C. Bregant, F. Carloni, M. Balestra, B.T. Linaldeddu, S. Murolo (2023) Pathogenicity of *Botryosphaeriaceae* and *Phytophthora* species associated with *Paulownia* dieback, canker and root rot in Italy. *Phytopathologia Mediterranea* 62(3): 381–412. doi: 10.36253/phyto-14910

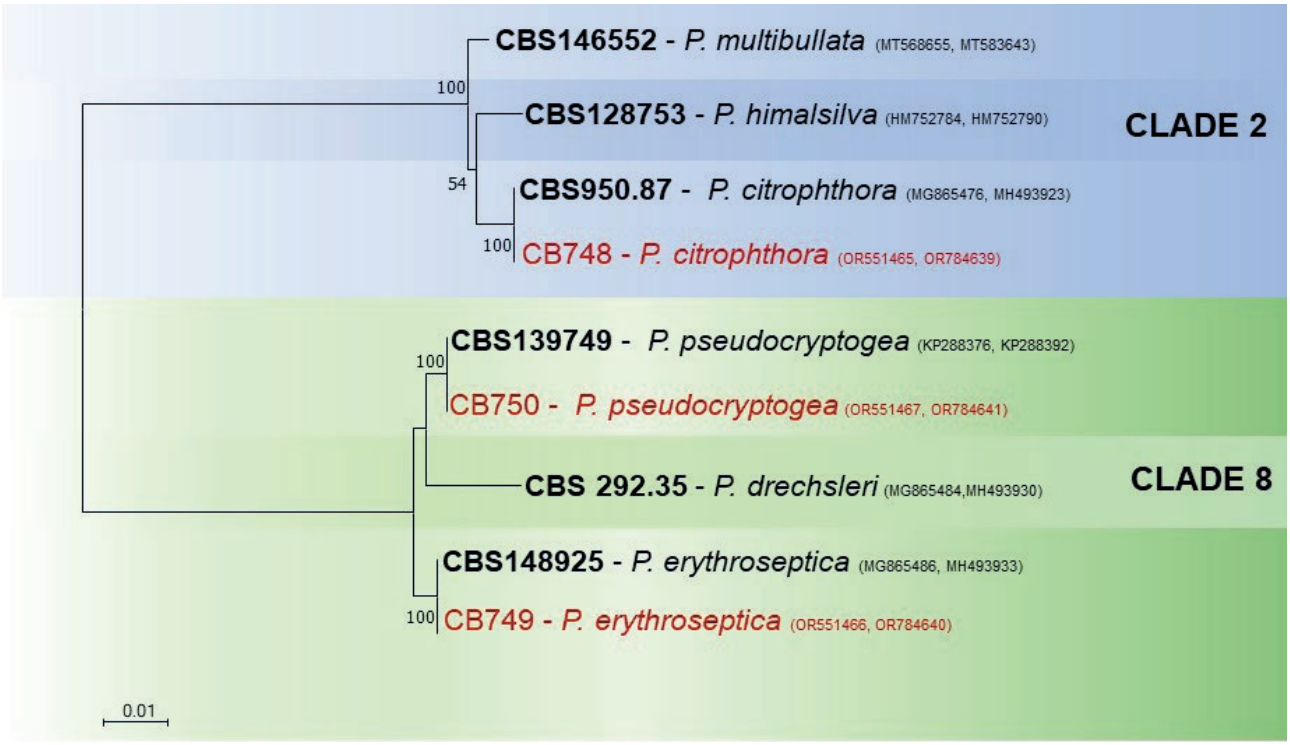

Figure S1. Maximum likelihood tree obtained from concatenated internal transcribed spacer (ITS) and beta tubulin (Btub) sequences of *Phytophthora* species. Data are based on the General Time Reversible model. A discrete Gamma distribution was used to model evolutionary rate differences among sites. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Bootstrap support values in percentage (1000 replicates) are given at the nodes. Ex-type cultures are in bold, and isolates obtained in this study in red. GenBank accession numbers are in brackets.

