

Figure S1. Phylogram generated from Maximum Likelihood analysis based on combined ITS sequence data from *Diaporthe* species. The ML tree is drawn to scale with branch lengths measured in the number of substitutions per site and rooted to *Diaporthella corylina*. Maximum Likelihood and Maximum Parsimony bootstrap values greater than 70% and posterior probabilities (PPs) inferred by Bayesian analysis greater than 0.80 are shown at the nodes. The ex-type strains are in bold.

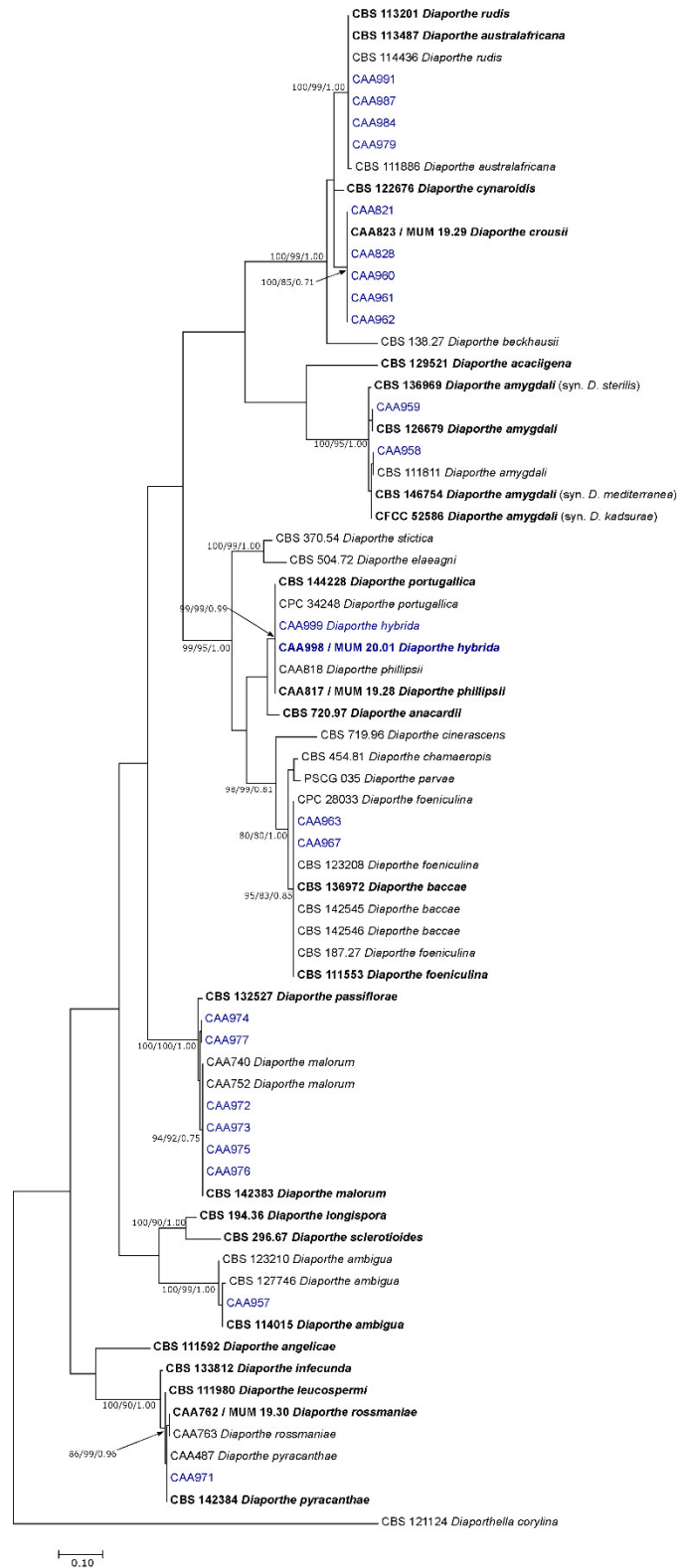


Figure S2. Phylogram generated from Maximum Likelihood analysis based on *tef1-α* sequence data from *Diaporthe* species. The ML tree is drawn to scale with branch lengths measured in the number of substitutions per site and rooted to *Diaporthella corylina*. Maximum Likelihood and Maximum Parsimony bootstrap values greater than 70% and posterior probabilities (PPs) inferred by Bayesian analysis greater than 0.80 are shown at the nodes. The ex-type strains are in bold.

