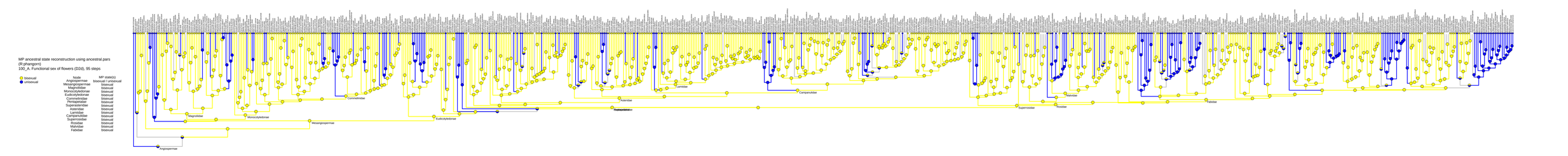
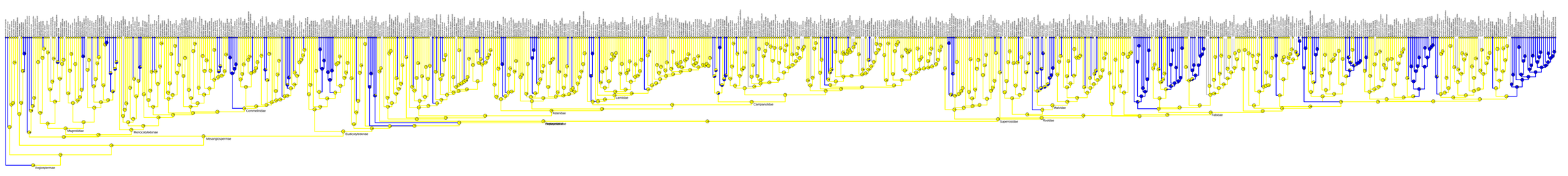

MP ancestral state reconstruction using ancestral.pars
(R phangorn)
100_A: Functional sex of flowers (02d), 95 steps
bisexual
unisexual
Node
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledonae
Eudicotyledonae
Commelinidae
Ceratophyllidae
Santalales incertae sedis
Asteridae
Lamiidae
Campanulidae
Superrosidae
Malvidae
Fabidae
MP state(s)
bisexual
bisexual
bisexual
bisexual
bisexual
bisexual
bisexual
bisexual
bisexual
bisexual
bisexual
bisexual
bisexual
bisexual
bisexual
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledonae
Eudicotyledonae
Commelinidae
Ceratophyllidae
Santalales incertae sedis
Asteridae
Lamiidae
Campanulidae
Superrosidae
Rosidae
Malvidae
Fabidae

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

bisexual
unisexual

Model	LogL	Npar	AIC	AICc	q12	q21
ARD	-311.75	2	627.5	627.59	0.0028	0.0028
ARDeq*	-311.12	2	626.24	626.25	0	0.45
ER	-314.19	1	630.38	630.38	4.13	0.06
UNI01	-312.72	1	627.44	627.45	1.19	0.25
UNI10	-358.95	1	719.9	719.9	93.65	0

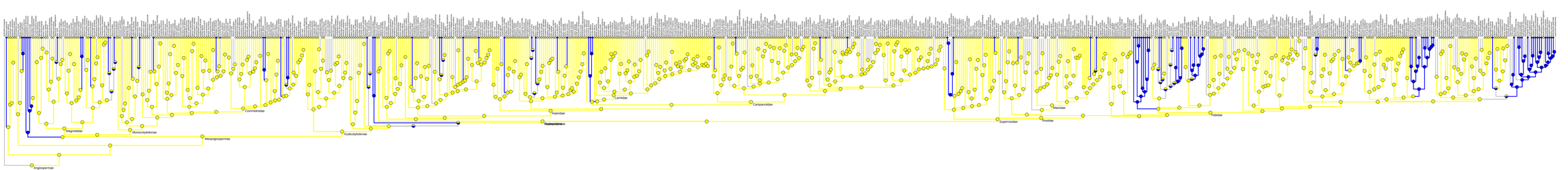
Node	ML state	Prob
Angiospermae	bisexual	1
Mesangiospermae	bisexual	1
Magnoliidae	bisexual	1
Monocotyledonae	bisexual	1
Eudicotyledonae	bisexual	1
Commelinidae	bisexual	0.9997
Pentapetalae	bisexual	1
Superrosidae	bisexual	1
Asteridae	bisexual	1
Lamiidae	bisexual	1
Campanulidae	bisexual	0.9991
Superasteridae	bisexual	1
Asterales	bisexual	1
Menyanthaceae	bisexual	0.7933

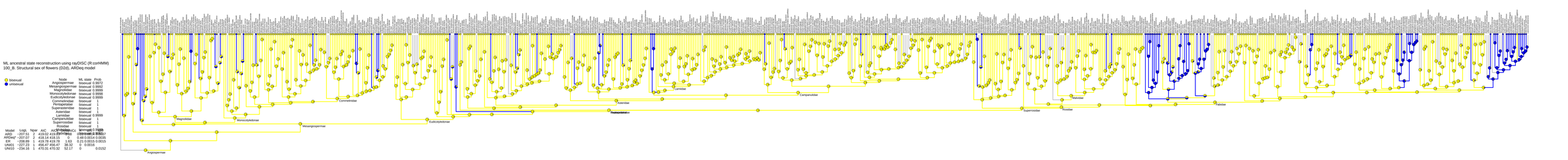


MP ancestral state reconstruction using ancestral.pars
(R phangorn)
100_B. Structural sex of flowers (0/2d), 54 steps

bisexual
unisexual

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

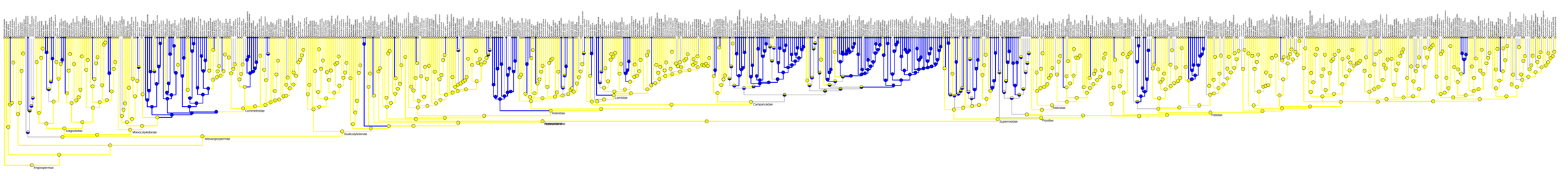


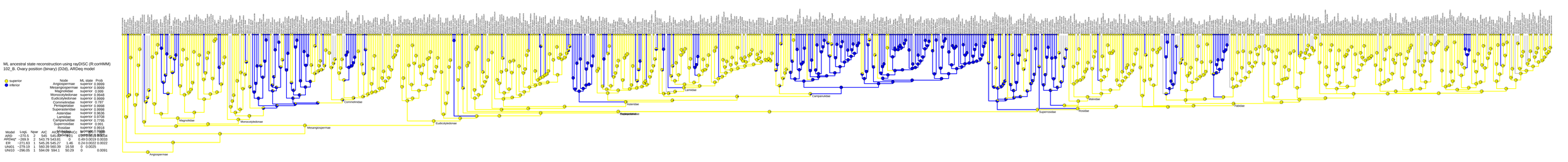

ML ancestral state reconstruction using ratyDISC (R:corHMM)
100_B. Structural sex of flowers (Ord), ARDeq model
bisexual
unisexual
Node ML state Prob
Angiospermae bisexual 0.9999
Mesangiospermae bisexual 0.9992
Magnoliidae bisexual 0.9999
Monocotyledoneae bisexual 0.9998
Eudicotyledoneae bisexual 0.9999
Commelinidae bisexual 1
Pentapetalae bisexual 1
Superasteridae bisexual 1
Asteridae bisexual 1
Lamiidae bisexual 0.9999
Campanuliidae bisexual 1
Superrosidae bisexual 1
Rosidae bisexual 1
Malvidae bisexual 0.9999
Fabidae bisexual 1
Model LogL Npar AIC AICc ΔAICc AICw
ARD −207.51 2 419.02 419.15 0 0.48
ARDeq* −207.07 2 418.14 418.15 0 0.48
ER −208.89 1 419.78 419.78 1.63 0.21
UNI01 −227.23 1 456.47 456.47 38.32 0
UNI10 −234.16 1 470.31 470.32 52.17 0
0.0014 0.0035
0.0014 0.0035
0.0015 0.0015
0.0016
0.0152
Angiospermae
Mesangiospermae
Monocotyledoneae
Magnoliidae
Eudicotyledoneae
Commelinidae
Pentapetalae
Superasteridae
Asteridae
Lamiidae
Campanuliidae
Superrosidae
Rosidae
Malvidae
Fabidae

MP ancestral state reconstruction using ancestral.pars
(R phangorn)
102_B. Ovary position (binary) (0|2d), 78 steps

superior
inferior

Node	MP state(s)
Angiospermae	superior
Mesangiospermae	superior
Magnoliidae	superior
Monocotyledonae	superior
Eudicotyledonae	superior
Commelinidae	superior
Ceratophyllidae	superior
Nymphaeaceae	superior
Asteridae	superior
Lamiidae	superior
Campanulidae	superior
Superrosidae	superior
Rosidae	superior
Malvidae	superior
Fabidae	superior

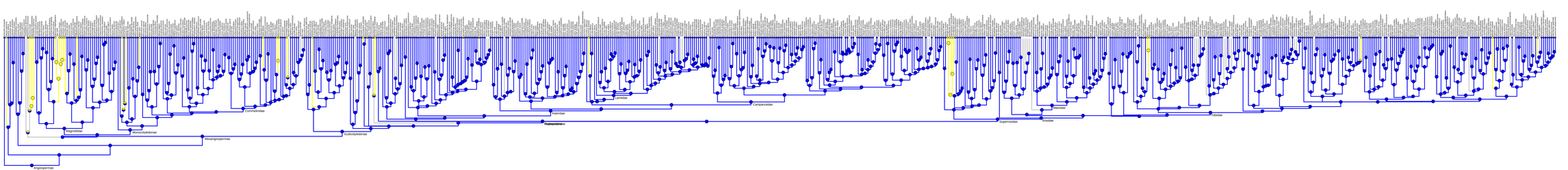



ML ancestral state reconstruction using rayDISC (R:corHMM)
102_B. Ovary position (binary) (D2d), ARDeq model
superior
inferior
Node ML state Prob
Angiospermae superior 1
Mesangiospermae superior 0.9999
Magnoliidae superior 0.999
Monocotyledoneae superior 0.9948
Eudicotyledonae superior 0.9999
Commelinidae superior 0.787
Ceratophyllales superior 0.9998
Superasteridae superior 0.9998
Asteridae superior 0.9636
Lamiidae superior 0.9708
Campanulidae superior 0.7795
Supersonidae superior 0.991
Myrtidae superior 0.9999
Malvidae superior 0.9999
Rosidae superior 0.9999
Model LogL Npar AIC AICc ΔAICc AICw
ARD -270.5 2 545 545.01 0 0.9914
ARDeq* -269.9 2 543.79 543.81 0 0.49
ER -271.63 1 545.26 545.27 1.45 0.24
UN01 -279.19 1 560.39 560.39 16.58 0
UN10 -296.05 1 594.09 594.1 50.29 0
0.0019 0.0033
0.0019 0.0033
0.0022 0.0022
0.0025
0.0091
Angiospermae
Magnoliidae
Monocotyledoneae
Mesangiospermae
Eudicotyledoneae
Commelinidae
Ceratophyllales
Superasteridae
Asteridae
Lamiidae
Campanulidae
Supersonidae
Myrtidae
Malvidae
Rosidae

MP ancestral state reconstruction using ancestral.pars (R:phangorn)
201_A. Perianth presence (D2c), 20 steps

absent
present

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

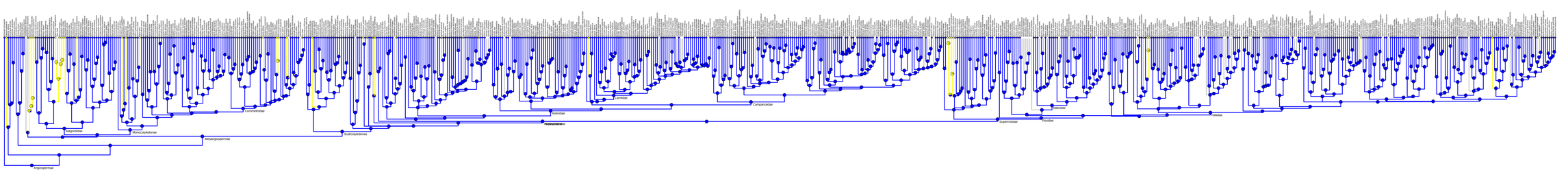


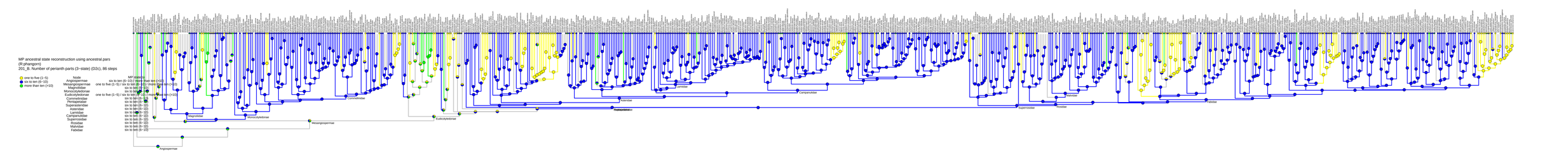
ML ancestral state reconstruction using rayDISC (R:corHMM) 203_A. Perianth presence (DDc), UNI10 model

