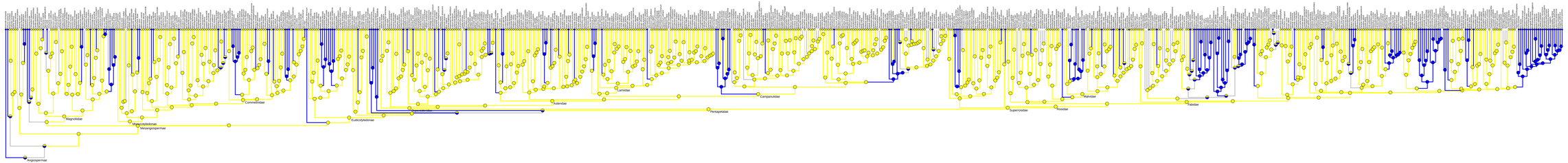
MP ancestral state reconstruction using ancestral pars
(R phangorn)
100_A: Functional sex of flowers (D2d), 96 steps

bisexual
unisexual

Node	MP state(s)
Angiospermae	bisexual / unisexual
Mesangiospermae	bisexual
Magnoliidae	bisexual
Monocotyledonae	bisexual
Eudicotyledonae	bisexual
Commelinidae	bisexual
Pentapetalae	bisexual
Superrosidae	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 (D2d), ARDeq model

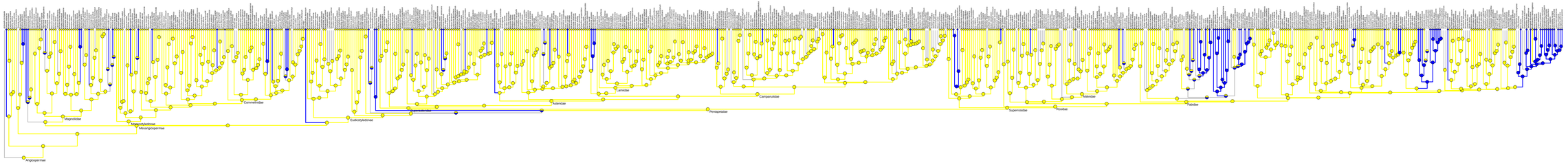
- bisexual
- unisexual

Node	ML state	Prob
Angiospermae	bisexual	1
Magnoliidae	bisexual	1
Magnoliidae	bisexual	1
Monocotyledonae	bisexual	1
Eudicotyledonae	bisexual	1
Commelinidae	bisexual	1
Pentapetalae	bisexual	1
Superrosidae	bisexual	1
Asteridae	bisexual	1
Lamiidae	bisexual	1
Campanulidae	bisexual	0.9996
Superrosidae	bisexual	1
Fabidae	bisexual	1
Malvidae	bisexual	1
Malvidae	bisexual	1
Malv

MP ancestral state reconstruction using ancestral.pars
(R phangorn)
100_B. Structural sex of flowers (D2d), 55 steps

bisexual
unisexual

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

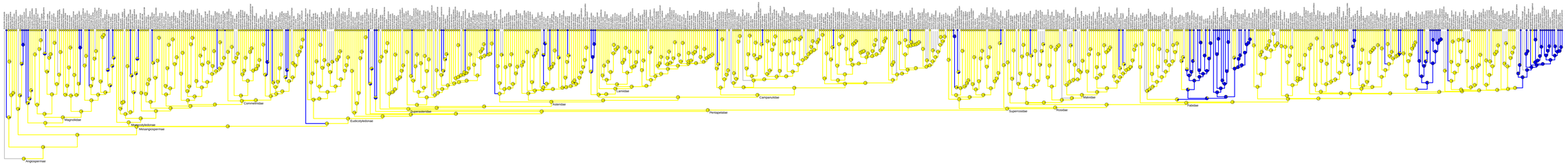


ML ancestral state reconstruction using rayDISC (R:corHMM) 100_B. Structural sex of flowers (D2d), ARDeq model

- bisexual
- unisexual

Node	ML state	Prob
Angiospermae	bisexual	0.9954
Mesangiospermae	bisexual	0.9997
Magnoliidae	bisexual	0.9999
Monocotyledonae	bisexual	0.9998
Eudicotyledonae	bisexual	0.9999
Commelinidae	bisexual	0.9999
Pentapetalae	bisexual	1
Superasterids	bisexual	1
Asteridae	bisexual	1
Lamidae	bisexual	0.9999
Campanulidae	bisexual	1
Superrosidae	bisexual	1
Rosidae	bisexual	1
Malvidae	bisexual	1
Fabidae	bisexual	1
Fabales	bisexual	1

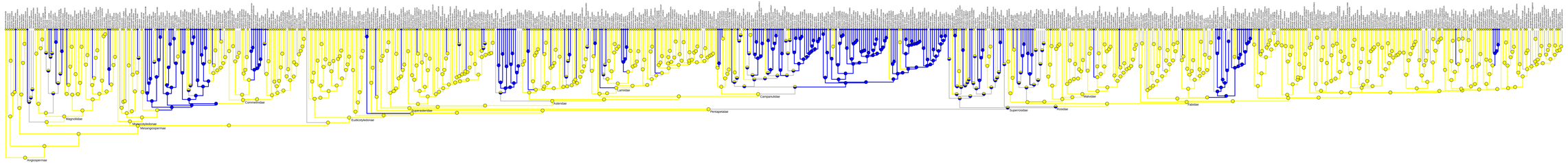
Model	Logl.	Npar	AIC	AICc	ΔAIC	ΔAICc	w AIC	w AICc
ARD	−207.08	2	418.16	418.21	0.01	0.01	0.4994	0.4989
ARDeq**	−206.68	2	417.35	417.37	0	0	0.55	0.5014
ER	−209.56	1	421.13	421.13	3.76	3.76	0.08	0.0015
UN01	−224.83	1	451.66	451.66	34.29	34.29	0	0.0016
UN10	−235.26	1	472.51	472.52	55.15	55.15	0	0.0155



MP ancestral state reconstruction using ancestral pars
(R phangorn)
102_B. Ovary position (binary) (D2d), 81 steps

superior
inferior

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

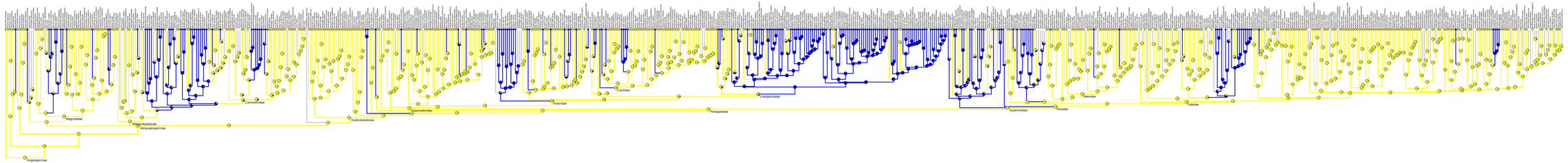


ML ancestral state reconstruction using rayDISC (R:corHMM)
102_B_Ovary position (binary) (02rd), ARDeq model

- superior
- inferior

Node	ML state	Prob
Angiospermae	superior	0.9998
Magnoliidae	superior	0.9997
Magnoliidae	superior	0.9997
Monocotyledonae	superior	0.9937
Eudicotyledonae	superior	0.9999
Commelinidae	superior	0.7959
Pentapetalae	superior	0.9996
Superasteridae	superior	0.9999
Asteridae	superior	0.9521
Lamiidae	superior	0.9575
Campanulidae	superior	0.781
Superrosidae	superior	0.9917
Rosidae	superior	0.9999
Malvidae	superior	0.9999
Fabidae	superior	0.9999
Fabidae	superior	0.9999
Malvidae	superior	0.9999
Rosidae	superior	0.9999
Superrosidae	superior	0.9999
Campanulidae	superior	0.9999
Lamiidae	superior	0.9999
Asteridae	superior	0.9999
Pentapetalae	superior	0.9999
Superasteridae	superior	0.9999
Eudicotyledonae	superior	0.9999
Commelinidae	superior	0.9999
Magnoliidae	superior	0.9999
Magnoliidae	superior	0.9999
Monocotyledonae	superior	0.9999
Magnoliidae	superior	0.9999
Angiospermae	superior	0.9998

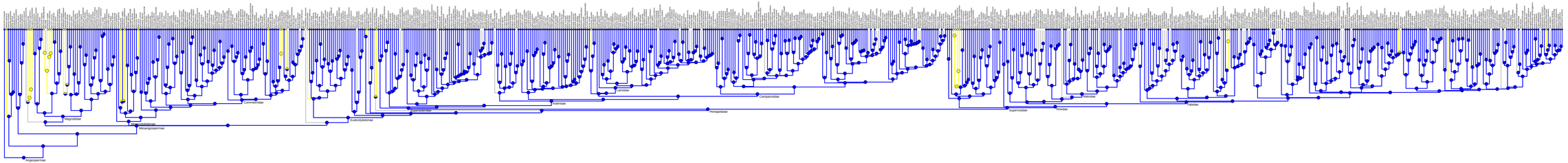
Model	LogL	Nopar	AIC	AICc	ΔAICc	AICc wt	q.10	q.01	σ²
ARD	−271.03	2	546.07	546.16	0	0.9999	0.0035	0.0035	0.0036
ARDeq**	−270.45	2	544.9	544.92	0	0	0.52	0.0019	0.0035
ER	−272.51	1	547.03	547.03	2.12	0.3	18	0.0022	0.0022
UN01	−280.77	1	563.55	563.55	18.64	0	0	0.0025	
UN10	−298.66	1	599.33	599.33	54.41	0		0.0095	



