

Supplementary figures

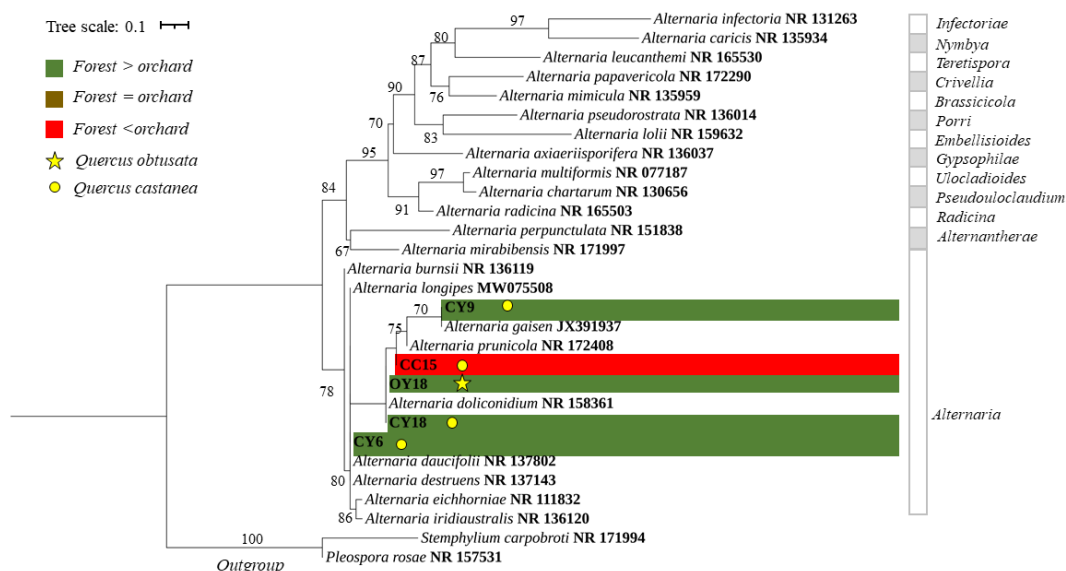


Figure S1. Phylogenetic tree based on ITS sequences of species in the genus *Alternaria*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the TIMe+I+G4 evolutionary model. *Stemphylium carpobroti* (NR 171994) served as the outgroup. At the ends of the terminal branches, the corresponding sections of the genus are indicated. Bootstrap values of 50 or higher, obtained from 1000 iterations, are shown at each node. Isolates from this study are in bold.

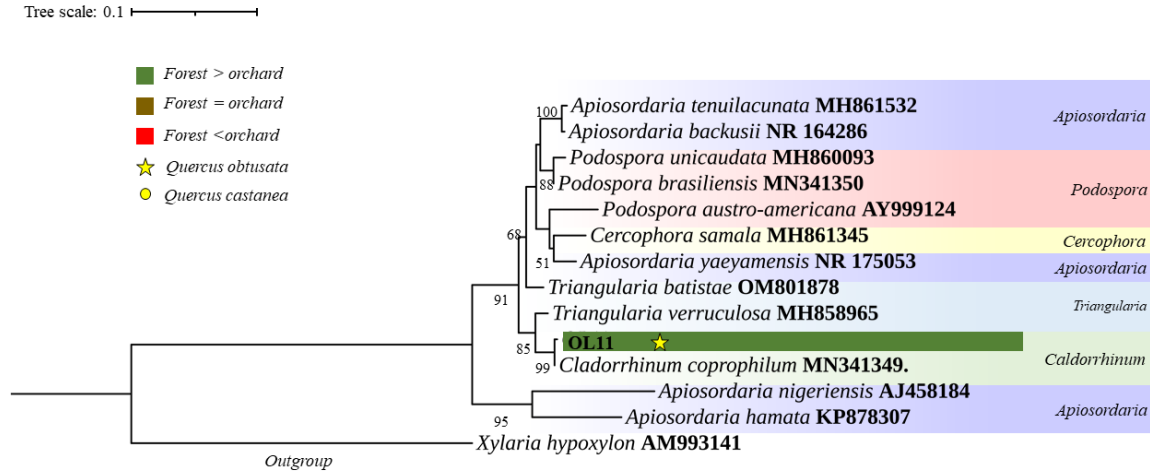


Figure S2. Phylogenetic tree based on ITS sequences of species in the genus *Apiosordaria*. The tree was inferred using the Maximum Likelihood (ML) criterion with the TIM2e+G4 evolutionary model. *Xylaria hypoxylon* (AM993141) served as the outgroup. At the ends of the terminal branches, the corresponding sections of the genus are indicated. Bootstrap values of 50 or higher, obtained from 1000 iterations, are shown at each node. Isolates from this study are in bold.

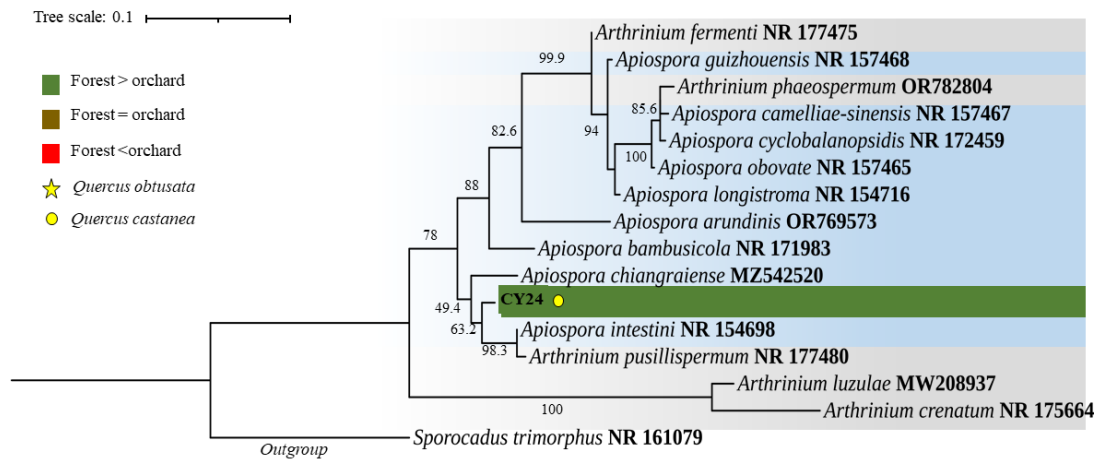


Figure S3. Phylogenetic tree based on ITS sequences of species from the genera *Apiospora* and *Arthrinium*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the TNe+G4 evolutionary model. *Sporocadus trimorphus* (NR 161079) served as the outgroup. Bootstrap values of 50 or higher, obtained from 1000 iterations, are shown at each node. Isolates from this study are in bold.

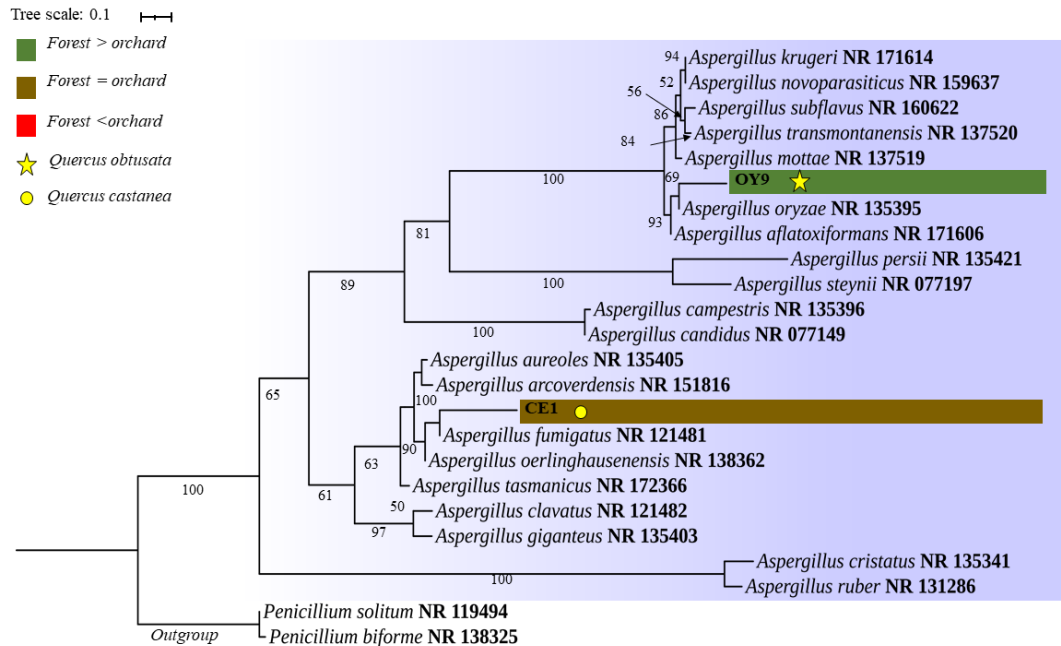


Figure S4. Phylogenetic tree based on ITS sequences of species in the genus *Aspergillus*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the TNe+I+G4 evolutionary model. *Penicillium solitum* (NR 119494) and *Penicillium biforme* (NR 138325) served as the outgroup. Bootstrap values of 50 or higher, obtained from 1000 iterations, are shown at each node. Isolates from this study are in bold.

