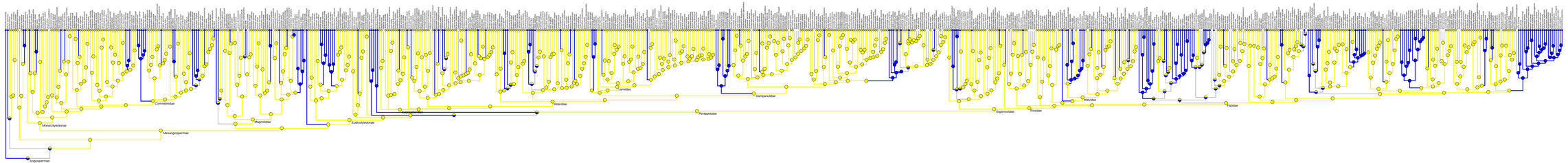
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
100_A. Functional sex of flowers (D2d), 98 steps

bisexual
unisexual

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

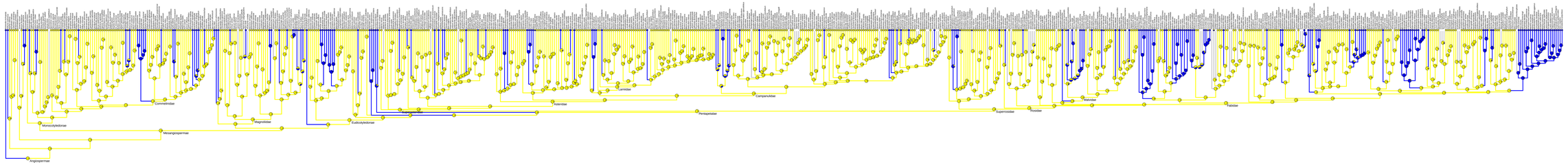


ML ancestral state reconstruction using rayDISC (R:corHMM) 100_A. Functional sex of flowers (D2d), ARDeq model

- bisexual
- unisexual

Model	Logl.	Npar	AIC	AICc	ΔAICc	AICc wt	q01	q10
ARD	−312.08	2	628.16	628.32	0	0.9991	0.0028	9.001
ARDeq	−311.46	2	626.92	626.94	0	0.46	0.0028	9e−04
ER	−313.98	1	629.96	629.96	3.02	0.1	0.0028	0.0028
UNI01	−313.34	1	628.68	628.68	1.74	0.19	0.0029	
UNI10	−359.8	1	721.61	721.61	94.68	0		0.0112

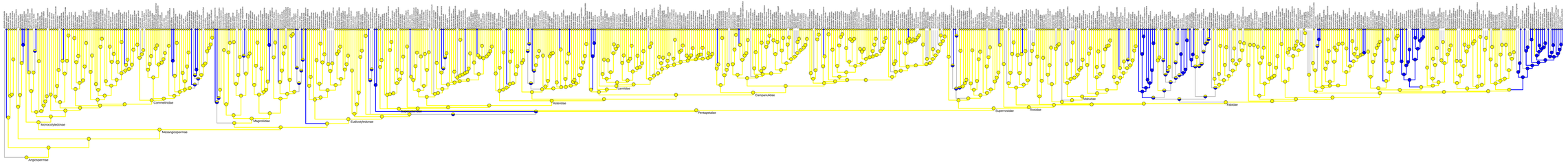
Node	ML state	Prob
Angiospermae	bisexual	0.9999
Mesangiospermae	bisexual	1
Magnoliidae	bisexual	1
Monocotyledonae	bisexual	0.9999
Eudicotyledonae	bisexual	1
Commelinidae	bisexual	0.9997
Pentapetalae	bisexual	1
Superrosidae	bisexual	1
Asteridae	bisexual	1
Lamiidae	bisexual	1
Campanulidae	bisexual	0.9991
Superasteridae	bisexual	1
Rosidae	bisexual	1
Malvidae	bisexual	1
Fabidae	bisexual	1



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

bisexual
unisexual

Node	MP state(s)
Angiosperms	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

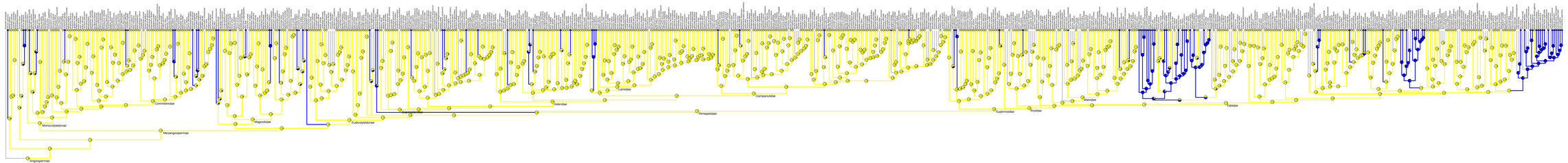


ML ancestral state reconstruction using rayDISC (R:corHMM) 100_B. Structural sex of flowers (D0d), ARDeq model

- bisexual
- unisexual

Node	ML state	Prob
Angiospermae	bisexual	0.9999
Mesangiospermae	bisexual	0.9995
Magnoliidae	bisexual	0.9996
Monocotyledonae	bisexual	0.9995
Eudicotyledonae	bisexual	0.9998
Commelinidae	bisexual	0.9999
Pentapetalae	bisexual	1
Superrosidae	bisexual	1
Asteridae	bisexual	1
Lamiidae	bisexual	0.9999
Campanulidae	bisexual	1
Superrosidae	bisexual	1
Rosidae	bisexual	1
Malvidae	bisexual	1
Fabidae	bisexual	1

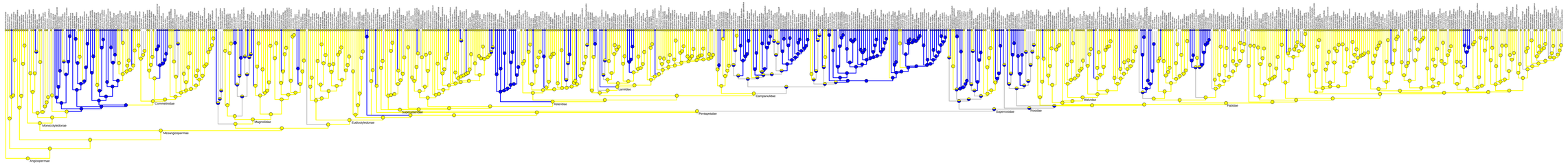
Model	Logl.	Npar	AIC	AICc	ΔAICc	AICw	ΔAICw	q01	q10
ARD	−206.91	2	417.82	417.84	0.05	0.6	0.6	0.0041	0.0041
ARDeq**	−206.48	2	416.97	416.98	0	0.54	0.0015	0.0039	
ER	−209.08	1	420.16	420.16	3.18	0.11	0.0015	0.0015	
UN01	−223.23	1	448.46	448.47	31.48	0	0	0.0016	
UN10	−234.37	1	470.74	470.74	53.76	0		0	0.0154



MP ancestral state reconstruction using ancestral pars
(R:phangorn)
102_B. Ovary position (binary) (D2d), 79 steps

superior
inferior

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

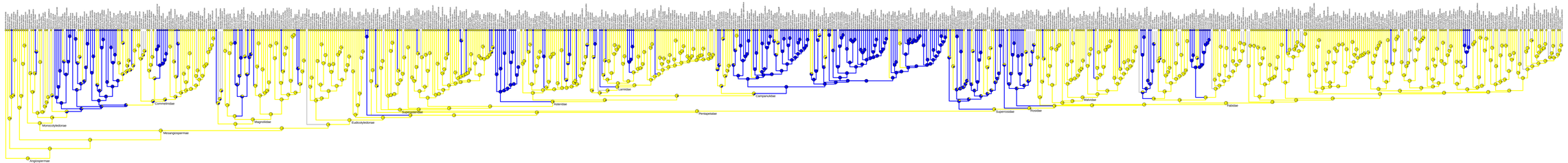


ML ancestral state reconstruction using rayDISC (R:corHMM)
102_B. Ovary position (binary) (02d), ARDeq model

- superior
- inferior

Model	Logl.	Npar	AIC	AICc	ΔAIC	ΔAICc	w.AIC	w.AICc
ARD	−271.06	2	546.11	546.19	0.18	0	0.9996	0.9997
ARDeq**	−270.47	2	544.93	544.95	0	0.55	0.0019	0.0037
ER	−272.76	1	547.53	547.53	2.59	0.15	0.0023	0.0003
UNI01	−281.98	1	565.95	565.96	21.01	0	0.0026	1
UNI10	−295.2	1	592.4	592.4	47.46	0	0	0.0004

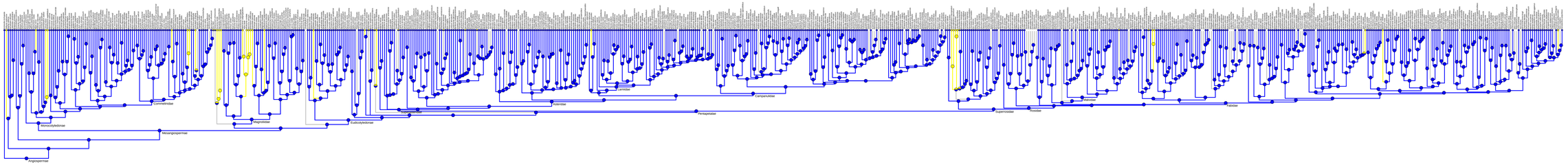
Node	ML state	Prob
Angiospermae	superior	0.9999
Mesangiospermae	superior	0.9991
Magnoliidae	superior	0.9958
Monocotyledonae	superior	0.9835
Eudicotyledonae	superior	0.9999
Commelinidae	superior	0.9642
Pentapetalae	superior	0.9973
Superrosidae	superior	0.9999
Asteridae	superior	0.9399
Lamiidae	superior	0.9519
Campanulidae	superior	0.7333
Superrosidae	superior	0.9569
Fabidae	superior	0.9999
Malvidae	superior	1
Rosidae	superior	0.9999
Fabidae	superior	0.9999



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

absent
present

hode	MP state(s)
Angiospermae	present
Mesangiospermae	present
Magnoliidae	present
Monocotyledonae	present
Eudicotyledonae	present
Commelinidae	present
Pentapetalae	present
Superrosidae	present
Asteridae	present
Lamidae	present
Campanulidae	present
Superrosidae	present
Rosidae	present
Malvidae	present
Fabidae	present

