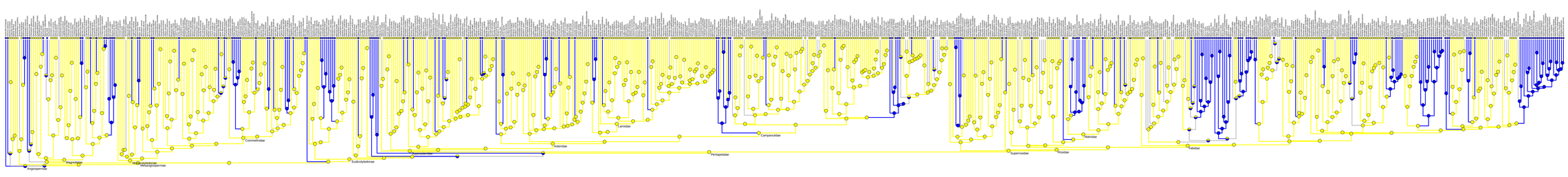
MP ancestral state reconstruction using ancestral pars
(R phangorn)
100_A. Functional sex of flowers (D2d), 96 steps

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

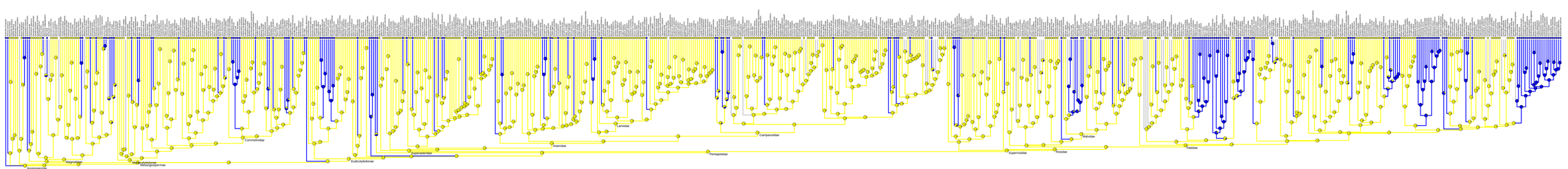


ML ancestral state reconstruction using rayDISC (R:corHMM) 100_A. Functional sex of flowers (0/2d), ARDeq model

bisexual
unisexual

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

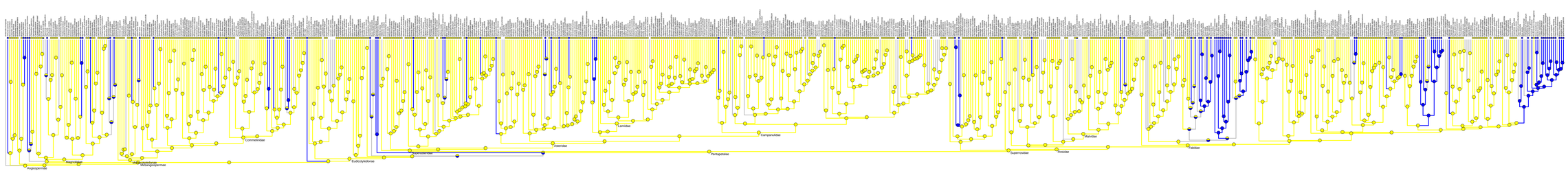
Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	-311.35	2	626.69	626.71	1.38	0.21	0.0029	6e−04
ARDeq*	-310.95	2	625.91	625.32	0	0.42	0.0029	6e−04
ER	-314.41	1	630.81	630.82	5.49	0.03	0.0029	0.0029
UN01	-311.97	1	625.73	625.74	0.41	0.34	0.003	
UN10	-354.14	1	710.28	710.29	84.96	0		0.012



MP ancestral state reconstruction using ancestral pars
(R phangorn)
100_B. Structural sex of flowers (02d), 55 steps

bisexual
unisexual

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

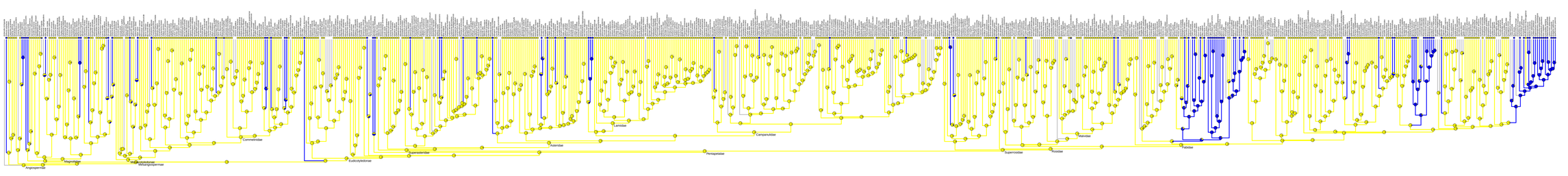


ML ancestral state reconstruction using rayDISC (R:corHMM) 100_B. Structural sex of flowers (D2d), ARDeq model

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
Ceratophyllidae	bisexual	1
Superasteridae	bisexual	1
Asteridae	bisexual	1
Lamidae	bisexual	0.9999
Campanulidae	bisexual	1
Superrosidae	bisexual	1
Rosidae	bisexual	1
Malvidae	bisexual	1
Fabidae	bisexual	0.9998

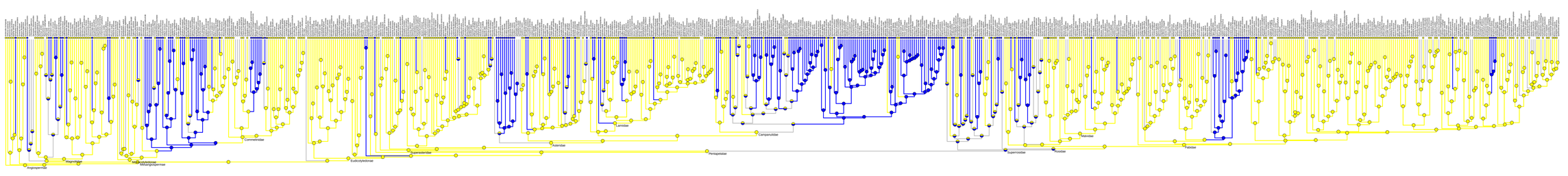
Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	−206.94	2	417.87	417.89	1.36	0.3	0.0015	0.0039
ARDeq**	−206.26	2	416.51	416.53	0	0.59	0.0015	0.0038
ER	−208.93	1	419.85	419.86	3.33	0.11	0.0016	0.0016
UNI01	−223.89	1	449.78	449.79	33.26	0	0.0017	
UNI10	−230.84	1	463.67	463.68	47.15	0		0.0167



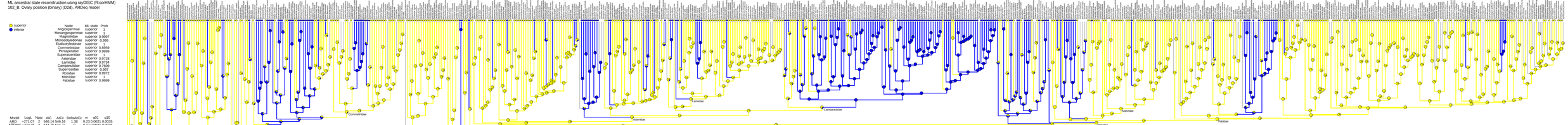
MP ancestral state reconstruction using ancestral pars
(R phangorn)
102_B. Ovary position (binary) (0≥0), 81 steps

superior
inferior

Node	MP state(s)
Angiospermae	superior
Mesangiospermae	superior
Magnoliidae	superior
Monocotyledoneae	superior
Eudicotyledoneae	superior
Commelinidae	superior
Ceratophyllidae	superior
Superasteridae	superior
Asteridae	superior
Lamiidae	superior
Campanulidae	superior
Superrosidae	superior / inferior
Rosidae	superior / inferior
Malvidae	superior
Fabidae	superior



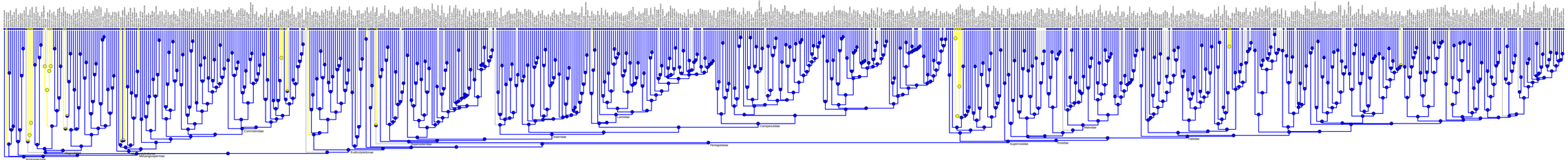
ML ancestral state reconstruction using rayDISC (R:corHMM)
102_B. Ovary position (binary) (D2d), ARDeq model



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

absent
present

node	MP state(s)
Angiospermae	present
Mesangiospermae	present
Magnoliidae	present
Monocotyledoneae	present
Eudicotyledoneae	present
Commelinidae	present
Ceratophyllum	present
Superasteridae	present
Asteridae	present
Lamiidae	present
Campanulidae	present
Superrosidae	present
Rosidae	present
Malvidae	present
Fabidae	present

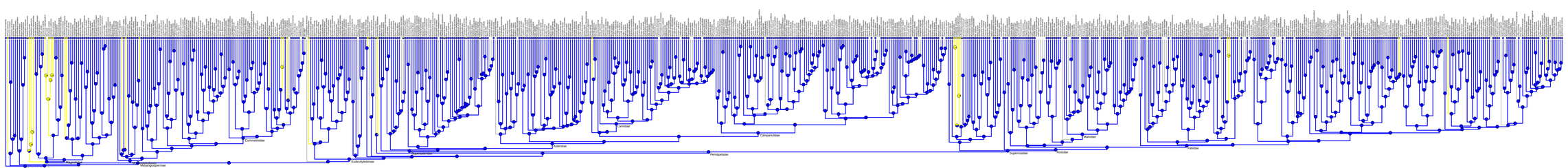


ML ancestral state reconstruction using ray[DISC (R:corHMM)
201_A. Perianth presence (D2c), UNI10 model