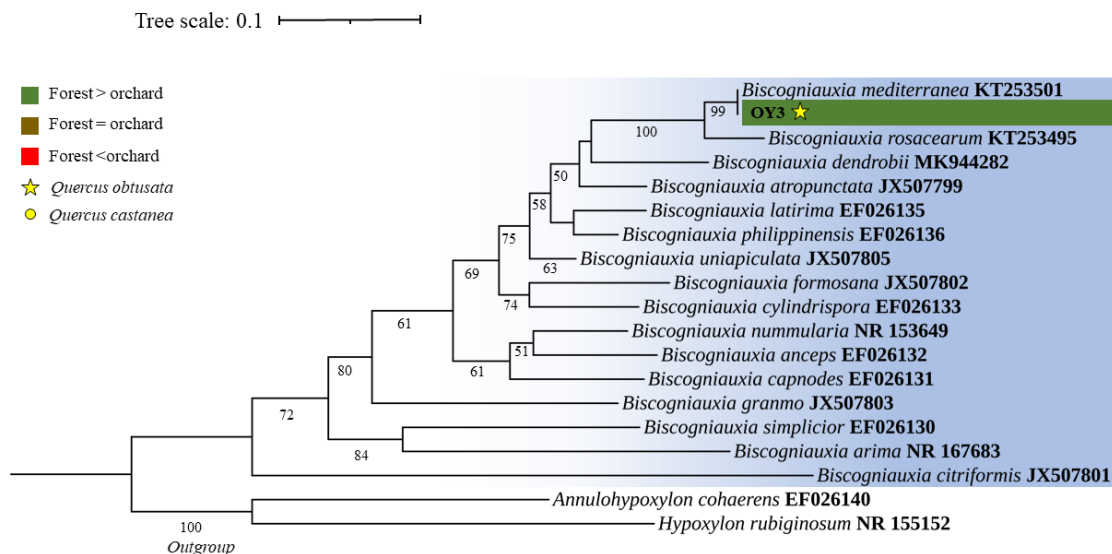


Figure S5. Phylogenetic tree based on ITS sequences of species in the genus *Biscogniauxia*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML)

criterion with the TNe+G4 evolutionary model. *Anulohypoxylon cohaerens* (EF026140) and *Hypoxylon rubiginosum* (NR 155152) served as the outgroup. Bootstrap values of 50 or higher, obtained from 1000 iterations, are shown at each node. Isolates from this study are in bold.

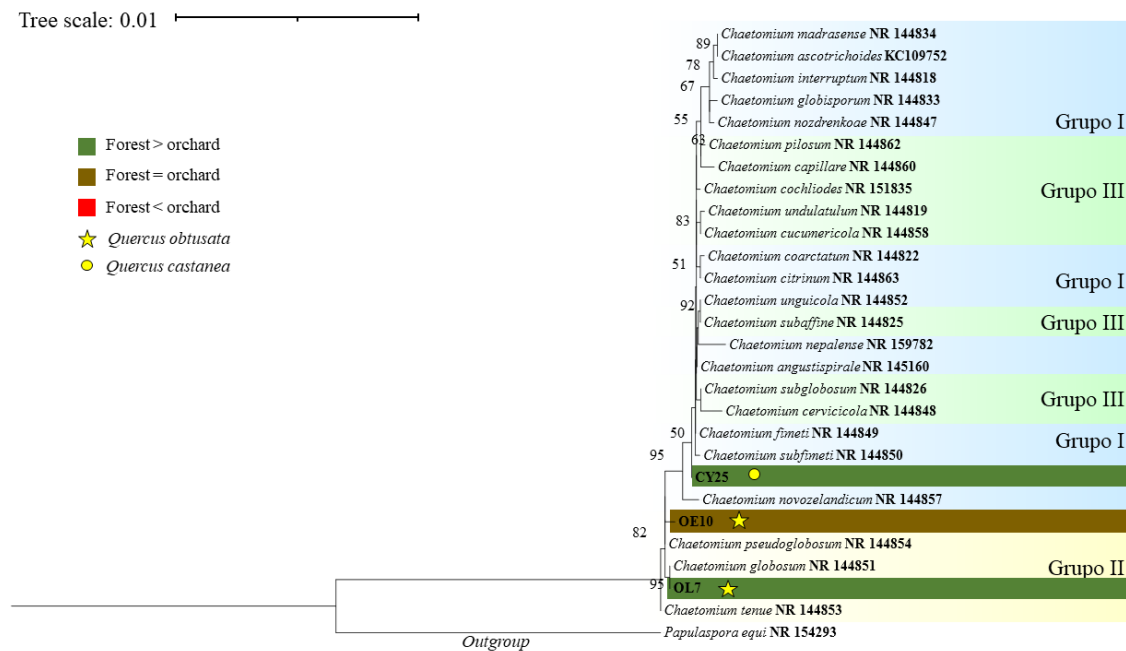


Figure S6. Phylogenetic tree based on ITS sequences of species in the genus *Chaetomium*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the TNe+G4 evolutionary model. *Papulaspora equi* (NR 154293) served as the outgroup. At the ends of the terminal branches, the corresponding Groups of the genus are indicated. Bootstrap values of 50 or higher, obtained from 1000 iterations, are shown at each node. Isolates from this study are in bold.

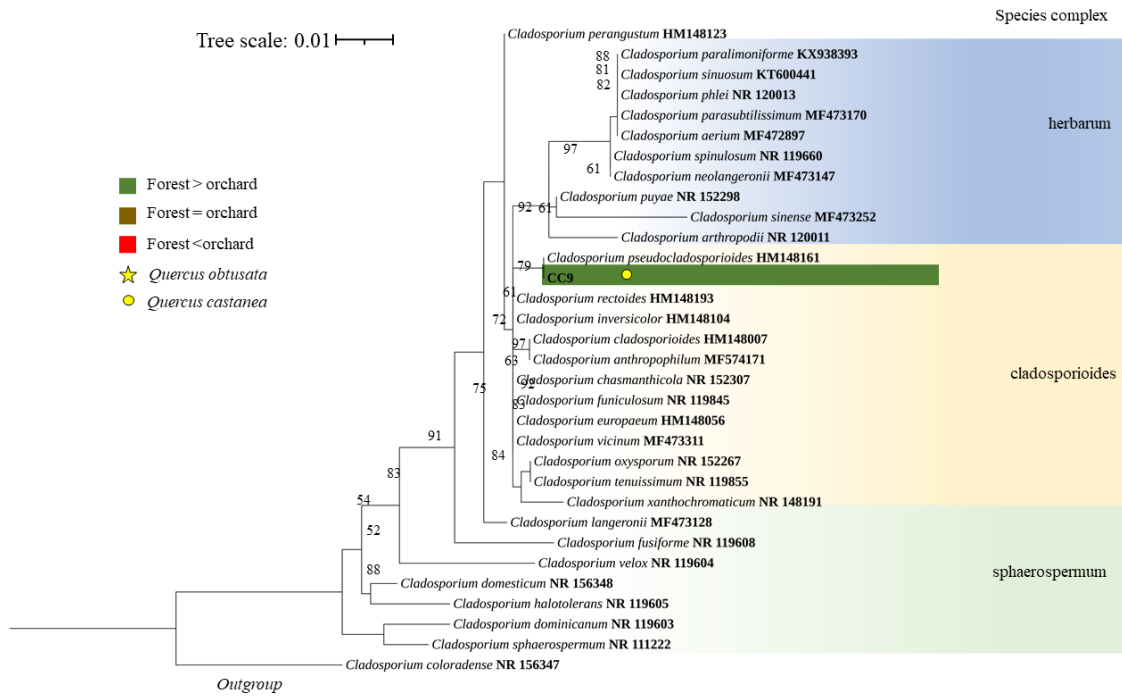


Figure S7. Phylogenetic tree based on ITS sequences of species in the genus *Cladosporium*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the TNe+I+G4 evolutionary model. *Cladosporium coloradense* (NR 156347) served as the outgroup. At the ends of the terminal branches, the corresponding species complexes are indicated. Bootstrap values of 50 or higher, obtained from 1000 iterations, are shown at each node. Isolates from this study are in bold.