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

absent
present

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

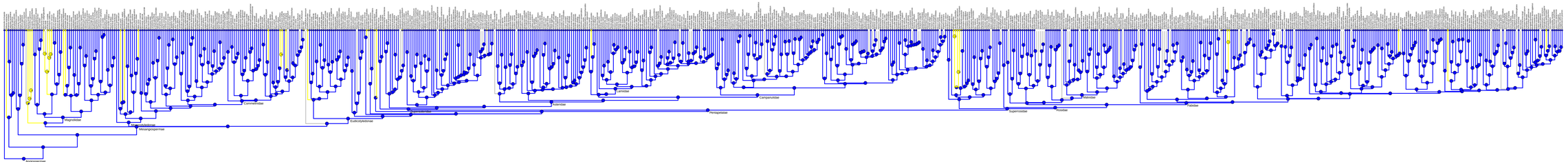


ML ancestral state reconstruction using rayDISC (R:corHMM)
201_A. Perianth presence (D2c), UNI10 model

absent
present

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

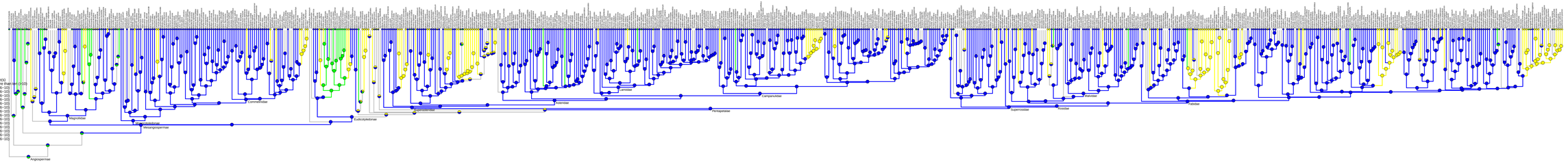
Model	Logl.	Npar	AIC	AICc	delta AICc	AICw	delta AICw	ER	Prob
ARD	−95.9	2	195.8	195.94	0.141	0.87	0	5e−04	1e10
ARDeq	−95.21	2	194.41	194.43	0.62	0.25	0	5e−04	
ER	−96.13	1	194.26	194.26	0.45	0.28	5e−04	5e−04	
UNI01	−113.81	1	229.62	229.63	35.82	0	0.0201		
UNI10*	−95.9	1	193.8	193.81	0	0.35		5e−04	



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

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

Node	MP state(s)
Angiospermae	six to ten (6–10) / more than ten (>10)
Magnoliopsidae	six to ten (6–10)
Magnoliidae	six to ten (6–10)
Monocotyledonae	six to ten (6–10)
Eudicotyledonae	six to ten (6–10)
Commelinidae	six to ten (6–10)
Pentapetalae	six to ten (6–10)
Superasteridae	six to ten (6–10)
Asteridae	six to ten (6–10)
Lamiidae	six to ten (6–10)
Campanulidae	six to ten (6–10)
Superrosidae	six to ten (6–10)
Rosidae	six to ten (6–10)
Malvidae	six to ten (6–10)
Fabidae	six to ten (6–10)

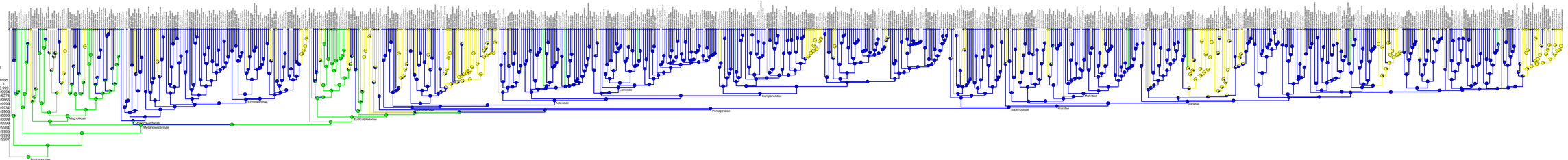


ML ancestral state reconstruction using rayDISC (R:corHMM)
201_8, Number of perianth parts (3~state) (O2c), ARDeq model

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

Node	ML state	Prob
Angiospermae	more than ten (>10)	1
Magnoliidae	more than ten (>10)	0.9998
Mesangiospermae	more than ten (>10)	0.9999
Monocotyledoneae	six to ten (6~10)	0.5214
Eudicotyledoneae	more than ten (>10)	0.9998
Commelinidae	six to ten (6~10)	0.9999
Pentapetalae	six to ten (6~10)	0.9931
Superrosidae	six to ten (6~10)	0.9999
Malvidae	six to ten (6~10)	0.9999
Rosidae	six to ten (6~10)	0.9998
Fabaceae	six to ten (6~10)	0.9998
Rosaceae	six to ten (6~10)	0.9998
Myrtales	six to ten (6~10)	0.9981
Lythraceae	six to ten (6~10)	0.9995
Lythrum	six to ten (6~10)	0.9998
Lythrum salicaria	six to ten (6~10)	0.9998

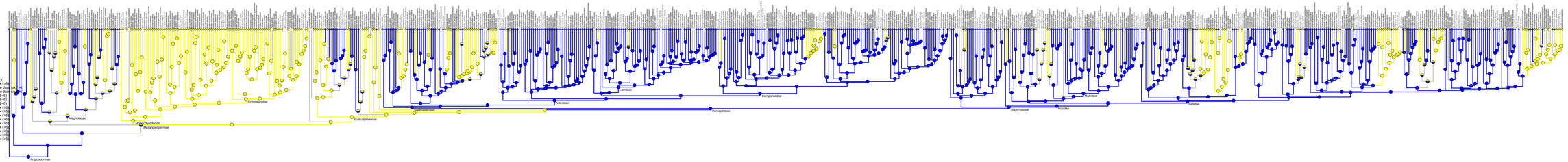
Model	Logl.	Npar	AIC	AICc	ΔAICc	ΔAICc rel.	AICc wt
ARD	~330.02	6	672.03	672.16	2.12	0.20	0.0499
ARDeq*	~328.96	6	669.92	670.04	0	0	0.9999
ER	~356.53	1	715.06	715.08	45.05	4.29	0.0010
ERdeq	~355.47	1	712.94	712.96	42.93	4.09	0.0035
SYMeq	~343.6	3	693.19	693.41	23.3	2.22	0.0000
ORD	~335.62	4	679.25	679.46	9.28	0.88	0.0010
ORDeq	~334.55	4	677.11	677.26	7.14	0.68	0.0047
ORDSYM	~347.04	2	698.09	698.1	28.0	2.67	0.0002
ORDSYMeq	~346.29	2	696.57	696.59	26.57	2.53	0.0002
ORDER	~357.37	1	716.75	716.75	46.73	4.45	0.0014



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

one to six (1–6)
more than six (>6)

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



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

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

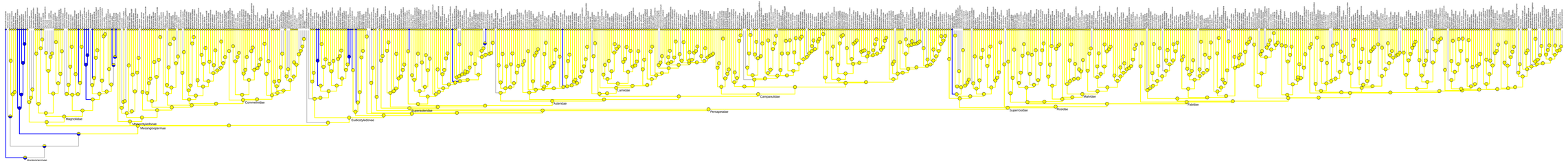
Model	Logl.	Npar	AIC	AICc	ΔAICc	AICc w
ARD	−251.87	2	507.74	507.82	0.00	0.9999
ARDeqr	−251.18	2	506.36	506.38	0	0.5
ER	−257.84	1	517.69	517.69	11.31	0
UN01	−328.53	1	659.07	659.07	152.69	0
UN10	−252.86	1	507.72	507.72	1.34	0.25

Node	ML state	Prob
Angiospermae	more than six (>6)	1
Mesangiospermae	more than six (>6)	0.9998
Magnoliidae	more than six (>6)	1
Monocotyledonae	one to six (1-6)	0.7415
Eudicotyledonae	more than six (>6)	0.9999
Commelinidae	one to six (1-6)	1
Pentapetalae	more than six (>6)	1
Superrosidae	more than six (>6)	1
Asteridae	more than six (>6)	1
Lamidae	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

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

whorled
spiral

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

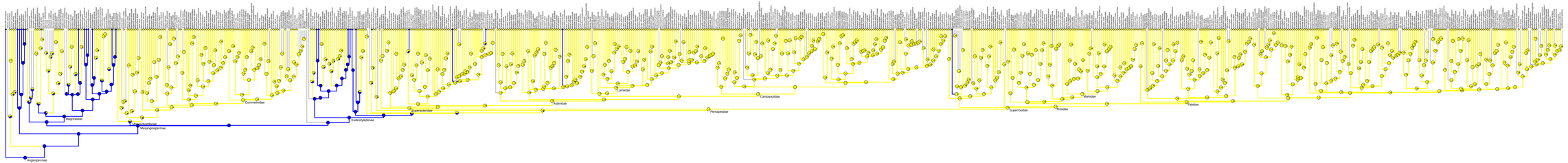


ML ancestral state reconstruction using rayDISC (R:corHMM)
230_A. Perianth phyllotaxy (binary) (D2d), ARDeq model

- whorled
- spiral

Model	Logl.	Npar	AIC	AICc	AICc_wt
ARD	−70.62	2	145.24	145.36	0.3
ARDeq**	−69.93	2	143.86	143.88	0
ER	−76.48	1	154.96	154.97	11.09
UNI01	−76.87	1	155.74	155.75	11.87
UNI10	−79.49	1	160.97	160.98	17.1

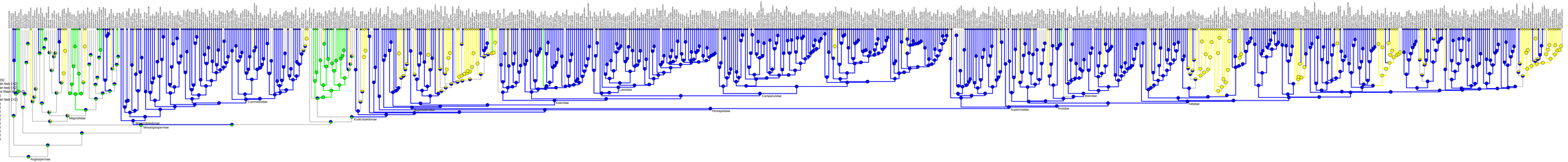
Node	ML state	Prob
Angiospermae	spiral	1
Mesangiospermae	spiral	0.9997
Magnoliidae	spiral	0.9997
Monocotyledonae	spiral	0.514
Eudicotyledonae	spiral	0.998
Commelinidae	whorled	0.9999
Pentapetalae	whorled	0.9876
Superasteridae	whorled	0.9999
Asteridae	whorled	0.9998
Lamiidae	whorled	1
Campanulidae	whorled	1
Superrosidae	whorled	0.9943
Rosidae	whorled	0.9
Malvidae	whorled	0.57
Fabidae	whorled	0.9994
Malvanae	whorled	0.9994
Fabanae	whorled	0.0094
Malvoidae	whorled	0.0094
Faboidae	whorled	0.0161



