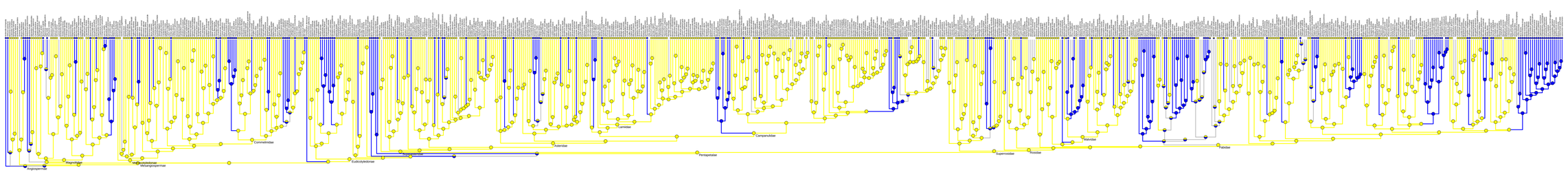
MP ancestral state reconstruction using ancestral.pars
(R phangorn)
100_A. Functional sex of flowers (D2d), 98 steps

bisexual
unisexual

Node	MP state(s)
Angiospermae	bisexual / unisexual
Mesangiospermae	bisexual
Magnoliidae	bisexual
Monocotyledonae	bisexual
Eudicotyledonae	bisexual
Commelinidae	bisexual
Ceratophyllidae	bisexual
Superasteridae	bisexual
Asteridae	bisexual
Lamidae	bisexual
Campanulidae	bisexual
Superrosidae	bisexual
Rosidae	bisexual
Malvidae	bisexual
Fabidae	bisexual

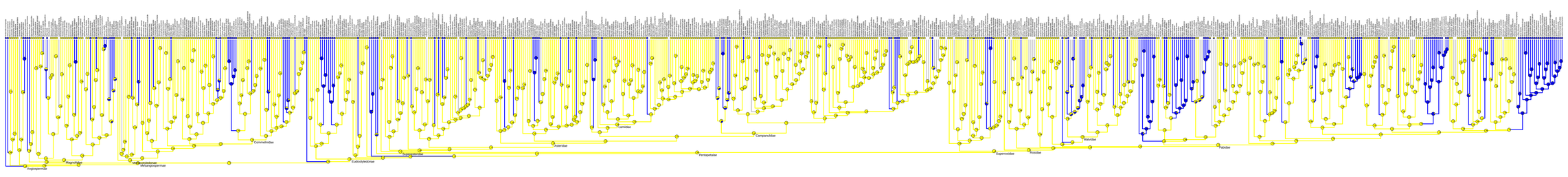


ML ancestral state reconstruction using rayDISC (R:corHMM)
100_A. Functional sex of flowers (0/2d), ARDeq model

bisexual
unisexual

Node	ML state	Prob
Angiospermae	bisexual	1
Mesangiospermae	bisexual	1
Magnoliidae	bisexual	1
Monocotyledonae	bisexual	1
Eudicotyledonae	bisexual	1
Commelinidae	bisexual	1
Gunneridae	bisexual	1
Superasteridae	bisexual	1
Asteridae	bisexual	1
Lamidae	bisexual	1
Campanulidae	bisexual	0.9993
Asteridae	bisexual	1
Rosidae	bisexual	1
Malvidae	bisexual	0.9997
Fabidae	bisexual	1

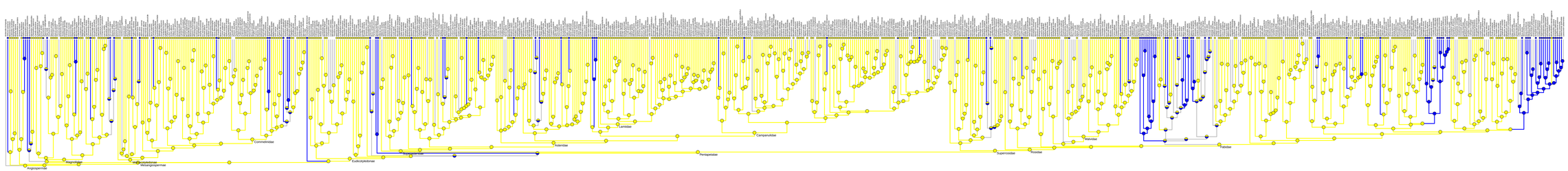
Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	-312.55	2	629.11	629.12	1.38	0.24	0.003	8e−04
ARDeq*	-311.86	2	627.73	627.74	0	0.47	0.003	8e−04
ER	-315.27	1	632.54	632.54	4.8	0.04	0.0029	0.0029
UN01	-313.49	1	628.98	628.98	1.24	0.25	0.003	
UN10	-354.49	1	710.98	710.99	83.24	0		0.0119



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

bisexual
unisexual

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

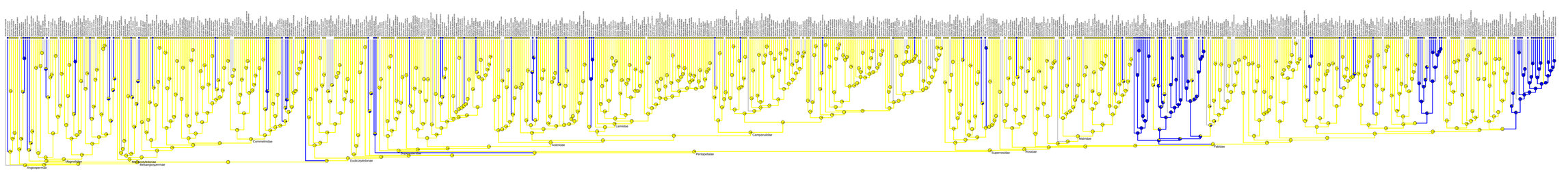


ML ancestral state reconstruction using rayDISC (R:corHMM)
100_B. Structural sex of flowers (D2d), ARDeq model

bisexual
unisexual

Node	ML state	Prob
Angiospermae	bisexual	1
Mesangiospermae	bisexual	1
Magnoliidae	bisexual	1
Monocotyledonae	bisexual	1
Eudicotyledonae	bisexual	1
Commelinidae	bisexual	0.9999
Ceratophyta	bisexual	1
Superasteridae	bisexual	1
Asteridae	bisexual	1
Lamidae	bisexual	0.9999
Campanulidae	bisexual	1
Pentapetalae	bisexual	1
Rosidae	bisexual	1
Malvidae	bisexual	1
Fabidae	bisexual	0.9977

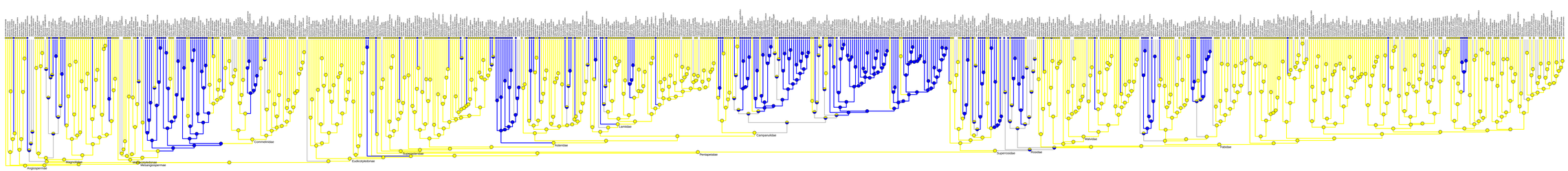
Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	−208.28	2	420.56	420.56	1.36	0.28	0.0015	0.0039
ARDeq**	−207.9	1	419.2	419.22	0	0.55	0.0015	0.0039
ER	−209.74	1	421.47	421.48	2.26	0.18	0.0016	0.0016
UN01	−226.92	1	455.84	455.85	35.63	0	0.0017	
UN10	−231.58	1	465.15	465.16	45.94	0		0.0167



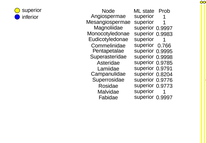
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
102_B. Ovary position (binary) (0/2d), 79 steps

superior
inferior

Node	MP state(s)
Angiospermae	superior
Mesangiospermae	superior
Magnoliidae	superior
Monocotyledonae	superior
Eudicotyledonae	superior
Commelinidae	superior
Ceratophyllum	superior
Superasteridae	superior
Asteridae	superior
Lamiidae	superior
Campanulidae	superior
Superrosidae	superior
Rosidae	superior / inferior
Malvidae	superior
Fabidae	superior

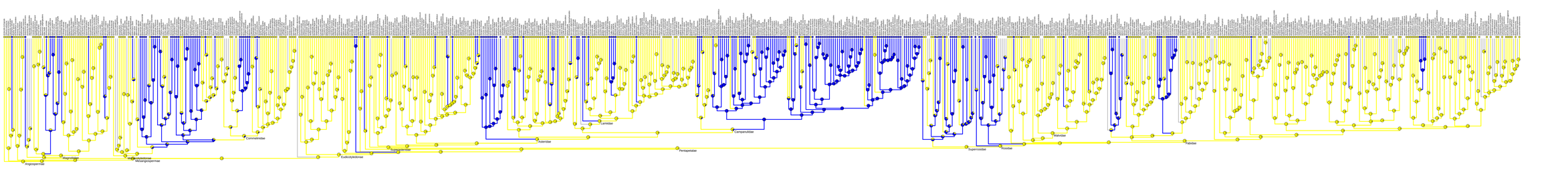


ML ancestral state reconstruction using rayDISC (R:corHMM)
102_B. Ovary position (binary) (02d), ARDeq model



Node	ML state	Prob
Angiospermae	superior	1
Mesangiospermae	superior	1
Magnoliidae	superior	0.9997
Monocotyledonae	superior	0.9983
Eudicotyledonae	superior	1
Commelinidae	superior	0.765
Gunneridae	superior	0.9998
Superasteridae	superior	0.8568
Asteridae	superior	0.9785
Lamidae	superior	0.9791
Campanulidae	superior	0.8204
Asteridae	superior	0.9785
Rosidae	superior	0.9773
Malvidae	superior	1
Fabidae	superior	0.9997

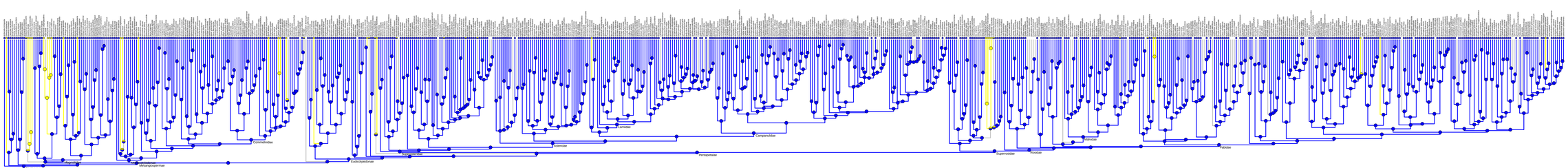
Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	-272.01	2	548.03	548.04	1.38	0.25	0.0021	0.0036
ARDeq*	-271.32	2	546.65	546.66	0	0.49	0.0021	0.0036
ER	-272.95	1	547.89	547.9	1.24	0.26	0.0024	0.0024
UN01	-281.44	1	564.88	564.89	18.23	0	0.0027	
UN10	-294.63	1	591.27	591.27	44.61	0		0.0099



