

Table S1. Multilocus phylogeny parameters used in the study.

Parameter	Details
Analysis*	PhyML
Model	GTR
Branch Support	Bootstrap with 1000 replicates
Nucleotide equilibrium frequencies	Empirical
Invariable sites	None
Across site rate variation	Optimized, classes 4
Tree searching operations	NNI
Starting tree	BioNJ, Optimize tree topology

* The analysis was performed with Seaview5 program only for *Diaporthe*, *Neofusicoccum* spp. (*ITS+tub-2+ACT*) and *Pestalotiopsis* spp. (*ITS+tub-2*) isolates obtained in the study along with reference species downloaded from NCBI nucleotide database.

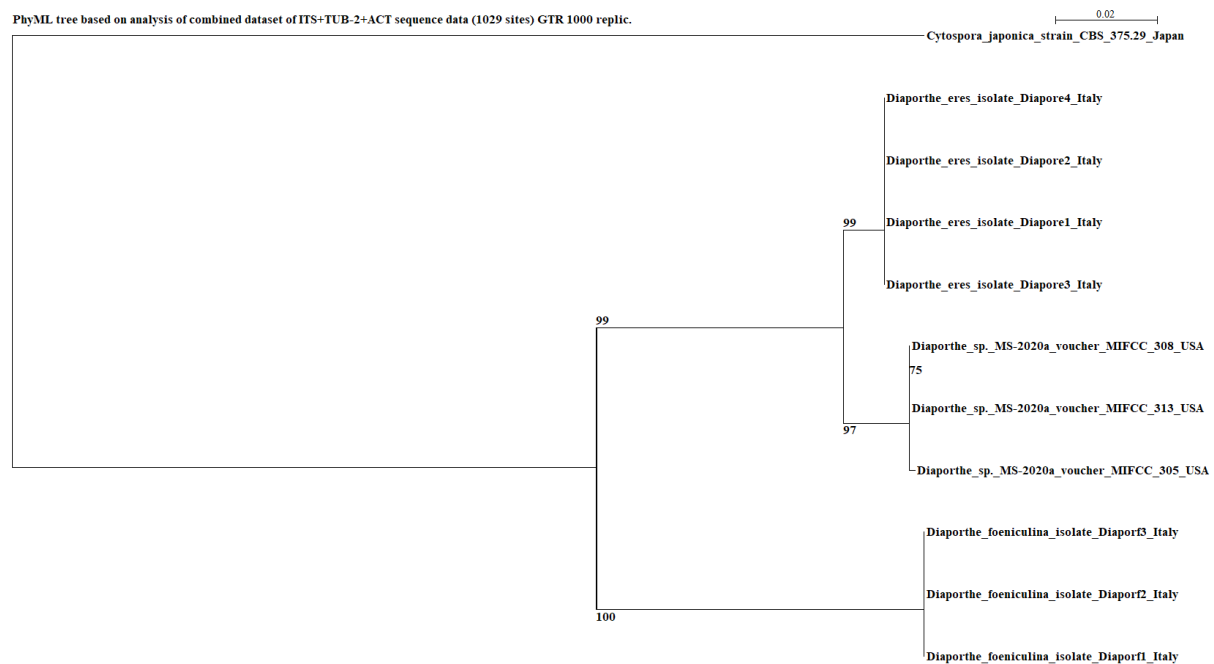


Figure S1.PhyML tree (ITS + tub-2 + ACT) for *Diaporthe* spp.

PhyML tree based on analysis of a combined dataset of ITS+TUB-2+ACT sequence data (1053 sites) GTR 1000 replic.