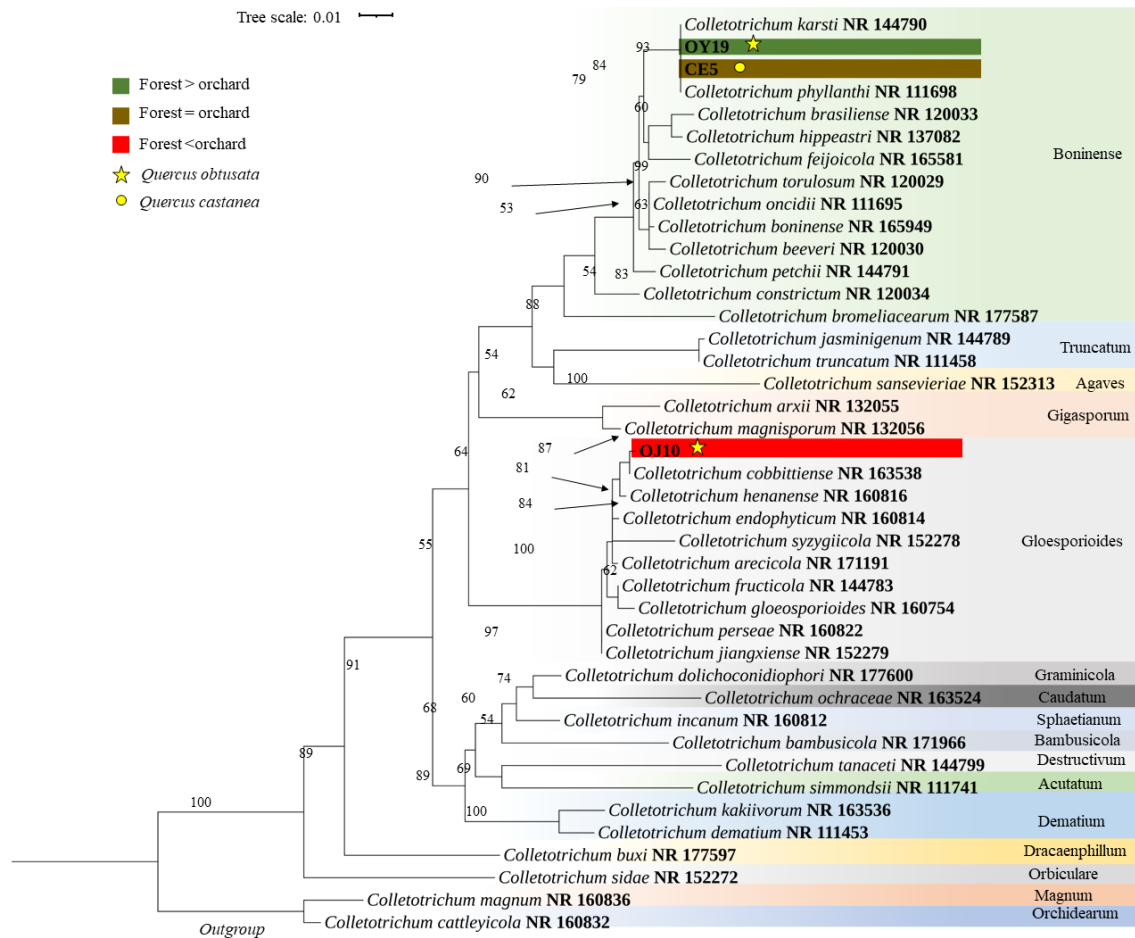


Figure S8. Phylogenetic tree based on ITS sequences of species in the genus *Colletotrichum*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the SYM+I+G4 evolutionary model. *Colletotrichum magnum* (NR 160836) and *Colletotrichum cattleiicola* (NR 160832) served as the outgroup. At the ends of the terminal branches, the corresponding clades of the genus are indicated. Bootstrap values of 50 or higher, obtained from 1000 iterations, are shown at each node. Isolates from this study are in bold.

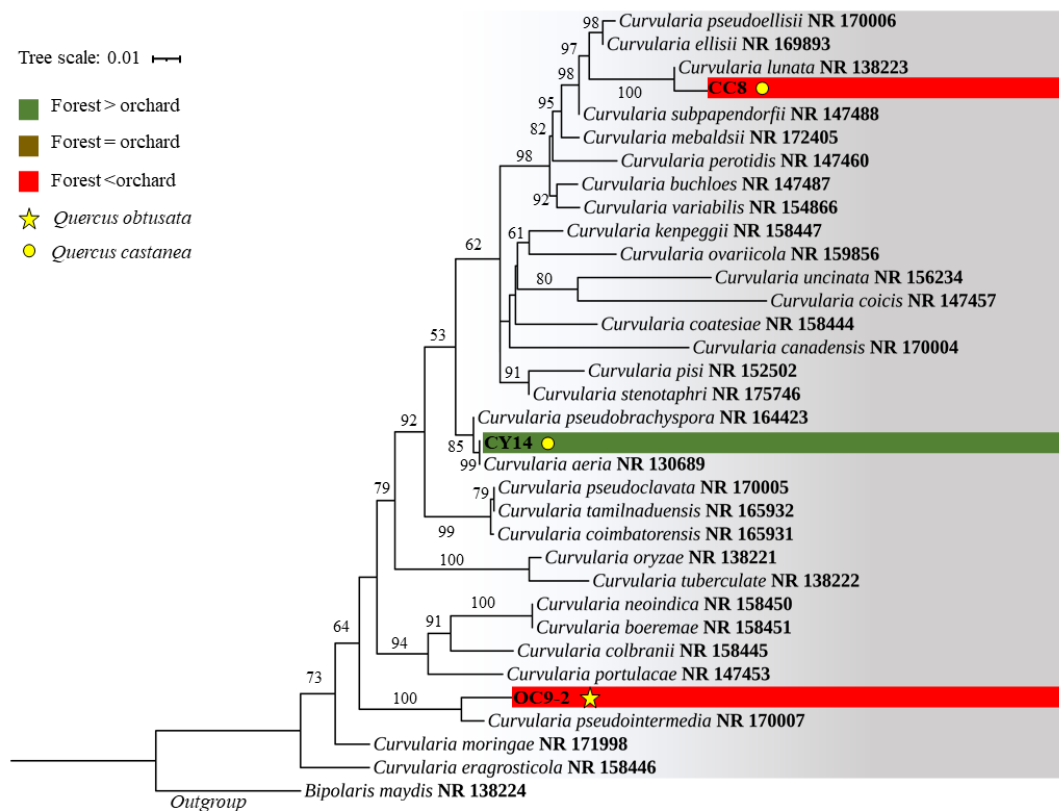


Figure S9. Phylogenetic tree based on ITS sequences of species in the genus *Curvularia*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the TNe+I+G4 evolutionary model. *Bipolaris maydis* (NR 138224) served as the outgroup. Bootstrap values of 50 or higher, obtained from 1000 iterations, are shown at each node. Isolates from this study are in bold.

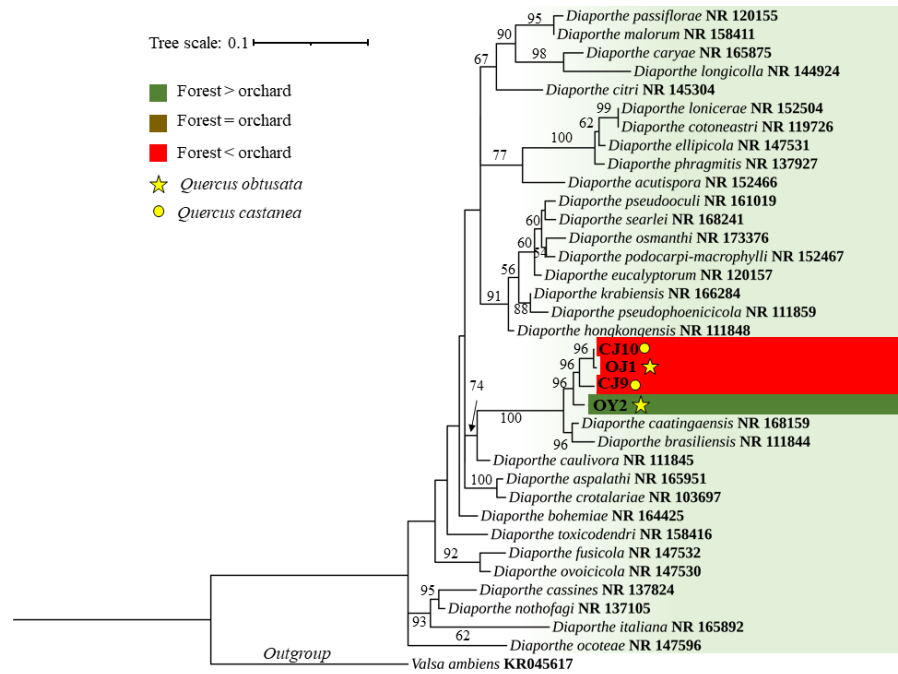


Figure S10. Phylogenetic tree based on ITS sequences of species in the genus *Diaporthe*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the TIM2e+I+G4 evolutionary model. *Valsa ambiens* (KR045617) served as the outgroup. Bootstrap values of 50 or higher, based on 1000 iterations, are shown at each node. Isolates from this study are in bold.

