

Genetic variability among ‘*Candidatus Phytoplasma ulmi*’ strains infecting elms in Serbia and survey of potential vectors

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Presence of elm yellows phytoplasmas (EY) belonging to 16Sr DNA group 16SrV-A infecting *Ulmus minor* and *U. laevis* in Serbia was reported in 2008 (Jović *et al.*, Plant Pathology, 57, 1174). Molecular characterization of these strains and additionally collected samples of different geographical origin in Serbia was performed. RFLP and nucleotide sequence analyzes of four conserved genes: 16S rDNA, *rpl22-rps3*, *SecY* and *map* were carried out. Comparison of obtained sequences with representative phytoplasma strains in the EY phytoplasma group (Lee *et al.*, Int. J. Syst. Bacteriol., 54, 337-347. 2004; Arnaud *et al.*, Appl. Environ. Microbiol., 73, 4001-4010. 2007) revealed presence of five different strains. Four strains exhibited nucleotide changes located inside a range of unique regions of 16S, *rp* and *SecY* genes determined by Lee *et al.* (2004), while the fifth strain had sequences most similar to strain EY626. Based on sequence analyses of FD9 genetic loci and virtual digestion of FD9f3/r2 amplicons with *MseI* endonuclease, a routine typing method was determined for all five strains. Topology of phylogenetic trees constructed for the *rp*, *SecY* and *map* genes was the same with EY phytoplasma strains from Serbia forming a separate cluster inside the ‘*Candidatus Phytoplasma ulmi*’ branch. Survey of potential hemipteran vectors on two localities in East Serbia where symptomatic, phytoplasma infected elm trees were present resulted in identifying 14 species of planthoppers and leafhoppers which were analyzed for EY phytoplasma presence. Most abundant species were *Reptalus quinquecostatus* and *Hyalesthes luteipes*. On both sites only *H. luteipes* individuals regularly present on elms, proved to be infected (6% and 10%). RFLP analyses of FD9 amplicons with *MseI* endonuclease showed that all phytoplasma strains from *H. luteipes* had a profile similar to the fifth strain described above and therefore related to EY strain EY626.