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
Ceratophyllum	present
Superasteridae	present
Asteridae	present
Lamiidae	present
Campanulidae	present
Superrosidae	present
Rosidae	present
Malvidae	present
Fabidae	present

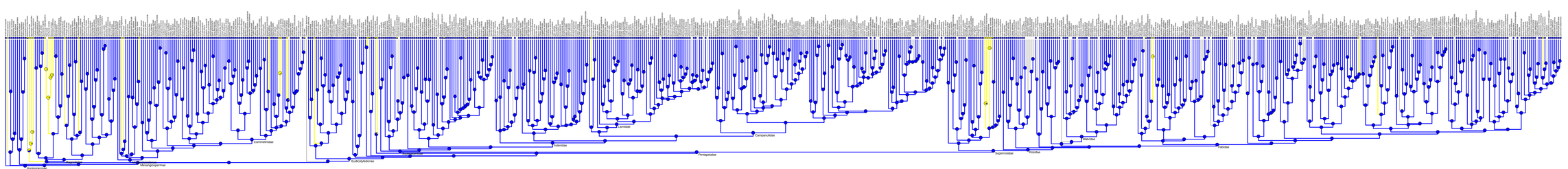


ML ancestral state reconstruction using rayDISC (R:corHMM)
201_A. Perianth presence (D2c), UNI10 model

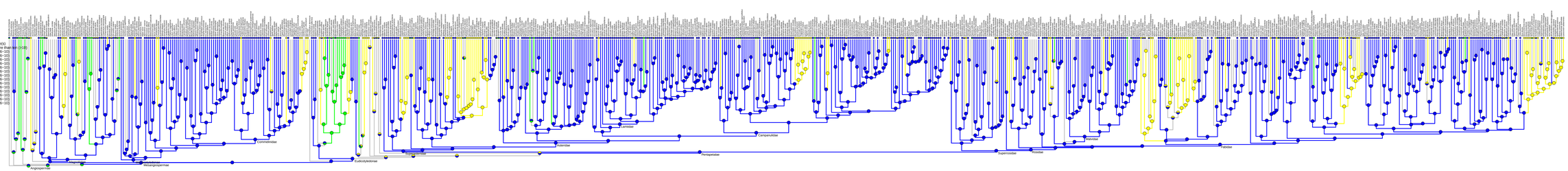
absent
present

Node	ML state	Prob
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
Lamidae	present	1
Campanulidae	present	1
Pentapetalae	present	1
Rosidae	present	1
Malvidae	present	1
Fabidae	present	1

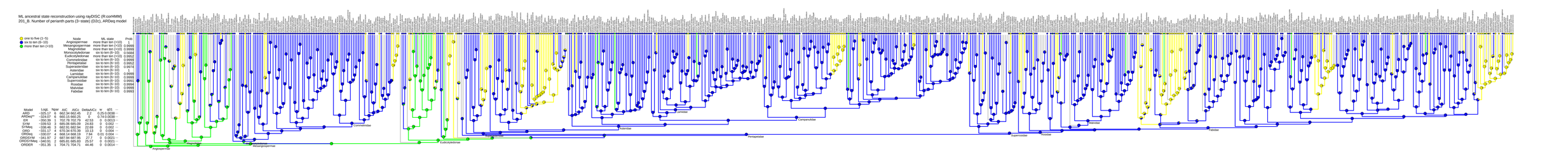
Model	LogL	Nparam	AICc	AICc_Delta	AICc_w	q01	q10
ARD	-96.83	2	197.67	197.69	2.01	0.13	0 5e−04
ARDeq	-96.14	2	196.28	196.3	0.62	0.26	0 5e−04
ER	-97.11	1	196.21	196.22	0.54	0.27	5e−04 5e−04
UNI01	-109.88	1	221.76	221.76	26.09	0	0.0224
UNI10*	-96.83	1	195.67	195.67	0	0.35	5e−04



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



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



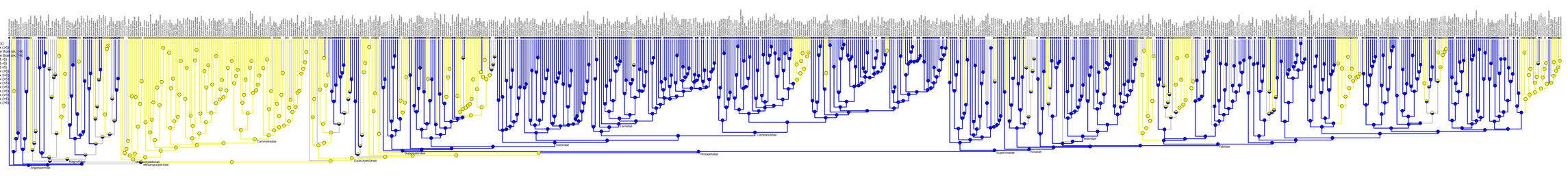
Node	ML state	Prob
Angiospermae	more than ten (>10)	1
Mesangiospermae	more than ten (>10)	0.9998
Magnoliidae	more than ten (>10)	0.9998
Monocotyledonae	six to ten (6–10)	0.5684
Eudicotyledonae	more than ten (>10)	0.9952
Commelinidae	six to ten (6–10)	0.9998
Gunneridae	six to ten (6–10)	0.9998
Superasteridae	six to ten (6–10)	0.9974
Asteridae	six to ten (6–10)	1
Lamiidae	six to ten (6–10)	0.9998
Campanulidae	six to ten (6–10)	0.9998
Caryophyllales	six to ten (6–10)	0.9994
Rosidae	six to ten (6–10)	0.9994
Malvidae	six to ten (6–10)	0.9998
Fabidae	six to ten (6–10)	0.9993

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	--
ARD	-325.17	6	662.34	662.45	2.2	0.25	0.0038	--
ARDeq**	-324.07	6	660.15	660.25	0	0.74	0.0038	--
ER	-350.39	1	702.78	702.79	42.53	0	0.0013	--
SYM	-338.46	3	682.92	682.94	22.69	0	0.002	--
SYMeq	-338.46	3	682.91	682.94	22.69	0	0.002	--
ORD	-331.17	4	670.34	670.39	10.13	0	0.004	--
ORDeq	-330.07	4	668.14	668.19	7.94	0.01	0.004	--
ORDSYM	-341.97	2	687.94	687.95	27.7	0	0.0021	--
ORDSYMeq	-340.91	2	685.81	685.83	25.57	0	0.0021	--
ORDER	-351.35	1	704.71	704.71	44.46	0	0.0014	--

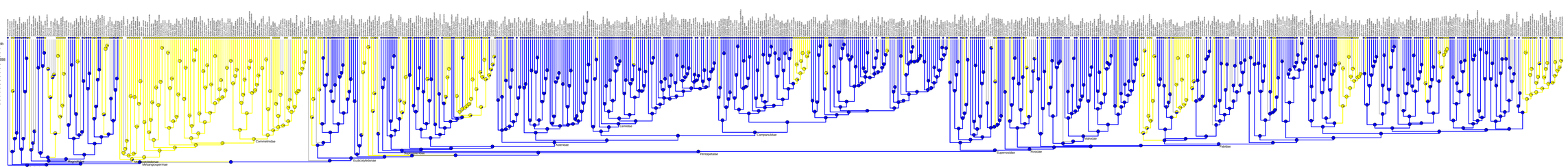
MP ancestral state reconstruction using ancestral pars
(R phangorn)
201_C. Number of perianth parts (binary) (D/2c), 69 steps

one to six (1–6)
more than six (>6)

Node	MP state(s)
Angiospermae	more than six (>6)
Mesangiospermae	one to six (1–6) / 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	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 periianth parts (binary) (D2c), ARDeq model

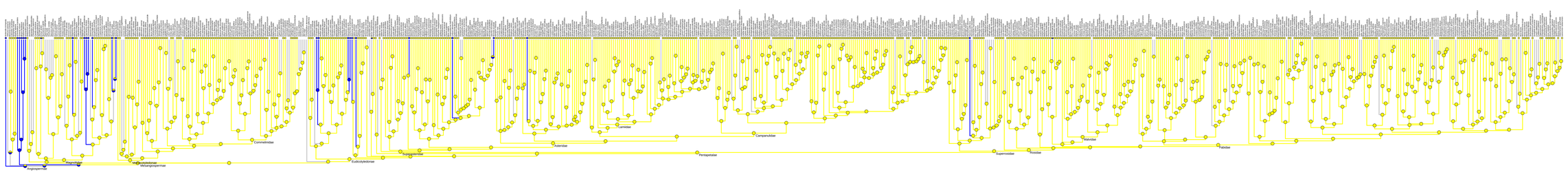


Model	LogL	Nopr	AIC	AICc	DeltaAICc	w	q01	q10
ARD	−247.75	2	499.51	499.52	1.39	0.33	6e−04	0.0026
ARDeq**	−247.06	2	498.12	498.14	0	0.66	6e−04	0.0026
ER	−254.33	1	510.67	510.67	12.54	0	0.0022	0.0022
UN01	−323.73	1	649.46	649.46	151.32	0	0.0083	
UN10	−252.79	1	507.58	507.59	9.45	0.01		0.0029

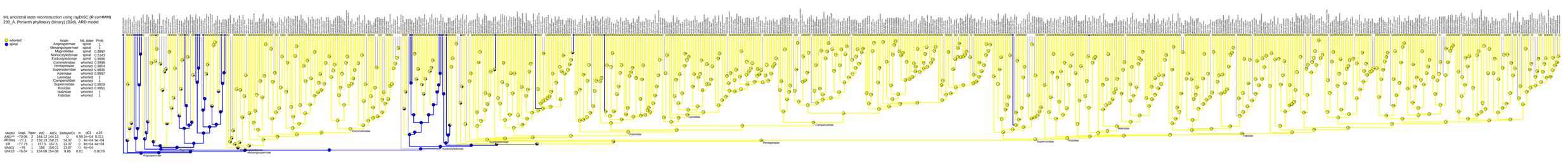
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
230_A. Perianth phyllotaxy (binary) (D2d), 16 steps

verticil
spiral

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



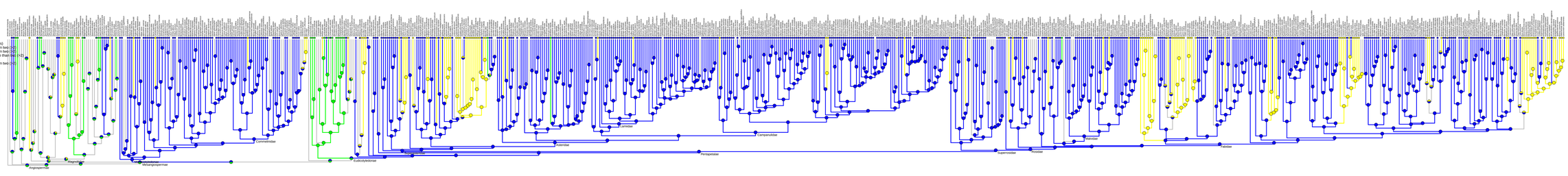
ML ancestral state reconstruction using rayDISC (R:corHMM)
230_A. Perianth phyllotaxy (binary) (D2d), ARD model

