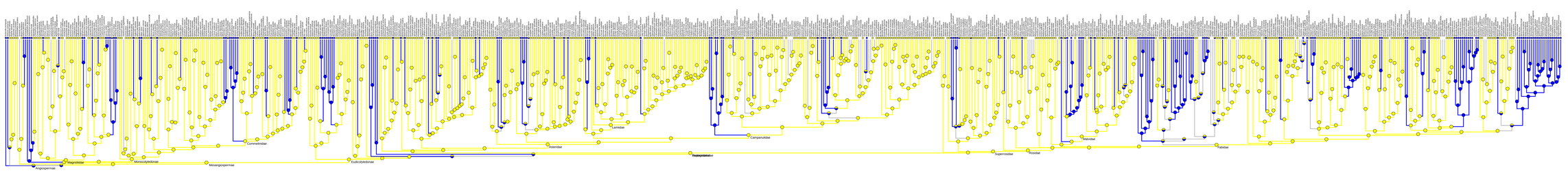
MP ancestral state reconstruction using ancestral pars
(R phangorn)
100_A. Functional sex of flowers (02d), 97 steps

bisexual
unisexual

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

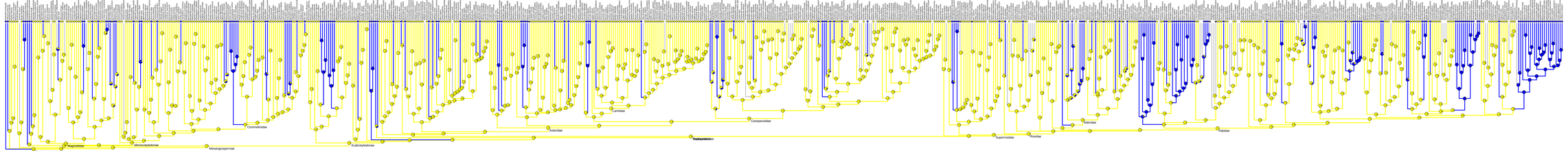


ML ancestral state reconstruction using rayDISC (R:corHMM) 100_A. Functional sex of flowers (02d), ARDeq model

bisexual
unisexual

Node	ML state	Prob
Angiospermae	bisexual	1
Mesangiospermae	bisexual	1
Magnoliidae	bisexual	1
Monocotyledonae	bisexual	1
Eudicotyledonae	bisexual	1
Commelinidae	bisexual	0.9999
Ranunculidae	bisexual	1
Superasteridae	bisexual	1
Asteridae	bisexual	1
Lamidae	bisexual	1
Campanulidae	bisexual	0.9996
Caryophyllidae	bisexual	1
Rosidae	bisexual	1
Malvidae	bisexual	0.9997
Fabidae	bisexual	1

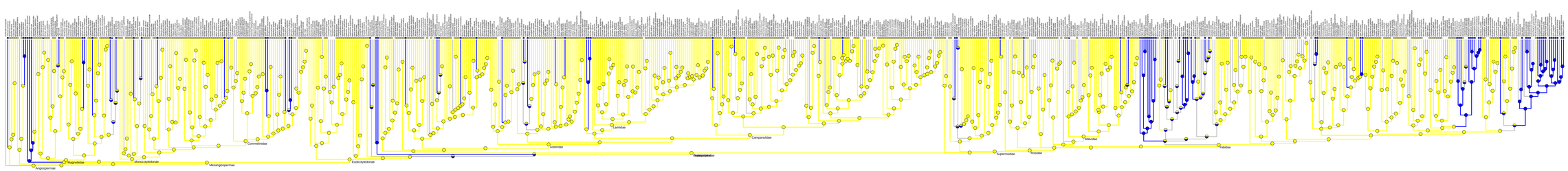
Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	-313.25	2	630.5	630.52	1.38	0.23	0.003	7e−04
ARDeq*	-312.56	2	629.12	629.14	0	0.46	0.003	7e−04
ER	-316.07	1	634.13	634.14	5	0.04	0.0029	0.0029
UNI01	-314.06	1	630.12	630.12	0.99	0.28	0.003	
UNI10	-354.64	1	711.27	711.28	82.14	0		0.0118



MP ancestral state reconstruction using ancestral pars
(R phangorn)
100_B. Structural sex of flowers (D2d), 56 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

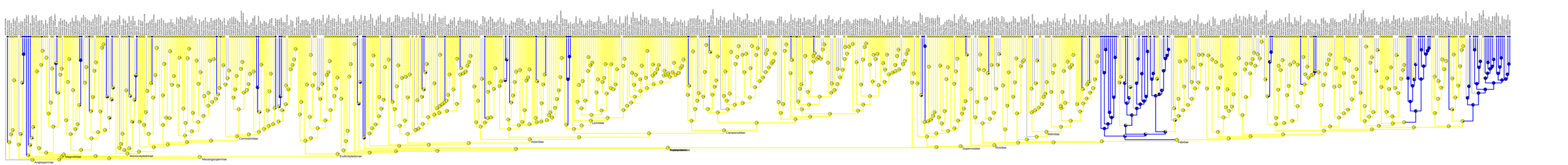


ML ancestral state reconstruction using rayDISC (R:corHMM) 100_B. Structural sex of flowers (D2d), ARDeq model

bisexual
unisexual

Node	ML state	Prob
Angiospermae	bisexual	1
Mesangiospermae	bisexual	1
Magnoliidae	bisexual	1
Monocotyledonae	bisexual	1
Eudicotyledonae	bisexual	1
Commelinidae	bisexual	1
Gentianidae	bisexual	1
Superasteridae	bisexual	1
Asteridae	bisexual	1
Lamidae	bisexual	0.9999
Campanulidae	bisexual	1
Asteridae	bisexual	1
Rosidae	bisexual	1
Malvidae	bisexual	1
Fabidae	bisexual	0.9975

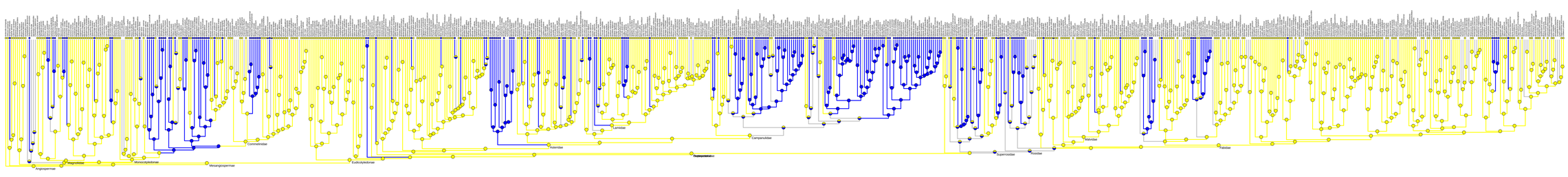
Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	−209.05	2	422.1	422.11	1.36	0.28	0.0015	0.004
ARDeq**	−208.37	2	420.74	420.75	0	0.56	0.0015	0.004
ER	−210.62	1	423.23	423.24	2.48	0.16	0.0016	0.0016
UN01	−223.81	1	449.61	449.62	28.87	0	0.0017	
UN10	−230.41	1	462.81	462.82	42.06	0	0	0.0165



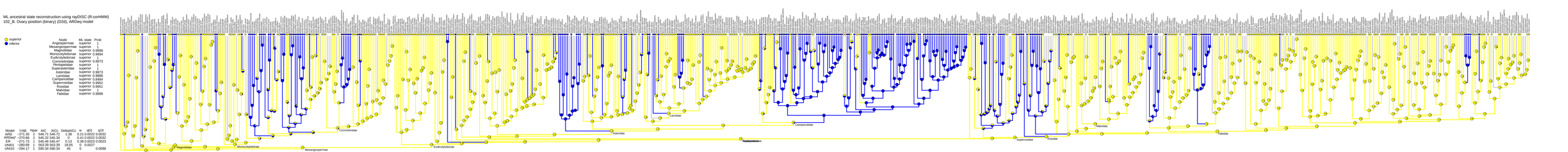
MP ancestral state reconstruction using ancestral.pars
(R phangorn)
102_B. Ovary position (binary) (0/d), 78 steps

superior
inferior

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



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



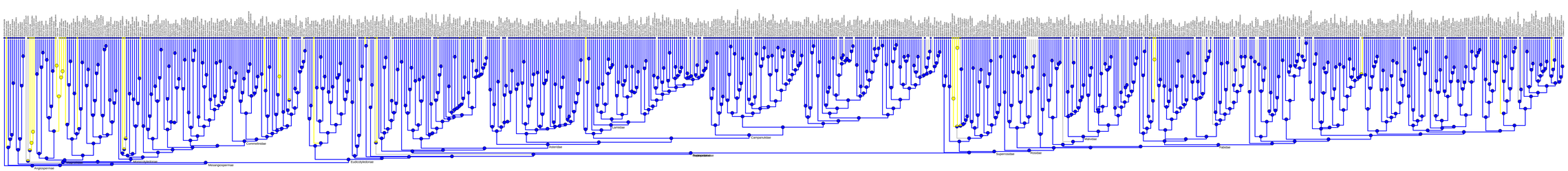
Node	ML state	Prob
Angiospermae	superior	1
Mesangiospermae	superior	1
Magnoliidae	superior	0.9999
Monocotyledonae	superior	0.9994
Eudicotyledonae	superior	1
Gunneridae	superior	0.8973
Pentapetalae	superior	1
Superasteridae	superior	1
Asteridae	superior	0.9873
Lamidae	superior	0.9898
Campanulidae	superior	0.8484
Superrosidae	superior	0.9953
Rosidae	superior	0.9953
Malvidae	superior	1
Fabidae	superior	0.9999

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	−271.35	2	546.71	546.72	1.38	0.21	0.0032	0.0032
ARDeq*	−270.66	2	545.32	545.34	0	0.41	0.0032	0.0032
ER	−271.73	1	545.46	545.47	0.13	0.38	0.0023	0.0023
UNI01	−280.89	1	563.78	563.79	18.05	0	0.0027	
UNI10	−294.17	1	590.34	590.34	45	0		0.0098

