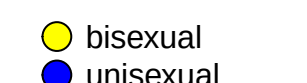
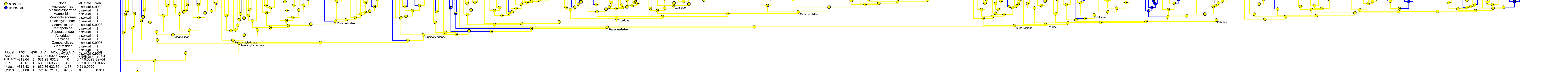


ML ancestral state reconstruction using rayDISC (R:corHMM)
100 A. Functional sex of flowers (D2d), ARDeg model

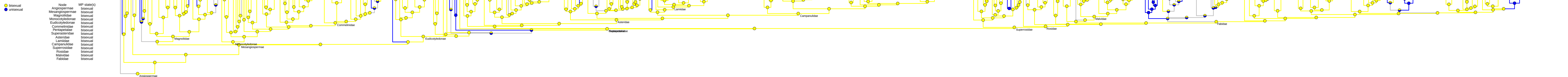


Node	ML state	Prob
Angiospermae	bisexual	0.9999
Gesangiospermae	bisexual	1
Magnoliidae	bisexual	1
Eumecotyledonae	bisexual	1
Audicotyledonae	bisexual	1
Commelinidae	bisexual	0.9998
Pentapetalae	bisexual	1
Superasteridae	bisexual	1
Asteridae	bisexual	1
Lamiidae	bisexual	1
Campanulidae	bisexual	0.9995
Sunspirocridae	bisexual	1

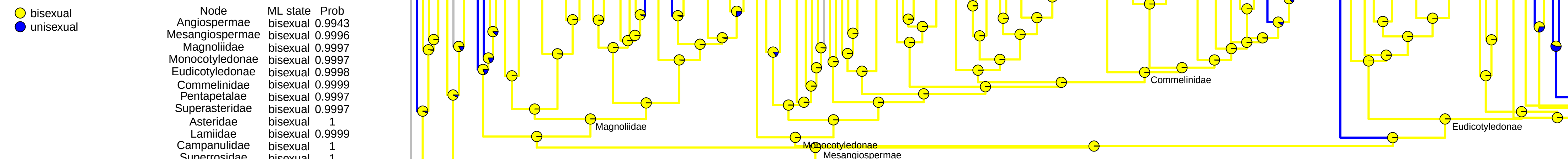
Model	LogL	Npar	AIC	AICc	Rosidae	Maridae	AICc	Sexual	1
ARD	-314.26	2	632.51	632.51	0.0028	0.0028	0.0028	0.0028	0.0028
ARDeq*	-313.64	2	631.28	631.3	0	0.47	0.0028	0.0028	0.0028
ER	-316.61	1	635.21	635.22	3.92	0.07	0.0027	0.0027	0.0027
UNI01	-315.43	1	632.86	632.86	1.57	0.21	0.0029		
UNI10	-361.08	1	724.16	724.16	92.87	0		0.011	



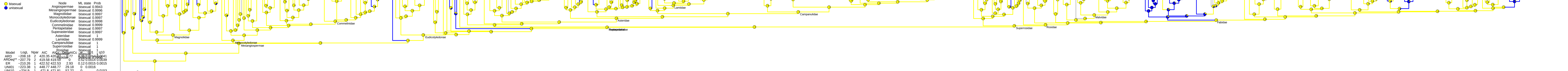
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
100_B. Structural sex of flowers (D2d), 56 steps



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

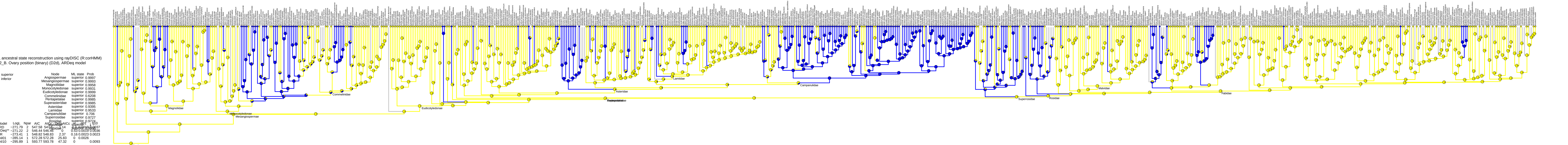


Model	LogL	Npar	AIC	AICc	ΔAICc	Weight	2ΔAICc	Prob > 0.95
ARD	-208.18	2	420.35	420.44	0.09	0.38	0.0014	0.0041
ARDeq**	-207.79	2	419.58	419.59	0	0.52	0.0014	0.0039
ER	-210.26	1	422.52	422.53	2.93	0.12	0.0015	0.0015
UNI01	-223.38	1	448.77	448.77	29.18	0	0.0016	
UNI10	-234.9	1	471.8	471.81	52.22	0	0.0153	



2. B. Ovary position (binary) (D2d), ARDeq model

Model	LogL	Npar	AIC	AICc	Residual deviance	Superior to null	Superior to null	Superior to null
RD	-271.79	2	547.58	547.58	14	0.0019	0.0037	0.0023
Deq**	-271.22	2	546.44	546.46	0	0.53	0.0019	0.0036
R	-273.41	1	548.82	548.83	2.37	0.16	0.0023	0.0023
NI01	-285.14	1	572.28	572.28	25.83	0	0.0026	
NI10	-295.89	1	593.77	593.78	47.32	0		0.0093

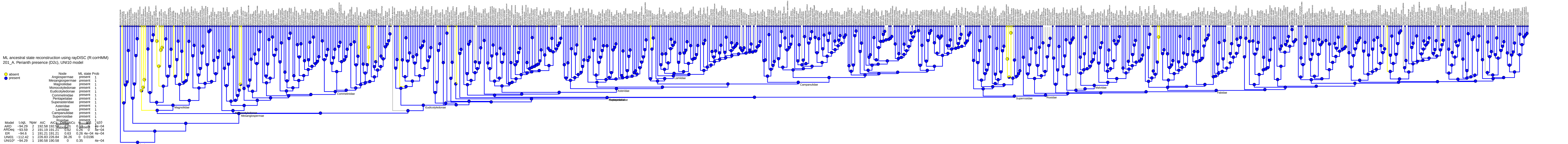


ML ancestral state reconstruction using rayDISC (R:corHMM)
201. A. Perianth presence (D2c), UNI10 model