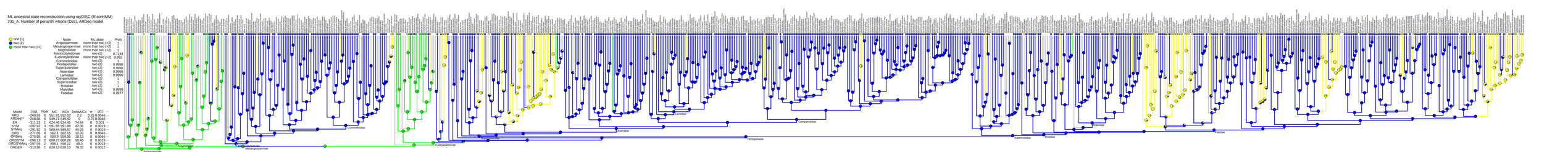


MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
231_A. Number of perianth whorls (D2c), 73 steps

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

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

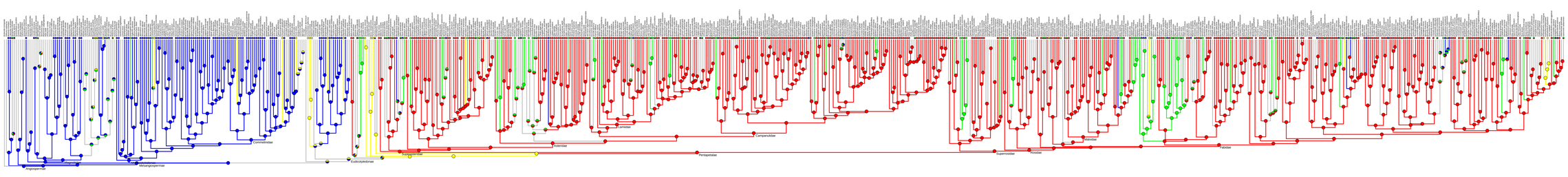



ML ancestral state reconstruction using rayDISC (R corHMM)
231_A. Number of perianth whorls (D2c), ARDeq model
one (1)
two (2)
more than two (>2)
Node ML state Prob
Angiospermae more than two (>2) 1
Mesangiospermae more than two (>2) 1
Magnoliidae more than two (>2) 1
Monocotyledonae two (2) 0.7194
Eudicotyledonae more than two (>2) 0.992
Commelinidae two (2)
Ceratophyllum two (2) 0.9998
Superasteridae two (2) 0.9998
Asteridae two (2) 0.9998
Lamiidae two (2) 0.9999
Campanulidae two (2) 1
Saxifragales two (2) 1
Rosidae two (2) 1
Malvidae two (2) 0.9999
Fabidae two (2) 0.9977
Model LogL Npar AIC AICc DeltaAICc w q01 ...
ARD ~269.95 6 551.91 552.02 2.2 0.25 0.0046 ...
ARDeq** ~268.86 6 549.71 549.82 0 0.75 0.0046 ...
ER ~311.23 1 624.46 624.46 74.64 0 0.001 ...
SYM ~311.23 3 628.46 628.57 78.75 0 0.0019 ...
SYMeq ~291.92 3 589.84 589.97 40.05 0 0.0019 ...
ORD ~277.05 4 562.1 562.15 12.33 0 0.0045 ...
ORDeq ~275.95 4 559.9 559.95 10.13 0 0.0045 ...
ORDSYM ~298.13 2 600.27 600.28 50.46 0 0.0019 ...
ORDSYMeq ~297.05 2 598.1 598.12 48.3 0 0.0019 ...
ORDER ~313.56 1 629.13 629.13 79.32 0 0.0012 ...
Angiospermae
Magnoliidae
Mesangiospermae
Commelinidae
Monocotyledonae
Eudicotyledonae
Ceratophyllum
Superasteridae
Asteridae
Lamiidae
Campanulidae
Saxifragales
Pentapetalae
Rosidae
Fabidae
Malvidae
Rosales
Fabales

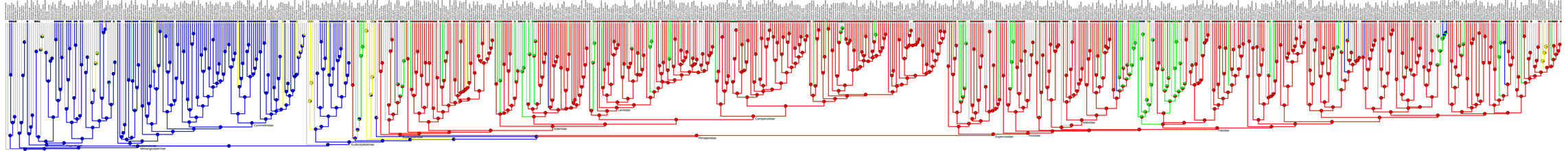
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
232_A. Perianth merism (4–state) (D2c), 84 steps

- dimerous
- trimerous
- tetramerous
- pentamerous

Node	MP state(s)
Angiospermae	trimerous
Mesangiospermae	trimerous
Magnoliidae	trimerous
Monocotyledonae	trimerous
Eudicotyledonae	dimerous / trimerous
Commelinidae	trimerous
Gunneridae	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)
232_A. Perianth merism (4–state) (D2c), SYMeq model

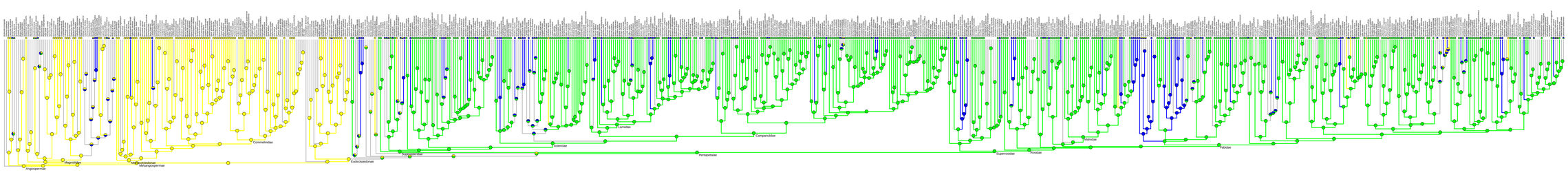


Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	...
ARD	-323.65	12	671.31	671.71	10.48	0	0	---
ARDeq	-322.29	12	668.57	669.08	7.75	0.02	0	---
ER	-360.68	1	723.35	723.36	62.13	0	8e−04	---
SYM	-324.56	6	661.12	661.22	0	0.98	0.0013	---
SYMeq	-324.56	6	661.12	661.22	0	0.98	0.0013	---
ORD	-336.72	6	685.43	685.54	24.32	0	0	---
ORDeq	-335.4	6	682.81	682.92	21.69	0	0	---
ORDSYM	-344.43	3	694.87	694.9	33.68	0	0.002	---
ORDSYMeq	-343.06	3	692.12	692.15	30.93	0	0.002	---
ORDER	-345.97	1	693.93	693.94	32.71	0	0.0025	---

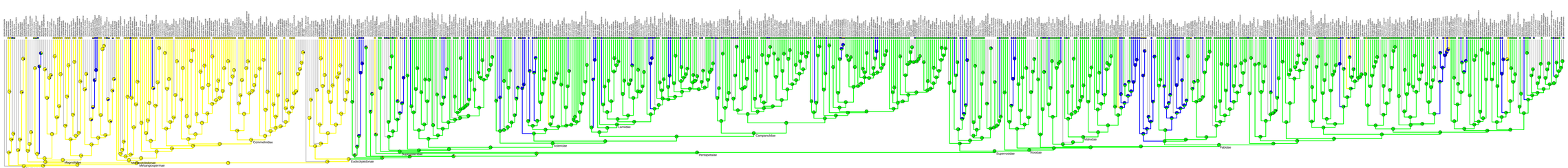
MP ancestral state reconstruction using ancestral.pars (R:phangorn)
232_B. Perianth merism (3–state) (D2c), 70 steps

trimerous
tetramerous
pentamerous

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

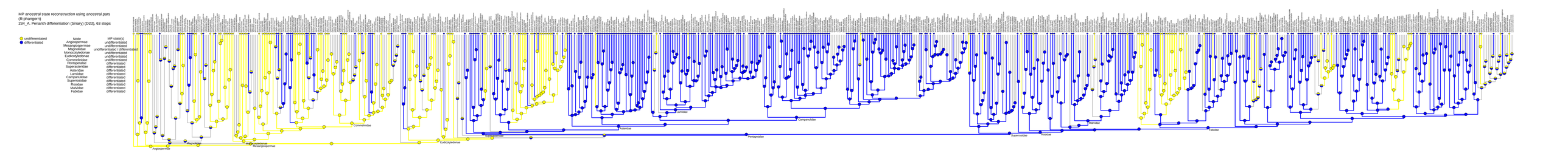


ML ancestral state reconstruction using ratDISC (R:corHMM)
232_8. Perianth merism (3–state) (D2c), SYMeq model

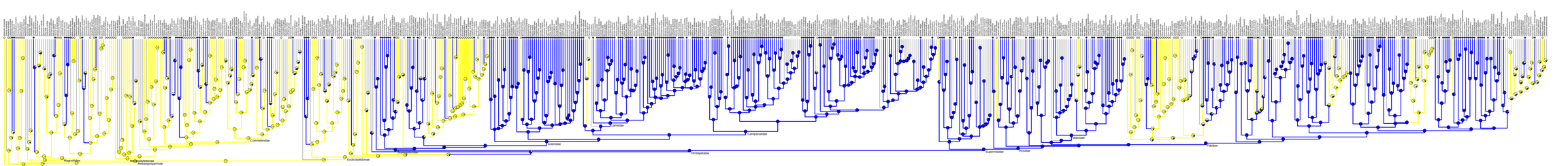


Node	ML state	Prob
Angiospermae	trimerous	1
Mesangiospermae	trimerous	1
Magnoliidae	trimerous	1
Monocotyledonae	trimerous	1
Eudicotyledonae	trimerous	0.9795
Commelinidae	trimerous	1
Core Eudicots	pentamerous	0.9998
Superasteridae	pentamerous	1
Asteridae	pentamerous	0.9999
Lamiidae	pentamerous	1
Campanulidae	pentamerous	1
Caryophyllales	pentamerous	1
Rosidae	pentamerous	1
Malvidae	pentamerous	1
Fabidae	pentamerous	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	...
ARD	-256.15	6	524.3	524.41	6.05	0.02	8e−04	...
ARDeq	-255.07	6	522.14	522.25	3.89	0.06	8e−04	...
ER	-291.41	1	564.83	564.83	46.47	0	0.0013	...
SYM	-256.17	3	518.33	518.36	0	0.42	0.001	...
SYMeq	-256.17	3	518.33	518.36	0	0.42	0.001	...
ORD	-256.99	4	521.98	522.03	3.67	0.07	0.001	...
ORDeq	-255.92	4	519.84	519.89	1.52	0.19	0.001	...
ORDSYM	-259.98	2	523.96	523.98	5.62	0.03	0.0015	...
ORDSYMeq	-258.89	2	521.79	521.79	3.43	0.07	0.0015	...
ORDER	-262.3	1	526.59	526.6	8.24	0.01	0.0024	...


MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
234_A. Periamth differentiation (binary) (D2d), 63 steps
undifferentiated
differentiated
Node
MP state(s)
Angiospermae
undifferentiated
Mesangiospermae
undifferentiated
Magnoliidae
undifferentiated / differentiated
Monocotyledonae
undifferentiated
Eudicotyledonae
undifferentiated
Commelinidae
undifferentiated
Ceratophyllidae
undifferentiated
Superasteridae
differentiated
Asteridae
differentiated
Lamiidae
differentiated
Campanulidae
differentiated
Superrosidae
differentiated
Rosidae
differentiated
Malvidae
differentiated
Fabidae
differentiated
Angiospermae
Magnoliidae
Mesangiospermae
Monocotyledonae
Eudicotyledonae
Commelinidae
Ceratophyllidae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Superrosidae
Rosidae
Malvidae
Fabidae

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



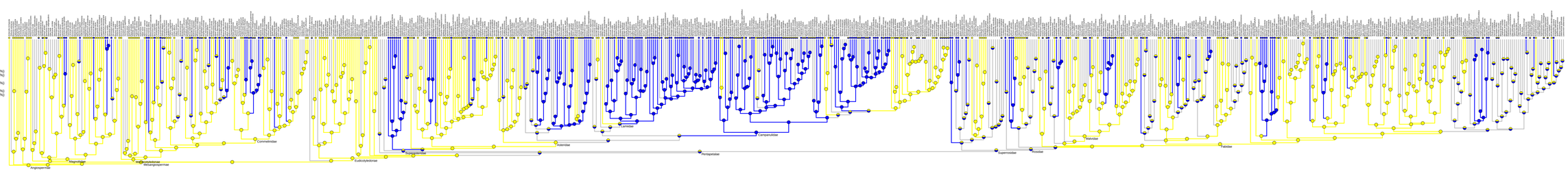
Node	ML state	Prob
Angiospermae	undifferentiated	1
Melanganospermae	undifferentiated	1
Magnoliidae	undifferentiated	0.9999
Monocotyledonae	undifferentiated	1
Eudicotyledonae	undifferentiated	0.9999
Commelinidae	undifferentiated	1
Caryophyllales	differentiated	0.9479
Superasteridae	differentiated	0.9402
Asteridae	differentiated	0.9982
Lamiidae	differentiated	0.9999
Campanulidae	differentiated	1
Santalales	differentiated	0.9921
Rosidae	differentiated	0.9953
Malvidae	differentiated	0.9989
Fabidae	differentiated	0.9872

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	−199.39	2	402.77	402.79	1.38	0.33	0.0045	0.0015
ARDeq**	−199.89	2	401.39	401.4	0	0.67	0.0045	0.0015
ER	−208.5	1	419	419	17.6	0	0.0025	0.0025
UN01	−225.54	1	453.09	453.09	51.69	0	0.0086	
UN10	−234.01	1	470.02	470.02	68.62	0		0.0034

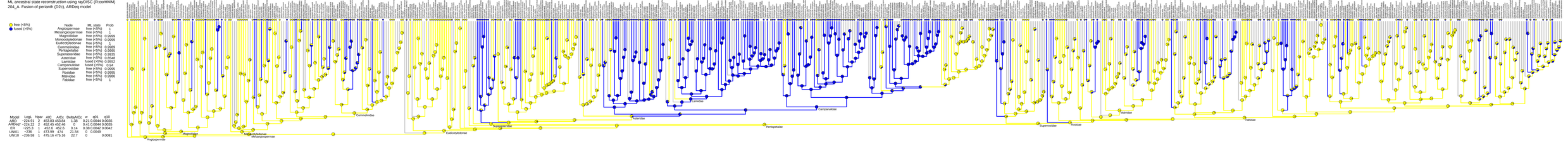
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
204_A. Fusion of perianth (D2c), 77 steps

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

Node	MP state(s)
Angiospermae	free (<5%)
Mesangiospermae	free (<5%)
Magnoliidae	free (<5%)
Monocotyledoneae	free (<5%)
Eudicotyledoneae	free (<5%)
Commelinidae	free (<5%)
Zingiberidae	free (<5%) / fused (>5%)
Superasteridae	free (<5%) / fused (>5%)
Asteridae	free (<5%)
Lamidae	free (<5%) / fused (>5%)
Campanulidae	fused (>5%)
Tetracoccae	free (<5%) / fused (>5%)
Rosidae	free (<5%) / fused (>5%)
Malvidae	free (<5%)
Fabidae	free (<5%)



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



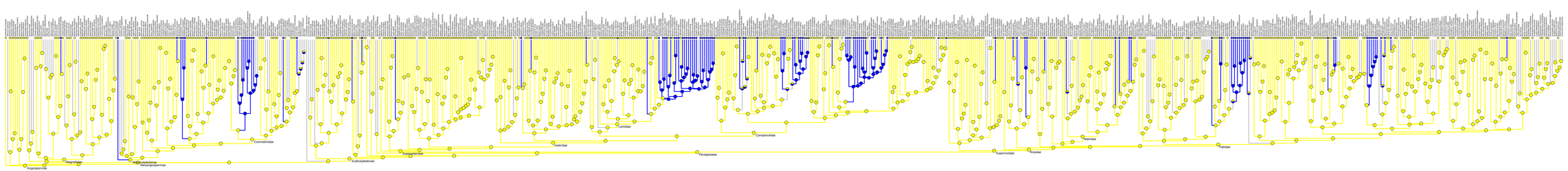
Node	ML state	Prob
Angiospermae	free (<5%)	1
Mesangiospermae	free (<5%)	1
Magnoliidae	free (<5%)	0.9999
Monocotyledonae	free (<5%)	0.9999
Eudicotyledonae	free (<5%)	1
Gunneridae	free (<5%)	0.9999
Pentapetalae	free (<5%)	0.9995
Superasteridae	free (<5%)	0.9935
Asteridae	free (<5%)	0.8548
Lamidae	fused (>5%)	0.9552
Campanulidae	fused (>5%)	0.94
Lamiidae	fused (>5%)	0.9945
Rosidae	free (<5%)	0.9995
Malvidae	free (<5%)	0.9986
Fabidae	free (<5%)	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	−224.91	2	453.83	453.84	1.38	0.21	0.0044	0.0035
ARDeq*	−224.22	2	452.45	452.46	0	0.41	0.0044	0.0035
ER	−225.3	1	452.6	452.6	0.14	0.38	0.0042	0.0042
UNI01	−236	1	473.99	474	21.54	0	0.0049	
UNI10	−236.58	1	475.16	475.16	22.7	0		0.0081

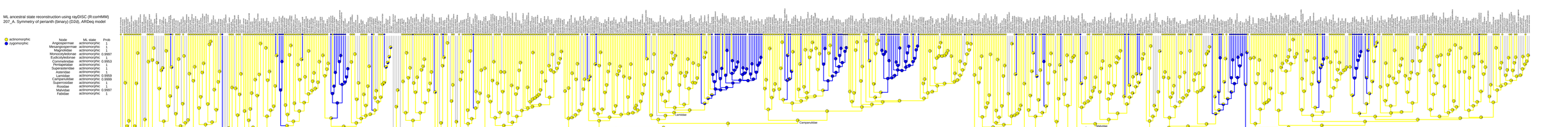
MP ancestral state reconstruction using ancestral.pars (R phangorn)
207_A. Symmetry of perianth (binary) (D2d), 55 steps

actinomorphic
zygomorphic

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



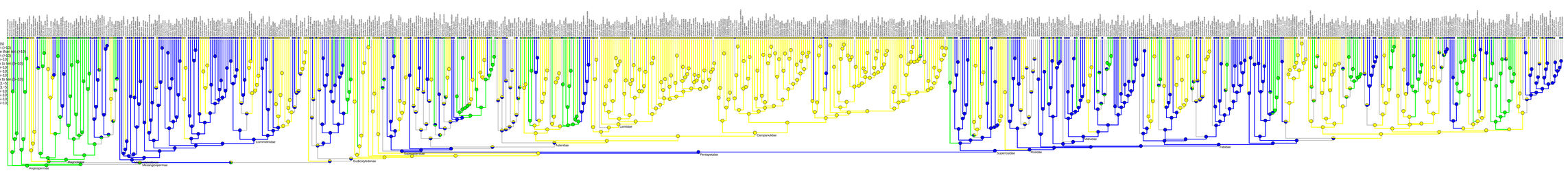
ML ancestral state reconstruction using ray|DISC (R:corHMM) 207_A: Symmetry of perianth (binary) (D2d), ARDeq model



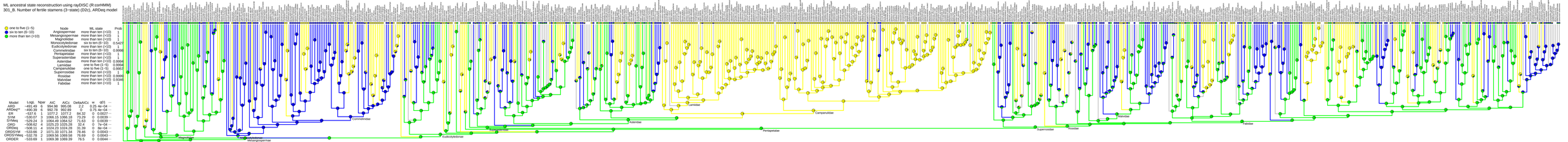
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
301_B. Number of fertile stamens (3–state) (D2c), 156 steps