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

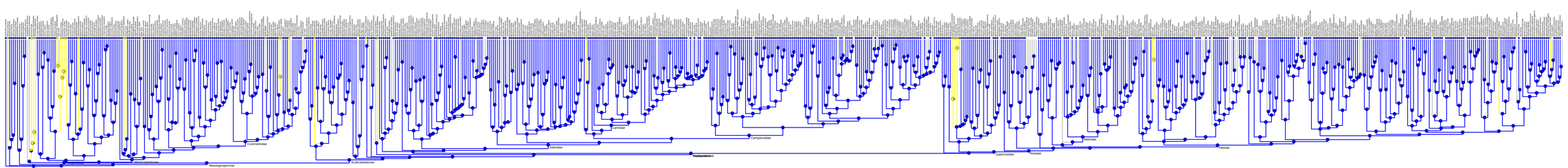


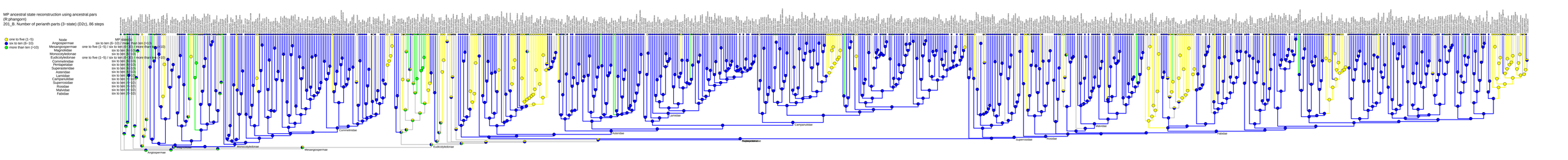
ML ancestral state reconstruction using rayDISC (R:corHMM)
201_A. Perianth presence (D2c), UNI10 model

absent
present

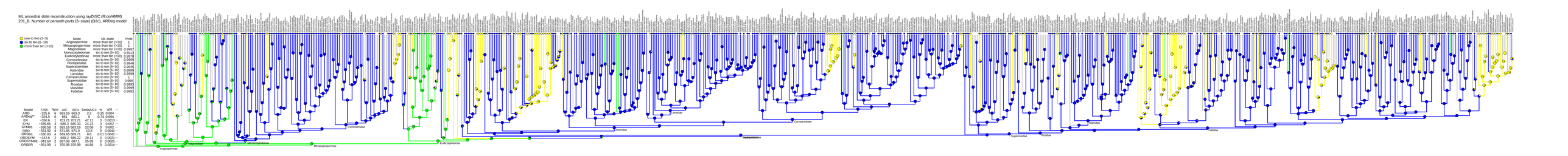
Node	ML state	Prob
Angiospermae	present	1
Mesangiospermae	present	1
Magnoliidae	present	1
Monocotyledonae	present	1
Eudicotyledonae	present	1
Commelinidae	present	1
Gunneridae	present	1
Superasteridae	present	1
Asteridae	present	1
Lamidae	present	1
Campanulidae	present	1
Superrosidae	present	1
Rosidae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

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	−97.4	2	198.81	198.82	2.01	0.13	0	5e−04
ARDeq	−96.71	2	197.42	197.44	0.62	0.25	0	5e−04
ER	−97.65	1	197.3	197.31	0.5	0.27	5e−04	5e−04
UNI01	−109.2	1	220.4	220.41	23.59	0	0.0221	
UNI10*	−97.4	1	196.81	196.81	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
one to five (1–5)
six to ten (6–10)
more than ten (>10)
Node
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledonae
Eudicotyledonae
Commelinidae
Ranunculidae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Santalanae
Rosidae
Malvidae
Fabidae
MP-state(s)
six to ten (6–10) / more than ten (>10)
one to five (1–5) / six to ten (6–10) / more than ten (>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)
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)
six to ten (6–10)
six to ten (6–10)
six to ten (6–10)
Angiospermae
Magnoliidae
Monocotyledonae
Commelinidae
Mesangiospermae
Eudicotyledonae
Ranunculidae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Santalanae
Rosidae
Malvidae
Fabidae

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



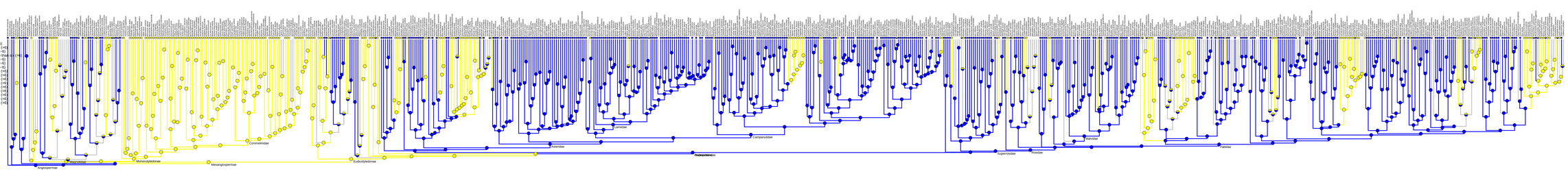
Node	ML state	Prob
Angiospermae	more than ten (>10)	1
Mesangiospermae	more than ten (>10)	1
Magnoliidae	more than ten (>10)	0.9997
Monocotyledonae	six to ten (6–10)	0.5913
Eudicotyledonae	more than ten (>10)	0.9978
Gunneridae	six to ten (6–10)	0.9998
Pentapetalae	six to ten (6–10)	0.9998
Superasteridae	six to ten (6–10)	0.9946
Asteridae	six to ten (6–10)	0.9998
Lamidae	six to ten (6–10)	0.9999
Campanulidae	six to ten (6–10)	1
Asteranthe	six to ten (6–10)	0.999
Rosidae	six to ten (6–10)	0.9993
Malvidae	six to ten (6–10)	0.9998
Fabidae	six to ten (6–10)	0.9992

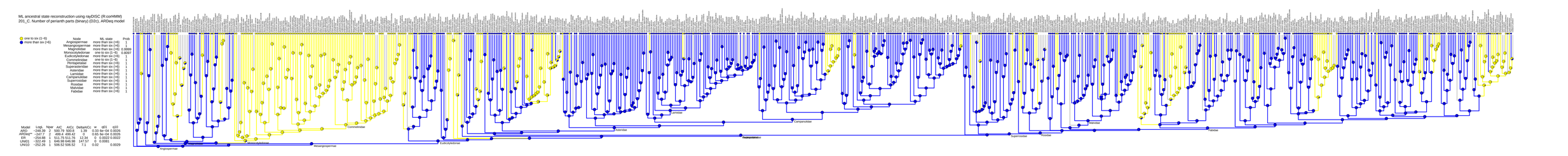
Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	--
ARD	−325.6	6	663.19	663.3	2.2	0.25	0.0004	--
ARDeq**	−324.5	6	661	661.1	0	0.74	0.004	--
ER	−350.6	1	703.21	703.21	42.11	0	0.0013	--
SYM	−338.58	3	683.16	683.23	22.04	0	0.0022	--
SYMeq	−338.58	3	683.16	683.23	22.03	0	0.002	--
ORD	−331.92	4	671.85	671.9	10.8	0	0.0041	--
ORDeq	−330.83	4	669.65	669.71	8.6	0.01	0.0041	--
ORDSYM	−342.6	2	689.2	689.22	28.11	0	0.0021	--
ORDSYMeq	−341.54	2	687.08	687.1	25.99	0	0.0021	--
ORDER	−351.99	1	705.98	705.98	44.88	0	0.0014	--

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	one to six (1–6)
Ceratophyllidae	more than six (>6)
Superasteridae	more than six (>6)
Asteridae	more than six (>6)
Lamiidae	more than six (>6)
Campanulidae	more than six (>6)
Superrosidae	more than six (>6)
Rosidae	more than six (>6)
Malvidae	more than six (>6)
Fabidae	more than six (>6)

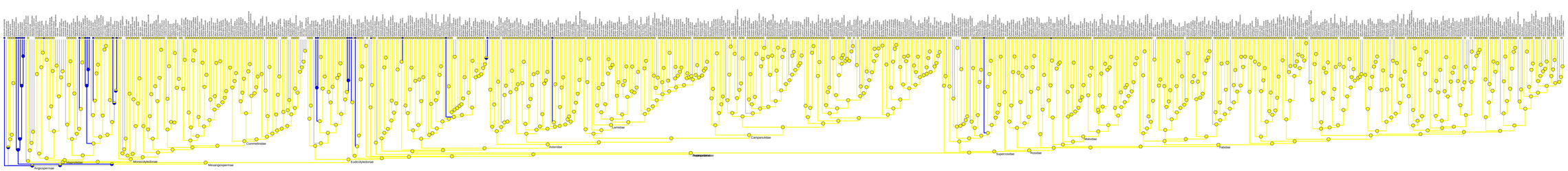



ML ancestral state reconstruction using ray/DISC (R:corHMM)
201_C. Number of perianth parts (binary) (D2c), ARDeq model
one to six (1–6)
more than six (>6)
Node ML state Prob
Angiospermae more than six (>6) 1
Mesangiospermae more than six (>6) 1
Magnoliidae more than six (>6) 0.9999
Monocotyledonae one to six (1–6) 0.8097
Eudicotyledonae more than six (>6) 1
Commelinidae one to six (1–6) 1
Gunneridae 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
Asterales 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 Nstr AIC ΔIC Delta ΔIC w q01 q10
ARD −248.39 2 500.79 500.8 1.39 0.33 6e−04 0.0026
ARDeq** −247.7 2 499.4 499.42 0 0.65 6e−04 0.0026
ER −254.88 1 511.75 511.76 12.34 0 0.0022 0.0022
UN01 −322.49 1 646.98 646.98 147.57 0 0.0081
UN10 −252.26 1 506.52 506.52 7.1 0.02 0.0029
Angiospermae
Magnoliidae
Monocotyledonae
Mesangiospermae
Commelinidae
Eudicotyledonae
Gunneridae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Asterales
Asterideae
Rosidae
Fabidae
Malvidae
Superrosidae
Malvideae
rabideae

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

alt verticillate
spiral

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

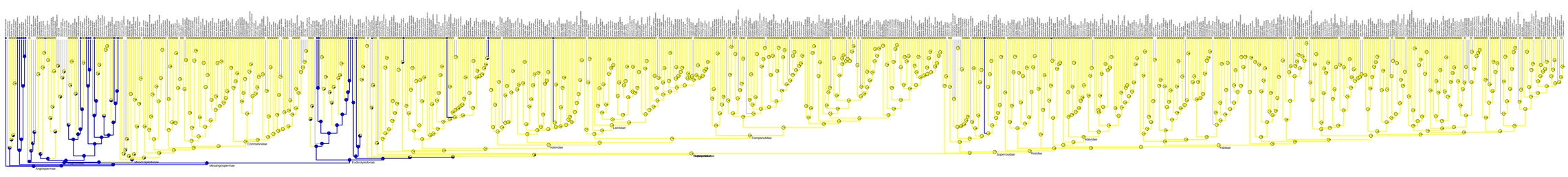


ML ancestral state reconstruction using rayDISC (R:corHMM)
230_A. Perianth phyllotaxy (binary) (D2d), ARD model

whorled
spiral

Node	ML state	Prob
Angiospermae	spiral	1
Mesangiospermae	spiral	1
Magnoliidae	spiral	0.9985
Monocotyledonae	whorled	0.5128
Eudicotyledonae	spiral	0.9998
Commelinidae	whorled	0.9997
Ceratophyta	whorled	0.9999
Superasteridae	whorled	0.9777
Asteridae	whorled	0.9995
Lamidae	whorled	1
Campanulidae	whorled	1
Superrosidae	whorled	0.9916
Rosidae	whorled	0.9545
Malvidae	whorled	1
Fabidae	whorled	1