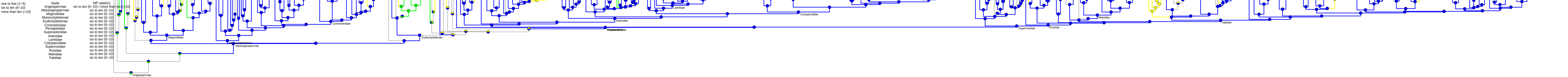
● absent
● present

Node Angiospermae ML state Prob present 1

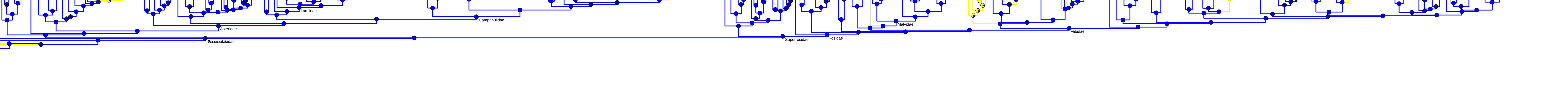
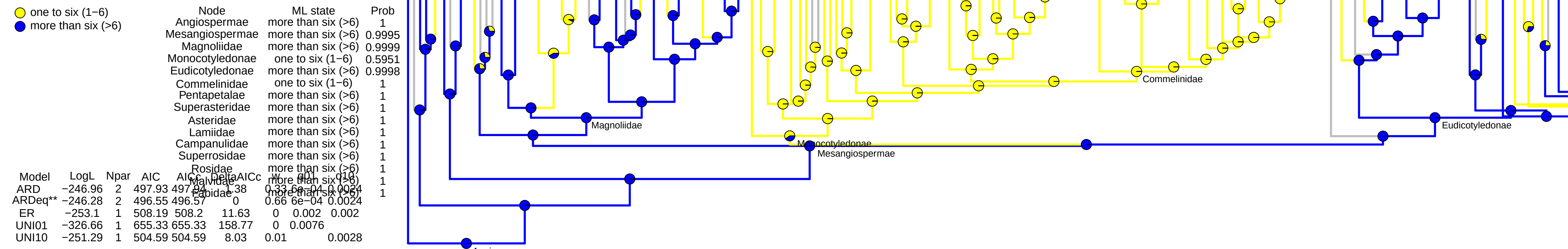
Model	LogL	Npar	AIC	AIC _{Rosidae}	AIC _{Malvales}	AIC _{ClCc}	present	1
ARD	-94.29	2	192.58	192.58	0.01	0	0	1e-04
ARDeq	-93.59	2	191.19	191.21	0.62	0.26	0	4e-04
ER	-94.6	1	191.21	191.21	0.63	0.26	4e-04	4e-04
UNI01	-112.42	1	226.83	226.84	36.26	0	0.0196	
UNI10*	-94.29	1	190.58	190.58	0	0.35		4e-04



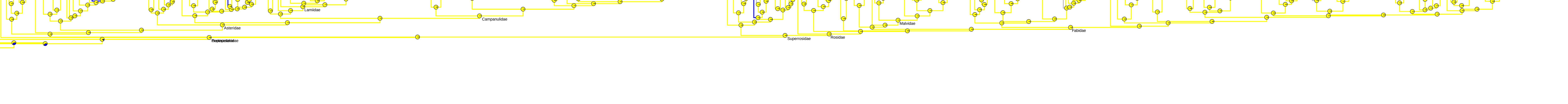
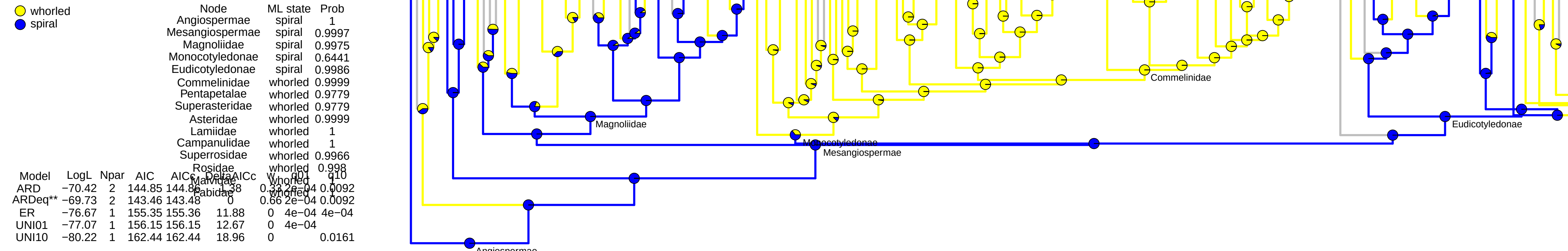
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
201_B. Number of perianth parts (3–state) (D2c), 86 steps



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



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



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	ΔAIC	Weight	Posterior Prob
ARD	-268.31	6	548.61	2.17	0.26	0.0045
ARD ^{eq}	-267.22	6	546.44	0	0.74	0.9945
ER	-308.97	1	619.99	65.55	0.00	0.001
SYM	-291.07	3	588.13	41.62	0.00	0.0018
SYM ^{eq}	-290.62	3	587.24	40.72	0.00	0.0018
ORD	-274.98	4	557.96	11.46	0.01	0.0043
ORD ^{eq}	-273.88	4	555.77	9.27	0.01	0.0043
ORDSYM	-297.42	2	598.83	52.3	0	0.0018
ORDSYM ^{eq}	-296.69	2	597.39	50.86	0	0.0018
ORDER	-312.18	1	626.36	626.36	0	0.0011