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

Node	MP state(s)
Angiospermae	more than ten (>10)
Mesangiospermae	one to five (1–5) / more than ten (>10)
Magnoliidae	more than ten (>10)
Monocotyledonae	six to ten (6–10)
Eudicotyledonae	one to five (1–5) / six to ten (6–10)
Commelinidae	six to ten (6–10)
Gunneridae	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 (RcorHMM)
301_B. Number of fertile stamens (3–state) (D2c), ARDeq model



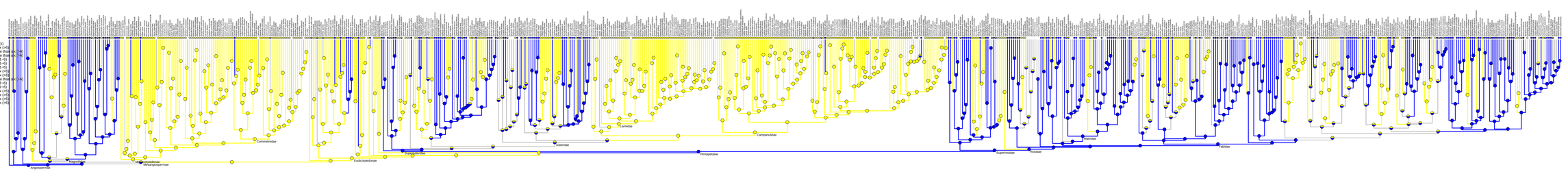
Node	ML state	Prob
Angiospermae	more than ten (>10)	1
Mesangiospermae	more than ten (>10)	1
Magnoliidae	more than ten (>10)	1
Monocotyledonae	six to ten (6–10)	0.5427
Eudicotyledonae	more than ten (>10)	1
Commelinidae	six to ten (6–10)	0.9996
Gunneridae	more than ten (>10)	1
Superasteridae	more than ten (>10)	1
Asteridae	more than ten (>10)	0.9994
Lamidae	one to five (1–5)	0.9958
Campanulidae	one to five (1–5)	0.9957
Caryophyllidae	more than ten (>10)	1
Rosidae	more than ten (>10)	0.9996
Malvidae	more than ten (>10)	0.9346
Fabidae	more than ten (>10)	1

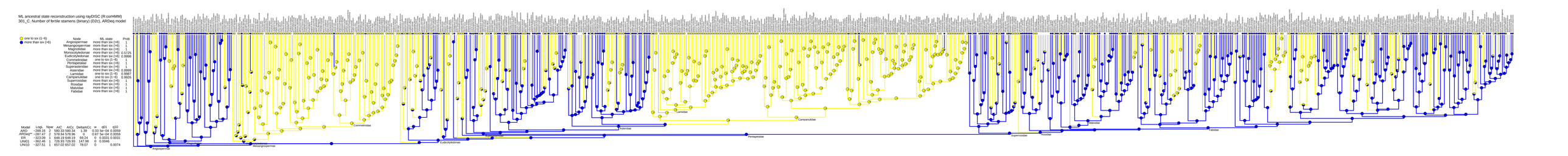
Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01
ARD	−491.49	6	994.98	995.08	2.2	0.25	4e−04
ARDeq**	−490.39	6	992.78	992.89	0	0.75	4e−04
ER	−537.6	1	1077.2	1077.3	84.32	0	0.0027
SYM	−529.34	3	1064.68	1064.82	71.83	0	0.0039
SYMeq	−529.34	3	1064.68	1064.82	71.83	0	0.0039
ORD	−508.62	4	1025.23	1025.28	32.4	0	7e−04
ORDeq	−508.11	4	1024.23	1024.28	31.39	0	8e−04
ORDSYM	−533.66	2	1071.33	1071.34	78.46	0	0.0043
ORDSYMeq	−532.78	2	1069.56	1069.58	76.69	0	0.0043
ORDER	−533.69	1	1069.38	1069.39	76.5	0	0.0044

MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
301_C. Number of fertile stamens (binary) (02c), 94 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) / 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	more than six (>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)

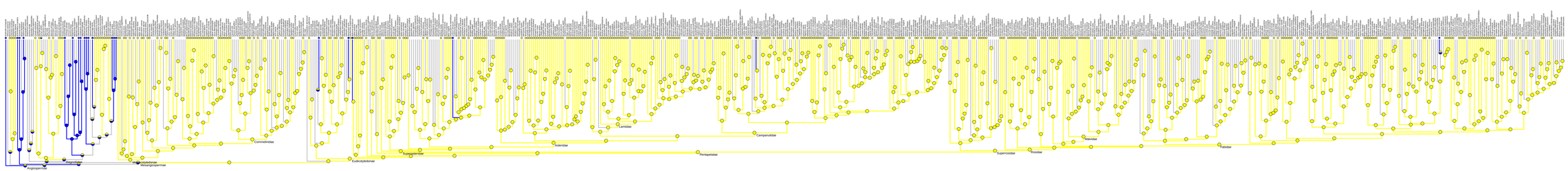



ML ancestral state reconstruction using ratDISC (RcorHMM)
301_C. Number of fertile stamens (binary) (02c), ARDeq model
one to six (1–6)
more than six (>6)
Node
ML state
Prob
Angiospermae more than six (>6) 1
Mesangiospermae more than six (>6) 1
Magnoliidae more than six (>6) 1
Monocotyledonae more than six (>6) 0.5725
Eudicotyledonae more than six (>6) 0.9998
Commelinidae one to six (1–6) 1
Ceratophyllum one to six (1–6) 1
Superasteridae more than six (>6) 1
Asteridae more than six (>6) 0.9999
Lamiidae one to six (1–6) 0.9997
Campanulidae one to six (1–6) 0.9926
Gunneridae more than six (>6) 1
Rosidae more than six (>6) 1
Malvidae more than six (>6) 1
Fabidae more than six (>6) 1
Model LogL Npar AIC AICc DeltaAICc w q01 q10
ARD −288.16 2 580.33 580.34 1.39 0.33 5e−04 0.0059
ARDeq** −287.47 2 578.94 578.96 0 0.67 5e−04 0.0059
ER −323.09 1 648.19 648.19 69.24 0 0.0031 0.0031
UN01 −362.46 1 726.93 726.93 147.98 0 0.0046
UN10 −327.51 1 657.02 657.02 78.07 0 0.0074
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledonae
Eudicotyledonae
Commelinidae
Ceratophyllum
Superasteridae
Asteridae
Lamiidae
Gunneridae
Rosidae
Malvidae
Fabidae
Campanulidae
Pentapetalae

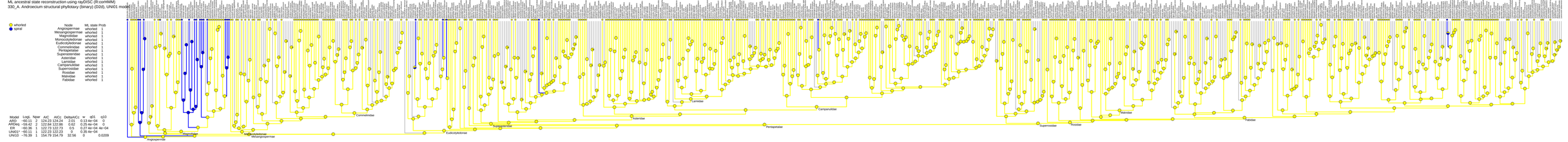
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
330_A. Androecium structural phyllotaxy (binary) (D2d), 12 steps

whorled
spiral

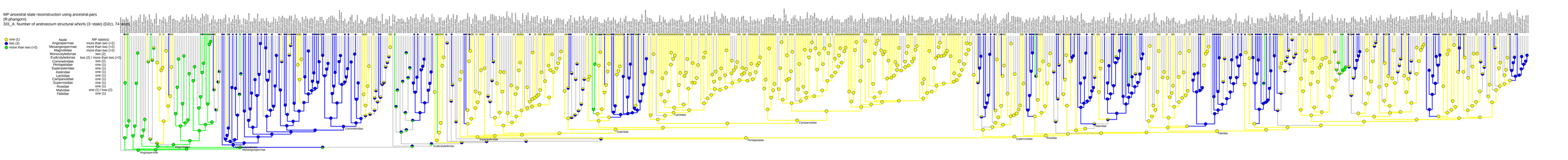
Node	MP state(s)
Angiospermae	whorled / spiral
Mesangiospermae	whorled / spiral
Magnoliidae	whorled / spiral
Monocotyledonae	whorled
Eudicotyledonae	whorled
Commelinidae	whorled
Ranunculidae	whorled
Superasteridae	whorled
Asteridae	whorled
Lamidae	whorled
Campanulidae	whorled
Superrosidae	whorled
Rosidae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



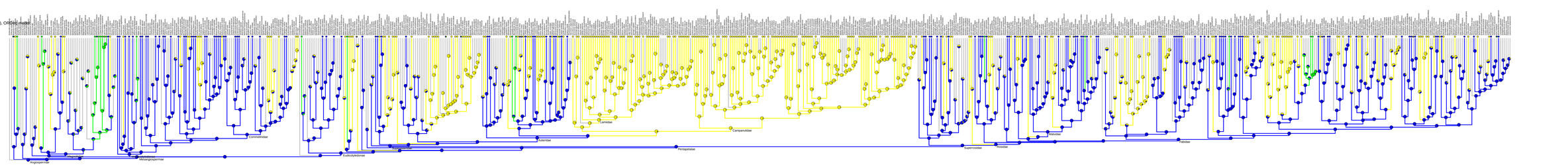
ML ancestral state reconstruction using rayDISC (R:corHMM)
330_A. Androcium structural phylotaxy (binary) (D2d), UNI01 model



MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
331_A. Number of androecium structural whorls (3–state) (D2c), 74 taxa

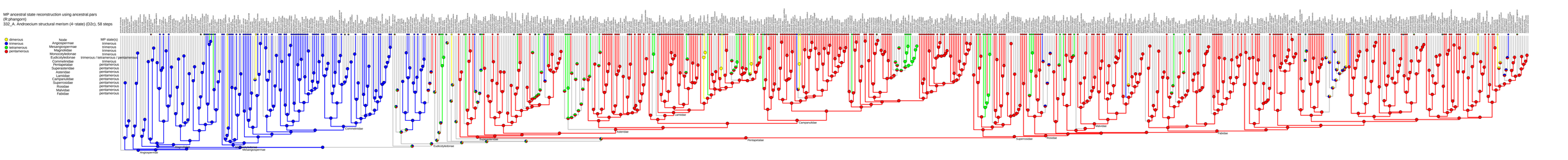


ML ancestral state reconstruction using rayDISC (R:corHMM)
331_A. Number of androecium structural whorls (3–state) (D2c), ORDER model