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

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

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

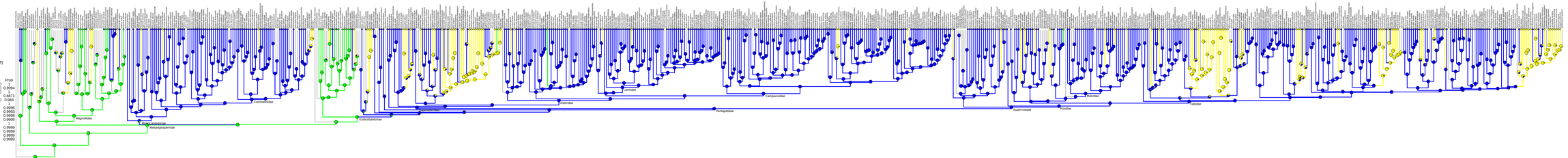


ML ancestral state reconstruction using rayDISC (R:corHMM)
231_A. Number of perianth whorls (D2c), ARDeq model

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

Node	ML state	Prob
Angiospermae	more than two (>2)	1
Magnoliidae	more than two (>2)	0.9994
Mesangiospermae	more than two (>2)	1
Monocotyledonae	two (2)	0.6571
Eudicotyledonae	more than two (>2)	0.984
Commelinidae	two (2)	1
Pentapetalae	two (2)	0.9996
Superrosidae	more than two (>2)	0.9998
Rosidae	more than two (>2)	0.9998
Fabidae	more than two (>2)	0.9999
Malvidae	more than two (>2)	1
Lamiidae	two (2)	0.9999
Campanulidae	two (2)	0.9999
Asteridae	more than two (>2)	0.9999
Lamiidae	more than two (>2)	0.9999
Campanulidae	more than two (>2)	0.9999

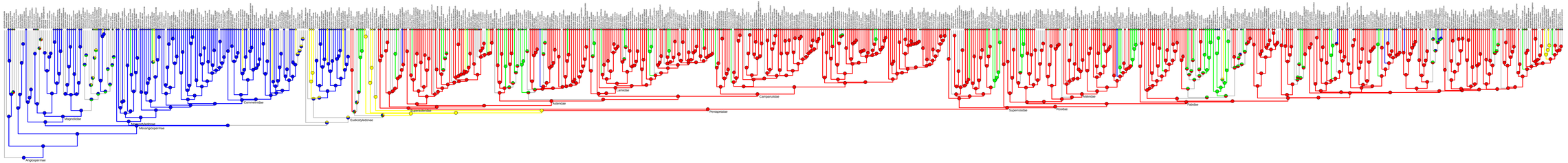
Model	Logl.	Npar	AIC	AICc	delta AICc	wheight	Prob
ARD	~269.55	6	551.09	551.58	0	0.9999	~
ARDeq*	~266.46	6	544.92	545.41	6.17	0.0457	1
ER	~311.54	1	625.08	625.09	74.01	0	0.9999
SYM	~292.09	3	590.18	590.36	39.28	0	0.9999
SYMeq	~292.09	3	590.18	590.36	41.18	0	0.9999
ORD	~272.79	4	553.58	553.82	4.46	0.0495	0.9999
ORDeq	~276.7	4	561.39	561.44	12.42	0	0.0048 ~
ORDSYM	~300.34	2	604.69	604.7	55.68	0	0.0018 ~
ORDSYMeq	~299.54	2	603.07	603.09	54.06	0	0.0018 ~
ORDER	~316.28	1	634.55	634.56	85.53	0	0.0011 ~



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
Pentapetalae	pentamerous
Superrosidae	pentamerous
Asteridae	pentamerous
Lamidae	pentamerous
Campanulidae	pentamerous
Superasteridae	pentamerous
Rosidae	pentamerous
Malvidae	pentamerous
Fabidae	pentamerous

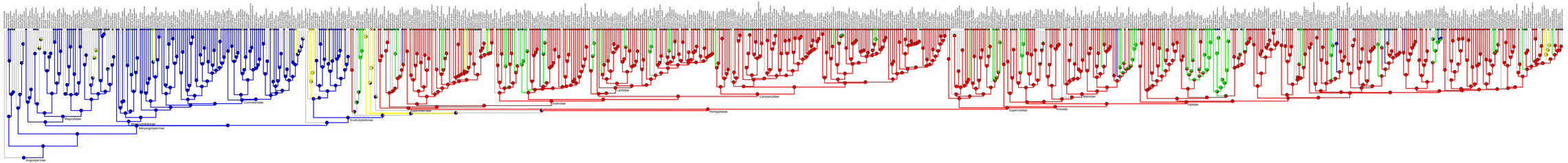


ML ancestral state reconstruction using rayDISC (R:corHMM) 232_A. Perianth merism (4–state) (D2c), SYMeq model

- dimerous
- trimerous
- tetramerous
- pentamerous

Node	ML state	Prob
Angiospermae	trimerous	1
Mesangiospermae	trimerous	1
Magnoliidae	trimerous	1
Monocotyledonae	trimerous	1
Eudicotyledonae	trimerous	0.8914
Commelinidae	trimerous	1
Pentapetalae	pentamerous	0.9993
Superrosidae	pentamerous	0.9999
Asteridae	pentamerous	0.9999
Lamiidae	pentamerous	1
Campanulidae	pentamerous	1
Asterids	pentamerous	1
Superasterids	pentamerous	1
Rosidae	pentamerous	1
Fabidae	pentamerous	1

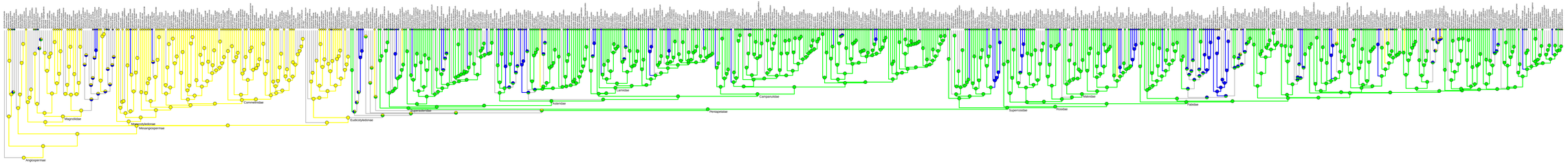
Model	Logl.	Npar	AIC	AICc	ΔAICc	ΔAICc rel.	AICc wt
ARD	-322.95	12	669.89	670.26	0.00	0.00	1
ARDeq	-321.84	12	667.68	667.94	5.92	0.0296	0.04
ER	-362.02	1	726.04	726.05	56.11	2.8e+04	0
ERdeq	-362.02	1	724.04	724.05	54.11	2.8e+04	0
SYMeq*	-326.13	6	664.26	664.38	0.44	0.2209	0.2
ORD	-337.6	6	687.2	687.32	23.38	1.2e-05	0
ORDeq	-336.69	6	685.38	685.48	21.11	0	0
ORDSYM	-348.2	3	698.39	698.42	34.05	0	0.0019
ORDSYMeq	-345.06	3	696.11	696.14	31.77	0	0.0018
ORDER	-348.11	1	698.22	698.22	33.85	0	0.0024



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
Pentapetalae	pentamerous
Superrosidae	pentamerous
Asteridae	pentamerous
Lamidae	pentamerous
Campanulidae	pentamerous
Superrosidae	pentamerous
Rosidae	pentamerous
Malvidae	pentamerous
Fabidae	pentamerous

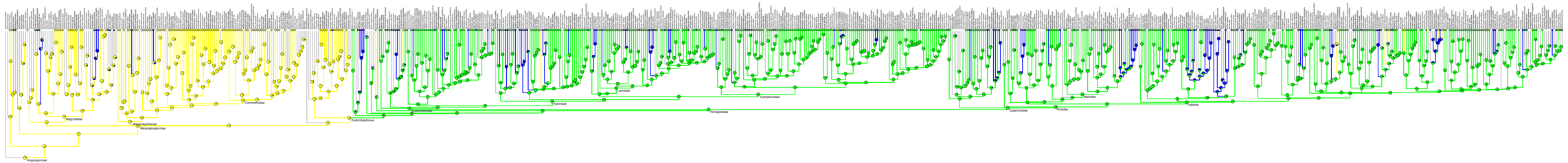


ML ancestral state reconstruction using rayDISC (R:corHMM)
232_8. Perianth merism (3–state) (D2c), SYMeq model

- trimerous
- tetramerous
- pentamerous

Node	ML state	Prob
Angiospermae	trimerous	1
Mesangiospermae	trimerous	1
Magnoliidae	trimerous	1
Monocotyledonae	trimerous	1
Eudicotyledonae	trimerous	0.9574
Commelinidae	trimerous	1
Pentapetalae	pentamerous	0.9996
Superrosidae	pentamerous	0.9999
Superasteridae	pentamerous	0.9999
Asterales	pentamerous	0.9999
Dipsacales	pentamerous	1
Caprifoliaceae	pentamerous	1
Lamiales	pentamerous	1
Lamiidae	pentamerous	1
Ericales	pentamerous	1
Ericaceae	pentamerous	1
Vaccinieae	pentamerous	1
Vaccinium	pentamerous	1
Vaccinium_macrocarpon	pentamerous	1

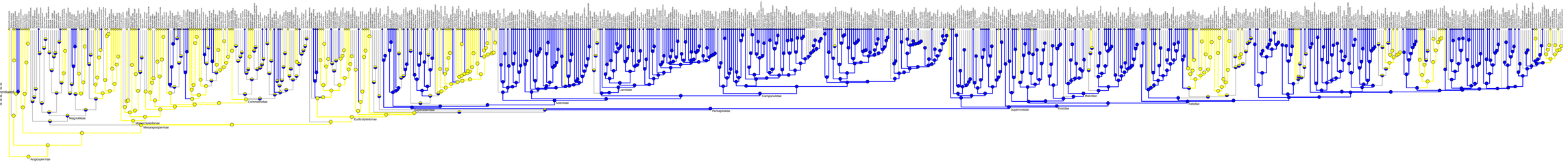
Model	Logl.	Npar	AIC	AICc	ΔAICc	AICcw	ΔAICc rel.	AICcw rel.
ARD	-256.75	6	525.5	526.15	0	0.7	0.00e+00	1
ARDeq	-255.83	6	523.67	524.32	-1.83	0.28	0.00e+00	1
ER	-282.3	1	566.6	566.65	40.5	7.9e-09	4.09e-01	1
SYM	-256.9	3	521.8	522.15	-4	2.06e-01	1.06e-04	1
SYMeq*	-256.9	3	519.8	520.15	-6	7.6e-02	3.92e-04	1
ORD	-256.97	4	521.93	522.39	-3.76	1.16e-01	5.96e-04	1
ORDeq	-256.08	4	520.15	520.2	0.38	0.28	1e-04	1
ORDSYM	-260.53	2	525.05	525.07	5.24	0.02	0.0014	1
ORDSYMeq	-258.53	2	523.05	523.07	3.25	0.07	0.0014	1
ORDER	-263.17	1	528.33	528.34	8.51	0	0.0023	1