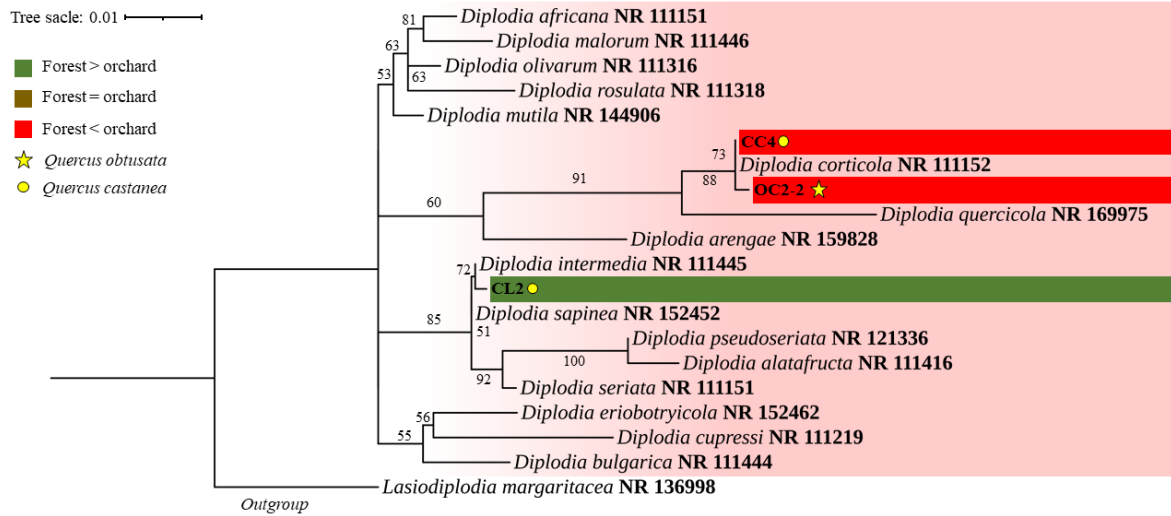


Figure S11. Phylogenetic tree based on ITS sequences of species in the genus *Diplodia*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the K2P+I evolutionary model. *Lasiodiplodia margaritacea* (NR 136998) served as the outgroup. Bootstrap values of 50 or higher, based on 1000 iterations, are shown at each node. Isolates from this study are in bold.

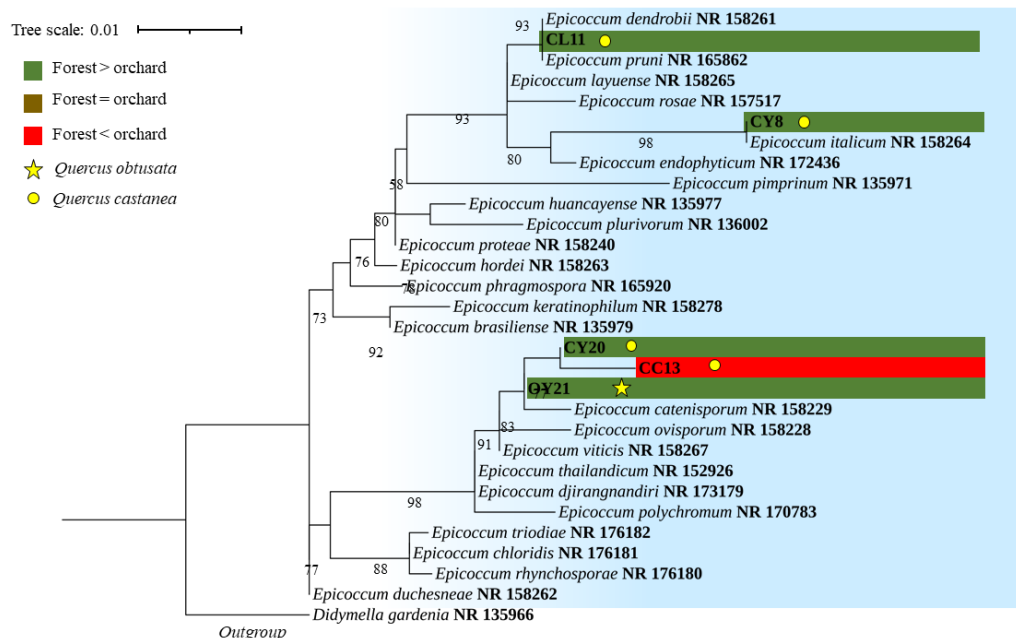


Figure S12. Phylogenetic tree based on ITS sequences of species in the genus *Epicoccum*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the TNe+I evolutionary model. *Didymella gardenia* (NR 135966) served as the outgroup. Bootstrap values of 50 or higher, based on 1000 iterations, are shown at each node. Isolates from this study are in bold.

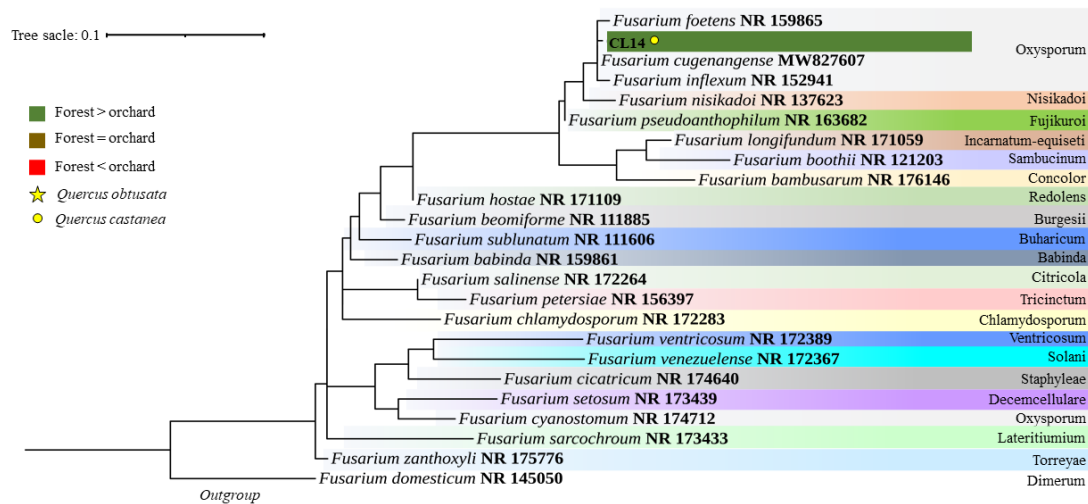


Figure S13. Phylogenetic tree based on ITS sequences of species in the genus *Fusarium*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the TIM2e+I+G4 evolutionary model. *Fusarium domesticum* (NR 145050) served as the outgroup. Bootstrap values of 50 or higher, based on 1000 iterations, are shown at each node. Isolates from this study are in bold.

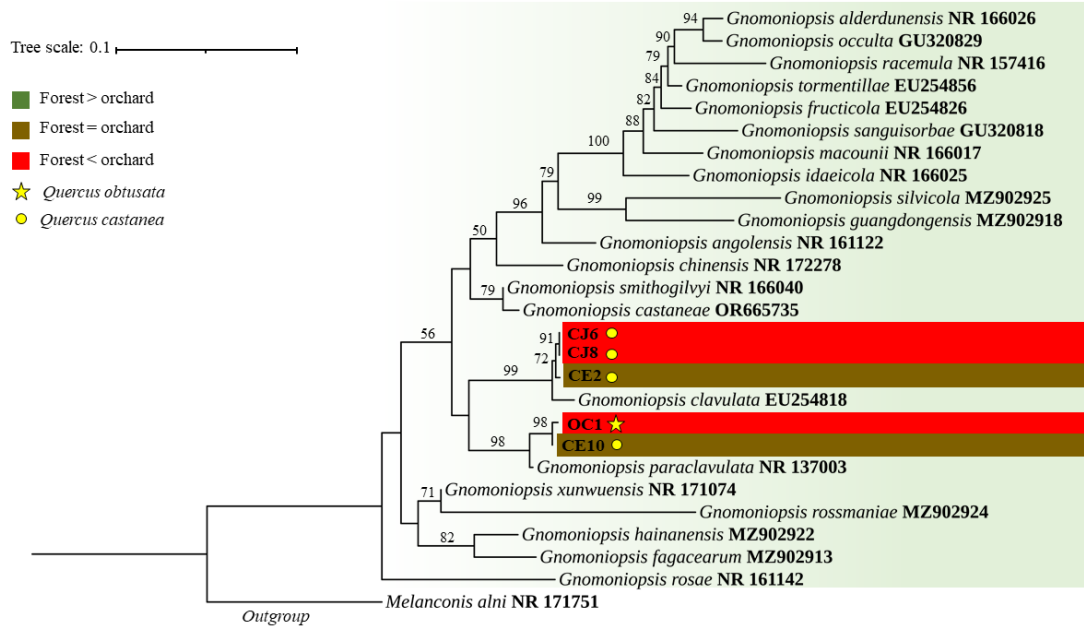


Figure S14. Phylogenetic tree based on ITS sequences of species in the genus *Gnomoniopsis*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the TNe+I+G4 evolutionary model. *Melanconis alni* (NR 171751) served as the outgroup. Bootstrap values of 50 or higher, based on 1000 iterations, are shown at each node. Isolates from this study are in bold.

