Supplementary Table S1. Statistical values of datasets for maximum parsimony and maximum likelihood analyses in this study.

Dataset	No. of taxa	No. of bp[1]	Maximum parsimony						
			PIC[2]	No. of trees	Tree length	CI[3]	RI[4]	RC[5]	HI[6]
tef1	71	523	226	160	545	0.708	0.961	0.68	0.292
tub2	57	598	253	4	644	0.675	0.936	0.632	0.325
cmdA	70	692	263	72	536	0.711	0.965	0.686	0.289
his3	69	466	168	468	598	0.545	0.905	0.493	0.455
tef1/tub2/cmdA/his3	71	2279	911	30	2461	0.621	0.938	0.583	0.379

Dataset	Maximum likelihood							
	Subst. mode[7]	NST[8]	Rate matrix					Rates
tef1	TIM2+G	6	1.6996	2.6313	1.6996	1.0000	5.2900	Gamma
tub2	TPM2uf+I+G	6	1.4626	4.1347	1.4626	1.0000	4.1347	Gamma
cmdA	TIM1+G	6	1.0000	3.3878	0.6980	0.6980	6.0097	Gamma
his3	TIM2+I+G	6	1.6118	5.5754	1.6118	1.0000	8.4960	Gamma
tef1/tub2/cmdA/his3	TIM2+I+G	6	1.5289	1.5289	1.5289	1.0000	5.7636	Gamma

[1] bp = base pairs.

[2] PIC = number of parsimony informative characters.

[3] CI = consistency index.

[4] RI = retention index.

[5] RC = rescaled consistency index.

[6] HI = homoplasy index.

[7] Subst. model = best fit substitution model.

[8] NST = number of substitution rate categories.