TABLE S4. BEAST settings of 16 individual molecular dating analyses. Analysis names corresponding to Fig. 3, letters provided in column "Constraints used" refer to Table S1 and Fig. 1. Individual prior distribution means are provided in detail in Table S1.

Analysis	Site Model	Clock	Constraints used	prior distribution	Mean	Speciation:	Root	taxa	number of runs	burnin (each)	generations (each)	sample frequency
Ref	GTR+G	UCLN	A, B, C, D, E, G, H, I, J, K, L, M, N, O, P, Q, R, S, T, U	Lognormal	individual	Birth Death incomlete sampling	uniform 323-400 mya	full sampling	2	5,000,000	250,000,000	5,000
root 500	GTR+G	UCLN	A, B, C, D, E, G, H, I, J, K, L, M, N, O, P, Q, R, S, T, U	Lognormal	individual	Birth Death incomlete sampling	uniform 323-500 mya	full sampling	1	5,000,000	250,000,000	5,000
noRoot	GTR+G	UCLN	A, B, C, D, E, G, H, I, J, K, L, M, N, O, P, Q, R, S, T, U	Lognormal	individual	Birth Death incomlete sampling	no constraint	full sampling	1	5,000,000	250,000,000	5,000
mean2	GTR+G	UCLN	A, B, C, D, E, G, H, I, J, K, L, M, N,	Lognormal	all 2	Birth Death incomlete e	uniform 323-400 mya	full sampling	1	5,000,000	250,000,000	5,000

			O, P, Q, R, S, T, U			samp ling						
exp	GT R+ G	U CL N	A, B, C, D, E, G, H, I, J, K, L, M, N, O, P, Q, R, S, T, U	Expo nenti al	all 2	Birth Deat h inco mlet e samp ling	unifo rm 323- 400 mya	full sampling	1	5,000 ,000	250,0 00,00 0	5,00 0
Chlo rA	GT R+ G	U CL N	A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q, R, S, T, U	Logno rmal	indiv idual	Birth Deat h inco mlet e samp ling	unifo rm 323- 400 mya	full sampling	1	5,000 ,000	250,0 00,00 0	5,00 0
Chlo rB	GT R+ G	U CL N	A, B, C, D, E, f, G, H, I, J, K, L, M, N, O, P, Q, R, S, T, U	Logno rmal	indiv idual	Birth Deat h inco mlet e samp ling	unifo rm 323- 400 mya	full sampling	1	10,00 0,000	250,0 00,00 0	5,00 0
notr icol p	GT R+ G	U CL N	A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q, S, T, U	Logno rmal	indiv idual	Birth Deat h inco mlet e samp ling	unifo rm 323- 400 mya	full sampling	1	5,000 ,000	250,0 00,00 0	5,00 0
no Wal k	GT R+ G	U CL N	A, B, C, D, E, F,	Logno rmal	indiv idual	Birth Deat h	unifo rm 323-	full sampling	1	25,00 0,000	250,0 00,00 0	5,00 0

			H, I, J, K, L, M, N, O, P, Q, R, S, T, U			incomlete sampling	400 mya					
noLac	GTR+G	UCLN	A, B, C, D, E, G, I, J, K, L, M, N, O, P, Q, R, S, T, U	Lognormal	individual	Birth Death incomlete sampling	uniform 323-400 mya	full sampling	1	5,000,000	250,000,000	5,000
Pip13	GTR+G	UCLN	A, B, C, D, E, G, H, I, J, K, L, M, N, O, P, Q, R, S, T, U	Lognormal	individual	Birth Death incomlete sampling	uniform 323-400 mya	13 Piperales (Asarum, Saruma, Lactoris, Aristolochia serpentaria, Thottea, Houttuynia, Gymnotheca, Saururus, Verhuellia, Zippelia, Manekia, Piper hostmannianum, Peperomia hispidula)	1	5,000,000	250,000,000	5,000
Pip9	GTR+G	UCLN	A, B, C, D, E, G, H, I, J, K, L, M, N, O, P, Q, R, S, T, U	Lognormal	individual	Birth Death incomlete sampling	uniform 323-400 mya	9 Piperales no Piperaceae (Asarum, Saruma, Lactoris, Aristolochia serpentaria, Thottea, Houttuynia, Gymnotheca, Saururus, Verhuellia)	1	5,000,000	250,000,000	5,000
5A	GT	U	C, D,	Logno	indiv	Birth	unifo	full sampling	1	3,000	250,0	5,00

	R+ G	CL N	E, O, S	rmal	idual	Deat h inco mlet e samp ling	rm 323- 400 mya			,000	00,00 0	0
5B	GT R+ G	U CL N	I, K, P, Q, S,	Logno rmal	indiv idual	Birth Deat h inco mlet e samp ling	unifo rm 323- 400 mya	full sampling	1	5,000 ,000	250,0 00,00 0	5,00 0
10A	GT R+ G	U CL N	A, B, C, D, H, M, N, Q, S, T	Logno rmal	indiv idual	Birth Deat h inco mlet e samp ling	unifo rm 323- 400 mya	full sampling	1	5,000 ,000	250,0 00,00 0	5,00 0
10B	GT R+ G	U CL N	A, D, E, I, K, L, M, P, T, U	Logno rmal	indiv idual	Birth Deat h inco mlet e samp ling	unifo rm 323- 400 mya	full sampling	1	5,000 ,000	250,0 00,00 0	5,00 0