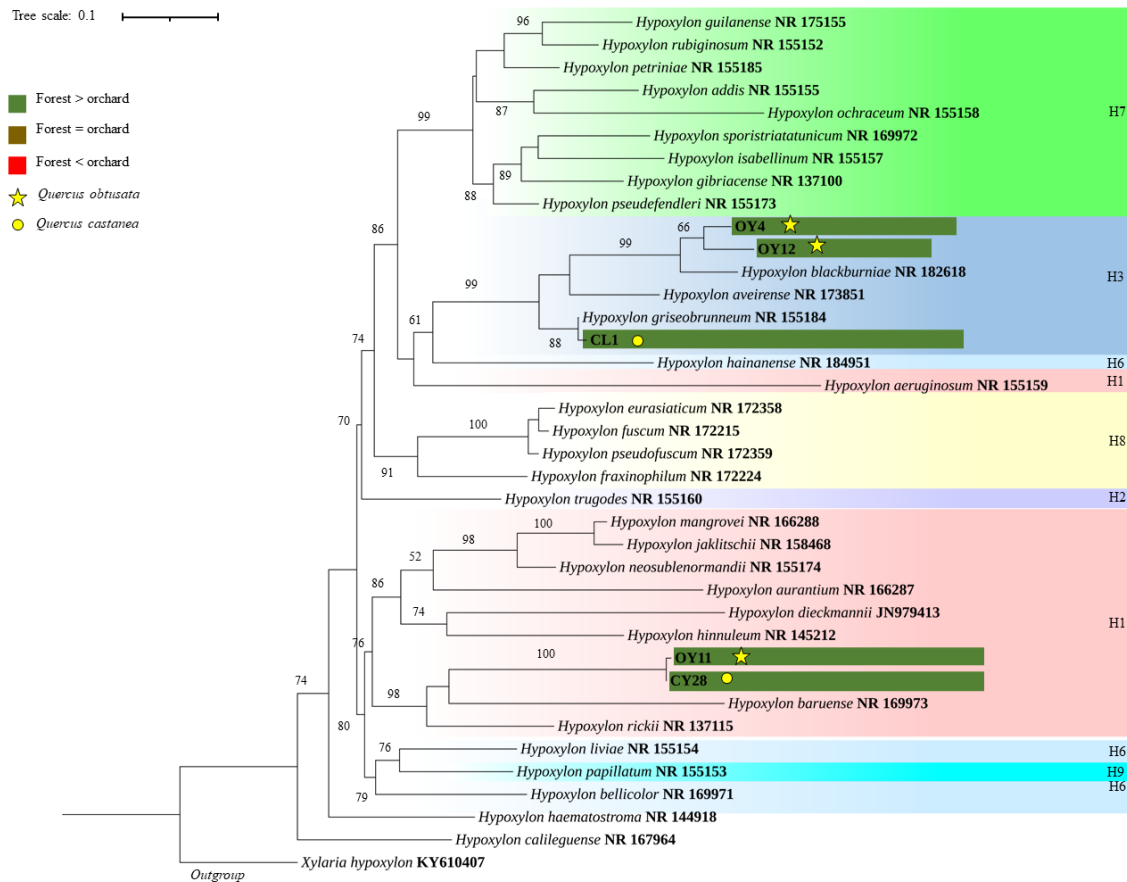


Figure S15. Phylogenetic tree based on ITS sequences of species in the genus *Hypoxylon*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the SYM+I+G4 evolutionary model. *Xylaria hypoxylon* (KY610407) served as the outgroup. At the ends of the terminal branches, the corresponding subclades of the genus are indicated. Bootstrap values of 50 or higher, based on 1000 iterations, are shown at each node. Isolates from this study are in bold.

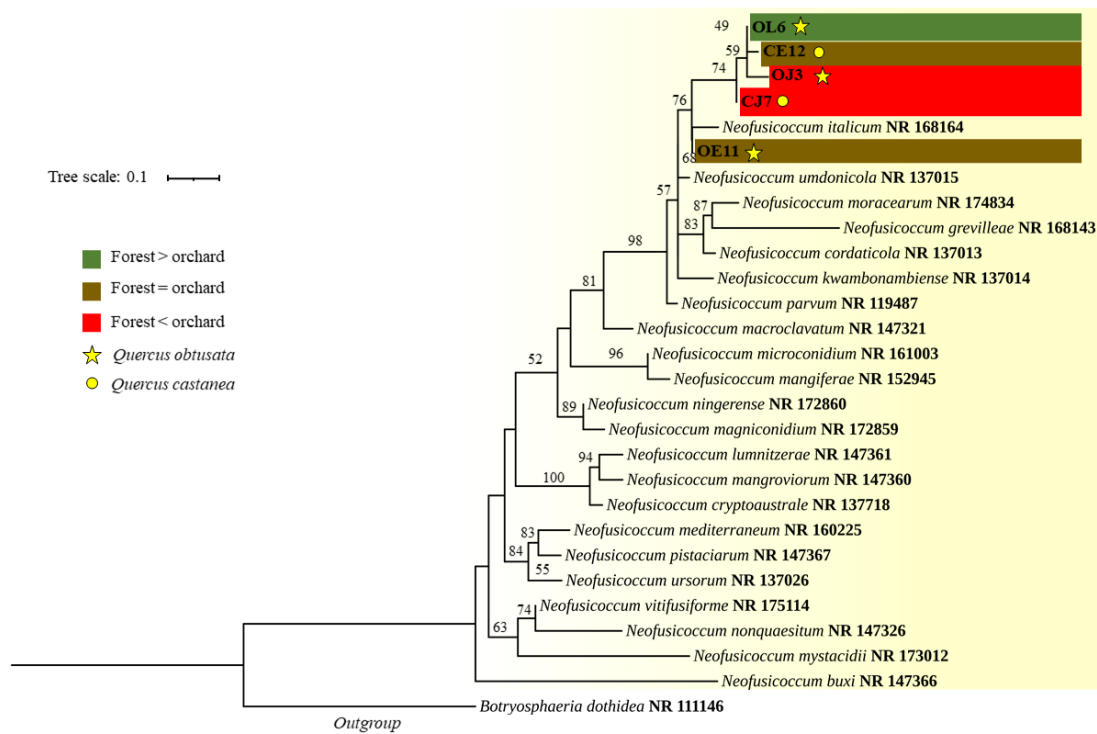


Figure S16. Phylogenetic tree based on ITS sequences of species in the genus *Neofusicoccum*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the TIMe+I+G4 evolutionary model. *Botryosphaeria dothidea* (NR 111146) served as the outgroup. Bootstrap values of 50 or higher, based on 1000 iterations, are shown at each node. Isolates from this study are in bold.

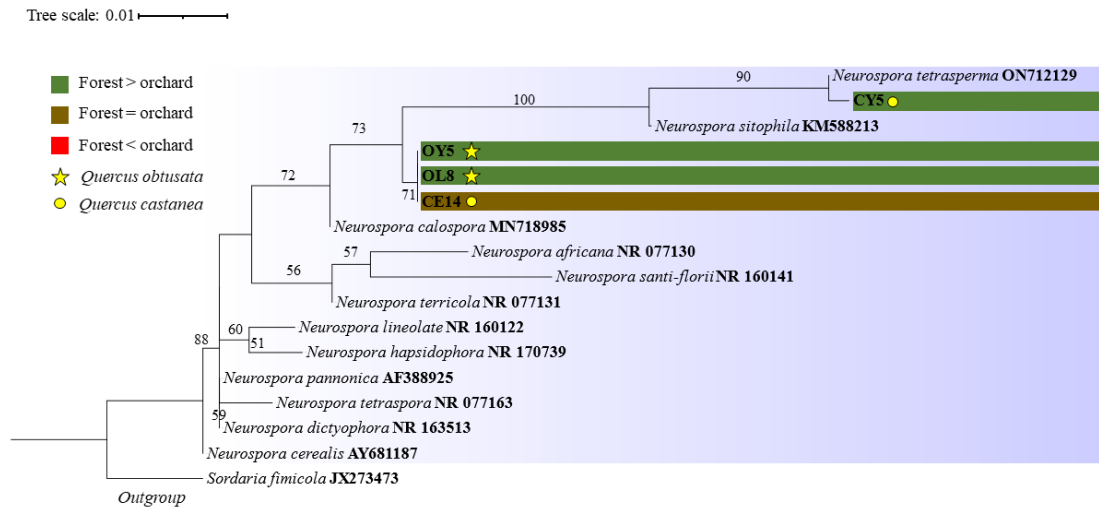


Figure S17. Phylogenetic tree based on ITS sequences of species in the genus *Neurospora*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the K2P+I evolutionary model. *Sordaria fimicola* (NR JX273473) served as the outgroup. Bootstrap values of 50 or higher, based on 1000 iterations, are shown at each node. Isolates from this study are in bold.