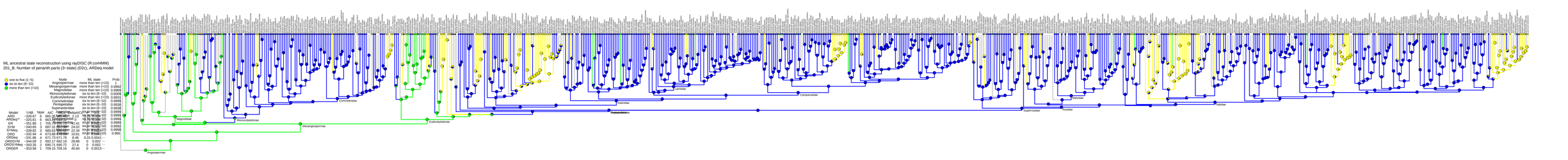
absent
present

Node	ML state Prob
Angiospermae	present 1
Mesangiospermae	present 1
Magnoliidae	present 1
Monocotyledonae	present 1
Eudicotyledonae	present 1
Commelinidae	present 1
Gunneridae	present 1
Superasteridae	present 1
Asteridae	present 1
Lamiidae	present 1
Campanulidae	present 1
Superrosidae	present 1
Rosidae	present 1
Malvidae	present 1

Model	LogL	Npar	AIC	AICc	d	e	Mean Anc	1q10
ARD	-95.31	2	194.62	194.82	0.61	0	0.99	5e−04
ARDeq	-94.62	2	193.24	193.25	0.62	0.25	0	5e−04
ER	-95.51	1	193.03	193.03	0.4	0.28	5e−04	5e−04
UNI01	−112.16	1	226.32	226.32	33.69	0	0.0193	
UNI10*	-95.31	1	192.62	192.63	0	0.34		5e−04



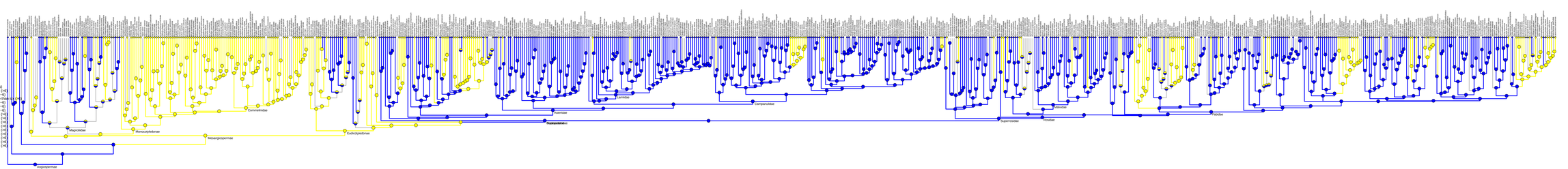

MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
201_B. Number of perianth parts (3–state) (02c), 86 steps
one to five (1–5)
six to ten (6–10)
more than ten (>10)
MP states(s)
Angiospermae six to ten (6–10) / more than ten (>10)
Mesangiospermae one to five (1–5) / six to ten (6–10) / more than ten (>10)
Magnoliidae six to ten (6–10)
Monocotyledonae six to ten (6–10)
Eudicotyledonae one to five (1–5) / six to ten (6–10) / more than ten (>10)
Commelinidae six to ten (6–10)
Gentianidae six to ten (6–10)
Solanidae 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)
Angiospermae
Magnoliidae
Monocotyledonae
Mesangiospermae
Eudicotyledonae
Commelinidae
Gentianidae
Solanidae
Asteridae
Lamiidae
Campanulidae
Superrosidae
Rosidae
Malvidae
Fabidae

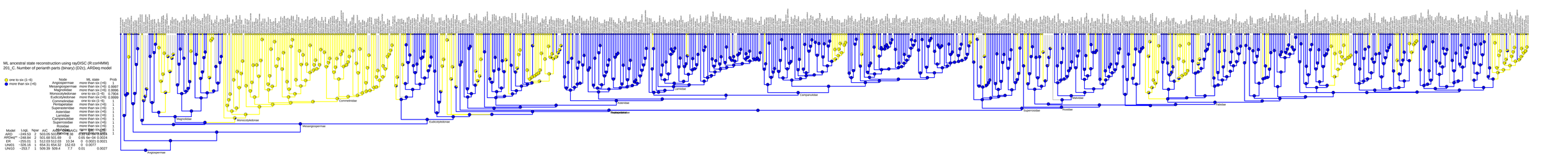

ML ancestral state reconstruction using ratDISC (R::corHMM)
201_B. Number of periarith parts (3–state) (D2c), ARDeq model
one to five (1–5)
six to ten (6–10)
more than ten (>10)
Model LogL Npar AIC AICc ΔAICc AICw
ARD -326.67 6 665.35 665.69 2.13 0.1
ARDeq* -325.61 6 663.22 663.56 0 0.2999
ER -351.86 1 705.73 705.77 42.41 0
SYM -339.82 3 685.64 685.81 22.34 0
SYMeq -339.82 3 685.63 685.81 22.34 0
ORD -332.94 4 673.88 674.09 10.61 0.0016
ORDeq -331.86 4 671.73 671.74 8.46 0.01
ORDSYM -344.09 2 692.17 692.19 28.86 0
ORDSYMeq -343.35 2 690.71 690.72 27.4 0
ORDER -353.58 1 709.15 709.16 45.84 0
Angiospermae more than ten (>10) 0.9992
Mesangiospermae more than ten (>10) 0.9988
Magnoliidae more than ten (>10) 0.9988
Monocotyledoneae six to ten (6–10) 0.6009
Eudicotyledoneae more than ten (>10) 0.9931
Commelinidae six to ten (6–10) 0.9999
Ceratophyllidae six to ten (6–10) 0.9999
Superasteridae six to ten (6–10) 0.9938
Asteridae more than ten (>10) 0.9999
Lamiidae six to ten (6–10) 0.9999
Campanulidae six to ten (6–10) 0.9999
Rosidae more than ten (>10) 0.9988
Fabidae more than ten (>10) 0.9988
Malvidae six to ten (6–10) 0.9958
Superrosidae six to ten (6–10) 0.995
Angiospermae
Magnoliidae
Monocotyledoneae
Mesangiospermae
Eudicotyledoneae
Commelinidae
Ceratophyllidae
Superasteridae
Asteridae
Lamiidae
Lamiidae
Campanulidae
Campanulidae
Rosidae
Fabidae
Malvidae
Malvidae
Superrosidae
Rosidae
Fabidae

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	one to six (1–6)
Magnoliidae	one to six (1–6) / more than six (>6)
Monocotyledonae	one to six (1–6)
Eudicotyledonae	one to six (1–6)
Commelinidae	more than six (>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)

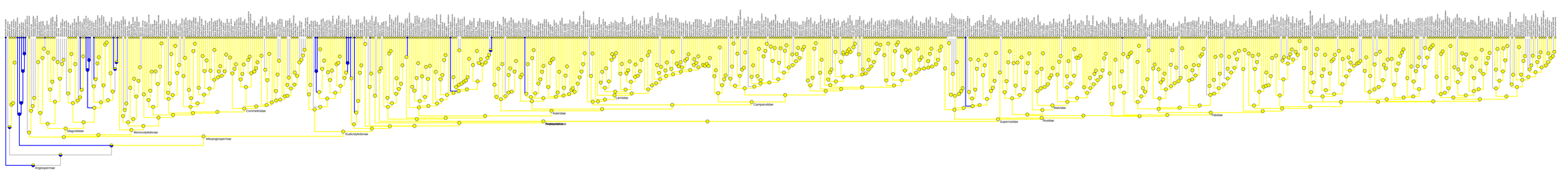


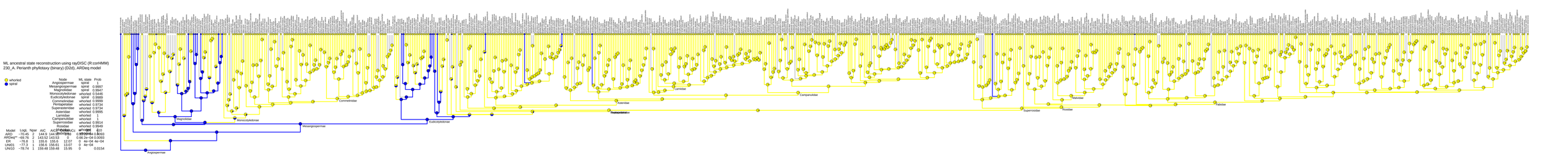

ML ancestral state reconstruction using ray/DISC (R corHMM)
201_C: Number of perianth parts (binary) (D1c), ARDeq model
one to six (1-6)
more than six (>6)
ML state Prob
Angiosperm more than six (>6) 1
Mesangiosperm more than six (>6) 0.9997
Magnoliidae more than six (>6) 0.9996
Monocotyledonae one to six (1-6) 0.7504
Eudicotyledonae more than six (>6) 0.9999
Commelinidae more than six (>6) 1
Ceratophyllidae more than six (>6) 1
Superasteridae more than six (>6) 1
Asteridae more than six (>6) 1
Lamiidae more than six (>6) 1
Campanulidae more than six (>6) 1
Superrosidae more than six (>6) 1
Rosidae more than six (>6) 1
Malvidae more than six (>6) 1
Model LogL Npar AIC AICc BIC
ARD -249.53 2 503.05 503.38 512.63
ARDeq** -248.84 2 501.68 501.89 510.99
ER -255.01 1 512.03 512.03 10.34
UN01 -326.16 1 654.31 654.32 152.63
UN10 -253.7 1 509.39 509.4 7.7
Likelihood ratio test
0 0.0021
0.65 6e-04 0.0024
0 0.0021 0.0021
0 0.0077
0.01 0.0027
Angiosperm
Magnoliidae
Monocotyledonae
Mesangiosperm
Commelinidae
Eudicotyledonae
Ceratophyllidae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Superrosidae
Rosidae
Malvidae

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
Ceratophyllidae	whorled
Nymphaeidae	whorled
Schisandraceae	whorled
Asteridae	whorled
Lamiidae	whorled
Campanulidae	whorled
Superrosidae	whorled
Rosidae	whorled
Malvidae	whorled
Fabidae	whorled

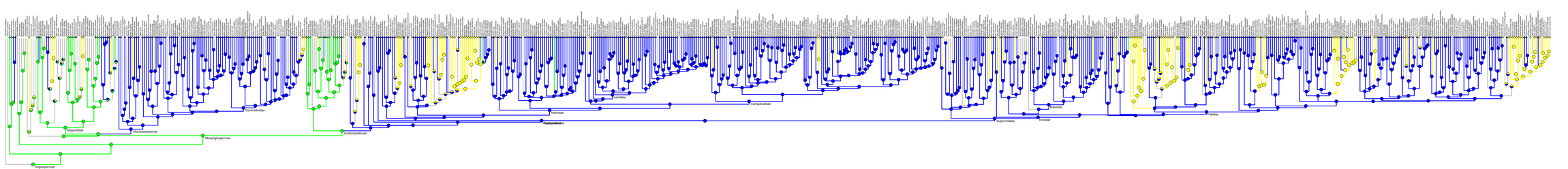


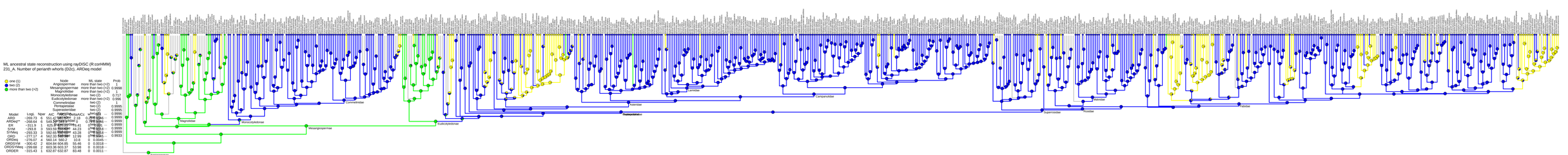

ML ancestral state reconstruction using rayDISC (R:corHMM)
230_A. Perianth phylotaxy (binary) (D2d), ARDeq model
whorled
spiral
Model LogL Npar AIC AICc ΔAICc AICw
ARD -70.45 2 144.9 144.9 0 0.8693
ARDeq** -69.76 2 143.52 143.53 0 0.86
ER -76.8 1 155.6 155.6 12.07 0
UN01 -77.3 1 156.6 156.61 13.07 0
UN10 -78.74 1 159.48 159.5 0 0
Node ML state Prob
Angiospermae spiral 1
Mesangiospermae spiral 0.9997
Magnoliidae spiral 0.9947
Monocotyledoneae whorled 0.5446
Eudicotyledoneae spiral 0.9989
Commelinidae whorled 0.9999
Ceratophyllidae whorled 0.9999
Santalanae whorled 0.9734
Asteridae whorled 0.9995
Lamiidae whorled 1
Campanulidae whorled 1
Superrosidae whorled 0.9914
Malvidae whorled 0.9999
Rosidae whorled 410
Fabidae whorled 0.9993
Angiospermae
Magnoliidae
Monocotyledoneae
Mesangiospermae
Commelinidae
Eudicotyledoneae
Santalanae
Asteridae
Lamiidae
Campanulidae
Superrosidae
Malvidae
Rosidae
Fabidae