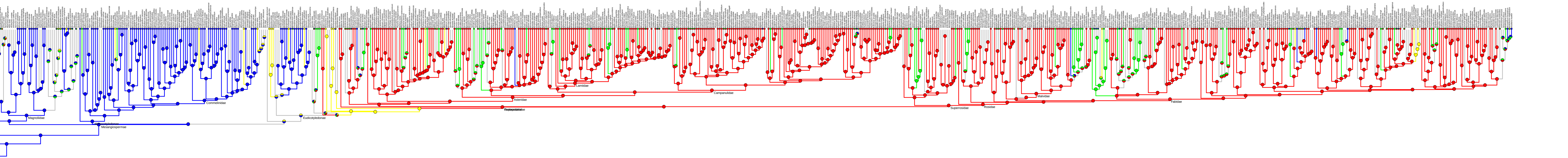
Node	ML state	Prob
Angiospermae	more than two (>2)	1
Mesangiospermae	more than two (>2)	0.9995
Magnoliidae	more than two (>2)	1
Monocotyledonae	two (2)	0.4988
Eudicotyledonae	more than two (>2)	0.9846
Commelinidae	two (2)	1
Pentapetalae	two (2)	0.9992
Superasteridae	two (2)	0.9992
Asteridae	two (2)	0.9992
Campanulidae	two (2)	0.9998
Superrosidae	two (2)	0.9999
Rosidae	two (2)	1
Malvidae	two (2)	1
Fabidae	two (2)	1

Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledonae
Eudicotyledonae

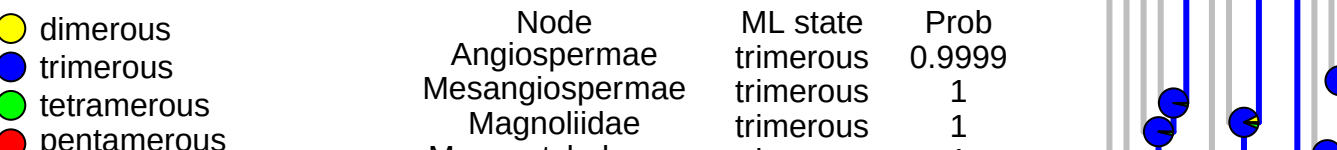


MP ancestral state reconstruction using ancestral.pars
R:phangorn)
32_A. Perianth merism (4-state) (D2c), 84 steps

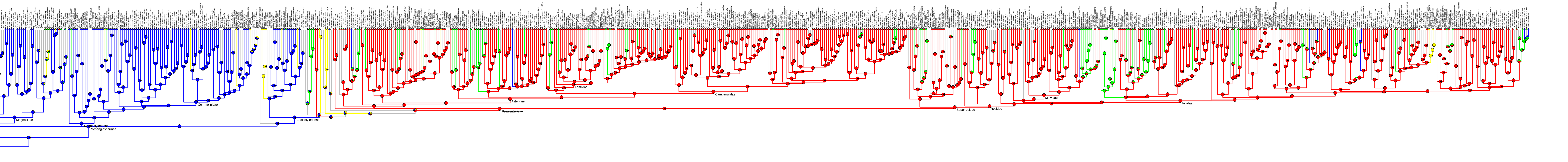
Node	MP state(s)
Angiospermae	trimerous
Mesangiospermae	trimerous
Magnoliidae	trimerous
Monocotyledonae	trimerous
Eudicotyledonae	dimerous / trimerous
Commelinidae	trimerous
Pentapetalae	pentamerous
Superasteridae	pentamerous
Asteridae	pentamerous
Lamiidae	pentamerous
Campanulidae	pentamerous
Superrosidae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



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

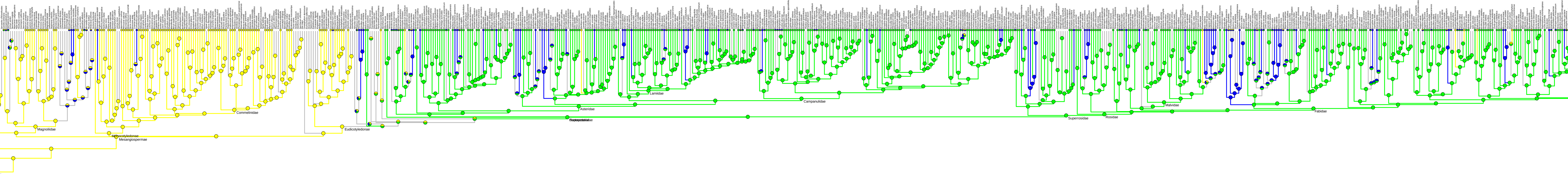


Model	LogL	Npar	AIC	DeltaAIC	Bayes	Posterior
ARD	-320.01	12	664.02	5.05	0.999	0.999
ARDeq	-318.98	12	661.97	2.05	0.994	0.994
ER	-359.78	1	721.59	57.57	0.001	0.001
SYM	-324.89	6	661.78	2.21	0.994	0.994
SYMeq**	-323.63	6	659.26	0.48	0.999	0.999
ORD	-334.77	6	681.55	22.21	0.001	0.001
ORDeq	-334.31	6	680.62	21.36	0	0
ORDSYM	-342.93	3	691.86	691.89	32.52	0 0.0018 ...
ORDSYMeq	-341.81	3	689.61	689.64	30.27	0 0.0018 ...
ORDER	-344.71	1	691.41	691.42	32.05	0 0.0023 ...

