0.9459 |

| Model | Logl. | Npar | AIC | AICc | ΔAICc | ΔAICc rel. | AICc wt |
|---|---|---|---|---|---|---|---|
| ARD | −264.16 | 2 | 532.33 | 532.54 | 0.00 | 0.00 | 0.9974 |
| ARDeq** | −263.9 | 2 | 531.79 | 531.99 | 4.55 | 0.0045 | 0.0026 |
| ER | −267.34 | 1 | 536.68 | 536.68 | 4.88 | 0.05 | 0.0053 |
| UN01 | −300.74 | 1 | 603.48 | 603.49 | 71.69 | 0 | 0.0057 |
| UN10 | −276.35 | 1 | 554.69 | 554.7 | 22.89 | 0 | 0.0074 |

MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
313_A_Anther dehiscence (3–state) (D2d), 10 steps



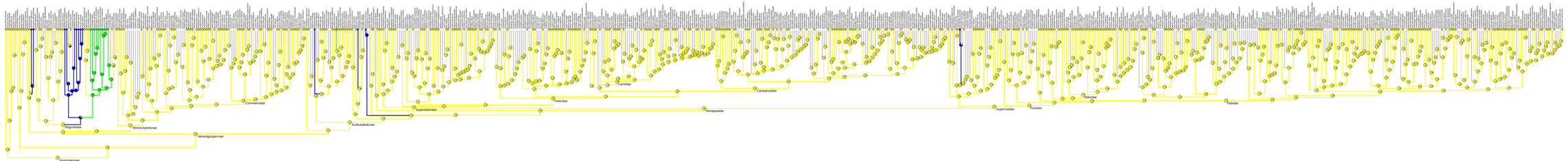

| Node | MP state(s) |
|---|---|
| Angiospermae | longitudinal slit |
| Mesangiospermae | longitudinal slit |
| Magnoliidae | longitudinal slit |
| Monocotyledonae | longitudinal slit |
| Eudicotyledonae | longitudinal slit |
| Cornoidae | longitudinal slit |
| Superasteridae | longitudinal slit |
| Asteridae | longitudinal slit |
| Lamiidae | longitudinal slit |
| Campanulidae | longitudinal slit |
| Superrosidae | longitudinal slit |
| Rosidae | longitudinal slit |
| Malvidae | longitudinal slit |
| Fabidae | longitudinal slit |

ML ancestral state reconstruction using rayDISC (R:corHMM) 313_A. Anther dehiscence (3-state) (D2d), ARDeq model

- longitudinal slit
- H–valvate
- flap–valvate

| Node | ML state | Prob |
|---|---|---|
| Angiospermae | longitudinal slit | 1 |
| Mesangiospermae | longitudinal slit | 1 |
| Magnoliidae | longitudinal slit | 0.992 |
| Monocotyledonae | longitudinal slit | 0.9999 |
| Eudicotyledonae | longitudinal slit | 1 |
| Commelinidae | longitudinal slit | 1 |
| Superasteridae | longitudinal slit | 1 |
| Superrosteridae | longitudinal slit | 1 |
| Asteridae | longitudinal slit | 1 |
| Lamiidae | longitudinal slit | 1 |
| Campanulidae | longitudinal slit | 1 |
| Supersolanidae | longitudinal slit | 1 |
| Solanaceae | longitudinal slit | 1 |
| Solanum | longitudinal slit | 1 |
| Solanum | longitudinal slit | 1 |

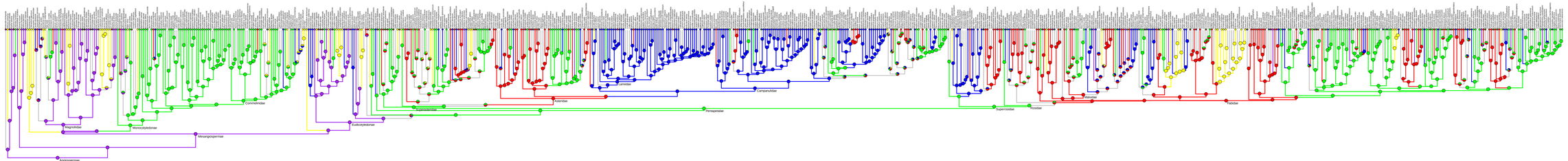
| Model | Logl. | Npar | AIC | AICc | ΔAICc | AICw |
|---|---|---|---|---|---|---|
| ARD | −55.17 | 6 | 122.33 | 122.46 | 0.00 | 0.99 |
| ARDeq | −54.09 | 6 | 120.18 | 120.31 | 2.15 | 0.34 |
| ER | −60.31 | 1 | 122.62 | 122.63 | 2.34 | 0.15 |
| SYM | −59.3 | 3 | 124.61 | 124.64 | 4.35 | 0.05 |
| SYMeq | −58.21 | 3 | 122.41 | 122.44 | 2.15 | 0.16 |