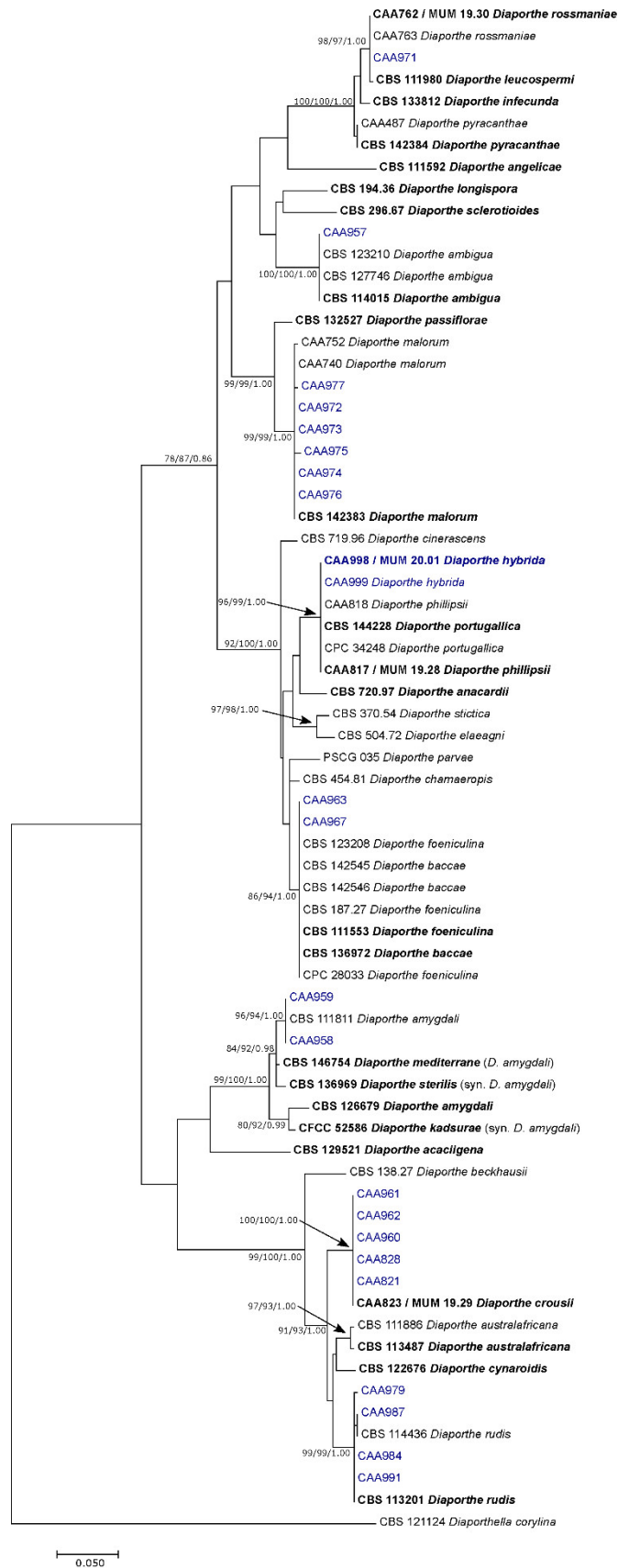


Figure S3. Phylogram generated from Maximum Likelihood analysis based on *tub2* sequence data from *Diaporthe* species. The ML tree is drawn to scale with branch lengths measured in the number of substitutions per site and rooted to *Diaporthella corylina*. Maximum Likelihood and Maximum Parsimony bootstrap values greater than 70% and posterior probabilities (PPs) inferred by Bayesian analysis greater than 0.80 are shown at the nodes. The ex-type strains are in bold.

