

BOOK OF ABSTRACTS



CONGRESS

OF THE SERBIAN GENETIC SOCIETY

2019 | October
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VRNJAČKA BANJA • SERBIA





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Abstracts of the 6th CONGRESS OF THE SERBIAN GENETIC SOCIETY



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WELCOME TO VI CONGRESS OF THE SERBIAN GENETIC SOCIETY!

Dear colleagues,

Welcome to the 6th Congress of the Serbian Genetic Society. The Serbian Genetic Society (SGS) has been founded in 1968 and the first Congress organized by the SGS was held in 1994 in Vrnjacka Banja. Since then, the Congress of Serbian Genetic Society is held every five years. Over the past years, the Congress has grown from a national to an international meeting.

The experience of the past meetings motivated our efforts to continue with this series with a clear tendency to strengthen the scientific connections among researchers from different European countries.

The Congress will focus on the most recent advances in genetics and on wide range of topics organized in 9 sessions and two workshops. Many of the presentations will be in lecture-like settings, but we hope that there will also be ample opportunities for informal interaction outside the scheduled sessions.

The successful organization of the Congress has required the talents, dedication and time of many members of the Scientific and Organizing committees and strong support from our sponsors. I hope that you will find the Congress both pleasant and valuable, and also enjoy the cultural and natural beauty of Vrnjacka Banja.

Yours sincerely,



Branka Vasiljevic
President of the Serbian Genetic Society



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07 – 13 Poster

GENODIVERSITY OF *XANTHOMONAS CAMPESTRIS PV. CAMPESTRIS* ISOLATED FROM LEAVES OF BRASSICACEAE PLANTS

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Brassicas are a significant source of edible vegetables and is the third most important source of oil on the world level. Black rot, caused by the bacterium *Xanthomonas campestris pv. campestris* (XCC) represents the most destructive Brassicas diseases, generally. The bacteria is widespread on all continents, and is present in our country, especially at the places where Brassicas are grown in monoculture. Particularly susceptible are cabbage local genotypes, which are highly appreciated by consumers. Given the importance, frequency and distribution of XCC, there was a need to study the diversity of this pathogen on cabbage, cauliflower, kale, broccoli and oil seed rape. Monitoring was conducted from 2014 to 2017 on the territory of the Republic of Serbia. From different Brassicas 82 bacterial isolates from leaves were collected. All isolates form yellow colonies on the YDC medium and based on biochemical-physiological characteristics were identified preliminarily as XCC. Further identification was done using m-PCR by primer sets Zup 2309/2310 and DLH 120/125, showing amplicons of 370 and 619 bp in all tested isolates, as well as in reference strain NCPPB 1144, and confirmed isolates as XCC. Characterization of isolates by rep-PCR (BOX A1R and (GTG)₅ primers) and RAPD (SPH1, OPA8, DJ15 and DJ16 primers) was done. In both cases, all tested XCC isolates and reference strain NCPPB 1144 formed one cluster, while the second cluster contained reference strains belonging to *Xanthomonas* genera (*X. axonopodis pv. phaseoli*, *X. perforans*, *X. vesicatoria* and *X. euvesicatoria*), but other than XCC, showing 56% and 57% differences for BOX and RAPD, respectively. At the 95% level of similarity, 9 different BOX patterns and 14 different RAPD patterns were obtained. Characterization of XCC isolated from leaves in Serbia will enable the comparison of isolates from different origin and facilitate the monitoring in epidemiological studies of this pathogen.

XANTHOMONAS CAMPESTRIS PV. CAMPESTRIS (XCC), REP-PCR, RAPD, M-PCR, BRASSICAS DISEASES

07 – 14 Poster

EFFECT OF COLD STORAGE ON THE PRESENCE OF FUNGAL SPECIES

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The occurrence of fungal species was examined in four maize grain accessions which were kept for different time under gene bank conditions. Samples were regenerated three times, e.g. in 1985, 2012 and 2016, and afterwards 12 samples in total, were stored in a cold room under medium storage conditions. The aim was to determine the occurrence of fungal species.

The 2012 maize growing season was characterised by extremely hot and dry conditions. A significantly lower amount of precipitation was recorded in this year than in the remaining two years. The recorded drought conditions were favourable for the growth of certain *Aspergillus* species, which resulted in the presence of *Aspergillus* section Flavi in 75% of the examined maize samples, while *Fusarium* species section Liseola, were detected in 33.23% of the samples. The highest amount of precipitation in the 2016 maize growing season in combination with temperatures close to optimum levels resulted in the presence of *Fusarium* species in 65.28% of maize samples, while *Aspergillus* species were not detected. In samples from 1985, the most dominate *Aspergillus* species belonged to the section Niger (44.80%) which were registered in all investigated samples.

The occurrence of fungal species was not affected by storage conditions (temperatures 4°-10°C, relative humidity of 40%). Significant differences in the appearance of fungal species were observed under various weather conditions during all years of investigation. The obtained results indicate that the occurrence of *Fusarium* section Liseola is characteristic for years with high precipitation sums, such as 2016. Maize grain contamination with *Aspergillus* section Flavi was recorded in dry and hot year of 2012.

Maize is continually exposed to the toxigenic fungi whose species can produce highly toxic compounds-mycotoxins. The presence of mycotoxins in maize should be recognised as a significant concern since these contaminants may have negative impact on human and animal health.

FUNGAL SPECIES, COLD STORAGE, MAIZE