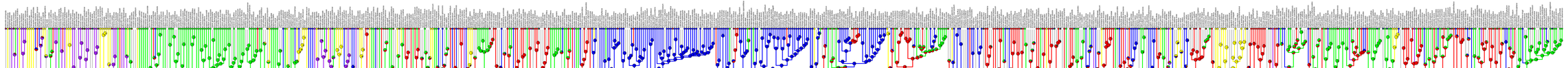


MP ancestral state reconstruction using ancestral pars
(R phangorn)
401_B, Number of structural carpels (5–state) (D2c), 188 steps

- one (1)
- two (2)
- three (3)
- four or five (4–5)
- more than five (>5)

| Node | MP state(s) |
|---|---|
| Angiospermae | more than five (>5) |
| Mesangiospermae | more than five (>5) |
| Magnoliidae | more than five (>5) |
| Monocotyledonae | three (3) |
| Eudicotyledonae | more than five (>5) |
| Commelinidae | three (3) |
| Ranunculidae | three (3) |
| Superasteridae | three (3) |
| Asteridae | four or five (4–5) |
| Lamiidae | two (2) |
| Campanulidae | two (2) |
| Superrosidae | three (3) |
| Rosidae | three (3) |
| Malvidae | four or five (4–5) |
| Fabidae | four or five (4–5) |





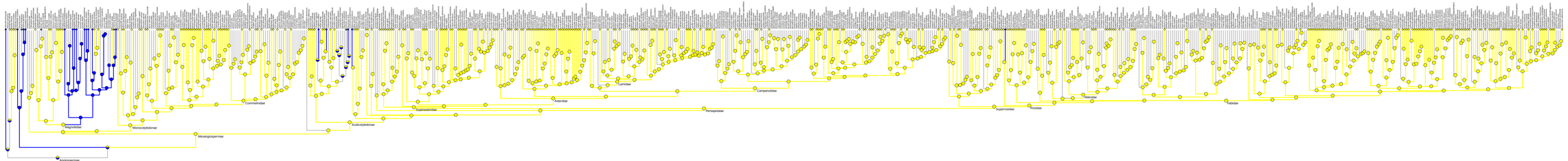

| Model | Logl. | Npar | AIC | AICc | ΔAICc | ΔAICc rel. | w |
|---|---|---|---|---|---|---|---|
| ARD | −665.46 | 20 | 1370.93 | 1372.7 | 3.2 | 0.0049 | 0.0917 |
| ARDeq* | −663.85 | 20 | 1367.7 | 1369.47 | 0 | 0.0015 | 0.0976 |
| ER | −715.93 | 1 | 1433.86 | 1433.87 | 65.08 | 0.0015 | 0.9641 |
| SYM | −681.58 | 10 | 1383.16 | 1384.16 | 14.69 | 0.0015 | 0.0004 |
| SYMeq | −681.58 | 10 | 1383.16 | 1384.16 | 14.69 | 0.0015 | 0.0003 |
| ORD | −756.03 | 8 | 1528.06 | 1528.47 | 159.00 | 0.0015 | 0.0991 |
| ORDeq | −755.01 | 8 | 1526.03 | 1526.43 | 157.96 | 0.0015 | — |
| ORDSYM | −759.28 | 4 | 1526.56 | 1526.6 | 157.81 | 0 | 0.0039 |
| ORDSYMeq | −758.45 | 4 | 1524.91 | 1524.96 | 156.17 | 0 | 0.0039 |
| ORDER | −765.02 | 1 | 1532.04 | 1532.05 | 163.25 | 0 | 0.0055 |