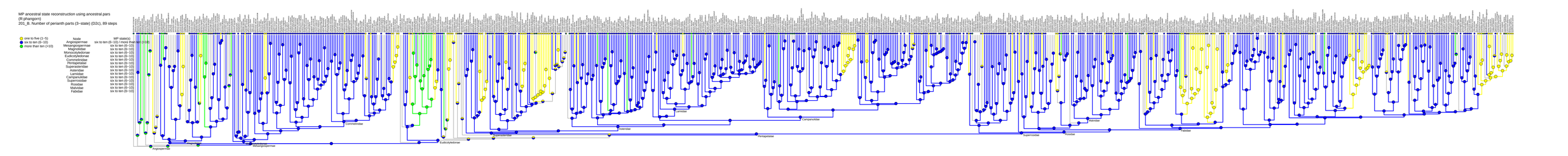
absent
present

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	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	−95.82	2	195.63	195.65	2.01	0.13	0	5e−04
ARDeq	−95.12	2	194.25	194.26	0.62	0.26	0	5e−04
ER	−96.11	1	194.22	194.22	0.58	0.26	5e−04	5e−04
UNI01	−109.95	1	221.9	221.91	28.27	0	0.0225	
UNI10*	−95.82	1	193.63	193.64	0	0.35		5e−04



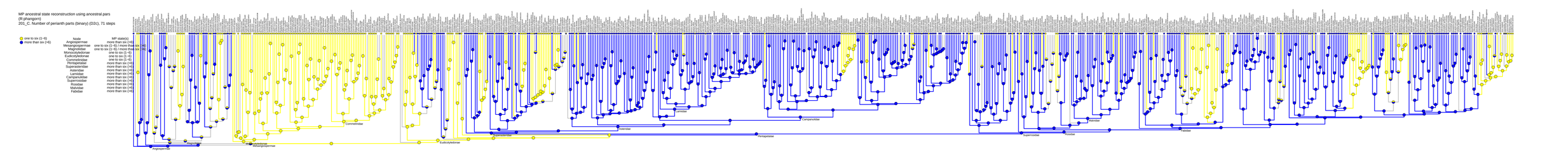
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
201_B. Number of perianth parts (3–state) (D2c), 89 steps



Node	ML state	Prob
Angiospermae	more than ten (>10)	1
Mesangiospermae	more than ten (>10)	0.9998
Magnoliidae	more than ten (>10)	0.9999
Monocotyledonae	six to ten (6–10)	0.5214
Eudicotyledonae	more than ten (>10)	0.995
Commelinidae	six to ten (6–10)	0.9998
Lamiidae	six to ten (6–10)	0.9999
Superasteridae	six to ten (6–10)	0.9979
Asteridae	six to ten (6–10)	0.9999
Lamiidae	six to ten (6–10)	0.9998
Campanulidae	six to ten (6–10)	0.9998
Superrosidae	six to ten (6–10)	0.9993
Rosidae	six to ten (6–10)	0.9993
Malvidae	six to ten (6–10)	0.9998
Fabidae	six to ten (6–10)	0.9994

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	--
ARD	−329	6	670	670.11	2.2	0.25	0.0047	--
ARDeq**	−327.9	6	667.81	667.91	0	0.74	0.0047	--
ER	−356.1	1	714.2	714.2	46.29	0	0.0013	--
SYM	−340.98	3	687.96	688.06	20.15	0	0.0022	--
SYMeq	−342.98	3	691.95	691.95	24.03	0	0.0022	--
ORD	−334.95	4	677.9	677.95	10.03	0	0.0048	--
ORDeq	−333.85	4	675.7	675.75	7.84	0.01	0.0048	--
ORDSYM	−346.35	2	696.69	696.71	28.79	0	0.0022	--
ORDSYMeq	−345.29	2	694.58	694.6	26.68	0	0.0022	--
ORDER	−356.72	1	715.44	715.44	47.53	0	0.0015	--

MP ancestral state reconstruction using ancestral.pars
(R phangorn)
201_C. Number of perianth parts (binary) (D2c), 71 steps



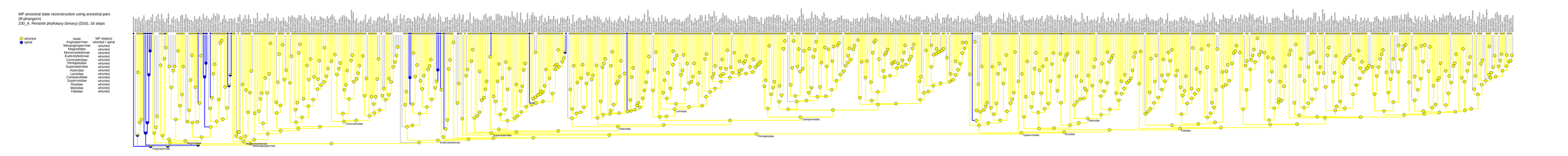
ML ancestral state reconstruction using rayDISC (R:corHMM)
201_C. Number of perianth parts (binary) (D2c), ARDeq model

- one to six (1−6)
- more than six (>6)

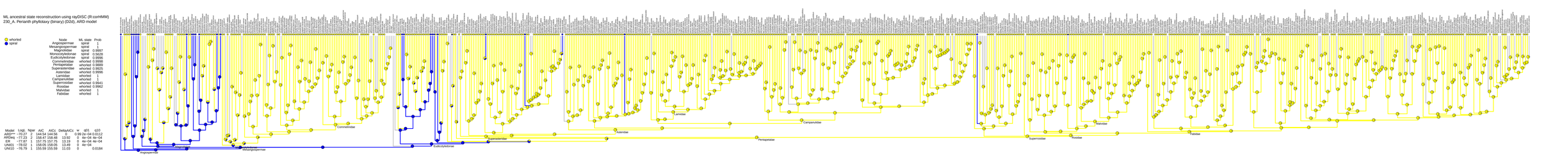
Node	ML state	Prob
Angiospermae	more than six (>6)	1
Mesangiospermae	more than six (>6)	1
Magnoliidae	more than six (>6)	1
Monocotyledonae	one to six (1−6)	0.7668
Eudicotyledonae	more than six (>6)	1
Commelinidae	one to six (1−6)	1
Pentapetalae	more than six (>6)	1
Superasteridae	more than six (>6)	1
Asteridae	more than six (>6)	1
Lamiidae	more than six (>6)	1
Campanulidae	more than six (>6)	1
Superrosidae	more than six (>6)	1
Rosidae	more than six (>6)	1
Malvidae	more than six (>6)	1
Fabidae	more than six (>6)	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	−252.06	2	508.11	508.13	1.39	0.25	5e−04	0.0027
ARDeq*	−251.36	2	506.72	506.74	0	0.49	5e−04	0.0027
ER	−258.22	1	518.45	518.45	11.71	0	0.0022	0.0022
UNI01	−324.04	1	650.07	650.08	143.34	0	0.0083	
UNI10	−253.02	1	508.03	508.04	1.3	0.26		0.0029

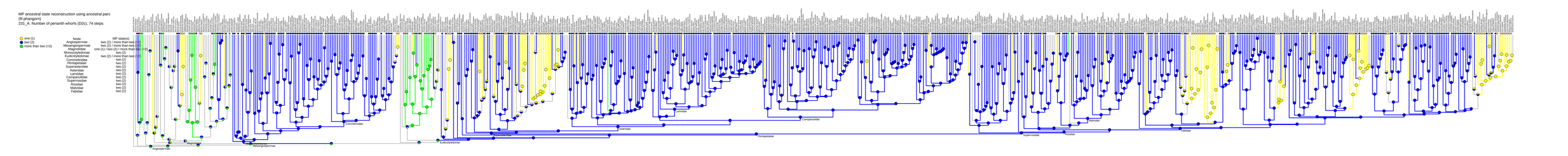
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
230_A. Perianth phyllotaxy (binary) (D2d), 16 steps



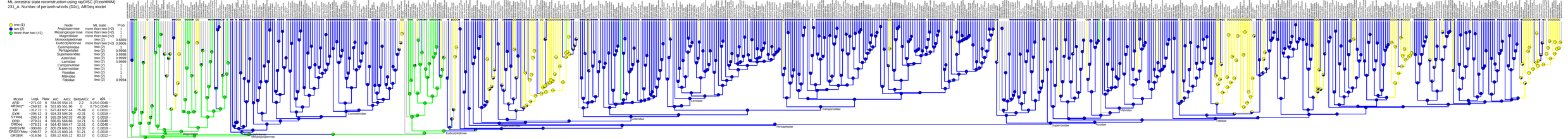
ML ancestral state reconstruction using rayDISC (R:corHMM)
230_A. Perianth phyllotaxy (binary) (D2d), ARD model



MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
231_A. Number of perianth whorls (D2c), 74 steps



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



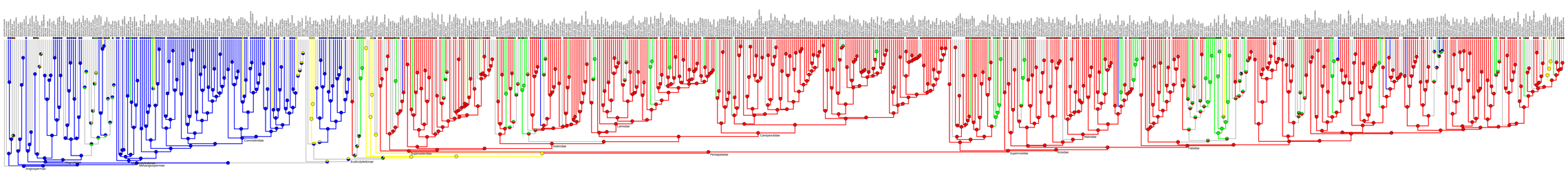
Node	ML state	Prob
Angiospermae	more than two (>2)	1
Mesangiospermae	more than two (>2)	1
Magnoliidae	more than two (>2)	1
Monocotyledonae	two (2)	0.6869
Eudicotyledonae	more than two (>2)	0.9905
Gunneridae	two (2)	1
Pentapetalae	two (2)	0.9998
Superrosidae	two (2)	0.9998
Asteridae	two (2)	0.9999
Lamiidae	two (2)	0.9999
Campanulidae	two (2)	1
Asteranae	two (2)	1
Rosidae	two (2)	1
Malvidae	two (2)	1
Fabidae	two (2)	0.9994