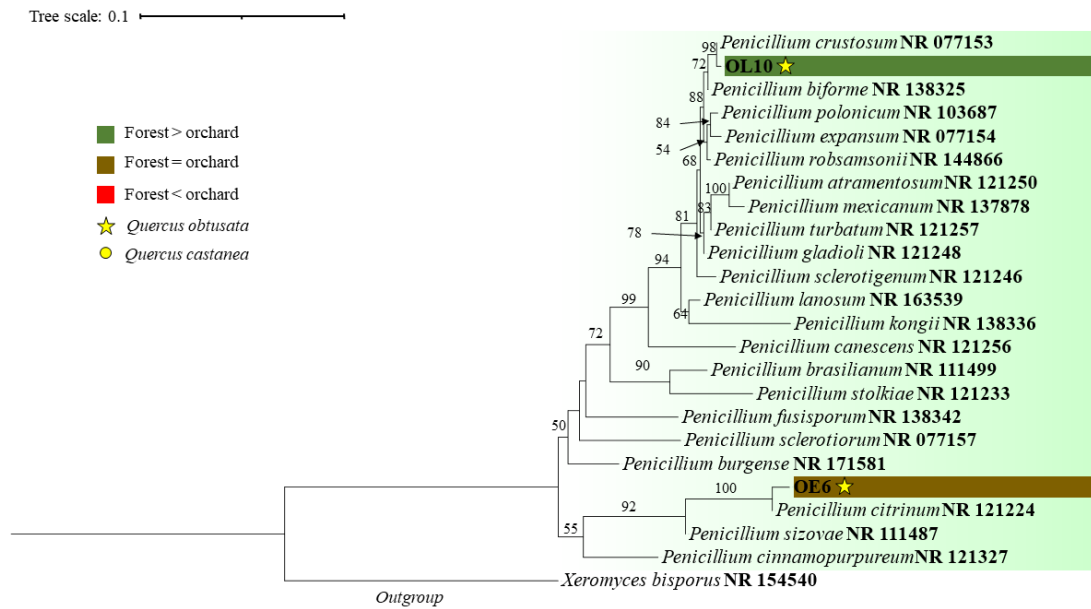


Figure S18. Phylogenetic tree based on ITS sequences of species in the genus *Penicillium*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the evolutionary model $TIN2e+I+G4$. *Xeromyces bisporus* (NR 154540) served as the outgroup. Bootstrap values of 50 or higher, based on 1000 iterations, are shown at each node. Isolates from this study are in bold.

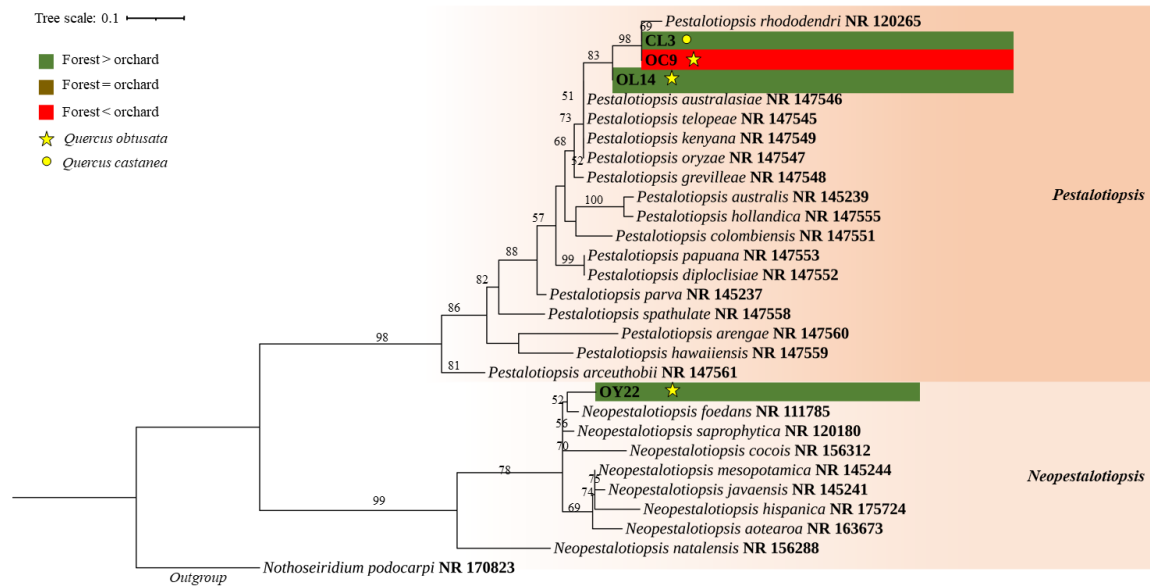


Figure S19. Phylogenetic tree based on ITS sequences of species from the genera *Pestalotiopsis* and *Neopestalotiopsis*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the TIM3e+G4 evolutionary model. *Nothoseridium podocarpi* (NR 170823) served as the outgroup. Bootstrap values of 50 or higher, based on 1000 iterations, are shown at each node. Isolates from this study are in bold.

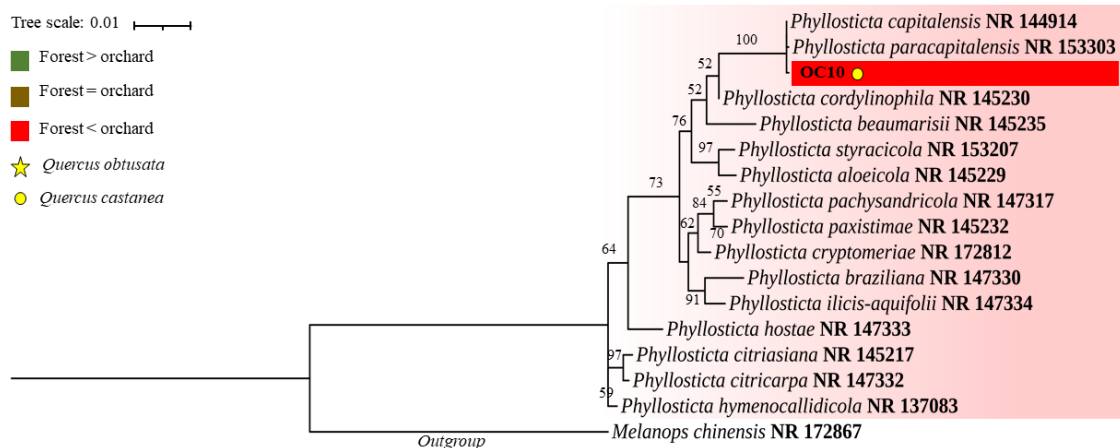


Figure S20. Phylogenetic tree based on ITS sequences of species in the genus *Phyllosticta*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML)

criterion with the TNe+I+G4 evolutionary model. *Melanops chinensis* (NR 172867) served as the outgroup. Bootstrap values of 50 or higher, based on 1000 iterations, are shown at each node. Isolates from this study are in bold.

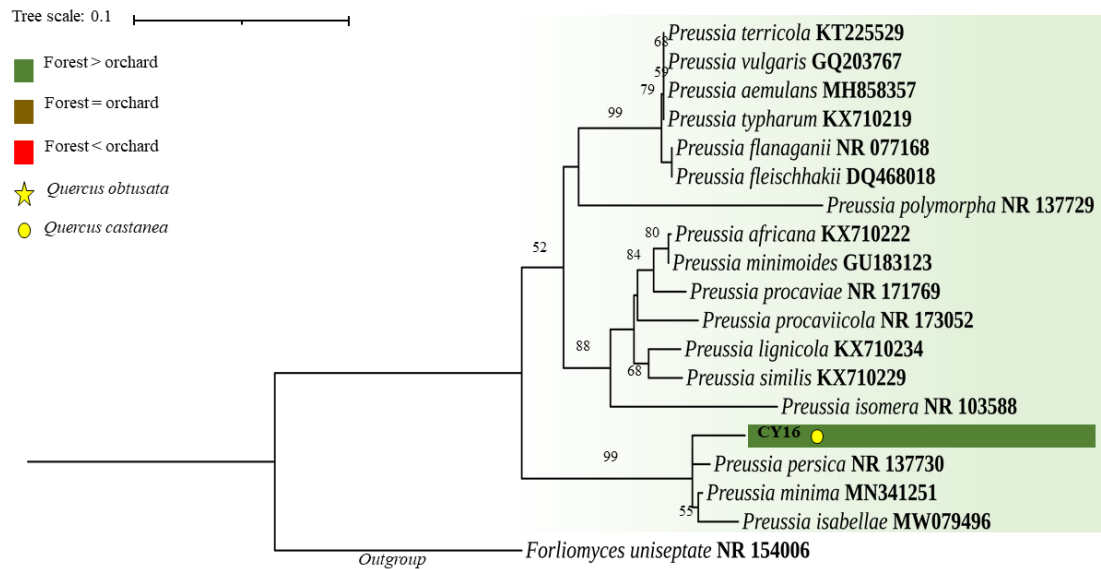


Figure S18. Phylogenetic tree based on ITS sequences of species in the genus *Preussia*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the TNe+I+G4 evolutionary model. *Forliomyces uniseptate* (NR 154006) served as the outgroup. Bootstrap values of 50 or higher, based on 1000 iterations, are shown at each node. Isolates from this study are in bold.