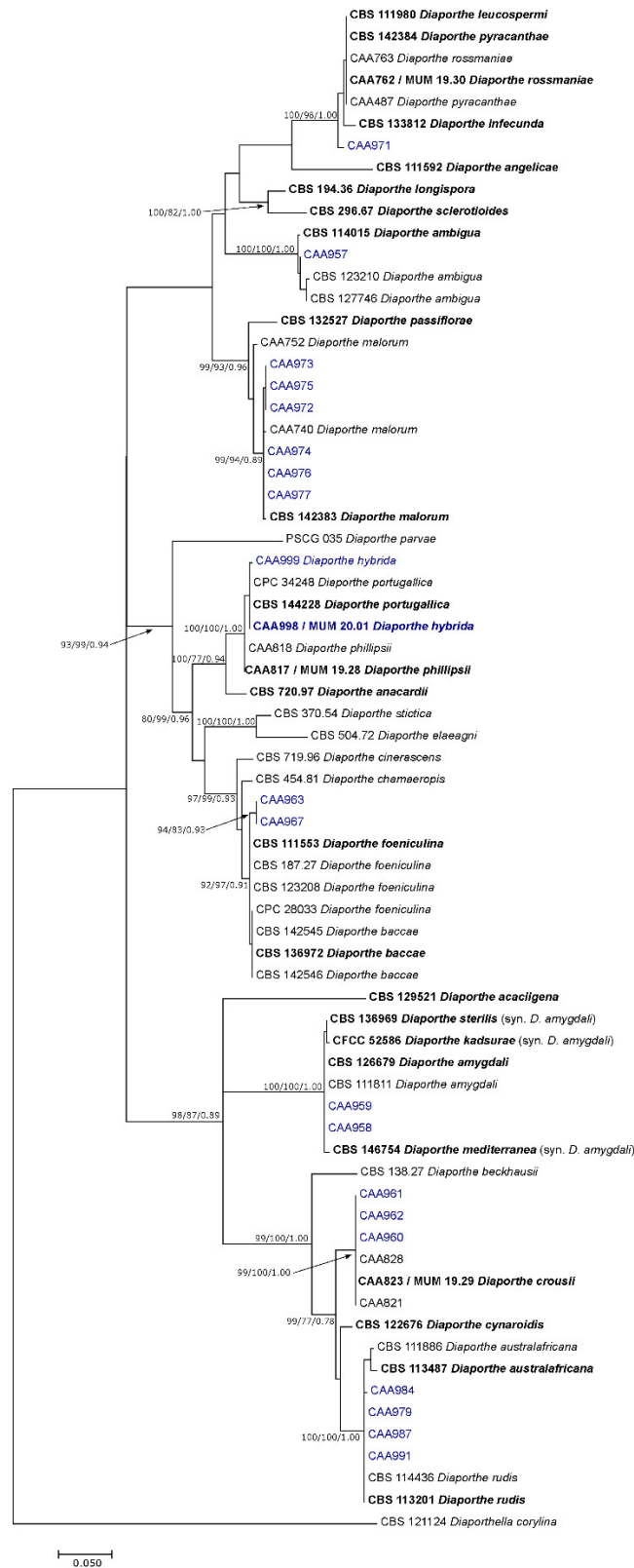


Figure S4. Phylogram generated from Maximum Likelihood analysis based on *cal* sequence data from *Diaporthe* species. The ML tree is drawn to scale with branch lengths measured in the number of substitutions per site and rooted to *Diaporthella corylina*. Maximum Likelihood and Maximum Parsimony bootstrap values greater than 70% and posterior probabilities (PPs) inferred by Bayesian analysis greater than 0.80 are shown at the nodes. The ex-type strains are in bold.