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	--
ARD	-271.02	6	554.05	554.15	2.2	0.25	0.0048	--
ARDeq**	-269.92	6	551.85	551.96	0	0.75	0.0048	--
ER	-312.72	1	627.43	627.44	75.48	0	0.0011	--
SYM	-310.14	3	626.28	626.42	74.46	0	0.0019	--
SYMeq	-309.14	3	625.29	625.42	73.46	0	0.0019	--
ORD	-279.31	4	566.61	566.66	14.71	0	0.0048	--
ORDeq	-278.21	4	564.42	564.47	12.51	0	0.0048	--
ORDSYM	-300.65	2	605.29	605.31	53.35	0	0.0019	--
ORDSYMeq	-299.57	2	603.15	603.16	51.21	0	0.0019	--
ORDER	-316.56	1	635.12	635.12	83.17	0	0.0012	--

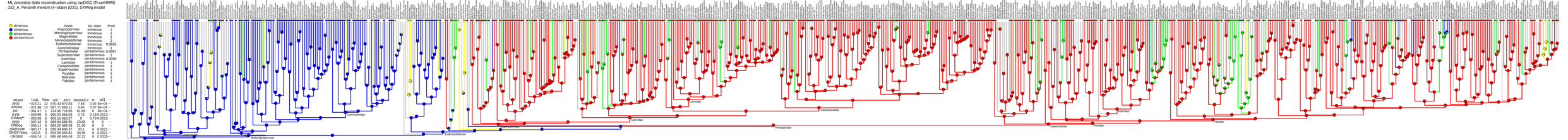
MP ancestral state reconstruction using ancestral pars
(R:phangorn)
232_A. Perianth merism (4–state) (D2c), 84 steps

- dimerous
- trimerous
- tetramerous
- pentamerous

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



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



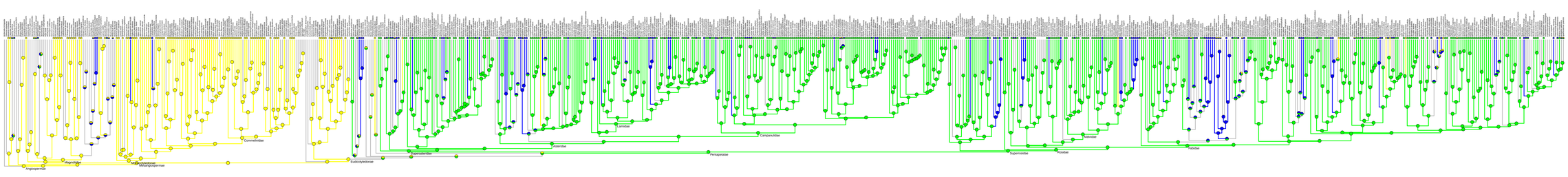
Node	ML state	Prob
Angiospermae	trimerous	1
Mesangiospermae	trimerous	1
Magnoliidae	trimerous	1
Monocotyledonae	trimerous	1
Eudicotyledonae	trimerous	0.9626
Commelinidae	trimerous	1
Ranunculidae	pentamerous	0.9997
Superasteridae	pentamerous	1
Asteridae	pentamerous	0.9999
Lamiidae	pentamerous	1
Campanulidae	pentamerous	1
Rosidae	pentamerous	1
Rosidae	pentamerous	1
Malvidae	pentamerous	1
Fabidae	pentamerous	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	--
ARD	-323.21	12	670.43	670.83	7.56	0.02	8e−04	--
ARDeq	-321.86	12	667.71	668.11	4.84	0.07	8e−04	--
ER	-361.47	1	724.95	724.95	61.69	0	8e−04	--
SYM	-325.58	6	663.16	663.27	0	0.18	0.0013	--
SYMeq	-325.58	6	663.16	663.27	0	0.18	0.0013	--
ORD	-337.42	6	686.84	686.95	23.68	0	0	--
ORDeq	-336.11	6	684.22	684.33	21.06	0	0	--
ORDSYM	-345.17	3	696.34	696.37	33.1	0	0.0021	--
ORDSYMeq	-343.8	3	693.59	693.62	30.36	0	0.0021	--
ORDER	-346.74	1	695.48	695.48	32.22	0	0.0025	--

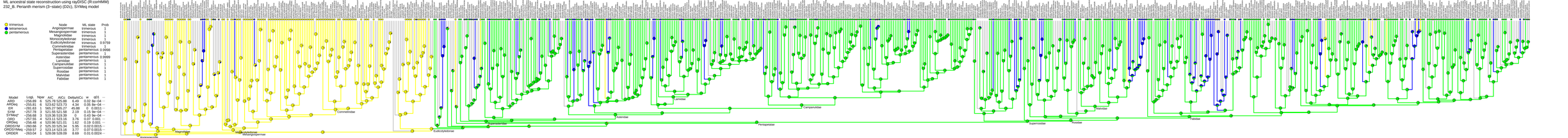
MP ancestral state reconstruction using ancestral pars
(R:phangorn)
232_B. Perianth merism (3–state) (D2c), 70 steps

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 rayDISC (R:corHMM)
232_8. Perianth merism (3–state) (D2c), SYMeq model



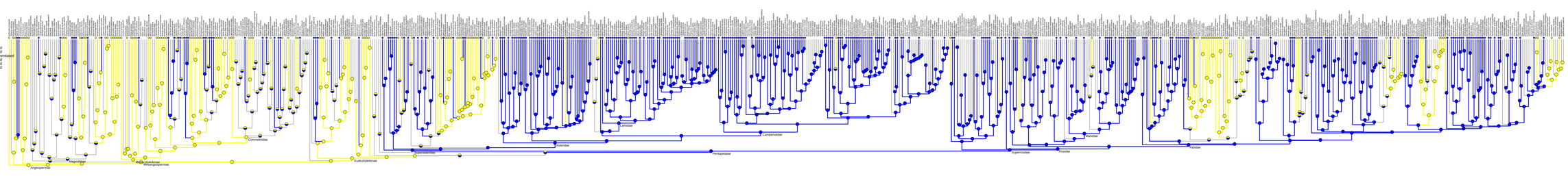
Node	ML state	Prob
Angiospermae	trimerous	1
Mesangiospermae	trimerous	1
Magnoliidae	trimerous	1
Monocotyledonae	trimerous	1
Eudicotyledonae	trimerous	0.9759
Commelinidae	trimerous	1
Ceratophyllaceae	pentamerous	0.9998
Superasteridae	pentamerous	1
Asteridae	pentamerous	0.9999
Lamiidae	pentamerous	1
Campanulidae	pentamerous	1
Caryophyllidae	pentamerous	1
Rosidae	pentamerous	1
Malvidae	pentamerous	1
Fabidae	pentamerous	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	...
ARD	-256.89	6	525.78	525.88	6.49	0.02	8e−04	...
ARDeq	-255.81	6	523.62	523.73	4.34	0.05	8e−04	...
ER	-281.63	1	565.27	565.27	45.88	0	0.0011	...
SYM	-256.68	3	519.36	519.48	0	0.43	8e−04	...
SYMeq	-256.68	3	519.35	519.48	0	0.43	8e−04	...
ORD	-257.55	4	523.11	523.16	3.76	0.07	0.001	...
ORDeq	-256.48	4	520.96	521.01	1.62	0.19	0.001	...
ORDSYM	-260.66	2	525.33	525.34	5.95	0.02	0.0015	...
ORDSYMeq	-259.57	2	523.14	523.16	3.77	0.07	0.0015	...
ORDER	-263.04	1	528.08	528.09	8.69	0.01	0.0024	...

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

undifferentiated
differentiated

Node	MP state(s)
Angiospermae	undifferentiated
Mesangiospermae	undifferentiated
Magnoliidae	undifferentiated / 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

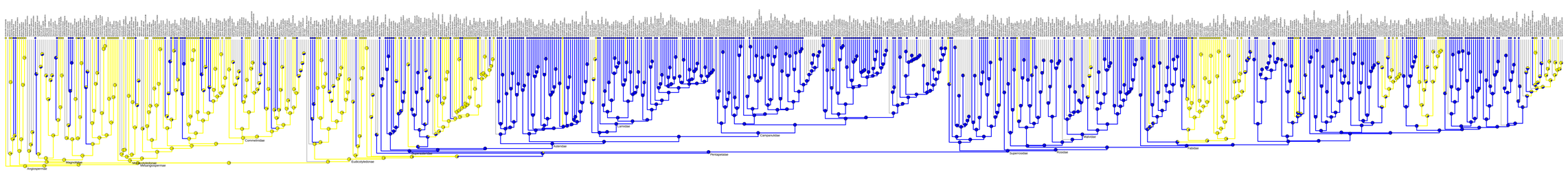


ML ancestral state reconstruction using rayDISC (R:corHMM)
234_A. Perianth differentiation (binary) (D2d), ARDeq model

undifferentiated
differentiated

Node	ML state	Prob
Angiospermae	undifferentiated	1
Mesangiospermae	undifferentiated	1
Magnoliidae	undifferentiated	0.999
Monocotyledonae	undifferentiated	1
Eudicotyledonae	undifferentiated	0.9998
Commelinidae	undifferentiated	1
Ceratophyllidae	differentiated	0.9645
Superasteridae	differentiated	0.9956
Asteridae	differentiated	0.9988
Lamidae	differentiated	0.9999
Campanulidae	differentiated	1
Gentianidae	differentiated	0.9938
Rosidae	differentiated	0.9961
Malvidae	differentiated	0.9995
Fabidae	differentiated	0.9967