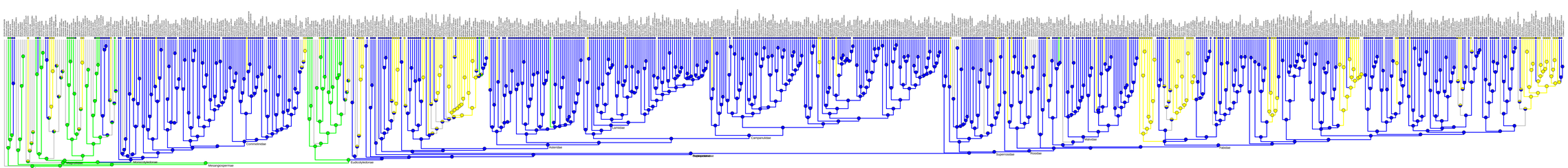
Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD***	-70.5	2	145	145.01	0	0.99	2e-04	0.0111
ARDeq	-77.64	2	159.29	159.3	14.29	0	4e-04	2e-04
ER	-78.3	1	158.6	158.61	13.6	0	4e-04	4e-04
UN01	-78.36	1	158.72	158.73	13.71	0	4e-04	
UN10	-77.59	1	157.18	157.18	12.17	0		0.0185



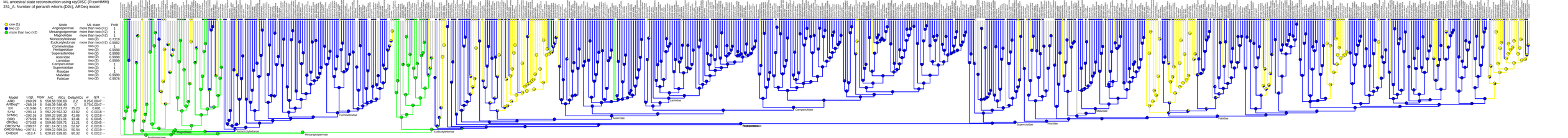
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
231_A. Number of perianth whorls (D2c), 73 steps

- 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)
Monocotyledoneae	two (2)
Eudicotyledoneae	more than two (>2)
Commelinidae	two (2)
Ranunculidae	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 ray|DISC (R corHMM)
231_A. Number of perianth whorls (D2c), ARDeq model



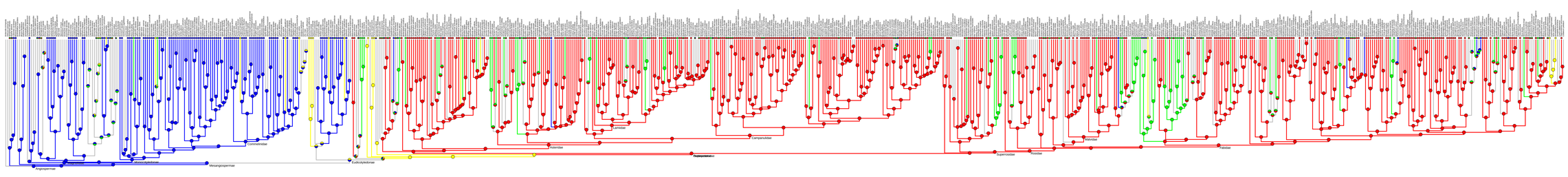
Node	ML state	Prob
Angiospermae	more than two (>2)	1
Mesangiospermae	more than two (>2)	1
Magnoliidae	more than two (>2)	1
Monocotyledonae	two (2)	0.7319
Eudicotyledonae	more than two (>2)	0.9982
Gunneridae	two (2)	1
Pentapetalae	two (2)	0.9998
Superasteridae	two (2)	0.9998
Asteridae	two (2)	0.9998
Lamidae	two (2)	0.9999
Campanulidae	two (2)	1
Lamiidae	two (2)	1
Rosidae	two (2)	1
Malvidae	two (2)	0.9999
Fabidae	two (2)	0.9976

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	--
ARD	-269.29	6	550.58	550.69	2.2	0.25	0.0047	--
ARDeq**	-268.19	6	548.39	548.49	0	0.75	0.0047	--
ER	-310.86	1	623.72	623.73	75.23	0	0.001	--
SYM	-292.14	3	590.28	590.35	41.86	0	0.0018	--
SYMeq	-292.14	3	590.28	590.35	41.86	0	0.0018	--
ORD	-276.93	4	561.85	561.91	13.41	0	0.0045	--
ORDeq	-275.83	4	559.65	559.71	11.21	0	0.0045	--
ORDSYM	-298.57	2	601.14	601.16	52.67	0	0.0019	--
ORDSYMeq	-297.51	2	599.02	599.04	50.54	0	0.0019	--
ORDER	-313.4	1	628.81	628.81	80.32	0	0.0012	--

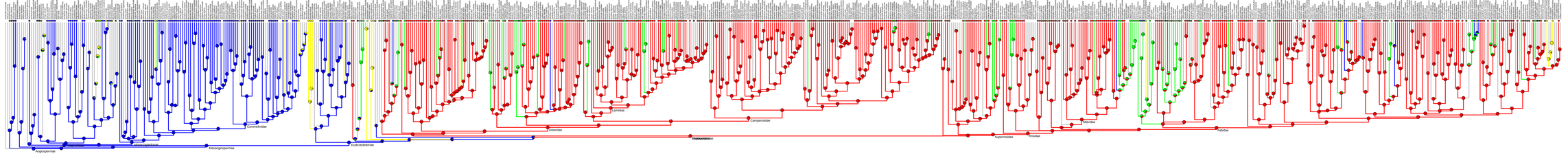
MP ancestral state reconstruction using ancestral pars
(R:phangorn)
232_A. Perianth merism (4–state) (D2c), 84 steps

- dimerous
- trimerous
- tetramerous
- pentamerous

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



ML ancestral state reconstruction using rayDISC (R:corHMM)
232_A. Perianth merism (4–state) (D2c), SYMeq model



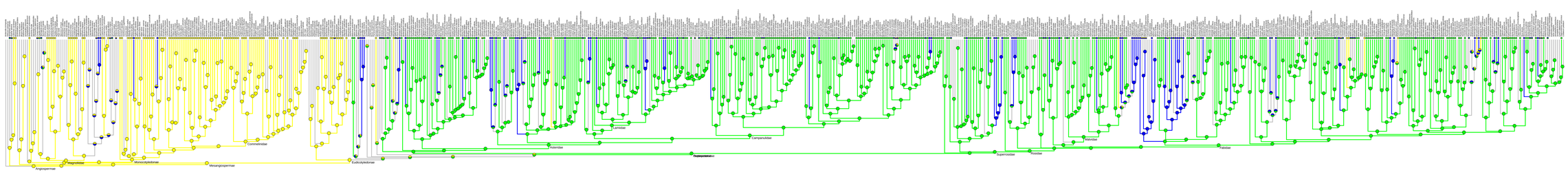
Node	ML state	Prob
Angiospermae	trimerous	1
Mesangiospermae	trimerous	1
Magnoliidae	trimerous	1
Monocotyledoneae	trimerous	1
Eudicotyledoneae	trimerous	0.9742
Commelinidae	trimerous	1
Superasteridae	pentamerous	0.9998
Superasteridae	pentamerous	0.9998
Asteridae	pentamerous	1
Lamidae	pentamerous	1
Campanulidae	pentamerous	1
Superrosidae	pentamerous	1
Rosidae	pentamerous	1
Malvidae	pentamerous	1
Fabidae	pentamerous	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	--
ARD	-321.85	12	667.7	668.1	7.62	0.02	6e−04	--
ARDeq	-326.5	12	665	665.4	4.92	0.09	5e−04	--
ER	-360.15	1	722.29	722.3	61.81	0	8e−04	--
SYM	-324.19	6	660.38	660.49	2.9	0.19	0.0013	--
SYMeq**	-324.19	6	660.38	660.49	2.9	0.19	0.0013	--
ORD	-336.7	6	685.4	685.51	25.02	0	0	--
ORDeq	-336.17	6	684.33	684.44	23.95	0	0	--
ORDSYM	-344.42	3	694.85	694.88	34.39	0	0.002	--
ORDSYMeq	-343.05	3	692.1	692.14	31.65	0	0.002	--
ORDER	-345.93	1	693.86	693.86	33.38	0	0.0025	--

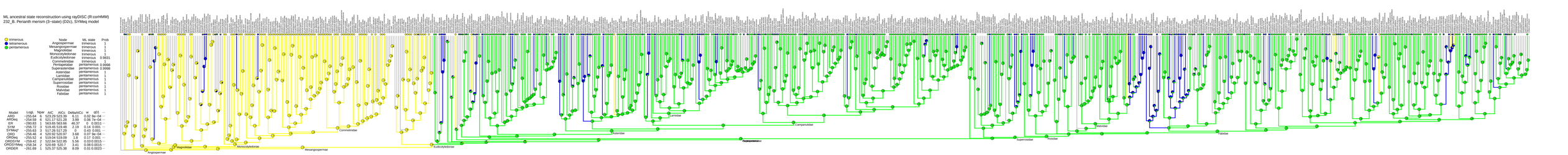
MP ancestral state reconstruction using ancestral pars (R:phangorn)
232_B. Perianth merism (3–state) (D2c), 70 steps

trimerous
tetramerous
pentamerous

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

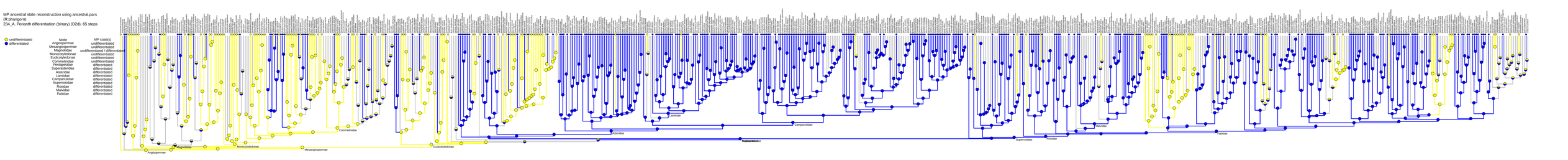


ML ancestral state reconstruction using rayDISC (R:corHMM)
232_B. Perianth merism (3–state) (D2c), SYMeq model



