

Supplementary Table 2. Datasets used and the statistics resulting from the phylogenetic analyses.

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
ITS+ <i>BTI</i>	117	1069	505	76	2239	0.442	0.886	0.392	0.558
ITS	29	512	97	552	138	0.841	0.944	0.794	0.159
<i>BTI</i>	29	416	56	15	79	0.873	0.940	0.821	0.127
TEF	25	280	75	6	95	0.895	0.953	0.853	0.105
ITS+BT2+TEF	29	1208	228	11	322	0.839	0.933	0.782	0.161

Dataset	Maximum likelihood										
	Subst. model ⁷	NST ⁸	Rate matrix					Ti/Tv ratio ⁹	p-inv	Gamma	Rates
ITS+ <i>BTI</i>	TPM3uf+I+G	6	0.748	3.191	1.000	0.748	3.191	–	0.365	0.484	gamma
ITS	TrNef+G	6	1.000	1.930	1.000	1.000	3.417	–	0	0.267	gamma
<i>BTI</i>	TrN+I	6	1.000	2.024	1.000	1.000	5.567	–	0.772	–	equal
TEF	TPM2uf	6	2.828	6.412	2.828	1.000	6.412	–	0	–	equal
ITS+ <i>BTI</i> +TEF	TrN+G	6	1.000	2.527	1.000	1.000	3.722	–	0	0.154	gamma

¹bp = base pairs.

²PIC = number of parsimony informative characters.

³CI = consistency index.

⁴RI = retention index.

⁵RC = rescaled consistency index.

⁶HI = homoplasy index.

⁷model = best-fit substitution model.

⁸NST = number of substitution rate categories.

⁹Ti/Tv ratio = transition/transversion ratio.