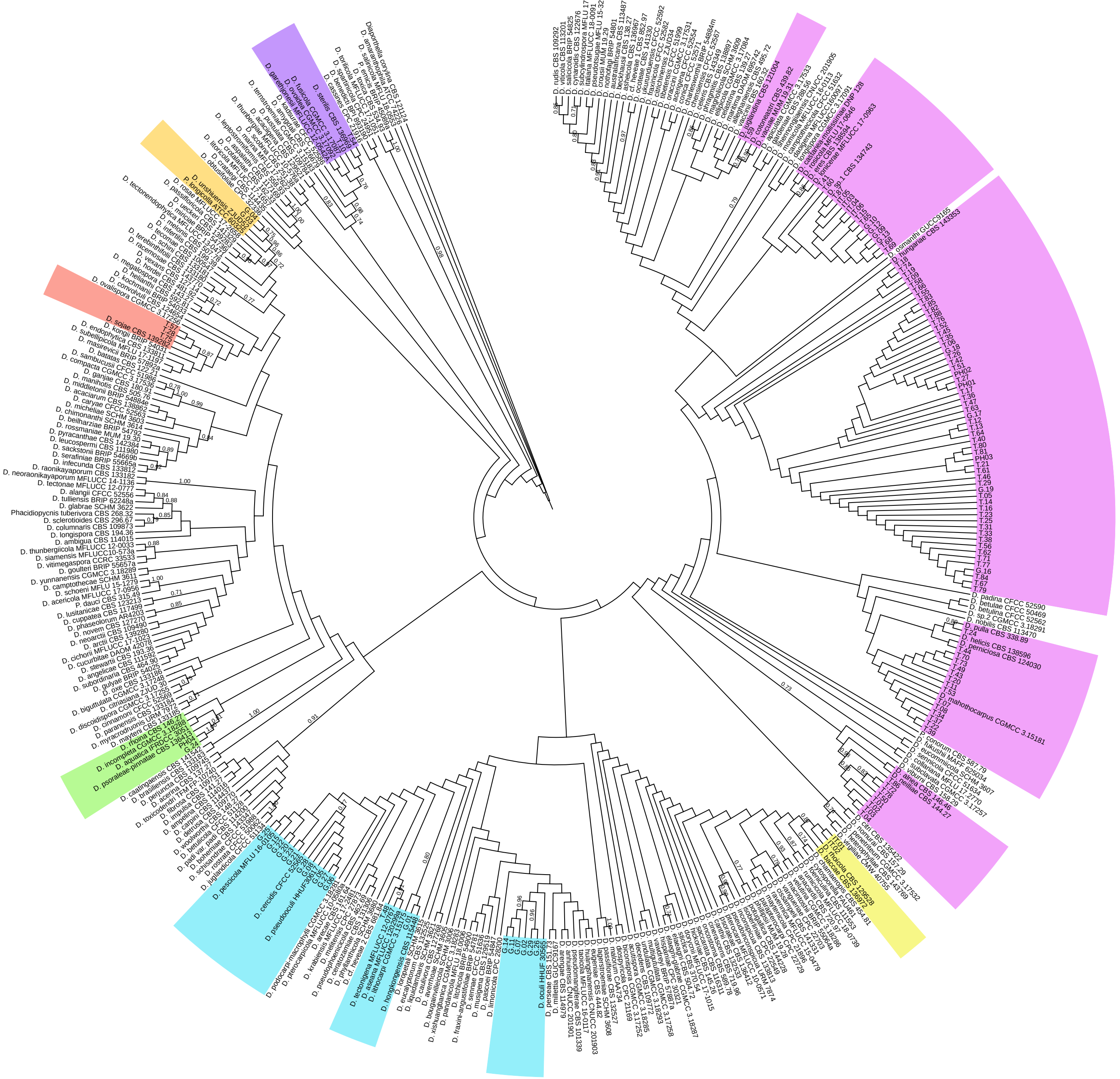
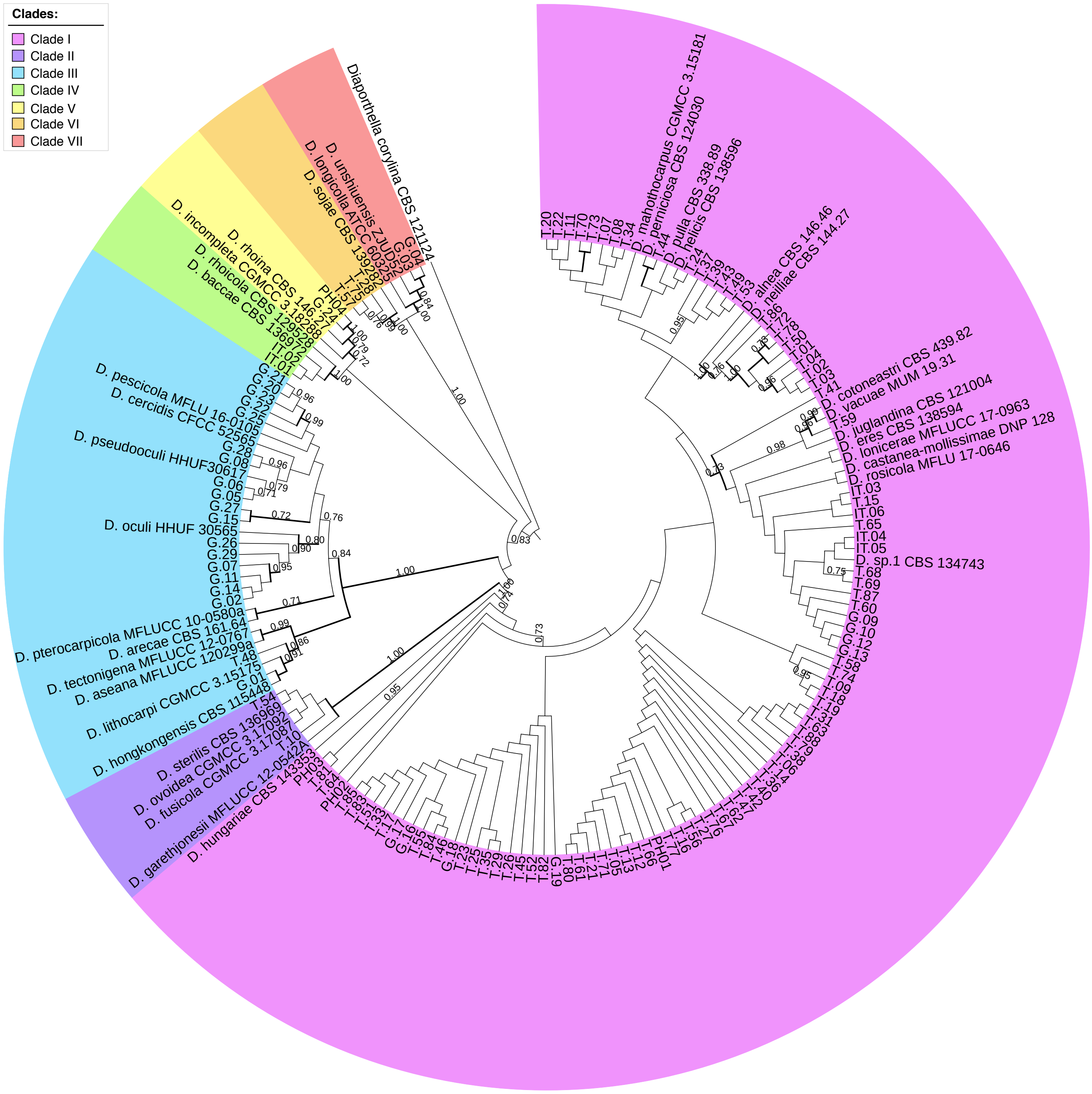


Supplementary Figure 1. Tree branch topology representation of the combined phylogeny for ITS, *EF1-α*, and *tub* sequence data of the 125 strains isolated from hazelnuts with other *Diaporthe* strains selected from the literature and detailed in Supplementary Table 1. *Diaporthella corylina* CBS 121124^{T} was used as the outgroup. Selected model: TN93+G+I. The percentage of trees in which the associated taxa cluster together in the bootstrap test (1,000 replicates) is shown above the branches. All positions with less than 90% site coverage were eliminated. The final dataset included 406 nucleotide sequences and a total of 684 positions.



Supplementary Figure 2. Tree branch topology representation of the tree presented in Figure 3. Combined phylogeny for ITS, *EF1-α*, and *tub* sequence data of the 125 strains isolated from hazelnuts with other *Diaporthe* strains selected from the results presented in Supplementary Figure 1 and detailed in Supplementary Table 1. *Diaporthella corylina* CBS 121124^T was used as the outgroup. Selected model: TN93+G+I. The percentage of trees in which the associated taxa cluster together in the bootstrap test (1,000 replicates) is shown above the branches. Bold branches are supported with ≥ 0.95 Bayesian posterior probability. All positions with less than 95% site coverage were eliminated. The final dataset included 162 nucleotide sequences and a total of 981 positions.