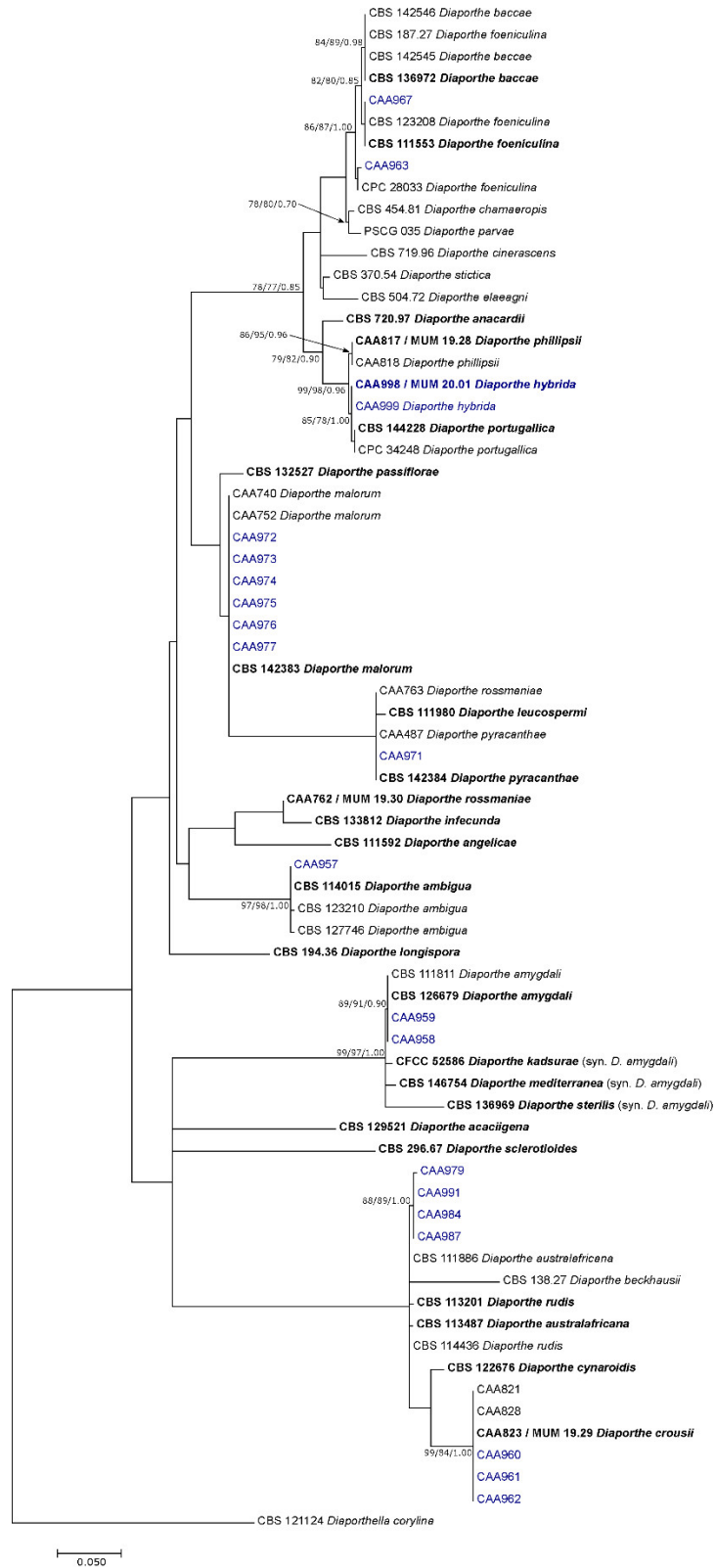


Figure S5. Phylogram generated from Maximum Likelihood analysis based on combined *his3* sequence data from *Diaporthe* species. The ML tree is drawn to scale with branch lengths measured in the number of substitutions per site and rooted to *Diaporthella corylina*. Maximum Likelihood and Maximum Parsimony bootstrap values greater than 70% and posterior probabilities (PPs) inferred by Bayesian analysis greater than 0.80 are shown at the nodes. The ex-type strains are in bold.