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

undifferentiated
differentiated

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

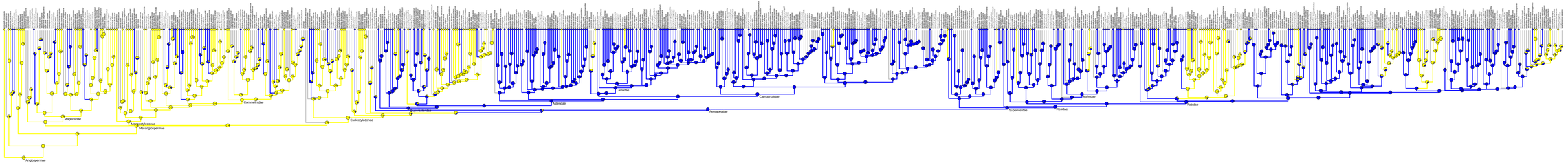


ML ancestral state reconstruction using rayDISC (R:corHMM)
234_A. Periantth differentiation (binary) (D2d), ARDeq model

- undifferentiated
- differentiated

Node	ML state	Prob
Angiospermae	undifferentiated	1
Mesangiospermae	undifferentiated	1
Magnoliidae	undifferentiated	0.9993
Monocotyledonae	undifferentiated	0.9999
Eudicotyledonae	undifferentiated	0.9759
Commelinidae	undifferentiated	0.9999
Pentapetalae	differentiated	0.9522
Superrosidae	differentiated	0.9984
Asteridae	differentiated	0.9984
Lamidae	differentiated	0.9999
Campanulidae	differentiated	1
Superrosidae	differentiated	0.9908
Rosidae	differentiated	0.9943
Malvidae	differentiated	0.9999

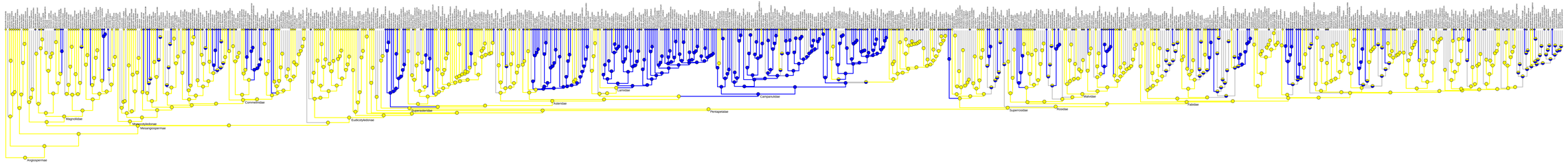
Model	Logl.	Nobr	AIC	AICc	AICc_wt	q01	q10	rate
ARD	−198.71	2	401.43	401.63	0.3	0.0041	0.0014	0.0055
ARDeq**	−198.06	2	400.13	400.14	0	0.0041	0.0014	
ER	−207.3	1	416.59	416.6	16.46	0	0.0024	0.0024
UN01	−231.39	1	464.78	464.79	64.65	0	0.0083	
UN10	−233.32	1	468.64	468.65	68.51	0		0.0032



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

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

Node	MP state(s)
Angiospermae	free (<5%)
Magnoliopsidae	free (<5%)
Magnoliidae	free (<5%)
Monocotyledonae	free (<5%)
Eudicotyledonae	free (<5%)
Commelinidae	free (<5%)
Pentapetalae	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%)

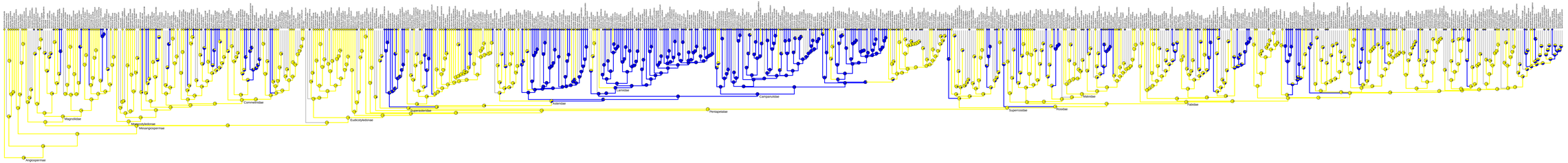


ML ancestral state reconstruction using rayDISC (R:corHMM)
204_A. Fusion of perianth (D2c), ER model

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

Node	ML state	Prob.
Angiospermae	free (<5%)	0.9237
Magnoliidae	free (<5%)	0
Mesangiospermae	free (<5%)	0.9988
Monocotyledonae	free (<5%)	0.9995
Eudicotyledonae	free (<5%)	0.9998
Commelinidae	free (<5%)	0.9968
Pentapetalae	free (<5%)	0.9943
Superasteridae	free (<5%)	0.9997
Asteridae	free (<5%)	0.997
Lamidae	fused (>5%)	0.9779
Campanulidae	fused (>5%)	0.9765
Superrosidae	free (<5%)	0.9949
Rosidae	free (<5%)	0.9994
Malvidae	free (<5%)	0.9994
Fabidae	free (<5%)	0.9994
Fagidae	free (<5%)	0.9998

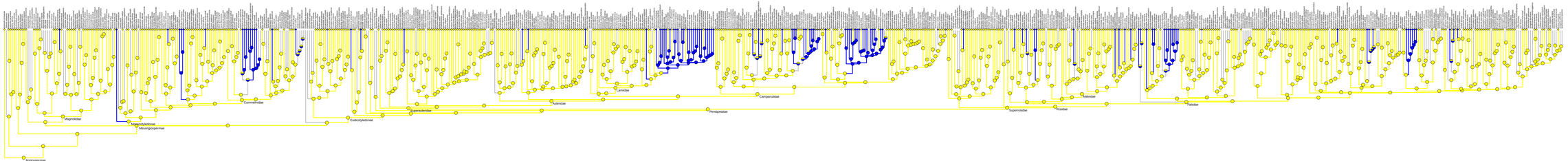
Model	Logl.	Npar	AIC	AICc	delta AIC	delta AICc	w AIC	w AICc	ER
ARD	−225.72	2	455.45	455.49	0.00	0.04	0.39	0.39	0.0008
ARDeq	−225.16	2	454.31	454.35	0.56	0.39	0.0041	0.0035	
ER*	−225.69	1	453.77	453.78	0	0.46	0.004	0.004	
UN01	-241	1	484	484	30.23	0	0.0046		
UN10	−237.57	1	477.15	477.15	23.38	0		0.0078	



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
Pentapetalae	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) (D2d), ARDeq model

actinomorphic
zygomorphic

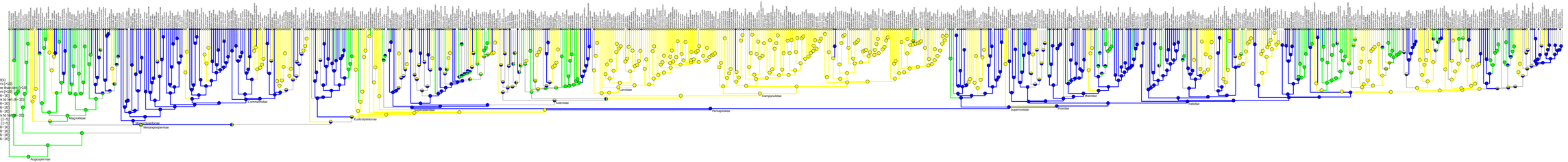
Model	Logl.	Nopar	AIC	AICc	ΔAIC	ΔAICc	w AIC	w AICc
ARD	-211.34	2	426.69	426.69	0	0	0.9974	0.9974
ARDeq**	-210.89	2	425.79	425.8	0	0	0.6311	0.6311
ER	-221.54	1	445.08	445.09	19.28	19.28	0.0015	0.0015
UN01	-270.67	1	543.34	543.34	117.54	117.54	0	0.0018
UN10	-221.29	1	444.57	444.58	18.77	18.77	0	0.0158

Node	ML state	Prob
Angiospermae	actinomorphic	0.9974
Magnoliidae	actinomorphic	0.9999
Mesangiospermae	actinomorphic	0.9999
Eudicotyledonae	actinomorphic	0.9999
Monocotyledonae	actinomorphic	0.9983
Eudicotyledonae	actinomorphic	0.9997
Commelinidae	actinomorphic	0.9961
Pentapetalae	actinomorphic	1
Superasteridae	actinomorphic	1
Asteridae	actinomorphic	1
Lamiidae	actinomorphic	0.9988
Campanulidae	actinomorphic	1
Superrosidae	actinomorphic	1
Rosidae	actinomorphic	0.9999
Malvidae	actinomorphic	0.9999
Fabidae	actinomorphic	0.9994

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)
Magnoliopsidae	one to five (1–5) / more than ten (>10)
Mesangiospermae	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)
Pentapetalae	six to ten (6–10)
Superrosidae	six to ten (6–10)
Asteridae	one to five (1–5) / six to ten (6–10)
Lamiidae	one to five (1–5)
Campanulidae	one to five (1–5)
Superrosidae	six to ten (6–10)
Rosidae	six to ten (6–10)
Malvidae	six to ten (6–10)
Fabidae	six to ten (6–10)

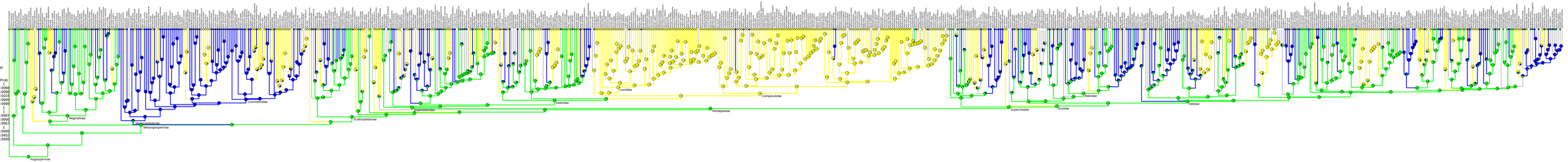


ML ancestral state reconstruction using rayDISC (R:corHMM)
301_8. Number of fertile stamens (3–state) (D2c), ARDeq model

