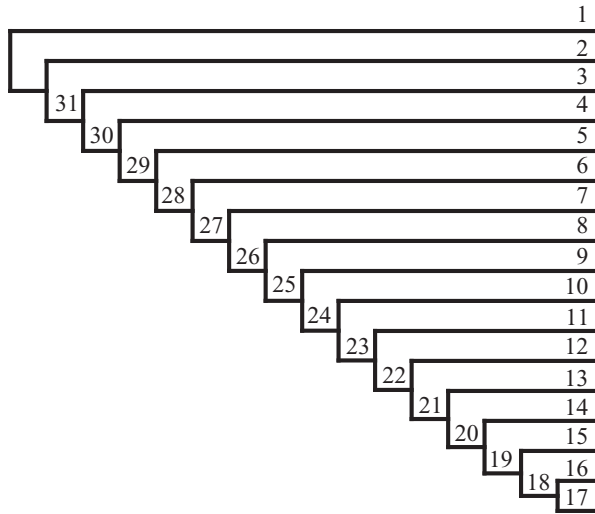


Figure 1. Seventeen-taxon topologies used for simulations assuming a molecular clock in this study. Pectinate (A) and symmetric (B) topologies with branches enumerated. See Table 1 for relative branch lengths used in each scenario.

A



B

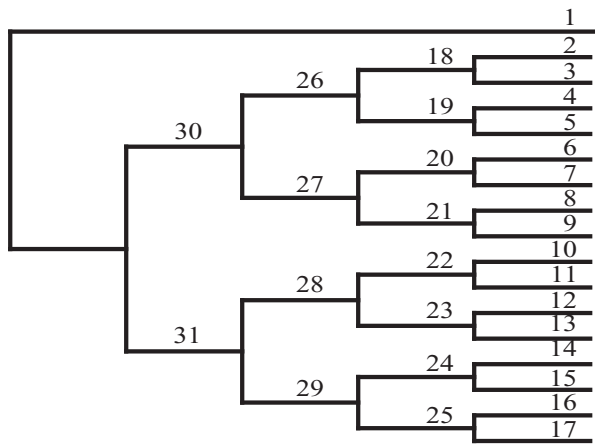


Table 1. Tree lengths and relative branch lengths of the 18 simulated topologies used in this study.

simulation ¹	length ²	Relative Branch Length ³													
		1	2	3	4	5	6	7	8	9	10	11	12	13	14
lpe	0.08	15.0	15.0	14.0	13.0	12.0	11.0	10.0	9.0	8.0	7.0	6.0	5.0	4.0	3.0
lpsb	0.08	60.0	60.0	59.5	58.5	57.0	55.0	52.5	49.5	46.0	42.0	37.5	32.5	27.0	21.0
lplb	0.08	60.0	60.0	53.0	46.5	40.5	35.0	30.0	25.5	21.5	18.0	15.0	12.5	10.5	9.0
lpsm	0.08	32.0	32.0	28.5	25.5	23.0	21.0	19.5	18.5	18.0	17.5	16.5	15.0	13.0	10.5
lplm	0.08	28.5	28.5	28.0	27.0	25.5	23.5	21.0	18.0	14.5	11.0	8.0	5.5	3.5	2.0
hpe	0.30	15.0	15.0	14.0	13.0	12.0	11.0	10.0	9.0	8.0	7.0	6.0	5.0	4.0	3.0
hpsb	0.30	60.0	60.0	59.5	58.5	57.0	55.0	52.5	49.5	46.0	42.0	37.5	32.5	27.0	21.0
hplb	0.30	60.0	60.0	53.0	46.5	40.5	35.0	30.0	25.5	21.5	18.0	15.0	12.5	10.5	9.0
hpsm	0.30	32.0	32.0	28.5	25.5	23.0	21.0	19.5	18.5	18.0	17.5	16.5	15.0	13.0	10.5
hplm	0.30	28.5	28.5	28.0	27.0	25.5	23.5	21.0	18.0	14.5	11.0	8.0	5.5	3.5	2.0
lse	0.08	4.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
lssb	0.08	20.0	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5
lslb	0.08	20.0	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5
lncl	0.08	50.0	18.0	3.0	15.0	2.0	6.0	17.0	7.0	8.0	1.2	0.8	1.5	0.5	5.0
hse	0.30	4.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
hssb	0.30	20	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.5
hslb	0.30	20.0	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5
hncl	0.30	50.0	18.0	3.0	15.0	2.0	6.0	17.0	7.0	8.0	1.2	0.8	1.5	0.5	0.5