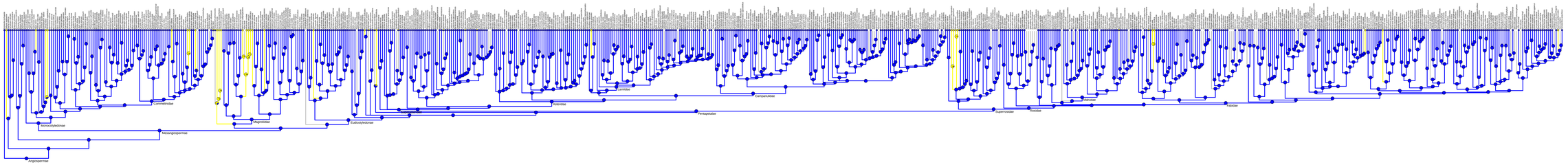


ML ancestral state reconstruction using rayDISC (R:corHMM) 201_A. Periantth presence (D2c), UNI10 model

absent
present

Model	Logl.	Npar	AIC	AICwt	AICc	AICcwt	q01	q10
ARD	−95.77	2	195.54	195.54	0	0.65	0.26	5e−04
ARDeq	−95.08	2	194.15	194.17	0.62	0.26	0	5e−04
ER	−96.05	1	194.09	194.1	0.56	0.27	5e−04	5e−04
UNI01	−114.11	1	230.21	230.22	36.67	0	0.02	
UNI10*	−95.77	1	193.54	193.54	0	0.35		5e−04

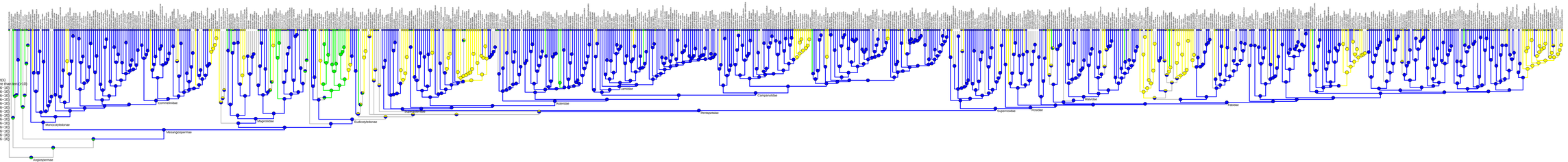
Node	ML state	Prob
Angiosperme	present	1
Mesangiosperme	present	1
Magnoliidae	present	1
Monocotyledonae	present	1
Eudicotyledonae	present	1
Commelinidae	present	1
Pentapetalae	present	1
Superrosidae	present	1
Asteridae	present	1
Lamiidae	present	1
Campanulidae	present	1
Superrosidae	present	1
Rosidae	present	1
Malvidae	present	1
Fabidae	present	1



MP ancestral state reconstruction using ancestral pars
(R:phangorn)
201_B. Number of perianth parts (3–state) (D2c), 85 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)
Mesangiospermae	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)
Superrosidae	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)

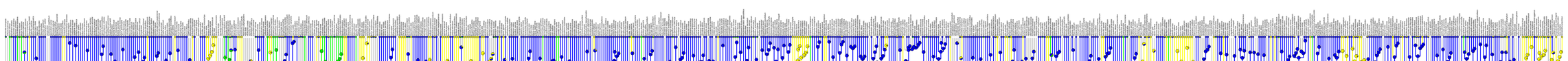


ML ancestral state reconstruction using rayDISC (R:corHMM)
201_8. Number of perianth parts (3~state) (D2c), ARDeq model

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

Model	Logl.	Npar	AIC	AICc	ΔAICc	ΔAICc rel	AICc wt
ARD	-323.1	6	658.2	658.3	0	0	0.9999
ARDeq*	-322.03	6	656.06	656.2	2.14	0.0033	0.0999
ER	-348.35	1	698.7	698.74	40.54	0.0622	0.0988
ERdeq	-336.14	2	676.28	676.38	18.18	0.0279	0.0999
SYMeq	-336.16	3	678.32	678.52	22.19	0.0341	0.0999
ORD	-326.91	4	665.83	666.07	9.71	0.0149	0.0999
ORDeq	-327.84	4	663.67	663.72	7.56	0.0116	0.1041
ORDSYM	-339.89	2	683.78	683.8	27.63	0	0.002
ORDSYMeq	-339.14	2	682.27	682.29	26.12	0	0.002
ORDER	-349.6	1	701.21	701.21	45.05	0	0.0014

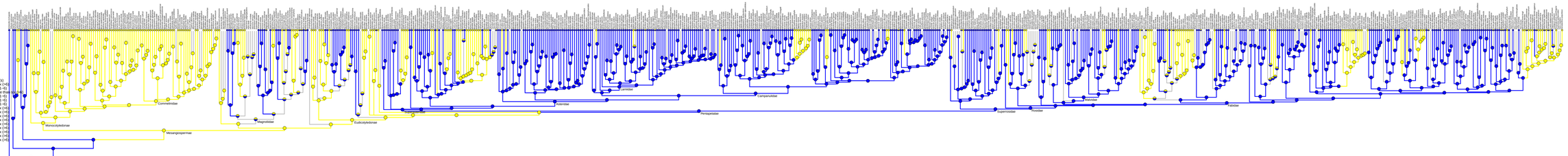
Node	ML state	Prob.
Angiospermae	more than ten (>10)	1
Mesangiospermae	more than ten (>10)	0.9977
Magnoliidae	more than ten (>10)	0.9999
Monocotyledonae	six to ten (6~10)	0.6429
Eudicotyledonae	more than ten (>10)	0.9896
Commelinidae	six to ten (6~10)	0.9999
Pentapetalae	six to ten (6~10)	0.9927
Superrosidae	six to ten (6~10)	0.9999
Superasteridae	six to ten (6~10)	0.9999
Lamiidae	six to ten (6~10)	0.9999
Campanulidae	six to ten (6~10)	0.9999
Asterales	six to ten (6~10)	0.9999
Asteroidae	six to ten (6~10)	0.9999
Asterids	six to ten (6~10)	0.9999
Rosids	six to ten (6~10)	0.9999
Fabidae	six to ten (6~10)	0.9999
Fabales	six to ten (6~10)	0.9999
Papilionoideae	six to ten (6~10)	0.9999
Phaseoleae	six to ten (6~10)	0.9999
Phaseolinae	six to ten (6~10)	0.9999
Vigna	six to ten (6~10)	0.9999
Vigna unguiculata	six to ten (6~10)	0.9999



MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
201_C: Number of perianth parts (binary) (D2c), 69 steps

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

node	MP state(s)
Angiospermae	more than six (>6)
Mesangiospermae	one to six (1-6)
Magnoliidae	one to six (1-6) / more than six (>6)
Monocotyledonae	one to six (1-6)
Eudicotyledonae	one to six (1-6)
Commelinidae	one to six (1-6)
Pentapetalae	more than six (>6)
Superrosidae	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)

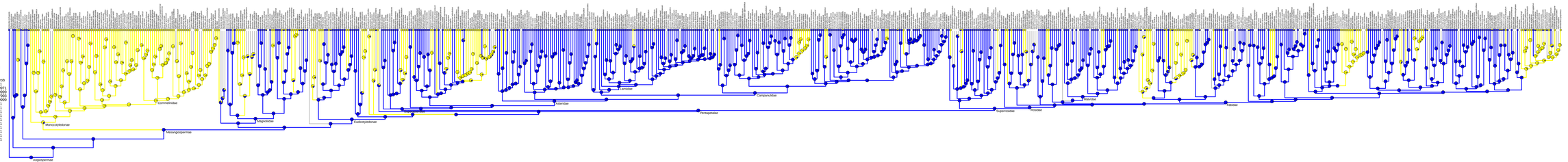


ML ancestral state reconstruction using rayDISC (R:corHMM)
201_C: Number of perianth parts (binary) (D1c), ARDeq model

one to six (1−6)
more than six (>6)

Node	ML state	Prob
Angiospermae	more than six (>6)	1
Mesangiospermae	more than six (>6)	0.9871
Magnoliidae	more than six (>6)	0.9999
Monocotyledonae	one to six (1−6)	0.7955
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
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

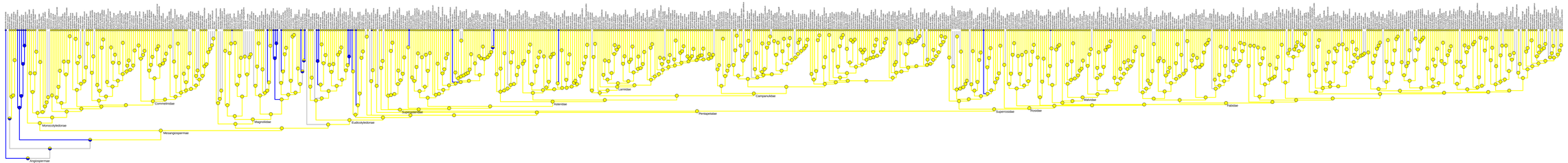
Model	Logl.	Npar.	AIC	AICc	ΔAICc	AICw	ΔAICw	ΔAICw/ΔAICc
ARD	−245.96	2	495.91	495.96	0.04	0.38	0.38	9.5
ARDeq**	−246.27	2	494.53	494.55	0	0.66	0.66	0.0025
ER	−251.67	1	505.34	505.35	10.8	0	0.0021	0.0001
UNI01	−319.59	1	641.18	641.19	146.64	0	0	0.0076
UNI10	−251.65	1	505.3	505.3	10.75	0	0	0.0028



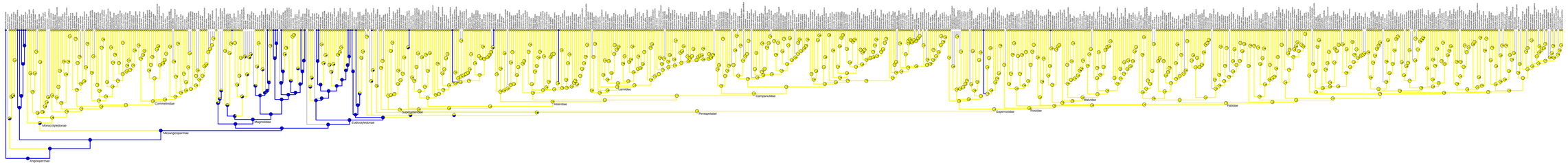
MP ancestral state reconstruction using ancestral pars
(R:phangorn)
230_A. Perianth phyllotaxy (binary) (D2d), 16 steps

whorled
spiral

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



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



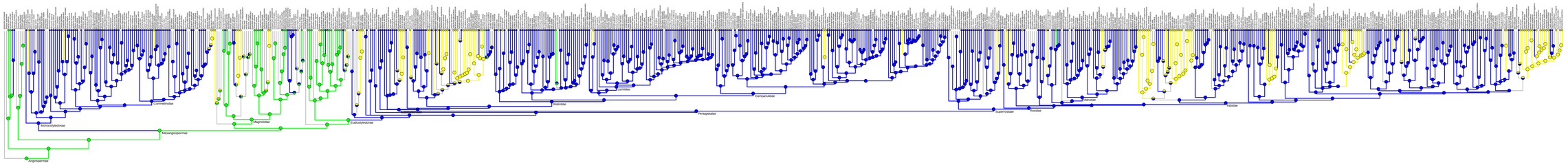
Model	LogL	Npar	AIC	AICc	Weight
ARD***	-69.87	2	143.75	143.78	0.9994
ARDeq	-75.71	2	155.42	155.43	11.67
ER	-76.18	1	154.37	154.37	10.61
UN01	-78.4	1	154.8	154.81	11.04
UN10	-78.94	1	159.89	159.89	16.13

node	ML state	Prob
Angiospermae	whorled	0.0006
Mesangiospermae	spiral	0.9991
Magnoliidae	spiral	0.9975
Monocotyledonae	whorled	0.6224
Eudicotyledonae	spiral	0.9985
Commelinidae	whorled	0.9999
Pentapetalae	whorled	0.9794
Superasteridae	whorled	0.9997
Asteridae	whorled	0.9997
Lamiidae	whorled	1
Campanulidae	whorled	1
Superrosidae	whorled	0.9945
Rosidae	whorled	0.9997
Malvidae	whorled	1
Fabidae	whorled	0.0161