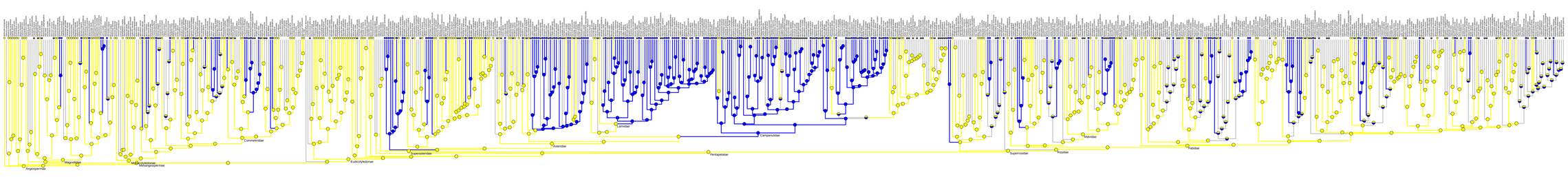
Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	-198.28	2	400.56	400.58	1.38	0.33	0.0045	0.0015
ARDeq**	-197.59	2	399.18	399.19	0	0.67	0.0045	0.0015
ER	-207.61	1	417.23	417.23	18.04	0	0.0025	0.0025
UN01	-228.28	1	458.56	458.56	59.36	0	0.0089	
UN10	-233.57	1	469.15	469.15	69.96	0		0.0034



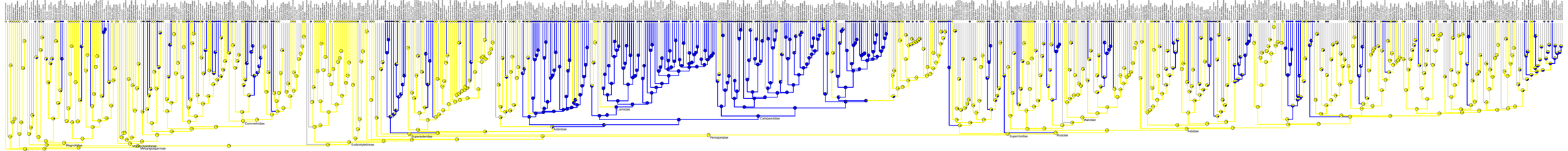
MP ancestral state reconstruction using ancestral pars (R:phangorn)
204_A. Fusion of perianth (D2c), 76 steps

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%)
Gunneridae	free (+5%)
Superasteridae	free (+5%)
Asteridae	free (+5%)
Lamiidae	free (+5%)
Campanulidae	fused (+5%)
Superrosidae	free (+5%)
Rosidae	free (+5%)
Malvidae	free (+5%)
Fabidae	free (+5%)



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



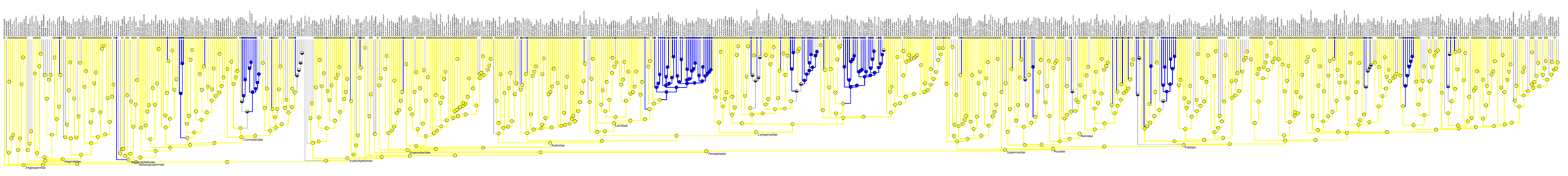
Node	ML state	Prob
Angiospermae	free (<5%)	0.9994
Mesangiospermae	free (<5%)	1
Magnoliidae	free (<5%)	0.9998
Monocotyledonae	free (<5%)	0.9999
Eudicotyledonae	free (<5%)	1
Commelinidae	free (<5%)	0.9971
Gunneridae	free (<5%)	0.9963
Superasteridae	free (<5%)	0.763
Asteridae	free (<5%)	0.7569
Lamiidae	fused (>5%)	0.9777
Campanulidae	fused (>5%)	0.9755
Caryophyllales	free (<5%)	0.9977
Rosidae	free (<5%)	0.9977
Malvidae	free (<5%)	0.9964
Fabidae	free (<5%)	0.9999

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	−224.97	2	453.94	453.95	1.39	0.2	0.0044	0.0036
ARDeq	−224.28	2	452.55	452.57	0	0.41	0.0044	0.0036
ER*	−225.28	1	452.56	452.56	0	0.4	0.0043	0.0043
UN01	−237.97	1	477.94	477.95	25.38	0	0.005	
UN10	−237.8	1	477.61	477.61	25.05	0		0.0084

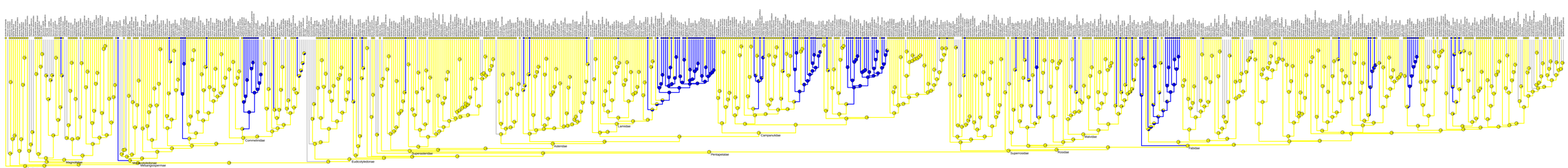
MP ancestral state reconstruction using ancestral.pars (R phangorn)
207_A. Symmetry of perianth (binary) (D2d), 57 steps

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) (2Dd), ARDeq model



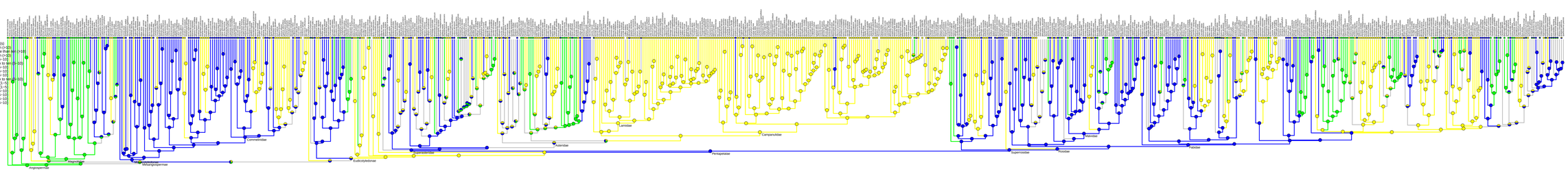
Node	ML state	Prob
Angiospermae	actinomorphic	1
Mesangiospermae	actinomorphic	1
Magnoliidae	actinomorphic	1
Monocotyledonae	actinomorphic	0.9997
Eudicotyledonae	actinomorphic	1
Commelinidae	actinomorphic	0.9959
Ceratophyllidae	actinomorphic	1
Superasteridae	actinomorphic	1
Asteridae	actinomorphic	1
Lamiidae	actinomorphic	0.9988
Campanulidae	actinomorphic	1
Pentapetalidae	actinomorphic	1
Rosidae	actinomorphic	1
Malvidae	actinomorphic	0.9998
Fabidae	actinomorphic	0.9997

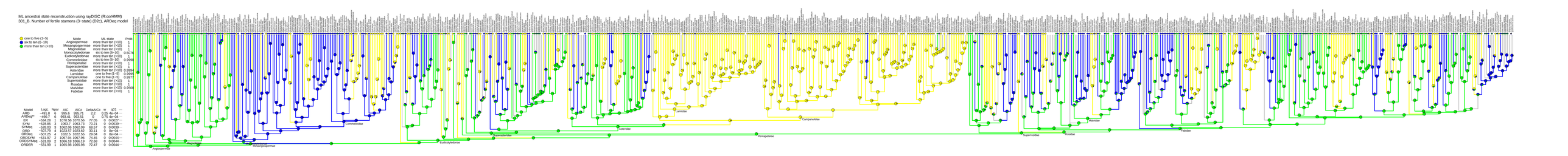
Model	LogL	Nopr	AIC	AICc	DeltaAICc	w	q01	q10
ARD	-210.43	2	424.85	424.87	1.37	0.33	0.0014	0.0065
ARDeq**	-209.74	2	423.48	423.5	0	0.66	0.0014	0.0065
ER	-220.76	1	443.52	443.53	20.03	0	0.0016	0.0016
UN01	-269.97	1	541.95	541.95	118.46	0	0.0019	0
UN10	-217.94	1	437.89	437.89	14.4	0	0	0.0171

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

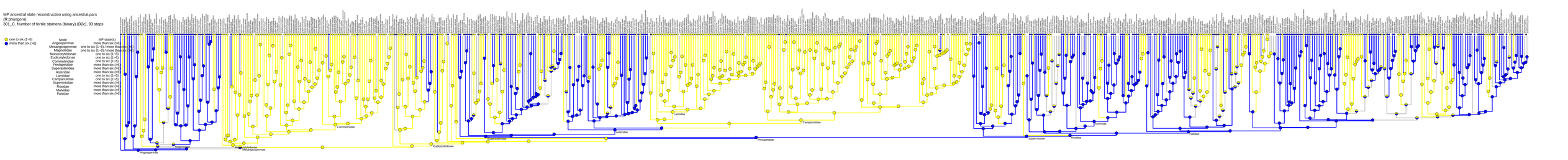
one to five (1–5)
six to ten (6–10)
more than ten (>10)

