CONGRESS OF THE SERBIAN GENETIC SOCIETY

BOOK OF ABSTRACTS

2024 | October 2 - 5

ZLATIBOR · SERBIA

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2024 | October 2–5

ZLATIBOR, SERBIA

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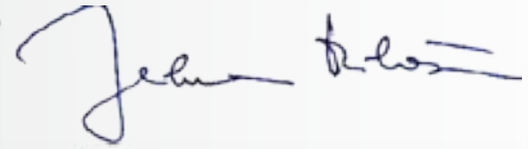
WELCOME TO VII CONGRESS OF THE SERBIAN GENETIC SOCIETY!

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.

The VII Congress of the Serbian Genetic Society has gathered over 250 scientists from different European countries and this collection of abstracts showcases cutting-edge research in the field of genetics, exploring the vast complexity of life. The abstracts contained in this book reflect the diversity and dynamism of the field. A wide range of topics have been covered including molecular genetics and genomics, medical genetics and personalized medicine, population and evolutionary genetics, microbial genetics, crop and livestock breeding, bioinformatics, genotoxicology, new technologies, and others, bringing significant contributions to our understanding of the genetic foundations that shape organisms.

We hope this collection will inspire and foster interdisciplinary collaboration, spark new ideas, and most generally, contribute to the advancement of genetics for the benefit of both science and society.



Jelena Milašin
President of the Serbian Genetic Society

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06 – 15 Oral

BACTERIAL TREATMENT ENHANCES THE GROWTH OF ONE-YEAR-OLD SESSILE OAK (*QUERCUS PETRAEA* (MATT.) LIEBL) SEEDLINGS OF TWO SERBIAN PROVENANCES

Sanja Jovanović [1], Aleksandar Lučić [1], Aleksandar Vemić [1], Ljubinko Rakonjac[1], Vanja Daničić [2], Tanja Berić [3], Vladan Popović [1]

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The root rhizosphere is one of the densest habitats on the planet, where significant intimate interactions between plants and their recruited rhizomicrobiota are implemented. Plant genetics impacts community composition. However, this communication is a two-way process regarding microorganisms modulating plants's physiological processes as well, which are eventually manifested in plant vigor, growth, and development.

One-year-old sessile oak seedlings of provenances Đerdap and Goč were treated with *Bacillus* sp. (treatment 1) and *Pseudomonas* sp. (treatment 2) in order to study their effect on the enhancement of seedling growth. Sessile oak seedlings were monitored for one growing season in semi-controlled conditions in the nursery of the Institute of Forestry. At the end of the experiment, seedling height and root collar diameter were measured by a ruler and Vernier's caliper as the standard morphological parameters of seedling growth. The obtained data were analyzed statistically in GraphPad Prism, and ANOVA and Dunnett's test were applied. The results indicate the enhancement of seedlings' growth treated with bacteria. Seedlings of Đerdap provenance treated with treatment 1 were 35% higher, and the ones treated with treatment 2 were 32% higher compared to the control. Seedlings of Goč provenance treated with treatment 1 were 85% higher than control. The effect of bacterial treatments on seedling root collar diameter of both provenances was not statistically significant, although it enhanced their mean values.

The obtained results indicate the potential of bacterial treatments to increase seedling growth, which should be researched comprehensively in the future, especially in the context of biological fertilizer commercialization.

Acknowledgments: This study was carried out under the Agreement on realization and funding of scientific research activity of scientific research organizations in 2024, funded by the Ministry of Science, Technological Development and Innovation. No. 451-03-66/2024-03/200027 and 451-03-65/2024-03/200178.

BACTERIA, SEEDLINGS, SESSILE OAK, PROVENANCES

06 – 16 Oral

CUTTING-EDGE BREEDING TOOLS FOR SOYBEAN YIELD PREDICTION

Vuk Djordjevic [1], Marina Ceran [1], Jegor Miladinovic [1], Predrag Randjelovic [1], Vojin Djukic [1], Simona Jacimovic [1], Marjana Vasiljevic [1]

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Soybean is a crop of major economic and environmental importance. Due to its broad importance, there is a need for developing long-term breeding strategies based on state-of-the-art technologies that involve breeding predictive tools. Genomic prediction (GP), high-throughput phenotyping prediction (HTPP), and Fourier transformed near-infrared reflectance spectroscopy (FT-NIRS) are selected as the three main pillars for predictive models because they reflect certain parts of soybean plant biology. Single-nucleotide polymorphism (SNP) data describes molecular differences between genotypes, while NIR spectra can be considered as surrogates for overall tissue chemical composition and reflect the culmination of physiological processes, and HTPP can detect subtle differences in canopy growth and developmental changes. Implementation of these prediction models through their compilation has the potential for application in a cost-effective manner. Estimating the accuracy and effectiveness of each specific model and describing their interaction is an essential step in understanding the complicated relationships between yield predictors. For that purpose, two sets of field trials are established to simulate the real breeding evaluation process (early and late-stage panels). For prediction model compilations, several strategies are used. The first strategy treats all data sets equally, while the second and third approaches take into account data set hierarchy and the application of different algorithms. Using all the strategies for combining prediction models should provide an answer to whether it is possible to improve the precision and accuracy of soybean phenotype prediction within and between environments as a key indicator for increasing genetic gain.

Acknowledgments: This research was supported by the Science Fund of the Republic of Serbia, 6788, Soybean Yield Prediction Using Multi-omics Data Integration – SoyPredict.

PREDICTION TOOLS, YIELD, SOYBEAN

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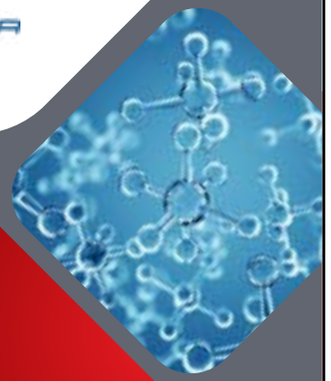

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