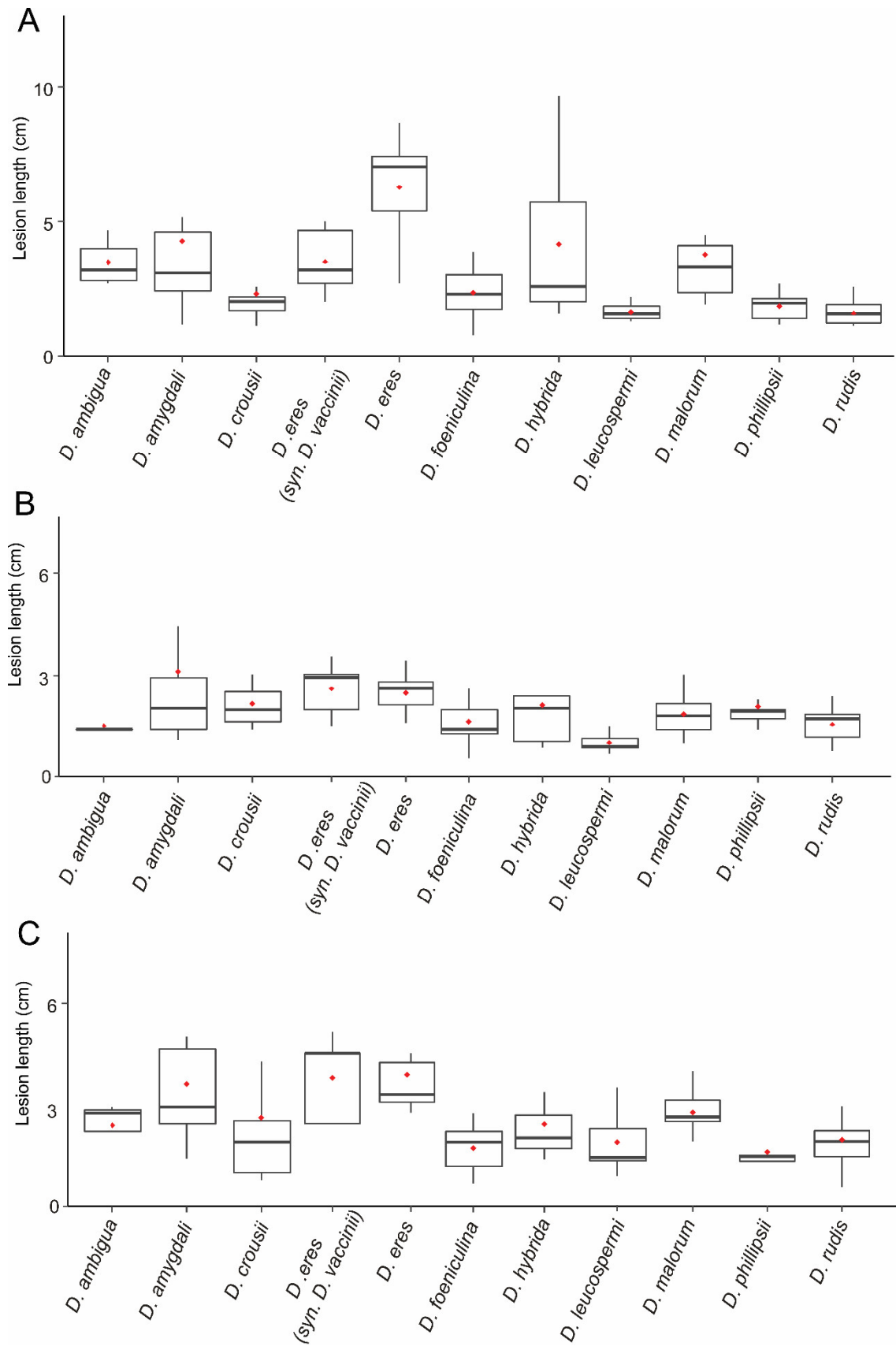


Figure S6. Box plot of lesion length (cm) caused by *Diaporthe* species on twigs of cultivars ‘Duke’ (A), ‘Legacy’ (B) and ‘Spartan’ (C). Black lines in the boxes show medians, and red dots represent the means. Species were compared according to the Wilcoxon rank sum test.

