

Title:

Identification and characterization of *Neofusicoccum Stellenboschiana* in branch and twig dieback-affected olive trees in Italy and comparative pathogenicity with *N. mediterraneum*

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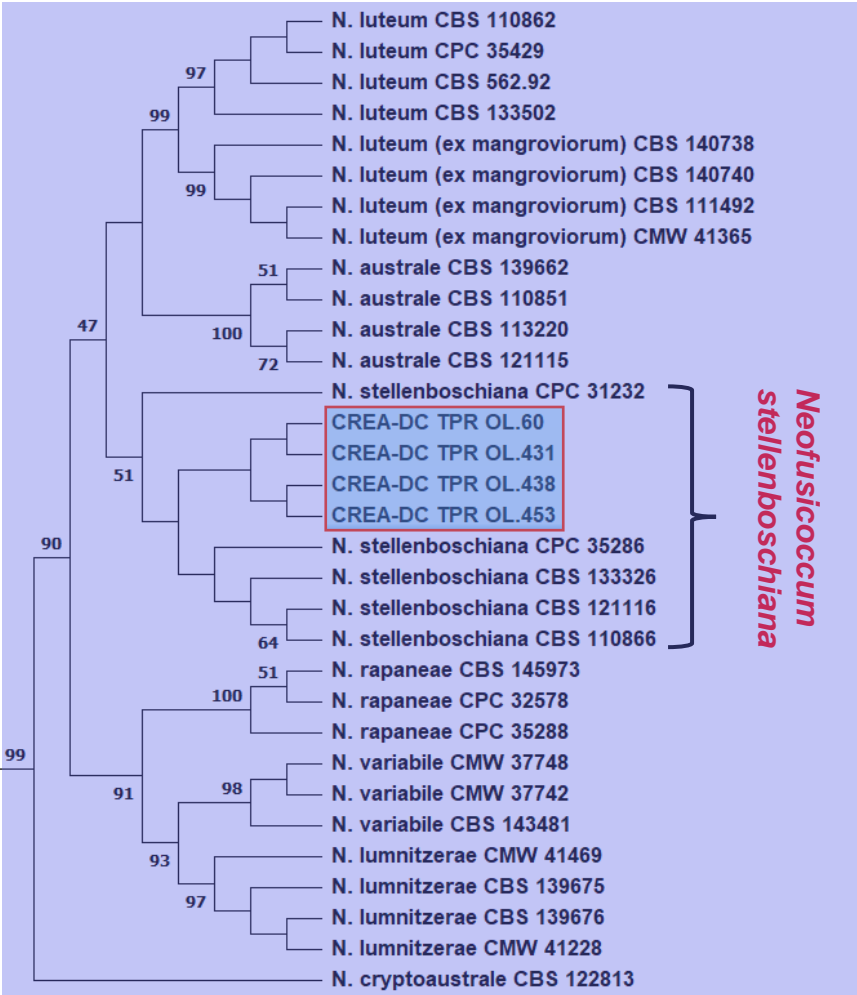
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Figure S1 Phylogeny of the *Neofusicoccum* genus, based on ITS + TEF1- α + TUB2 + RPB2 data set and including the botryosphaeriaceous isolates from Apulia, Latium and Tuscany (Italy), CREA-DC TPR OL.431, 438, 60, 453 (shaded in blue-sky within a red frame). The phylogeny was inferred using the ML method and General Time Reversible model [34], with 1000 bootstraps. The evolutionary history was inferred by using the Maximum Likelihood method and General Time Reversible model [34]. The tree with the highest log likelihood (-10197.21) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches (values > 40). Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. This analysis involved 78 nucleotide sequences. There were a total of 2420 positions in the final dataset. Evolutionary analyses were conducted in MEGA X [33]

References

33. Kumar, S.; Stecher, G.; Li, M.; Knyaz, C.; Tamura, K. MEGA X: molecular evolutionary genetics analysis across computing platforms. *Mol. Biol. Evol.* 2018, 35(6), 1547-1549. Doi: 10.1093/molbev/msy096.
34. Nei, M.; Kumar, S. *Molecular evolution and phylogenetics*. Oxford University Press Inc., Oxford, 2000; pp. 333.

Neofusicoccum australe complex



Neofusicoccum

