Additional file 4. Summary statistics for phylogenetic dataset.
Sampling, sequence length and model selection for data partitions.

	ITS	matK	psbA	rbcL	rps16	trnLF intron	trnLF spacer
Sequence alignment length	799	1622	765	1362	1041	1143	530
Number of taxa	175	207	64	92	159	55	55
Model selected by Akaike Information Criterion	HKY+G	GTR+G	HKY+I+G	GTR+I+G	HKY+G	HKY+G	HKY+G