

# BOOK OF ABSTRACTS



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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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## 06 – 03 Invited lectures

**BREEDING OF MAIZE HYBRIDS WITH SPECIFIC TRAITS FOR ENHANCED AGRONOMIC AND NUTRITIONAL PROPERTIES**

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Maize stands out by its high genetic variability, thus it provides the possibility to develop different types for various purposes in the breeding process. Maize breeding provides significant modifications in the grain composition in the respect of quantity and quality of certain components. It is mainly grown as an energetic crop, but there is a broad use of types with specific traits, such as sweet corn and popcorn that are primarily used for human consumption. Although breeding methods are the same as in breeding standard quality grain, special attention is necessary in the process of breeding, seed production, but also in the commercial production and processing. Breeding strategies are based on the application of conventional breeding methods and also on the application of molecular markers, especially due to the fact that the genetic base of these two types of maize is very narrow. Beside the increase in yielding potential and other agronomic traits, great challenge is the improvement of quality parameters and nutritional composition of sweet corn and popcorn. Quality and sensory characteristics are of great importance for the commercial value, therefore several methods are applied in order to estimate them. On the other hand these traits are often in negative correlation with the yield, which presents a great challenge in breeding of specialty maize. Popcorn and sweet corn are very popular in diet because of their high nutritional values. Popcorn contains very powerful antioxidants such as tocopherols and carotenoids, and the compounds with the highest biological activity like tocopherols, are mainly retained in popcorn after heat treatment. Sweet corn also has very rich nutrient composition containing main nutrients, such as: starch, sugar, protein, oil and cellulose, and phenolic acids: galic, protocatechuic, vanilic, sinapic, p-coumaric, ferulic and cinnamic.

SPECIFIC TRAITS, SWEET CORN, POPCORN, NUTRITIONAL PROPERTIES

## 06 – 04 Invited lectures

**GENOMIC PREDICTION – NEW TOOL IN SOYBEAN BREEDING**

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Yield and most of the agronomical important traits are quantitatively inherited, influenced by many loci with a small effect and affected by environmental conditions. When dealing with the improvement of quantitative traits, it is not particularly useful to perform the selection by using few major-effect loci as in traditional marker-assisted selection, but to simultaneously use genome-wide molecular markers able to capture all small effect loci influencing a trait.

The training population consisted of 227 diverse soybean lines that were used for genomic prediction model development. Training population was evaluated for yield at three consecutive years. DNA of each genotype was sequenced on Illumina HiSeq 2500, using GBS Discovery Pipeline for SNP calling. Prediction ability was evaluated using six mathematical models, including parametric and non-parametric and were validated on three different levels: self-prediction, cross-validation (5-fold) and external validation (historical data).

Overall, genomic prediction ability for soybean yield was relatively high (0.60) and the results indicate a modest influence of mathematical model and marker number on the prediction ability using cross-validation and external validation. However, model had variable ability to predict phenotypic performance in separate environments, with especially high prediction ability in years not impacted by yield-limiting factors, when the genetic potential was fully achieved. Improvement of model performance in cross-validation and external validation was achieved by increasing the phenotyping intensity that must reflect the target environment variability.

Obtained results indicate that genomic prediction can be integrating part of breeding process as useful tool that can increase breeding efficiency and decrease breeding time. Particular implementations are diverse, from germplasm screening and parental choice to the forward breeding and direct selection based on genomic prediction.

SOYBEAN, GENOMIC PREDICTION, YIELD, MODEL