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

Node	ML state	Prob
Angiospermae	more than ten (>10)	1
Magnoliidae	more than ten (>10)	0.9998
Eudicotyledonae	more than ten (>10)	0.9998
Monocotyledonae	six to ten (6–10)	0.5016
Eudicotyledonae	more than ten (>10)	0.9999
Commelinidae	six to ten (6–10)	0.9998
Pentapetalae	more than ten (>10)	1
Superrosidae	more than ten (>10)	1
Superasteridae	more than ten (>10)	0.9997
Lamiidae	more than ten (>10)	0.9998
Campanulidae	more than ten (>10)	0.9998
Asteridae	more than ten (>10)	0.9998
Rosidae	more than ten (>10)	0.9998
Fabidae	more than ten (>10)	0.9998
Malvidae	more than ten (>10)	0.9998
Superrosidae	more than ten (>10)	0.9998
Mesangiospermae	more than ten (>10)	0.9998

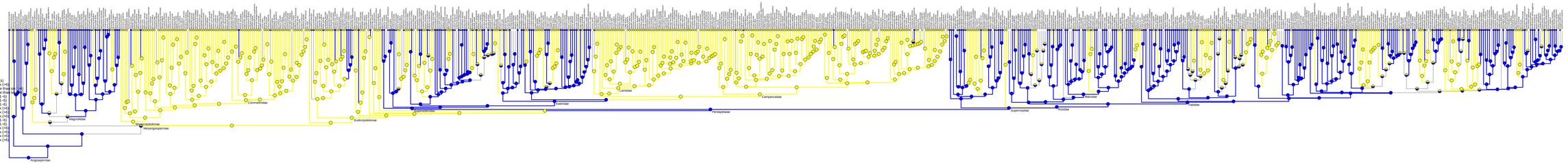
Model	Logl.	Npar	AIC	AICc	Delta AICc	AICw	LRT	p-value
ARD	−495.2	6	1002.4	1002.6	2.1	0.26	0.9998	0.9998
ARDeq**	−494.12	6	1000.24	1000.45	0	0.74	1	0.9997
ER	−533.11	1	1068.22	1068.22	67.78	0	0.9258	1
SYM	−528.16	3	1062.32	1062.52	67.98	0	1.9	0.9258
SYMeq	−528.16	3	1062.32	1062.52	67.98	0	0.9258	0.9453
ORD	−506.42	4	1024.84	1024.97	24.46	0	0.9258	0.9958
ORDeq	−507.88	4	1023.75	1023.9	23.46	0	5e−04	—
ORDSYM	−532.73	2	1069.47	1069.48	69.14	0	0.0041	—
ORDSYMeq	−532.38	2	1068.76	1068.77	68.44	0	0.0041	—
ORDER	−532.74	1	1067.48	1067.48	67.14	0	0.0042	—



MP ancestral state reconstruction using ancestral.pars
(R phangorn)
301_C: Number of fertile stamens (binary) (D2c), 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) / more than six (>6)
Magnoliidae	one to six (1–6) / more than six (>6)
Monocotyledonae	one to six (1–6)
Eudicotyledonae	one to six (1–6)
Commelinidae	one to six (1–6)
Pentapetalae	more than six (>6)
Superasteridae	more than six (>6)
Asteridae	more than six (>6)
Lamiidae	one to six (1–6)
Campanulidae	one to six (1–6)
Superrosidae	more than six (>6)
Rosidae	more than six (>6)
Malvidae	more than six (>6)
Fabidae	more than six (>6)

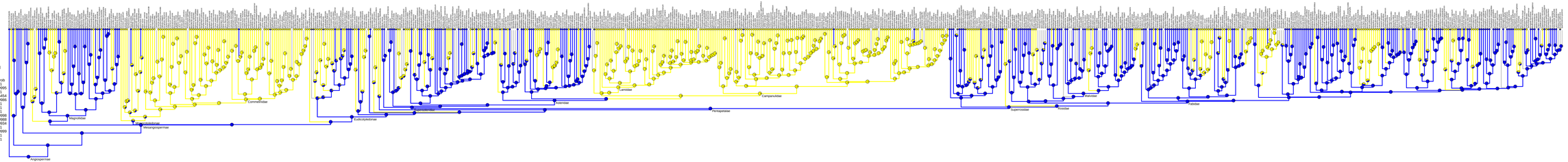


ML ancestral state reconstruction using rayDISC (R:corHMM)
301_C. Number of fertile stamens (binary) (D2c), ARDeq model

one to six (1–6)
more than six (>6)

Node	ML state	Prob
Angiospermae	more than six (>6)	1
Magnoliophytae	more than six (>6)	0.9995
Magnoliidae	more than six (>6)	1
Monocotyledonae	more than six (>6)	0.5454
Eudicotyledonae	more than six (>6)	0.9986
Commelinidae	one to six (1–6)	1
Pentapetalae	more than six (>6)	1
Superrosidae	more than six (>6)	1
Asteridae	more than six (>6)	0.9998
Lamiidae	one to six (1–6)	0.9968
Campanulidae	one to six (1–6)	0.9934
Superrosidae	more than six (>6)	1
Rosidae	more than six (>6)	0.9999
Fabidae	more than six (>6)	1
Malvidae	more than six (>6)	1

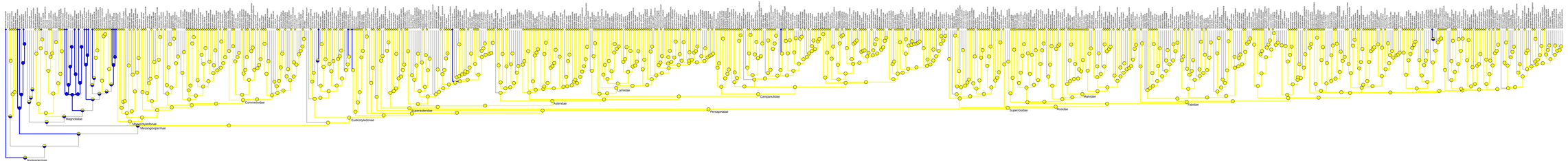
Model	Logl.	Npar	AIC	AICc	ΔAICc	AICc wt	Pchi2	ΔP	Omnibus
ARD	−291	2	585.99	586.02	0.38	0.3338	0.0000	0	1
ARDeq**	−290.31	2	584.62	584.63	0	0.67	Se−04	0.0005	
ER	−322.94	1	647.87	647.88	63.24	0	0.0029	0.0029	
UN01	−365.41	1	734.83	734.83	150.2	0	0.0044		
UN10	−330.35	1	662.7	662.7	78.07	0		0.0069	



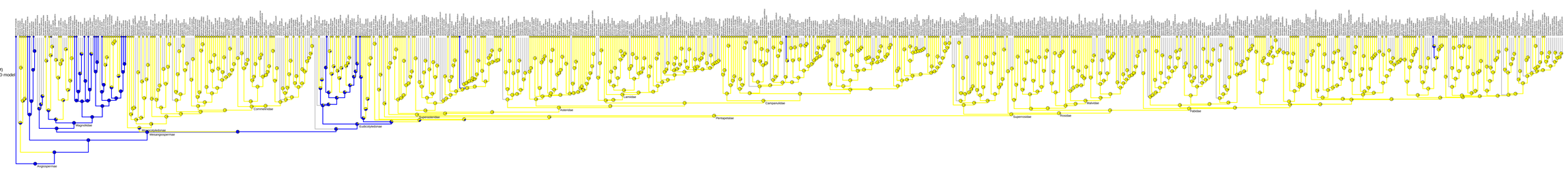
MP ancestral state reconstruction using ancestral pars
(R:phangorn)
330_A. Androecium structural phylotaxy (binary) (D2d), 12 steps

whorled
spiral

Node	MP state(s)
Angiospermae	whorled / spiral
Mesangiospermae	whorled / spiral
Magnoliidae	whorled / spiral
Monocotyledonae	whorled
Eudicotyledonae	whorled
Commelinidae	whorled
Pentapetalae	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) (D20, ARD model)



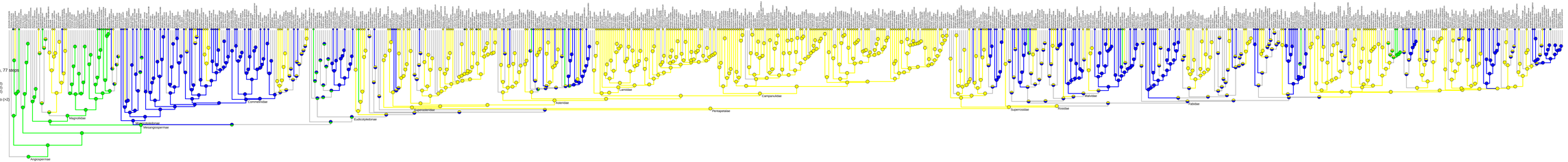
Node	ML state	Prob
Angiospermae	spiral	0.9888
Mesangiospermae	spiral	0.9794
Magnoliidae	wholed	0.9999
Monocotyledonae	wholed	0.5501
Eudicotyledonae	spiral	0.8243
Cornoideae	wholed	0.9999
Pentapetalae	wholed	0.9983
Superrosidae	wholed	0.9992
Asteridae	wholed	1
Lamidae	wholed	1
Campanulidae	wholed	1
Superrosidae	wholed	0.9996
Fabidae	wholed	0.9998

Model	Logl.	Npar	AIC	AICc	Weight	w-AIC	w-AICc
ARD**	-54.43	2	112.86	112.87	Fabidae	0.99	0.99
ARDeq	-57.81	2	119.62	119.64	5.76	0.03	4e-04
ER	-58.55	1	119.1	119.11	6.23	0.04	4e-04
UN01	-58.5	1	119.01	119.01	6.14	0.04	4e-04
UN10	-79.63	1	161.25	161.26	48.38	0	0.0181

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)
Eudicotyledonae	more than two (>2)
Monocotyledonae	two (2)
Eudicotyledonae	two (2) / more than two (>2)
Commelinidae	two (2)
Pentapetalae	one (1)
Superasterideae	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), ORDER model

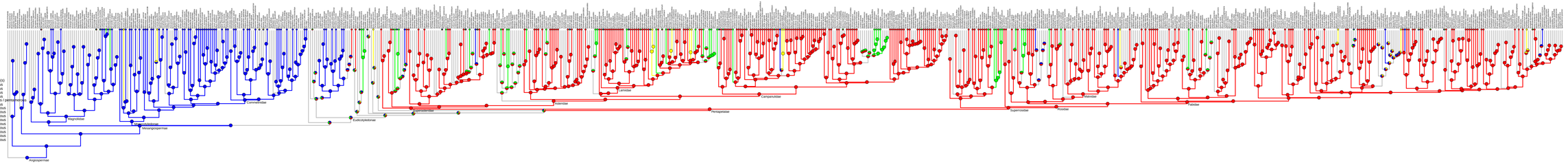
- one (1)
- two (2)
- more than two (>2)