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

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

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

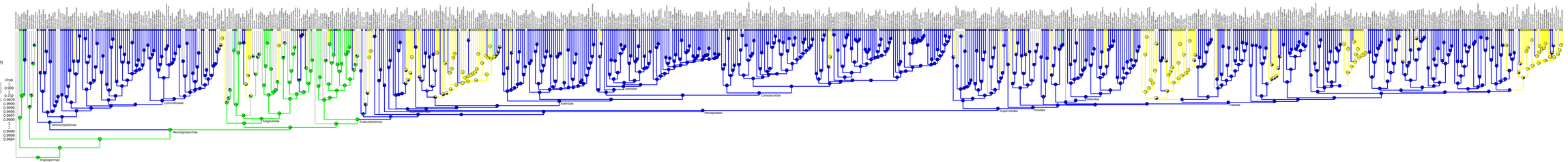


ML ancestral state reconstruction using rayDISC (R:corHMM)
231_A. Number of perianth whorls (D2c), ARDeq model

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

Model	Logl.	Npar	AIC	AICc	ΔAICc	wAIC	ΔwAIC
ARD	−267.02	6	546.03	546.18	2.18	0.2667	0.2667
ARDeq*	−266.93	6	543.86	543.99	0	0.7333	1
ER	−309.43	1	620.86	620.89	76.9	0	0.0000
SYM	−290.13	3	586.26	586.39	42.41	0	0.0000
SYMeq	−290.83	3	587.66	587.79	43.71	0	0.0000
ORD	−274.16	4	556.32	556.47	12.41	0	0.0015
ORDeq	−273.06	4	554.13	554.18	10.22	0	0.0045
ORDSYM	−297.48	2	598.96	598.98	55.02	0	0.0018
ORDSYMeq	−296.71	2	597.43	597.44	53.48	0	0.0018
ORDER	−312.45	1	626.89	626.9	82.94	0	0.0011

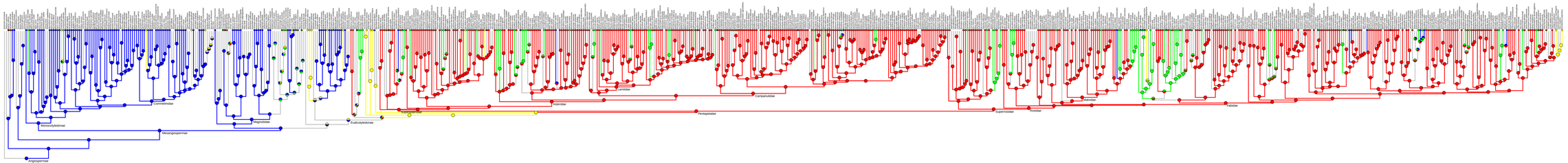
Node	ML state	Prob
Angiospermae	more than two (>2)	1
Mesangiospermae	more than two (>2)	0.99
Magnoliidae	more than two (>2)	1
Monocotyledonae	two (2)	0.732
Eudicotyledonae	more than two (>2)	0.9929
Commelinidae	two (2)	0.9999
Ptyrospermae	two (2)	0.9996
Strelitziaceae	two (2)	0.9999
Zingiberales	two (2)	0.9997
Lamiidae	two (2)	0.9999
Lamiales	two (2)	1
Gesneriaceae	two (2)	1
Lamiales	two (2)	0.9999
Lamiales	two (2)	0.9999
Lamiales	two (2)	0.9984



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

- dimerous
- trimerous
- tetramerous
- pentamerous

hode	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
Superrosidae	pentamerous
Rosidae	pentamerous
Malvidae	pentamerous
Fabidae	pentamerous



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

- dimerous
- trimerous
- tetramerous
- pentamerous

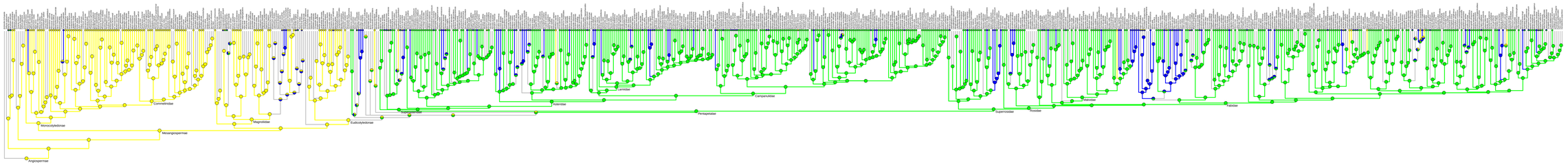
Model	Logl.	Npar	AIC	AICc
ARD	−320.6	12	665.2	666.1
ARDeq	−319.49	12	662.98	663.88
ER	−360.2	1	722.39	722.42
SYM	−324.3	6	660.6	661.5
SYMeq**	−324.3	6	660.6	661.5
ORD	−336.09	6	684.18	685.08
ORDeq	−335.22	6	682.44	682.55
ORDSYM	−344.53	3	695.05	695.08
ORDSYMeq	−343.36	3	692.73	692.76
ORDER	−346.22	1	694.45	694.45

Node	ML state	Prob
Asteranthemum	trimerous	1
Mesangiospermae	trimerous	0.9999
Magnoliidae	trimerous	1
Monocotyledonae	trimerous	0.9999
Eudicotyledonae	trimerous	0.8465
Commelinidae	trimerous	1
Pentapetalae	pentamerous	0.9999
Superrosidae	pentamerous	0.9999
Asterids	pentamerous	0.9999
Lamiidae	pentamerous	1
Solanaceae	pentamerous	1
Rubiaceae	pentamerous	1
Asterales	pentamerous	1
Campanulidae	pentamerous	1
Asteraceae	pentamerous	1
Rosidae	pentamerous	1
Fabaceae	pentamerous	1
Malvaceae	pentamerous	1
Brassicaceae	pentamerous	1
Malpighiales	pentamerous	1
Ericales	pentamerous	1
Caryophyllales	pentamerous	1
Cucurbitales	pentamerous	1
Fagales	pentamerous	1
Rosales	pentamerous	1
Fabales	pentamerous	1
Malvales	pentamerous	1
Brassicales

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

- trimerous
- tetramerous
- pentamerous

hode	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

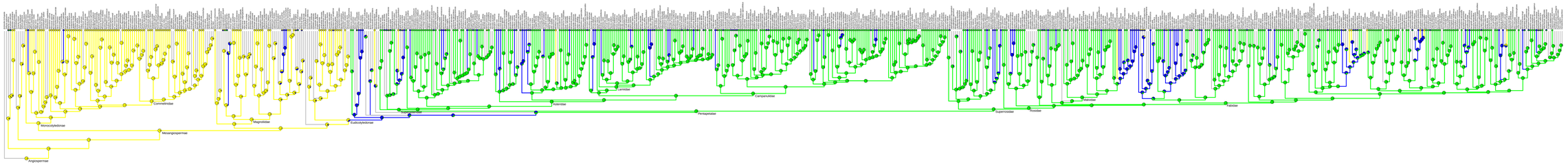


ML ancestral state reconstruction using rayDISC (R:corHMM) 232_B. Perianth merism (3–state) (D2c), ORDeq model

- trimerous
- tetramerous
- pentamerous

Node	ML state	Prob
Angiospermae	trimerous	0.9998
Mesangiospermae	trimerous	0.9976
Magnoliidae	trimerous	0.9977
Monocotyledonae	trimerous	0.9996
Eudicotyledonae	trimerous	0.7392
Commelinidae	trimerous	1
Pentapetalae	pentamerous	0.9809
Superrosidae	pentamerous	0.9969
Asteridae	pentamerous	0.9991
Lamiidae	pentamerous	0.9998
Campanulidae	pentamerous	0.9999
Asterids	pentamerous	0.9999
Rosidae	pentamerous	0.9981
Fabidae	pentamerous	0.9998
Malvidae	pentamerous	0.9998
Fabidae	pentamerous	0.9997

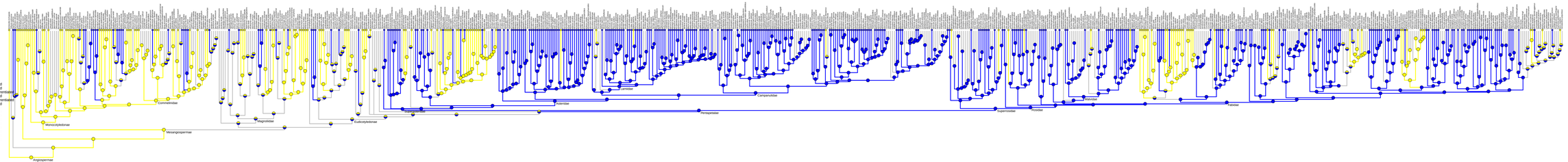
Model	Logl.	Npar	AIC	AICc	ΔAICc	ΔAICc_Rank	wAICc
ARD	−254.32	6	520.65	520.85	0	0	0.9998
ARDeq	−253.42	6	518.84	519.04	5.44	1	0.0645
ER	−280.25	1	562.5	562.59	43.74	2	0.0001
SYM	−254.17	3	514.34	514.54	48.94	3	0.0001
SYMeq	−254.17	3	512.35	512.55	49.01	4	0.0001
ORD	−254.52	4	517.05	517.25	51.64	5	0.0000
ORDeq*	−253.83	4	515.27	515.32	0	0.31	5e−04
ORDSYM	−257.91	2	519.82	519.83	4.51	6	0.0001
ORDSYMeq	−258.9	2	517.8	517.82	2.5	7	0.0001
ORDER	−260.43	1	522.85	522.86	7.54	8	0.0100



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 / differentiated
Commelinidae	undifferentiated
Pentapetalae	differentiated
Superrosidae	differentiated
Asteridae	differentiated
Lamiidae	differentiated
Campanulidae	differentiated
Superrosidae	differentiated
Rosidae	differentiated
Malvidae	differentiated
Fabidae	differentiated

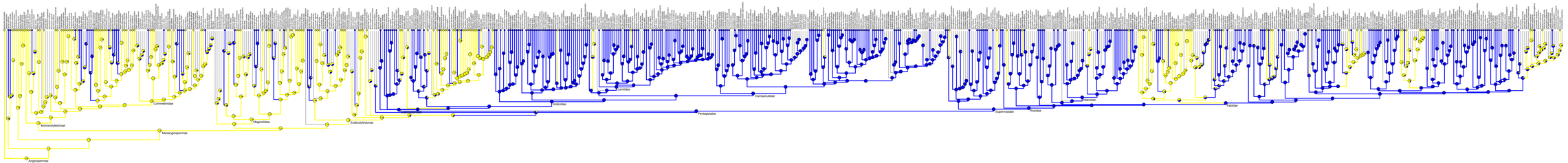


ML ancestral state reconstruction using rayDISC (R:corHMM) 234_A. Perianth differentiation (binary) (D2/D, ARDeq model

