

# 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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**PERFORMANCE OF SUNFLOWER HYBRIDS INTERCROPPED WITH LEGUMES  
REVELED BY AMMI ANALYSIS**

Brankica Babec<sup>1</sup>, Nada Hladni<sup>1</sup>, Srdjan Šeremešić<sup>2</sup>, Nemanja Ćuk<sup>1</sup>, Milan Jocković<sup>1</sup>, Bojan Vojnov<sup>2</sup>

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Intercropping, as ecologically designed agricultural system, could help in agriculture advancement for many crops. The aim of research was to evaluate the effects of legume-sunflower intercropping and their interaction on the sunflower seed yield during 2017 and 2018 vegetation seasons. A field experiment was set up by intercropping three sunflower hybrids (Dukat, Rimi PR, and NS Gricko) with three types of legumes (*Vicia sativa* L., *Medicago sativa* L., and *Trifolium pratense* L.), whereas sole crops of sunflower were used as control. The Additive Main Effects and Multiplicative Interaction Analysis (AMMI) was used to test the main effects and interaction of intercrops. Year × crop combinations were examined as 8 environments. Analysis of Variance (ANOVA) tests of seed yield in 8 environments indicated highly significant effects of genotype, environment and their interaction, with the following share: genotype 61.78%, environment 27.69%, and interaction 10.53%. Mean seed yield of the hybrids varied from 3 t/ha (Dukat), 3.5 t/h (Rimi PR), to 4.4 t/ha (NS Gricko). Knowing that hybrid Dukat, which had the smallest seed yield, is a short vegetation hybrid, while NS Gricko, which had the highest seed yield, is a confectionary hybrid, the results were expected. The AMMI ANOVA test showed high significance of IPC1 with the contribution of 94.39%. The interaction was detected using the AMMI1 biplot. The correlation of main effects and IPCA scores can be used in making predictions of yield performance. Small IPCA scores indicate more stable genotypes. Therefore, hybrid NS Gricko had the highest stability of seed yield. Hybrid Rimi PR was the most unstable for the examined trait, but interacted best with red clover in 2017 and alfalfa in 2018, respectively. Hybrid Dukat interacted best with red clover in 2018. The obtained results could be important for the recommendation of sunflower hybrids that are stable and high yielding when intercropped with different legumes.

SUNFLOWER, LEGUMES, INTERCROPPING, AMMI

06 – 46 Poster

**GENOMIC PREDICTION IN MAIZE BREEDING**

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In recent years the availability of cheap genome-wide markers resulted in a novel approach in maize breeding called genomic prediction (GP). Genomic prediction is a special form of marker assisted breeding, in which genetic markers covering the whole genome are used for estimation genomic breeding value of individuals under selection. Genomic estimated breeding value (GEBV) of an individual represents the sum of effects associated with all the marker alleles present in an individual and included in the GP model applied to the population under selection. The GP is based on training (TP) and breeding (BP) populations. The TP is used for training of the GP model and for estimation of the marker effects required for estimation of GEBV of the individuals in the BP. The BP is the population subjected to GP for identification of the superior lines for use as parents for new hybrid combinations. In real maize breeding programs, successful implementation of the GP is based on data from multi-environment trials. Thus, appropriate modeling and statistical approaches are required to deal with the complexity of the multi-environment grain yield data coupled with genomic and environmental data to speed-up maize breeding.

MAIZE BREEDING, GENOMIC PREDICTION, GEBV, TRAINING AND BREEDING POPULATION