

Table S3. Datasets, partitions where applicable, models selected under AIC criterion, and parameters estimated on the best ML tree.

Data Set	Partition	Aligned		Invariant (I)	Shape (α)	Base frequencies		Rate Matrix
		Length	Model (AIC)			(A, C, G, T)		
cpDNA	trnT-L-F	2163	GTR+G	0.0 (fixed)	0.1962	0.3665, 0.1347,	AC=1.063, AG=0.722,	
						0.1596, 0.3391	AT=0.440, CG=0.546,	
	rpoA	1375	GTR+G	0.0 (fixed)	0.0500	0.3576, 0.1578,	CT=0.794, GT=1.000	
						0.1805, 0.3041	AC=1.568, AG=2.219,	
β -Amylase	Exons	608	K80+G	0.0 (fixed)	0.4921	Equal (fixed)	AT=0.469, CG=1.295,	
	Introns	936	GTR+I+G	0.0 (est.)	1.2874	0.3306, 0.2033,	CT=4.065, GT=1.000	
						0.1925, 0.2736	ti/tv=2.7048	
							AC=1.307, AG=3.529,	
							AT=0.993, CG=2.193,	
							CT=4.594, GT=1.000	
pepC	Single	1348	HK+G	0.0 (fixed)	1.0202	0.2307, 0.2211,	ti/tv=1.8002	
						0.2363, 0.3120		
GBSSI-Triticeae	Exons	759	GTR+G	0.0 (fixed)	0.3759	0.2307, 0.3074,	AC=0.619, AG=3.290,	
						0.3089, 0.1531	AT=0.620, CG=1.063,	
	Introns	507	GTR+G	0.0 (fixed)	0.9455	0.2604, 0.2194,	CT=6.661, GT=1.000	
						0.2379, 0.2823	AC=1.226, AG=2.735,	
							AT=0.642, CG=1.350,	
							CT=3.323, GT=1.000	
GBSSI exons- Pooideae and Bambusoideae	Single	719	GTR+I+G	0.3077	0.7833	0.2208, 0.2929,	AC=1.172, AG=2.858,	
						0.3290, 0.1574	AT=0.730, CG=1.245,	
							CT=4.357, GT=1.000	