- undifferentiated
- differentiated

Node	ML state	Prob
Angiospermae	undifferentiated	1
Mesangiospermae	undifferentiated	0.9999
Magnoliidae	undifferentiated	0.9992
Monocotyledonae	undifferentiated	0.9998
Eudicotyledonae	undifferentiated	0.9651
Commelinidae	undifferentiated	0.9998
Pentapetalae	differentiated	0.9414
Superrosidae	differentiated	0.9998
Asteridae	differentiated	0.9984
Lamidae	differentiated	0.9999
Campanulidae	differentiated	1
Superasterids	differentiated	0.9916
Rosidae	differentiated	0.9998
Malvidae	differentiated	0.9993
Fabidae	differentiated	0.9993

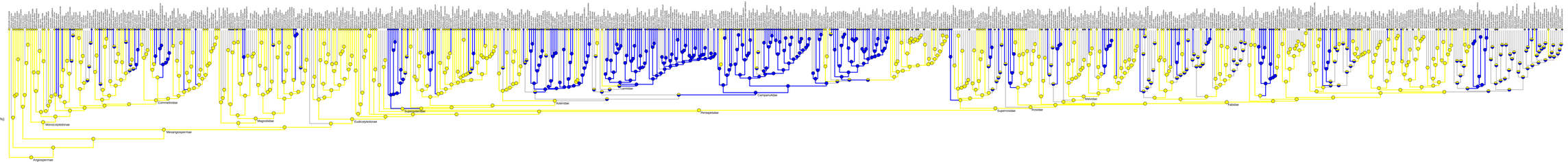
Model	Logl.	Npar	AIC	AICc	ΔAIC	ΔAICc	AICc wt	AIC wt
ARD	−200.3	2	404.59	404.62	0.73	0.73	0.3333	0.6993
ARDeq**	−199.64	2	403.28	403.29	0	0	0.6667	0.3007
ER	−208.52	1	419.04	419.04	15.75	15.75	0	0.0024
UN001	−231.57	1	465.14	465.15	61.86	61.86	0	0.0082
UN10	−234.38	1	470.76	470.76	67.47	67.47	0	0.0032



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

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

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

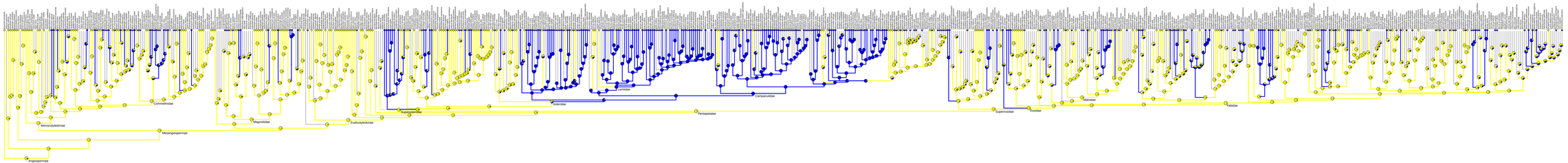


ML ancestral state reconstruction using rayDISC (R:corHMM) 204_A. Fusion of perianth (D2c), ER model

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

Node	ML state	Prob.
Angiospermae	free (<5%)	0.9931
Mesangiospermae	free (<5%)	0.9997
Magnoliidae	free (<5%)	0.9986
Monocotyledonae	free (<5%)	0.9986
Eudicotyledonae	free (<5%)	0.9998
Commelinidae	free (<5%)	0.9958
Pentapetalae	free (<5%)	0.9961
Superrosidae	free (<5%)	0.9998
Asteridae	free (<5%)	0.7090
Lamiidae	fused (>5%)	0.9799
Campanulidae	fused (>5%)	0.9731
Superrosidae	free (<5%)	0.995
Rosidae	free (<5%)	0.9955
Malvidae	free (<5%)	0.9955
Fabidae	free (<5%)	0.9996

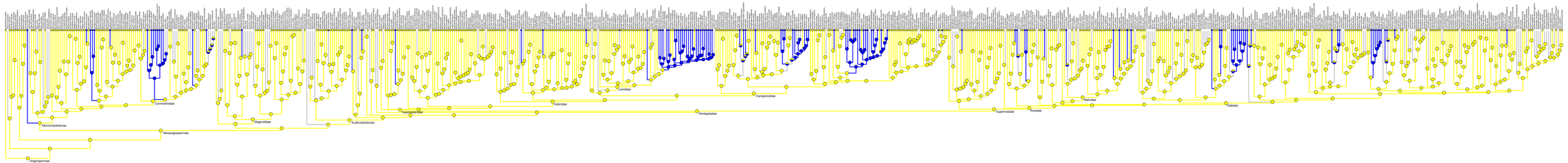
Model	Logl.	Npar	AIC	AICc	AICc weight	q01	q10	pi0	pi1
ARD	−225.91	2	455.81	455.87	0.99	0.18	0.18	0.5000	0.5000
ARDeq	−225.33	2	454.65	454.87	0.62	0.34	0.0042	0.0037	
ER*	−226.02	1	454.04	454.05	0	0.47	0.0041	0.0041	
UN01	−238.92	1	479.85	479.85	25.81	0	0.0046		
UN10	−235.97	1	473.95	473.95	19.91	0		0.0077	



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

actinomorphic
zygomorphic

hode	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

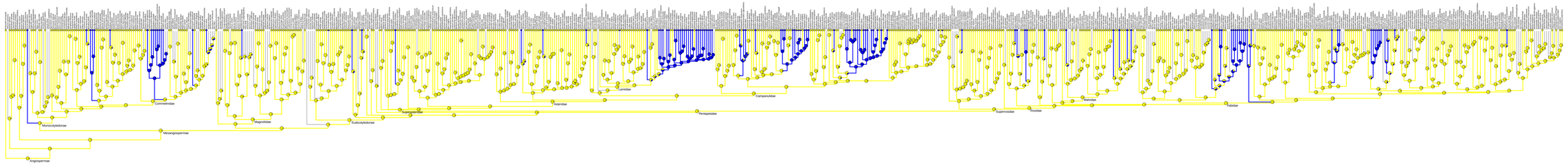


ML ancestral state reconstruction using rayDISC (R:corHMM) 207_A. Symmetry of perianth (binary) (D2d), ARDeq model

- actinomorphic
- zygomorphic

Model	Logl.	Npar	AIC	AICc	AICc w
ARD	−209.31	2	422.62	422.63	0.9999
ARDeq**	−208.81	2	421.62	421.63	0
ER	−217.31	1	436.62	436.63	15
UNI01	−263.32	1	528.64	528.65	107.01
UNI10	−218.34	1	438.68	438.69	17.06

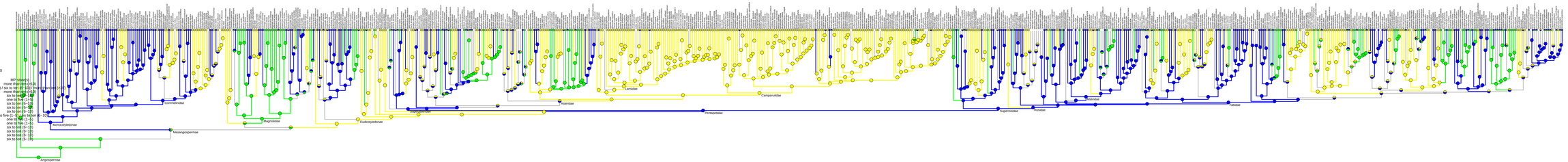
Node	ML state	Prob
Angiospermae	actinomorphic	0.9997
Mesangiospermae	actinomorphic	0.9997
Magnoliidae	actinomorphic	0.9998
Monocotyledonae	actinomorphic	0.9961
Eudicotyledonae	actinomorphic	0.9997
Commelinidae	actinomorphic	0.9951
Pentapetalae	actinomorphic	1
Superasterids	actinomorphic	1
Asteridae	actinomorphic	1
Lamiidae	actinomorphic	0.9978
Campanulidae	actinomorphic	1
Superrosidae	actinomorphic	1
Rosidae	actinomorphic	1
Malvidae	actinomorphic	0.9997
Fabidae	actinomorphic	0.9999



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	
Angiospermae	MP ambiguous
Mesangiospermae	more than ten (>10)
Magnoliidae	one to five (1–5)
Monocotyledonae	one to five (1–5)
Eudicotyledonae	more than ten (>10)
Commelinidae	six to ten (6–10)
Pentapetalae	one to five (1–5)
Superrosidae	six to ten (6–10)
Asteridae	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)

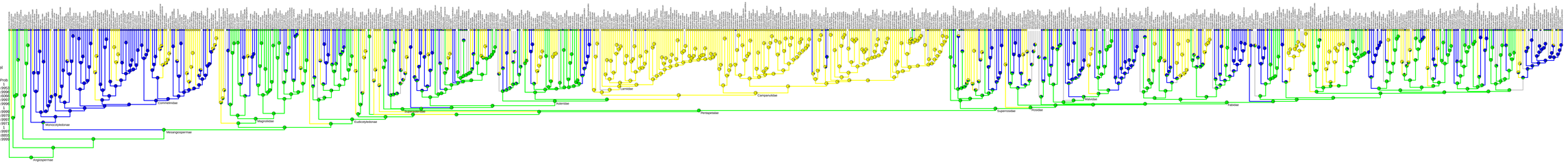


ML ancestral state reconstruction using rayDISC (R:corHMM)
301_B. Number of fertile stamens (3–state) (D2c), ARDeq model

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

Node	ML state	Prob.
Angiospermae	more than ten (>10)	0.9999
Mesangiospermae	more than ten (>10)	0.9999
Magnoliidae	more than ten (>10)	0.9998
Monocotyledonae	six to ten (6–10)	0.6068
Eudicotyledonae	more than ten (>10)	0.9997
Commelinidae	six to ten (6–10)	0.9996
Pentapetalae	more than ten (>10)	0.9999
Superrosidae	more than ten (>10)	0.9998
Asteridae	more than ten (>10)	0.9979
Lamiidae	more than ten (>10)	0.9997
Campanulidae	more than ten (>10)	0.9997
Asterids	more than ten (>10)	0.9973
Rosidae	more than ten (>10)	0.9997
Fabidae	more than ten (>10)	0.9999
Malvidae	more than ten (>10)	0.9855
Fabidae	more than ten (>10)	0.9999
Malvidae	more than ten (>10)	0.9999