Node	ML state	Prob
Angiospermae	more than two (>2)	1
Magnoliidae	more than two (>2)	0.9982
Eudicots	more than two (>2)	0.9999
Monocotyledonae	more than two (>2)	0.3288
Eudicotyledonae	more than two (>2)	0.8079
Commelinidae	two (2)	0.968
Pentapetalae	two (2)	0.9915
Superrosidae	two (2)	0.9999
Rosidae	two (2)	0.9999
Malvidae	two (2)	0.9982
Rutidae	two (2)	0.9504
Sapindidae	two (2)	0.9976
Sapindales	two (2)	0.9986
Malpighiales	two (2)	0.9997
Fabidae	two (2)	0.9999
Fabales	two (2)	1
Rosales	two (2)	1
Cucurbitales	two (2)	1
Fagales	two (2)	1
Cucurbitales	two (2)	1
Mesangiospermae	two (2)	1
Lamiidae	two (2)	1
Lamiales	two (2)	1
Lamiales	two (2)	1
Lamiales

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



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

- dimerous
- trimerous
- tetramerous
- pentamerous

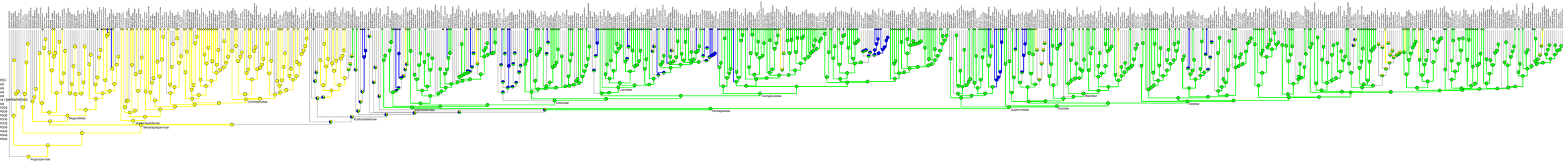
Model	Logλ	Npar	AIC	AICc	ΔAICc	ΔAICc rel	AICw
ARD	-222.76	12	469.52	469.82	0	1	0.9993
ARDeq	-221.86	12	467.72	467.92	10.39	0.0103	0.0007
ER	-237.93	1	477.86	477.91	58.08	0.0577	0.0000
SYM	-225.73	3	457.46	457.61	0	0	0.5204
SYMeq*	-225.73	6	459.46	459.82	2.21	0.3333	0.1734
ORD	-236.95	6	485.9	486.26	26.64	0.0000	0.0000
ORDeq	-236.69	6	485.39	485.5	25.93	0	100
ORDSYM	-260.13	3	526.27	526.3	66.73	0	0.002
ORDSYMeq	-259.23	3	524.47	524.5	64.93	0	0.0019
ORDER	-261.09	1	524.18	524.18	64.62	0	0.0029

Node	ML state	Prob
Angiospermae	trimerous	1
Mesangiospermae	trimerous	1
Eudicotyledonae	trimerous	1
Monocotyledonae	trimerous	1
Eudicotyledonae	trimerous	0.8208
Commelinidae	trimerous	1
Pentapetalae	pentamerous	0.9999
Superrosidae	pentamerous	1
Superasteridae	pentamerous	0.3993
Lamiidae	pentamerous	0.9967
Asterids	pentamerous	0.9956
Campanulidae	pentamerous	1
Asterids	pentamerous	0.9004
Asterids	pentamerous	0.9004
Asterids	pentamerous	0.9004

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
Monocotyledonae	trimerous
Eudicotyledonae	trimerous / tetramerous / pentamerous
Cornoideae	trimerous
Pentapetalae	pentamerous
Superasterideae	pentamerous
Asteridae	pentamerous
Lamiidae	pentamerous
Campanulidae	pentamerous
Superrosidae	pentamerous
Rosidae	pentamerous
Malvidae	pentamerous
Fabidae	pentamerous



ML ancestral state reconstruction using rayDISC (R:corHMM)
332_8. Androecium structural merism (3–state) (D2c), ARDeq model

- trimerous
- tetramerous
- pentamerous

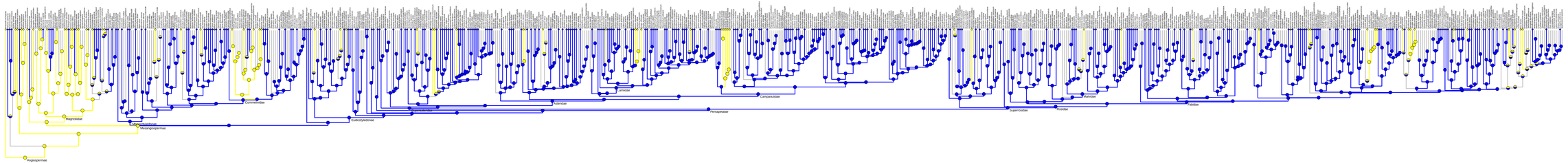
Model	Logl.	Npar	AIC	AICc	ΔAICc	ΔAICc rel.	AICc wt
ARD	−170.44	6	352.88	353.06	1.97	0.00	0.9919
ARDeq*	−169.46	6	350.92	351.10	0	1	0.9624
ER	−186.52	1	375.04	375.07	24.01	0.0169	0.0061
SYM	−176	3	358.01	358.16	7.09	0.2024	0.0294
SYMeq	−176	3	358.01	358.16	7.09	0.2024	0.0294
ORD	−178.86	4	365.72	365.92	14.75	0.0104	0.0474
ORDeq	−178.69	4	365.37	365.43	14.41	0	1e−04
ORDSYM	−186.31	2	376.62	376.64	25.62	0	0.0019
ORDSYMeq	−185.41	2	374.83	374.84	23.82	0	0.0018
ORDER	−187.22	1	376.44	376.44	25.42	0	0.0026

Node	ML state	Prob
Angiospermae	trimerous	0.9999
Mesangiospermae	trimerous	1
Eudicotyledonae	trimerous	1
Monocotyledonae	trimerous	1
Eudicotyledonae	trimerous	0.8752
Commelinidae	trimerous	1
Pentapetalae	tetramerous	0.9999
Superrosidae	tetramerous	1
Malvidae	tetramerous	1
Rosidae	tetramerous	1
Superasteridae	tetramerous	1
Asteridae	tetramerous	1
Lamiidae	tetramerous	1
Campanulidae	tetramerous	1
Asterids	tetramerous	1
Lamiidae	tetramerous	1
Lamiidae	tetramerous	1
Lamiidae

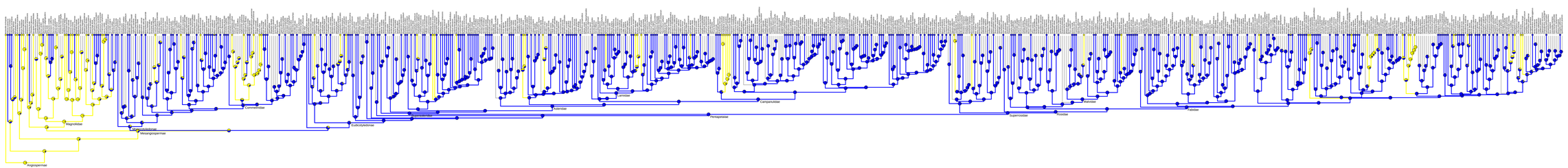
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
305_A. Filament (binary) (D2d), 52 steps

- laminar (wide)
- typical (narrow)

Node	MP state(s)
Angiospermae	laminar (wide)
Magnoliopsmae	laminar (wide)
Magnoliidae	laminar (wide)
Monocotyledonae	typical (narrow)
Eudicotyledonae	typical (narrow)
Commelinidae	typical (narrow)
Pentapetalae	typical (narrow)
Superrosidae	typical (narrow)
Asteridae	typical (narrow)
Lamiidae	typical (narrow)
Campanulidae	typical (narrow)
Superrosidae	typical (narrow)
Rosidae	typical (narrow)
Malvidae	typical (narrow)
Fabidae	typical (narrow)



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



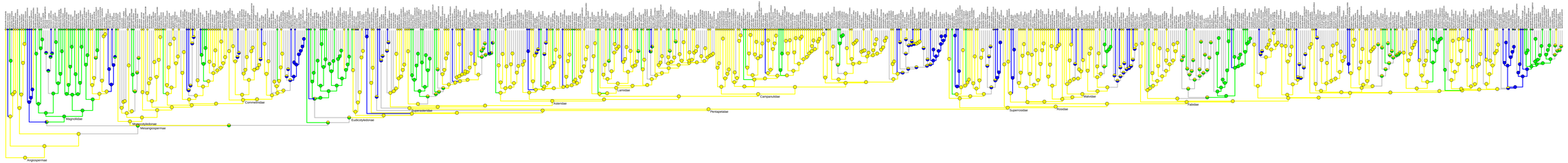
Node	ML state	Prob
Angiospermae	laminar (wide)	0.9845
Magnoliopsida	laminar (wide)	0.7691
Mesangiospermae	laminar (wide)	0.9999
Monocotyledonae	typical (narrow)	0.6794
Eudicotyledonae	typical (narrow)	0.9083
Commelinidae	typical (narrow)	0.9614
Pentapetalae	typical (narrow)	0.9999
Superrosidae	typical (narrow)	0.9999
Asteridae	typical (narrow)	0.9999
Lamiidae	typical (narrow)	0.9992
Campanulidae	typical (narrow)	0.996
Superrosidae	typical (narrow)	0.9999
Rosidae	typical (narrow)	0.9999
Asterales	typical (narrow)	0.9997
Asteraceae	typical (narrow)	0.9999

Model	Logl.	Npar	AIC	AICc	ΔAIC	ΔAICc	w.AIC	w.AICc
ARD	−171.41	2	346.82	346.82	0.58	0.58	0.4423	0.4423
ARDeq**	−171.12	2	346.24	346.26	0	0	0.5710	0.5577
ER	−176.86	1	355.71	355.72	9.46	9.46	0.0100	0.0022
UN01	−188.13	1	378.27	378.27	32.02	32.02	0	0.0135
UN10	−188.56	1	379.11	379.12	32.86	32.86	0	0.0022

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	introrse
Monocotyledonae	introrse
Eudicotyledonae	introrse / extrorse
Commelinidae	introrse
Pentapetalae	introrse
Superasteridae	introrse
Asteridae	introrse
Lamiidae	introrse
Campanulidae	introrse
Superrosidae	introrse
Rosidae	introrse
Malvidae	introrse
Fabidae	introrse