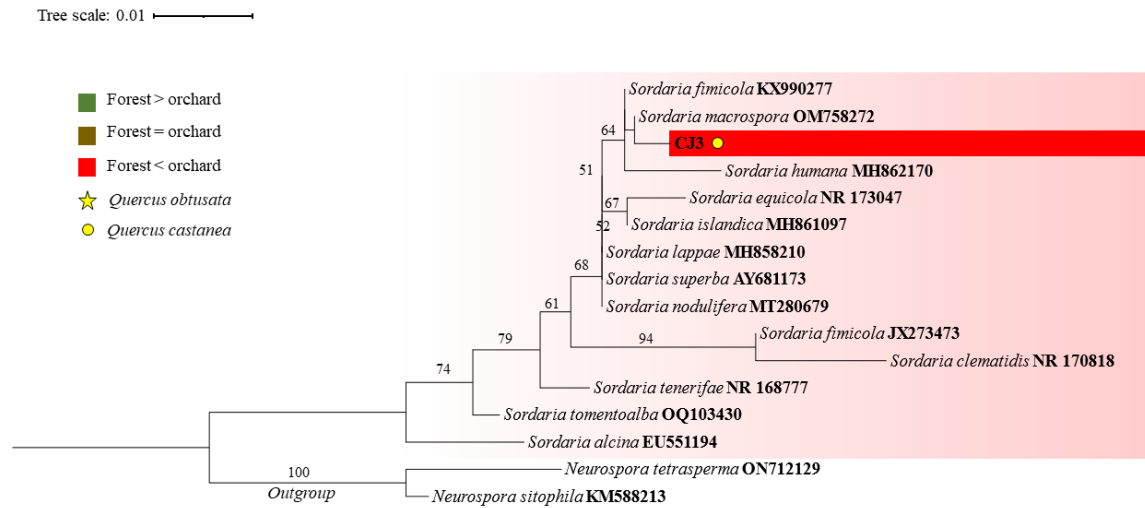


Figure S22. Phylogenetic tree based on ITS sequences of species in the genus *Sordaria*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the TNe+G4 evolutionary model. *Neurospora sitophila* (KM588213) served as the outgroup. Bootstrap values of 50 or higher, based on 1000 iterations, are shown at each node. Isolates from this study are in bold.

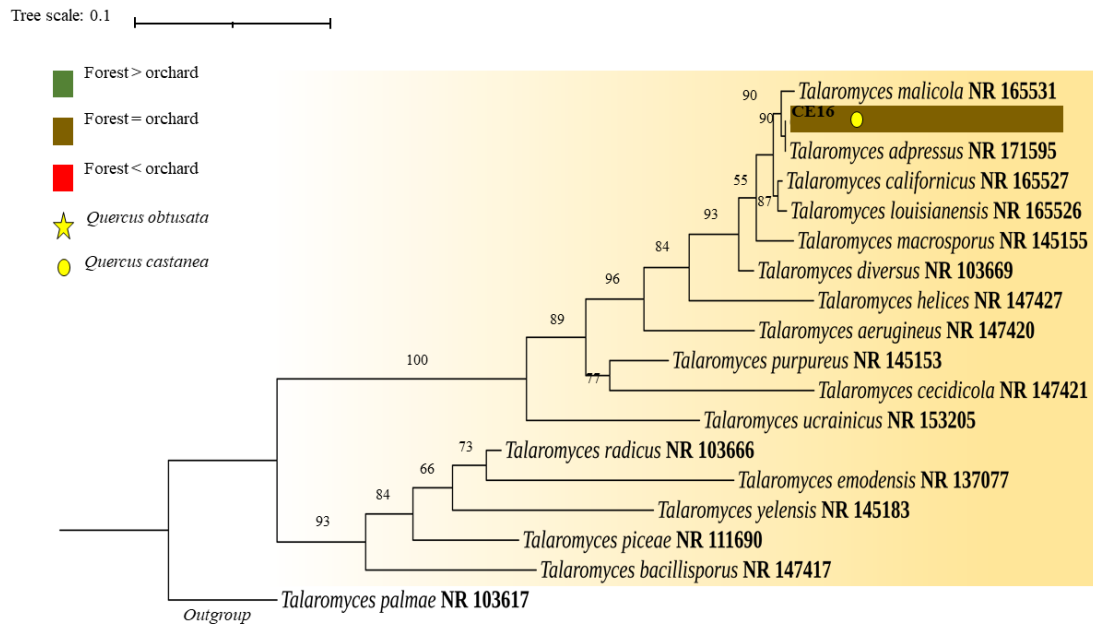


Figure S19. Phylogenetic tree based on ITS sequences of species in the genus *Talaromyces*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the TNe+I+G4 evolutionary model. *Talaromyces palmae* (NR 103617) served as the outgroup. Bootstrap values of 50 or higher, based on 1000 iterations, are shown at each node. Isolates from this study are in bold.

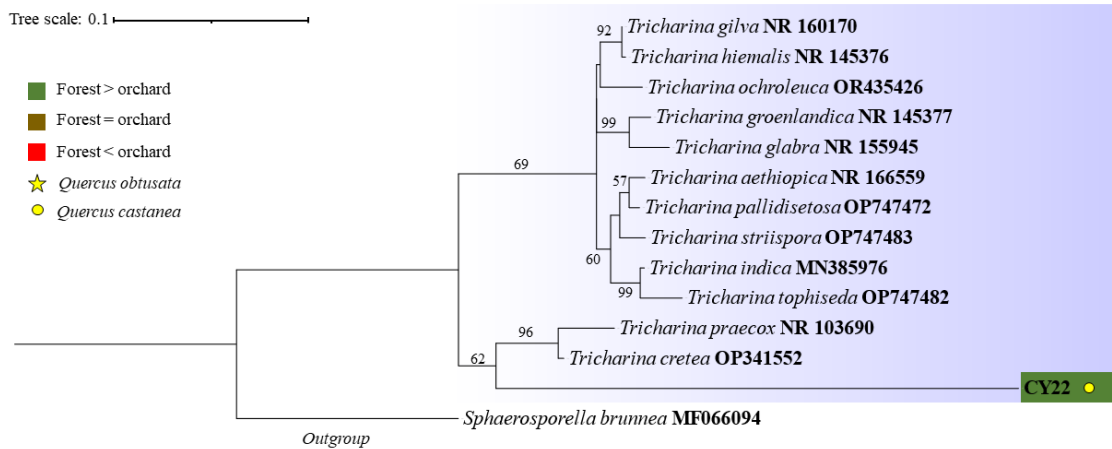


Figure S20. Phylogenetic tree based on ITS sequences of species in the genus *Tricharina*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the TIM2e+I+G4 evolutionary model. *Sphaerospora brunnea* (MF066094)

served as the outgroup. Bootstrap values of 50 or higher, based on 1000 iterations, are shown at each node. Isolates from this study are in bold.