| Node | ML state | Prob |
|---|---|---|
| Angiospermae | more than five (>5) | — |
| Mesangiospermae | more than five (>5) | 0.9999 |
| Magnoliidae | more than five (>5) | 0.9998 |
| Monocotyledonae | more than five (>5) | 0.7033 |
| Eudicotyledonae | more than five (>5) | 0.9845 |
| Commelinidae | three (3) | 0.9999 |
| Ceratophyllidae | four or five (4–5) | 0.9999 |
| Chloranthaceae | four or five (4–5) | 0.9993 |
| Piperales | four or five (4–5) | 0.9917 |
| Saururaceae | four or five (4–5) | 0.9976 |
| Nymphaeales | more than five (>5) | 0.9641 |
| Amborellales | more than five (>5) | 0.9994 |
| Gentianidae | more than five (>5) | 0.9993 |
| Lamiidae | more than five (>5) | 0.9991 |
| Campanulidae | more than five (>5) | — |
| Asterales | more than five (>5) | — |
| Dipsacidae | more than five (>5) | — |
| Pentapetalae | more than five (>5) | — |
| Rosidae | more than five (>5) | — |
| Fabidae | more than five (>5) | — |
| Malvidae | more than five (>5) | — |
| Superrosidae | more than five (>5) | — |

MP ancestral state reconstruction using ancestral pars
(R phangorn)
400_A_Gynoecium phyllotaxy (D2d), 10 steps

whorled
spiral

| Node | MP state(s) |
|---|---|
| Angiospermae | whorled / spiral |
| Mesangiospermae | whorled |
| Magnoliidae | whorled |
| Monocotyledonae | whorled |
| Eudicotyledonae | whorled |
| Commelinidae | whorled |
| Ranunculidae | whorled |
| Superasteridae | whorled |
| Asteridae | whorled |
| Lamiidae | whorled |
| Campanulidae | whorled |
| Superrosidae | whorled |
| Rosidae | whorled |
| Malvidae | whorled |
| Fabidae | whorled |

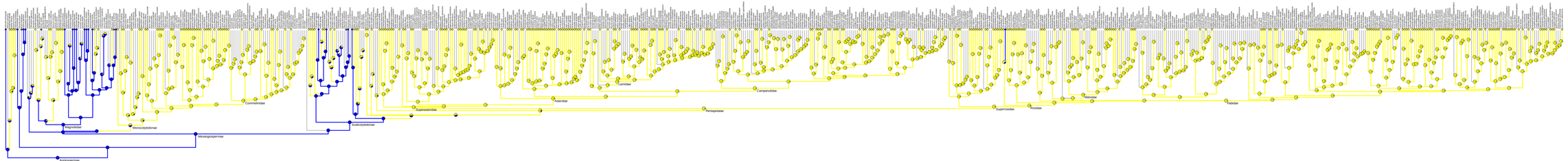


ML ancestral state reconstruction using rayDISC (R:corHMM)
400_A. Gynoecium phyllotaxy (D2d), ARDeq model

whorled
spiral

| Node | ML state | Prob |
|---|---|---|
| Angiospermae | spiral | |
| Mesangiospermae | spiral | 0.9999 |
| Magnoliidae | spiral | 0.9988 |
| Monocotyledonae | whorled | 0.5576 |
| Eudicotyledonae | spiral | 0.998 |
| Commelinidae | whorled | 0.9999 |
| Ranunculidae | whorled | 0.9794 |
| Superasteridae | whorled | 0.9952 |
| Asteridae | whorled | 1 |
| Lamiidae | whorled | 1 |
| Campanulidae | whorled | 1 |
| Superrosidae | whorled | 0.9133 |
| Asterophyllitidae | whorled | 0.9993 |
| Rosidae | whorled | 0.9664 |
| Malvidae | whorled | 0.9664 |
| Fabidae | whorled | 0.9664 |