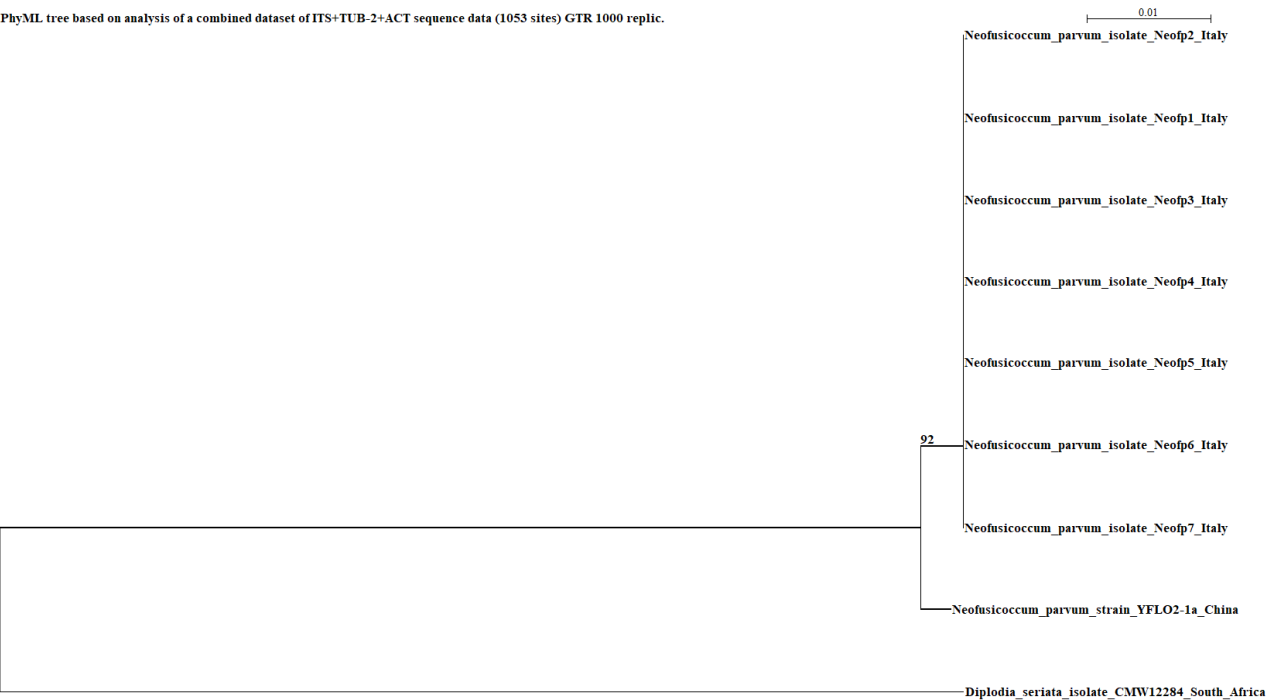


Figure S2. PhyML tree (ITS + tub-2 + ACT) for *Neofusicoccum* spp.

PhyML tree based on analysis of a combined dataset of ITS+TUB-2 sequences data (834 sites) GTR 1000 replic.

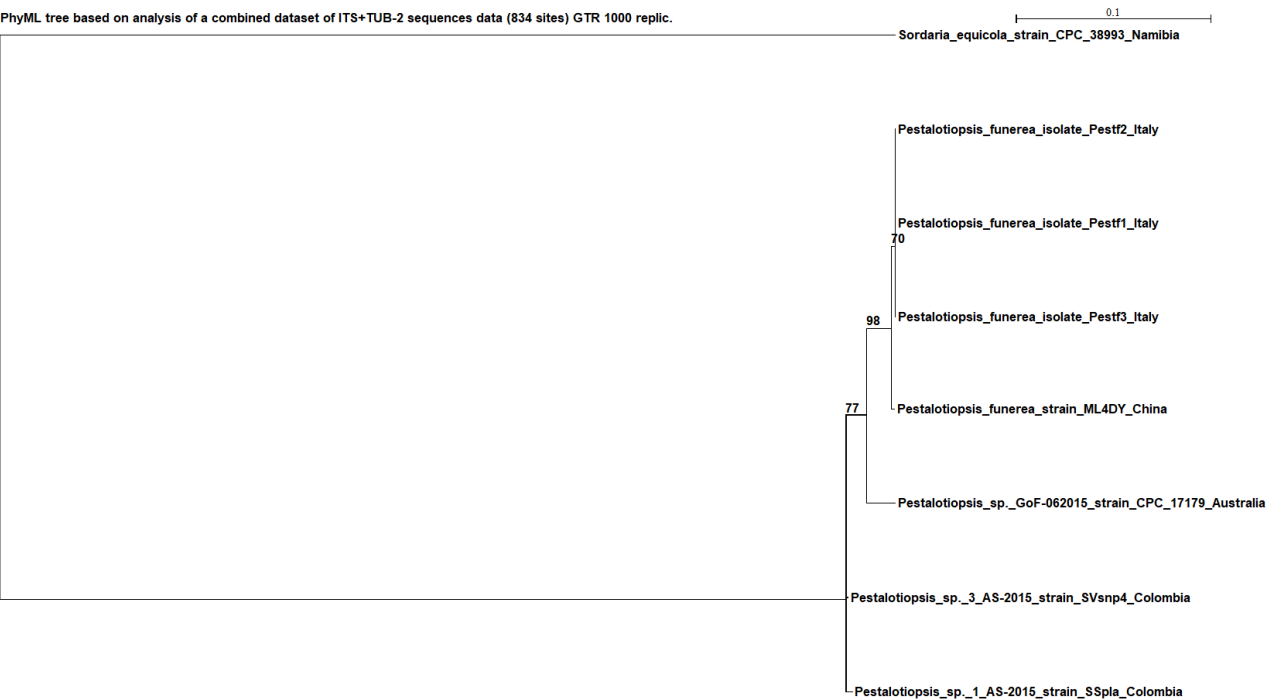


Figure S3. PhyML tree (ITS + tub-2) for *Pestalotiopsis* spp.