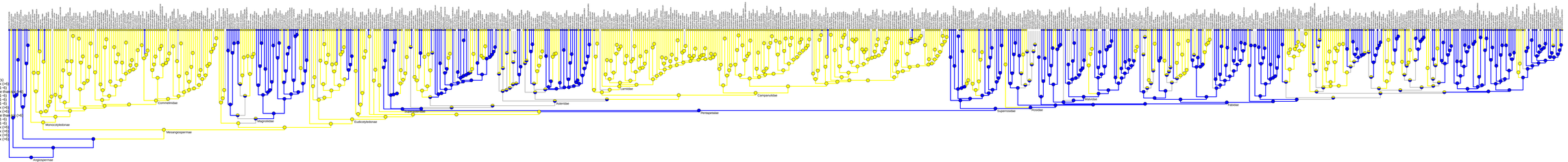
Model	Logl.	Npar	AIC	AICc	Delta AICc	AICw	LRT	df	Prob.
ARD	−495.55	6	1003.1	1003.23	2.13	0.2918	0.0000	0	1
ARDeq*	−494.47	6	1000.94	1001.06	0	0.8782	0.0000	0	1
ER	−534.45	1	1070.9	1070.92	69.86	0	0.0041	1	0.9497
SYM	−527.84	3	1061.68	1061.82	60.76	0	0.0041	3	0.8955
SYMeq	−527.84	3	1061.68	1061.82	60.76	0	0.0041	3	0.8955
ORD	−510.04	4	1028.09	1028.21	27.15	0	0.0041	2	0.9999
ORDeq	−509.49	4	1026.97	1027.02	25.97	0	7e−04	1	1
ORDSYM	−533.58	2	1071.16	1071.17	70.11	0	0.0041	—	—
ORDSYMeq	−533.2	2	1070.41	1070.42	69.36	0	0.0041	—	—
ORDER	−533.61	1	1069.23	1069.23	68.17	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)
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)
Superrosidae	more than six (>6)
Asteridae	one to six (1–6) / more than six (>6)
Lamiidae	one to six (1–6)
Campanulidae	one to six (1–6)
Superrosidae	more than six (>6)
Rosidae	more than six (>6)
Malvidae	more than six (>6)
Fabidae	more than six (>6)

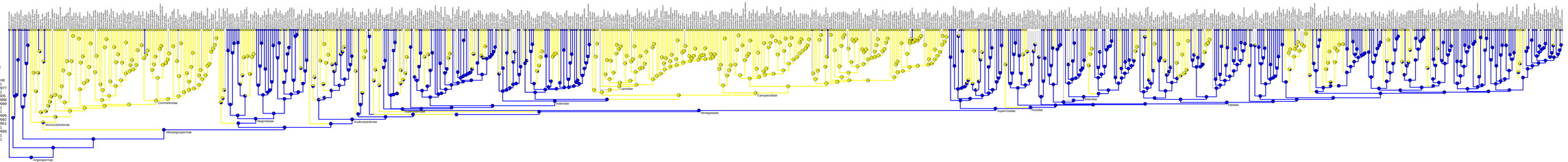


ML ancestral state reconstruction using rayDISC (R:corHMM)
301_C: Number of fertile stamens (binary) (D2c), ARDeq model

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

Node	ML state	Prob
Angiospermae	more than six (>6)	1
Mesangiospermae	more than six (>6)	0.9877
Magnoliidae	more than six (>6)	1
Monocotyledonae	one to six (1-6)	0.025
Eudicotyledonae	more than six (>6)	0.9968
Commelinidae	one to six (1-6)	0.9999
Pentapetalae	more than six (>6)	1
Superrosidae	more than six (>6)	1
Asteridae	more than six (>6)	0.9999
Lamiidae	one to six (1-6)	0.9992
Campanulidae	one to six (1-6)	0.9951
Superrosidae	more than six (>6)	1
Rosidae	more than six (>6)	0.9999
Malvidae	more than six (>6)	1
Fabidae	more than six (>6)	1

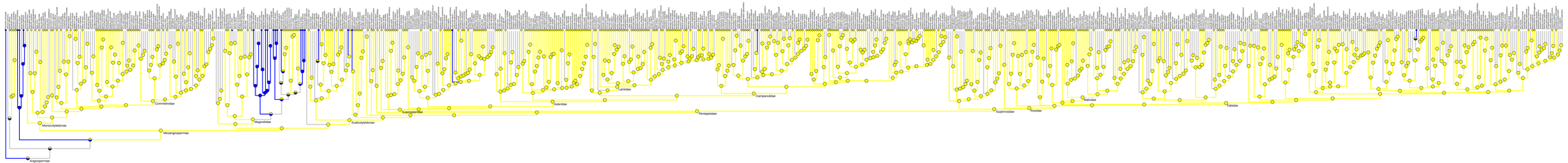
Model	Logl.	Nobr	AIC	AICc	AICc Wt	Delta AICc	Akaike Wt	Delta Wt	Conditional AIC
ARD	−289.19	2	582.37	582.41	0.38	0	0.38	0	1
ARDeq**	−288.5	2	580.99	581.03	0	0	0.87	Se-04	0.0005
ER	−321.11	1	644.23	644.23	63.22	0	0.003	0.003	
UN001	−365.05	1	732.1	732.1	151.09	0	0.0044		
UN10	−326.48	1	654.97	654.97	73.96	0		0.0069	



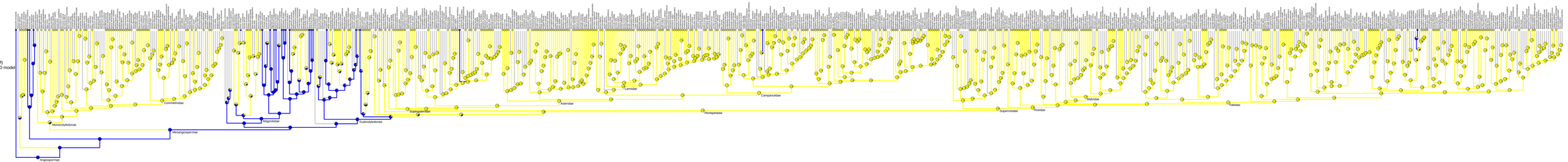
MP ancestral state reconstruction using ancestral pars
(R:phangorn)
330_A. Androecium structural phyllotaxy (binary) (D2d), 12 steps

whorled
spiral

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



ML ancestral state reconstruction using rayDISC (R:corHMM)
S30_A. Androecium structural phylotaxy (binary) (D2d), ARD model



Model	Logl.	Npar	AIC	AICc	Weight
ARD**	-53.93	2	111.87	111.88	0.9999
ARDeq	-58	2	119.99	120.01	8.12
ER	-58.76	1	119.53	119.53	7.65
UNI01	-58.69	1	119.38	119.38	7.5
UNI10	-79.36	1	160.73	160.73	48.85

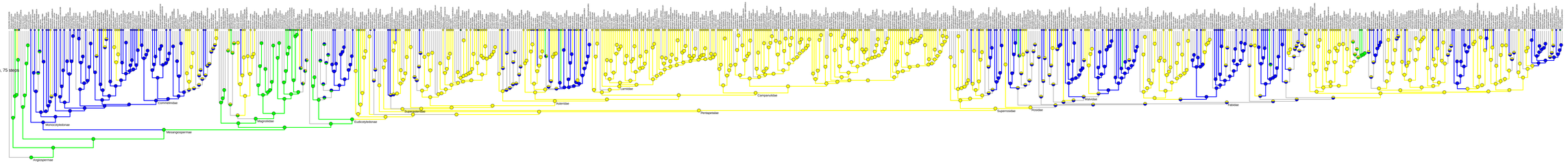
node	ML state	Prob
Angiospermae	whorled	0.9999
Mesangiospermae	spiral	0.9913
Magnoliidae	spiral	0.9934
Monocotyledonae	whorled	0.6499
Eudicotyledonae	spiral	0.9224
Commelinidae	whorled	0.9999
Pentapetalae	whorled	0.9977
Superasteridae	whorled	0.9994
Asteridae	whorled	1
Lamiidae	whorled	1
Campanulidae	whorled	1
Superrosidae	whorled	0.9997
Rosidae	whorled	0.9998
Malvidae	whorled	0.9998
Fabidae	whorled	0.9998

Parameter	Estimate	95% CI lower	95% CI upper
Forward	0.0102	0.0102	0.0102
Reverse	0.02	4e-04	0
Forward	0.02	4e-04	4e-04
Reverse	0.02	4e-04	
Forward	0		0.0183

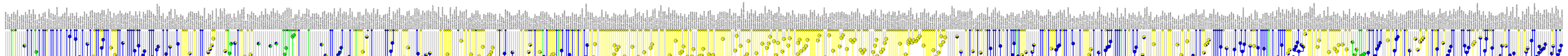
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
331_A. Number of androecium structural whorls (3–state) (D2c), 75 taxa

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

hode	MP state(s)
Angiospermae	more than two (>2)
Mesangiospermae	more than two (>2)
Magnoliidae	more than two (>2)
Monocotyledonae	two (2)
Eudicotyledonae	more than two (>2)
Commelinidae	two (2)
Pentapetalae	one (1)
Superrosidae	one (1)
Asteridae	one (1)
Lamidae	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) (DDo), ARDer model



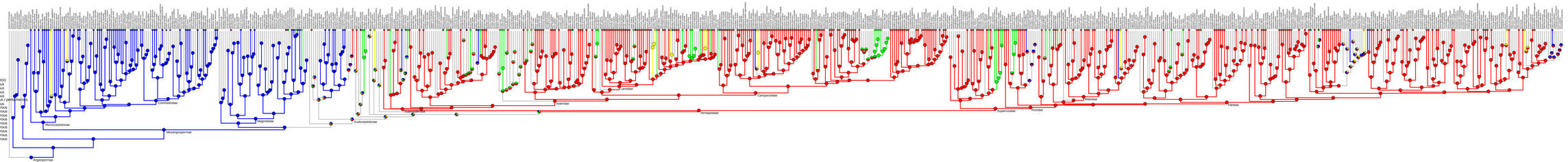
Node	ML state	Prob
Angiospermae	more than two (>2)	1
Mesangiospermae	more than two (>2)	0.9874
Magnoliidae	more than two (>2)	0.8889
Monocotyledonae	more than two (>2)	0.8839
Eudicotyledonae	more than two (>2)	0.8062
Ceratophyllales	two (2)	0.9733
Lamiidae	two (2)	0.9932
Campanulidae	two (2)	0.9999
Asteraceae	two (2)	0.9999
Asterales	two (2)	0.999
Pentapetalae	two (2)	0.9935
Superrosidae	two (2)	0.9987
Rosidae	two (2)	0.9993
Malvaceae	two (2)	0.9997
Fabaceae	two (2)	1

