

# BOOK OF ABSTRACTS



CONGRESS

OF THE SERBIAN GENETIC SOCIETY

2019 | October  
13–17

VRNJAČKA BANJA • SERBIA





*Publisher*  
Serbian Genetic Society,  
Belgrade, Serbia  
[www.dgsgenetika.org.rs](http://www.dgsgenetika.org.rs)

*Editors*  
Branka Vasiljević  
Aleksandra Patenković  
Nađa Nikolić

*Printing*  
Serbian Genetic Society,  
Belgrade, Serbia

*Number of copies printed*  
300

*Design*  
Ivan Strahinić  
Ana Kričko

ISBN  
978-86-87109-15-5

# BOOK OF ABSTRACTS

Abstracts of the 6th CONGRESS OF THE SERBIAN GENETIC SOCIETY



2019 | October  
2019

VRNJAČKA BANJA • SERBIA

05 – 21 Poster

### MULTILOCUS SEQUENCE ANALYSIS OF *RALSTONIA SOLANACEARUM* ISOLATES ORIGINATED FROM POTATO IN SERBIA

Sanja Marković<sup>1</sup>, Slaviša Stanković<sup>2</sup>, Aleksandra Jelušić<sup>1</sup>, Renata Iličić<sup>3</sup>, Tatjana Popović<sup>4</sup>

<sup>1</sup> University of Belgrade, Institute for Multidisciplinary Research, Belgrade, Serbia

<sup>2</sup> University of Belgrade, Faculty of Biology, Belgrade, Serbia

<sup>3</sup> University of Novi Sad, Faculty of Agriculture, Novi Sad, Serbia

<sup>4</sup> Institute for Plant Protection and Environment, Belgrade, Serbia

[janjatovics@gmail.com](mailto:janjatovics@gmail.com)

*Ralstonia solanacearum* is a soil borne bacterium which affects more than 450 plant species including a wide range of crop plants, ornamentals and weeds. This bacterium is causing bacterial wilt disease which leads to severe economic losses. On potato, disease is known as brown rot. Even though this phytopathogen originates from tropic, subtropics and warm temperate regions, in recent years cold-adapted strains dramatically enhanced the threat of European potato crops, including Serbia. *R. solanacearum* is at A2 list of quarantine plant pathogens in Europe. During six year period (2013-2018), isolates from diseased potato tubers were collected, identified using Multilocus sequence analysis (MLSA) and checked for certain phylotype affiliation. DNA from the obtained isolates was amplified using seven housekeeping genes (*adk*, *fliC*, *gapA*, *gdhA*, *gyrB*, *hrpB*, *ppsA*) and sequenced. Phylogenetic analysis was performed with concatenated sequences of all tested isolates, and compared with the most similar *R. solanacearum* strains from PAMDB database. All Serbian isolates were identified as *R. solanacearum* using PAMDB BLAST. Neighbor-joining phylogenetic analysis placed tested isolates in the same cluster with *R. solanacearum* strains belonging to race 3, biovar 2, and phylotype II obtained from PAMDB. Although, bacterial wilt caused by this plant pathogenic bacteria is appearing in different locations and on different potato cultivars in Serbia it remained genetically homogenous. Currently, *R. solanacearum* is a quarantine bacteria occurring only on potato in our country, but considering its wide host range, there is a possibility of it causing disease on other significant crops with devastating consequences. Therefore, its fast and accurate identification and mapping is of main interest for stopping the disease spread.

This work was supported by the Ministry of Education, Science and Technological Development, Republic of Serbia (Project No. III43010).

*RALSTONIA SOLANACEARUM*, BACTERIAL WILT, BROWN ROT, MULTILOCUS SEQUENCE ANALYSIS (MLSA)

05 – 22 Poster

### GENETIC INSIGHT INTO THE ISOLATES CAUSING BLACKLEG DISEASE ON POTATO

Sanja Marković<sup>1</sup>, Tatjana Popović<sup>2</sup>, Aleksandra Jelušić<sup>1</sup>, Renata Iličić<sup>3</sup>, Slaviša Stanković<sup>4</sup>

<sup>1</sup> University of Belgrade, Institute for Multidisciplinary Research, Belgrade, Serbia

<sup>2</sup> Institute for Plant Protection and Environment, Belgrade, Serbia

<sup>3</sup> University of Novi Sad, Faculty of Agriculture, Novi Sad, Serbia

<sup>4</sup> University of Belgrade, Faculty of Biology, Belgrade, Serbia

[janjatovics@gmail.com](mailto:janjatovics@gmail.com)

Blackleg disease, caused by pectolytic bacteria from genus *Dickeya* and *Pectobacterium* is currently being one of the main concerns in potato production. Yield loss and reduced quality, visible through potato black rotting at the stem base, as well as whole plant decaying, makes potato cultivation less profitable. Blackleg disease outbreak was observed in potato field (cv. Lady Claire) in Bačka (northern Serbia) in June 2018. The percent of the infected plants, estimated during the vegetation season was 45%, with yield reduction of about 20%. In this study the causal pathogens were genetically characterized using multilocus sequence analysis (MLSA). DNA of the obtained isolates was amplified with primers made based on the sequences of five housekeeping genes - *gapA*, *icdA*, *mdh*, *pgi* and *proA* and sequenced. Phylogenetic analysis was performed to compare the obtained isolates with the ones already deposited in NCBI database. NCBI BLAST identified isolates as *Dickeya dianthicola* and *Pectobacterium carotovorum* subsp. *brasiliensis*, indicating on the persistence of mix infection on observed potato crop. According to all genes, isolates appeared to be the most similar (99-100%) to the reference strains - *D. dianthicola* (CFBP 1200) and *P. carotovorum* subsp. *brasiliensis* (BC1). Blast results were confirmed after phylogenetic analysis, where isolates of both identified species were clustering with the rest of the strains of the same species, obtained from NCBI. Our findings confirm the presence of new blackleg causal agents, *D. dianthicola* and *P. carotovorum* subsp. *brasiliensis* on potato in Serbia. Their isolation and localization is of great importance, especially *D. dianthicola* which has quarantine status, and therefore it gives a signal for pathogen eradication and prevention of its future spreading.

This work was supported by the Ministry of Education, Science and Technological Development, Republic of Serbia (Project No. III43010).

POTATO, BLACKLEG, *DICKEYA*, *PECTOBACTERIUM*, MULTILOCUS SEQUENCE ANALYSIS (MLSA)