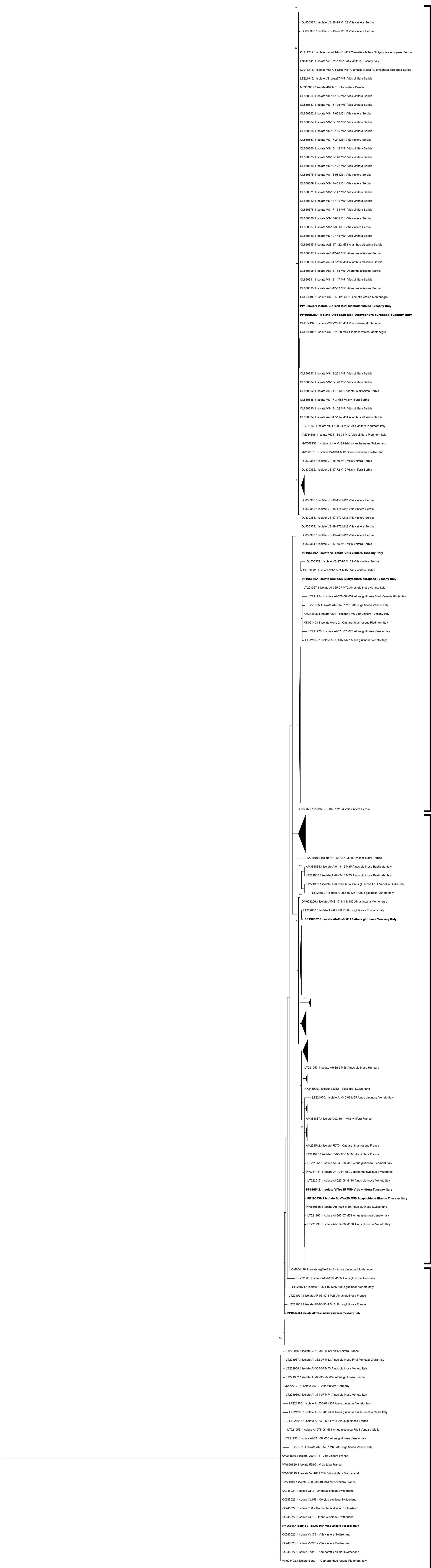




map-FD3

map-FD1

map-FD2

Supplementary Figure S2. Phylogenetic tree of 247 flavescence doré phytoplasma (FDp) isolates from Europe reconstructed from partial *map* gene. The tree was generated by Maximum Likelihood (ML) method, using the Jukes-Cantor model of evolution for nucleotide. The significance of each branch was evaluated by constructing 1,000 trees in bootstrap analysis. Bootstrap values are shown. The scale represents a distance of 0.050 substitutions per site. The branches that do not contain the identified sequences have been collapsed. The isolates sequenced in this study are in bold and the subdivisions between clusters are reported on the right. For sequences from Italy, the specific region of origin is also mentioned. Bois noir phytoplasma (BNp) isolate (AM990988) was used as outgroup.