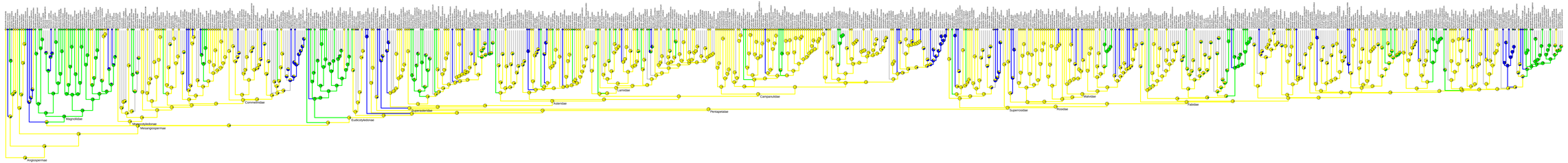


ML ancestral state reconstruction using rayDISC (R:corHMM)
311_A. Anther orientation (D2d), ER model

- introrse
- latrorse
- extrorse

Node	ML state	Prob
Angiospermae	introrse	0.8346
Mesangiospermae	introrse	0.9161
Magnoliidae	introrse	0.9999
Monocotyledonae	introrse	0.8488
Eudicotyledonae	introrse	0.9321
Commelinidae	introrse	0.9939
Pentapetalae	introrse	1
Superasteridae	introrse	0.9998
Asteridae	introrse	0.9997
Lamiidae	introrse	0.9998
Campanulidae	introrse	1
Superrosidae	introrse	1
Rosidae	introrse	1
Malvidae	introrse	0.9999
Fabidae	introrse	0.9997

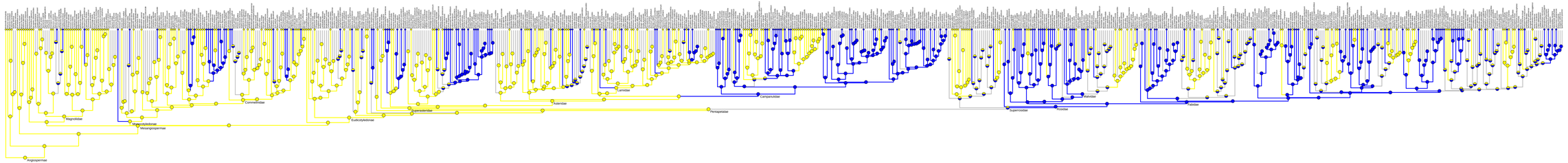
Model	LogL	Npar	AIC	AICc	delta AICc	wt AICc	ER
ARD	−344.54	6	701.08	701.19	0	0.9999	--
ARDeq	−344.25	6	700.5	700.6	1.61	0.14	0.0036 --
ER*	−348.5	1	698.99	699	0	0.32	0.0028 --
SYM	−347.33	3	700.65	700.68	1.68	0.14	0.003 --
SYMeq	−346.55	3	699.11	699.14	0.14	0.3	0.0029 --



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
Pentapetalae	basifixed
Superasteridae	basifixed
Asteridae	basifixed
Lamiidae	basifixed
Campanulidae	basifixed
Superrosidae	basifixed / dorsifixed
Rosidae	dorsifixed
Malvidae	dorsifixed
Fabidae	dorsifixed



ML ancestral state reconstruction using rayDISC (R:corHMM)
312_A. Anther attachment (binary) (D2/d), ARDeq model

- basifixed
- dorsifixed

Node	ML state	Prob
Angiospermae	basifixed	0.9776
Magnoliidae	basifixed	0.9575
Magnoliidae	basifixed	0.9575
Monocotyledonae	basifixed	0.9448
Eudicotyledonae	basifixed	0.6833
Commelinidae	basifixed	0.9554
Pentapetalae	dorsifixed	0.9515
Superrosidae	dorsifixed	0.9534
Asteridae	dorsifixed	0.9534
Lamidae	dorsifixed	0.7834
Campanulidae	dorsifixed	0.5902
Superrosidae	dorsifixed	0.9558
Rosidae	dorsifixed	0.9558
Asteridae	dorsifixed	0.9558
Asteridae	dorsifixed	0.9558
Asterales	dorsifixed	0.9558
Asteraceae	dorsifixed	0.9558
Asteraceae	dorsifixed	0.9558
Asteraceae

MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
313_A. Anther dehiscence (3-state) (D2d), 10 steps

- longitudinal slit
- int–valvate
- flap–valvate

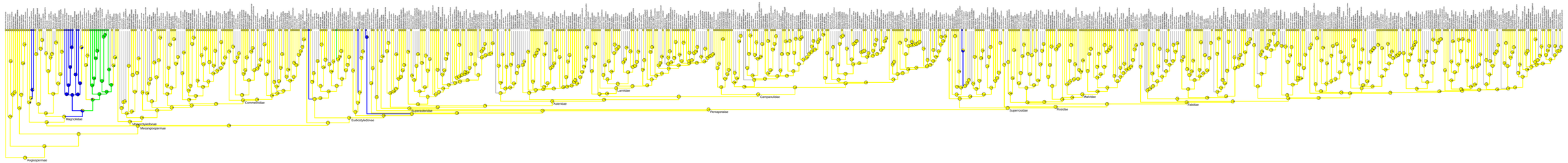
Node	MP state(s)
Angiospermae	longitudinal slit
Magnoliidae	longitudinal slit
Magnoliidae	longitudinal slit
Magnoliid

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

- longitudinal slit
- 1+–valvate
- flap–valvate

Node	ML state	Prob
Angiospermae	longitudinal slit	1
Magnoliopsermae	longitudinal slit	0.9999
Magnoliidae	longitudinal slit	0.9999
Monocotyledonae	longitudinal slit	1
Eudicotyledonae	longitudinal slit	1
Commelinidae	longitudinal slit	1
Pentapetalae	longitudinal slit	1
Superasteridae	longitudinal slit	1
Asteridae	longitudinal slit	1
Lamidae	longitudinal slit	1
Campanulidae	longitudinal slit	1
Superrosidae	longitudinal slit	1
Rosidae	longitudinal slit	1
Malvidae	longitudinal slit	1
Fabidae	longitudinal slit	1

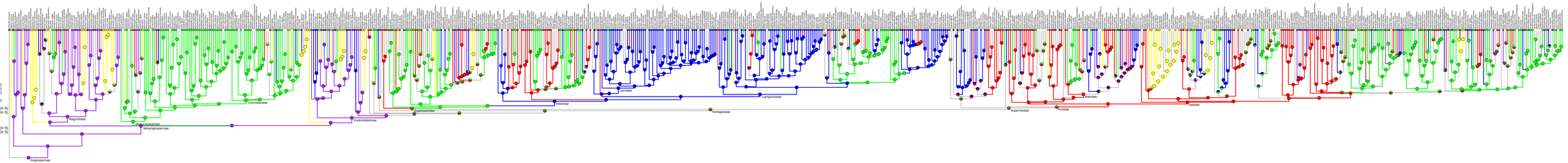
Model	Logl.	Npar	AIC	AICc	delta AIC	AICw	ER
ARD	−55.6	6	123.19	123.39	0.00	0.38	1e+00
ARDeq	−54.57	6	121.13	121.24	0	0.36	2e−04
ER	−60.2	1	122.39	122.4	1.16	0.2	1e−04
SYM	−59.16	3	124.32	124.35	3.11	0.08	2e−04
SYMeq	−58.06	3	122.13	122.16	0.92	0.23	2e−04



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)
Monocotyledonae	three (3)
Eudicotyledonae	more than five (>5)
Commelinidae	three (3)
Pentapetalae	three (3) / four or five (4–5)
Superrosidae	three (3) / four or five (4–5)
Asteridae	two (2)
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)

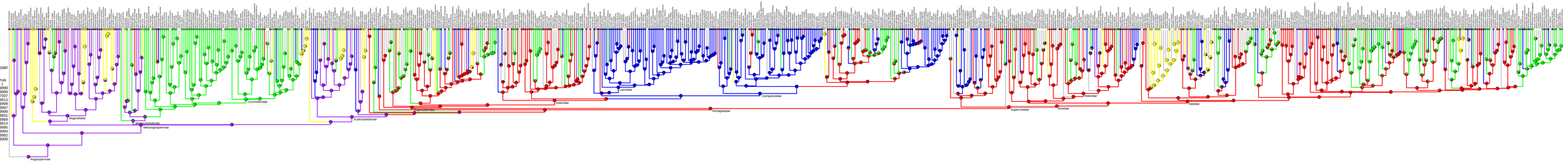


ML ancestral state reconstruction using rayDISC (R:corHMM)
401_8. Number of structural carpels (5~state) (D2ci), ARDeq model

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

Node	ML state	Prob
Angiospermae	more than five (>5)	1
Magnoliidae	more than five (>5)	0.9999
Chloranthaceae	more than five (>5)	0.9999
Monocotyledonae	more than five (>5)	0.7337
Eudicotyledonae	more than five (>5)	0.9913
Commelinidae	three (3)	0.9999
Pentapetalae	four or five (4~5)	0.9997
Superrosidae	four or five (4~5)	0.9999
Rosidae	four or five (4~5)	0.9931
Fabidae	four or five (4~5)	0.9969
Malvidae	four or five (4~5)	0.9614
Malvidae	four or five (4~5)	0.9995
Malvidae	four or five (4~5)	0.9994
Malvidae	four or five (4~5)	0.9992
Malvidae	four or five (4~5)	0.9999

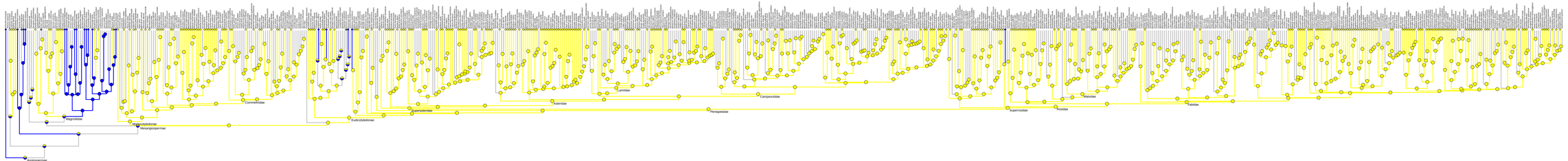
Model	Logl.	Npar	AIC	AICc	Delta AICc	AICc wt	Prob
ARD	−665.1	20	1370.2	1374.0	3.13	0.0177	0.9969
ARDeq*	−663.53	20	1367.06	1370.88	0	0.8513	0.9614
ER	−719.31	1	1440.62	1440.65	72.76	0	0.9995
SYM	−684.52	10	1389.04	1391.04	23.16	0	0.9994
SYMeq	−683.52	10	1387.04	1389.04	21.16	0	0.9992
ORD	−763.1	8	1542.19	1543.87	162.99	0	0.9999
ORDeq	−756.05	8	1528.11	1529.29	160.14	0	1
ORDSYM	−762.95	4	1533.89	1533.94	165.79	0	0.0038
ORDSYMeq	−762.22	4	1532.44	1532.5	164.34	0	0.0038
ORDER	−768.94	1	1539.87	1539.88	171.73	0	0.0055