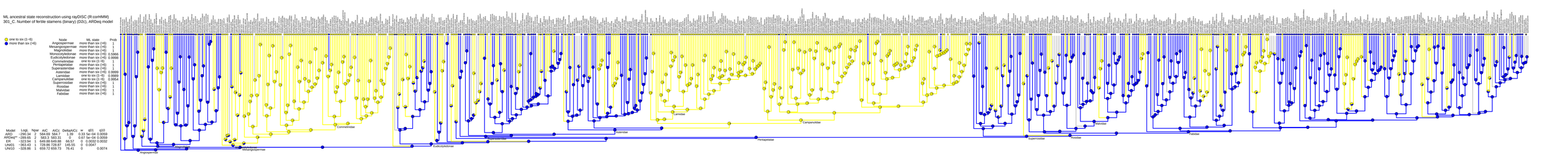
Node	MP state(s)
Angiospermae	more than ten (>10)
Mesangiospermae	one to five (1–5) / more than ten (>10)
Magnoliidae	more than ten (>10)
Monocotyledonae	six to ten (6–10)
Eudicotyledonae	one to five (1–5) / six to ten (6–10)
Commelinidae	six to ten (6–10)
Ceratophyllum	six to ten (6–10)
Superasteridae	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)
Pentapetalae	six to ten (6–10)
Rosidae	six to ten (6–10)
Malvidae	six to ten (6–10)
Fabidae	six to ten (6–10)



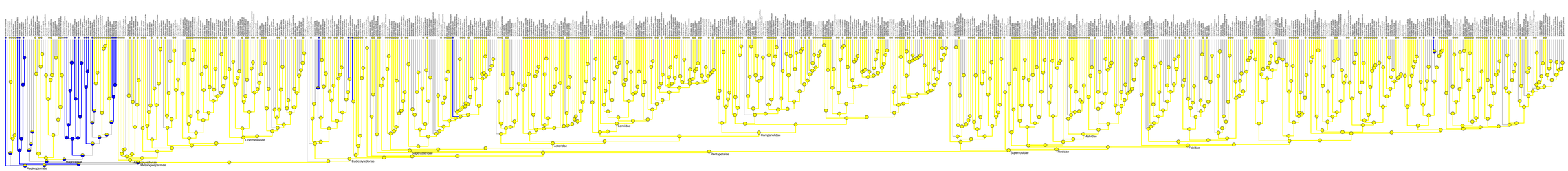

ML ancestral state reconstruction using rayDISC (R:corHMM)
301_B. Number of fertile stamens (3–state) (D2c), ARDeq model
one to five (1–5)
six to ten (6–10)
more than ten (>10)
Node | ML state | Prob
Angiospermae | more than ten (>10) | 1
Mesangiospermae | more than ten (>10) | 1
Magnoliidae | more than ten (>10) | 1
Monocotyledonae | six to ten (6–10) | 0.5078
Eudicotyledonae | more than ten (>10) | 1
Commelinidae | six to ten (6–10) | 0.9996
Ceratophyllidae | more than ten (>10) | 1
Superasteridae | more than ten (>10) | 1
Asteridae | more than ten (>10) | 0.9994
Lamiidae | one to five (1–5) | 0.9995
Campanulidae | one to five (1–5) | 0.9977
Pentapetalae | more than ten (>10) | 1
Rosidae | more than ten (>10) | 1
Malvidae | more than ten (>10) | 0.9508
Fabidae | more than ten (>10) | 1
Model | LogL | Npar | AIC | AICc | DeltaAICc | w | q01
ARD | −491.8 | 6 | 995.6 | 995.71 | 2.2 | 0.25 | 4e−04
ARDeq** | −492.7 | 6 | 993.41 | 993.51 | 0 | 0.75 | 4e−04
ER | −534.28 | 1 | 1070.56 | 1070.56 | 77.05 | 0 | 0.0027
SYM | −526.03 | 3 | 1058.06 | 1058.19 | 64.67 | 0 | 0.0039
SYMeq | −528.03 | 3 | 1062.06 | 1062.19 | 68.67 | 0 | 0.0039
ORD | −507.79 | 4 | 1023.57 | 1023.62 | 30.11 | 0 | 8e−04
ORDeq | −507.25 | 4 | 1022.5 | 1022.55 | 29.04 | 0 | 8e−04
ORDSYM | −531.97 | 2 | 1067.94 | 1067.96 | 74.45 | 0 | 0.0044
ORDSYMeq | −531.09 | 2 | 1066.18 | 1066.19 | 72.68 | 0 | 0.0044
ORDER | −531.99 | 1 | 1065.98 | 1065.98 | 72.47 | 0 | 0.0044
Angiospermae
Magnoliidae
Mesangiospermae
Monocotyledonae
Eudicotyledonae
Commelinidae
Ceratophyllidae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Pentapetalae
Rosidae
Fabidae
Malvidae
Superrosidae
Malvidae

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

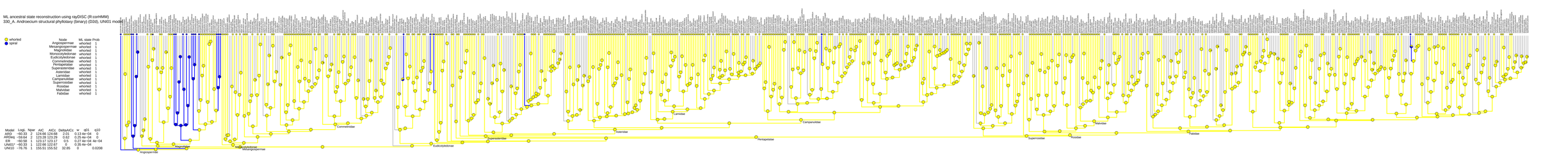



ML ancestral state reconstruction using ray/DISC (R corHMM)
301_C. Number of fertile stamens (binary) (02c), ARDeq model
one to six (1–6)
more than six (>6)
Node | ML state | Prob
Angiospermae | more than six (>6) | 1
Mesangiospermae | more than six (>6) | 1
Magnoliidae | more than six (>6) | 1
Monocotyledonae | more than six (>6) | 0.5966
Eudicotyledonae | more than six (>6) | 0.9998
Commelinidae | one to six (1–6) | 1
Ceratophyllidae | 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) | 0.9998
Campanulidae | one to six (1–6) | 0.9954
Superrosidae | 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 | Nopr | AIC | AICc | DeltaAICc | w | q01 | q10
ARD | -290.34 | 2 | 584.69 | 584.7 | 1.39 | 0.33 | 5e−04 | 0.0059
ARDeq** | -289.65 | 2 | 583.3 | 583.31 | 0 | 0.67 | 5e−04 | 0.0059
ER | -323.94 | 1 | 649.88 | 649.88 | 66.57 | 0 | 0.0032 | 0.0032
UN01 | -363.43 | 1 | 728.86 | 728.87 | 145.55 | 0 | 0.0047
UN10 | -328.86 | 1 | 659.72 | 659.73 | 76.41 | 0 | 0 | 0.0074
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledonae
Eudicotyledonae
Commelinidae
Ceratophyllidae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Superrosidae
Rosidae
Malvidae
Fabidae

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



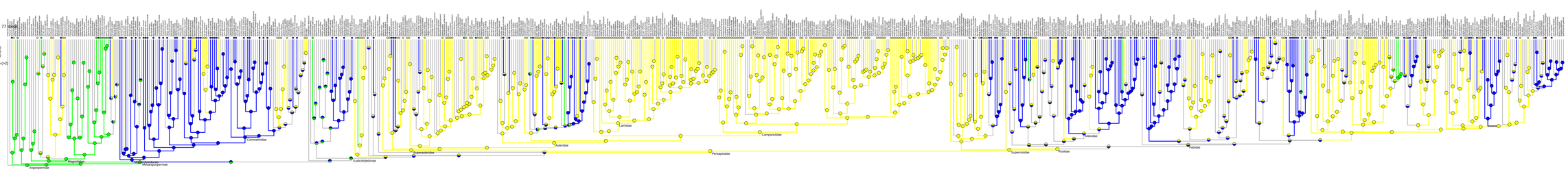
ML ancestral state reconstruction using ray(DISC (R:corHMM)
330_A. Androecium structural phylotaxy (binary) (D2d), UNI01 model



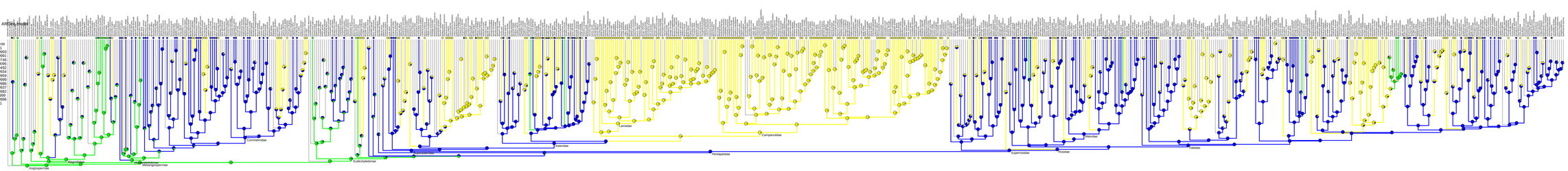
MP ancestral state reconstruction using ancestral pars
(R:phangorn)
331_A. Number of androecium structural whorls (3–state) (D2c), 77 taxa

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	two (2) / more than two (>2)
Commelinidae	two (2)
Ceratophyllidae	one (1)
Superasteridae	one (1)
Asteridae	one (1)
Lamiidae	one (1)
Campanulidae	one (1)
Superrosidae	one (1)
Rosidae	one (1)
Malvidae	one (1) / two (2)
Fabidae	one (1) / two (2)

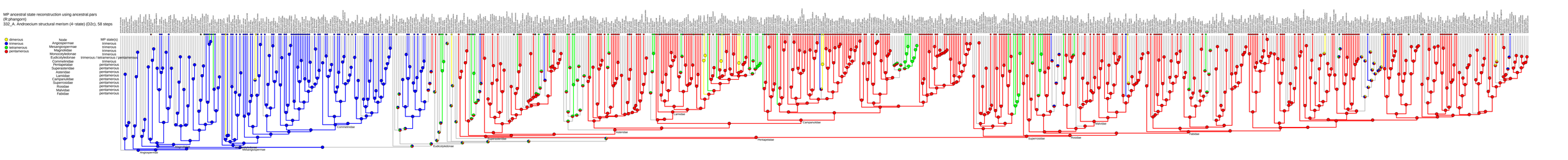


ML ancestral state reconstruction using rayDISC (R:corHMM)
331_A. Number of androecium structural whorls (3–state) (D2c), AR3eq model

