

BOOK OF ABSTRACTS



CONGRESS

OF THE SERBIAN GENETIC SOCIETY

2019 | October
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VRNJAČKA BANJA • SERBIA





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Branka Vasiljević
Aleksandra Patenković
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Abstracts of the 6th CONGRESS OF THE SERBIAN GENETIC SOCIETY



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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



TABLE OF CONTENTS

Human omics variation

Medical genetics

Genetic toxicology: from cell to ecosystem

Adaptation and ecological genetics

Genetic diversity, phylogeny and conservation

Breeding for changing environments

Microbial genetics

Bioinformatics and big data analysis

Miscellaneous topics

Personalized medicine: promise and reality

The truth is in wine and DNA
– applications of molecular methods in viticulture

09 – 03 Poster (Plant breeding)

**RATIO OF DOMINANT AND RECESSIVE GENES
OF IMPORTANT QUANTITATIVE TRAITS IN SUNFLOWER**

Milan Jocković¹, Slaven Prodanović², Sandra Cvejić¹, Siniša Jocić¹,
Petar Čanak¹, Ana Marjanović-Jeromela¹, Vladimir Miklič¹, Jelena Ovuka¹

¹ *Institute of Field and Vegetable Crops, Novi Sad, Serbia*

² *Agriculture Faculty, University of Belgrade, Belgrade, Serbia*

jockovic@gmail.com

For designing efficient breeding procedure adequate information on the genetic structure of the parents and mode of gene action affecting the yield and its related traits are prerequisite for progress in breeding. The objective of this research was to evaluate heritability, components of genetic variance as well as ratio of dominant and recessive genes in parental genotypes of sunflower. The plant material selected for this research consisted of sunflower genotypes distinguished by important characteristics for the production of sunflower. Quantitative traits evaluated in this study were seed yield/plant, oil content, 1000 seed weight, head diameter and plant height. Presented results showed significant variability of evaluated quantitative traits. Phenotypic variance was higher than genotypic demonstrating strong environment effect in expression of evaluated traits. The values of broad sense heritability for evaluated traits were very high for plant height, high for 1000 seed weight, moderate for seed yield/plant and head diameter, while low for oil content. The analysis of components of genetic variance indicated prevalence of dominant component (H) compared to additive (D) and higher concentration of dominant genes (u) compared to recessive (v), in all investigated traits. Position of expected line of regression pointed over dominance in inheritance for seed yield/plant, oil content and head diameter, while for 1000 seed weight and plant height was found that additive gene action played role in inheritance suggesting that selection in early generations for these traits will be effective. Comparing the sequences of the scattering diagrams indicated the presence of interallelic interaction which was discarded after testing the coefficients of regression.

HERITABILITY, PHENOTYPIC VARIANCE, GENOTYPIC VARIANCE, DOMINANT COMPONENT

09 – 04 Poster (Modulation of gene expression: Pharmacological Aspects)

**GENE EXPRESSION OF PREFRONTAL DOPAMINE BIOSYNTHETIC ENZYME
IN CHRONICALLY STRESSED RATS TREATED WITH LITHIUM**

Nataša Popović, Vesna Stojiljković, Snežana Pejić, Ana Todorović,
Ivan Pavlović, Snežana B. Pajović, [Ljubica Gavrilović](mailto:gljubica@vin.bg.ac.rs)

*Institute of Nuclear Sciences "Vinča", Laboratory of Molecular Biology and
Endocrinology, University of Belgrade, Belgrade, Serbia*

gljubica@vin.bg.ac.rs

Our earlier research confirmed that chronic restraint stress (CRS) induced decreased gene expression of tyrosine hydroxylase (TH) a "rate-limiting" enzyme of dopamine biosynthesis and decreased concentrations of dopamine (DA) in the prefrontal cortex (PFC). In addition, we confirm that CRS influenced anxiety and depressive-like behavior in rats. In pathophysiology of mood disorders lithium is known as an effective drug in the long-term stabilization of moods. However, very little is known about gene expression of TH and concentration of DA in the PFC in chronically stressed rats treated with lithium. Therefore, this study aimed to investigate the effects of mood stabilizer lithium on gene expression of TH, as well as concentration of DA in the PFC in animals exposed to CRS (2 hours × 14 days). The investigated parameters were quantified by real-time RT-PCR, Western blot analyses and ELISA kits. In the present study we found that lithium treatment increased levels of TH mRNA by 56% ($p < 0.05$), TH protein by 22% ($p < 0.01$) and concentration of DA by 72% ($p < 0.001$) in chronically stressed rats to the levels found in unstressed animals, which indicates that lithium enabled de novo synthesis of prefrontal DA in chronically stressed rats. Lithium may have induced gene expression of TH in stress condition through the activator protein-1 (AP-1) transcription factor pathway. The results presented here suggest that lithium treatment may modulate gene expression of prefrontal TH and increase concentration of prefrontal DA in chronically stressed rats to the levels found in unstressed animals.

GENE EXPRESSION, LITHIUM, CHRONIC RESTRAINT STRESS, DOPAMINE