

Appendix S8. Plastome alignment statistics. Data shows number of sequences, trimming mode, the number of loci retained for coalescent analysis after checking for excessive gene tree branch lengths, alignment length, number of informative and constant sites, pairwise identity, average GC content, percentage of gaps, and average locus length for the exon, intron and intergenic regions.

	Exons (ex)		Introns (in)		Intergenic (it)		Combined plastome (al)	
Number of taxa	151	125	151	125	151	125	151	125
Trimming mode	visual	visual	visual	visual	strict (trimAl)	strict (TrimAl)	strict & visual	strict & visual
Total sites	64,117	64,117	15,881	15,881	51,358	51,358	131,356	131,356
Parsimony informative sites	3,561 (5.6%)	3,197 (4.9%)	1,496 (9.4%)	1,364 (8.6%)	4,309 (8.4%)	3,984 (7.7%)	9,359 (7.1%)	8,545 (6.5%)
Constant sites	56,604 (88%)	57,665 (90%)	12,864 (81%)	13,187 (83%)	42,024 (82%)	42,898 (84%)	111,523 (85%)	113,731 (87%)
Pairwise identity (%)	94	99	90	98	90	97	91	97
Average GC content (%)	38.8	38.8	34.7	34.6	35.6	35.4	37.1	36.8
Gaps (%)	4	2	14	10	6	2	6.5	10
Average locus length	823	823	1,058	1,058	740	740	816	816
Loci retained for ASTRAL analysis	76	76	15	15	69	69	160	160