

Supplementary files

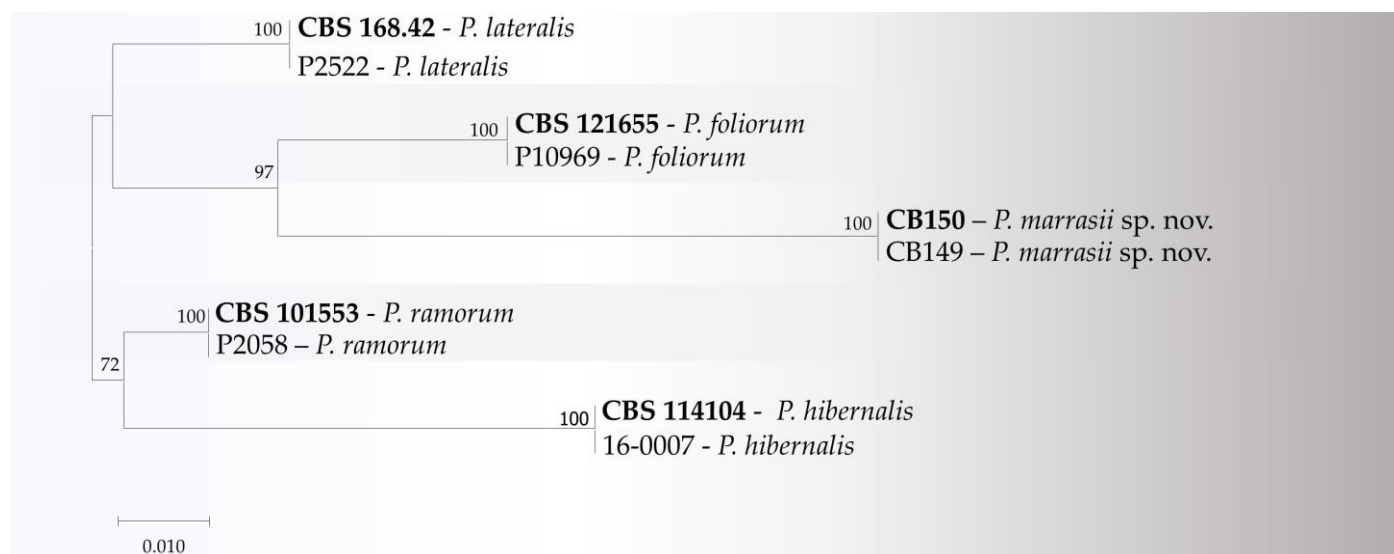


Figure S1. Maximum likelihood tree obtained from concatenated ITS and *cox1* sequences of *Phytophthora* species belonging to clade 8c. Data are based on the General Time Reversible model. A discrete Gamma distribution was used to model evolutionary rate differences among sites. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Bootstrap support values in percentage are given at the nodes. Ex-type cultures are in bold.

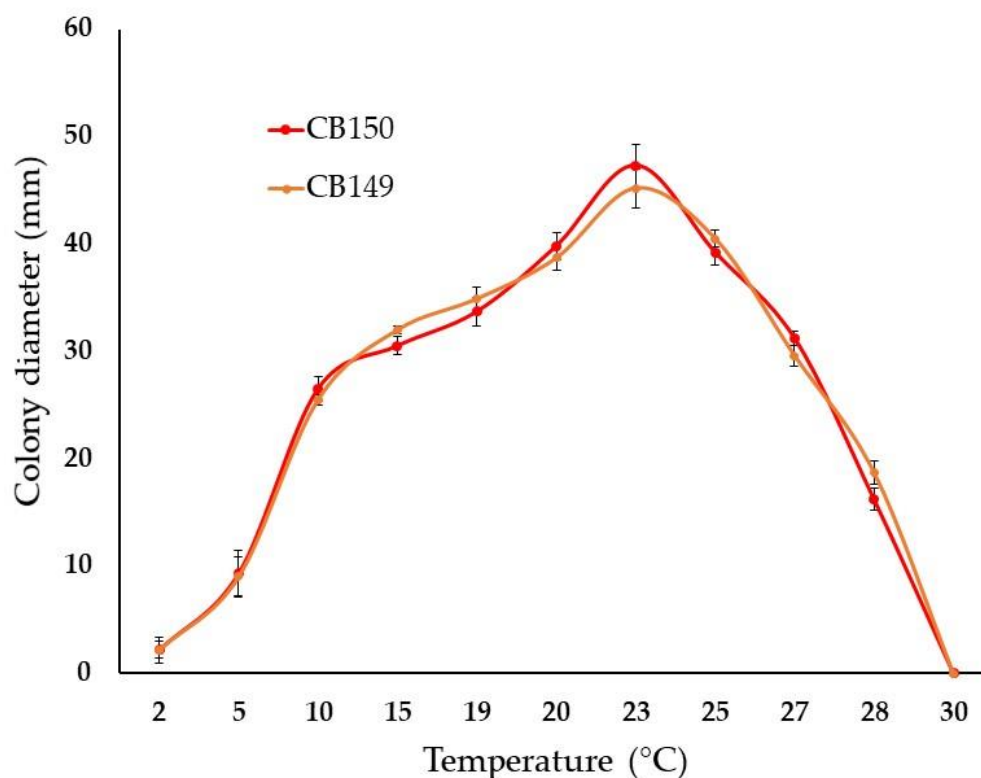


Figure S2. Mean colony diameter (\pm standard deviation) of *P. marrasii* (isolates CB149 and CB150) after 96 h on CA in the dark at different temperatures.