Node	ML state	Prob
Angiospermae	trimerous	1
Mesangiospermae	trimerous	1
Magnoliidae	trimerous	1
Monocotyledoneae	trimerous	1
Eudicotyledoneae	trimerous	0.9831
Commelinidae	trimerous	1
Gunneridae	pentamerous	0.9998
Superasteridae	pentamerous	0.998
Asteridae	pentamerous	1
Lamiidae	pentamerous	1
Campanulidae	pentamerous	1
Superrosidae	pentamerous	1
Rosidae	pentamerous	1
Malvidae	pentamerous	1
Fabidae	pentamerous	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	…
ARD	-255.64	6	523.29	523.39	6.11	0.02	8e−04	…
ARDeq	-254.59	4	521.17	521.28	3.99	0.06	7e−04	…
ER	-260.83	1	563.65	563.66	46.37	0	0.0013	…
SYM	-255.63	3	517.25	517.29	2.19	0.19	0.001	…
SYMeq	-255.63	3	517.25	517.29	2.19	0.43	0.001	…
ORD	-256.46	4	520.92	520.97	3.68	0.07	9e−04	…
ORDeq	-255.52	4	519.04	519.09	1.8	0.17	0.001	…
ORDSYM	-259.42	2	522.84	522.85	5.56	0.03	0.0015	…
ORDSYMeq	-258.34	2	520.69	520.7	3.41	0.08	0.0015	…
ORDER	-261.69	1	525.37	525.38	8.09	0.01	0.0023	…

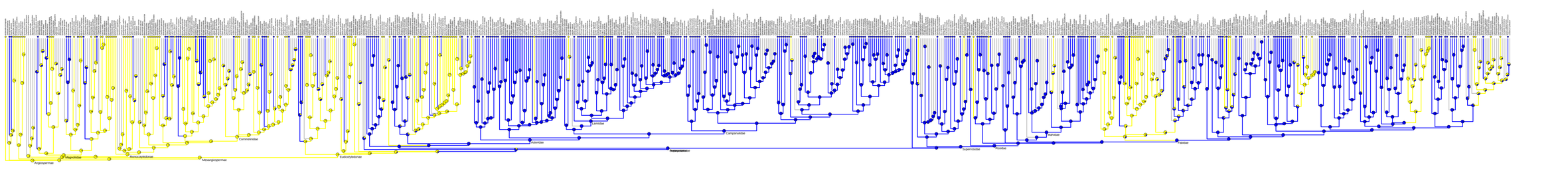

MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
234_A. Periamth differentiation (binary) (D2d), 65 steps
undifferentiated
differentiated
Node
MP state(s)
Angiospermae
undifferentiated
Mesangiospermae
undifferentiated
Magnoliidae
undifferentiated / differentiated
Monocotyledonae
undifferentiated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

undifferentiated
differentiated

Node	ML state	Prob
Angiospermae	undifferentiated	1
Mesangiospermae	undifferentiated	1
Magnoliidae	undifferentiated	1
Monocotyledonae	undifferentiated	1
Eudicotyledonae	undifferentiated	0.9915
Commelinidae	undifferentiated	0.9999
Ceratophyllidae	undifferentiated	0.9429
Superasteridae	differentiated	0.9429
Asteridae	differentiated	0.9977
Lamidae	differentiated	0.9999
Campanulidae	differentiated	1
Gentianidae	differentiated	0.9913
Rosidae	differentiated	0.9985
Malvidae	differentiated	0.9988
Fabidae	differentiated	0.9985

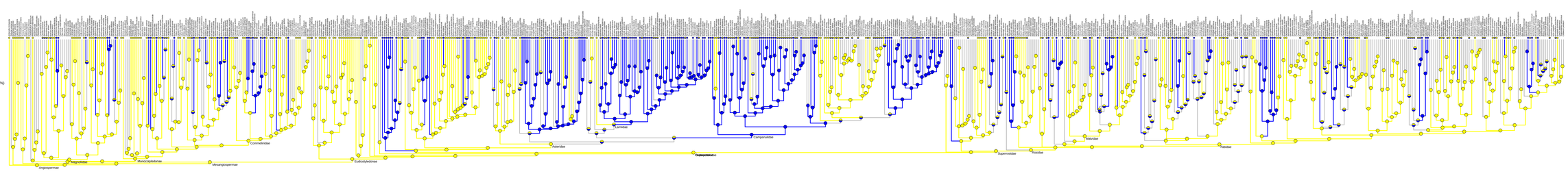
Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	-199.82	2	403.64	403.66	1.38	0.33	0.0046	0.0015
ARDeq**	-199.13	2	402.26	402.27	0	0.67	0.0046	0.0015
ER	-209.24	1	420.48	420.48	18.21	0	0.0025	0.0025
UN01	-229.29	1	458.58	458.59	56.32	0	0.0089	
UN10	-233.78	1	469.55	469.56	67.28	0		0.0034



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%)
Monocotyledonae	free (<5%)
Eudicotyledonae	free (<5%)
Commelinidae	free (<5%)
Ranunculidae	free (<5%)
Superasteridae	free (<5%)
Asteridae	free (<5%)
Lamidae	free (<5%) / fused (>5%)
Campanulidae	fused (>5%)
Rosanae	free (<5%)
Rosidae	free (<5%)
Malvidae	free (<5%)
Fabidae	free (<5%)



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

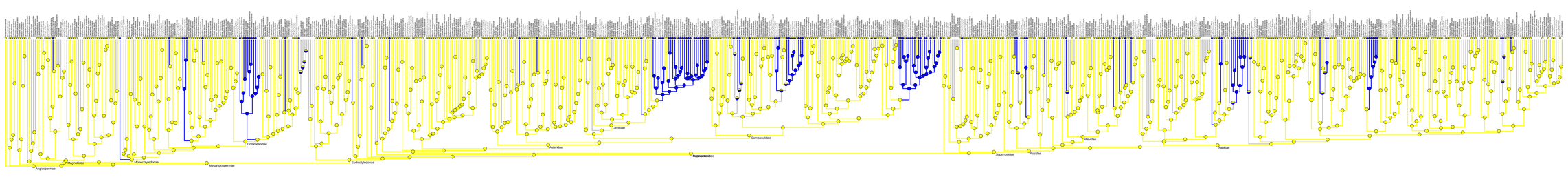
Node	ML state	Prob
Angiospermae	free (<5%)	1
Mesangiospermae	free (<5%)	1
Magnoliidae	free (<5%)	0.9999
Monocotyledoneae	free (<5%)	1
Eudicotyledoneae	free (<5%)	1
Commelinidae	free (<5%)	0.9991
Gunneridae	free (<5%)	0.9994
Superasteridae	free (<5%)	0.9994
Asteridae	free (<5%)	0.8583
Lamiidae	fused (>5%)	0.9506
Campanulidae	fused (>5%)	0.9276
Superrosidae	free (<5%)	0.9994
Rosidae	free (<5%)	0.9994
Malvidae	free (<5%)	0.9983
Fabidae	free (<5%)	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	-224.54	2	453.08	453.1	1.38	0.21	0.0044	0.0035
ARDeq*	-223.85	2	451.7	451.71	0	0.42	0.0044	0.0035
ER	-225.01	1	452.01	452.02	0.3	0.36	0.0042	0.0042
UN01	-236.28	1	474.56	474.57	22.85	0	0.0049	
UN10	-236.29	1	474.58	474.59	22.87	0		0.008

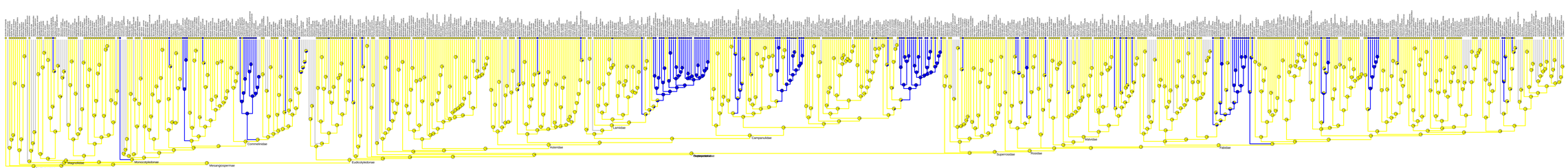
MP ancestral state reconstruction using ancestral.pars (R:phangorn)
207_A. Symmetry of perianth (binary) (D2d), 55 steps

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 rayDISC (R corHMM)
207_A. Symmetry of perianth (binary) (02d), ARDeq model



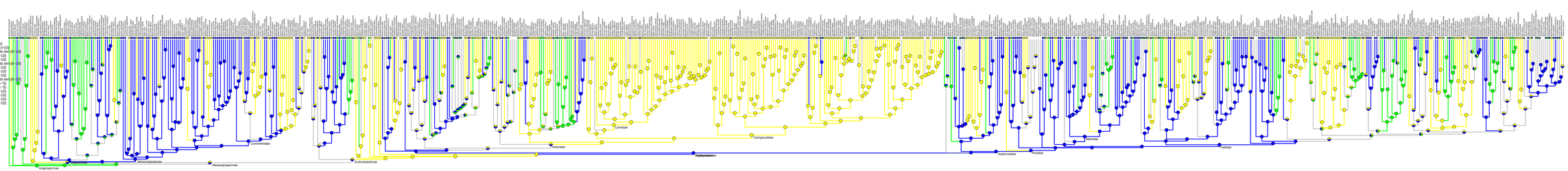
Node	ML state	Prob
Angiospermae	actinomorphic	1
Mesangiospermae	actinomorphic	1
Magnoliidae	actinomorphic	1
Monocotyledonae	actinomorphic	0.9997
Eudicotyledonae	actinomorphic	1
Commelinidae	actinomorphic	0.9978
Gunneridae	actinomorphic	1
Superasteridae	actinomorphic	1
Asteridae	actinomorphic	1
Lamiidae	actinomorphic	0.9998
Campanulidae	actinomorphic	1
Superrosidae	actinomorphic	1
Rosidae	actinomorphic	1
Malvidae	actinomorphic	0.9998
Fabidae	actinomorphic	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	−209.77	2	423.55	423.56	1.37	0.33	0.0014	0.0059
ARDeq**	−209.99	2	422.17	422.19	0	0.66	0.0014	0.0059
ER	−217.62	1	437.24	437.24	15.06	0	0.0015	0.0015
UN01	−258.94	1	519.88	519.88	97.7	0	0.0018	0
UN10	−216.82	1	435.64	435.64	13.45	0	0	0.0167

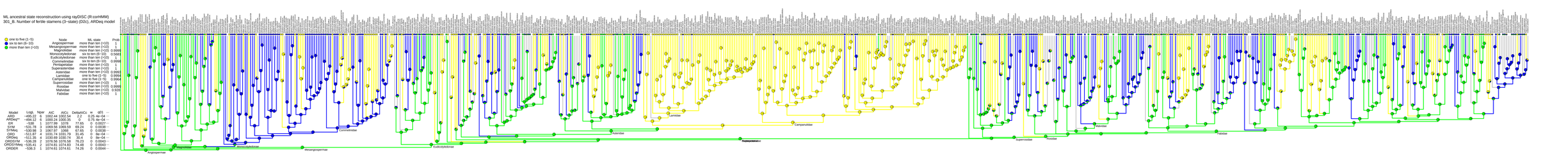
MP ancestral state reconstruction using ancestral pars
(R:phangorn)
301_B. Number of fertile stamens (3–state) (D2c), 157 steps