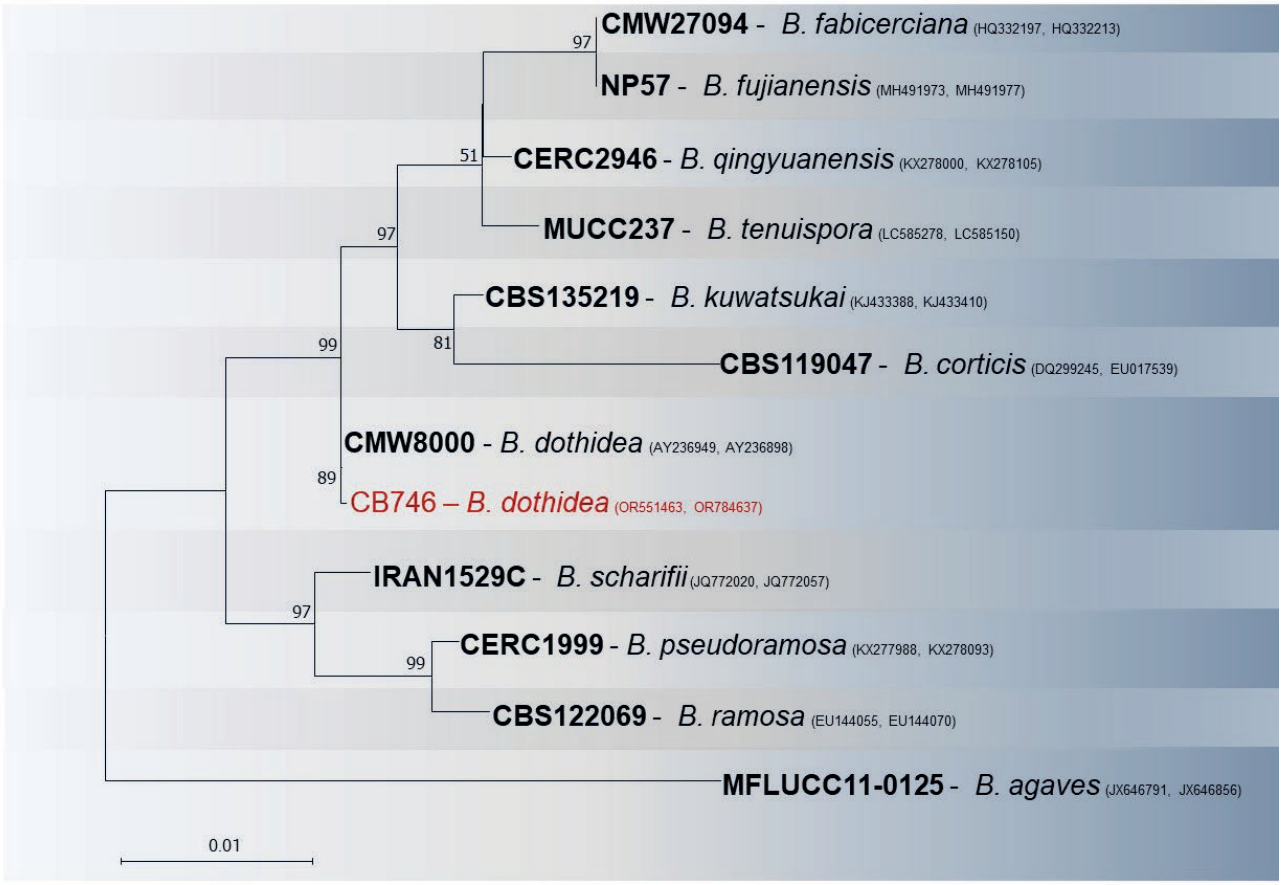

Figure S2. Maximum likelihood tree obtained from concatenated internal transcribed spacer (ITS) and transcription elongation factor (*tef1-α*) sequences of *Botryosphaeria* species. Data are based on the General Time Reversible model. A discrete Gamma distribution was used to model evolutionary rate differences among sites. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Bootstrap support values in percentage (1000 replicates) are given at the nodes. Ex-type cultures are in bold, and isolates obtained in this study in red. GenBank accession numbers are in brackets.