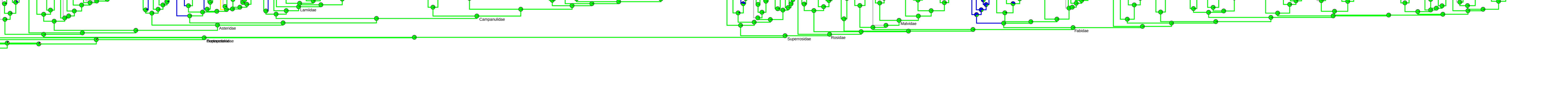
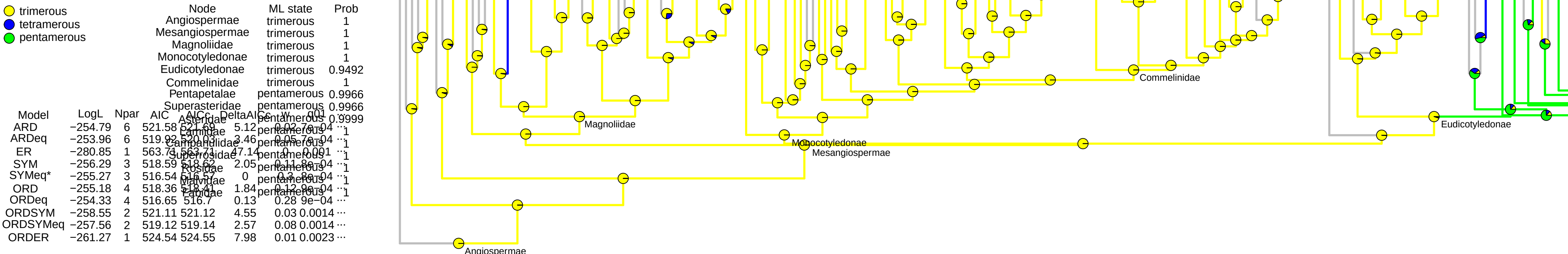


MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
232_B. Perianth merism (3-state) (D2c), 70 steps

- | | | |
|---|--|---|
| <div><div></div>trimerous</div> <div><div></div>tetramerous</div> <div><div></div>pentamerous</div> | <div>Node</div> <div>Angiospermae</div> <div>Mesangiospermae</div> <div>Magnoliidae</div> <div>Monocotyledonae</div> <div>Eudicotyledonae</div> <div>Commelinidae</div> <div>Pentapetalae</div> <div>Superasteridae</div> <div>Asteridae</div> <div>Lamiidae</div> <div>Campanulidae</div> <div>Superrosidae</div> <div>Rosidae</div> <div>Malvidae</div> <div>Fabidae</div> | <div>MP state(s)</div> <div>trimerous</div> <div>trimerous</div> <div>trimerous</div> <div>trimerous</div> <div>trimerous</div> <div>trimerous</div> <div>pentamerous</div> <div>pentamerous</div> <div>pentamerous</div> <div>pentamerous</div> <div>pentamerous</div> <div>pentamerous</div> <div>pentamerous</div> <div>pentamerous</div> <div>pentamerous</div> |
|---|--|---|



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



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

- undifferentiated
- differentiated

	Node	ML state	Prob
● undifferentiated	Angiospermae	undifferentiated	1
● differentiated	Mesangiospermae	undifferentiated	1
	Magnolidae	undifferentiated	0.9992
	Monocotyledonae	undifferentiated	0.9999
	Eudicotyledonae	undifferentiated	0.978
	Commelinidae	undifferentiated	0.9998
	Pentapetalae	differentiated	0.9441
	Superasteridae	differentiated	0.9441
	Asteridae	differentiated	0.999
	Lamiidae	differentiated	0.9999
	Campanulidae	differentiated	1
	Superrosidae	differentiated	0.9949

Model	LogL	Npar	AIC	AICc	Posterior Probability	BayesAICc	Dimension	Integrated Probability	95% Credible Interval
ARD	-199.02	2	402.04	402.04	0.0000	0.0000	0	0.9993	0.9993
ARD ^{eq} **	-198.37	2	400.74	400.75	0.0000	0.0000	0	0.9993	0.9993
ER	-207.02	1	416.04	416.05	15.29	0	0.0024	0.0024	0.0024
UNI01	-231.24	1	464.48	464.48	63.73	0	0.0082		
UNI10	-231.65	1	465.3	465.3	64.55	0	0.0032		



MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
204_A. Fusion of perianth (D2c), 78 steps

- free (<5%)

● fused (>5%)

Node

Angiospermae

Mesangiospermae

Magnoliidae

Monocotyledonae

Eudicotyledonae

Commelinidae

Pentapetalae

Superasteridae

Asteridae

Lamiidae

Campanulidae

Superrosidae

Rosidae

Malvidae

Fabidae
- MP state(s)

free (<5%)

free (<5%)

free (<5%)

free (<5%)

free (<5%)

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

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

free (<5%)

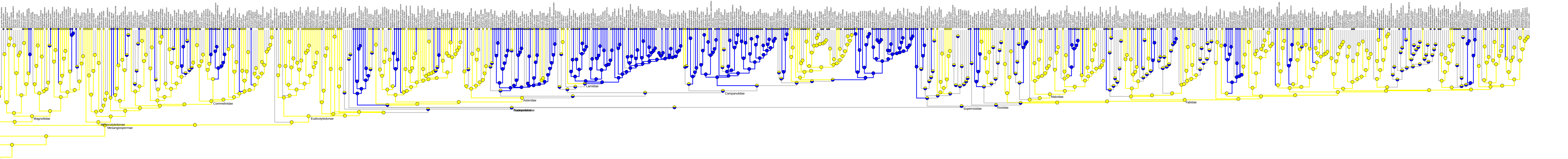
free (<5%) / fused (>5%)