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)
Ranunculidae	two (2)
Santalopsiidae	two (2)
Asteridae	two (2)
Lamiidae	two (2)
Campanulidae	two (2)
Superrosidae	two (2)
Rosidae	two (2)
Malvidae	two (2)
Fabidae	two (2)

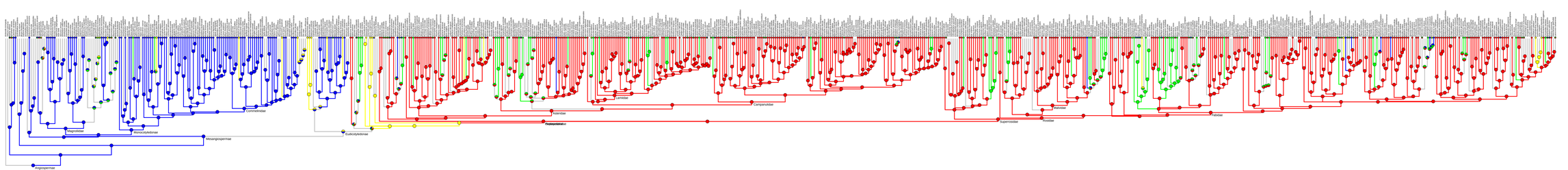


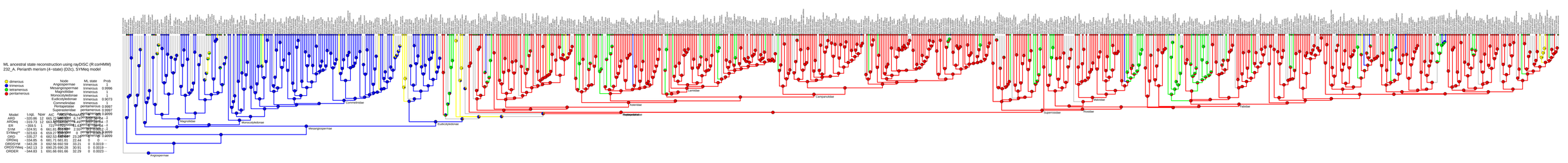

ML ancestral state reconstruction using ratDISC (R:corHMM)
231_A. Number of perianth whorls (02c), ARDeq model
one (1)
two (2)
more than two (>2)
Model LogL Nparam AIC AICc ΔAICc AICw
ARD -269.73 6 551.47 552.18 0.25 0.0046
ARDeq* -268.64 6 549.28 549.99 0 0.9999
ER -311.9 1 625.8 625.81 76.41 0
SYM -310.33 3 626.66 626.81 77.23 0
SYMeq -310.33 3 626.66 626.81 77.23 0
ORD -277.17 4 562.33 562.59 12.99 0.0001
ORDeq -276.07 4 560.14 560.2 10.6 0.0045
ORDSYM -300.42 2 604.84 604.85 55.46 0
ORDSYMeq -299.68 2 603.36 603.37 53.98 0
ORDER -315.43 1 632.87 632.87 83.48 0
Node Pr(>0
Angiospermae more than two (>2) 0.998
Mesangiospermae more than two (>2) 0.998
Magnoliidae more than two (>2) 1
Monocotyledoneae two (2) 0.717
Eudicotyledonae more than two (>2) 0.996
Commelinidae two (2) 0
Ceratophyllidae two (2) 0.995
Superasteridae two (2) 0.995
Asteridae whorl 0.996
Lamiidae 2.18 0.9999
Campanulidae 0 0.9999
Asteranthidae 76.41 0.9999
Caryophyllidae 77.23 0.9999
Rosidae 43.28 0.9999
Malvidae 12.99 0.9933
Fabidae 10.6 0
Malvanae 55.46 0
Rosanae 53.98 0
Pentapetalae 83.48 0
Angiospermae
Magnoliidae
Monocotyledoneae
Mesangiospermae
Eudicotyledoneae
Commelinidae
Ceramiidae
Lamiidae
Campanulidae
Asteridae
Caryophyllidae
Rosidae
Malvidae
Malvanae
Fabidae

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	pentamerous
Magnoliidae	pentamerous
Superasteridae	pentamerous
Asteridae	pentamerous
Lamiidae	pentamerous
Campanulidae	pentamerous
Superrosidae	pentamerous
Rosidae	pentamerous
Malvidae	pentamerous
Fabidae	pentamerous

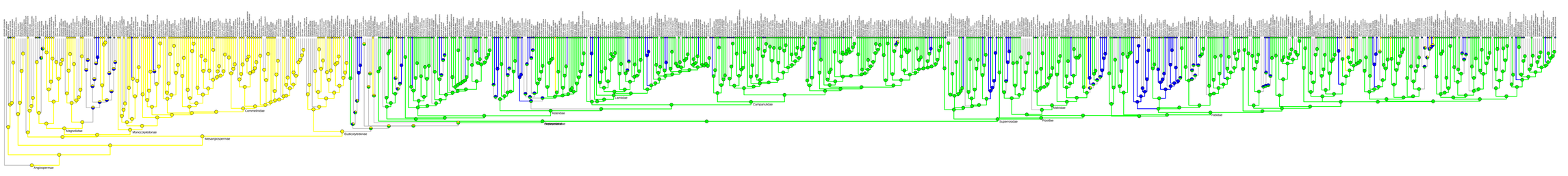



ML ancestral state reconstruction using rayDISC (R:corHMM)
232_A. Perianth merism (4–state) (D2c), SYMeq model
dimerous
trimerous
tetramerous
pentamerous
Model LogL Npar AIC AICc
ARD ~320.86 12 665.72 666.08
ARDeq ~319.73 12 663.46 663.82
ER ~359.5 1 721.01 721.02
ERSYM ~321.63 6 655.26 655.46
SYMeq** ~323.63 6 659.27 659.47
ORD ~335.27 6 682.53 682.73
ORDeq ~334.85 6 681.71 681.91
ORDSYM ~343.28 3 692.56 692.59
ORDSYMeq ~342.13 3 690.25 690.28
ORDER ~344.83 1 691.66 691.66
Node ML state Prob
Angiospermae trimerous 1
Mesangiospermae trimerous 0.9596
Magnoliidae trimerous 1
Monocotyledonae trimerous 1
Eudicotyledonae trimerous 0.9073
Dilleniidae pentamerous 1
Gunneridae pentamerous 0.9997
Superasteridae pentamerous 0.9997
Asteridae pentamerous 0.9999
Lamiidae pentamerous 1
Campanulidae pentamerous 1
Asterales pentamerous 1
Rosidae pentamerous 0.9999
Fabidae pentamerous 0.9999
Malvidae pentamerous 1
Superrosidae pentamerous 0.9999
Rosales pentamerous 1
Malvoidae pentamerous 1
Fabidae pentamerous 1
Angiospermae
Magnoliidae
Monocotyledonae
Mesangiospermae
Eudicotyledonae
Gunneridae
Dilleniidae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Asterales
Rosidae
Superrosidae
Rosales
Malvoidae
Malvidae
Fabidae

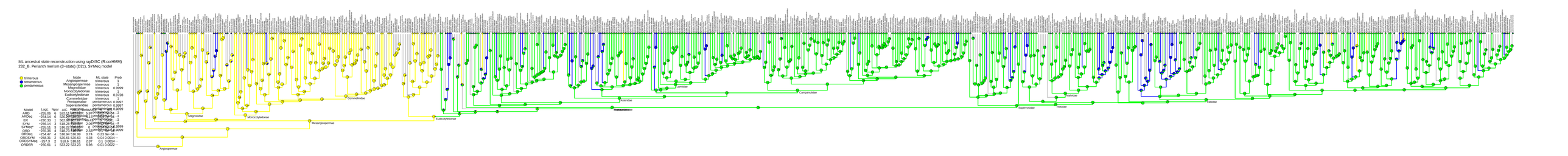
MP ancestral state reconstruction using ancestral.pars (R:phangorn)
232_B. Perianth merism (3–state) (D2c), 70 steps

trimerous
tetramerous
pentamerous

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

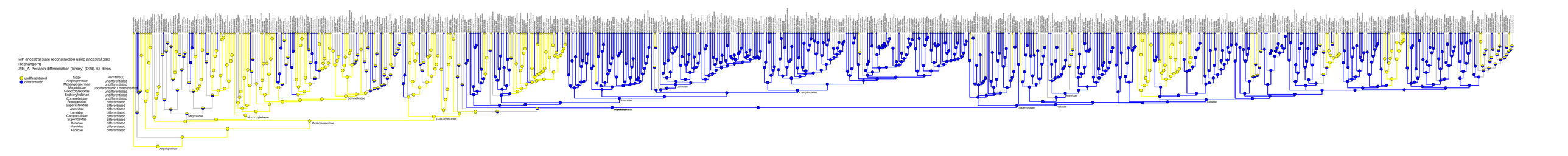


ML ancestral state reconstruction using rayDISC (R:corHMM)
232_B. Perianth merism (3=state) (D2c), SYMeq model



Node	ML state	Prob
Angiospermae	trimerous	1
Mesangiospermae	trimerous	1
Magnoliidae	trimerous	0.9999
Monocotyledonae	trimerous	1
Eudicotyledonae	trimerous	0.9728
Commelinidae	pentamerous	1
Hexangiospermae	pentamerous	0.9997
Superasteridae	pentamerous	0.9997
Asteridae	pentamerous	0.9999
Lamiidae	pentamerous	1
Campanulidae	pentamerous	1
Pentapetalae	pentamerous	0.9999
Superrosidae	pentamerous	0.9999
Rosidae	pentamerous	1
Malvidae	pentamerous	1

Model	LogL	Npar	AIC	AICc	ΔAICc	AICcWt	Q	wAICc
ARD	-255.06	6	522.12	523.01	5.07	0.0369	0.4	1
ARDeq	-254.14	6	520.28	521.17	3.23	0.0924	0.4	1
ER	-260.33	1	562.66	562.69	44.75	0	0.4	1
SYM	-255.11	3	516.21	516.51	0	0.8499	0.4	0.9999
SYMeq	-256.11	3	518.23	518.53	2	0.3119	0.4	0.9999
ORD	-255.36	4	518.73	519.09	2.57	0.2357	0.4	0.9999
ORDeq	-254.47	4	516.94	517.29	0.78	0.23	9e-04	---
ORDSYM	-258.31	2	520.61	520.63	4.38	0.0412	0.4	0.9914
ORDSYMeq	-257.3	2	518.6	518.61	2.37	0.1	0.4	0.9914
ORDER	-260.61	1	523.22	523.23	6.98	0.0102	0.4	---

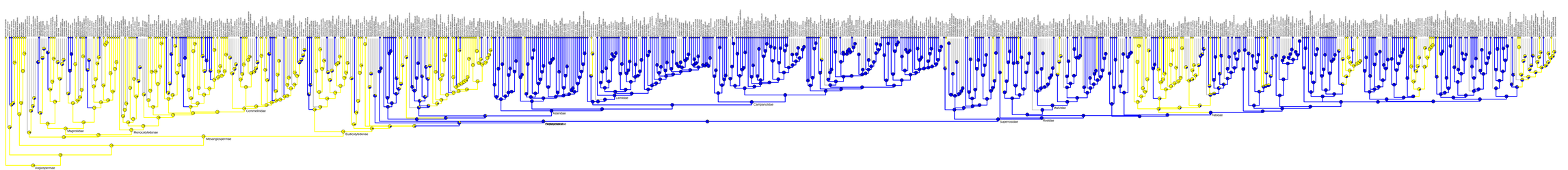

MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
234_A. Perianth differentiation (binary) (D2d), 65 steps
undifferentiated
differentiated
Node
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledonae
Eudicotyledonae
Commelinidae
Ceratophyllales
Santalales
Asteridae
Lamiidae
Campanulidae
Superrosidae
Rosidae
Malvidae
Fabidae
MP state(s)
undifferentiated
undifferentiated
undifferentiated / differentiated
undifferentiated
undifferentiated
undifferentiated
differentiated
differentiated
differentiated
differentiated
differentiated
differentiated
differentiated
differentiated
differentiated
differentiated
Angiospermae
Magnoliidae
Monocotyledonae
Mesangiospermae
Commelinidae
Eudicotyledonae
Ceratophyllales
Santalales
Asteridae
Lamiidae
Campanulidae
Superrosidae
Rosidae
Malvidae
Fabidae