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) / six to ten (6–10)
Magnoliidae	six to ten (6–10)
Monocotyledonae	six to ten (6–10)
Eudicotyledonae	one to five (1–5) / six to ten (6–10)
Commelinidae	six to ten (6–10)
Ceratophyllum	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



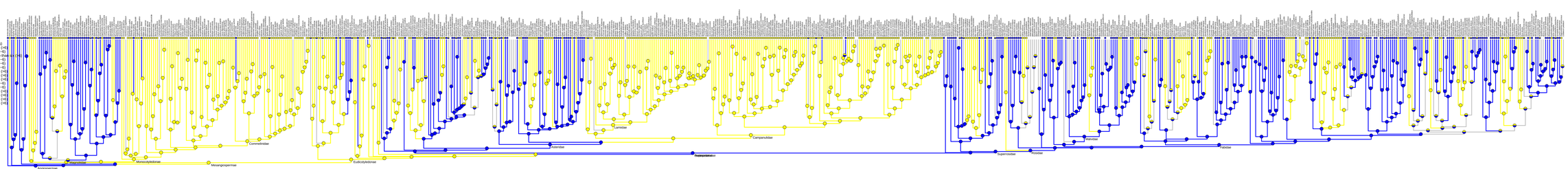
Node	ML state	Prob
Angiospermae	more than ten (>10)	1
Mesangiospermae	more than ten (>10)	1
Magnoliidae	more than ten (>10)	0.9998
Monocotyledoneae	six to ten (6–10)	0.5681
Eudicotyledoneae	more than ten (>10)	1
Commelinidae	six to ten (6–10)	0.9996
Gunneridae	more than ten (>10)	1
Superasteridae	more than ten (>10)	1
Asteridae	more than ten (>10)	0.9992
Lamiidae	one to five (1–5)	0.9994
Campanulidae	one to five (1–5)	0.9964
Superrosidae	more than ten (>10)	1
Rosidae	more than ten (>10)	0.9998
Malvidae	more than ten (>10)	0.938
Fabidae	more than ten (>10)	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01
ARD	−495.22	6	1002.44	1002.54	2.2	0.25	4e−04
ARDeq**	−494.12	6	1000.24	1000.35	0	0.75	4e−04
ER	−538	1	1077.99	1078	77.65	0	0.0037
SYM	−538.98	3	1083.96	1084.05	83.71	0	0.0038
SYMeq	−538.98	3	1067.95	1068	67.65	0	0.0038
ORD	−511.87	4	1031.74	1031.79	31.45	0	8e−04
ORDeq	−511.35	4	1030.69	1030.74	30.4	0	8e−04
ORDSYM	−536.28	2	1076.56	1076.58	76.23	0	0.0043
ORDSYMeq	−535.41	2	1074.81	1074.83	74.48	0	0.0043
ORDER	−536.3	1	1074.61	1074.61	74.26	0	0.0044

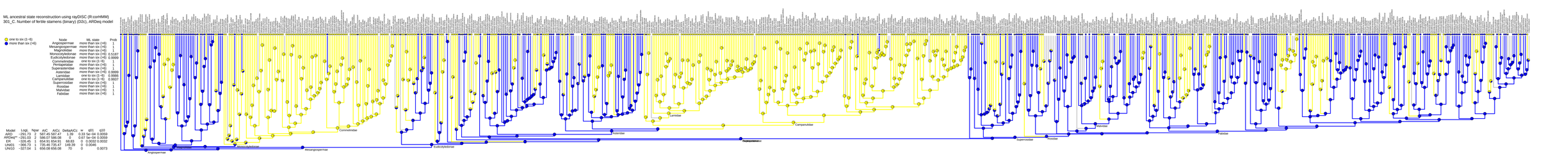
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
301_C. Number of fertile stamens (binary) (02c), 93 steps

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	one to six (1–6)
Ceratophyllidae	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) (02c), ARDeq model



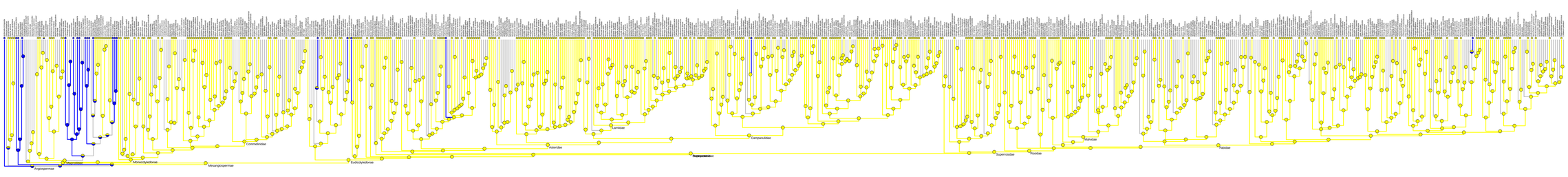
Node	ML state	Prob
Angiospermae	more than six (>6)	1
Mesangiospermae	more than six (>6)	1
Magnoliidae	more than six (>6)	1
Monocotyledonae	more than six (>6)	0.5187
Eudicotyledonae	more than six (>6)	0.9999
Commelinidae	one to six (1–6)	1
Gunneridae	more than six (>6)	1
Superasteridae	more than six (>6)	1
Asteridae	more than six (>6)	0.9999
Lamiidae	one to six (1–6)	0.9996
Campanulidae	one to six (1–6)	0.9937
Caryophyllidae	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	−291.73	2	587.45	587.47	1.39	0.33	5e−04	0.0059
ARDeq**	−291.03	2	586.07	586.08	0	0.67	5e−04	0.0059
ER	−326.45	1	654.91	654.91	68.83	0	0.0032	0.0032
UN01	−365.73	1	735.46	735.47	149.39	0	0.0046	
UN10	−327.04	1	656.08	656.08	70	0		0.0073

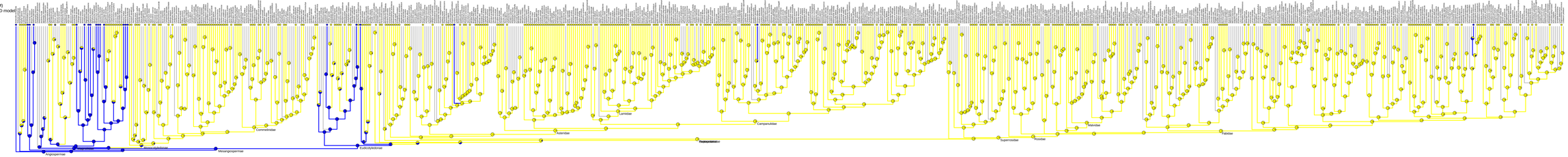
MP ancestral state reconstruction using ancestral pars
(R:phangorn)
330_A. Androecium structural phyllotaxy (binary) (D2d), 12 steps

whorled
spiral

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



ML ancestral state reconstruction using rayDISC (R:corHMM)
330_A. Androecium structural phylotaxy (binary) (D2z), ARD model



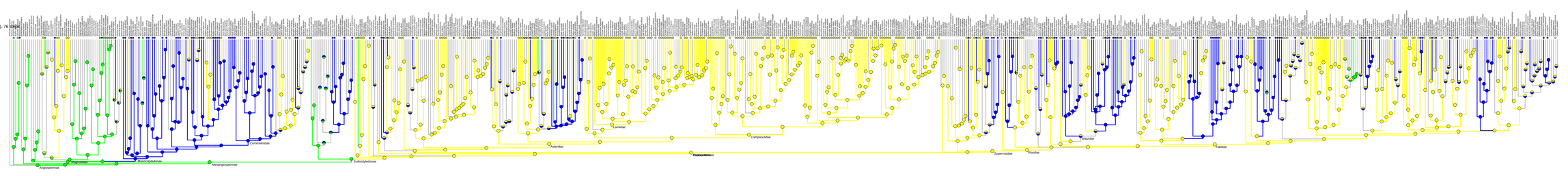
Node	ML state	Prob
Angiospermae	spiral	1
Mesangiospermae	spiral	0.9992
Magnoliidae	spiral	0.9982
Monocotyledonae	whorled	0.5792
Eudicotyledonae	spiral	0.9844
Commelinidae	whorled	0.9997
Gunneridae	whorled	0.9975
Superasteridae	whorled	0.9975
Asteridae	whorled	1
Lamiidae	whorled	1
Campanulidae	whorled	1
Superasteridae	whorled	0.9996
Rosidae	whorled	0.9997
Malvidae	whorled	1
Fabidae	whorled	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD***	-55.27	2	114.54	114.65	0	0.97	1e-04	0.0087
ARDeq	-59.88	2	123.77	123.78	9.23	0.01	4e-04	0
ER	-60.81	1	123.62	123.62	9.07	0.01	4e-04	4e-04
UN01	-60.58	1	123.16	123.16	8.61	0.01	4e-04	
UN10	-76.52	1	155.04	155.04	40.49	0		0.0211

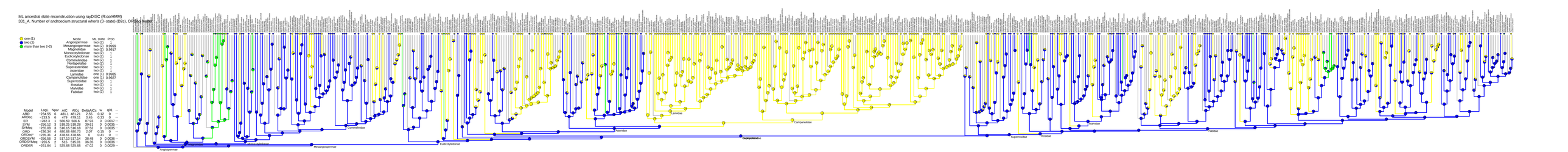
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
331_A. Number of androecium structural whorls (3–state) (D2c), 76 taxa

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

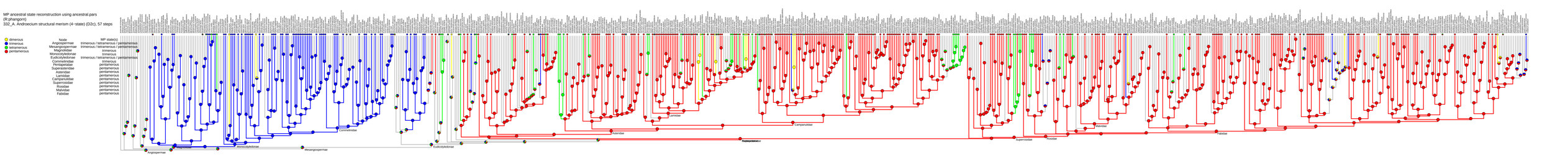
Node	MP state(s)
Angiospermae	more than two (>2)
Mesangiospermae	more than two (>2)
Magnoliidae	more than two (>2)
Monocotyledonae	two (2)
Eudicotyledonae	more than two (>2)
Commelinidae	two (2)
Ceratophyllum	two (2)
Superasteridae	one (1)
Asteridae	one (1)
Lamiidae	one (1)
Campanulidae	one (1)
Superrosidae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