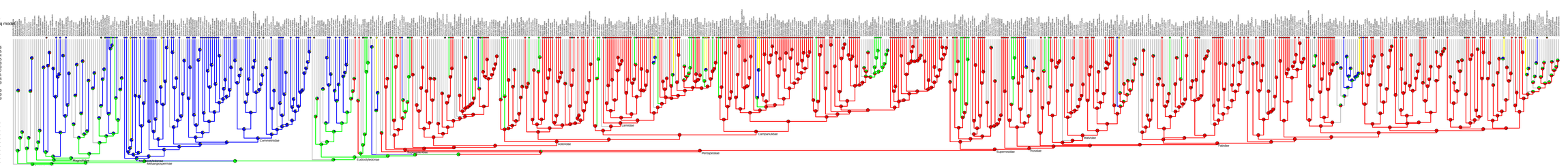


Node	ML state	Prob
Angiospermae	two (2)	1
Mesangiospermae	two (2)	0.9999
Magnoliidae	two (2)	0.9917
Monocotyledoneae	two (2)	1
Eudicotyledoneae	two (2)	1
Commelinidae	two (2)	1
Ceratophyllidae	two (2)	1
Superasteridae	two (2)	1
Asteridae	two (2)	1
Lamiidae	one (1)	0.9986
Campanulidae	one (1)	0.9916
Gentianidae	two (2)	1
Rosidae	two (2)	1
Malvidae	two (2)	1
Fabidae	two (2)	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	---
ARD	-230.47	6	472.95	473.06	0.19	0.32	0	---
ARDeq	-230.91	4	473.82	473.92	1.06	0.21	0	---
ER	-260.24	1	562.49	562.49	89.63	0	0.0017	---
SYM	-254.09	3	514.19	514.36	41.49	0	0.0035	---
SYMeq	-254.18	2	512.35	512.41	39.54	0	0.0035	---
ORD	-233.46	4	474.93	474.98	2.11	0.12	0	---
ORDeq*	-232.41	4	472.82	472.87	0	0.35	0	---
ORDSYM	-255.12	7	514.24	514.26	41.39	0	0.0036	---
ORDSYMeq	-254.05	2	512.09	512.11	39.24	0	0.0036	---
ORDER	-260.45	1	522.9	522.9	50.04	0	0.0029	---

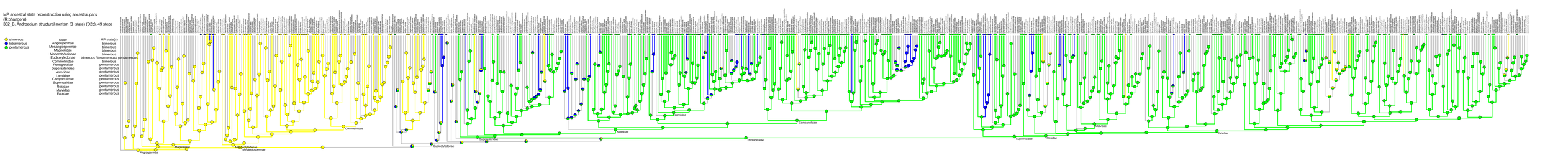

MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
332_A. Androecium structural merism (4–state) (D2c), 58 steps
dimerous
trimerous
tetramerous
pentamerous
Node
MP state(s)
Angiospermae
trimerous
Mesangiospermae
trimerous
Magnoliidae
trimerous
Monocotyledoneae
trimerous
Eudicotyledoneae
trimerous / tetramerous / pentamerous
Commelinidae
trimerous
Gunneridae
pentamerous
Superasteridae
pentamerous
Asteridae
pentamerous
Lamiidae
pentamerous
Campanulidae
pentamerous
Rosidae
pentamerous
Malvidae
pentamerous
Fabidae
pentamerous
Poales
Commelinidae
Angiospermae
Mesangiospermae
Eudicotyledonae
Gunneridae
Pentapetalae
Lamiidae
Asteridae
Campanulidae
Superasteridae
Rosidae
Malvidae
Fabidae

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

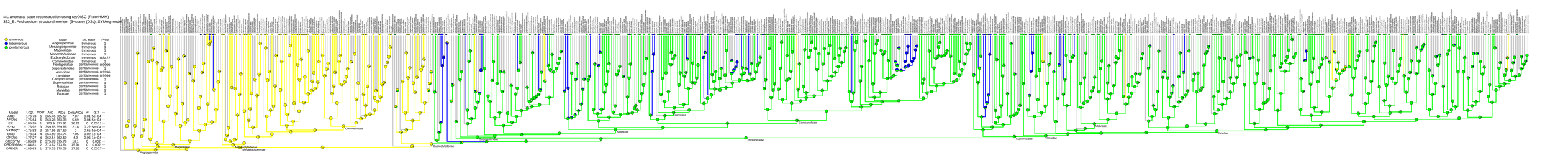


Node	ML state	Prob
Angiospermae	tetramerous	0.9846
Mesangiospermae	tetramerous	0.9215
Magnoliidae	tetramerous	0.8424
Monocotyledoneae	trimerous	0.5155
Eudicotyledoneae	tetramerous	0.9628
Commelinidae	trimerous	0.8489
Gunneridae	tetramerous	0.9691
Superasteridae	pentamerous	0.9901
Asteridae	pentamerous	0.9998
Lamiidae	pentamerous	0.9999
Campanulidae	pentamerous	1
Asterales	pentamerous	0.9999
Rosidae	pentamerous	0.9999
Malvidae	pentamerous	0.9999
Fabidae	pentamerous	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	—
ARD	−222.8	12	469.59	469.99	348.76	0	0.0071	—
ARDeq	−221.46	12	466.92	467.32	346.09	0	0.0069	—
ER	−236.77	1	475.53	475.54	354.3	0	9e−04	—
SYM	−236.77	2	477.53	477.55	356.31	0	9e−04	—
SYMeq	−223.38	6	458.77	458.92	337.68	0	6e−04	—
ORD	−56.67	6	125.34	125.44	4.21	0.11	99.9998	—
ORDeq*	−54.56	6	121.13	121.24	0	0.89	100	—
ORDSYM	−256.73	3	519.46	519.49	398.26	0	0.0021	—
ORDSYMeq	−255.4	3	516.8	516.83	395.59	0	0.0021	—
ORDER	−257.49	1	516.97	516.98	395.74	0	0.0031	—


MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
332_B. Androecium structural merism (3–state) (D2c), 49 steps
trimerous
tetramerous
pentamerous
Node
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledonae
Eudicotyledonae
Commelinidae
Ceratophyllidae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Santalales
Rosidae
Malvidae
Fabidae
MP state(s)
trimerous
trimerous
trimerous
trimerous
trimerous / tetramerous / pentamerous
trimerous
pentamerous
pentamerous
pentamerous
pentamerous
pentamerous
pentamerous
pentamerous
pentamerous
Angiospermae
Magnoliidae
Mesangiospermae
Ceratophyllidae
Monocotyledonae
Eudicotyledonae
Commelinidae
Superasteridae
Asteridae
Lamiidae
Santalales
Campanulidae
Pentapetalae
Superrosidae
Rosidae
Malvidae
Fabidae

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



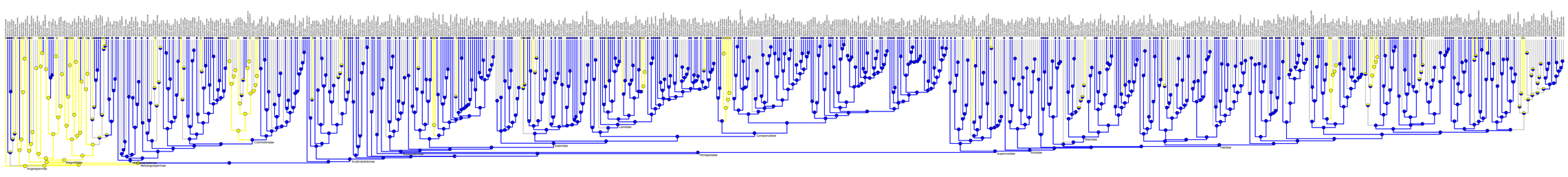
Node	ML state	Prob
Angiospermae	trimerous	1
Mesangiospermae	trimerous	1
Magnoliidae	trimerous	1
Monocotyledoneae	trimerous	1
Eudicotyledoneae	trimerous	0.8422
Commelinidae	trimerous	1
Gunneridae	pentamerous	0.9999
Superasteridae	pentamerous	1
Asteridae	pentamerous	0.9996
Lamidae	pentamerous	0.9999
Campanulidae	pentamerous	1
Pentapetalae	pentamerous	1
Rosidae	pentamerous	1
Malvidae	pentamerous	1
Fabidae	pentamerous	1

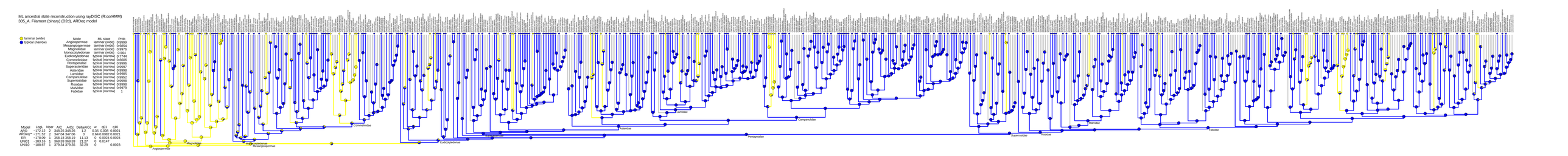
Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	---
ARD	-176.73	6	365.46	365.57	7.87	0.01	5e−04	--
ARDeq	-176.64	6	363.28	363.38	5.69	0.04	5e−04	--
ER	-185.95	1	373.9	373.91	16.21	0	0.0011	--
SYM	-176.73	3	359.46	359.57	2.07	0.26	5e−04	--
SYMeq*	-176.83	3	357.65	357.69	0	0.65	5e−04	--
ORD	-178.34	4	364.69	364.74	7.05	0.02	1e−04	--
ORDeq	-177.27	4	362.54	362.59	4.9	0.06	1e−04	--
ORDSYM	-185.89	2	375.79	375.79	18.1	0	0.002	--
ORDSYMeq	-184.81	2	373.62	373.64	15.94	0	0.002	--
ORDER	-186.63	1	375.25	375.26	17.56	0	0.0027	--

MP ancestral state reconstruction using ancestral.pars
(R phangorn)
305_A. Filament (binary) (D2d), 52 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	typical (narrow)
Ranunculidae	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)