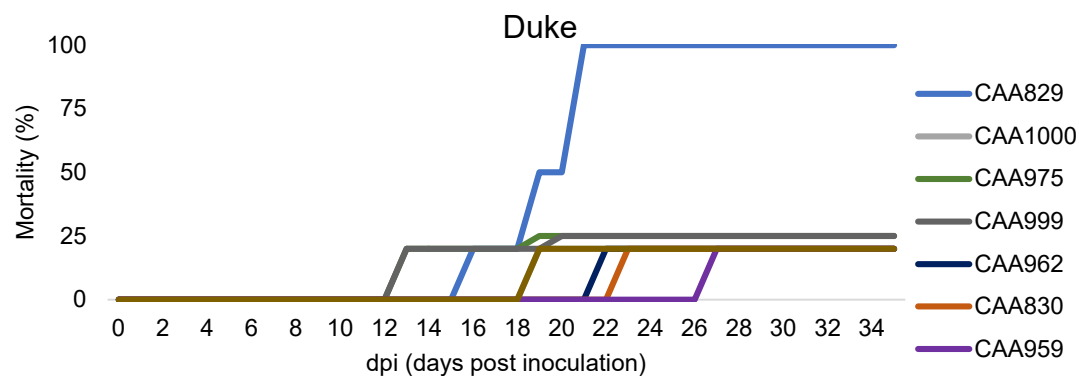


Figure S7. Time course percentage of mortality of Duke cultivar, after inoculation with different isolates.

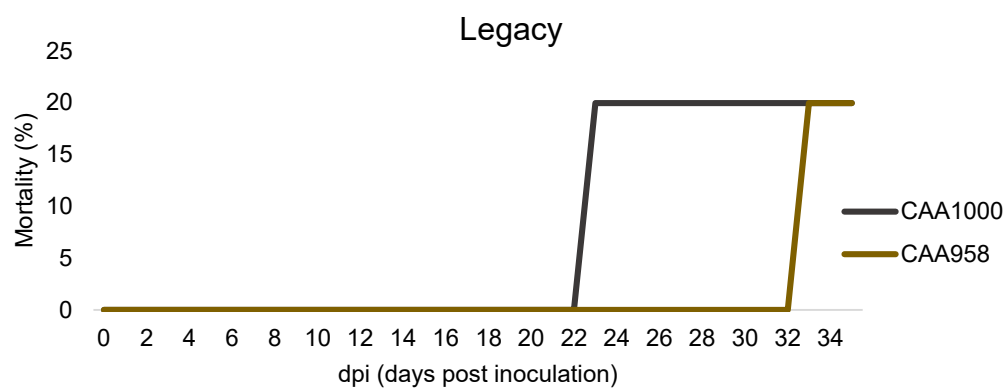


Figure S8. Time course percentage of mortality of Legacy cultivar, after inoculation with different isolates.

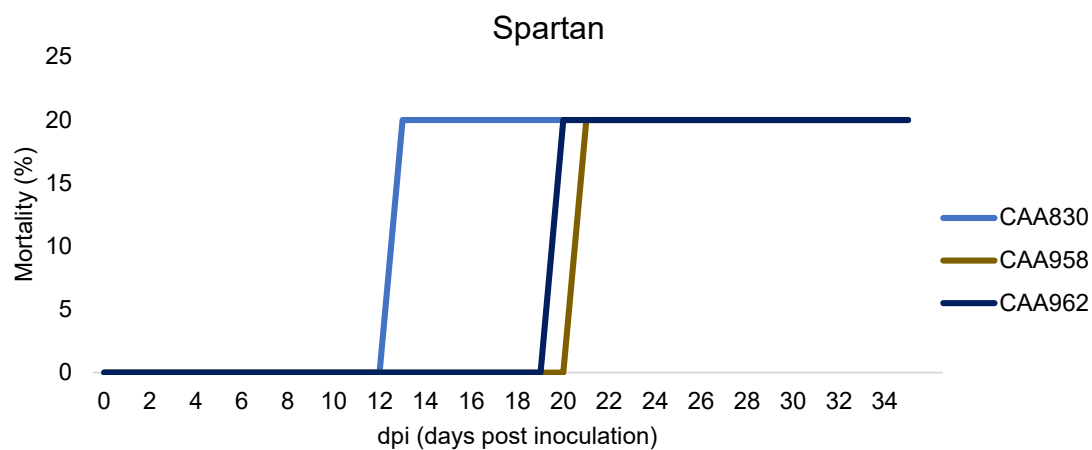


Figure S9. Time course percentage of mortality of Spartan cultivar, after inoculation with different isolates.