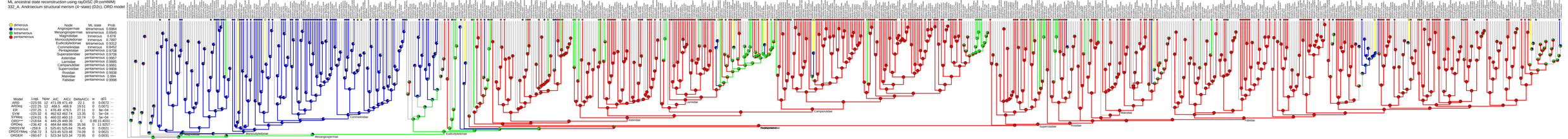
ML ancestral state reconstruction using rayDISC (R:corHMM)
331_A. Number of androecium structural whorls (3–state) (D2c), OR0deg model



Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	...
ARD	-234.55	6	481.1	481.21	2.55	0.12	0	...
ARDeq	-233.5	6	479	479.11	0.45	0.32	0	...
ER	-282.3	1	566.59	566.6	87.93	0	0.0017	...
SYM	-256.08	3	518.15	518.28	37.52	0	0.0035	...
SYMeq	-256.08	3	518.15	518.28	37.52	0	0.0035	...
ORD	-236.34	4	480.68	480.73	2.07	0.11	0	...
ORDeq*	-236.31	4	478.61	478.66	0	0.41	0	...
ORDSYM	-256.56	2	517.13	517.14	38.48	0	0.0036	...
ORDSYMeq	-255.5	2	515	515.01	36.35	0	0.0036	...
ORDER	-261.84	1	525.68	525.68	47.02	0	0.0029	...


MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
332_A. Androecium structural merism (4–state) (D2c), 57 steps
dimerous
trimerous
tetramerous
pentamerous
Node
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledoniae
Eudicotyledoniae
Commelinidae
Ranunculidae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Santalanae
Rosidae
Malvidae
Fabidae
MP state(s)
trimerous / tetramerous / pentamerous
trimerous / tetramerous / pentamerous
trimerous
trimerous
trimerous / tetramerous / pentamerous
trimerous
pentamerous
pentamerous
pentamerous
pentamerous
pentamerous
pentamerous
pentamerous
pentamerous
Angiospermae
Magnoliidae
Monocotyledoniae
Commelinidae
Mesangiospermae
Eudicotyledoniae
Asteridae
Lamiidae
Campanulidae
Superasteridae
Rosidae
Malvidae
Fabidae

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



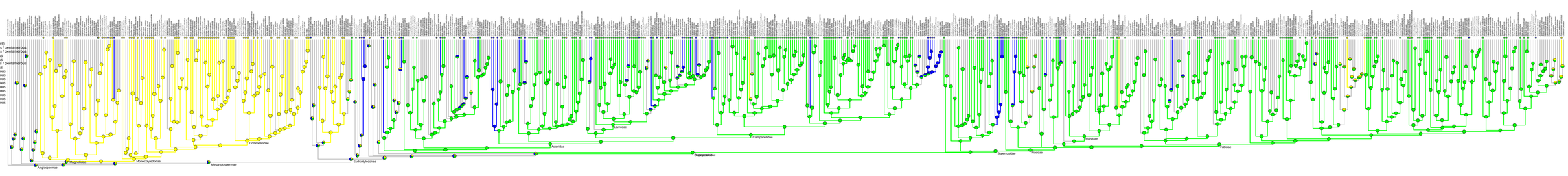
Node	ML state	Prob
Angiospermae	tetramerous	0.6854
Mesangiospermae	tetramerous	0.6945
Magnoliidae	trimerous	0.678
Monocotyledoneae	trimerous	0.7897
Eudicotyledoneae	tetramerous	0.9312
Commelinidae	trimerous	0.8452
Gunneridae	pentamerous	0.9708
Superasteridae	pentamerous	0.9728
Asteridae	pentamerous	0.9957
Lamiidae	pentamerous	0.9985
Campanulidae	pentamerous	0.9991
Superrosidae	pentamerous	0.9938
Rosidae	pentamerous	0.9938
Malvidae	pentamerous	0.994
Fabidae	pentamerous	0.9998

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	--
ARD	-223.55	12	471.09	471.49	22.1	0	0.0072	--
ARDeq	-222.25	12	468.5	468.9	19.51	0	0.0071	--
ER	-237.35	1	476.69	476.7	27.11	0	8e-04	--
SYM	-224.01	6	460.02	460.33	10.74	0	5e-04	--
SYMeq	-224.01	6	460.02	460.13	10.74	0	5e-04	--
ORD**	-218.64	6	449.28	449.39	0	0.99	15.4031	--
ORDeq	-236.42	6	484.84	484.95	35.56	0	11.9257	--
ORDSYM	-259.8	3	525.81	525.84	76.45	0	0.0021	--
ORDSYMeq	-258.72	3	523.45	523.48	74.09	0	0.0021	--
ORDER	-260.67	1	523.34	523.34	73.95	0	0.0031	--

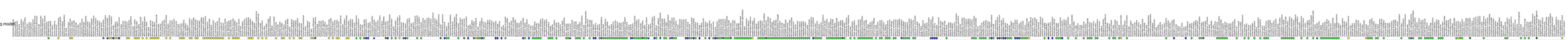
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
332_B. Androecium structural merism (3–state) (D2c), 48 steps

trimerous
tetramerous
pentamerous

Node	MP state(s)
Angiospermae	trimerous / tetramerous / pentamerous
Mesangiospermae	trimerous / tetramerous / pentamerous
Magnoliidae	trimerous
Monocotyledoneae	trimerous
Eudicotyledoneae	trimerous / tetramerous / pentamerous
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)
332_B. Androecium structural merism (3–state) (D2c), SYMeq model



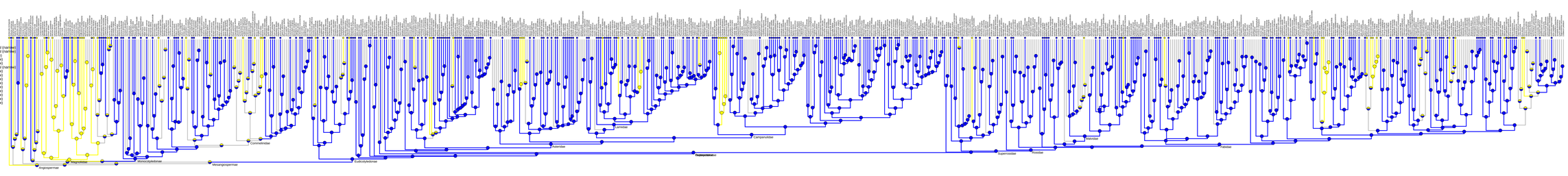
Node	ML state	Prob
Angiospermae	trimerous	0.9999
Mesangiospermae	trimerous	0.9985
Magnoliidae	trimerous	1
Monocotyledoneae	trimerous	1
Eudicotyledoneae	trimerous	0.9633
Commelinidae	trimerous	1
Gunneridae	pentamerous	0.9999
Superasteridae	pentamerous	0.9999
Asteridae	pentamerous	0.9997
Lamiidae	pentamerous	0.999
Campanulidae	pentamerous	1
Superrosidae	pentamerous	1
Rosidae	pentamerous	1
Malvidae	pentamerous	1
Fabidae	pentamerous	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	...
ARD	-176.92	6	365.85	365.96	7.74	0.01	5e−04	...
ARDeq	-176.95	6	363.89	364	5.78	0.03	5e−04	...
ER	-185.99	1	373.98	373.98	15.77	0	0.0011	...
SYM	-176.9	3	359.8	359.88	1.67	0.31	5e−04	...
SYMeq*	-176.09	3	358.19	358.22	0	0.62	5e−04	...
ORD	-178.11	4	364.22	364.27	6.05	0.03	5e−04	...
ORDeq	-177.21	4	362.42	362.47	4.25	0.07	3e−04	...
ORDSYM	-186.25	2	376.49	376.51	18.29	0	0.002	...
ORDSYMeq	-185.32	2	374.64	374.66	16.44	0	0.002	...
ORDER	-186.96	1	375.91	375.92	17.7	0	0.0027	...

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

laminar (wide)
typical (narrow)

Node	MP state(s)
Angiospermae	laminar (wide) / typical (narrow)
Mesangiospermae	laminar (wide) / typical (narrow)
Magnoliidae	laminar (wide)
Monocotyledonae	typical (narrow)
Eudicotyledonae	typical (narrow)
Commelinidae	laminar (wide) / 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)

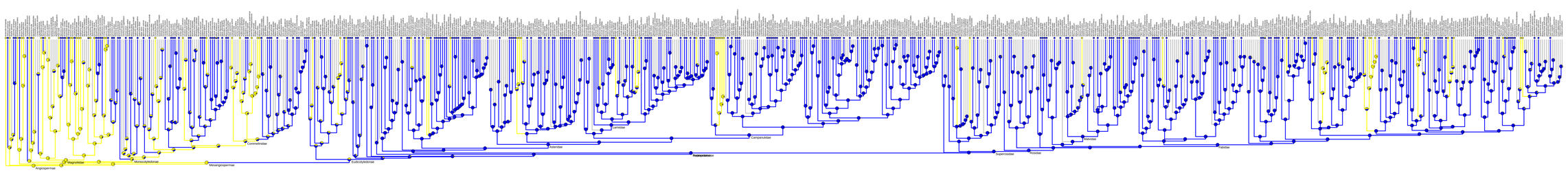


ML ancestral state reconstruction using rayDISC (R:corHMM)
305_A. Filament (binary) (D2d), ARDeq model

laminar (wide)
typical (narrow)

Node	ML state	Prob
Angiospermae	laminar (wide)	1
Mesangiospermae	laminar (wide)	0.9953
Magnoliidae	laminar (wide)	0.5978
Monocotyledonae	laminar (wide)	0.851
Eudicotyledonae	typical (narrow)	0.5337
Commelinidae	laminar (wide)	0.6355
Ceratophyllum	laminar (wide)	0.9981
Superasteridae	typical (narrow)	0.9981
Asteridae	typical (narrow)	0.9995
Lamidae	typical (narrow)	0.9971
Campanulidae	typical (narrow)	0.9945
Superrosidae	typical (narrow)	0.9993
Rosidae	typical (narrow)	0.9993
Malvidae	typical (narrow)	0.997
Fabidae	typical (narrow)	1

