

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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VRNJAČKA BANJA • SERBIA

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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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THE EVALUATION OF DONORS OF FAVOURABLE ALLELES FOR THE IMPROVEMENT OF F1 MAIZE HYBRIDS

Mile Sečanski¹, Goran Todorović¹, Jelena Srdić¹, Nikola Grčić¹, Snežana Jovanović¹, Jelena Golijan², Marijenka Tabaković¹, Aleksandar Popović¹

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The basic aim of maize breeding programs is the development of new hybrids that will exceed the existing commercial hybrids. The purpose of this study was to estimate which inbreds derived from the BSSS and BSCB1 populations had the highest relative values of favourable alleles for the improvement of the number of kernels per row in an elite maize hybrid. Inbreds B73 (C5), B97 (C9) and B99 (C10) had the highest values of favourable alleles μG^* for the improvement of the number of kernels per row. The inbred line B73 (C5) originating from the synthetic population BSSS had a significant and positive difference $\mu G^* - (\mu D^* \text{ or } \mu F^*)$, hence in the breeding process, the F1 generation should be crossed to an inbred donor and then self-pollinated to develop an improved inbred line. Inbred lines B97 (C9), B99 (C10) and B84 (C7) had high values of μG^* but did not have high differences $\mu G^* - (\mu D^* \text{ or } \mu F^*)$, not significantly higher than null. Ranking of inbreds as donors of favourable alleles over four applied parameters (μG^* , UBND, PTC and NI) shows congruence. The best ranked inbred line B73 (C5) was the best over all four parameters, while remaining inbreds expressed identical ranking confirming high and significant rank correlations.

INBRED LINES, MAIZE, DONORS, HYBRID, ALLELES, RANK CORRELATIONS

06 – 42 Poster

SCREENING EARLY SOYBEAN GERMLASM FOR YIELD AND AGRONOMIC IMPORTANT TRAITS

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The objective of this study was screening of soybean germplasm with reference to yield and other agronomical important traits, as novel source of genetic variability in soybean breeding program. The focus is on early soybean germplasm as a potential genetic source for breeding in the light of global climate changes and to increase diversity of early varieties that can be grown as a second crop in Vojvodina province.

The trial was conducted in 2018 year, established as row-column design, at experimental fields of Institute of field and vegetable crops, Novi Sad. A 262 genotypes from three maturity groups (MG 000, MG 00, MG 0) were included in this research. Number of soybean genotypes per MG was 85, 93 and 84, respectively. Sowing was conducted in early April while harvesting start from July and lasting till September. The earliest genotype matures in 65 days, while the latest one mature after 125 days. This extremely early genotype can be very useful source in breeding program for earliness. It was identifying several genotypes with 1000 seed weight over 300 grams. This is good genetic source in breeding programs dedicating to food soybean and edamame production. Wide yield variability was observed, in the range 0.3-3.9 t/ha, indicating on potential source of useful germplasm for introducing in elite breeding program.

The results showed a good correlation between maturity group and yield, but also with length of phases VE-R8, VE-R1 and R1-R8, respectively. Genotypes from MG 0 had longer vegetation than genotypes from MG 00 and MG 000, which resulted in higher plants, more nodes, higher 1000 seed weight and after all a higher total yield per plot. Also, number of fertile nods can be used as indicator for productive trials of soybean germplasm. The trial will be repeated for obtaining more precise results in the year of 2019.

SOYBEAN; MATURITY GROUP; YIELD