

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



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– applications of molecular methods in viticulture

06 – 05 Oral

MOLECULAR MARKERS FOR DETECTION OF Rf1 GENE DEVELOPED FROM BAC-END SEQUENCES IN SUNFLOWER

Aleksandra Radanović¹, Renate Horn², Yves Sprycha², Sonia Hamrit³, Milan Jocković¹, Sandra Cvejić¹, Siniša Jocić¹, Vladimir Miklič¹, Dragana Miladinović¹

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Sunflower is the second most common crop among hybrids, worldwide. Development of cytoplasmic male sterile and fertility restoration lines enables creation of hybrids. Sunflower hybrid breeding most frequently relies on the combination of the CMS PET1 cytoplasm and the fertility restoration gene Rf1. Use of molecular markers can accelerate creation of restorer lines. Previous work on this subject included mapping of the Rf1 gene on chromosome 13 and development of bacterial artificial chromosome (BAC) libraries for the restorer line RHA325 and the maintainer line HA383, which enabled positioning of BAC clones surrounding the Rf1 gene in the cross RHA325 x HA342. In this study, BAC-end sequences were used to derive primers in order to amplify selected regions from RHA325 and the maintainer line, HA342. While the majority of primer combinations were monomorphic, some were polymorphic between RHA325 and HA342. Previously reported markers for detection of Rf1 gene and newly developed ones based on BAC-end sequences were further tested on hybrids and its components (A, B and R lines) created at the Institute of Field and Vegetable Crops, Novi Sad.

So far, the majority of markers designed for identification of Rf1 gene are dominant, with just a few being co-dominant. In the present research we increased the number of available markers that can be used for detection of the Rf1 gene in marker assisted selection (MAS). However, none of the newly designed markers could be universally used for all tested restorer lines, thus verification of the reported markers is required before application in MAS in a specific cross combination.

This study was supported by German-Serbian bilateral cooperation project - (No. 451-03-01732/2017-09/3 and project code 57393592), Deutsche Forschungsgemeinschaft (DFG) projects HO 1593/5-1 and HO 1593/5-2, Ministry of Education, Science and Technological Development of Republic of Serbia, project TR31025 and COST Action CA18111.

HELIANTHUS ANNUUS L., MARKER ASSISTED SELECTION, FERTILITY RESTORATION, HYBRID, BREEDING

06 – 06 Oral

EFFECT OF GENOTYPE AND ENVIRONMENT ON VARIABILITY OF PRODUCTIVE TILLERING IN BREAD WHEAT (*TRITICUM AESTIVUM L.*)

Desimir Knežević¹, Dušan Urošević², Aleksandar Paunović³, Jelica Živić, Danica Mićanović⁵, Nevena Djukić⁶, Stefan Marković⁶, Mirela Matković Stojšin², Veselinka Zečević²

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Productive tillering of wheat plants has impact on determination of crop density, number of spikes and number of kernels per unit area (m⁻²), which is related with grain yield. The aim of the work was to investigate variability of productive tillering of genetically divergent wheat cultivars grown under different environmental conditions. Twenty genetically divergent winter wheat cultivars were investigated during a two-year period in a randomized block design experiment, in three replications. Seeds of the cultivars were sown in rows 1.0 m in length. The distance between seeds was 0.10 m in rows and the distance between rows was 0.2m. The 60 plants in full maturity stage (20 plants per replication) were used for analysis of the number of productive tillers plant⁻¹. The analysis of variance of obtained data were processed using MSTAT C (5.0 version). The significant differences between values were estimated by F-test and LSD (0.01; 0.05). The results showed differences among genotypes for productive tillering and significant differences between years. In the first year of experiment, the number of productive tillers varied between 6.13 in Proteinka and 9.01 in Kompas, and in the second between 8.26 in Tanjugovka and 10.68 tillers in Kompas cultivar. The average productive tillering was 7.39 in the first year, while in the second it was 9.40. The differences between cultivars were affected by genetic and environmental factors with greater influence by the latter.

WHEAT, GENOTYPE, VARIABILITY, TILLERS, ENVIRONMENT