

Supplemental Table S4: Best substitutional model for generating phylogenetic trees

Type of phylogeny	Tree generating method	Selected substitutional model	Parameters
	Maximum likelihood	GTR+G	partition : 12345, -lnL 309613.5545, K 43 freqA 0.307 R(a) 0.9552 freqC 0.1927 R(b) 1.9375 freqG 0.1869 R(c) 0.6822 freqT 0.3134 R(d) 0.8165 ti/tv - R(e) 1.8111 R(f) 1 p-inv - gamma 0.782
Chloroplast	Bayesian inference method	TPM1uf+G	partition 12210, -lnL 309625.2399, K 40 freqA 0.3069 R(a) 1 freqC 0.1926 R(b) 1.9139 freqG 0.1875 R(c) 0.7339 freqT 0.3129 R(d) 0.7339 ti/tv - R(e) 1.9139 R(f) 1 p-inv - gamma 0.782
	Maximum likelihood		partition 12345, -lnL 175579.5668, K 46 freqA 0.2869 R(a) 0.9773 freqC 0.1937 R(b) 4.5495 freqG 0.2414 R(c) 1.1012 freqT 0.278 R(d) 1.3391 ti/tv - R(e) 5.1218 R(f) 1 p-inv 0.787 gamma 0.623
Nuclear gene-based phylogeny	Bayesian inference method		Partition 12230, -lnL 175587.0945, K 44 freqA 0.286 R(a) 1 freqC 0.1945 R(b) 4.592 freqG 0.2424 R(c) 1.2088 freqT 0.2772 R(d) 1.2088 ti/tv - R(e) 5.1657 R(f) 1 -inv 0.787 gamma 0.621