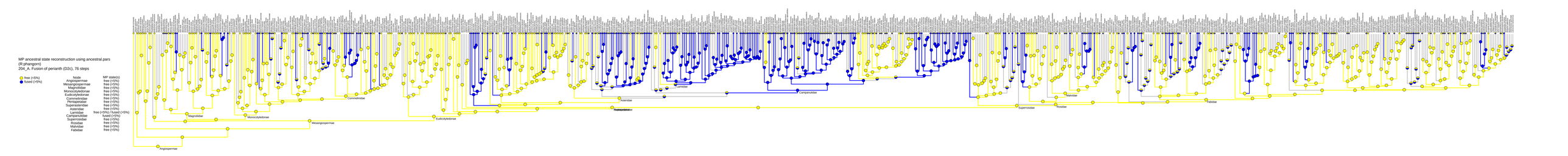
ML ancestral state reconstruction using rayDISC (R:corHMM)
234_A. Periamth differentiation (binary) (D2d), ARDeq model

undifferentiated
differentiated

Node	ML state	Prob
Angiospermae	undifferentiated	1
Mesangiospermae	undifferentiated	0.9998
Magnoliidae	undifferentiated	0.9995
Monocotyledoneae	undifferentiated	0.9999
Eudicotyledonae	undifferentiated	0.9851
Commelinidae	undifferentiated	0.9998
Pentapetalae	differentiated	0.9998
Superasteridae	differentiated	0.8866
Asteridae	differentiated	0.996
Lamiidae	differentiated	0.9998
Campanulidae	differentiated	1
Superrosidae	differentiated	0.9819
Rosidae	differentiated	0.9981
Fabidae	differentiated	0.9981
Malvidae	differentiated	0.9655

Model	LogL	Nrar	AIC	AICc	Akaike weight	Delta AIC	Delta AICc
ARD	-200.06	2	404.12	404.32	0.32	0	0
ARDeq**	-199.4	2	402.8	402.82	0	0.66	0.0043
ER	-209.3	1	420.59	420.6	17.78	0	0.0024
UN01	-235.15	1	458.29	458.3	55.48	0	0.0081
UN10	-234.54	1	471.09	471.09	68.28	0	0.0032



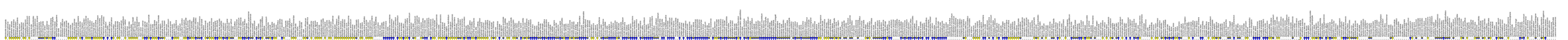

MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
204_A. Fusion of perianth (D2c), 76 steps
free (<5%)
fused (>5%)
Node
MP state(%)
Angiospermae
free (<5%)
Mesangiospermae
free (<5%)
Magnoliidae
free (<5%)
Monocotyledonae
free (<5%)
Eudicotyledonae
free (<5%)
Commelinidae
free (<5%)
Ceratophyllidae
free (<5%)
Superasteridae
free (<5%)
Asteridae
free (<5%)
Lamiidae
free (<5%) / fused (>5%)
Campanulidae
fused (>5%)
Superrosidae
free (<5%)
Rosidae
free (<5%)
Malvidae
free (<5%)
Fabidae
free (<5%)
Angiospermae
Magnoliidae
Monocotyledonae
Mesangiospermae
Eudicotyledonae
Commelinidae
Ceratophyllidae
Asteridae
Lamiidae
Campanulidae
Superrosidae
Rosidae
Malvidae
Fabidae

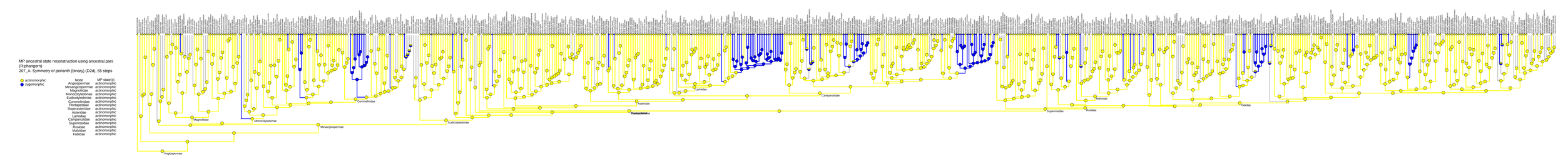
ML ancestral state reconstruction using rayDISC (R:corHMM) 204_A. Fusion of periianth (D2c), ER model

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

Node	ML state	Prob
Angiospermae	free (>5%)	0.9931
Mesangiospermae	free (>5%)	0.9999
Magnoliidae	free (>5%)	0.9987
Monocotyledonae	free (>5%)	0.9994
Eudicotyledonae	free (>5%)	0.9998
Commelinidae	free (>5%)	0.9975
Gunneridae	free (>5%)	0.993
Superasteridae	free (>5%)	0.993
Asteridae	free (>5%)	0.9804
Lamiidae	fused (>5%)	0.9782
Campanuliidae	fused (>5%)	0.9771
Superrosidae	free (>5%)	0.9944
Rosidae	free (>5%)	0.9971
Malvidae	free (>5%)	0.9971
Pentapetalae	free (>5%)	0.9993

Model	LogL	Npar	AIC	AICc	ΔAICc	AICcWt	Q01	Q10
ARD	−225.75	2	455.51	455.67	0.45	0.28	0.035	0.035
ARDeq	−225.17	2	454.34	454.35	0.48	0.39	0.0041	0.0035
ER*	−225.93	1	453.87	453.87	0	0.45	0.004	0.004
UN01	−239.31	1	480.61	480.62	26.74	0	0.0045	
UN10	−237.05	1	476.1	476.11	22.23	0		0.0076




MP ancestral state reconstruction using ancestral.pars
(R phangorn)
207_A. Symmetry of perianth (binary) (l2d2), 55 steps
actinomorphic
zygomorphic
Node MP state(s)
Angiospermae actinomorphic
Mesangiospermae actinomorphic
Magnoliidae actinomorphic
Monocotyledonae actinomorphic
Eudicotyledonae actinomorphic
Commelinidae actinomorphic
Gunneridae actinomorphic
Superrosidae actinomorphic
Rosidae actinomorphic
Asteridae actinomorphic
Lamiidae actinomorphic
Campanulidae actinomorphic
Superasteridae actinomorphic
Malvidae actinomorphic
Fabidae actinomorphic
Angiospermae
Magnoliidae
Monocotyledonae
Mesangiospermae
Commelinidae
Eudicotyledonae
Gunneridae
Asteridae
Lamiidae
Campanulidae
Superasteridae
Superrosidae
Rosidae
Malvidae
Fabidae

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

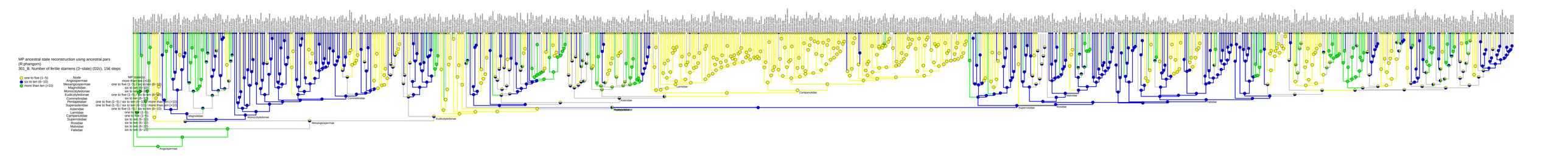
actinomorphic
zygomorphic

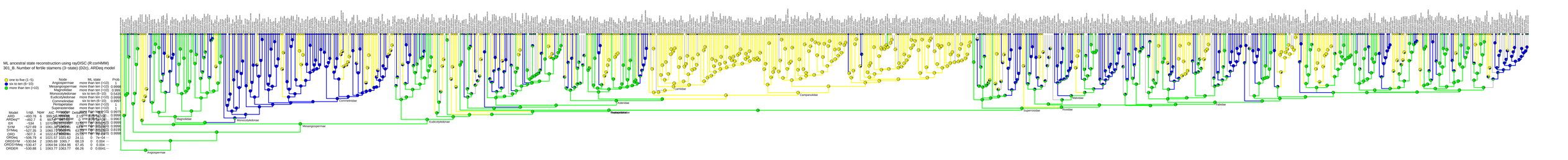
Node	ML state	Prob.
Angiospermae	actinomorphic	0.9971
Mesangiospermae	actinomorphic	1
Magnoliidae	actinomorphic	0.9998
Monocotyledonae	actinomorphic	0.9981
Eudicotyledonae	actinomorphic	0.9998
Commelinidae	actinomorphic	0.9979
Gunneridae	actinomorphic	1
Superasteridae	actinomorphic	1
Asteridae	actinomorphic	1
Lamiidae	actinomorphic	0.9982
Campanulidae	actinomorphic	0.9999
Superrosidae	actinomorphic	1
Rosidae	actinomorphic	0.9997
Malvidae	actinomorphic	0.9999

Model	LogL	Nopr	AIC	AICc	ΔAICc	AICw
ARD	-209.93	2	423.87	423.98	0.03	0.3317
ARDeq**	-209.42	2	422.84	422.86	0	0.631
ER	-217.33	1	436.66	436.66	13.81	0
UN01	-261.66	1	525.32	525.33	102.47	0
UN10	-219.78	1	441.57	441.57	18.72	0

Pairwise comparison	Mean	95% CI
actinomorphic,actinomorphic	0.9997	0.9997,0.9999
actinomorphic,zygomorphic	0.0003	0.0001,0.0003
zygomorphic,actinomorphic	0.0013	0.0005,0.0024
zygomorphic,zygomorphic	0.9987	0.9976,0.9995

Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledonae
Eudicotyledonae
Commelinidae
Gunneridae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Superrosidae
Rosidae
Malvidae
Malvaceae


MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
301_B. Number of fertile stamens (3-state) (D2c), 156 steps
one to five (1–5)
six to ten (6–10)
more than ten (>10)
Node
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledonae
Eudicotyledonae
Commelinidae
Ceratophyllaceae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Superrosidae
Malvidae
Fabidae
last common ancestor
more than ten (>10)
one to five (1–5) / six to ten (6–10)
six to ten (6–10)
six to ten (6–10)
one to five (1–5) / six to ten (6–10)
six to ten (6–10)
one to five (1–5) / six to ten (6–10) / more than ten (>10)
one to five (1–5) / six to ten (6–10) / more than ten (>10)
one to five (1–5) / six to ten (6–10) / more than ten (>10)
one to five (1–5) / six to ten (6–10)
one to five (1–5)
one to five (1–5)
six to ten (6–10)
six to ten (6–10)
six to ten (6–10)
six to ten (6–10)
six to ten (6–10)
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledonae
Eudicotyledonae
Commelinidae
Ceratophyllaceae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Superrosidae
Malvidae
Fabidae



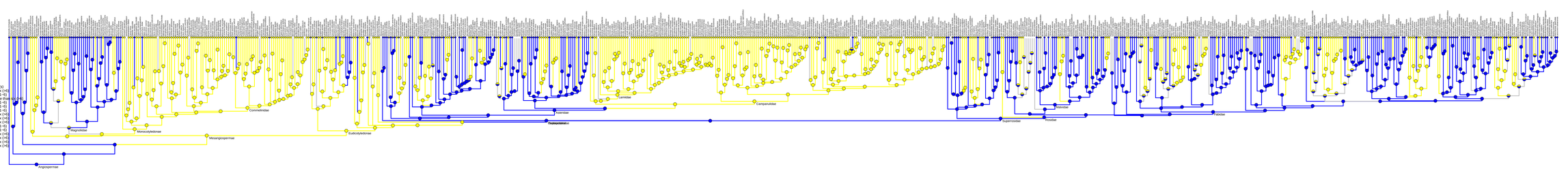
Model	LogL	Nparam	AIC	AICc	Delta AICc	AICc Weight
ARD	-493.78	6	999.56	999.68	2.15	0.2496
ARDeq**	-493.7	6	997.4	997.52	0	0.7504
ER	-534	1	1070.01	1070.03	72.51	0
SYM	-527.35	3	1060.71	1060.8	63.28	0.0169
SYMeq	-527.35	3	1061.19	1061.28	63.76	0.0133
ORD	-507.3	4	1022.61	1022.69	25.17	0.0998
ORDeq	-506.79	4	1021.57	1021.62	24.11	0
ORDSYM	-530.84	2	1065.69	1065.7	68.19	0
ORDSYMeq	-530.47	2	1064.94	1064.96	67.45	0
ORDER	-530.88	1	1063.77	1063.77	66.26	0