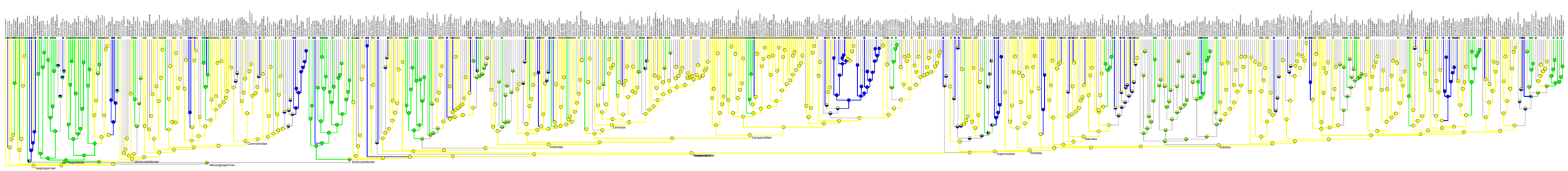
Model	LogL	Nopr	AIC	AICc	DeltaAICc	w	q01	q10
ARD	−173.1	2	350.21	350.22	1.32	0.34	0.0092	0.0022
ARDeq**	−172.45	2	348.89	348.91	0	0.66	0.0093	0.0021
ER	−176.67	1	359.33	359.34	10.43	0	0.0024	0.0024
UN01	−184.89	1	371.78	371.78	22.88	0	0.0147	
UN10	−187.98	1	377.95	377.96	29.05	0		0.0023



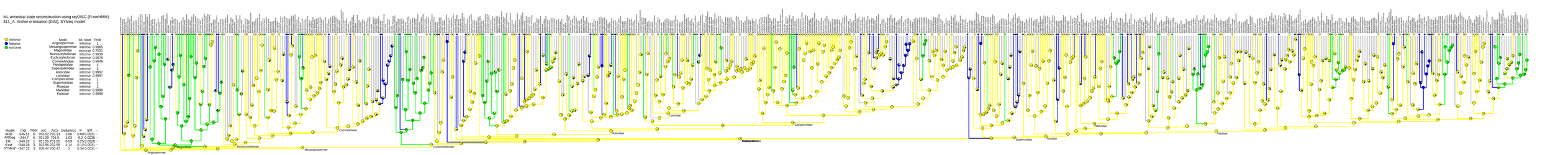
MP ancestral state reconstruction using ancestral.pars (R:phangorn)
311_A. Anther orientation (D2d), 110 steps

- introrse
- latrorse
- extrorse

Node	MP state(s)
Angiospermae	introrse
Mesangiospermae	introrse / extrorse
Magnoliidae	extrorse
Monocotyledoneae	introrse
Eudicotyledoneae	introrse / extrorse
Commelinidae	introrse
Ranunculidae	introrse
Superasteridae	introrse
Asteridae	introrse
Lamiidae	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

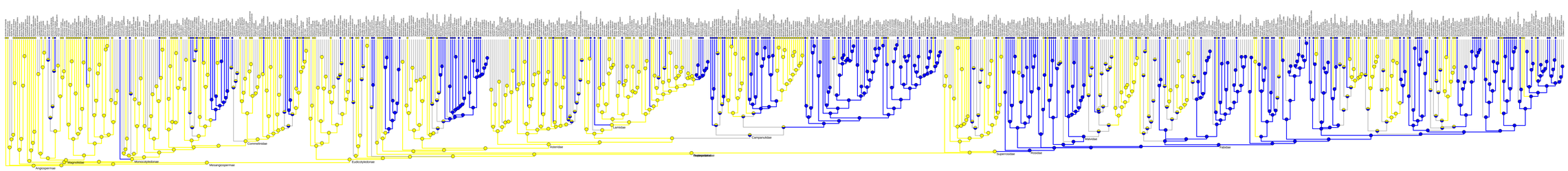


Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	--
ARD	-345.51	6	703.02	703.13	2.66	0.09	0.0031	---
ARDeq	-344.7	4	701.39	701.5	1.03	0.2	0.0038	---
ER	-349.52	1	701.05	701.05	0.59	0.25	0.0028	---
SYM	-348.28	3	702.56	702.59	2.12	0.12	0.0031	---
SYMeq*	-347.22	3	700.44	700.47	0	0.34	0.0031	---

MP ancestral state reconstruction using ancestral pars
(R:phangorn)
312_A. Anther attachment (binary) (D2d), 96 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
Lamiidae	basifixed
Campanulidae	basifixed / dorsifixed
Superrosidae	dorsifixed
Rosidae	dorsifixed
Malvidae	dorsifixed
Fabidae	dorsifixed

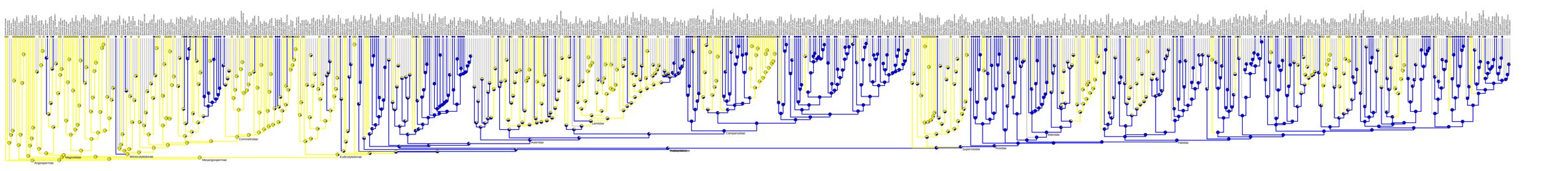


ML ancestral state reconstruction using ratDISC (R:corHMM)
312_A. Anther attachment (binary) (D2d), ARDeq model

basifixed
dorsifixed

Node	ML state	Prob
Angiospermae	basifixed	1
Mesangiospermae	basifixed	0.9994
Magnoliidae	basifixed	0.9993
Monocotyledonae	basifixed	0.9964
Eudicotyledonae	basifixed	0.9849
Commelinidae	basifixed	0.9857
Ranunculidae	basifixed	0.9638
Superasteridae	dorsifixed	0.7638
Asteridae	dorsifixed	0.7705
Lamidae	basifixed	0.5045
Campanulidae	dorsifixed	0.9267
Superrosidae	dorsifixed	0.8723
Rosidae	dorsifixed	0.8723
Malvidae	dorsifixed	0.9743
Fabidae	dorsifixed	0.9994

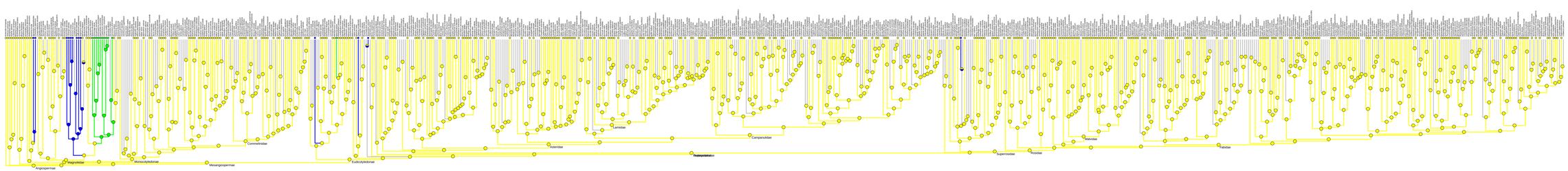
Model	LogL	Nstr	AIC	AICc	DeltaAICc	w	q01	q10
ARD	−265.7	2	535.4	535.41	1.34	0.27	0.0045	0.0073
ARDeq**	−265.03	2	534.06	534.08	0	0.53	0.0045	0.0073
ER	−266.99	1	535.98	535.99	1.91	0.2	0.0055	0.0055
UN01	−262.69	1	587.37	587.38	53.3	0	0.0061	
UN10	−277.87	1	557.73	557.74	23.66	0		0.008



MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
313_A. Anther dehiscence (3-state) (0/2d), 10 steps

longitudinal slit
N—valvate
flap—valvate

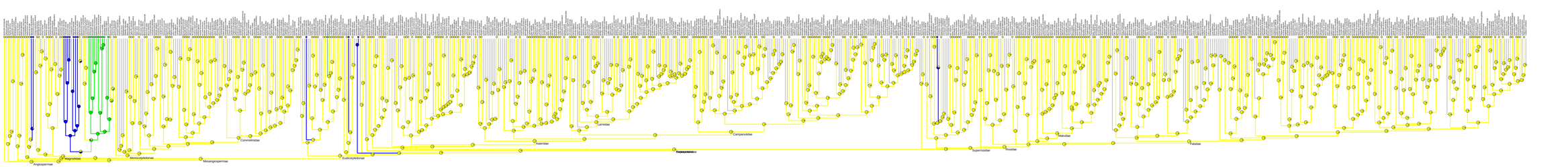
Node	MP state(s)
Angiospermae	longitudinal slit
Mesangiospermae	longitudinal slit
Magnoliidae	longitudinal slit
Monocotyledonae	longitudinal slit
Eudicotyledonae	longitudinal slit
Commelinidae	longitudinal slit
Ranunculidae	longitudinal slit
Superasteridae	longitudinal slit
Asteridae	longitudinal slit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



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

Node	ML state	Prob
Angiospermae	longitudinal slit	1
Mesangiospermae	longitudinal slit	1
Magnoliidae	longitudinal slit	0.9994
Monocotyledonae	longitudinal slit	1
Eudicotyledonae	longitudinal slit	1
Commelinidae	longitudinal slit	1
Ranunculidae	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
Fabidae	longitudinal slit	1

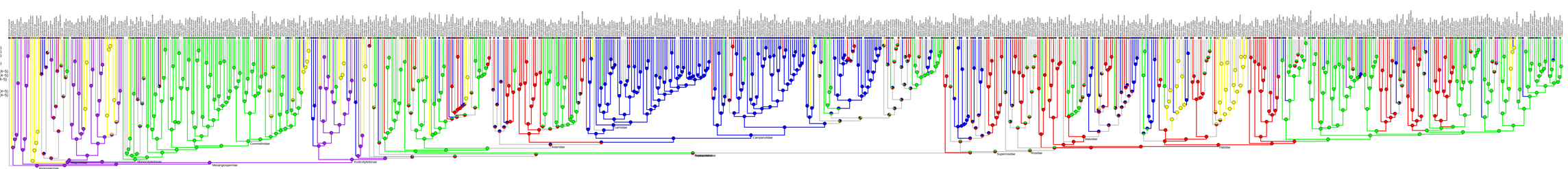
Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	···
ARD	−56.78	6	125.55	125.66	2.19	0.13	2e−04	···
ARDeq*	−55.68	6	123.36	123.47	0	0.38	2e−04	···
ER	−61.41	1	124.81	124.82	1.35	0.2	2e−04	···
SYM	−60.38	3	126.77	126.8	3.33	0.07	2e−04	···
SYMeq	−59.29	3	124.57	124.6	1.14	0.22	2e−04	···



