

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

BIOINFORMATICS PREDICTION OF MITOCHONDRIAL AND CHLOROPLAST TRANSCRIPTS POSSIBLY INVOLVED IN MAIZE ABIOTIC STRESS SIGNALING

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In plants, the expression of mitochondrial and chloroplast genomes is continuously changing to enable adequate functional adjustments related to overall metabolic changes needed for plant adaptation to fluctuating environmental conditions. In order to identify mitochondrial and chloroplast transcripts expressed prior to stresses, we have analyzed mitochondrial and chloroplast transcriptomes of 46 maize inbred lines chosen from three main heterotic groups (BSSS, Lancaster, Iowa dent) regularly used in elite maize breeding programs. Organelles' data were extracted from transcriptome data obtained by next generation sequencing of total leaf transcriptomes of 46 maize inbred lines grown under the optimal conditions in the greenhouse. All data manipulation and differential gene expression analysis were performed by using Galaxy software (<https://usegalaxy.eu/>). Detected organellar complex transcripts milieus were expected to contain candidates that modulate responses of their genomes by activating certain signaling pathways upon exposure to abiotic stresses. With the aim to identify such candidates we focused on selecting transcripts that were differentially expressed between 46 maize inbred lines grown under the optimal breeding conditions and also annotated as important for abiotic stresses response in different plant species. Selected transcripts/genes were then subjected to freely available tools for gene networking analysis with the aim to depict possible anterograde and retrograde signaling between nucleus and mitochondria/chloroplasts under the abiotic stresses. Obtained results are promising in terms of planning biological experiments for testing the roles of genes that were bioinformatically predicted as novel members of abiotic stress signaling network between nucleus and organelles in maize.

ORGANELLE, TRANSCRIPTOME, ABIOTIC STRESS, MAIZE