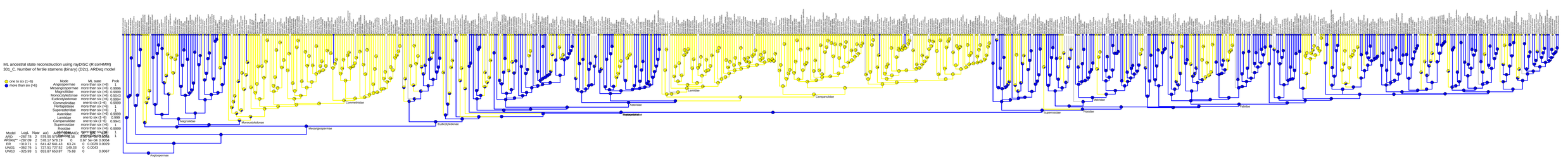
Angiospermae	more than ten (>10)	0.9998
Mesangiospermae	more than ten (>10)	0.9998
Magnoliidae	more than ten (>10)	0.999
Monocotyledoneae	six to ten (6–10)	0.5435
Eudicotyledoneae	more than ten (>10)	0.9998
Commelinidae	more than ten (>10)	0.9997
Gunneridae	more than ten (>10)	1
Superasteridae	more than ten (>10)	1
Asteridae	more than ten (>10)	0.9975
Lamiidae	more than ten (>10)	0.9998
Campanulidae	more than ten (>10)	0.9998
Rosidae	more than ten (>10)	0.9998
Malvidae	more than ten (>10)	0.9998
Superrosidae	more than ten (>10)	0.9998
Tracheophyta	more than ten (>10)	0.9998

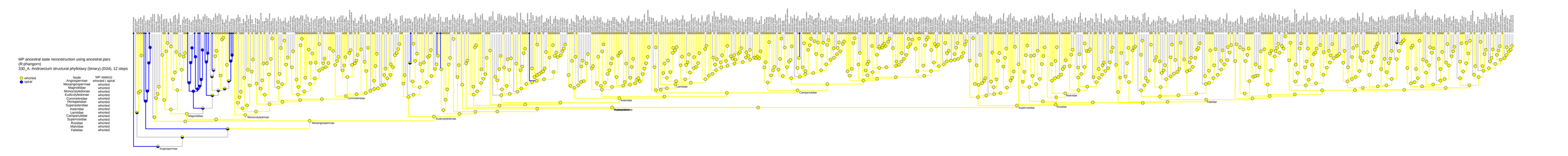
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
301_C: Number of fertile stamens (binary) (D2c), 92 steps

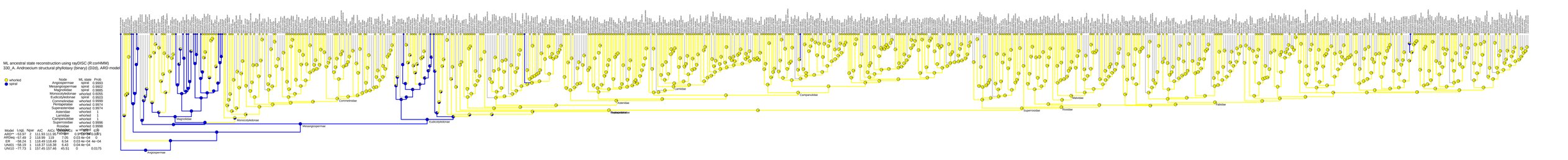
one to six (1–6)
more than six (>6)

Node	MP state(s)
Angiospermae	more than six (>6)
Mesangiospermae	one to six (1–6)
Magnoliidae	one to six (1–6) / more than six (>6)
Monocotyledonae	one to six (1–6)
Eudicotyledonae	one to six (1–6)
Commelinidae	more than six (>6)
Gunneridae	more than six (>6)
Superasteridae	more than six (>6)
Asteridae	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 (R corHMM)
301_C: Number of fertile stamens (binary) (D2c), ARDeq model
one to six (1-6)
more than six (>6)
ML state Prob
Angiospermae more than six (>6) 1
Mesangiospermae more than six (>6) 0.9996
Magnoliidae more than six (>6) 0.9999
Monocotyledoneae more than six (>6) 0.5043
Eudicotyledonae more than six (>6) 0.9994
Commelinidae more than six (>6) 0.9999
Ceratophyllidae more than six (>6) 1
Superasteridae more than six (>6) 1
Asteridae more than six (>6) 0.9999
Lamiidae one to six (1-6) 0.999
Campanulidae one to six (1-6) 0.9941
Supercluster more than six (>6) 1
Rosidae more than six (>6) 0.9699
Malvidae more than six (>6) 1
Model LogL Nparam AIC AICc ΔAICc AICcWt
ARD -287.78 2 579.55 579.78 0 0.67
ARDeq** -287.09 2 578.17 578.19 0 0.67
ER -319.71 1 641.42 641.43 63.24 0
UN01 -363.76 1 727.51 727.52 149.33 0
UN10 -325.93 1 653.87 653.87 75.68 0
Sa-0004 0.0054
Sa-0029 0.0029
Sa-0043 0
Sa-0067 0
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledoneae
Eudicotyledoneae
Commelinidae
Ceratophyllidae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Supercluster
Rosidae
Malvidae

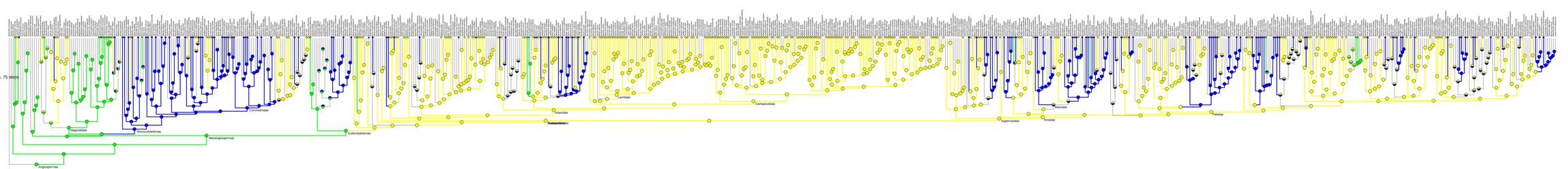

MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
330_A. Androecium structural phyllotaxy (binary) (D2d), 12 steps
whorled
spiral
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledonae
Eudicotyledonae
Commelinidae
Ceratophyllidae
Nymphaeidae
Schisandraceae
Asteridae
Lamiidae
Campanulidae
Supersrosidae
Rosidae
Malvidae
Fabidae
Node
MP state(s)
Angiospermae whorled/spiral
Mesangiospermae whorled
Magnoliidae whorled
Monocotyledonae whorled
Eudicotyledonae whorled
Commelinidae whorled
Ceratophyllidae whorled
Nymphaeidae whorled
Schisandraceae whorled
Asteridae whorled
Lamiidae whorled
Campanulidae whorled
Supersrosidae whorled
Rosidae whorled
Malvidae whorled
Fabidae whorled

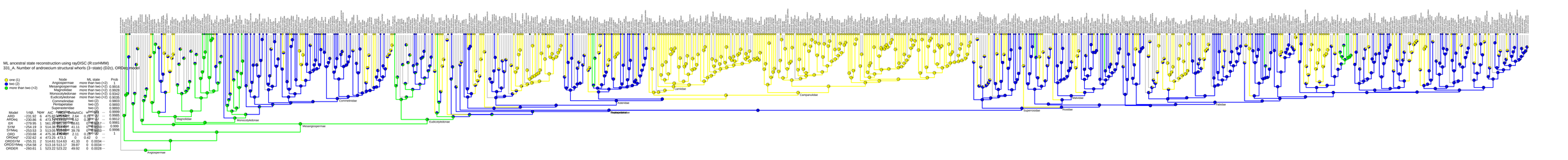

ML ancestral state reconstruction using rayDISC (R:corHMM)
330_A. Androecium structural phylotasy (binary) (D20), ARD model
whorled
spiral
Node ML state Prob
Angiospermae spiral 0.9999
Mesangiospermae spiral 0.9963
Magnoliidae spiral 0.9885
Monocotyledonae whorled 0.6055
Eudicotyledonae spiral 0.9503
Commelinidae whorled 0.9999
Ceratopsioids whorled 0.9974
Saxifragales whorled 0.974
Asteridae whorled 1
Lamiidae whorled 1
Campanulidae whorled 1
Superrosidae whorled 0.9996
Rosidae whorled 0.9999
Malvidae whorled 1
Fabidae whorled 0.9999
Model Logl Npar AIC AICc ΔAICc AICw
ARD** -53.97 2 111.93 111.95 0 0.9999
ARDeq -57.49 2 118.99 119 7.05 0.03
ER -58.24 1 118.49 118.49 6.54 0.03
UN01 -58.19 1 118.37 118.38 6.43 0.04
UN10 -77.73 1 157.45 157.46 45.51 0
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledonae
Eudicotyledonae
Commelinidae
Ceratopsioids
Saxifragales
Asteridae
Lamiidae
Campanulidae
Superrosidae
Rosidae
Malvidae
Fabidae

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	one (1)
Zingiberidae	one (1)
Syringaceae	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)

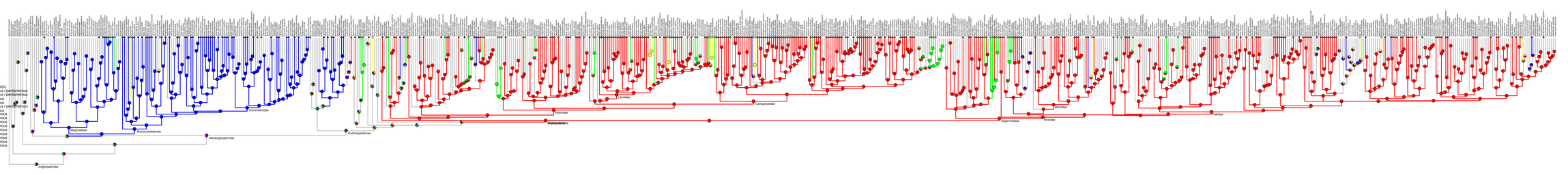


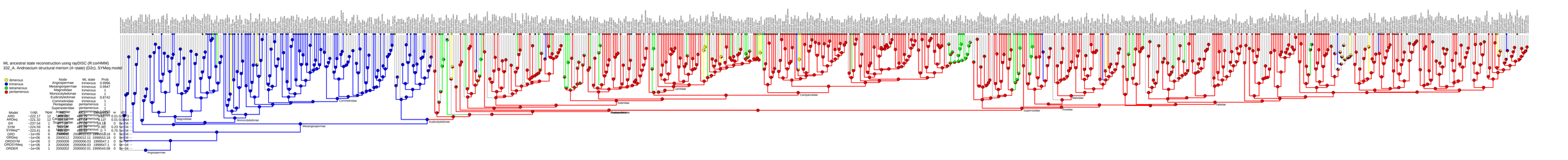

ML ancestral state reconstruction using rayDISC (R:corHMM)
331_A. Number of androecium structural whorls (3=state) (Ddo), ORDER.model
one (1)
two (2)
more than two (>2)
Node
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledoneae
Eudicotyledoneae
Commelinidae
Core Eudicotyledoneae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Superrosidae
Rosidae
Malvidae
Fabidae
ML state
more than two (>2)
more than two (>2)
more than two (>2)
more than two (>2)
two (2)
two (2)
two (2)
two (2)
two (2)
two (2)
Prob
0.9914
0.9928
0.9342
0.9035
0.9883
0.9883
0.9893
0.9999
0.9985
0.9912
0.9951
0.9999
0.9996
Model LogL Npar AIC AICc ΔAICc AICw
ARD −231.92 6 475.83 476.64 0.27 0.1
ARDeq −230.86 6 473.72 474.52 0 0.34
ER −279.95 1 561.89 561.91 87.39 0
ERSYM −253.53 3 513.06 513.15 38.63 0
SYMeq −253.53 3 513.06 513.15 38.63 0
ORD −233.68 4 475.36 475.61 0.98 0.21
ORDeq −232.62 4 473.25 473.5 0.87 0.21
ORDSYM −255.31 2 514.61 514.63 41.33 0
ORDSYMeq −254.58 2 513.16 513.17 39.87 0
ORDER −260.81 1 523.22 523.22 49.92 0
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledoneae
Eudicotyledoneae
Commelinidae
Core Eudicotyledoneae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Superrosidae
Rosidae
Malvidae
Fabidae

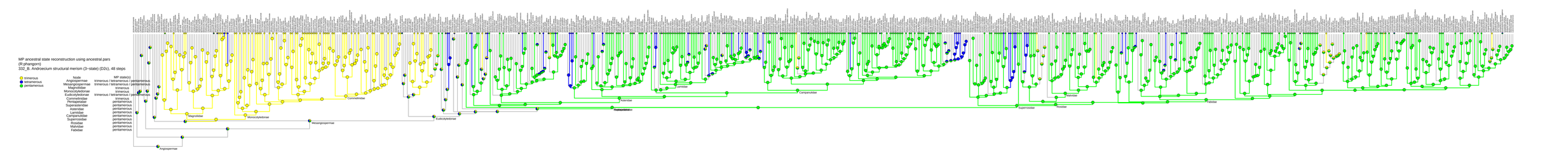
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
332_A. Androecium structural merism (4~state) (D2c), 57 steps