Model	Logl.	Npar	AIC	AICc	AICc_wt	q.01	q.10	q.21	q.12	q.31	q.13	q.32	q.23
ARD	−231.14	6	474.28	474.68	0.99	2.1	0.39	0	0	0	0	0	0.9935
ARDep*	−230.09	6	472.18	472.58	0.34	2.09	0.39	0	0.4	0	0	0	0.9935
ER	−278.88	1	559.76	559.79	0.01	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
SYM	−253.57	3	513.15	513.25	0.01	0.9993	0.9993	0.9993	0.9993	0.9993	0.9993	0.9993	0.9993
SYMeq	−253.57	3	513.15	513.25	0.01	0.9993	0.9993	0.9993	0.9993	0.9993	0.9993	0.9993	0.9993
ORD	−233.57	4	475.15	475.31	0.32	2.91	0.94	0.03	0.03	0.03	0.03	0.03	–
ORDeq	−232.53	4	473.05	473.1	0.62	0.3	0	–					
ORDSYM	−255.21	2	514.43	514.44	42.16	0	0.0034	–					
ORDSYMeq	−254.47	2	512.94	512.95	40.67	0	0.0034	–					
ORDER	−260.43	1	522.85	522.86	50.57	0	0.0027	–					

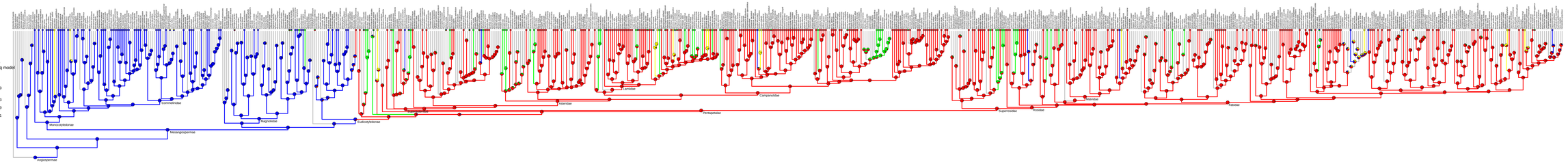
MP ancestral state reconstruction using ancestral.pars
(R phangorn)
332_A. Androecium structural merism (4–state) (D2c), 58 steps

- dimerous
- trimerous
- tetramerous
- pentamerous

Node	MP state(s)
Angiospermae	trimerous
Mesangiospermae	trimerous
Magnoliidae	trimerous
Monocotyledonae	trimerous
Eudicotyledonae	trimerous / tetramerous / pentamerous
Commelinidae	trimerous
Pentapetalae	pentamerous
Superrosidae	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



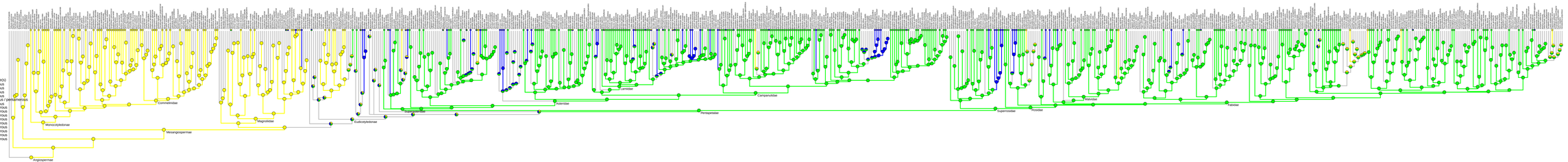
Model	Logl.	Npar	AIC	AICc	ΔAICc	AICc wt	Prob
ARD	-222.67	12	469.34	469.90	0.00	0.9979	1
ARDeq	-221.79	12	467.58	468.14	0.24	0.0887	1
ER	-238.24	1	476.48	476.52	6.62	0.0029	1
SYM	-237.24	2	478.48	478.56	8.66	0.0104	1
SYMeq*	-223.14	6	458.28	458.48	0.00	0.9999	1
ORD	-236.2	6	484.41	484.62	24.02	0.0010	1
ORDeq	-236.6	6	485.2	485.31	25.71	0	99.9737
ORDSYM	-259.1	3	524.2	524.23	64.64	0	0.002	--
ORDSYMeq	-258.18	3	522.35	522.38	62.79	0	0.002	--
ORDER	-260.1	1	522.21	522.21	62.62	0	0.003	--

Node	ML state	Prob
Angiospermae	trimerous	0.9999
Mesangiospermae	trimerous	1
Magnoliidae	trimerous	1
Monocotyledoneae	trimerous	1
Eudicotyledoneae	trimerous	0.7933
Commelinidae	trimerous	1
Pentapetalae	pentamerous	0.9999
Superrosidae	pentamerous	1
Asterids	pentamerous	0.3981

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
Commelinidae	trimerous
Pentapetalae	pentamerous
Superrosidae	pentamerous
Asteridae	pentamerous
Lamiidae	pentamerous
Campanulidae	pentamerous
Superrosidae	pentamerous
Rosidae	pentamerous
Malvidae	pentamerous
Fabidae	pentamerous

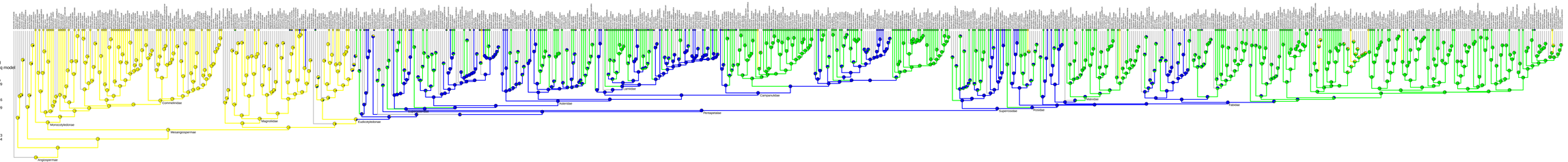


ML ancestral state reconstruction using rayDISC (R:corHMM)
332_B. Androecium structural merism (3–state) (D2c), ARDeq model

- trimerous
- tetramerous
- pentamerous

Node	ML state	Prob
Angiospermae	trimerous	0.9999
Mesangiospermae	trimerous	1
Magnoliidae	trimerous	1
Monocotyledonae	trimerous	1
Eudicotyledonae	trimerous	0.8316
Commelinidae	trimerous	1
Pentapetalae	tetramerous	0.9999
Superasteridae	tetramerous	1
Asteridae	tetramerous	1
Lamiidae	tetramerous	1
Campanulidae	tetramerous	1
Asterids	tetramerous	1
Rosidae	tetramerous	1
Fabidae	tetramerous	1

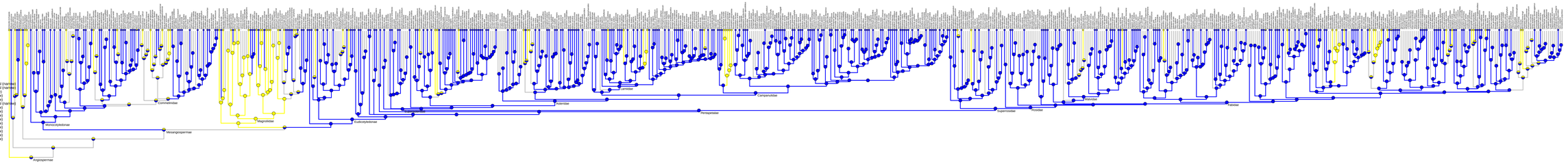
Model	Logl.	Npar	AIC	AICc	delta AICc	AICw	delta AICw	ER
ARD	−170.59	6	353.18	353.58	1.98	0.2929	0.04	1
ARDeq*	−169.6	6	351.2	351.6	0	0.7971	0	1
ER	−186.71	1	375.42	375.42	23.82	0	0.0011	1
SYM	−176.92	3	359.84	360.24	8.66	0.0066	0.0473	1
SYMeq	−176.92	3	357.83	358.23	6.65	0.0182	0.1294	1
ORD	−178.03	4	364.05	364.55	12.9	0.0008	0.9994	1
ORDeq	−177.5	4	362.99	363.05	11.74	0	2e−04	∞
ORDSYM	−185.53	2	375.06	375.07	23.77	0	0.0019	∞
ORDSYMeq	−184.62	2	373.24	373.26	21.95	0	0.0019	∞
ORDER	−186.47	1	374.94	374.94	23.64	0	0.0026	∞



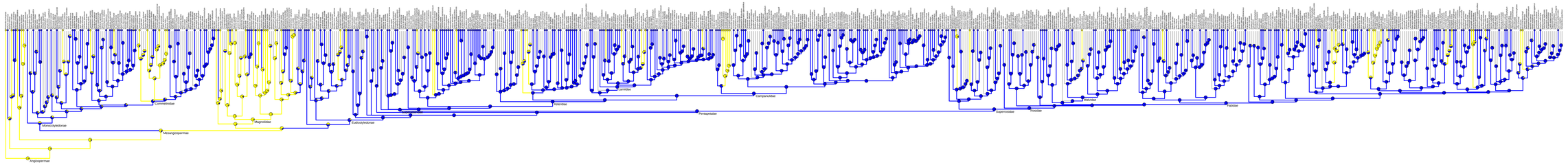
MP ancestral state reconstruction using ancestral pars
(R:phangorn)
305_A. Filament (binary) (D2d), 55 steps

laminar (wide)
typical (narrow)

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



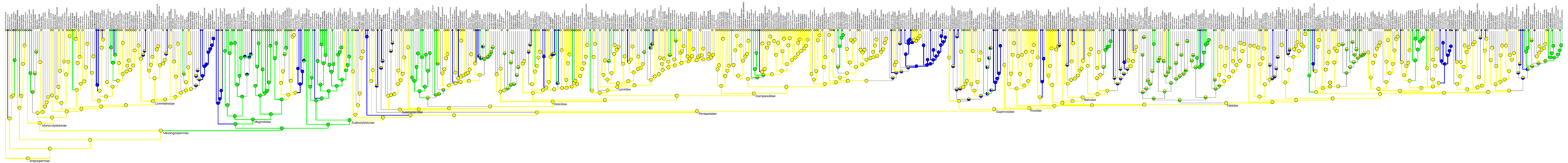
Model	Logl.	Npar	AIC	AICc	ΔAICc	AICc wt	q01	q10
ARD	−172.12	2	348.24	348.24	0.00	0.9977	0.0011	0.0011
ARDeq**	−171.79	2	347.57	347.59	0	0.58	0.0074	0.0021
ER	−177.98	1	357.96	357.97	10.38	0	0.0023	0.0023
UN01	−189.97	1	381.95	381.95	34.36	0	0.0136	0
UN10	−189.94	1	381.87	381.88	34.29	0	0	0.0022

Node	ML state	Prob.
Angiospermae	laminar (wide)	0.8188
Mesangiospermae	laminar (wide)	0.8135
Magnoliidae	laminar (wide)	0.961
Monocotyledonae	typical (narrow)	0.5102
Eudicotyledonae	typical (narrow)	0.8083
Commelinidae	typical (narrow)	0.7418
Pentapetalae	typical (narrow)	0.9996
Superrosidae	typical (narrow)	0.9999
Asteridae	typical (narrow)	0.9997
Lamiidae	typical (narrow)	0.9989
Campanulidae	typical (narrow)	0.9999
Superrosidae	typical (narrow)	0.9998
Rosidae	typical (narrow)	0.9999
Malvidae	typical (narrow)	0.9981
Fabidae	typical (narrow)	0.9911