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

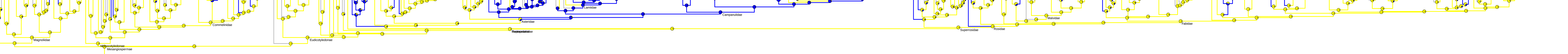
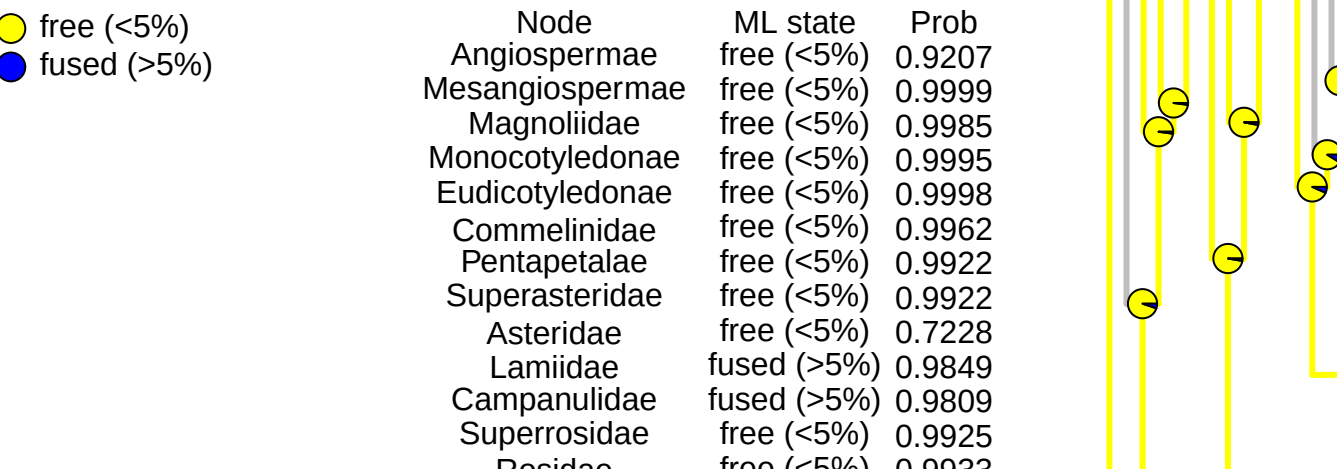
free (<5%) / fused (>5%)

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

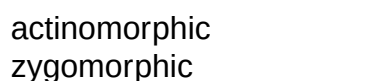
free (<5%)



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

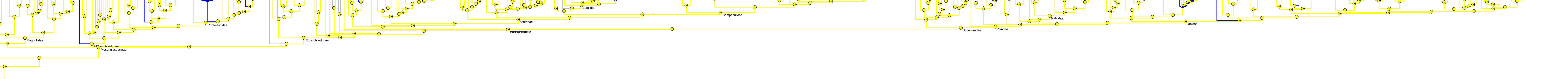


ancestral state reconstruction using rayDISC (R:corHMM)
7_ A. Symmetry of perianth (binary) (D2d), ARDeq model



Node	ML state	Prob
Angiospermae	actinomorph	0.9981
Nonangiospermae	actinomorph	0.9999
Magnoliidae	actinomorph	0.9997
Monocotyledonae	actinomorph	0.9985
Eudicotyledonae	actinomorph	0.9996
Commelinidae	actinomorph	0.9961
Pentapetalae	actinomorph	1
Superasteridae	actinomorph	1
Asteridae	actinomorph	1
Lamiidae	actinomorph	0.9985
Campanulidae	actinomorph	1

Model	LogL	Npar	AIC	AICc	BayesAICc	Relative Posterior Probability	Mean Posterior Probability	Mean Posterior Probability	Mean Posterior Probability
ARD	-210.26	2	424.51	424.51	0.94	0.98	0.98	0.98	0.98
ARDeq**	-209.79	2	423.57	423.59	0	0.02	0.01	0.01	0.01
ER	-218.48	1	438.97	438.97	15.38	0	0.0014	0.0014	0.0014
UNI01	-263.34	1	528.69	528.69	105.11	0	0.0018	0.0018	0.0018
UNI10	-219.81	1	441.62	441.62	18.03	0	0.0155	0.0155	0.0155



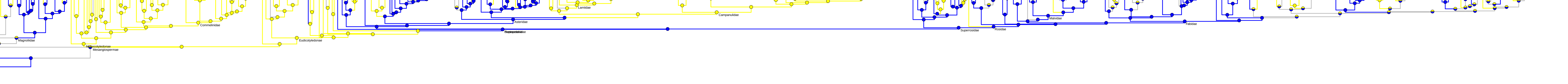
MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
301_C. Number of fertile stamens (binary) (D2c), 93 steps

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

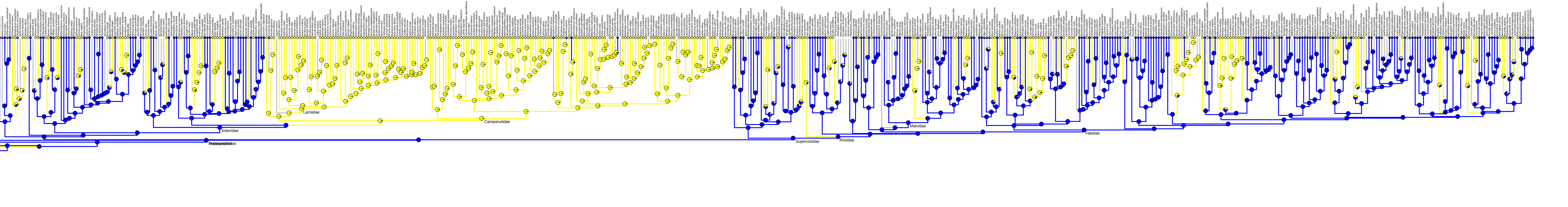
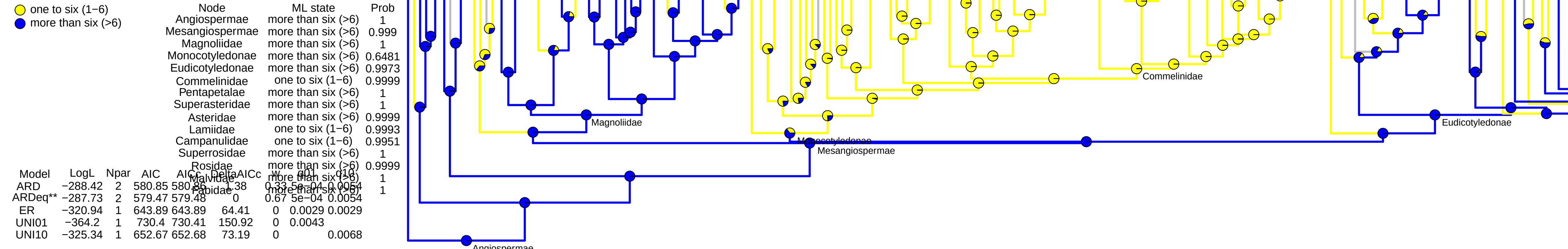
Node
Angiospermae
Mesangiospermae
Magnoliidae
Monocotyledonae
Eudicotyledonae
Commelinidae
Pentapetalae
Superasteridae
Asteridae
Lamiidae
Campanulidae
Superrosidae
Rosidae
Malvidae
Fabidae

