Table S1. Statistics for the different phylogenetic analyses performed in this study.

Analysis[1]	Number of strains (including outgroup)	Total number of characters (including gaps)	IQ-TREE analysis					Bayesian analysis		
			Distinct patterns	Parsimony-informative sites	Singleton sites	Constant sites	Best-fit model[2]	Unique site patterns	Trees sampled	Substitution model[3]
Fig. 1. *Dothideomycetes* (other orders) - LSU	161	872	478	317	64	491	TN+F+R4	n/a	n/a	n/a
Fig. 2. *Dothideomycetes* (*Pleosporales*) - LSU	97	880	267	151	90	639	TIM3e+I+G4	n/a	n/a	n/a
Fig. 3. *Eurotiomycetes*- LSU	34	958	208	95	129	734	TNe+R3	n/a	n/a	n/a
Fig. 4. *Leotiomycetes* - LSU	54	831	254	150	72	609	TN+F+I+G4	254	125 252 of 167 002	GTR + I + gamma with dirichlet state frequency distribution
Fig. 5. *Orbiliomycetes* - LSU	34	819	197	151	46	622	TIMe+I+G4	n/a	n/a	n/a
Fig. 6. *Sordariomycetes* (other orders) - LSU	53	899	320	242	63	594	TIMe+R3	n/a	n/a	n/a
Fig. 7. *Sordariomycetes* (*Hypocreales & Glomerales*) LSU	39	862	228	142	80	640	TIM3e+R2	n/a	n/a	n/a
Fig. 8. *Sordariomycetes* (*Xylariales*) - LSU	54	855	218	134	89	632	TIM3e+R3	n/a	n/a	n/a
Fig. 13. *Mycosphaerellales & Cladosporiales* - LSU/*rpb2*	155	1 461	778	631	81	748	GTR+F+I+G4 for both loci	n/a	n/a	n/a
Fig. 18. *Dactylella/Dactylellina* - ITS	42	684	451	275	123	286	TIM2e+I+G4	n/a	n/a	n/a
Fig. 22. *Exophiala* - ITS	15	629	185	93	70	466	TIM2e+G4	n/a	n/a	n/a
Fig. 24. *Teichosporaceae* - LSU/ITS/*tef1*	57	2 970	1 066	692	226	2 052	TNe+G4 (ITS), TN+F+I+G4 (*tef1*) and TIM3e+I+G4 (LSU)	n/a	n/a	n/a
Fig. 27. *Idriellomyces* - ITS	12	579	200	114	56	409	TIM2e+G4	n/a	n/a	n/a
Fig. 32. *Microcera* - ITS/*rpb1/rpb2/tub2*	11	2 812	605	402	351	2 059	TNe+G4 for all loci	n/a	n/a	n/a
Fig. 36. *Teratosphaeriaceae* - ITS	37	575	293	158	71	345	TIM2e+I+G4	n/a	n/a	n/a
Fig. 39. *Niesslia* - ITS	32	701	378	202	83	416	TIM2+F+G4	n/a	n/a	n/a
Fig. 44. *Nothotrimmatostroma* - ITS	21	565	180	116	50	399	TNe+G4	n/a	n/a	n/a
Fig. 50. *Phaeosphaeria* - ITS	21	609	279	114	126	369	TIM2+F+I+G4	n/a	n/a	n/a
Fig. 65. *Scytalidium* - ITS	28	630	203	105	50	475	TNe+G4	n/a	n/a	n/a

[1] ITS: internal transcribed spacers and intervening 5.8S nrDNA; LSU: large subunit (28S) of the nrRNA gene operon; *rpb1*: partial DNA-directed RNA polymerase II largest subunit gene; *rpb2*: partial DNA-directed RNA polymerase II second largest subunit gene; *tef1*: partial translation elongation factor 1-alpha gene; *tub2*: partial beta-tubulin gene.

[2] The best-fit model(s) identified for the alignment in IQ-TREE using the TESTNEW option.

[3] The best-fit model identified according to the Akaike Information Criterion as implemented in MrModeltest.