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

introrse
latrorse
extrorse

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

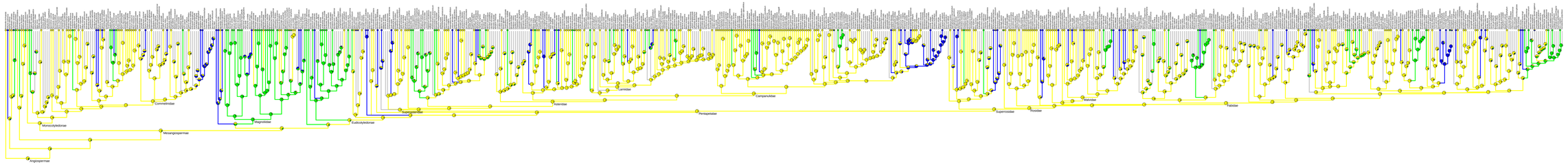


ML ancestral state reconstruction using rayDISC (R:corHMM)
311_A. Anther orientation (D2d), ER model

- introrse
- latrorse
- extrorse

Model	LogL	Npar	AIC	AICc	delta AIC	delta AICc	weight AIC	weight AICc
ARD	−342.48	6	696.95	697.06	0.95	0.95	0.3999	0.3999
ARDeq	−341.91	6	695.81	695.92	0.82	0.2	0.0033	–
ER*	−346.55	1	695.1	695.1	0	0.29	0.0026	–
SYM	−345.39	3	696.77	696.81	1.7	0.13	0.0029	–
SYMeq	−344.6	3	695.2	695.23	0.13	0.28	0.0029	–

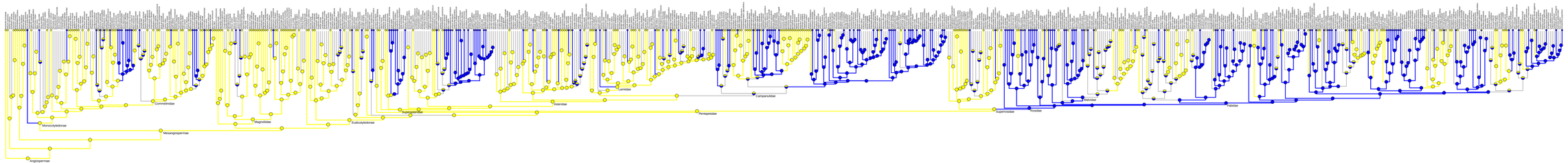
Node	ML state	Prob.
Angiospermae	introrse	0.8423
Mesangiospermae	introrse	1
Magnoliidae	extrorse	0.9042
Monocotyledonae	introrse	0.9489
Eudicotyledonae	introrse	0.8826
Commelinidae	introrse	0.9938
Pentapetalae	introrse	0.9999
Superrosidae	introrse	0.9999
Asteridae	introrse	0.9995
Lamiidae	introrse	0.9998
Campanulidae	introrse	1
Superrosidae	introrse	1
Rosidae	introrse	1
Malvidae	introrse	0.9999
Fabidae	introrse	0.9998



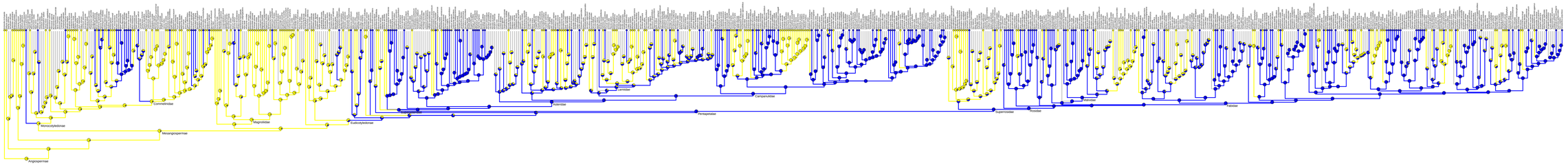
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
312_A. Anther attachment (binary) (D2d), 96 steps

basifixed
dorsifixed

node	MP state(s)
Angiospermae	basifixed
Mesangiospermae	basifixed
Magnoliidae	basifixed
Monocotyledonae	basifixed
Eudicotyledonae	basifixed
Commelinidae	basifixed
Pentapetalae	basifixed
Superrosidae	basifixed
Asteridae	basifixed
Lamidae	basifixed
Campanulidae	basifixed / dorsifixed
Superrosidae	basifixed
Rosidae	dorsifixed
Malvidae	dorsifixed
Fabidae	dorsifixed



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



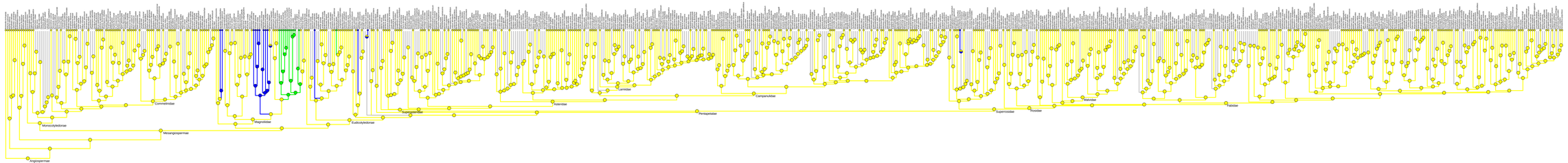
Model	Logl.	Npar	AIC	AICc	ΔAIC	ΔAICc	w AIC	w AICc
ARD	−264.88	2	533.76	533.78	0.00	0.00	0.9926	0.9926
ARDeq**	−264.62	2	533.25	533.26	0	0.52	0.004	0.0074
ER	−287.47	1	536.94	536.94	3.68	0.08	0.0006	0.0055
UN01	−295.34	1	592.68	592.69	59.43	0	0.0058	
UN10	−276.74	1	555.48	555.48	22.22	0		0.0076

Node	ML state	Prob.
Angiospermae	basifixed	0.9926
Mesangiospermae	basifixed	0.941
Magnoliidae	basifixed	0.972
Monocotyledonae	basifixed	0.9235
Eudicotyledonae	basifixed	0.6727
Commelinidae	basifixed	0.9329
Pentapetalae	dorsifixed	0.9377
Superrosidae	dorsifixed	0.9264
Asteridae	dorsifixed	0.9264
Lamiidae	dorsifixed	0.7008
Campanulidae	dorsifixed	0.9812
Superrosidae	dorsifixed	0.9456
Rosidae	dorsifixed	0.9188
Malvidae	dorsifixed	0.7188
Fabidae	dorsifixed	0.9188

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

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

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

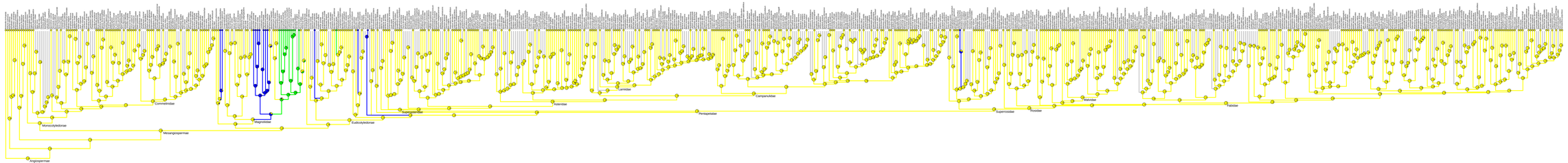


ML ancestral state reconstruction using rayDISC (R:corHMM)
313_A. Anther dehiscence (3-state) (0/20), ARDeq model

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

Node	ML state	Prob
Angiospermae	longitudinal slit	1
Mesangiospermae	longitudinal slit	1
Magnoliidae	longitudinal slit	0.9601
Monocotyledonae	longitudinal slit	1
Eudicotyledonae	longitudinal slit	1
Commelinidae	longitudinal slit	1
Pentapetalae	longitudinal slit	1
Superrosidae	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

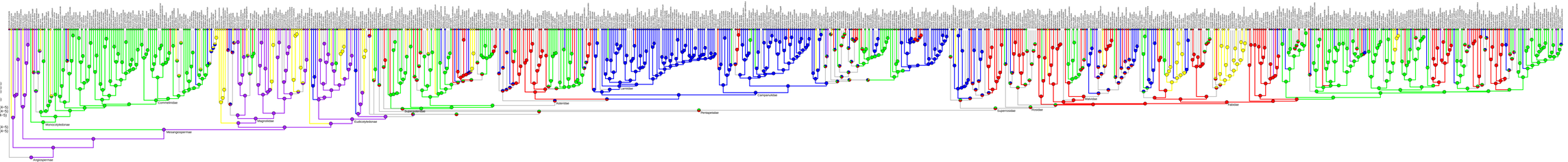
Model	LogL	Npar	AIC	AICc	delta AIC	AICc weight	delta AICc	AICc weight
ARD	−55.64	6	123.27	123.38	0.00	0.99	0.00	0.99
ARDeq	−54.61	6	121.22	121.33	6	0.45	2e−04	0.45
ER	−60.71	1	123.41	123.42	2.08	0.16	2e−04	0.16
SYM	−59.7	3	125.41	125.44	4.11	0.06	2e−04	0.06
SYMeq	−58.61	3	123.21	123.24	1.91	0.17	2e−04	0.17



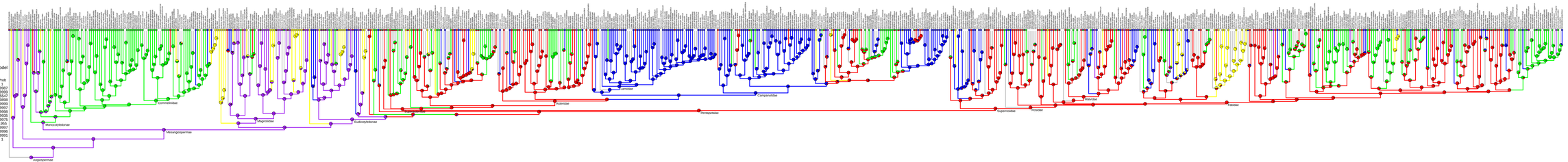
MP ancestral state reconstruction using ancestral pars
(R:phangorn)
401_B. Number of structural carpels (5~state) (D2c), 189 steps

- 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) / four or five (4~5)
Lamiidae	two (2)
Campanulidae	two (2)
Superrosidae	three (3) / four or five (4~5)
Rosidae	three (3) / four or five (4~5)
Malvidae	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) (02c), ARDeq model



