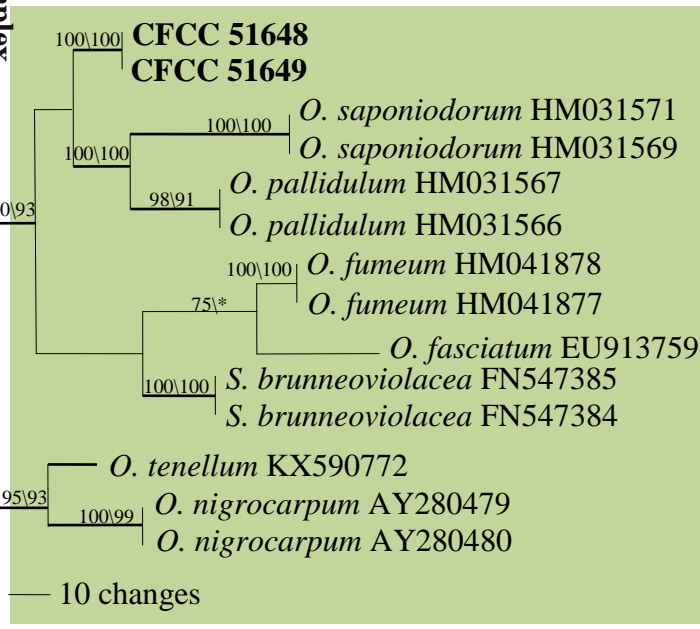
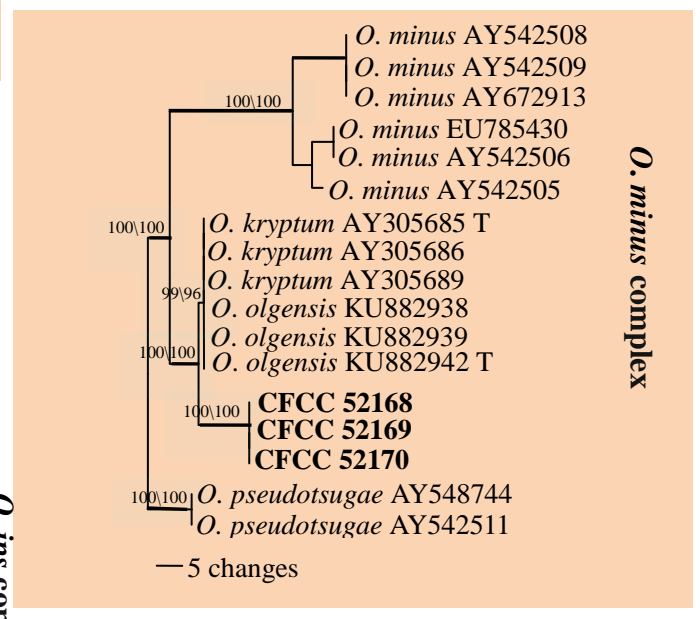
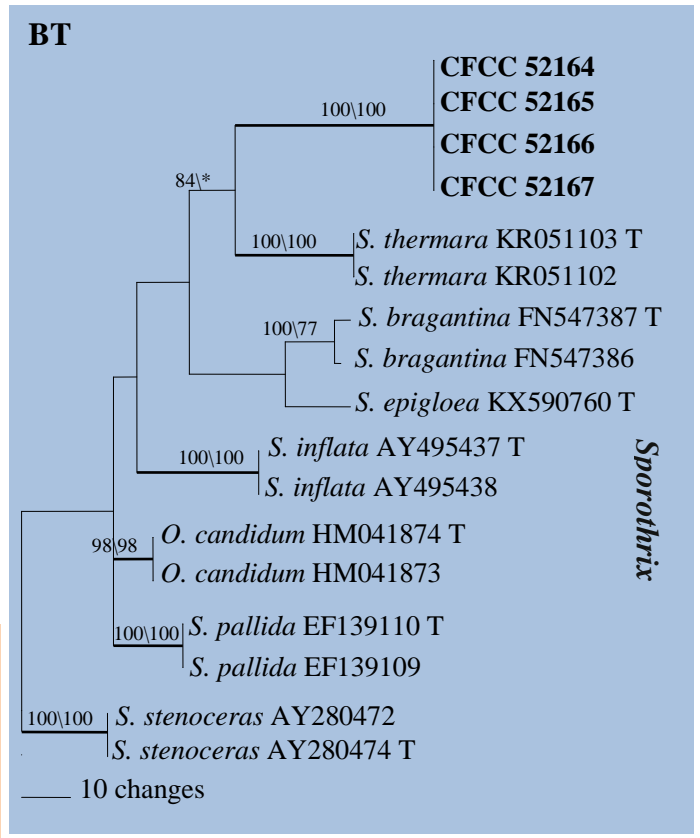


ITS



BT



CFCC 52164
CFCC 52165
CFCC 52166
CFCC 52167

Sporothrix

O. minus complex

O. ips complex

O. tenellum complex

— 10 changes

— 10 changes

— 5 changes

— 10 changes

Figure 1. Phylograms of fungal associates of pine infected by PWN and *Monochamus alternatus* in China. The phylograms were generated after MP analysis of the ITS1–5.8S–ITS2 rDNA and partial *tub2* sequences. Novel sequences obtained in the current study are indicated in bold type. MP bootstrap values (10,000 replicates) and ML bootstrap support values (1000 replicates) (normal type) above 70% are indicated at the nodes. Values below 70% are indicated by asterisk (*). Posterior probabilities (above 90%) obtained from BI are indicated by bold lines at the relevant branching points. Scale bar, total nucleotide differences between taxa; ML, maximum likelihood; MP, maximum parsimony; BI, Bayesian inference.