

Supplementary figures:

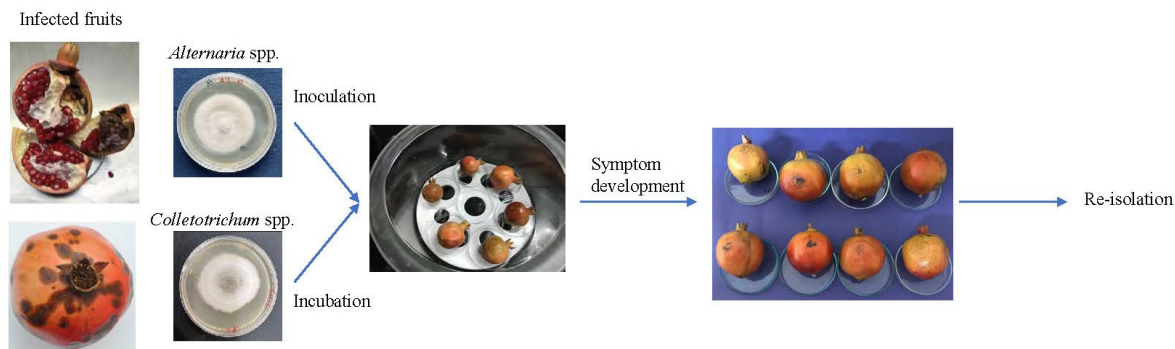


Figure S1. Flowchart depicting steps performed during pathogenicity tests

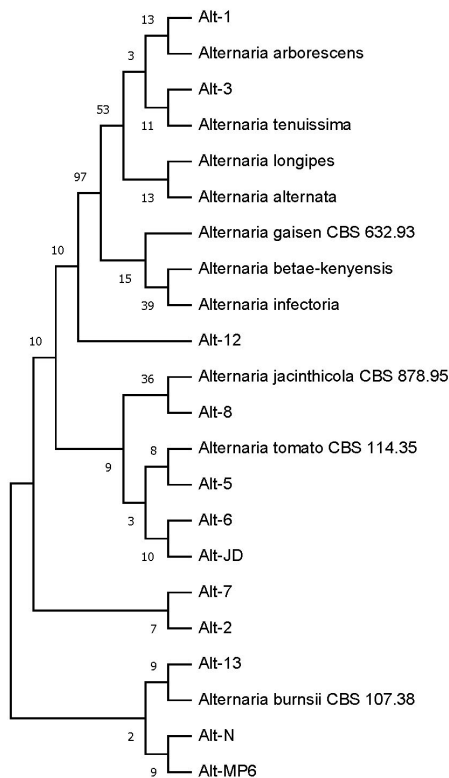


Figure S2. Phylogenetic analysis using elongation factor (*TEF-α*) gene amplified and sequenced from *Alternaria* isolates. Maximum Likelihood tree drawn using MEGA XI with 1000 bootstrap

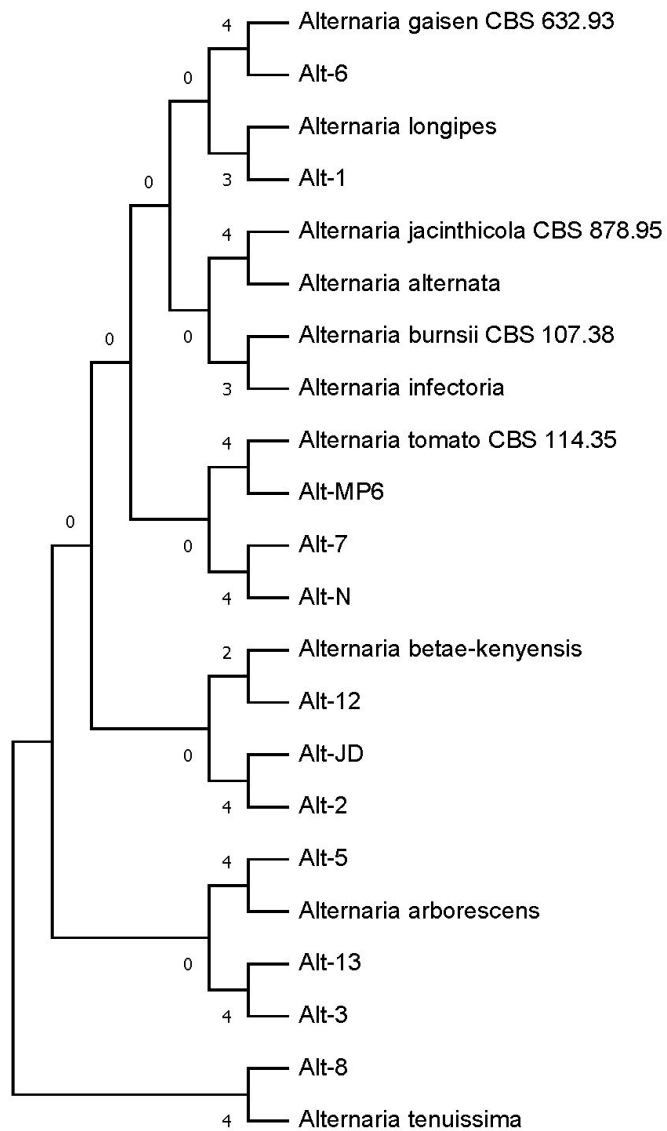


Figure S3. Phylogenetic analysis using *ITS* region amplified and sequenced from *Alternaria* isolates. Maximum Likelihood tree drawn using MEGA XI with 1000 bootstrap

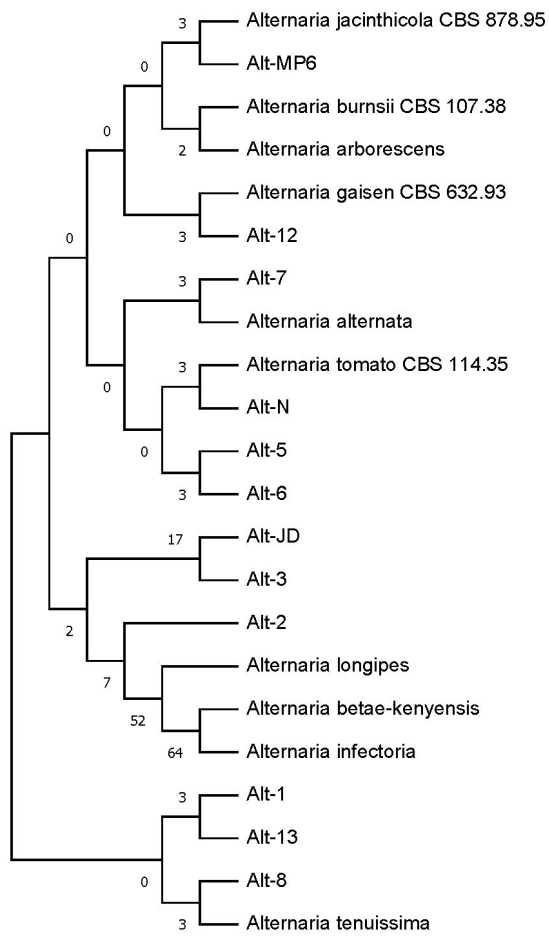


Figure S4. Phylogenetic analysis using nuclear ribosomal large subunit (LSU) region amplified and sequenced from *Alternaria* isolates. Maximum Likelihood tree drawn using MEGA XI with 1000 bootstrap