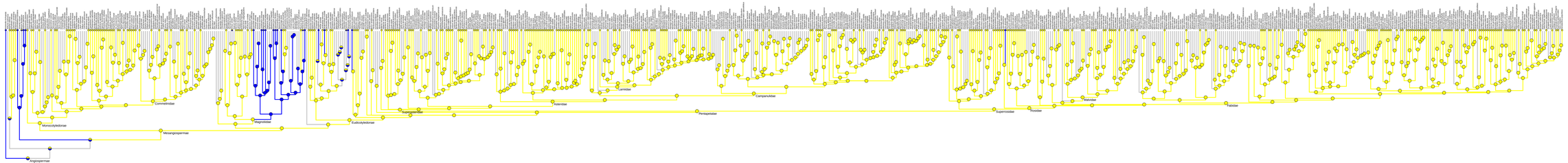
Model	Logl.	Npar	AIC	AICw	Delta AIC	Delta AICc	Delta BIC
ARD	−673.8	20	1387.6	1.000	0.000	19.5	0.000
ARDeq**	−664.05	20	1368.1	0.000	19.5	0	19.5
ER	−717.7	1	1437.4	0.000	68.9	0.07	68.9
SYM	−640.88	10	1301.8	0.000	86.3	16.4	86.3
SYMeq	−640.88	10	1301.8	0.000	86.3	16.4	86.3
ORD	−756.1	8	1528.1	0.000	159.6	159.7	159.6
ORDeq	−755.12	8	1526.24	0.000	157.8	157.22	157.8
ORDSYM	−759.4	4	1526.8	0.000	158.4	157.66	158.4
ORDSYMeq	−758.64	4	1525.29	0.000	156.9	156.14	156.9
ORDER	−764.7	1	1531.41	0.000	163.0	162.21	163.0

Node	ML state	Prob
Angiospermae	more than five (>5)	1
Mesangiospermae	more than five (>5)	0.9987
Magnoliidae	more than five (>5)	0.9999
Monocotyledonae	more than five (>5)	0.9347
Eudicotyledonae	more than five (>5)	0.9898
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)	0.9908
Malvaceae	four or five (4–5)	0.9975
Fabaceae	four or five (4–5)	0.955
Lamiidae	four or five (4–5)	0.9997
Asterales	four or five (4–5)	0.9996
Campanulidae	four or five (4–5)	0.9991

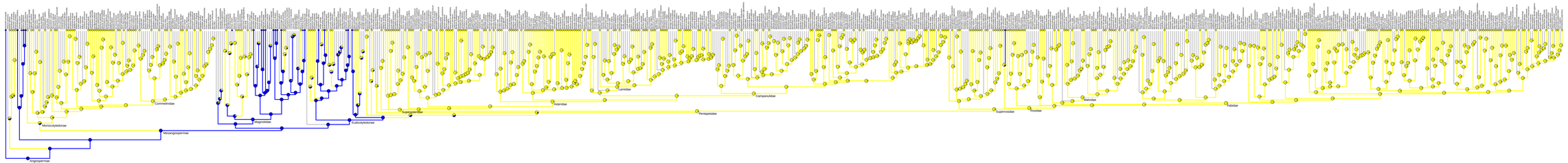
MP ancestral state reconstruction using ancestral pars
(R:phangorn)
400_A. Gynoecium phyllotaxy (D2d), 10 steps

whorled
spiral

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



ML ancestral state reconstruction using ratDISC (R:corHMM) 400_A_Cynoecium phylotaxy (D2d), ARDeq model



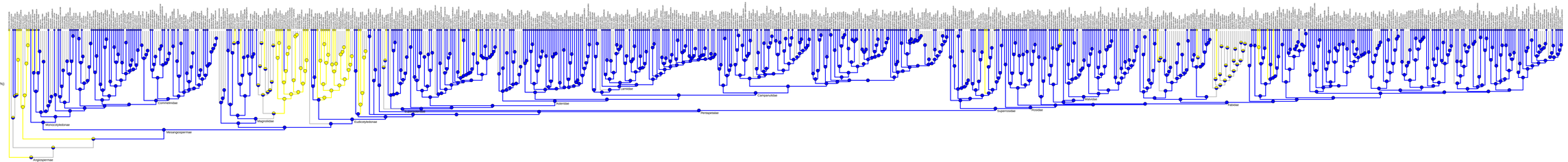
Node	ML state	Prob
Angiospermae	whorled	1
Mesangiospermae	spiral	0.9999
Magnoliidae	spiral	0.9997
Monocotyledonae	whorled	0.6307
Eudicotyledonae	spiral	0.9987
Commelinidae	whorled	0.9999
Pentapetalae	whorled	0.9748
Superrosidae	whorled	0.9943
Asteridae	whorled	1
Lamiidae	whorled	1
Campanulidae	whorled	1
Superrosidae	whorled	0.9786
Rosidae	whorled	0.9999
Malvidae	whorled	1
Fabidae	whorled	1

Model	Logl.	Npar	AIC	AICwt	AICc	AICcwt	q.10	q.01
ARD	−38.72	2	81.45	81.45	81.65	0.99	0.0068	0.0068
ARDeq**	−38.02	2	80.05	80.07	0	0.82	1e-04	0.0068
ER	−49.53	1	101.05	101.06	20.98	0	4e-04	4e-04
UNI01	−51.34	1	104.67	104.68	24.4	0	4e-04	
UNI10	−41.33	1	84.65	84.66	4.58	0.06		0.008

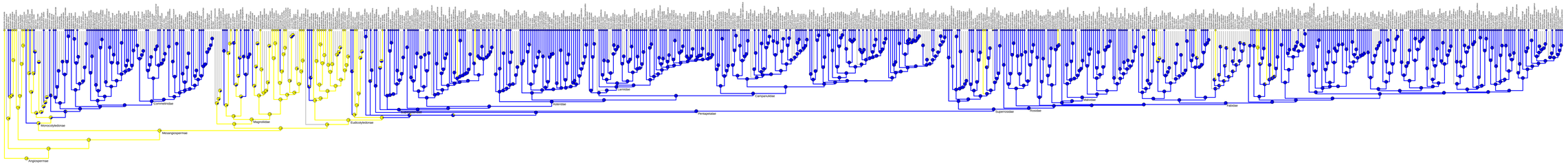
MP ancestral state reconstruction using ancestral pars
(R:phangorn)
403_A. Fusion of ovaries (binary) (D2c), 24 steps

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

Node	MP state(s)
Angiospermae	free (<5%) fused (>5%)
Mesangiospermae	fused (>5%)
Magnoliidae	fused (>5%)
Monocotyledonae	fused (>5%)
Eudicotyledonae	fused (>5%)
Commelinidae	fused (>5%)
Pentapetalae	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) (ID1), ARDeq model



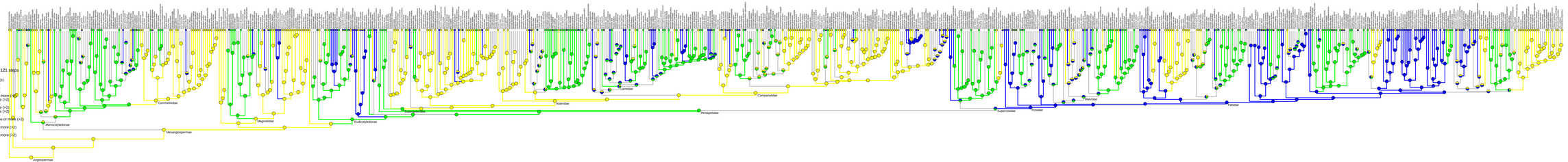
Node	ML state	Prob
Angiospermae	free (>5%)	1
Mesangiospermae	free (>5%)	0.9992
Magnoliidae	free (>5%)	0.9992
Monocotyledonae	free (>5%)	0.8142
Eudicotyledonae	free (>5%)	0.9956
Commelinidae	fused (>5%)	0.9999
Pentapetalae	fused (>5%)	0.9974
Superrosidae	fused (>5%)	0.9978
Asteridae	fused (>5%)	1
Lamiidae	fused (>5%)	1
Campanulidae	fused (>5%)	1
Superrosidae	fused (>5%)	0.9998
Rosidae	fused (>5%)	0.9999
Malvidae	fused (>5%)	0.18
Fabidae	fused (>5%)	0.9999

Model	Logl.	Nopr	AIC	AICc	ΔAICc	AICw	q01	q10
ARD	−94.72	2	193.43	193.58	0.38	0.46	0.0045	5e−04
ARDeq**	−94.03	2	192.05	192.07	0	0.66	0.0045	5e−04
ER	−100.22	1	202.44	202.44	10.38	0	7e−04	7e−04
UN01	−100.88	1	203.79	203.79	11.72	0	0.0102	0
UN10	−105.42	1	212.84	212.84	20.78	0	0	8e−04

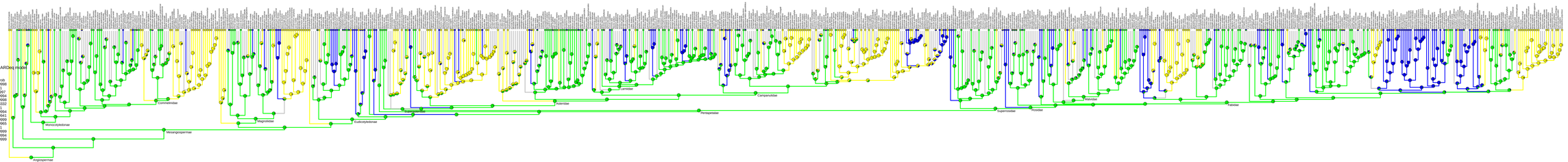
MP ancestral state reconstruction using ancestral pars
(R:phangorn)
411_A. Number of ovules per functional carpel (3–state) (D2c), 121 steps

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

Node	MP state(s)
Angiospermae	two (2)
Mesangiospermae	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)
Lamiidae	one (1) / two (2) / three or more (>2)
Campanulidae	one (1)
Superrosidae	two (2) / three or more (>2)
Rosidae	two (2)
Malvidae	two (2) / three or more (>2)
Fabidae	two (2)



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



Node	ML state	Prob
Angiospermae	three or more (>2)	0.9998
Mesangiospermae	three or more (>2)	1
Magnoliidae	three or more (>2)	0.997
Monocotyledonae	three or more (>2)	0.9994
Eudicotyledonae	three or more (>2)	0.9998
Commelinidae	three or more (>2)	0.8332
Hydrocharitales	three or more (>2)	1
Scrophulariales	three or more (>2)	0.9994
Asterales	three or more (>2)	0.9941
Lamiidae	three or more (>2)	0.9999
Campanulidae	three or more (>2)	0.9965
Asterids	three or more (>2)	1
Rosidae	three or more (>2)	0.9999
Fabidae	three or more (>2)	0.9994
Malvidae	three or more (>2)	0.9999

Model	Logl.	Npar	AIC	AICc	ΔAIC	ΔAICc	AICw	AICcw	
ARD	-388.9	6	789.8	789.9	0.00	0.00	1.00	1.00	
ARDeq*	-397.96	6	807.92	807.99	18.12	18.09	0.00	0.00	
ER	-400.35	1	802.7	802.72	12.91	12.82	0.07	0.07	
SYM	-398.19	3	802.38	802.49	12.59	12.59	0.08	0.08	
SYMeq	-399.09	3	804.18	804.29	14.39	14.39	0.03	0.03	
ORD	-399.51	4	807.02	807.14	17.23	17.24	0.01	0.01	
ORDeq	-398.86	4	805.73	805.78	17.75	0	0.0021	1	
ORDSYM	-410.55	2	825.09	825.11	37.08	0	0.0053	1	
ORDSYMeq	-410.31	2	824.62	824.64	36.61	0	0.0052	1	
ORDER	-411.55	1	825.11	825.11	37.09	0	0.0061	1	