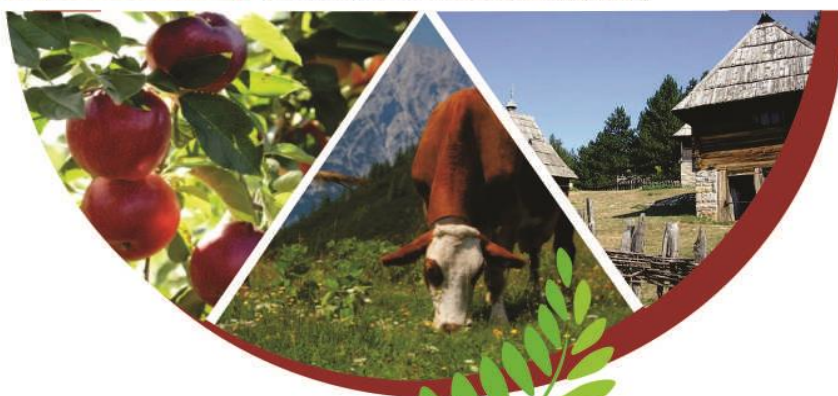


BOOK OF ABSTRACTS



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MOLECULAR CHARACTERIZATION OF *PSEUDOMONAS SYRINGAE* PV. *CORIANDRICALA* ORIGINATED FROM CARROT, PARSLEY AND PARSNIP

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Abstract

Recent studies have been made to investigate some molecular features of plant pathogenic bacteria *Pseudomonas syringae* pv. *coriandricola*. This pathogen causes bacterial leaf spot disease on some members of family *Apiaceae*, such as coriander, carrot, parsnip and parsley. Initial symptoms are small water-soaked lesions on foliage, which then develop into spots varying in shades, tan, brown or black. The spots are usually limited by leaf veins having an angular appearance, and visible from both sides of leaves. Under favorable conditions of high humidity, spots may spread and cause foliage blighting. *P. s.* pv. *coriandricola* strains used in this study originate from carrot, parsley and parsnip. Repetitive element PCR fingerprinting (rep-PCR), using REP, BOX, ERIC, (GTG)₅ and SERE primers, and randomly amplified polymorphic DNA-polymerase chain reaction (RAPD-PCR) using M13 primer were used to determinate genetic polymorphism between tested strains. Further molecular features were observed on the basis of a multilocus sequence analysis (MLSA) by sequencing key genes for *Pseudomonas syringae* (*gapA*, *gltA*, *gyrB*, *rpoD*). DNA profiling revealed identical banding patterns for all tested strains. The sequence and phylogenetic analysis of three MLSA genes (*gapA*, *gyrB*, *rpoD*) showed homology with pathotype strains *P. s.* pv. *coriandricola* deposited in PAMDB (<http://genome.ppws.vt.edu/cgi-bin/MLST/home.pl>). Sequencing of *gltA* gene determined the isolates above the species level (*P. syringae*). Our results indicate that *gapA*, *gyrB* and *rpoD* genes are more discriminatory than *gltA* and their usage is therefore suggested for further genotypic studies of this pathogen.

Keywords: *Bacterial leaf spot, Apiaceae, rep-PCR, MLSA.*

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