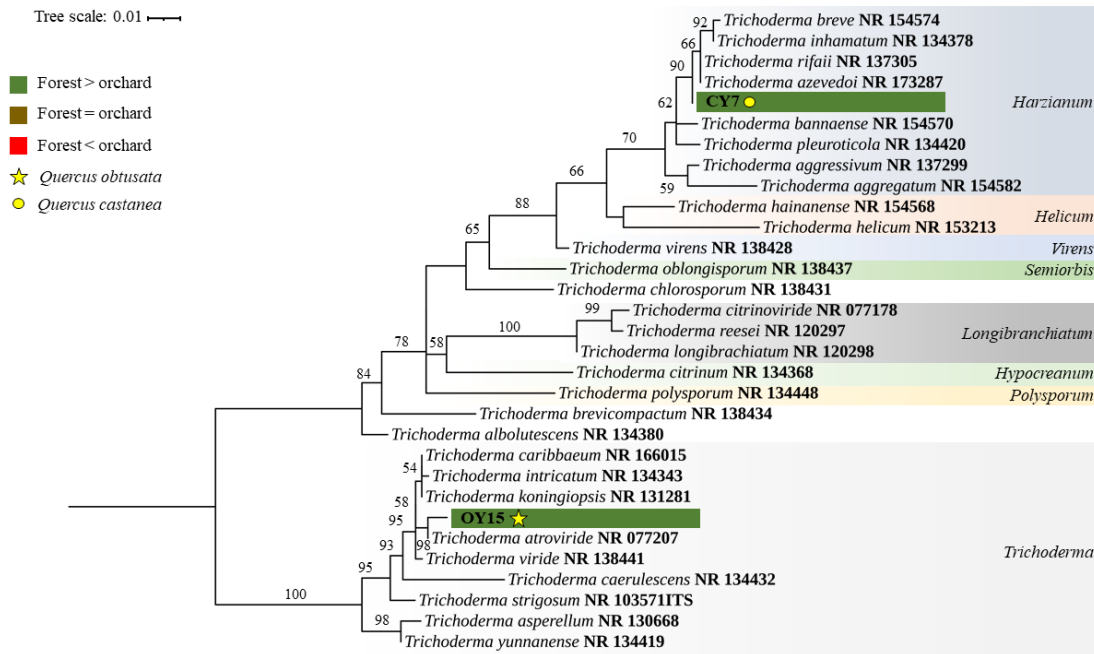


Figure S25. Phylogenetic tree based on ITS sequences of species in the genus *Trichoderma*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the TIM2e+I+G4 evolutionary model. The different *Trichoderma* sections served as outgroups and are shown at the ends of the terminal branches. Bootstrap values of 50 or higher, based on 1000 iterations, are shown at each node. Isolates from this study are in bold.

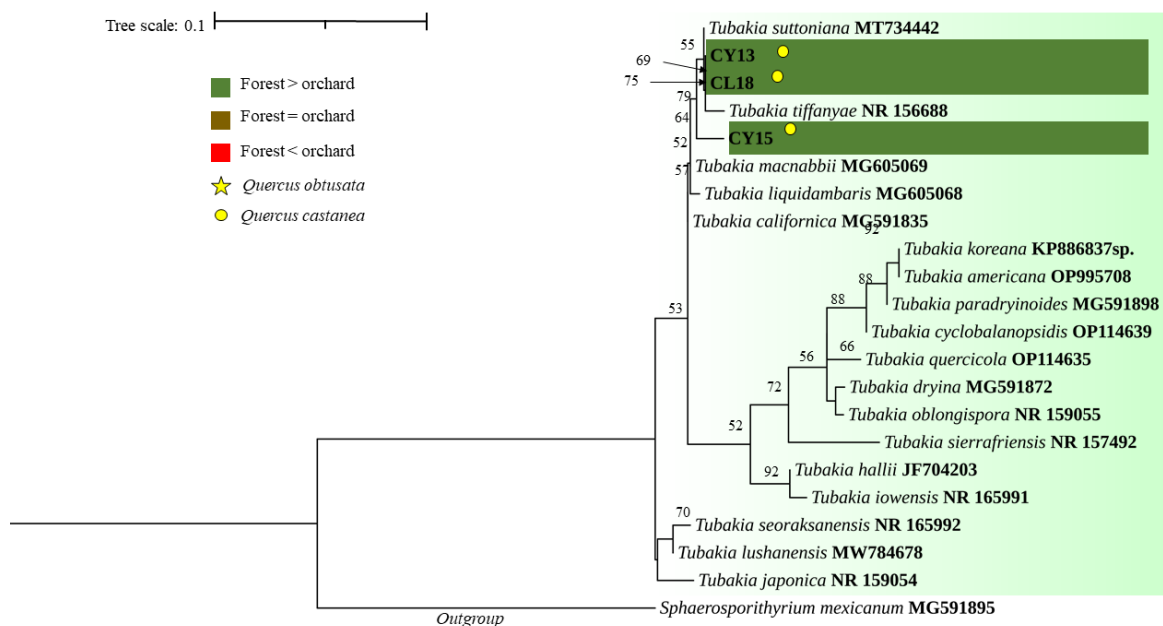


Figure S26. Phylogenetic tree based on ITS sequences of species in the genus *Tubakia*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the TIM2e+I+G4 evolutionary model. *Sphaerosporithyrium mexicanum* (MG591895) served as the outgroup. Bootstrap values of 50 or higher, based on 1000 iterations, are shown at each node. Isolates from this study are in bold.

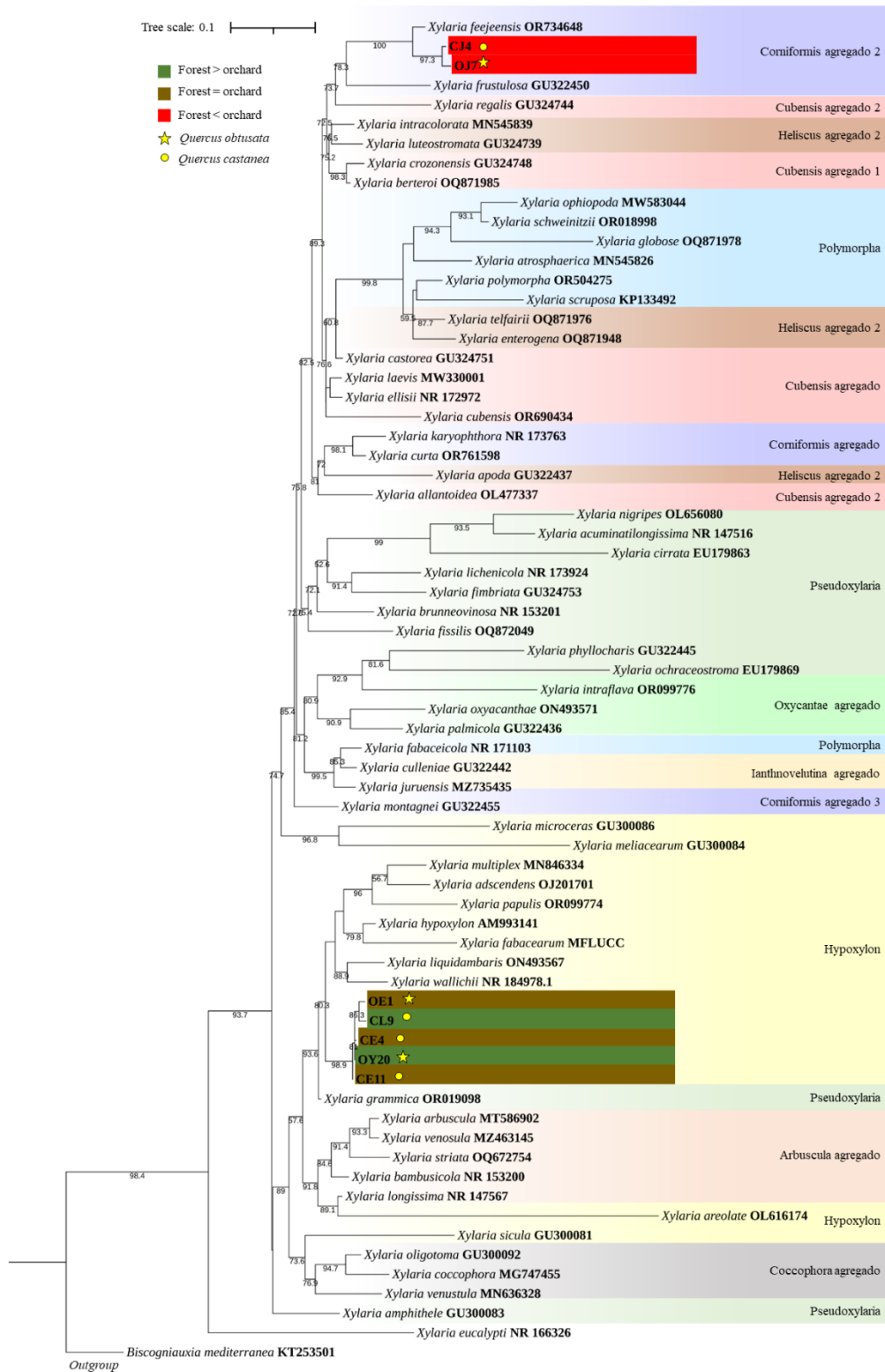


Figure S27. Phylogenetic tree based on ITS sequences of species in the genus *Xylaria*. The phylogenetic reconstruction was performed using the Maximum Likelihood (ML) criterion with the TIM2e+I+G4 evolutionary model. *Biscogniauxia mediterranea* (KT253501) served as the outgroup. At the ends of the terminal branches, the corresponding aggregates of the genus are indicated. Bootstrap values of 50 or higher, based on 1000 iterations, are shown at each node. Isolates from this study are in bold.