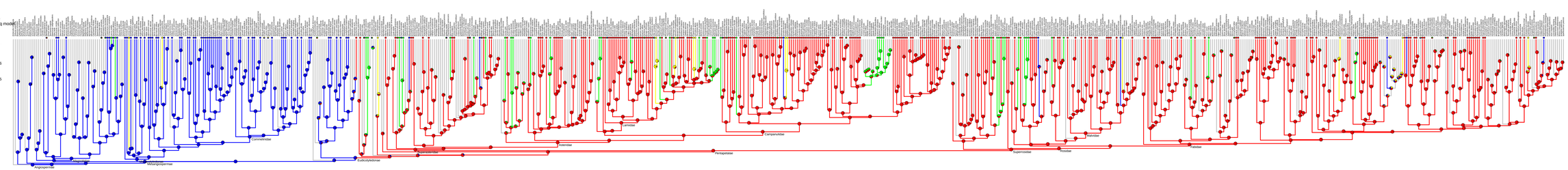


Node	ML state	Prob
Angiospermae	more than two (>2)	1
Mesangiospermae	more than two (>2)	0.9993
Magnoliidae	more than two (>2)	0.9991
Monocotyledoneae	more than two (>2)	0.9746
Eudicotyledoneae	more than two (>2)	0.9095
Commelinidae	two (2)	0.9492
Ranunculidae	two (2)	0.9997
Superasteridae	two (2)	0.9999
Asteridae	two (2)	0.9999
Lamiidae	one (1)	0.9988
Campanulidae	one (1)	0.9937
Gentianidae	one (1)	0.9999
Rosidae	two (2)	0.999
Malvidae	two (2)	0.9996
Fabidae	two (2)	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	---
ARD	-231.41	6	474.81	474.92	2.18	0.2	0	---
ARDeq**	-230.31	4	472.63	472.73	0	0.59	0	---
ER	-280.69	1	563.38	563.38	90.65	0	0.0017	---
SYM	-255.89	3	517.78	517.91	45.18	0	0.0035	---
SYMeq	-255.89	3	513.77	513.91	41.07	0	0.0035	---
ORD	-234.71	4	477.43	477.48	4.74	0.06	0	---
ORDeq	-233.68	4	475.35	475.4	2.67	0.16	0	---
ORDSYM	-255.53	2	515.06	515.07	42.34	0	0.0036	---
ORDSYMeq	-254.46	2	512.91	512.93	40.19	0	0.0036	---
ORDER	-261.1	1	524.2	524.2	51.47	0	0.0029	---

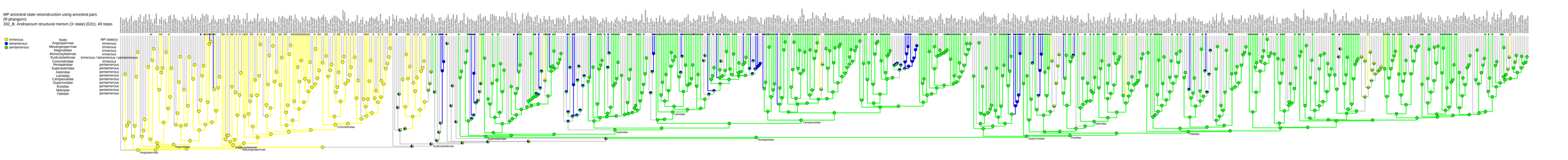

MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
332_A. Androecium structural merism (4–state) (D2c), 58 steps
dimerous
trimerous
tetramerous
pentamerous
Node
MP state(s)
Angiospermae
trimerous
Mesangiospermae
trimerous
Magnoliidae
trimerous
Monocotyledonae
trimerous
Eudicotyledonae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

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



Node	ML state	Prob
Angiospermae	trimerous	1
Mesangiospermae	trimerous	1
Magnoliidae	trimerous	1
Monocotyledoniae	trimerous	1
Eudicotyledoniae	trimerous	0.8426
Commelinidae	trimerous	1
Ceratophyllidae	pentamerous	1
Superasteridae	pentamerous	1
Asteridae	pentamerous	0.9995
Lamiidae	pentamerous	1
Campanulidae	pentamerous	1
Pentapetalae	pentamerous	1
Rosidae	pentamerous	1
Malvidae	pentamerous	1
Fabidae	pentamerous	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	...
ARD	-223.83	12	471.66	472.06	11.01	0	0.0068	---
ARDeq	-222.49	12	468.98	469.38	8.33	0.01	0.0066	---
ER	-238.3	1	478.6	478.6	17.55	0	9e-04	---
SYM	-224.47	6	460.94	461.05	0	0.79	6e-04	---
SYMeq*	-224.47	6	460.94	461.05	0	0.79	6e-04	---
ORD	-237.85	6	487.71	487.82	26.77	0	100	---
ORDeq	-237.24	6	486.48	486.59	25.54	0	100	---
ORDSYM	-260.66	3	527.31	527.34	66.29	0	0.0021	---
ORDSYMeq	-259.32	3	524.64	524.67	63.62	0	0.0021	---
ORDER	-261.5	1	525	525	63.95	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
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
Superrosidae
pentamerous
Rosidae
pentamerous
Malvidae
pentamerous
Fabidae
pentamerous
Angiospermae
Magnoliidae
Mesangiospermae
Eudicotyledoneae
Commelinidae
Gunneridae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Pentapetalae
Superrosidae
Rosidae
Malvidae
Fabidae

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

- trimerous
- tetramerous
- pentamerous

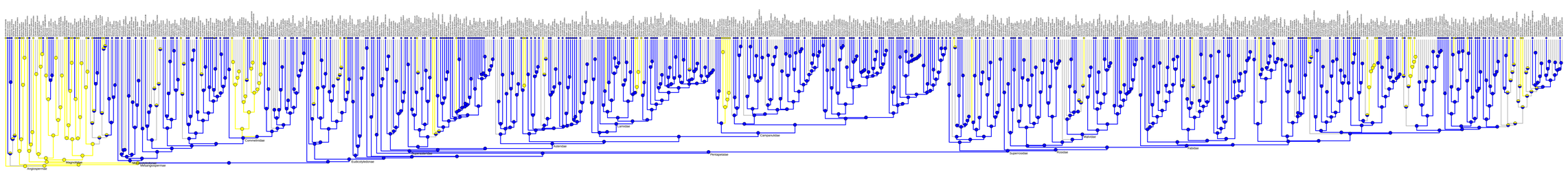
Node	ML state	Prob
Angiospermae	trimerous	1
Mesangiospermae	trimerous	1
Magnoliidae	trimerous	1
Monocotyledonae	trimerous	1
Eudicotyledonae	trimerous	0.9066
Commelinidae	trimerous	1
Pentapetalae	tetramerous	0.9999
Superasteridae	tetramerous	1
Asteridae	tetramerous	1
Lamiidae	tetramerous	0.9937
Campanulidae	tetramerous	0.9697
Superrosidae	tetramerous	1
Rosidae	tetramerous	0.9998
Malvidae	pentamerous	0.5684
Fabidae	tetramerous	0.9736

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	···
ARD	−171.02	6	354.04	354.15	2.18	0.25	0.001	···
ARDeq**	−169.93	6	351.86	351.97	0	0.73	0.001	···
ER	−186.89	1	375.78	375.78	23.82	0	0.0011	···
SYM	−177.93	3	361.85	361.88	9.92	0.01	4e−04	···
SYMeq	−176.84	3	359.67	359.7	7.74	0.02	4e−04	···
ORD	−180.2	4	368.4	368.45	16.48	0	2e−04	···
ORDeq	−179.15	4	366.29	366.34	14.38	0	1e−04	···
ORDSYM	−187.33	2	378.67	378.68	26.72	0	0.002	···
ORDSYMeq	−186.26	2	376.51	376.53	24.56	0	0.002	···
ORDER	−188.09	1	378.19	378.19	26.23	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)
Gunneridae	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)

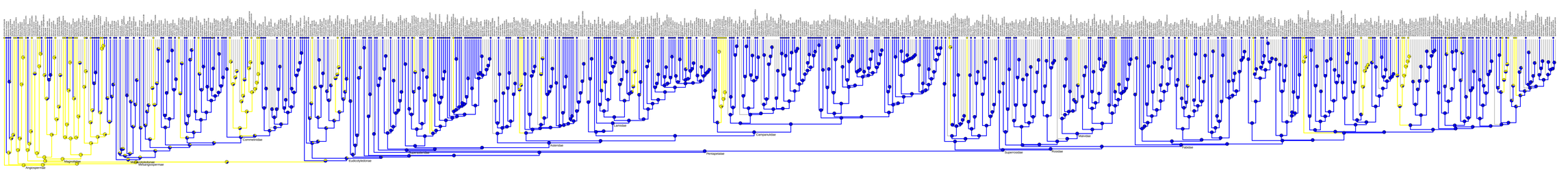


ML ancestral state reconstruction using rayDISC (R:corHMM)
305_A. Filament (binary) (D2d), ARDeq model

laminar (wide)
typical (narrow)

Node	ML state	Prob
Angiospermae	laminar (wide)	0.9999
Mesangiospermae	laminar (wide)	0.9823
Magnoliidae	laminar (wide)	0.9971
Monocotyledonae	laminar (wide)	0.5715
Eudicotyledonae	typical (narrow)	0.7656
Commelinidae	typical (narrow)	0.6933
Gunneridae	typical (narrow)	0.9997
Superasteridae	typical (narrow)	0.9997
Asteridae	typical (narrow)	0.9998
Lamidae	typical (narrow)	0.998
Campanulidae	typical (narrow)	0.9961
Lamiidae	typical (narrow)	0.9998
Rosidae	typical (narrow)	0.9998
Malvidae	typical (narrow)	0.9979
Fabidae	typical (narrow)	1