MP state(s)
more than six (>6)
one to six (1-6) / more than six (>6)
one to six (1-6)
one to six (1-6)
one to six (1-6)
one to six (1-6)
more than six (>6)
more than six (>6)
more than six (>6)
one to six (1-6)
one to six (1-6)
more than six (>6)
more than six (>6)
more than six (>6)

Magnoliidae
Monocotyledonae
Mesangiospermae



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



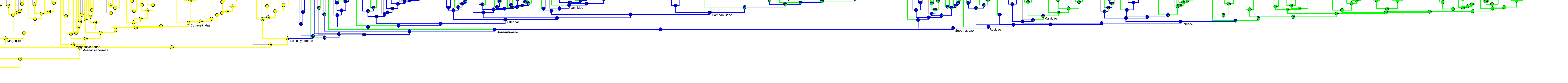
Model	LogL	Npar	AIC	AICc	Rosidae	whorled	0.998
ARD**	-54.27	2	112.53	112.55	Rosidae	whorled	0.999
ARDeq	-57.95	2	119.9	119.92	Malvaceae	whorled	0.007
ER	-58.67	1	119.34	119.34	Fabidae	whorled	0
UNI01	-58.64	1	119.29	119.29		0.03 e-04	4e-04
UNI10	-80.64	1	163.29	163.29		0.03 e-04	0.0186

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

● trimerous
● tetramerous
● pentamerous

Model	LogL	Npar	AIC	ΔAIC	Model	LogL	Npar	AIC	ΔAIC
ARD	-170.56	6	353.12	1.96	ARD	-170.56	6	353.12	1.96
ARD**	-169.58	6	351.16	0	ARD**	-169.58	6	351.16	0
ER	-185.95	1	373.26	22.10	ER	-185.95	1	373.26	22.10
SYM	-176.38	3	358.76	5.64	SYM	-176.38	3	358.76	5.64
SYMeq	-175.38	3	356.77	5.52	SYMeq	-175.38	3	356.77	5.52
ORD	-177.5	4	363.01	11.78	ORD	-177.5	4	363.01	11.78
ORDeq	-177.35	4	362.7	11.48	ORDeq	-177.35	4	362.7	11.48
ORDSYM	-185.19	2	374.38	23.12	ORDSYM	-185.19	2	374.38	23.12
ORDSYMeq	-184.29	2	372.57	21.32	ORDSYMeq	-184.29	2	372.57	21.32
ORDER	-186.13	1	374.26	23	ORDER	-186.13	1	374.26	23

Node	ML state	Prob
Angiospermae	trimerous	0.9999
Mesangiospermae	trimerous	1
Magnoliidae	trimerous	1
Monocotyledonae	trimerous	1
Eudicotyledonae	trimerous	0.8377
Commelinidae	trimerous	1
Pentapetalae	tetramerous	0.9993
Superasteridae	tetramerous	0.9993
Asteridae	tetramerous	1
Campanulidae	tetramerous	0.9929
Campanulidae	tetramerous	0.967
Superasteridae	tetramerous	1
Superasteridae	tetramerous	0.9996
Magnoliidae	pentamerous	0.5514
Monocotyledonae	tetramerous	0.9589



MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
305_A. Filament (binary) (D2d), 53 steps

- laminar (wide)

● typical (narrow)

Node

Angiospermae

Mesangiospermae

Magnoliidae

Monocotyledonae

Eudicotyledonae

Commelinidae

Pentapetalae

Superasteridae

Asteridae

Lamiidae

Campanulidae

Superrosidae

Rosidae

Malvidae

Fabidae
- MP state(s)

laminar (wide)

laminar (wide)

typical (narrow)

laminar (wide)

typical (narrow)

laminar (wide) / typical (narrow)

typical (narrow)

typical (narrow)

typical (narrow)

typical (narrow)

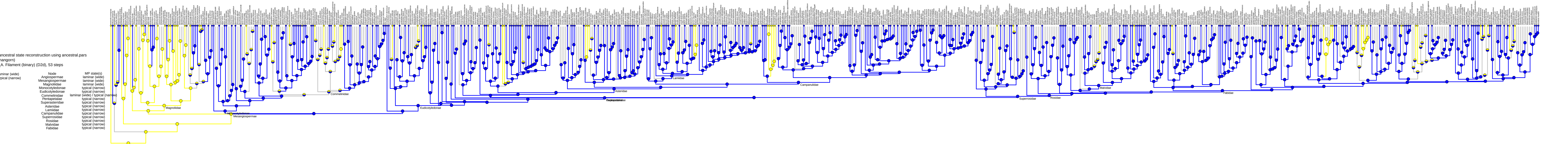
typical (narrow)

typical (narrow)

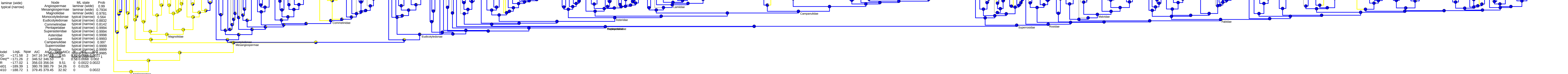
typical (narrow)

typical (narrow)

typical (narrow)