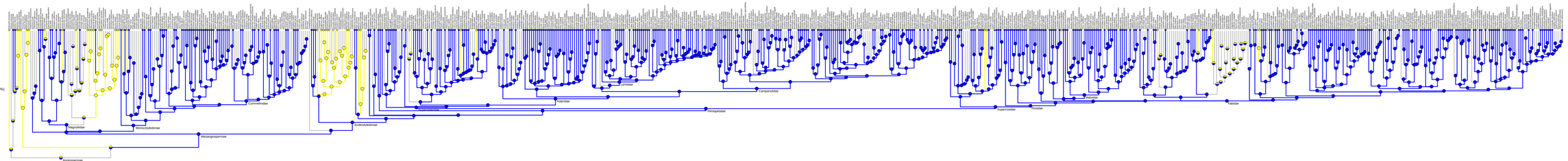
| Model | Logl. | Npar | AIC | AICc | AICc_wt | Prob |
|---|---|---|---|---|---|---|
| ARD | −38.98 | 2 | 81.97 | 81.97 | 0.99 | 0.9664 |
| ARDeq** | −38.29 | 2 | 80.58 | 80.58 | 0.5 | 0.9664 |
| ER | −49.14 | 1 | 100.29 | 100.29 | 19.7 | 0 4e−04 4e−04 |
| UNI01 | −51.05 | 1 | 104.11 | 104.11 | 23.52 | 0 4e−04 |
| UNI10 | −41.74 | 1 | 85.47 | 85.48 | 4.88 | 0.05 0.0075 |



MP ancestral state reconstruction using ancestral pars
(R phangorn)
403_A, Fusion of ovaries (binary) (D2c), 24 steps

free (<5%)
fused (>5%)

| Node | MP state(s) |
|---|---|
| Angiospermae | free (<5%) / fused (>5%) |
| Mesangiospermae | fused (>5%) |
| Magnoliidae | fused (>5%) |
| Monocotyledonae | fused (>5%) |
| Eudicotyledonae | fused (>5%) |
| Commelinidae | fused (>5%) |
| Ceratophyllidae | fused (>5%) |
| Superasterridae | fused (>5%) |
| Asteridae | fused (>5%) |
| Lamiidae | fused (>5%) |
| Campanulidae | fused (>5%) |
| Superrosidae | fused (>5%) |
| Rosidae | fused (>5%) |
| Malvidae | fused (>5%) |
| Fabidae | fused (>5%) |

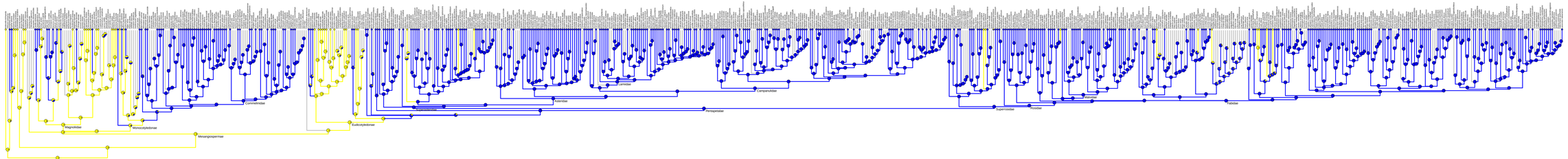


ML ancestral state reconstruction using rayDISC (R:corHMM) 403_A. Fusion of ovaries (binary) (D2c), ARDeq model

free (<5%)
fused (>5%)

| Node | ML state | Prob |
|---|---|---|
| Angiospermae | free (<5%) | 1 |
| Mesangiospermae | free (<5%) | 0.9995 |
| Magnoliidae | free (<5%) | 0.998 |
| Monocotyledonae | free (<5%) | 0.8807 |
| Eudicotyledonae | free (<5%) | 0.9935 |
| Commelinidae | fused (>5%) | 0.9999 |
| Ceratophyllidae | fused (>5%) | 0.9996 |
| Superasterridae | fused (>5%) | 0.9999 |
| Asteridae | fused (>5%) | 1 |
| Lamiidae | fused (>5%) | 1 |
| Campanulidae | fused (>5%) | 1 |
| Asterids incertae sedis | fused (>5%) | 1 |
| Rosidae | fused (>5%) | 0.9 |
| Superrosidae | fused (>5%) | 1 |
| Fabidae | fused (>5%) | 1 |