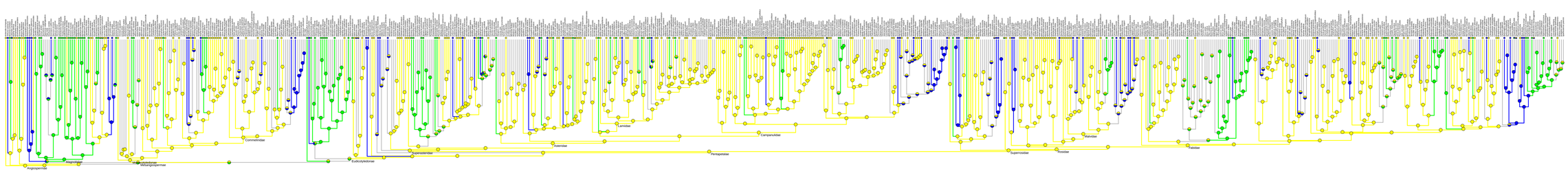
Model	LogL	Nopr	AIC	AICc	DeltaAICc	w	q01	q10
ARD	−171.88	2	347.76	347.77	1.16	0.36	0.008	0.0021
ARDeq**	−171.3	2	346.6	346.61	0	0.64	0.0083	0.0021
ER	−177.52	1	357.04	357.05	10.44	0	0.0024	0.0024
UN01	−184.44	1	370.88	370.88	24.27	0	0.0148	
UN10	−187.63	1	377.25	377.26	30.65	0		0.0023



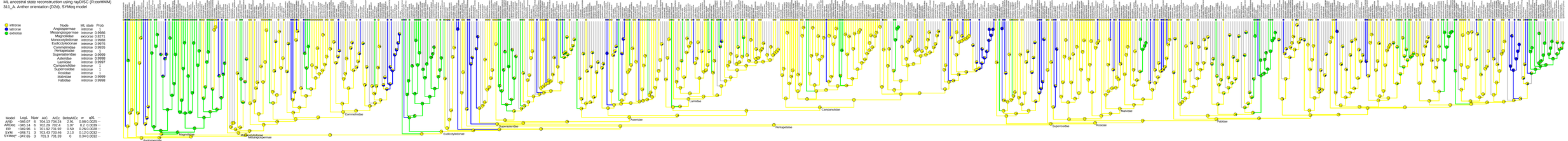
MP ancestral state reconstruction using ancestral pars (R:phangorn)
311_A. Anther orientation (D2d), 110 steps

	introrse
	latrorse
	extrorse

Node	MP state(s)
Angiospermae	introrse
Mesangiospermae	introrse / extrorse
Magnoliidae	extrorse
Monocotyledonae	introrse
Eudicotyledonae	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

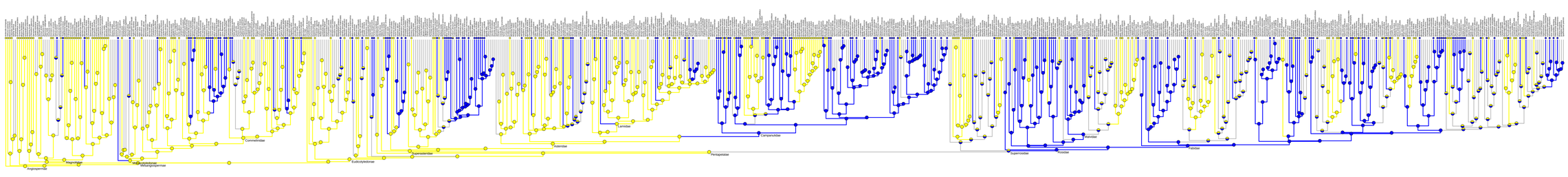


Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	···
ARD	-346.07	6	704.13	704.24	2.91	0.08	0.0025	···
ARDeq	-346.14	4	702.29	702.4	1.07	0.2	0.0039	···
ER	-349.96	1	701.92	701.92	0.59	0.26	0.0028	···
SYM	-348.71	3	703.43	703.46	2.13	0.12	0.0032	···
SYMeq*	-347.65	3	701.3	701.33	0	0.34	0.0032	···

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
Lamiidae	basifixed
Campanulidae	dorsifixed
Superrosidae	basifixed/dorsifixed
Rosidae	dorsifixed
Malvidae	dorsifixed
Fabidae	dorsifixed

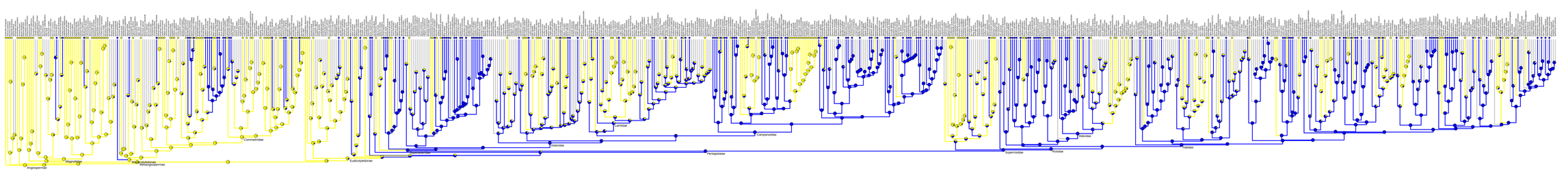


ML ancestral state reconstruction using ray|DISC (R:corHMM)
312_A. Anther attachment (binary) (D2d), ARDeq model

basifixed
dorsifixed

Node	ML state	Prob
Angiospermae	basifixed	1
Mesangiospermae	basifixed	0.9991
Magnoliidae	basifixed	0.9989
Monocotyledonae	basifixed	0.994
Eudicotyledonae	basifixed	0.9364
Commelinidae	basifixed	0.9823
Gunneridae	basifixed	0.9182
Superasteridae	dorsifixed	0.52
Asteridae	dorsifixed	0.9182
Lamidae	dorsifixed	0.7175
Campanulidae	dorsifixed	0.9855
Rosidae	dorsifixed	0.9182
Rosidae	dorsifixed	0.9546
Malvidae	dorsifixed	0.9897
Fabidae	dorsifixed	0.9994

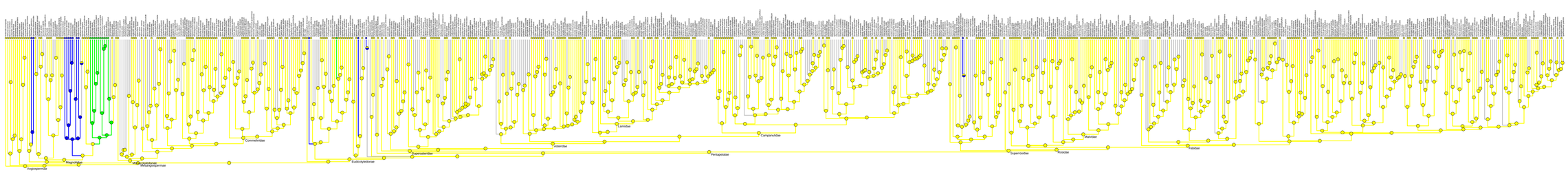
Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	q10
ARD	−266.03	2	536.05	536.07	1.32	0.3	0.0043	0.0077
ARDeq**	−265.37	2	534.74	534.75	0	0.59	0.0043	0.0077
ER	−268.08	1	538.16	538.17	3.42	0.11	0.0057	0.0057
UN01	−291.52	1	585.04	585.04	50.29	0	0.0061	
UN10	−277.64	1	557.28	557.28	22.53	0		0.0081



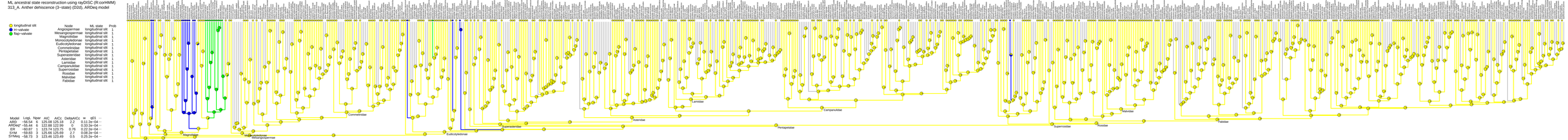
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
313_A. Anther dehiscence (3–state) (0\2d), 10 steps

longitudinal slit
H—ulvate
Rap—ulvate

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



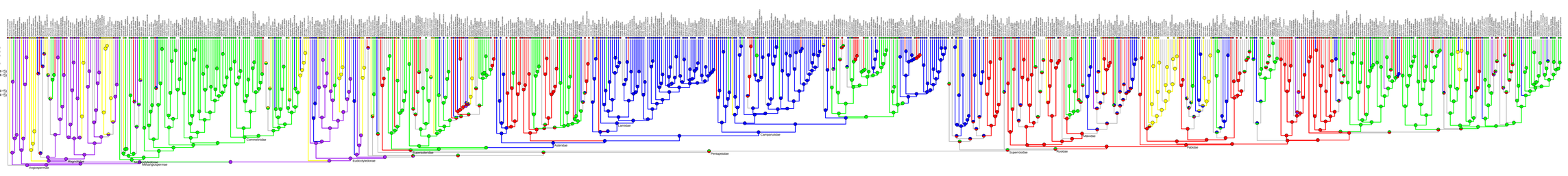
ML ancestral state reconstruction using rayDISC (R:corHMM)
313_A. Anther dehiscence (3–state) (D2d), ARDeq model



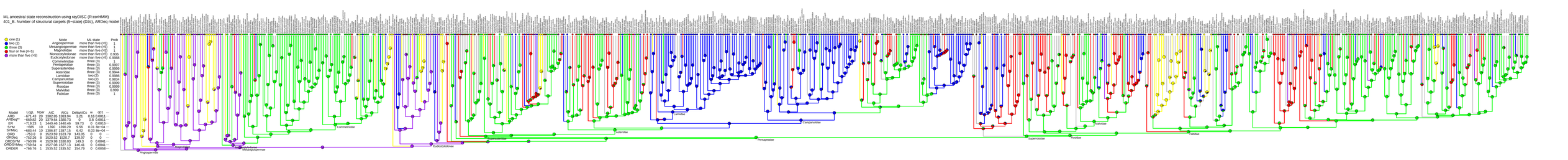
MP ancestral state reconstruction using ancestral.pars
(R phangorn)
401_B. Number of structural carpels (5~state) (D2c), 186 steps