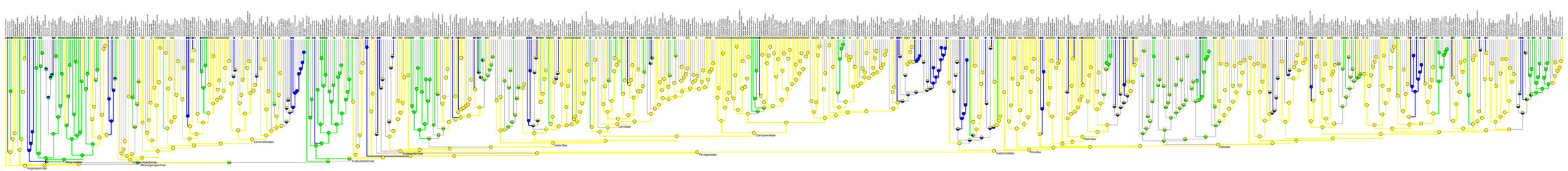



ML ancestral state reconstruction using rayDISC (R:corHMM)
305_A. Filament (binary) (D2d), ARDeq model
laminar (wide)
typical (narrow)
Node
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledonae
Eudicotyledonae
Commelinidae
Ceratophyllidae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Rosidae
Malvidae
Fabidae
ML state
laminar (wide) 0.9999
laminar (wide) 0.9854
laminar (wide) 0.5976
laminar (wide) 0.564
typical (narrow) 0.7744
typical (narrow) 0.6606
typical (narrow) 0.9997
typical (narrow) 0.9997
typical (narrow) 0.9998
typical (narrow) 0.9985
typical (narrow) 0.9952
typical (narrow) 0.9998
typical (narrow) 0.9998
typical (narrow) 0.9979
typical (narrow) 1
Model
ARD
ARDeq**
ER
UN01
UN10
LogL
−172.12
−171.52
−178.09
−183.16
−188.67
Npar
2
2
1
1
1
AIC
348.25
347.06
358.18
368.32
379.34
AICc
348.26
347.06
358.18
368.33
379.35
DeltaAICc
1.2
0
11.13
21.27
32.29
w
0.35
0.64
0
0
0
q01
0.008
0.0082
0.0024
0.0147
0
q10
0.0021
0.0021
0.0024
0.0147
0.0023
Angiospermae
Magnoliidae
Mesangiospermae
Monocotyledonae
Eudicotyledonae
Commelinidae
Ceratophyllidae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Pentapetalae
Rosidae
Malvidae
rabidae
Fabidae

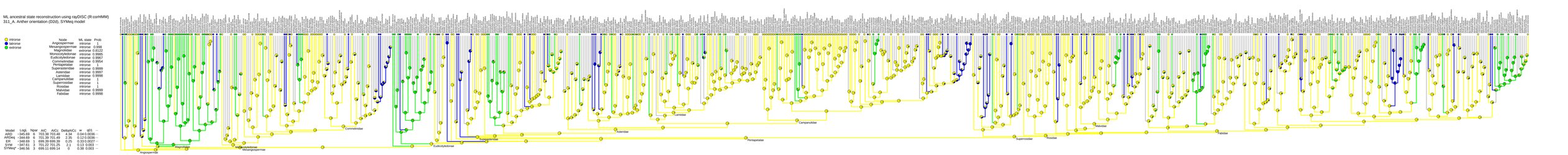
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
311_A. Anther orientation (D2d), 108 steps

- introrse
- latrorse
- extrorse

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



ML ancestral state reconstruction using ray/DISC (R:corHMM)
311_A. Anther orientation (D2d), SYMeq model

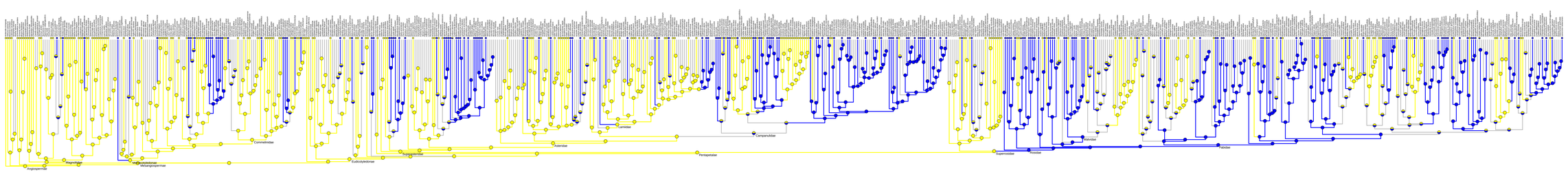


Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	---
ARD	-345.69	6	703.38	703.48	4.34	0.04	0.0036	---
ARDeq	-344.69	6	701.39	701.49	2.35	0.12	0.0036	---
ER	-348.69	1	699.39	699.39	0.25	0.33	0.0027	---
SYM	-347.81	3	701.22	701.25	2.1	0.13	0.003	---
SYMeq*	-346.56	3	699.11	699.14	0	0.38	0.003	---

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
Ceratophyllidae	basifixed
Superasteridae	basifixed
Asteridae	basifixed
Lamidae	basifixed
Campanulidae	basifixed / dorsifixed
Superrosidae	dorsifixed
Rosidae	dorsifixed
Malvidae	dorsifixed
Fabidae	dorsifixed

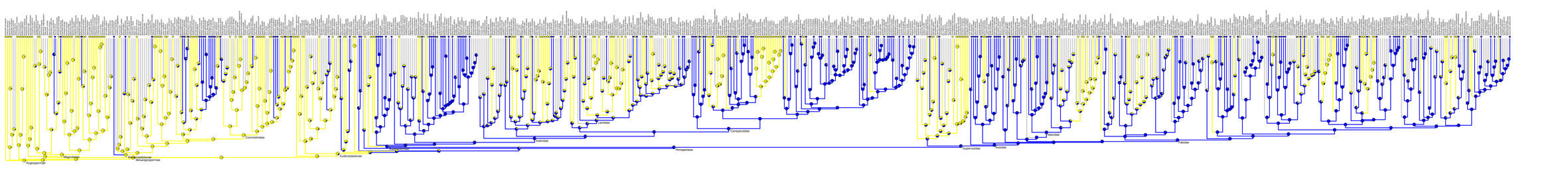


ML ancestral state reconstruction using ratyDISC (R corHMM)
312_A. Anther attachment (binary) (D2d), ARDeq model

basifixed
dorsifixed

Node	ML state	Prob
Angiospermae	basifixed	1
Mesangiospermae	basifixed	0.9991
Magnoliidae	basifixed	0.9989
Monocotyledonae	basifixed	0.9932
Eudicotyledonae	basifixed	0.9303
Commelinidae	basifixed	0.9823
Gunneridae	dorsifixed	0.8579
Superasteridae	dorsifixed	0.8979
Asteridae	dorsifixed	0.8989
Lamidae	dorsifixed	0.8781
Campanulidae	dorsifixed	0.9702
Pentapetalae	dorsifixed	0.9481
Rosidae	dorsifixed	0.9483
Malvidae	dorsifixed	0.9799
Fabidae	dorsifixed	0.9998

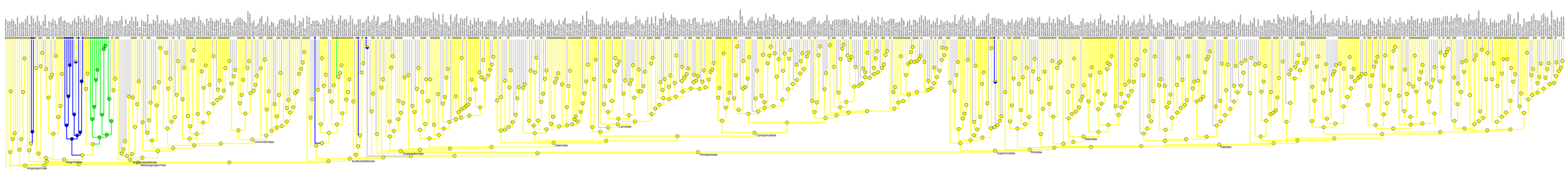
Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	−265.57	2	535.13	535.15	1.32	0.29	0.0043	0.0077
ARDeq**	−264.9	2	533.81	533.82	0	0.57	0.0043	0.0076
ER	−267.34	1	536.68	536.69	2.86	0.14	0.0056	0.0056
UN01	−293.27	1	588.54	588.55	54.73	0	0.0061	
UN10	−276.87	1	555.75	555.75	21.93	0		0.0081



MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
313_A. Anther dehiscence (3–state) (Ord), 10 steps

longitudinal slit
Fr–ulvate
Rap–valvate

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

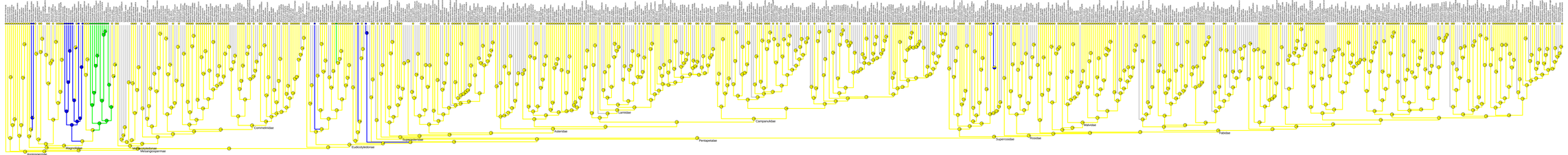


ML ancestral state reconstruction using ray|DISC (R:corHMM) 313_A. Anther dehiscence (3-state) (D2d), ARDeq model

- longitudinal slit
- hr--valvate
- flap--valvate

Node	ML state	Prob
Angiospermae	longitudinal slit	1
Mesangiospermae	longitudinal slit	1
Magnoliidae	longitudinal slit	1
Monocotyledonae	longitudinal slit	1
Eudicotyledonae	longitudinal slit	1
Commelinidae	longitudinal slit	1
Ceratophyta	longitudinal slit	1
Superasteridae	longitudinal slit	1
Asteridae	longitudinal slit	1
Lamidae	longitudinal slit	1
Campanulidae	longitudinal slit	1
Superrosidae	longitudinal slit	1
Rosidae	longitudinal slit	1
Malvidae	longitudinal slit	1
Fabidae	longitudinal slit	1

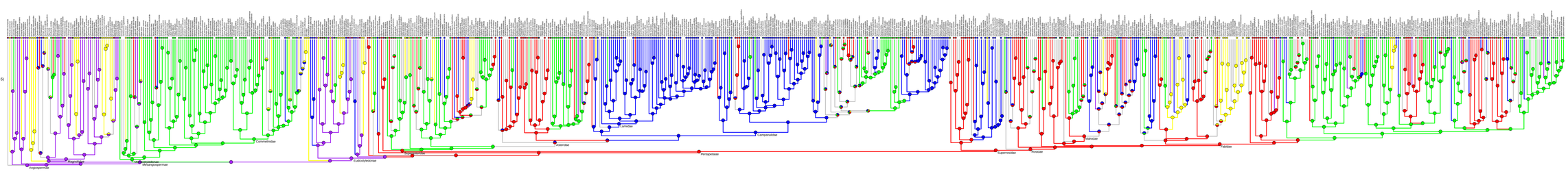
Model	Logl	Npar	AIC	AICc	DeltaAICc	w	q01	...
ARD	−56.51	6	125.03	125.13	2.2	0.11	2e−04	--
ARDeq*	−55.41	6	122.83	122.94	0	0.32	2e−04	--
ER	−60.8	1	123.6	123.61	0.67	0.23	2e−04	--
SYM	−59.75	3	125.51	125.54	2.6	0.09	2e−04	--
SYMeq	−58.65	3	123.31	123.34	0.4	0.26	2e−04	--



