

Supplementary Figures



Figure S1. Elm yellows (EY)-diseased *U. minor* (European field elm) (**a** through **d**) and *U. glabra* (Scots elm) (**e** and **f**) trees. (**a**) Trees showing foliar yellowing and decline. (**b**) Reduced terminal growth. (**c**) Tree showing yellowing and apical witches'-brooms. (**d**) Apical witches'-brooms with decreasing leaf size towards the top. (**e**) Branches with yellowing, small leaves and sparse foliage. (**f**) Localized yellowing which progressively spread overtime to other parts of the crown.

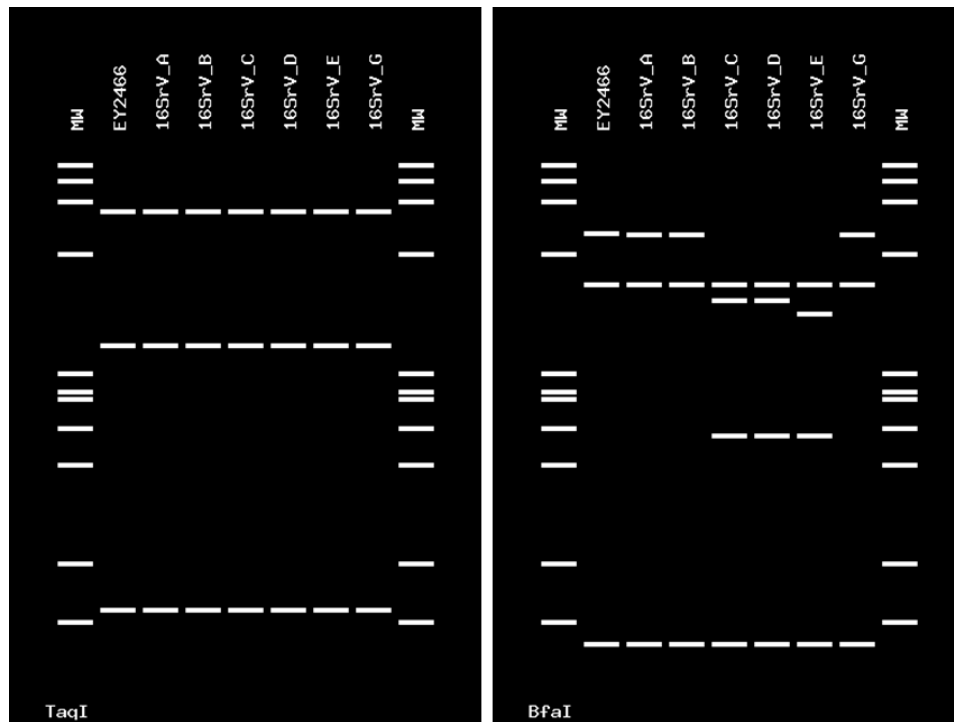


Figure S2. Virtual RFLP analysis performed through the *iPhyClassifier* online tool at <http://plantpathology.ba.ars.usda.gov/cgi-bin/resource/iphyclassifier.cgi> [1] using *TaqI* and *BfaI* restriction enzymes of the 16S rDNA R16F2n/R2 fragments from EY phytoplasma strains detected in the present study (example) and other 16SrV group phytoplasmas. MW, ϕ X174DNA *HaeIII* digest.

