

Supplementary Table S1. Summary of phylogenetic information for the different analyses in this study¹.

Alignment	Nuclear region	Length incl. gaps / number of taxa incl. outgroup	BI unique site patterns	Model (AIC)	BI sample frequency / temperature value	Number of sampled trees (BI)	ML -lnL (R)	IQ-TREE distinct patterns / parsimony informative sites / singleton sites / constant sites	ML (IQ)	-lnL	BI sample frequency / temperature value
Meristematic and meristem-like fungi in <i>Dothideomycetes</i>	LSU	836	465	GTR + - G	-	-	-10031.012864	465 / 321 / 81 / 434	-10030.410	-	
	SSU	1 008	291	GTR + - I + G	-	-	-4544.455785	287 / 171 / 77 / 760	-4543.764	-	
	<i>RPB2</i>	789	635	GTR + - I + G	-	-	-21587.985097	634 / 546 / 39 / 204	-21588.165	-	
	ITS	669	495	GTR + - I + G	-	-	-12896.045334	494 / 394 / 50 / 225	-12896.408	-	
	Combined	3 305 / 97	1 349	-	1 000 / 0.10	24 336	-50.865.307.601	1 878 / 1 432 / 247 / 1 626	-49.901.350	1 000 / 0.10	

¹ BI: Bayesian inference; Model (AIC): Evolutionary model selected by MrModeltest under the Akaike Information Criterion (superscript d is for dirichlet state frequencies and superscript f for fixed state frequencies); BI sample frequency: Number of nth generations sampled; ML -lnL (R): Log-likelihood of final tree in RAxML; ML -lnL(IQ): Log-likelihood of consensus tree in IQ-TREE.