5 A. Filament (binary) (D2d), ARDeq model



MP ancestral state reconstruction using ancestral.pars
(R:phangorn)
311_A. Anther orientation (D2d), 109 steps

introrse

latrorse

extrorse

Node

Angiospermae

Mesangiospermae

Magnoliidae

Monocotyledonae

Eudicotyledonae

Commelinidae

Pentapetalae

Superasteridae

Asteridae

Lamiidae

Campanulidae

Superrosidae

Rosidae

Malvidae

Fabidae

MP state(s)

introrse

introrse / extrorse

extrorse

introrse / extrorse

introrse

introrse / latrorse

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introrse

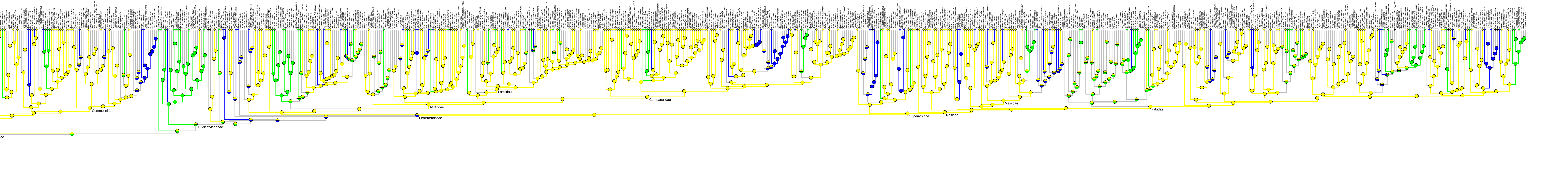
introrse

introrse

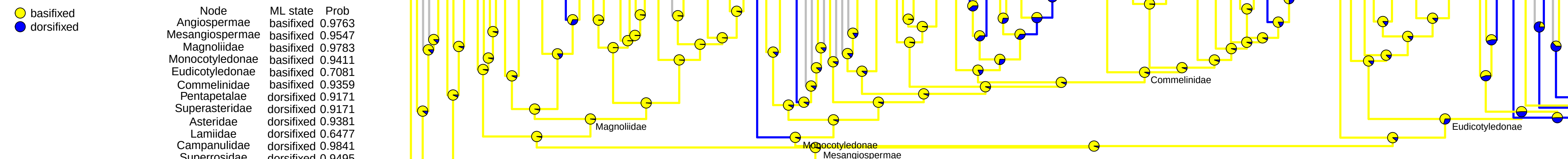
introrse

introrse

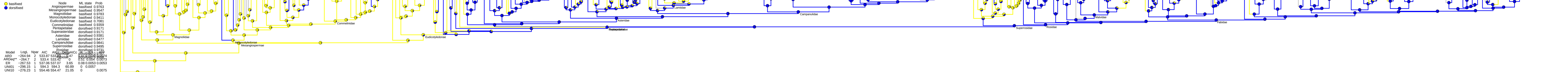
introrse



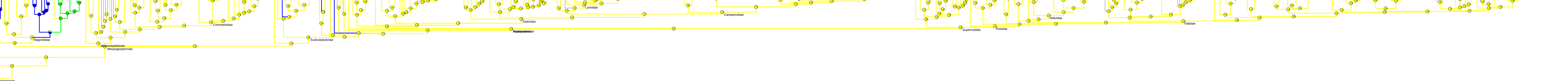
ML ancestral state reconstruction using rayDISC (R:corHMM)
312 A. Anther attachment (binary) (D2d), ARDeq model



Model	LogL	Npar	AIC	AICc	rusidae	maividae	capidae	unifixed	unifixed	unifixed
ARD	-264.94	2	533.87	533.87	0.47	0.0038	0.0074	0.51	0.004	0.0073
ARD _{eq} **	-264.7	2	533.4	533.42	0	0.0004	0.0073	0.51	0.004	0.0073
ER	-267.53	1	537.06	537.07	3.65	0.08	0.0053	0.0053	0	0.0057
UNI01	-296.15	1	594.3	594.3	60.89	0	0.0057	0	0.0075	0
UNI10	-276.23	1	554.46	554.47	21.05	0	0.0075	0	0.0075	0



Model	LogL	Npar	AIC	AIC _C	Delta AIC _C	Weight	Longitudinal slit	1
ARD	-55.71	6	123.41	123.52	0.11	0.90	Longitudinal slit	1
ARD _{eq}	-54.68	6	121.37	121.48	0	0.38	Longitudinal slit	1
ER	-60.41	1	122.82	122.83	1.35	0.19	1e-04	...
SYM	-59.39	3	124.78	124.81	1.34	0.07	2e-04	...
SYM _{eq}	-58.29	3	122.59	122.62	1.14	0.22	2e-04	...

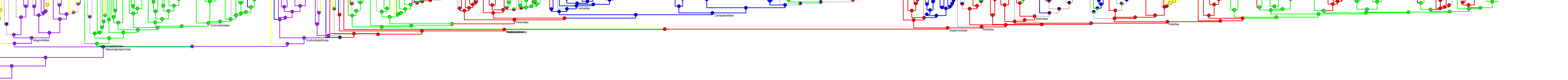


MP ancestral state reconstruction using ancestral.pars
(R:phangorn)