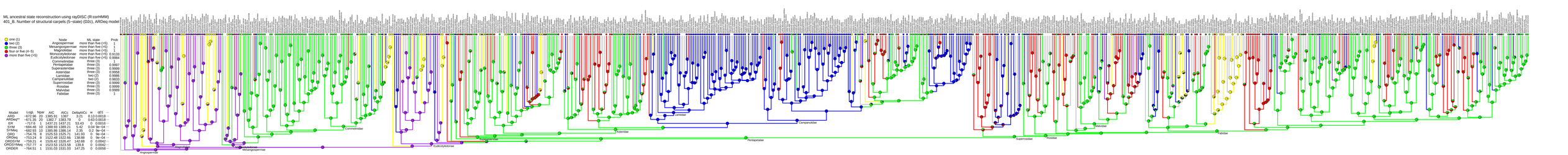
MP ancestral state reconstruction using ancestral.pars
(R phangorn)
401_B. Number of structural carpels (5~state) (D2c), 188 steps

- 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)
Monocotyledoneae	three (3)
Eudicotyledoneae	more than five (>5)
Commelinidae	one (1)
Ceratophyllidae	four or five (4~5)
Superasteridae	four or five (4~5)
Asteridae	two (2) / four or five (4~5)
Lamiidae	two (2)
Campanulidae	two (2)
Santalanae	four or five (4~5)
Rosidae	four or five (4~5)
Malvidae	four or five (4~5)
Fabidae	four or five (4~5)



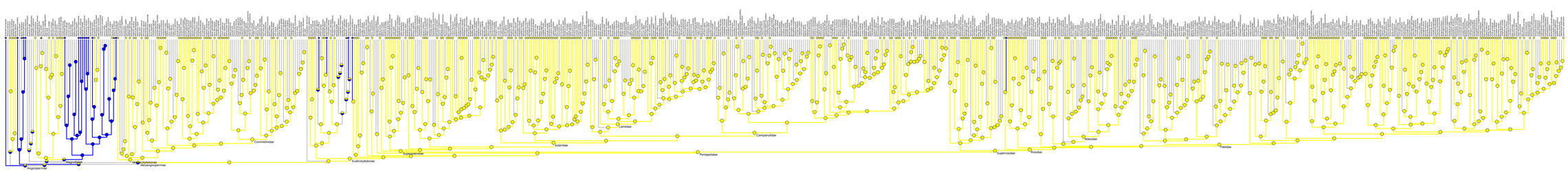
ML ancestral state reconstruction using rayDISC (R:corHMM)
401_B. Number of structural carpels (5-state) (D2c), ARDeq model



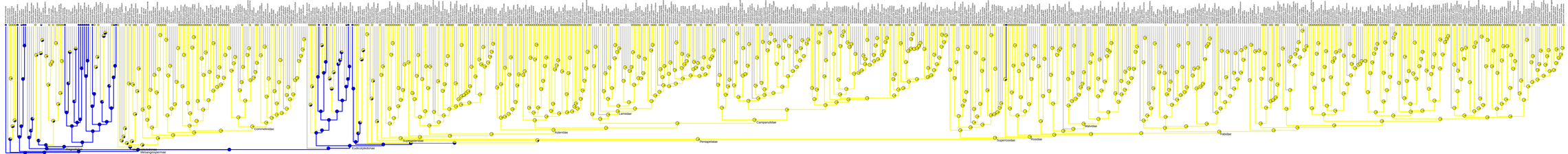
MP ancestral state reconstruction using ancestral.pars (R phangorn)
400_A. Gynoecium phyllotaxy (D2d), 10 steps

whorled
spiral

Node	MP state(s)
Angiospermae	whorled / spiral
Mesangiospermae	whorled / spiral
Magnoliidae	whorled / spiral
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



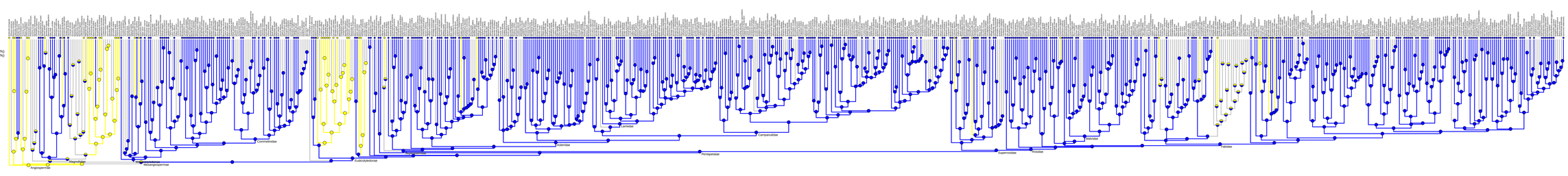
Node	ML state	Prob
Angiospermae	spiral	1
Mesangiospermae	spiral	1
Magnoliidae	spiral	1
Monocotyledonae	spiral	0.5145
Eudicotyledonae	spiral	0.9994
Commelinidae	whorled	0.9938
Ceratophyllidae	whorled	0.9976
Superasteridae	whorled	0.9976
Asteridae	whorled	1
Lamidae	whorled	1
Campanulidae	whorled	1
Pentapetalae	whorled	0.9795
Rosidae	whorled	0.9795
Malvidae	whorled	1
Fabidae	whorled	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	-39.93	2	83.86	83.87	1.39	0.31	1e-04	0.0084
ARDeq**	-39.24	2	82.47	82.49	0	0.63	1e-04	0.0084
ER	-51.55	1	105.1	105.1	22.61	0	4e-04	4e-04
UN01	-53.06	1	108.13	108.13	25.64	0	4e-04	
UN10	-42.6	1	87.21	87.21	4.73	0.06		0.0098

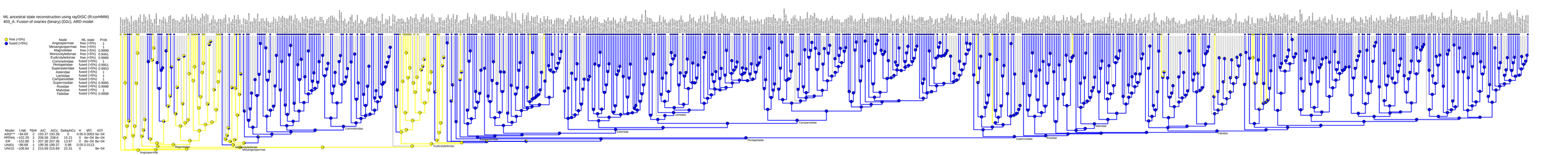
MP ancestral state reconstruction using ancestral.pars
(R phangorn)
403_A. Fusion of ovaries (binary) (D2c), 23 steps

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

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



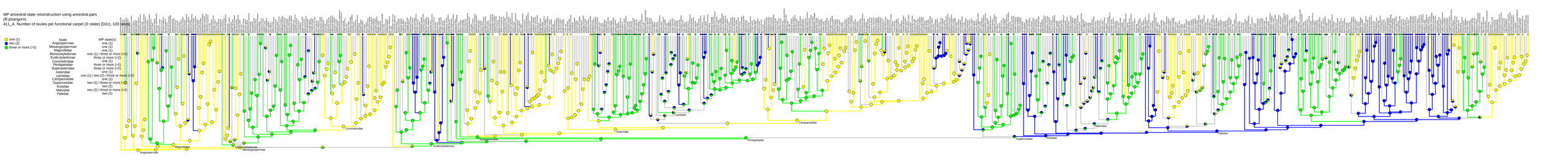
ML ancestral state reconstruction using rayDISC (R:corHMM)
403_A. Fusion of ovaries (binary) (D2c), ARD model



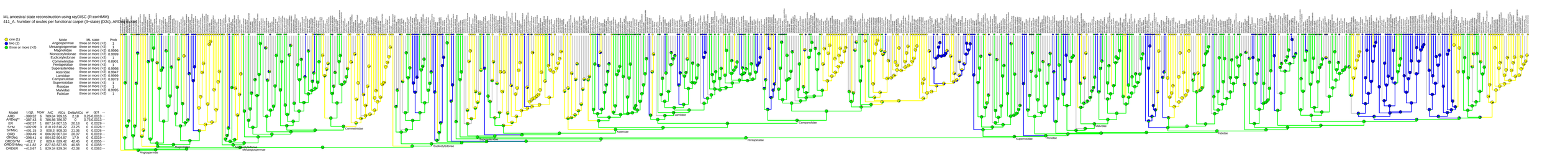
Node	ML state	Prob
Angiospermae	free (<5%)	1
Mesangiospermae	free (<5%)	1
Magnoliidae	free (<5%)	0.9999
Monocotyledoneae	free (<5%)	0.9461
Eudicotyledoneae	free (<5%)	0.9999
Commelinidae	fused (>5%)	1
Gunneridae	fused (>5%)	0.9951
Superasteridae	fused (>5%)	0.9953
Asteridae	fused (>5%)	1
Lamiidae	fused (>5%)	1
Campanulidae	fused (>5%)	1
Caryophyllales	fused (>5%)	0.9995
Rosidae	fused (>5%)	0.9998
Malvidae	fused (>5%)	1
Fabidae	fused (>5%)	0.9998

Model	LogL	Nparam	AICc	AICc_Delta	AICc_Weight	q01	q10
ARD***	-94.69	2	193.37	193.39	0	0.95	0.0053
ARDeq	-102.29	2	208.58	208.6	15.21	0	6e−04
ER	-102.68	1	207.36	207.36	13.97	0	8e−04
UN01	-98.68	1	199.36	199.37	5.98	0.05	0.0113
UN10	-106.84	1	215.69	215.69	22.31	0	9e−04

MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
411_A. Number of ovules per functional carpel (3–state) (D2c), 120 taxa



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



Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	---
ARD	-386.52	6	789.04	789.15	2.18	0.25	0.0013	---
ARDeq**	-387.43	6	786.86	786.97	0	0.75	0.0013	---
ER	-402.57	1	807.14	807.15	20.18	0	0.0029	---
SYM	-401.15	3	808.31	808.43	21.46	0	0.0026	---
SYMeq	-401.15	3	808.3	808.23	21.39	0	0.0026	---
ORD	-399.49	4	806.99	807.04	20.07	0	0.0019	---
ORDeq	-398.41	4	804.82	804.87	17.9	0	0.0019	---
ORDSYM	-412.7	2	829.4	829.42	42.45	0	0.0055	---
ORDSYMeq	-411.82	2	827.63	827.65	40.68	0	0.0055	---
ORDER	-413.67	1	829.34	829.34	42.38	0	0.0063	---