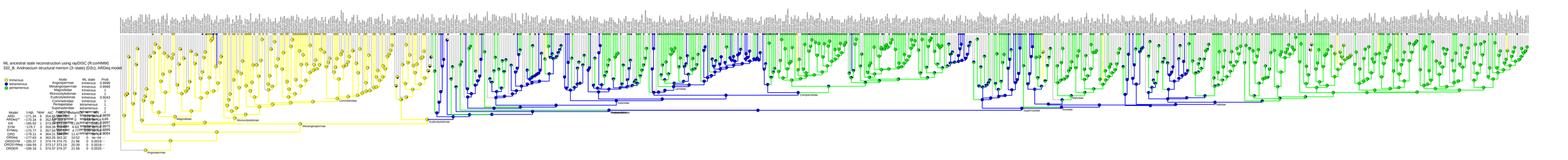
- dimerous
- trimerous
- tetramerous
- pentamerous

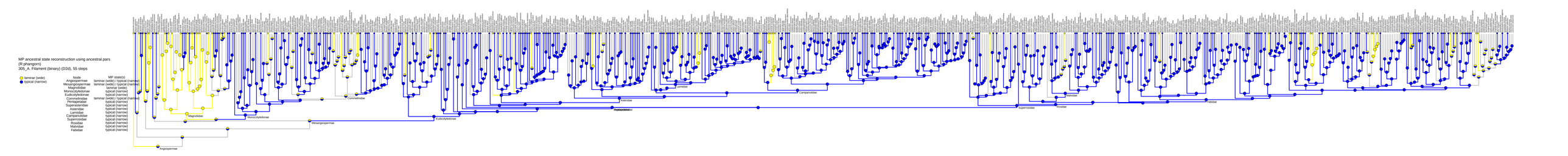
Node	MP state(s)
Angiospermae	trimerous / pentamerous
Mesangiospermae	trimerous / tetramerous / pentamerous
Magnoliidae	trimerous
Monocotyledoneae	trimerous
Eudicotyledoneae	trimerous / tetramerous / pentamerous
Commelinidae	trimerous
Ranunculidae	pentamerous
Superasteridae	pentamerous
Asteridae	pentamerous
Lamiidae	pentamerous
Campanulidae	pentamerous
Superrosidae	pentamerous
Rosidae	pentamerous
Malvidae	pentamerous
Fabidae	pentamerous

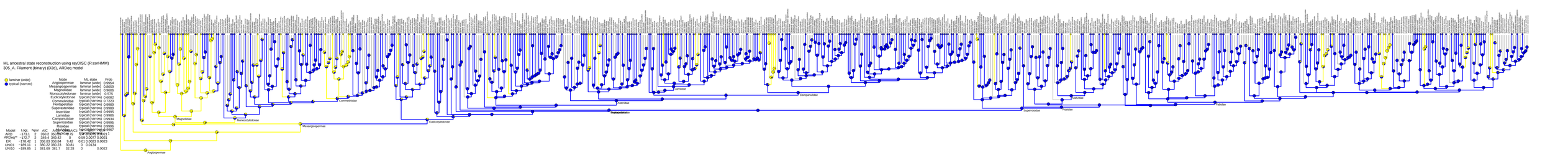



ML ancestral state reconstruction using ratDISC (R:corHMM)
332_A. Androecium structural merism (4−state) (Dzi), SYMeq model
dimerous
trimerous
tetramerous
pentamerous
Node ML state Prob
Angiospermae trimerous 0.9996
Mesangiospermae trimerous 0.947
Magnoliidae trimerous 1
Monocotyledonae trimerous 1
Eudicotyledonae trimerous 0.8742
Commelinidae trimerous 1
Dilleniidae pentamerous 1
Superasteridae pentamerous 1
Asteridae pentamerous 0.9999
Lamiidae pentamerous 1
Campanulidae pentamerous 1
Asterales pentamerous 1
Model LogL Npar AICc ΔAICc w wDZ
ARD −222.17 12 469.79 469.79 0.01 0.0013
ARDeq −221.32 12 467.98 467.98 0.01 0.0014
ER −237.54 1 477.08 477.08 0 9e−04
ERSYM −233.54 6 479.44 479.44 0 9e−04
SYMeq** −223.41 6 459.17 459.17 0.75 0.75
ORD −1e+06 6 2000002 2000002.01 1999553.18 0 9e−04
ORDeq −1e+06 6 2000012 2000012.11 1999553.18 0 9e−04
ORDSYM −1e+06 3 2000006 2000006.03 1999547.1 0 9e−04
ORDSYMeq −1e+06 3 2000006 2000006.03 1999547.1 0 9e−04
ORDER −1e+06 1 2000002 2000002.01 1999543.08 0 9e−04
Angiospermae
Magnoliidae
Monocotyledonae
Mesangiospermae
Eudicotyledonae
Commelinidae
Dilleniidae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Asterales
Superrosidae
Rosidae
Malvidae
Malvoidae
Rhoidae


MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
332_B. Androecium structural merism (3–state) (D2c), 48 steps
trimerous
tetramerous
pentamerous
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledonae
Eudicotyledonae
Commelinidae
Magnoliidae
Saxifragales
Rosidae
Asteridae
Lamiidae
Campanulidae
Superrosidae
Malvidae
Fabidae
MP state(s)
trimerous / pentamerous
trimerous / tetramerous / pentamerous
trimerous
trimerous
trimerous / tetramerous / pentamerous
trimerous
pentamerous
pentamerous
pentamerous
pentamerous
pentamerous
pentamerous
pentamerous
pentamerous
pentamerous
pentamerous
Commelinidae
Magnoliidae
Monocotyledonae
Mesangiospermae
Eudicotyledonae
Saxifragales
Rosidae
Asteridae
Lamiidae
Campanulidae
Superrosidae
Malvidae
Fabidae


ML ancestral state reconstruction using ratDISC (R:corHMM)
332_B. Androecium structural merism (3=state) (D2c), ARDeq model
trimerous
tetramerous
pentamerous
Node ML state Prob
Angiospermae trimerous 0.9999
Mesangiospermae trimerous 0.99
Magnoliidae trimerous 1
Monocotyledonae trimerous 1
Eudicotyledonae trimerous 0.9043
Commelinidae trimerous 1
Ceratophyllidae trimerous 1
Superasteridae tetramerous 1
Asteridae tetramerous 1
Rosidae tetramerous 0.8039
Saxifragales tetramerous 0.89
Vitales tetramerous 0.8997
Rosales tetramerous 0.8489
Fabidae tetramerous 0.8489
Malvidae tetramerous 0.8084
Model LogL Npar AIC AICc ΔAICc AICw
ARD −171.34 6 354.69 355.69 0 0.8039
ARDeq* −170.34 6 352.68 353.68 0 0.89
ER −185.92 1 373.84 373.87 20.19 0.0037
SYM −175.77 3 357.54 357.62 3.94 0.0257
SYMeq −175.77 3 357.54 357.62 3.94 0.0257
ORD −178.11 4 364.21 364.32 10.64 0.0084
ORDeq −177.63 4 363.26 363.32 10.52 0 4e−04 ~
ORDSYM −185.37 2 374.74 374.75 21.96 0 0.0019 ~
ORDSYMeq −184.59 2 373.17 373.19 20.39 0 0.0018 ~
ORDER −186.18 1 374.37 374.37 21.58 0 0.0026 ~
Angiospermae
Magnoliidae
Monocotyledonae
Commelinidae
Mesangiospermae
Eudicotyledonae
Ceratophyllidae
Superasteridae
Asteridae
Saxifragales
Vitales
Rosales
Fabidae
Malvidae
Malvidae
Rosidae
Fabidae
Vitales
Saxifragales
Asteridae
Superasteridae
Ceratophyllidae
Commelinidae
Eudicotyledonae
Monocotyledonae
Magnoliidae
Mesangiospermae
Angiospermae

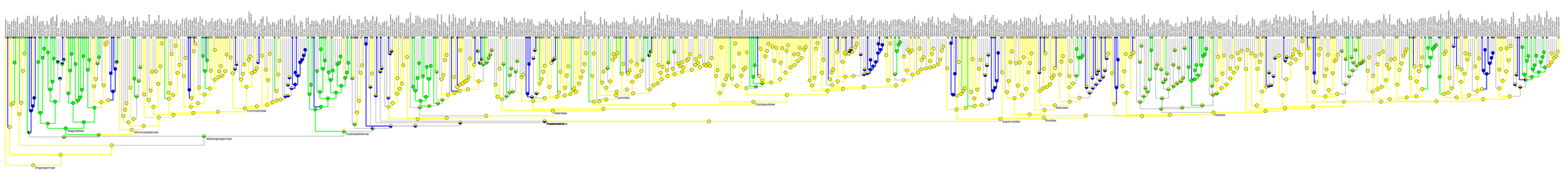

MP ancestral state reconstruction using ancestral.pars
(R phangorn)
305_A. Filament (binary) (D2d), 55 steps
laminar (wide)
typical (narrow)
Taxon
MP state(s)
Angiospermae
laminar (wide) / typical (narrow)
Mesangiospermae
laminar (wide) / typical (narrow)
Magnoliidae
laminar (wide)
Monocotyledonae
typical (narrow)
Eudicotyledonae
typical (narrow)
Commelinidae
laminar (wide) / typical (narrow)
Ceratophyllidae
typical (narrow)
Superasteridae
typical (narrow)
Asteridae
typical (narrow)
Lamiidae
typical (narrow)
Campanulidae
typical (narrow)
Superrosidae
typical (narrow)
Rosidae
typical (narrow)
Malvidae
typical (narrow)
Fabidae
typical (narrow)
Angiospermae
Magnoliidae
Monocotyledonae
Mesangiospermae
Eudicotyledonae
Commelinidae
Ceratophyllidae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Superrosidae
Rosidae
Malvidae
Fabidae

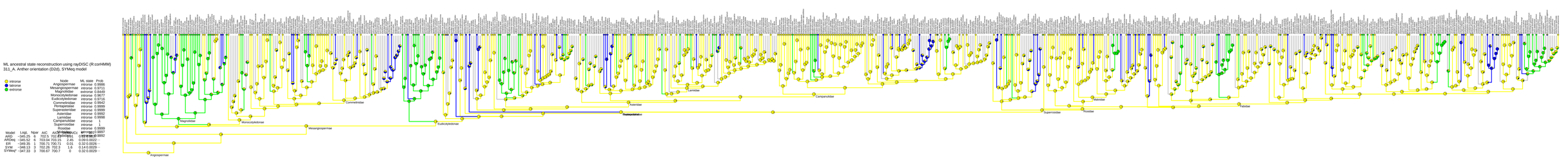

ML ancestral state reconstruction using rayDISC (R:corHMM)
305_A. Filament (binary) (D2d), ARDeq model
laminar (wide)
typical (narrow)
Node ML state Prob
Angiospermae laminar (wide) 0.7777
Mesangiospermae laminar (wide) 0.8659
Magnoliidae laminar (wide) 0.9606
Monocotyledonae laminar (wide) 0.575
Eudicotyledonae typical (narrow) 0.6082
Commelinidae typical (narrow) 0.7223
Ceratophyllum typical (narrow) 0.9999
Synapsiantheridae typical (narrow) 0.9999
Asteridae typical (narrow) 0.9999
Lamiidae typical (narrow) 0.9986
Campanulidae typical (narrow) 0.9934
Superasteridae typical (narrow) 0.9995
Asterales typical (narrow) 0.9997
Model LogL Nparam AIC AICc ΔAICc AICw
ARD −173.1 2 350.2 350.79 0 0.9999
ARDeq** −172.7 2 349.4 349.42 0 0.59
ER −176.42 1 358.83 358.84 9.42 0.01
UN01 −189.11 1 380.22 380.23 30.81 0
UN10 −189.85 1 381.69 381.7 32.28 0
0.0001
0.0001
0.0023
0.0023
0.0134
0.0002
Angiospermae
Magnoliidae
Monocotyledonae
Mesangiospermae
Eudicotyledonae
Commelinidae
Ceratophyllum
Synapsiantheridae
Asteridae
Lamiidae
Campanulidae
Superasteridae
Asterales
Rosidae
Malvidae
Malvaceae
Fabidae

MP ancestral state reconstruction using ancestral.pars
(R phangorn)
311_A. Anther orientation (D2d), 109 steps

- intorse
- latrorse
- extrorse

Node	MP state(s)
Angiospermae	intorse
Mesangiospermae	intorse / extrorse
Magnoliidae	extrorse
Monocotyledonae	intorse
Eudicotyledonae	intorse / extrorse
Commelinidae	intorse
Pentapetalae	intorse / latrorse
Superasteridae	intorse / latrorse
Asteridae	intorse
Lamiidae	intorse
Campanulidae	intorse
Superrosidae	intorse
Rosidae	intorse
Malvidae	intorse
Fabidae	intorse