¹lpe = low-rate pectinate equal length internodes, lpsb = low-rate pectinate short basal internodes, lplb = low-rate pectinate long basal internodes, lpsm = low-rate pectinate short middle internodes, lplm = low-rate pectinate long middle internodes, hpe = high-rate pectinate equal length internodes, hpsb = high-rate pectinate short basal internodes, hplb = high-rate pectinate long basal internodes, hpsm = high-rate pectinate short middle internodes, hplm = high-rate pectinate long middle internodes (Fig. 2); lse = low-rate symmetric equal length internodes, lssb = low-rate symmetric short basal internodes, lslb = low-rate symmetric long basal internodes, lncl = low-rate symmetric no clock, hse = high-rate symmetric equal length internodes, hssb = high-rate symmetric short basal internodes, hslb = high-rate symmetric long basal internodes, hncl = high-rate symmetric no clock (Fig. 3)

²Tree length corresponds to the number of expected substitutions across the tree from the root to any tip.

³Relative branch length corresponds to branch numbers on trees shown in Figure 1

Table 1 (cont.) Tree lengths and relative branch lengths of the 18 simulated topologies used in this study.

simulation ¹	length ²	Relative Branch Length																	
		15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	
lpe	0.08	2.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	
lpsb	0.08	14.5	7.5	7.5	7.0	6.5	6.0	5.5	5.0	4.5	4.0	3.5	3.0	2.5	2.0	1.5	1.0	0.5	
lplb	0.08	8.0	7.5	7.5	.5	1.0	1.5	2.0	2.5	3.0	3.5	4.0	4.5	5.0	5.5	6.0	6.5	7.0	
lpsm	0.08	7.5	4.0	4.0	3.5	3.0	2.5	2.0	1.5	1.0	0.5	.5	1.0	1.5	2.0	2.5	3.0	3.5	
lplm	0.08	1.0	0.5	0.5	0.5	1.0	1.5	2.0	2.5	3.0	3.5	3.5	3.0	2.5	2.0	1.5	1.0	0.5	
hpe	0.30	2.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	
hpsb	0.30	14.5	7.5	7.5	7.0	6.5	6.0	5.5	5.0	4.5	4.0	3.5	3.0	2.5	2.0	1.5	1.0	0.5	
hplb	0.30	8.0	7.5	7.5	0.5	1.0	1.5	2.0	2.5	3.0	3.5	4.0	4.5	5.0	5.5	6.0	6.5	7.0	
hpsm	0.30	7.5	4.0	4.0	3.5	3.0	2.5	2.0	1.5	1.0	0.5	0.5	1.0	1.5	2.0	2.5	3.0	3.5	
hplm	0.30	1.0	0.5	0.5	0.5	1.0	1.5	2.0	2.5	3.0	3.5	3.5	3.0	2.5	2.0	1.5	1.0	0.5	
lse	0.08	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	
lssb	0.08	13.5	13.5	13.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	1.5	1.5	1.5	1.5	0.5	0.5	
lslb	0.08	0.5	0.5	0.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	4.5	4.5	4.5	4.5	13.5	13.5	
lncl	0.08	18.0	13.0	12.0	1.0	1.5	2.5	1.5	.5	1.0	3.0	8.0	1.0	3.5	10	1.5	1.0	3.0	
hse	0.30	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	
hssb	0.30	13.5	13.5	13.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	1.5	1.5	1.5	1.5	0.5	0.5	
hslb	0.30	0.5	0.5	0.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	4.5	4.5	4.5	4.5	13.5	13.5	
hncl	0.30	18.0	13.0	12.0	1.0	1.5	2.5	1.5	0.5	1.0	3.0	8.0	1.0	3.5	10	1.5	1.0	3.0	