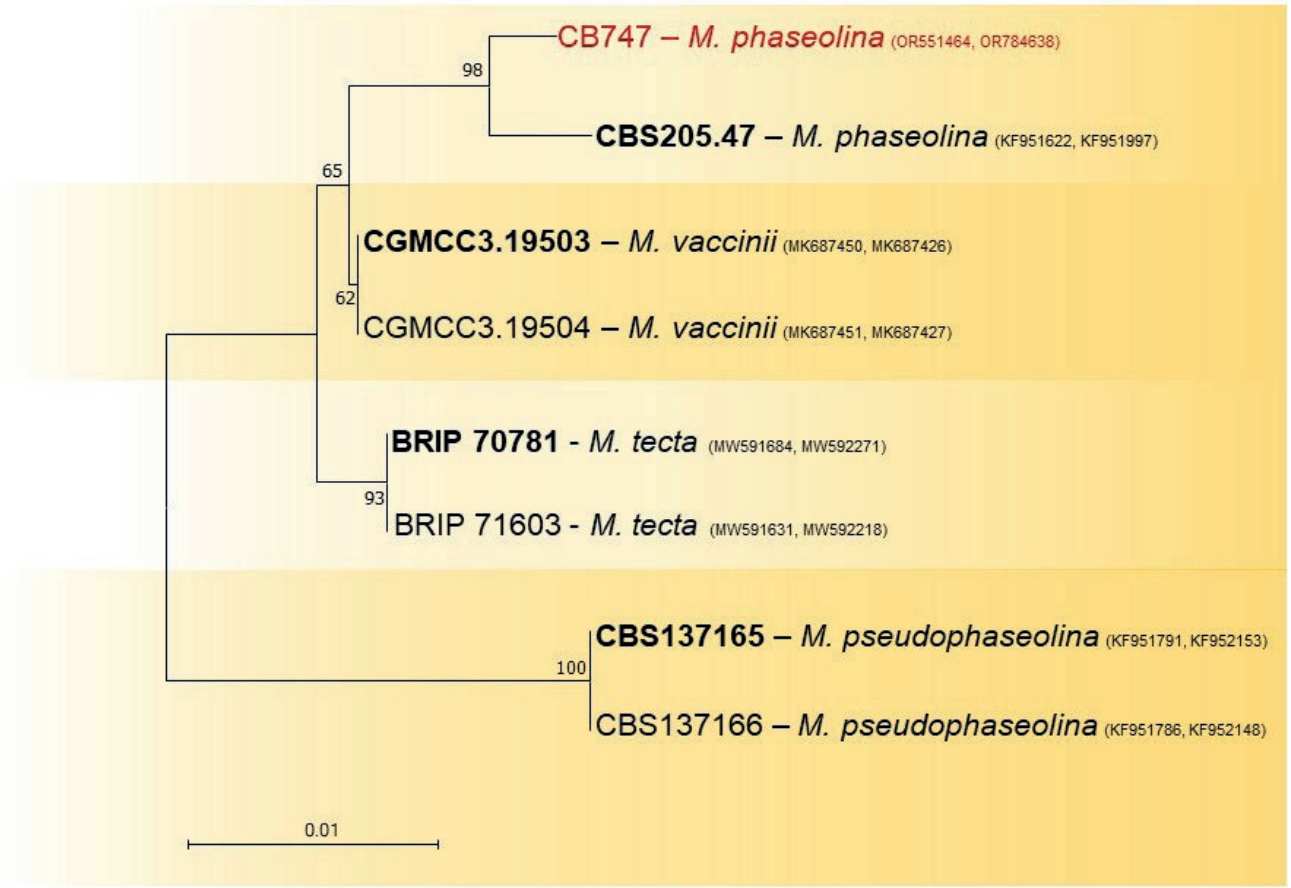

Figure S3. Maximum likelihood tree obtained from concatenated internal transcribed spacer (ITS) and transcription elongation factor (*tef1-α*) sequences of *Macrophomina* species. Data are based on the General Time Reversible model. A discrete Gamma distribution was used to model evolutionary rate differences among sites. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Bootstrap support values in percentage (1000 replicates) are given at the nodes. Ex-type cultures are in bold, and isolates obtained in this study in red. GenBank accession numbers are in brackets.