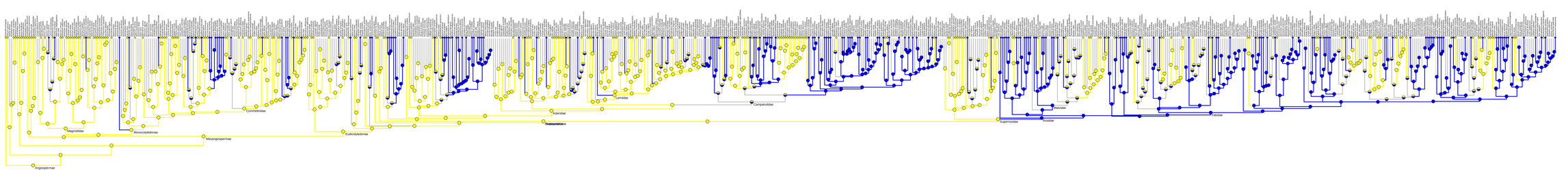


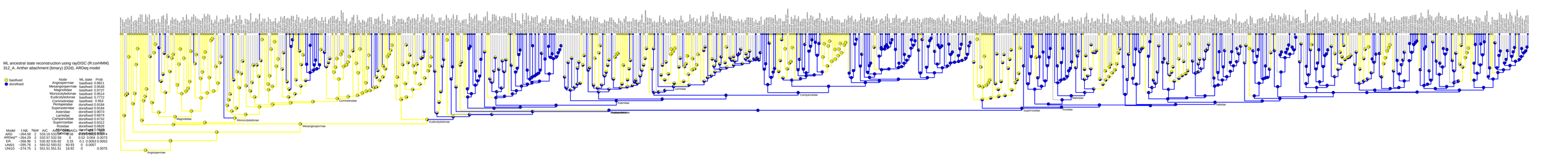

ML ancestral state reconstruction using ray.DISC (R::corHMM)
311_A. Anther orientation (D2d), SYMeq model
intorse
latorse
extorse
Model LogL Npar AIC AICc ΔAICc AICw
ARD −345.25 6 702.5 702.87 0.00 0.9992
ARDeq −345.52 6 703.04 703.15 2.45 0.0029
ER −349.35 1 700.71 700.71 0.01 0.32
SYM −348.13 3 702.26 702.3 1.6 0.14
SYMeq* −347.33 3 700.67 700.7 0 0.32
State ML state Prob
Angiospermae intorse 0.9999
Mesangiospermae intorse 0.9711
Magnoliidae extorse 0.8449
Monocotyledoneae intorse 0.9677
Eudicotyledoneae intorse 0.9716
Commelinidae intorse 0.9942
Ceratophyllales intorse 0.9999
Santalanae intorse 0.9999
Asteridae intorse 0.9992
Lamiidae intorse 0.9998
Campanuliidae intorse 1
Superrosidae intorse 1
Malvidae intorse 0.9999
Rosidae intorse 0.9997
Fabidae intorse 0.9992
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledoneae
Eudicotyledoneae
Commelinidae
Ceratophyllales
Santalanae
Asteridae
Lamiidae
Campanuliidae
Superrosidae
Malvidae
Rosidae
Fabidae

MP ancestral state reconstruction using ancestral.pars
(R phangorn)
312_A. Anther attachment (binary) (0/2d), 98 steps

basifixed
dorsifixed

Node	MP state(s)
Angiospermae	basifixed
Mesangiospermae	basifixed
Magnoliidae	basifixed
Monocotyledonae	basifixed
Eudicotyledonae	basifixed
Commelinidae	basifixed
Ceratophyllidae	basifixed
Santalales/Caryophyllidae	basifixed
Asteridae	basifixed
Lamiidae	basifixed
Campanuloidae	basifixed / dorsifixed
Superrosidae	basifixed
Rosidae	basifixed
Malvidae	dorsifixed
Fabidae	dorsifixed

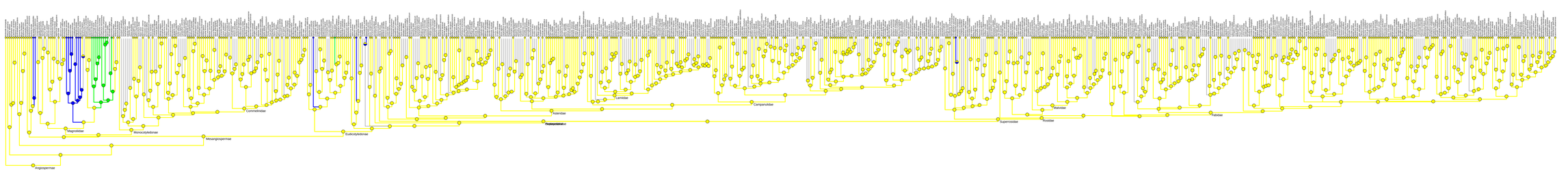


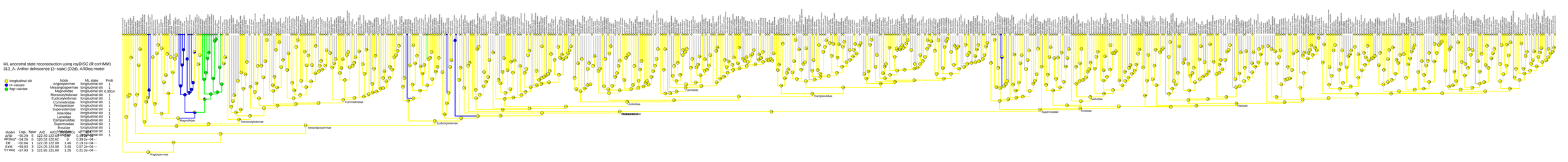

ML ancestral state reconstruction using rayDISC (R:corHMM)
312_A. Anther attachment (binary) (D2di), ARDeq model
basifixed
dorsifixed
Node ML state Prob.
Angiospermae basifixed 0.9999
Mesangiospermae basifixed 0.9548
Magnoliidae basifixed 0.9737
Monocotyledonae basifixed 0.9514
Eudicotyledonae basifixed 0.7772
Commelinidae basifixed 0.5533
Hamamelidae basifixed 0.9184
Superasteridae dorsifixed 0.9184
Asteridae dorsifixed 0.9073
Lamiidae dorsifixed 0.6674
Campanulidae dorsifixed 0.9732
Superrosidae dorsifixed 0.9312
Rosidae dorsifixed 0.9312
Malvidae dorsifixed 0.7428
Brassicales dorsifixed 0.6664
Model LogL Npar AIC AICc ΔAICc Weight
ARD -264.58 2 533.16 533.59 0.58 0.4286
ARDeq** -264.29 2 532.57 532.59 0 0.574
ER -266.96 1 535.92 535.92 3.33 0.1
UN01 -265.76 1 533.52 533.52 0.93 0.0653
UN10 -274.75 1 551.51 551.51 18.92 0.0007
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledonae
Eudicotyledonae
Commelinidae
Hamamelidae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Superrosidae
Rosidae
Malvidae
Brassicales

MP ancestral state reconstruction using ancestral.pars
(R phangorn)
313_A. Anther dehiscence (3-state) (02d), 10 steps

- longitudinal slit
- In−valvate
- Rap−valvate

Node	MP state(s)
Angiospermae	longitudinal slit
Mesangiospermae	longitudinal slit
Magnoliidae	longitudinal slit
Monocotyledonae	longitudinal slit
Eudicotyledonae	longitudinal slit
Commelinidae	longitudinal slit
Arecidae	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

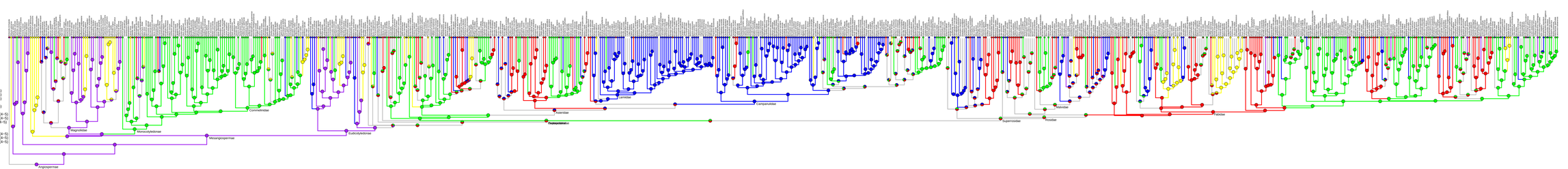



ML ancestral state reconstruction using rayDISC (R::corHMM)
313_A. Anther dehiscence (3=stam) (0203), ARDeq model
longitudinal slit
1= valvate
Rap= valvate
Model LogL Npar AIC AICc
ARD -55.29 6 122.59 122.69
ARDeq* -54.26 6 120.52 120.62
ER -60.04 1 122.08 122.09
SYM -59.03 3 124.05 124.08
SYMeq -57.93 3 121.85 121.89
Node ML state Prob
Angiospermae longitudinal slit 1
Mesangiospermae longitudinal slit 1
Magnoliidae longitudinal slit 0.9914
Monocotyledoneae longitudinal slit 1
Eudicotyledoneae longitudinal slit 1
Commelinidae longitudinal slit 1
Gunneridae longitudinal slit 1
Superasteridae longitudinal slit 1
Asteridae longitudinal slit 1
Lamiidae longitudinal slit 1
Campanulidae longitudinal slit 1
Superrosidae longitudinal slit 1
Rosidae longitudinal slit 1
Malvidae longitudinal slit 1
Rosidae longitudinal slit 1
Fabidae longitudinal slit 1
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledoneae
Eudicotyledoneae
Commelinidae
Gunneridae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Superrosidae
Rosidae
Malvidae
Fabidae

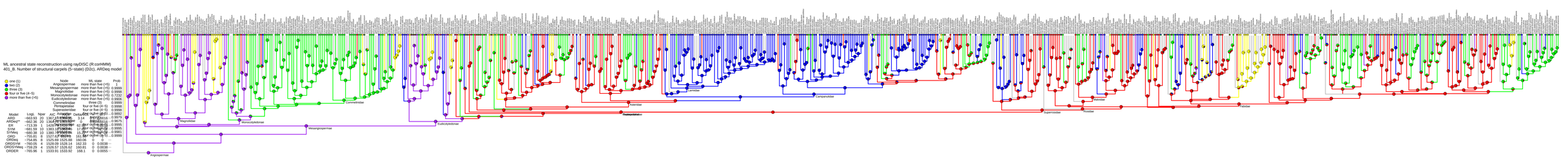
MP ancestral state reconstruction using ancestral.pars
(R phangorn)
401_B. Number of structural carpels (5–state) (D2c), 197 steps

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)
Monocotyledoneae	three (3)
Eudicotyledonae	more than five (>5)
Commelinidae	two (2)
Ceratophyllidae	three (3) / four or five (4–5)
Superasteridae	three (3) / four or five (4–5)
Asteridae	two (2) / four or five (4–5)
Lamiidae	two (2)
Campanulidae	two (2)
Superrosidae	three (3) / four or five (4–5)
Rosidae	three (3) / four or five (4–5)
Malvidae	three (3) / four or five (4–5)
Fabidae	four or five (4–5)



ML ancestral state reconstruction using rayDISC (R:corHMM)
401_B. Number of structural carpels (5-state) (0/2c), ARDeq model



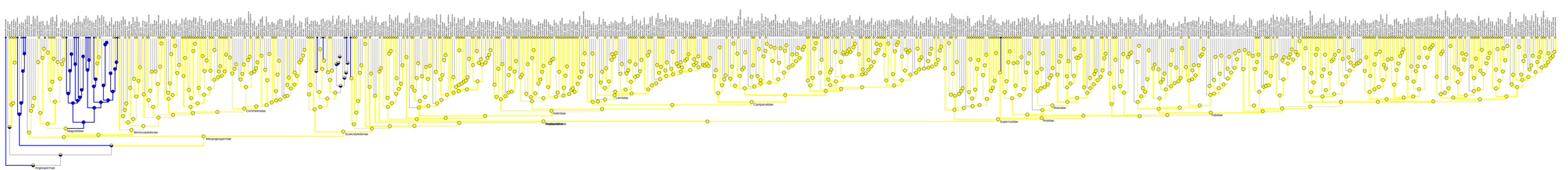
Model	LogL	Npar	AIC	AICc	Delta_AICc	AICw
ARD	-663.93	20	1367.87	1368.96	3.14	0.0016
ARDeq*	-662.36	20	1364.72	1365.81	0	0.0079
ER	-713.39	1	1428.78	1428.82	62.99	0.0000
SYM	-690.38	10	1400.76	1401.19	35.38	0.0000
SYMeq	-690.38	10	1380.76	1381.19	15.38	0.0061
ORD	-755.81	8	1527.62	1528.05	161.24	0.0000
ORDeq	-754.85	8	1525.69	1525.88	160.06	0
ORDSYM	-760.05	4	1528.09	1528.14	162.33	0
ORDSYMeq	-759.29	4	1526.57	1526.62	160.81	0
ORDER	-765.96	1	1533.91	1533.92	168.1	0