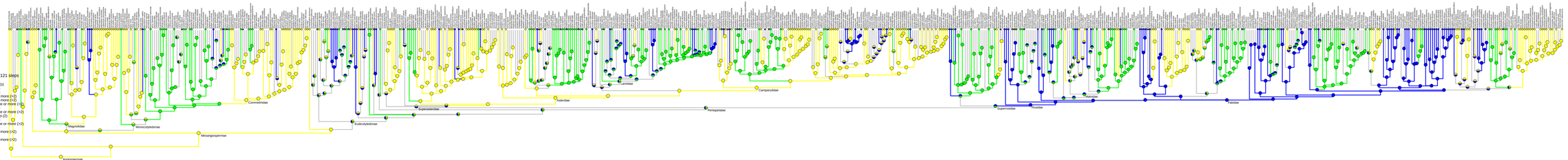
| Model | Logl. | Npar | AIC | AICc | q.fwd | q.rev |
|---|---|---|---|---|---|---|
| ARD | −95.11 | 2 | 194.21 | 194.26 | 0.0 | 0.0 |
| ARDeq** | −94.41 | 2 | 192.83 | 192.88 | 0.0 | 0.0 |
| ER | −100.26 | 1 | 202.51 | 202.52 | 9.68 | 0.01 |
| UN01 | −102.63 | 1 | 207.26 | 207.26 | 14.42 | 0 |
| UN10 | −105.98 | 1 | 213.97 | 213.97 | 21.13 | 0 |



MP ancestral state reconstruction using ancestral pars
(R phangorn)
411_A, Number of ovules per functional carpel (3–state) (D2c), 121 steps

one (1)
two (2)
three or more (>2)

| Node | MP state(s) |
|---|---|
| Angiospermae | one (1) |
| Mesangiospermae | one (1) |
| Magnoliidae | one (1) / three or more (>2) |
| Monocotyledonae | one (1) / three or more (>2) |
| Eudicotyledonae | one (1) / two (2) / three or more (>2) |
| Commelinidae | one (1) |
| Arecidae | one (1) / two (2) / three or more (>2) |
| Superasteridae | one (1) / two (2) |
| Asteridae | one (1) |
| Lamiidae | one (1) / two (2) / three or more (>2) |
| Campanulidae | one (1) |
| Superrosidae | two (2) / three or more (>2) |
| Rosidae | two (2) |
| Malvidae | two (2) / three or more (>2) |
| Fabidae | two (2) |



ML ancestral state reconstruction using rayDISC (R:corHMM)
411_A. Number of ovules per functional carpel (3-state) (D2c), ARDeq model

one (1)
two (2)
three or more (>2)

| Node | ML state | Prob |
|---|---|---|
| Angiospermae | three or more (>2) | 0.9998 |
| Mesangiospermae | three or more (>2) | 0.9996 |
| Magnoliidae | three or more (>2) | 0.9963 |
| Monocotyledonae | three or more (>2) | 0.9991 |
| Eudicotyledonae | three or more (>2) | 0.9994 |
| Commelinidae | three or more (>2) | 0.7727 |
| Caryophyllidae | three or more (>2) | 1 |
| Caryophyllales | three or more (>2) | 0.9985 |
| Pentapetalae | three or more (>2) | 0.9968 |
| Cornales | three or more (>2) | 0.9999 |
| Campanulidae | three or more (>2) | 0.9924 |
| Asterales | three or more (>2) | 1 |
| Supernosidae | three or more (>2) | 0.9999 |
| Rosidae | three or more (>2) | 0.9995 |
| Fabidae | three or more (>2) | 1 |

| Model | LogL | Npar | AIC | AICc | ΔAICc | AICcWt | Prob |
|---|---|---|---|---|---|---|---|
| ARD | -389.27 | 6 | 790.54 | 790.85 | 1.91 | 0.28 | 0.0000 |
| ARDeq** | -389.32 | 6 | 788.63 | 788.94 | 0 | 0.72 | 0.0000 |
| ER | -400.17 | 1 | 802.34 | 802.37 | 13.43 | 0.00 | 0.0000 |
| SYM | -398.85 | 3 | 803.69 | 803.82 | 14.88 | 0.00 | 0.0000 |
| SYMeq | -398.85 | 3 | 803.69 | 803.82 | 14.88 | 0.00 | 0.0000 |
| ORD | -397.11 | 4 | 802.22 | 802.39 | 13.53 | 0.00 | 0.0000 |
| ORDeq | -400.66 | 4 | 809.32 | 809.49 | 20.63 | 0.00 | 0.0000 |
| ORDSYM | -410.87 | 2 | 825.75 | 825.76 | 37.02 | 0 | 0.0052 |
| ORDSYMeq | -410.62 | 2 | 825.24 | 825.26 | 36.52 | 0 | 0.0052 |
| ORDER | -411.98 | 1 | 825.95 | 825.96 | 37.22 | 0 | 0.006 |