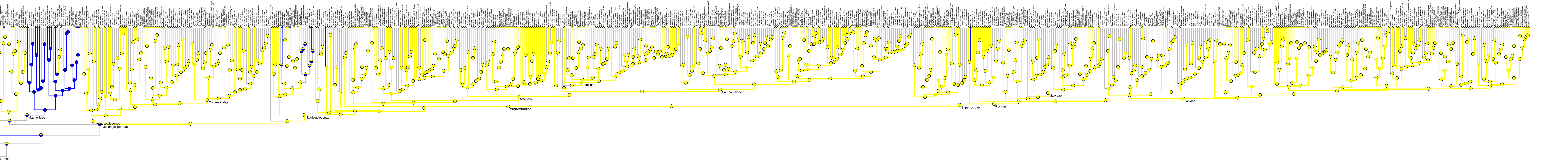
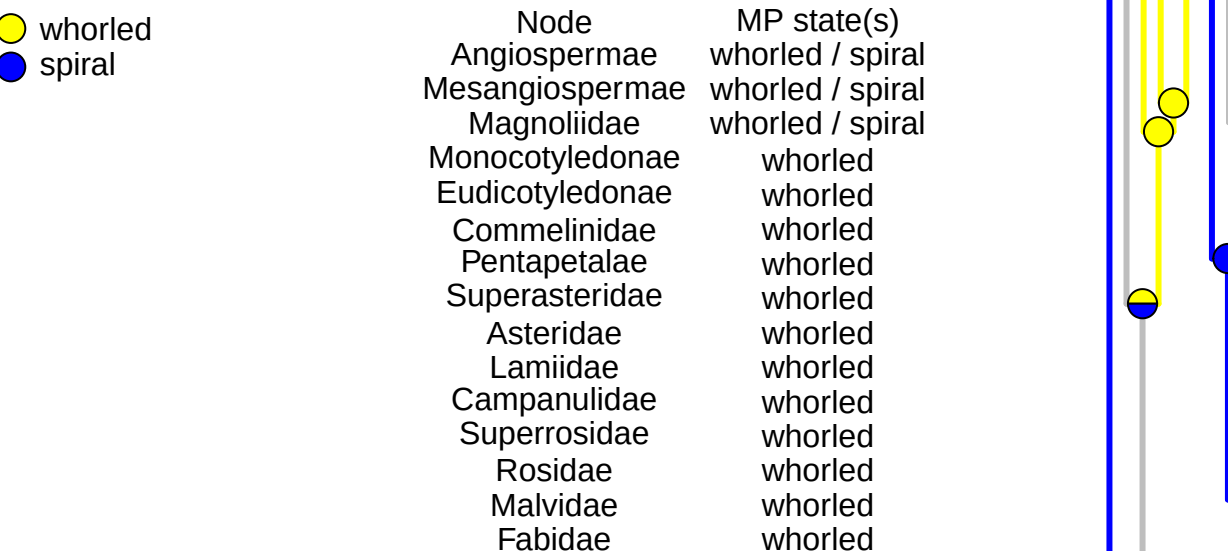
401_B. Number of structural carpels (5-state) (D2c), 187 steps

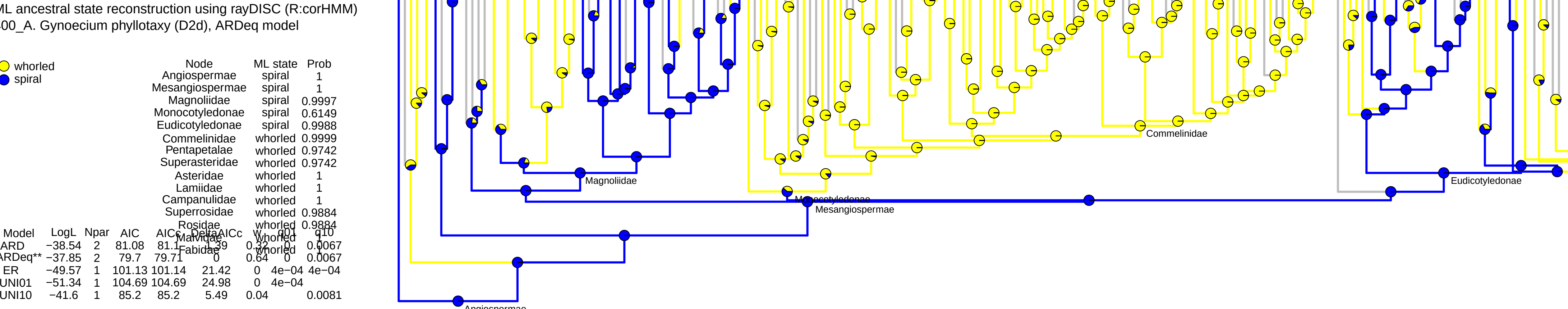
- one (1)
- two (2)
- three (3)
- four or five (4-5)

- | 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 | four or five (4-5) |
| Superasteridae | four or five (4-5) |
| Asteridae | four or five (4-5) |
| Lamiidae | two (2) |
| Campanulidae | two (2) |
| Superrosidae | four or five (4-5) |
| Rosidae | four or five (4-5) |
| Malvidae | four or five (4-5) |
| Fabidae | four or five (4-5) |



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



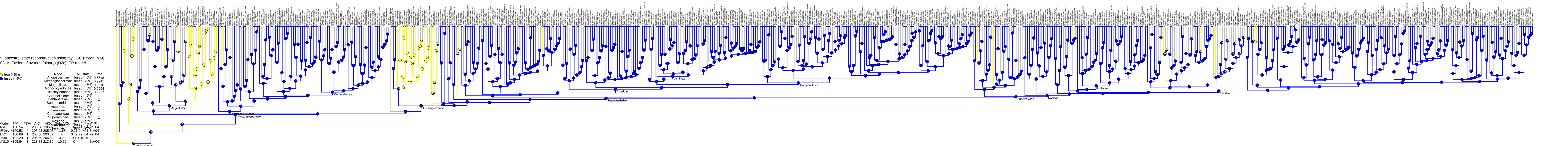


ML ancestral state reconstruction using rayDISC (R:corHMM)
403_A. Fusion of ovaries (binary) (D2c), ER model

● free (<5%)
● fused (>5%)

Node	ML state	Prob
Angiospermae	fused (>5%)	0.6618
Mesangiospermae	fused (>5%)	0.9941
Magnoliidae	fused (>5%)	0.9916
Monocotyledonae	fused (>5%)	0.9994
Eudicotyledonae	fused (>5%)	0.9957
Commelinidae	fused (>5%)	1
Pentapetalae	fused (>5%)	1
Superasteridae	fused (>5%)	1
Asteridae	fused (>5%)	1
Lamiidae	fused (>5%)	1
Campanulidae	fused (>5%)	1
Superrosidae	fused (>5%)	1

Model	LogL	Npar	AIC	AICc	BayesIC	IC
ARD	-100.54	2	205.08	205.05	0.21	1e-04
ARDc	-100.52	2	205.03	205.05	0.21	9e-04
ER*	-100.68	1	203.36	203.37	0	0.49
UNI01	-102.29	1	206.59	206.59	3.22	0.1
UNI10	-105.94	1	213.88	213.89	10.52	8e-04



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