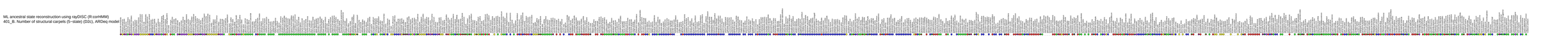
MP ancestral state reconstruction using ancestral pars
(R phangorn)
401_B. Number of structural carpels (5−state) (D2c), 187 steps

- 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	three (3)
Ceratophyllidae	three (3) / four or five (4–5)
Superasteridae	three (3) / four or five (4–5)
Asteridae	two (2) / four or five (4–5)
Lamidae	two (2)
Campanulidae	two (2)
Superrosidae	three (3) / four or five (4–5)
Rosidae	three (3) / four or five (4–5)
Malvidae	four or five (4–5)
Fabidae	four or five (4–5)



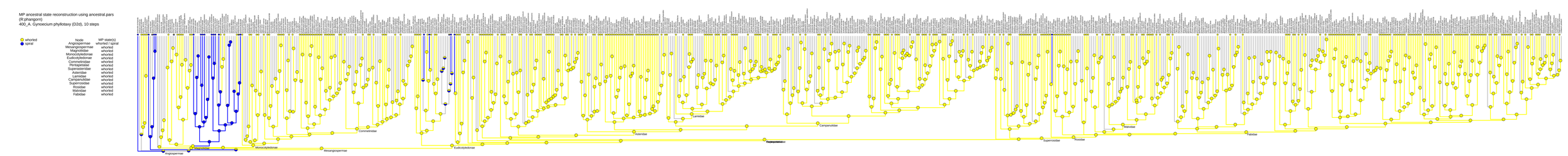
ML ancestral state reconstruction using rayDISC (R:corHMM)
401_B. Number of structural carpels (5-state) (D2c), ARDeq model



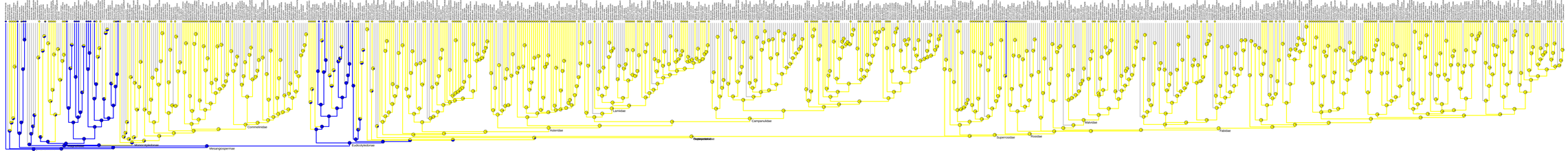
Node	ML state	Prob
Angiospermae	more than five (>5)	1
Mesangiospermae	more than five (>5)	1
Magnoliidae	more than five (>5)	1
Monocotyledoneae	more than five (>5)	0.8204
Eudicotyledoneae	more than five (>5)	0.9956
Commelinidae	three (3)	0.9999
Gunneridae	four or five (4–5)	0.9999
Superasteridae	four or five (4–5)	0.9999
Asteridae	four or five (4–5)	0.9953
Lamiidae	two (2)	0.9968
Campanulidae	two (2)	0.9551
Superrosidae	four or five (4–5)	0.9999
Rosidae	four or five (4–5)	0.9998
Malvidae	four or five (4–5)	0.9991
Fabidae	four or five (4–5)	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	—
ARD	−665.28	20	1370.55	1371.64	3.22	0.17	0.0017	—
ARDeq*	−669.67	20	1367.33	1368.42	0	0.83	0.0017	—
ER	−720.04	1	1442.09	1442.09	73.67	0	0.0016	—
SYM	−694.89	10	1409.77	1410.05	41.63	0	8e−04	—
SYMeq	−694.89	10	1399.78	1400.06	31.63	0	8e−04	—
ORD	−760.36	8	1536.72	1536.9	168.48	0	0.001	—
ORDeq	−758.84	8	1533.69	1533.87	165.45	0	0.001	—
ORDSYM	−764.3	4	1536.59	1536.64	168.22	0	0.0042	—
ORDSYMeq	−762.85	4	1533.7	1533.75	165.33	0	0.0042	—
ORDER	−769.83	1	1541.66	1541.67	173.25	0	0.0059	—

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



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



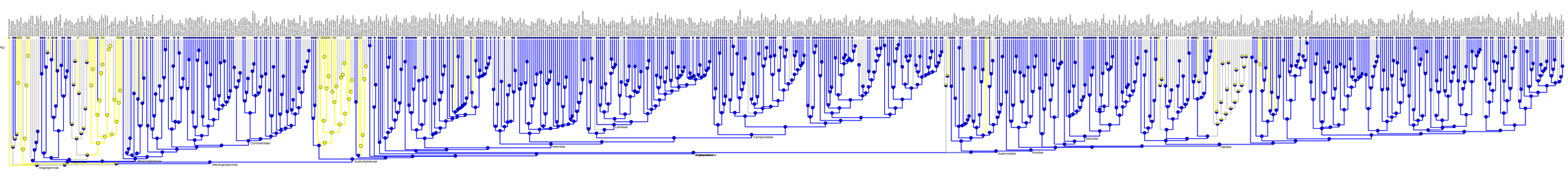
Node	ML state	Prob
Angiospermae	spiral	1
Mesangiospermae	spiral	1
Magnoliidae	spiral	0.9997
Monocotyledonae	whorled	0.5317
Eudicotyledonae	spiral	0.9997
Gunneridae	whorled	0.9997
Pentapetalae	whorled	0.9997
Superasteridae	whorled	0.9746
Asteridae	whorled	1
Lamidae	whorled	1
Campanulidae	whorled	1
Superrosidae	whorled	0.9775
Rosidae	whorled	0.9777
Malvidae	whorled	1
Fabidae	whorled	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	-39.73	2	83.46	83.48	1.39	0.31	1e-04	0.0083
ARDeq**	-39.04	2	82.07	82.09	0	0.62	1e-04	0.0083
ER	-51.33	1	104.66	104.66	22.57	0	4e-04	4e-04
UN01	-52.95	1	107.89	107.9	25.81	0	4e-04	
UN10	-42.27	1	86.55	86.55	4.46	0.07		0.0098

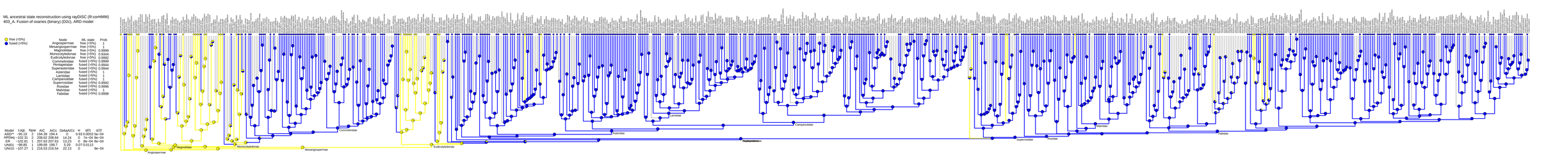
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
403_A. Fusion of ovaries (binary) (D2c), 24 steps

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%)
Ranunculidae	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 ray[DISC (R:corHMM)
403_A. Fusion of ovaries (binary) (D2c), ARD model

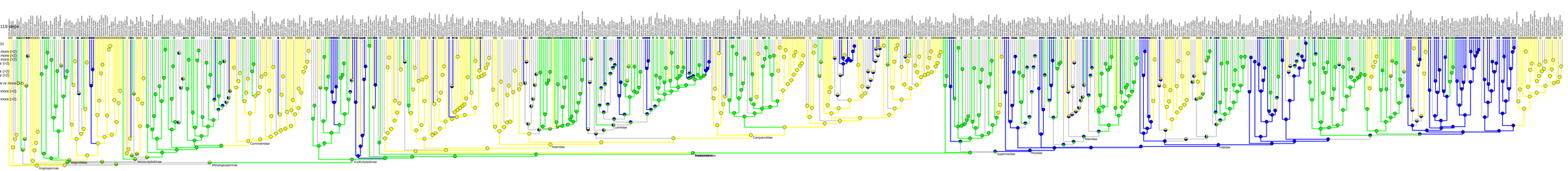


Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD**	-95.19	2	194.39	194.4	0	0.93	0.0053	5e−04
ARDeq	-102.31	2	208.62	208.64	14.24	0	7e−04	8e−04
ER	-102.81	1	207.63	207.63	13.23	0	8e−04	8e−04
UN01	-98.85	1	199.69	199.7	5.29	0.07	0.0113	
UN10	-107.27	1	216.53	216.54	22.13	0		9e−04

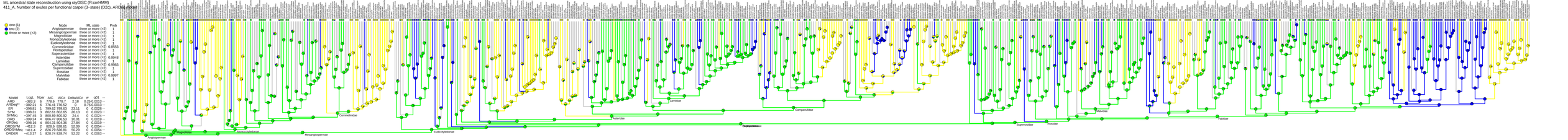
MP ancestral state reconstruction using ancestral pars
(R phangorn)
411_A. Number of ovules per functional carpel (3–state) (D2c), 119 taxa

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

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



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



Node	ML state	Prob
Angiospermae	three or more (>2)	1
Mesangiospermae	three or more (>2)	1
Magnoliidae	three or more (>2)	1
Monocotyledoneae	three or more (>2)	1
Eudicotyledoneae	three or more (>2)	1
Commelinidae	three or more (>2)	0.8553
Gunneridae	three or more (>2)	1
Superasteridae	three or more (>2)	1
Asteridae	three or more (>2)	0.9948
Lamiidae	three or more (>2)	1
Campanulidae	three or more (>2)	0.9983
Pentapetalae	three or more (>2)	1
Rosidae	three or more (>2)	1
Malvidae	three or more (>2)	0.9997
Fabidae	three or more (>2)	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	...
ARD	-383.3	6	778.6	779.7	2.18	0.25	0.0013	...
ARDeq**	-382.21	6	776.41	777.52	0	0.75	0.0013	...
ER	-398.81	1	799.62	799.63	23.11	0	0.0028	...
SYM	-397.45	3	800.9	800.93	24.41	0	0.0024	...
SYMeq	-397.45	3	800.89	800.92	24.4	0	0.0024	...
ORD	-399.24	4	806.47	806.53	30.01	0	0.0019	...
ORDeq	-399.16	4	804.31	804.36	27.84	0	0.0019	...
ORDSYM	-412.3	2	828.6	828.61	52.09	0	0.0054	...
ORDSYMeq	-411.4	2	826.79	826.81	50.29	0	0.0054	...
ORDER	-413.37	1	828.74	828.74	52.22	0	0.0063	...