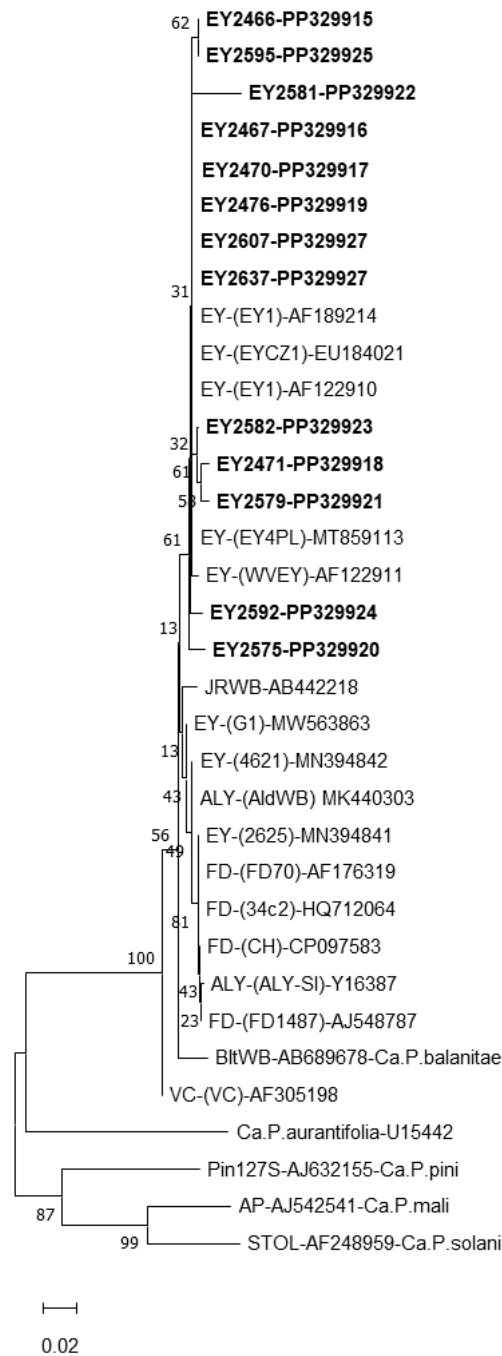
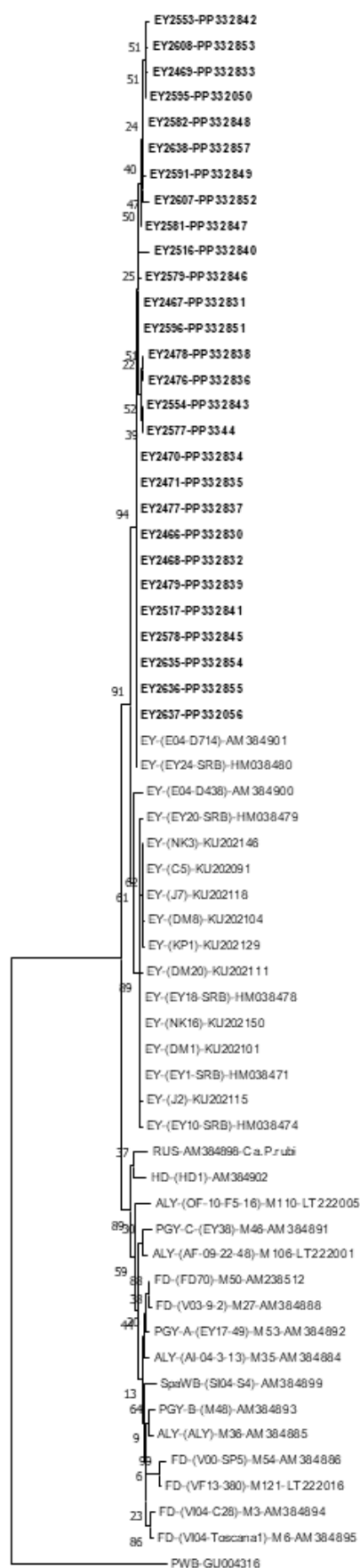


Figure S3. Phylogenetic tree constructed using the neighbor-joining method [2] with 16S/23S rDNA spacer region sequences from newly detected EY phytoplasma strains in southern Italy (in bold type), other EY strains previously detected in elm, 16SrV-B, -C, -D, and -F subgroup phytoplasmas, and a number of formally described ‘*Candidatus* Phytoplasma’ species. ‘*Ca. Phytoplasma solani*’ was used as the outgroup. Bar represents a phylogenetic distance of 0.02 nucleotide substitutions per site. GenBank accession number is provided for each phytoplasma. Bootstrap values are shown on branches of the phylogenetic tree.



0.02

Figure S4. Phylogenetic tree constructed using the neighbor-joining method [2] with *map* gene sequences from newly detected EY phytoplasma strains in southern Italy (in bold type), other EY strains previously detected in elm, flavescence dorée (FD), Palatinate grapevine yellows (PGY), spartium witches'-broom (SpaWB), rubus stunt (RUS) and hemp dogbane yellows (HD) strains. Potato witches'-broom (PWB) phytoplasma strain PWB was used as the outgroup. Bar represents a phylogenetic distance of 0.02 nucleotide substitutions per site. GenBank accession number is provided for each phytoplasma. Bootstrap values are shown on branches of the phylogenetic tree.

References

1. Zhao, Y.; Wei, W.; Lee, I.-M.; Shao, J.; Suo, X.; Davis, R.E. Construction of an interactive online phytoplasma classification tool, *iPhyClassifier*, and its application in analysis of the peach X-disease phytoplasma group (16SrIII). *Int. J. Syst. Evol. Microbiol.* **2009**, *59*, 2582-2593.
2. Tamura, K.; Stecher, G.; Kumar, S. MEGA 11: Molecular evolutionary genetics analysis version 11. *Mol. Biol. Evol.* **2021**, *38* (7), 3022-3027.