

Appendix S4. Supermatrix alignment details, with details about the nine regions selected for this study. Number of species sampled per region, accumulative percentage of species sampled per region, aligned length, proportions of parsimony informative characters (PI), and variable sites (VS) per region in the dataset are indicated. Values are calculated with outgroups, and with ambiguous regions and repeats excluded. bp=base pairs.

Region	Genome	Species (% of total)	% of total	Aligned length before exclusion (bp)	Excluded bp	Aligned length after exclusion (bp)	PI	PI of total (%)	VS	VS of total (%)
<i>trnT-L</i>	Plastid	622	84	2,077	164	1,913	593	31	928	45
ITS	Nuclear ribosomal	609	82	881	355	526	352	67	465	88
waxy	Nuclear	532	72	1,792	81	,711	923	54	1,195	70
<i>trnS-G</i>	Plastid	334	45	932	141	791	173	22	330	42
<i>ndhF</i>	Plastid	261	35	2,088	0	2,088	344	16	581	28
<i>ndhF- rpl32</i>	Plastid	261	35	899	16	883	232	26	404	46
<i>matK</i>	Plastid	242	32	1,148	0	1,148	220	19	409	36
<i>rpL32- trnL</i>	Plastid	206	27	1,377	124	1,253	282	23	494	39
<i>psbA- trnH</i>	Plastid	163	22	650	55	595	145	24	238	40
Total		746	--	11,844	936	10,908	3,263	30	5,044	46
Plastid only		678	91	9,171	500	8,671	1,989	23	3,384	39