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
Pentapetalae	whorled
Superasteridae	whorled
Asteridae	whorled
Lamiidae	whorled
Campanulidae	whorled
Superrosidae	whorled
Rosidae	whorled
Malvidae	whorled
Fabidae	whorled

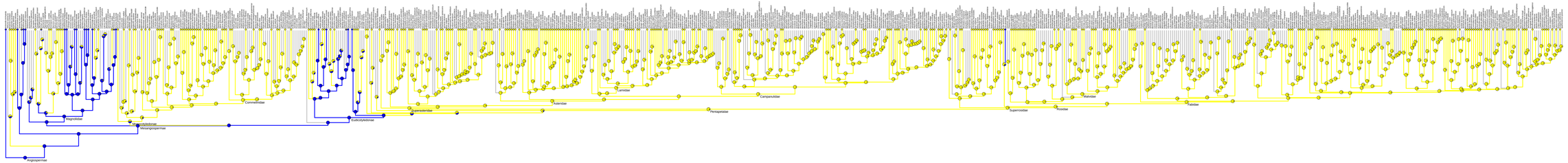


ML ancestral state reconstruction using rayDISC (R:corHMM)
400_A. Gynoecium phylotaxy (D2d), ARDeq model

- whorled
- spiral

Node	ML state	Prob
Angiospermae	spiral	1
Mesangiospermae	spiral	0.9999
Magnoliidae	whorled	1
Monocotyledonae	whorled	0.5215
Eudicotyledonae	spiral	0.9984
Commelinidae	whorled	1
Pentapetalae	whorled	0.9638
Superasterideae	whorled	0.964
Asteridae	whorled	1
Lamiidae	whorled	1
Campanulidae	whorled	1
Superrosidae	whorled	0.9668
Rosidae	whorled	1
Malvidae	whorled	1
Fabidae	whorled	1

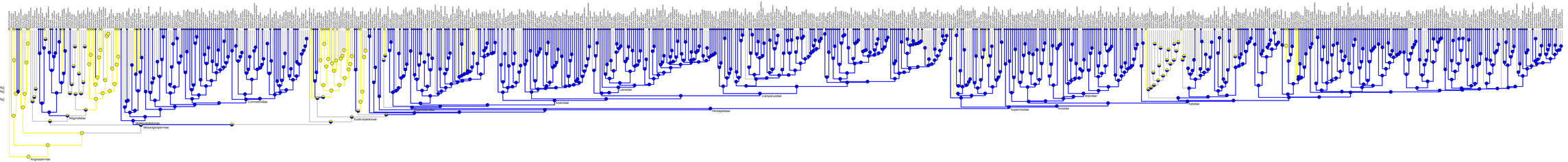
Model	Logl.	Npar	AIC	AICc	AICc_wt	Delta_AICc	AIC_wt	Delta_AIC	AIC_wt
ARD	−39.15	2	82.31	82.32	0.99	0	0.99	0	0.99
ARDeq**	−38.46	2	80.92	80.93	0	0.61	0	0.0068	
ER	−49.47	1	100.94	100.94	20.01	0	4e−04	4e−04	
UNI01	−51.93	1	105.1	105.11	24.17	0	4e−04		
UNI10	−41.36	1	84.73	84.73	3.8	0.09		0.0079	



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%)
Magnoliopsidae	free (<5%) / fused (>5%)
Magnoliidae	free (<5%) / fused (>5%)
Monocotyledonae	fused (>5%)
Eudicotyledonae	free (<5%) / fused (>5%)
Commelinidae	fused (>5%)
Pentapetalae	fused (>5%)
Superrosidae	fused (>5%)
Asteridae	fused (>5%)
Lamidae	fused (>5%)
Campanulidae	fused (>5%)
Superrosidae	fused (>5%)
Rosidae	fused (>5%)
Malvidae	fused (>5%)
Fabidae	fused (>5%)

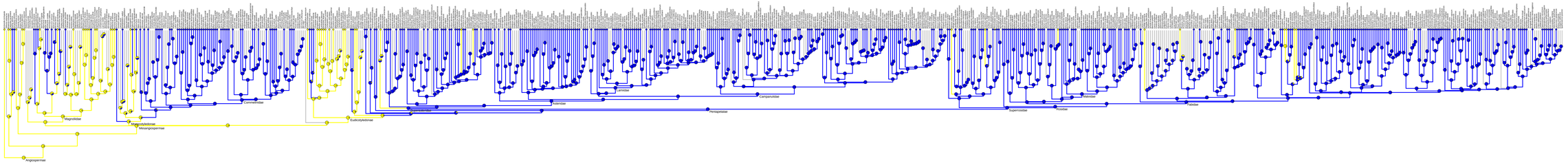


ML ancestral state reconstruction using rayDISC (R:corHMM) 403_A. Fusion of ovaries (binary) (D2c), ARDeq model

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

Node	ML state	Prob
Angiospermae	free (<5%)	1
Magnoliopsidae	free (<5%)	0.9998
Magnoliidae	free (<5%)	0.9998
Monocotyledonae	free (<5%)	0.9088
Eudicotyledonae	free (<5%)	0.9971
Commelinidae	fused (>5%)	1
Pentapetalae	fused (>5%)	0.9955
Superrosidae	fused (>5%)	0.9957
Asteridae	fused (>5%)	1
Lamidae	fused (>5%)	1
Campanulidae	fused (>5%)	1
Superrosidae	fused (>5%)	0.9994
Rosidae	fused (>5%)	0.9997
Fabidae	fused (>5%)	0.9
Malvidae	fused (>5%)	0.9999
Brassicales	fused (>5%)	0.9999
Brassicaceae	fused (>5%)	0.9999

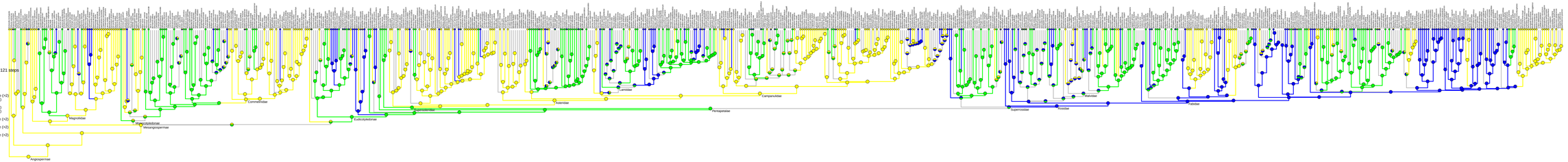
Model	Logl.	Nopr	AIC	AICc	ΔAIC	ΔAICc	AICw	AICcw
ARD	−95.14	2	194.29	194.31	0.00	0.00	0.99	0.99
ARDeq**	−94.45	2	192.91	192.93	0	0	0.66	0.0045
ER	−102	1	206	206.01	13.08	0	7e−04	7e−04
UN01	−102.29	1	206.58	206.59	13.66	0	0.0102	0
UN10	−107.41	1	216.81	216.82	23.89	0	0	8e−04



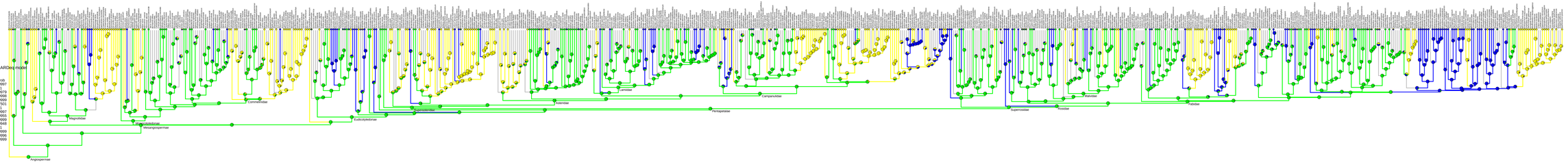
MP ancestral state reconstruction using ancestral pars
(R:phangorn)
411_A: Number of ovules per functional carpel (3-state) (D2c), 121 steps

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

Node	MP state(s)
Angiospermae	one (1)
Magnoliopsidae	one (1)
Magnoliidae	one (1)
Monocotyledonae	one (1) / three or more (>2)
Eudicotyledonae	three or more (>2)
Commelinidae	one (1)
Pentapetalae	three or more (>2)
Superrosidae	three or more (>2)
Asteridae	one (1)
Lamidae	two (2) / three or more (>2)
Campanulidae	one (1)
Superrosidae	two (2) / three or more (>2)
Rosidae	two (2)
Malvidae	two (2) / three or more (>2)
Fabidae	two (2)



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



Node	ML state	Prob.
Angiospermae	three or more (>2)	0.9997
Mesangiospermae	three or more (>2)	1
Eudicotyledonae	three or more (>2)	0.9979
Monocotyledonae	three or more (>2)	0.9998
Eudicotyledonae	three or more (>2)	0.9999
Commelinidae	three or more (>2)	0.7501
Pentapetalae	three or more (>2)	1
Superrosidae	three or more (>2)	0.9997
Malvidae	three or more (>2)	0.9955
Malvidae	three or more (>2)	0.9999
Malvidae	three or more (>2)	0.9999
Malvidae	three or more (>2)	0.9948
Malvidae	three or more (>2)	1
Malvidae	three or more (>2)	0.9999
Malvidae	three or more (>2)	0.9999
Malvidae	three or more (>2)	0.9996
Malvidae	three or more (>2)	0.9999

Model	Logl.	Npar	AIC	AICc	ΔAICc	AICcw	Prob.
ARD	−387.49	6	786.99	788.14	0	0.9999	0.9999
ARDeq**	−396.57	6	805.14	806.29	18.15	0.0001	0.0001
ER	−399.78	1	801.56	801.67	13.53	0.0011	0.0011
SYM	−393.13	3	792.26	792.61	4.47	0.0999	0.0999
SYMeq	−398.53	3	803.05	803.40	15.26	0.0005	0.0005
ORD	−394.33	4	796.66	797.02	8.88	0.0111	0.0111
ORDeq	−393.44	4	794.88	794.93	6.69	0.03	0.03
ORDSYM	−411.38	2	826.77	826.79	41.54	0	0.0052
ORDSYMeq	−411.17	2	826.33	826.35	41.1	0	0.0052
ORDER	−412.36	1	826.73	826.73	41.49	0	0.006