Node	ML state	Pr(d)
Angiospermae	more than five (>5)	—
Mesangiospermae	more than five (>5)	0.9999
Magnoliidae	more than five (>5)	0.9998
Monocotyledoneae	more than five (>5)	0.7232
Eudicotyledoneae	more than five (>5)	0.9906
Commelinidae	more than five (>5)	0.9999
Gunneridae	four or five (4–5)	0.9999
Superasteridae	four or five (4–5)	0.9998
Asteridae	four or five (4–5)	0.9992
Pentapetalae	four or five (4–5)	0.9979
Rosidae	four or five (4–5)	0.9975
Superrosidae	four or five (4–5)	0.9995
Malvidae	four or five (4–5)	0.9981
Rosidae	four or five (4–5)	0.9999

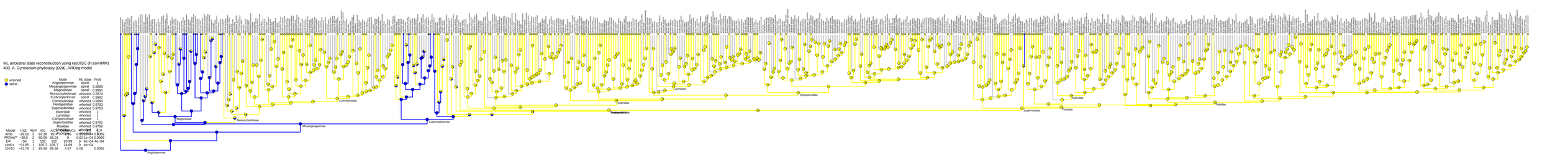
MP ancestral state reconstruction using ancestral.pars
(R phangorn)
400_A. Gynoecium phyllotaxy (D2d), 10 steps

whorled
spiral

Node	MP state(s)
Angiospermae	whorled / spiral
Mesangiospermae	whorled
Magnoliidae	whorled
Monocotyledonae	whorled
Eudicotyledonae	whorled
Commelinidae	whorled
Ceratophyllidae	whorled
Nymphaeidae	whorled
Schisandraceae	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. Cynoecium phylotaxy (D2d), ARDeq model



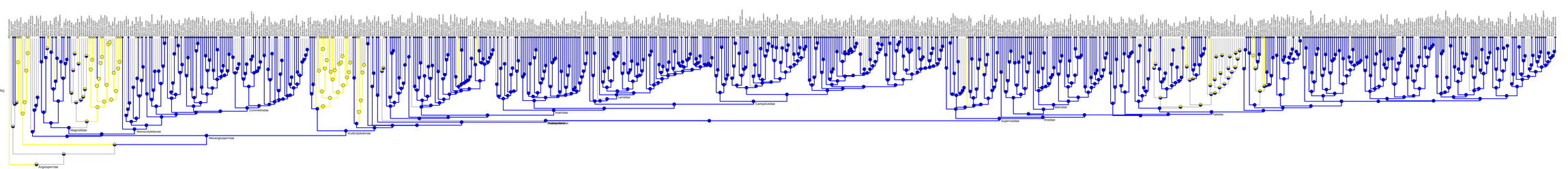
Node	ML state	Prob
Angiospermae	spiral	0.9999
Mesangiospermae	spiral	0.9999
Magnoliidae	spiral	0.9991
Monocotyledonae	whorled	0.5674
Eudicotyledonae	spiral	0.9992
Gunneridae	whorled	0.9999
Pentapetalae	whorled	0.9753
Superrosidae	whorled	0.9993
Asteridae	whorled	1
Lamiidae	whorled	1
Campanulidae	whorled	1
Superasteridae	whorled	0.9791
Rosidae	whorled	0.9999
Malvidae	whorled	410
Fabidae	whorled	0.9999

Model	LogL	Npar	AIC	AICc	ΔAICc	Weight	q12	q21
ARD	-39.19	2	82.38	82.77	0	0.99	0.0099	0.0099
ARDeq**	-38.5	2	80.99	81.01	0	0.82	1e-04	0.0099
ER	-50	1	102	102	20.99	0	4e-04	4e-04
UN01	-51.85	1	105.7	105.7	24.69	0	4e-04	
UN10	-41.79	1	85.58	85.58	4.57	0.06		0.0082

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%)
Gentianidae	fused (>5%)
Superasteridae	fused (>5%)
Asteridae	fused (>5%)
Lamiidae	fused (>5%)
Campanuliidae	fused (>5%)
Superrosidae	fused (>5%)
Rosidae	fused (>5%)
Malvidae	fused (>5%)
Fabidae	fused (>5%)



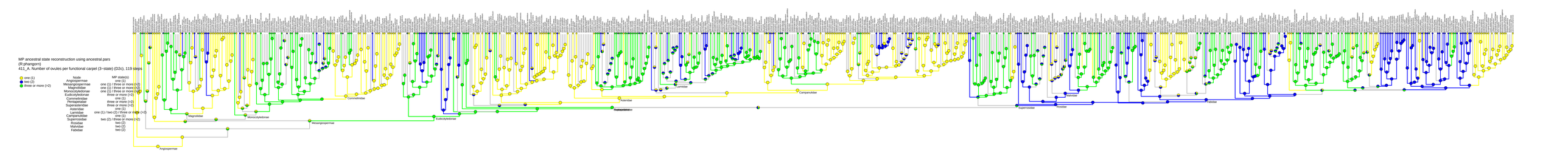
ML ancestral state reconstruction using rayDISC (R:corHMM) 403_A. Fusion of ovaries (binary) (DDJ), ARDeq model

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

Node	ML state	Prob
Angiospermae	free (>5%)	1
Mesangiospermae	free (>5%)	0.9998
Magnoliidae	free (>5%)	0.9991
Monocotyledonae	free (>5%)	0.9043
Eudicotyledonae	free (>5%)	0.9975
Commelinidae	free (>5%)	0.9999
Gentianidae	fused (>5%)	0.9864
Solanoplantiidae	fused (>5%)	1
Asteridae	fused (>5%)	1
Lamiidae	fused (>5%)	1
Campanulidae	fused (>5%)	1
Superrosidae	fused (>5%)	0.9995
Rosidae	fused (>5%)	0.9944
Malvidae	fused (>5%)	0.9918
Brassicales	fused (>5%)	0.9946

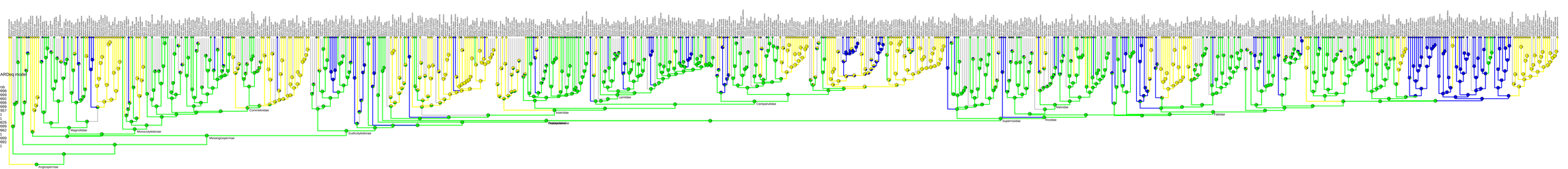
Model	LogL	Nparam	AIC	AICc	ΔAICc	AICcWt	Weight
ARD	−94.59	2	193.19	193.38	0	0.65	0.0047
ARDeq**	−93.9	2	191.81	191.82	0	0.65	0.0047
ER	−100.62	1	203.23	203.24	11.42	0	7e−04
UN01	−99.42	1	198.84	198.85	7.02	0.02	0.0098
UN10	−105.87	1	213.73	213.74	21.91	0	8e−04

Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledonae
Eudicotyledonae
Commelinidae
Gentianidae
Solanoplantiidae
Asteridae
Lamiidae
Campanulidae
Superrosidae
Rosidae
Malvidae
Brassicales


MP ancestral state reconstruction using ancestral.pars
(R phangorn)
411_A. Number of ovules per functional carpel (3–state) (D2c), 119 steps
one (1)
two (2)
three or more (>2)
Angiospermae
Amborellaceae
Mesangiospermae
Magnoliidae
Monocotyledonae
Eudicotyledonae
Commelinidae
Ceratophyllidae
Chloranthaceae
Piperales
Saxifragales
Asteridae
Lamiidae
Campanulidae
Dipsacales
Rosidae
Fabidae
Malvidae
Brassicaceae
Cleomaceae
Caricaceae
Malvaceae
Sapindaceae
Rutaceae
Geraniaceae
Vitaceae
Myrtaceae
Lythraceae
Onagraceae
Cucurbitaceae
Fabaceae
Rosaceae
Elaeagnaceae
Cannabaceae
Moraceae
Urticaceae
Fagaceae
Betulaceae
Juglandaceae
Salicaceae
Euphorbiaceae
Linaceae
Oxalidaceae
Celastraceae
Ericaceae
Primulaceae
Ebenaceae
Sapotaceae
Styracaceae
Oleaceae
Gentianaceae
Apocynaceae
Rubiaceae
Caprifoliaceae
Adoxaceae
Asteraceae
Solanaceae
Convolvulaceae
Boraginaceae
Lamiaceae
Orobanchaceae
Plantaginaceae
Bignoniaceae
Scrophulariaceae
Phrymaceae
Verbenaceae
Acanthaceae
Gesneriaceae
Campanulaceae
Goodeniaceae
Menyanthaceae
Asparagales
Liliales
Alismatales
Arecaceae
Poales
Commelinaceae
Zingiberales
Musaceae
Cannaceae
Marantaceae
Costaceae
Heliconiaceae
Strelitziaceae
Lowiaceae
Zingiberaceae
Costaceae
Hanguanaceae
Dasypogonaceae
Asteliaceae
Boryaceae
Hypoxidaceae
Ixioliriaceae
Tecophilaeaceae
Doryanthaceae
Iridaceae
Xeronemataceae
Asphodelaceae
Amaryllidaceae
Agavaceae
Anthericaceae
Hemerocallidaceae
Xanthorrhoeaceae
Alliaceae
Colchicaceae
Melanthiaceae
Petrosaviaceae
Nartheciaceae
Tofieldiaceae
Alismataceae
Araceae
Hydrocharitaceae
Potamogetonaceae
Juncaginaceae
Scheuchzeriaceae
Aponogetonaceae
Cymodoceaceae
Posidoniaceae
Ruppiaceae
Zannichelliaceae
Zosteraceae
Arecaceae
Dioscoreaceae
Pandanaceae
Stemonaceae
Cyclanthaceae
Typhaceae
Bromeliaceae
Rapateaceae
Xyridaceae
Eriocaulaceae
Mayacaceae
Juncaceae
Thurniaceae
Cyperaceae
Poaceae
Ecdeiocoleaceae
Centrolepidaceae
Restionaceae
Joinvilleaceae
Flagellariaceae
Hydatellaceae
Triuridaceae
Petrosaviaceae
Nartheciaceae
Tofieldiaceae
Alismataceae
Araceae
Hydrocharitaceae
Potamogetonaceae
Juncaginaceae
Scheuchzeriaceae
Aponogetonaceae
Cymodoceaceae
Posidoniaceae
Ruppiaceae
Zannichelliaceae
Zosteraceae
Arecaceae
Dioscoreaceae
Pandanaceae
Stemonaceae
Cyclanthaceae
Typhaceae
Bromeliaceae
Rapateaceae
Xyridaceae
Eriocaulaceae
Mayacaceae
Juncaceae
Thurniaceae
Cyperaceae
Poaceae
Ecdeiocoleaceae
Centrolepidaceae
Restionaceae
Joinvilleaceae
Flagellariaceae
Hydatellaceae
Triuridaceae

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

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

Model	LogL	Nparam	AIC	AICc	ΔAICc	AICcWt	Pchisq
ARD	-386.52	6	785.04	785.26	0	0.9999	1
ARDeq**	-385.58	6	783.16	783.38	-1.88	0.9999	0.9962
ER	-399.73	1	801.46	801.48	16.22	0	1
SYM	-398.54	3	803.08	803.19	17.93	0.0001	0.9999
SYMeq	-398.54	3	803.08	803.19	17.93	0.0001	0.9992
ORD	-395.26	4	798.52	798.67	13.41	0.0012	1
ORDeq	-399.2	4	806.4	806.45	21.18	0	0.0019
ORDSYM	-410.96	2	825.92	825.94	42.67	0	0.0051
ORDSYMeq	-410.72	2	825.43	825.45	42.18	0	0.0051
ORDER	-412.02	1	826.04	826.04	42.77	0	0.0059

ML state	Prob
Angiospermae three or more (>2)	0.9998
Menangiospermae three or more (>2)	0.9998
Magnoliidae three or more (>2)	0.9992
Monocotyledoneae three or more (>2)	0.9996
Eudicotyledoneae three or more (>2)	0.9999
Commelinidae three or more (>2)	0.7857
Liliidae three or more (>2)	1
Superasteridae three or more (>2)	1
Asteridae three or more (>2)	0.9826
Lamiidae three or more (>2)	0.9999
Campanulidae three or more (>2)	0.9962
Asterales three or more (>2)	1
Rosidae three or more (>2)	0.9999
Fabidae three or more (>2)	0.9992
Malvidae three or more (>2)	1