BOOK OF ABSTRACTS

CONGRESS
OF THE SERBIAN GENETIC SOCIETY

2019 | October 13–17

VRNJAČKA BANJA • SERBIA

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Abstracts of the 6th CONGRESS OF THE SERBIAN GENETIC SOCIETY

October
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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

08 – 03 Invited lecture

LEAF TOTAL TRANSCRIPTOME ANALYSIS ENRICHES INSIGHT INTO MAIZE ABIOTIC STRESS SIGNALING NETWORK

Bojana Banović Đeri [1], Dragana Dudić [2], Manja Božić [3], Pavle Janić [4], Lana Džodanović [4], Jelena Samardžić [1], Dragana Ignjatović-Micić [3], Jelena Vančetović [3], Sofija Božinović [3], Dejan Dodig [3], Nenad Delić [3], Ana Nikolić [3]

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Abiotic stresses cause great losses in crop production worldwide. Due to climatic changes temperatures higher than the average are frequently observed in temperate areas in the course of maize flowering and grain filling period, displaying detrimental effect on maize yield. In order to overcome this problem development of drought tolerant maize lines, but also cold tolerant maize lines that would allow earlier sowing and hence avoidance of extremely high temperatures during sensitive developmental phases in maize, became important goal of maize breeding programs in temperate areas. A set of 46 maize inbred lines was chosen from three main heterotic groups (BSSS, Lancaster, Iowa dent) important for commercial breeding programs. Plants were grown under the optimal conditions in the greenhouse and sampled upon entering V5 growth stage. A total RNA isolated from leaves of three plants of each inbred line was used for DNA library preparation by Illumina TruSeq Stranded RNA LT kit. Pair-end sequencing was performed on MiSeq Illumina sequencer using MiSeq Reagent kit v2 (2x150bp). For data manipulation and analysis a custom made bioinformatics pipeline was used. Differential gene expression analysis revealed a minimum of 21 genes that were strongly statistically supported for differential expression between the inbred lines and also annotated as involved in abiotic stress responses in other plant species. We tested 10 of these genes in maize by using qPCR on the subset of 8 inbred lines grown under optimal, cold and drought conditions. Real-time PCR results revealed significant change in the expression level of tested genes under abiotic stresses, supporting bioinformatics prediction. Verified genes were then submitted to free online gene networking tools and after determining relationships between predicted networks and inbred line phenotypes, possible novel gene candidates for enriching maize abiotic stress signaling network resolution were proposed.

MAIZE, TRANSCRIPTOME, DIFFERENTIAL GENE EXPRESSION, COLD, DROUGHT

08 – 04 Poster

FORWARD-IN-TIME METHOD VS. ARTIFICIAL NEURAL NETWORKING AS A TOOL FOR SIMULATION OF GENETIC DATA

Abdurahim Kalajdžić [1], Belma Kalamujić Stroil [1], Samim Konjicija [2], Naris Pojskić [1]

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Simulation studies in population and evolutionary genetics play a significant role in better understanding of different evolution scenarios and effects of different genetic models on genetic diversity. Forward-in-time method is designed in such a way that it starts with an initial population and follows entire evolution under different genetic models within multiple generations. On the other hand, artificial neural networks represent a formidable method for genetic simulation and prediction. In this project, we wanted to compare and corroborate results obtained with forward-in-time simulation which was done in a specialized simulation program with results attained from a specially designed strategy based on cluster analysis/ unsupervised learning using R programming language. As input data, alleles from 13 microsatellite loci from 219 specimens representing autochthonous Adriatic haplotype of *Salmo trutta* L. were used. This species was chosen as a model organism because it has been a center of many previous studies as well as because populations of *Salmo trutta* L. from the Neretva river were under the constant influence of major anthropogenic factors. Finally, genetic variation within these populations was disturbed due to hybridization and introduction of different allochthonous populations in its natural habitat. The main goal of this research is to reconstruct possible genetic structure of *Salmo trutta* L. population before major anthropogenic influence, and then make an assessment of possible deviation in genetic diversity of recent populations with populations from a period before human influence. The second goal was to compare precision and reliability of these two methods for different purposes. Our results are in concordance with other reports from literature which indicate that both of these approaches can be used as a reliable simulation tools. However, it is believed that artificial neural networks can represent more powerful simulation tools.

FORWARD-IN-TIME, ARTIFICIAL NEURAL NETWORK, SIMULATION, MICROSATELLITE