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)
Lamiidae	two (2)
Campanulidae	two (2)
Santalanae	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)



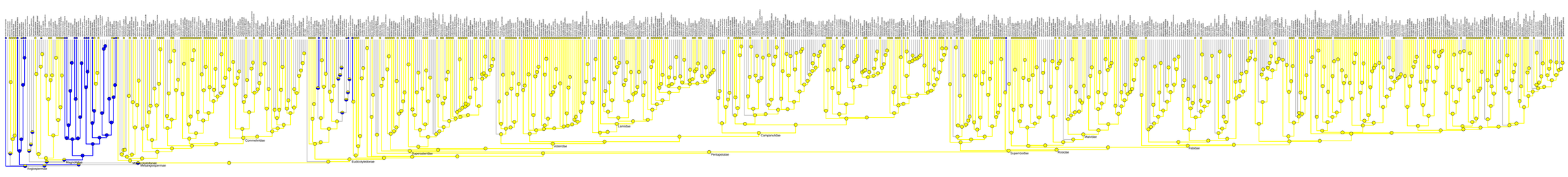
ML ancestral state reconstruction using ray[DISC (R:corHMM)
401_B. Number of structural carpels (5-state) (D2c), ARDeq model



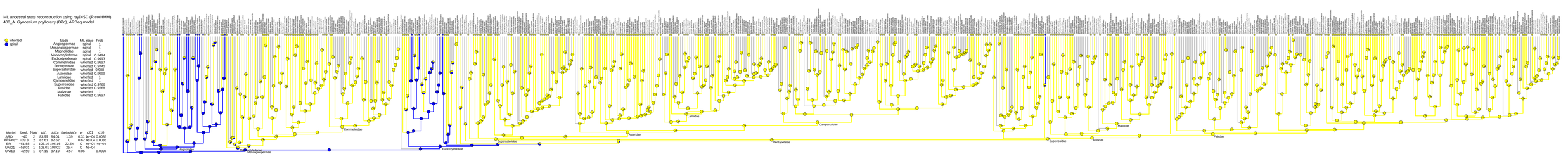
MP ancestral state reconstruction using ancestral pars (R phangorn)
400_A. Gynoecium phyllotaxy (D2d), 10 steps

whorled
spiral

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



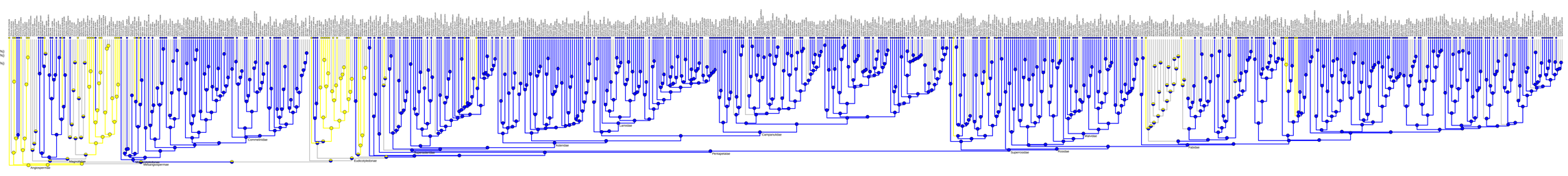
ML ancestral state reconstruction using ray[DISC (R:corHMM)
400_A. Gynoecium phyllotaxy (D2d), ARDeq model



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%)
Mesangiospermae	free (<5%) / fused (>5%)
Magnoliidae	free (<5%) / fused (>5%)
Monocotyledonae	fused (>5%)
Eudicotyledonae	free (<5%) / fused (>5%)
Commelinidae	fused (>5%)
Gunneridae	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%)

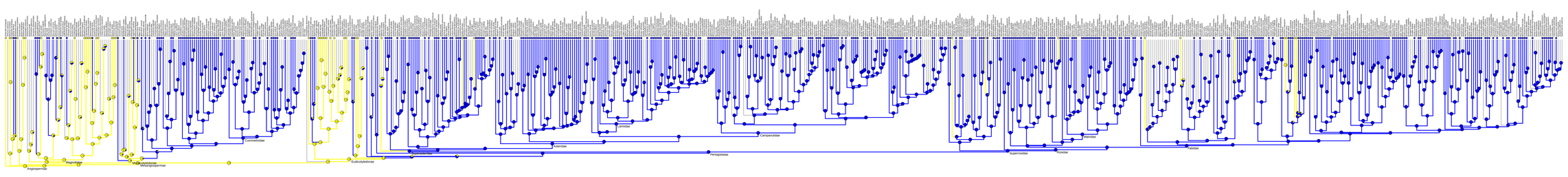


ML ancestral state reconstruction using rayDISC (R:corHMM)
403_A. Fusion of ovaries (binary) (Dr2c), ARDeq model

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

Node	ML state	Prob
Angiospermae	free (<5%)	1
Mesangiospermae	free (<5%)	1
Magnoliidae	free (<5%)	0.9999
Monocotyledonae	free (<5%)	0.9545
Eudicotyledonae	free (<5%)	0.9993
Commelinidae	fused (>5%)	1
Core Eudicots	fused (>5%)	0.9961
Superasteridae	fused (>5%)	0.9963
Asteridae	fused (>5%)	1
Lamiidae	fused (>5%)	1
Campanulidae	fused (>5%)	1
Superrosidae	fused (>5%)	0.9995
Rosidae	fused (>5%)	0.9997
Malvidae	fused (>5%)	1
Fabidae	fused (>5%)	0.9998

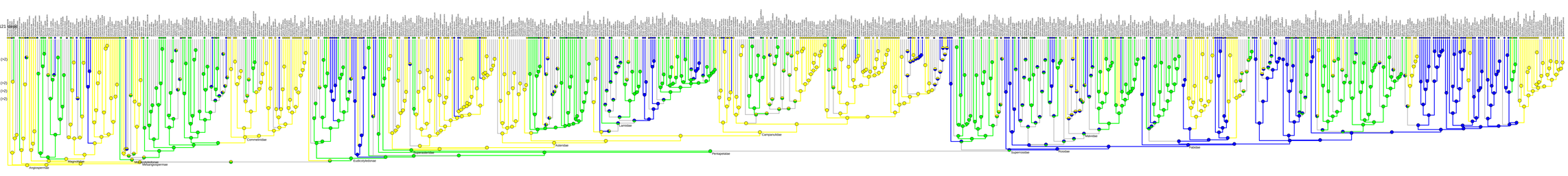
Model	LogL	Nopr	AIC	AICc	DeltaAICc	w	q01	q10
ARD	−94.6	2	193.19	193.21	1.39	0.33	0.0053	5e−04
ARDeq**	−93.9	2	191.81	191.82	0	0.66	0.0053	5e−04
ER	−103.17	1	208.34	208.34	16.52	0	8e−04	8e−04
UN01	−98.93	1	199.86	199.87	8.05	0.01	0.0114	
UN10	−107.51	1	217.02	217.02	25.2	0		8e−04



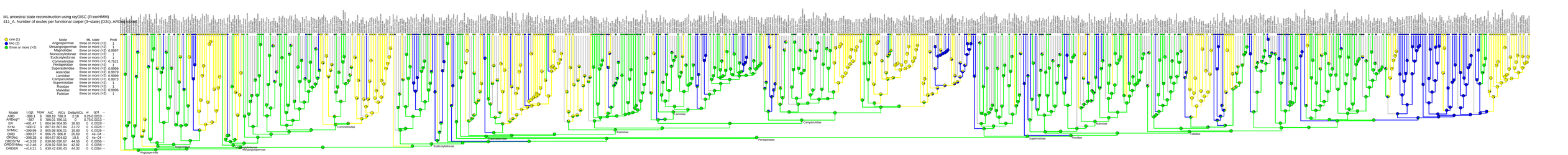
MP ancestral state reconstruction using ancestral pars
(R:phangorn)
411_A. Number of ovules per functional carpel (3–state) (D2c), 121 taxa

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

Node	MP state(s)
Angiospermae	one (1)
Mesangiospermae	one (1)
Magnoliidae	one (1)
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	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+its+equal



Node	ML state	Prob
Angiospermae	three or more (>2)	1
Mesangiospermae	three or more (>2)	1
Magnoliidae	three or more (>2)	0.9997
Monocotyledonae	three or more (>2)	1
Eudicotyledonae	three or more (>2)	1
Commelinidae	three or more (>2)	0.7521
Gunneridae	three or more (>2)	1
Superasteridae	three or more (>2)	0.9999
Asteridae	three or more (>2)	0.9979
Lamiidae	three or more (>2)	0.9999
Campanulidae	three or more (>2)	0.9973
Caryophyllidae	three or more (>2)	1
Rosidae	three or more (>2)	1
Malvidae	three or more (>2)	0.9996
Fabidae	three or more (>2)	1

Model	LogL	Npar	AIC	AICc	DeltaAICc	w	q01	---
ARD	-388.1	6	788.19	788.3	2.18	0.25	0.0013	---
ARDeq**	-387	6	786.01	786.11	0	0.75	0.0013	---
ER	-401.47	1	804.94	804.95	18.83	0	0.0029	---
SYM	-399.98	3	805.96	806.01	19.89	0	0.0025	---
SYMeq	-399.98	3	805.96	806.01	19.89	0	0.0025	---
ORD	-399.37	4	806.75	806.8	20.69	0	4e-04	---
ORDeq	-399.28	4	804.57	804.62	18.5	0	4e-04	---
ORDSYM	-413.33	2	830.66	830.67	44.56	0	0.0056	---
ORDSYMeq	-412.46	2	828.92	828.94	42.82	0	0.0056	---
ORDER	-414.21	1	830.42	830.43	44.32	0	0.0064	---