The Balkan Botanical Congress is an international meeting that has been held nearly every three years, since 1997. It brings together botanists from around the world who perform research on plants in the widest sense, as well as scientists who are engaged in the plant sciences and their applications. We were honored to host such an extraordinary scientific event this year in Serbia.

The 7th Balkan Botanical Congress – 7BBC 2018 took place in Novi Sad from September 10th to 14th 2018. The Congress was organized by the University of Novi Sad, Faculty of Sciences, Department of Biology and Ecology and the "Andreas Wolny" Botanical Society, along with the great help of 7 co-organizers and more than 30 supporters and sponsors. It truly was not possible to happen without exceptional help of our co-organizer - the Institute for Nature Conservation of Vojvodina Province who made this congress not only possible, but totally awesome.

7BBC 2018 placed a special emphasis on plants of the Balkan Peninsula and covered various research fields. The Congress was organized into ten sessions: Plant Anatomy and Physiology, Plant Taxonomy and Systematics, Plant Molecular Biology and Genetics, Floristics, Vegetation and Phytogeography, Conservation Botany and Plant Invasions, Phytochemistry and Plant Resources, Agronomy and Forestry, Botanical Collections and History, Ethnobotany and Cryptogam Biology. These topics were elaborated through five plenary lectures given by eminent scientists, as well as in the form of introductory lectures, oral and poster presentations. With an overall number of 387 abstracts presented on the very latest of botanical science, we shared knowledge, expertise and novel ideas. We welcomed nearly 400 scientists to Novi Sad, and we believe that we succeeded in our joint endeavor to make new networks and new connections among botanists. We hope that we contributed to advancements in the wide and beautiful field of botany, ranging from fundamental botanical research to applied botany.

It is our great pleasure to publish this Abstract Book in Botanica Serbica, in the same year that this international journal, a renamed continuation of the Bulletin of the Institute of Botany and Botanical Garden Belgrade, celebrates its 90 year jubilee. On behalf of the Scientific and Organizing committee of 7BBC 2018 we would like to express our gratitude to all contributors, colleagues and sponsors for taking part in the 7th Balkan Botanical Congress, as well as for their efforts and contributions to it's successful realization.

Goran Anačkov and Lana Zorić,
Co-presidents of the Scientific Committee of the 7 BBC
and guest editors of Botanica Serbica 42 (supplement 1).

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The 7th Balkan Botanical Congress consists of plenary lectures, introductory lectures of each session, as well as oral and poster presentations on the following topics:
Sessions 1. Plant Anatomy and Physiology
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Sessions 3. Plant Molecular Biology and Genetics
Sessions 4. Floristics, Vegetation and Phtytogeography
Sessions 5. Conservation Botany and Plant Invasion
Sessions 6. Phytochemistry and Plant Resources
Sessions 7. Agronomy and Forestry
Sessions 8. Botanical Collections and History
Sessions 9. Ethnobotany
Sessions 10. Cryptogam Biology

GENETIC DIVERSITY OF *POSIDONIA OCEANICA* MEADOWS IN THRACIAN (NORTHERN AEGEAN) SEA: PRELIMINARY RESULTS

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Posidonia oceanica is an endemic seagrass widespread in the Mediterranean Sea, forming continuous meadows and playing an important role in coastal ecosystem dynamics. Up to date, it is considered the most important and well-studied seagrass of the Mediterranean. *P. oceanica* meadows of the Thracian Sea (Northern Aegean Sea, Greece) is estimated as one of the largest in the Eastern Mediterranean. Growing along the Mediterranean coastline, they are subject to continuous anthropogenic pressure, occasionally leading to decline, which challenges the ecological stability of those coastal ecosystems. Genetic diversity and intra-meadow heterogeneity in *P. oceanica* is correlated with adaptability of its populations in variable environmental conditions (both natural and anthropogenic) and therefore is an indicator of meadow's sensitivity to these perturbations. *P. oceanica* meadows showing signs of decline during 2000-2012, mainly in the easternmost part of the Thracian Sea, motivated us to estimate its genetic diversity using highly variable dinucleotide microsatellite markers. Samples were collected from eight stations in the Thracian Sea at a depth range of 9-11 m. Fresh leaf tissues, cleaned from epiphytes were grounded using distilled water and genomic DNA was extracted from eight samples widely distributed through the study area using an isoamylic-chloroform protocol. Four microsatellite loci (Po5, Po5-10, Po5-49 and Po4-3) were amplified by Polymerase Chain Reaction and submitted to Sanger sequencing. Alleles were detected by manual and automated inspection (Mutation Surveyor software) of Sanger chromatograms in order to read superimposed base calls and identify the heterozygous alleles. Results were validated using 12% w/v polyacrylamide gel electrophoresis. Statistical analysis was conducted with appropriate software (GENCLONE v2.0, GeneAlEx, ARLEQUIN). Two loci were monomorphic (Po5, Po4-3) and two were polymorphic (Po5-10, Po5-49). Clonal diversity was found at 0.75 and levels of heterozygosity are exceeding the expected values. Our preliminary findings imply that the intra-meadow genotypic diversity is significant and provide an interesting insight concerning the correlation between genetic diversity and adaptability of *P. oceanica* in diverse environmental conditions.

KEYWORDS: *Posidonia oceanica*, marine angiosperm, intra-population genetic diversity, microsatellite

GENETIC DIVERSITY OF APRICOT CULTIVARS AND SELECTIONS FROM FACULTY OF AGRICULTURE, NOVI SAD BREEDING PROGRAM

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Apricot selection program at the Faculty of Agriculture in Novi Sad, Serbia, started in early 80s with selection goals including late flowering, late frosts resistance, high productivity and good fruit quality. Selection from natural populations resulted with five cultivars and two selections still in the process of registration. Cultivars released from the selection program are nowadays wide spreading in Serbia and surrounding countries, making traditionally grown Magyar kajszi and Kécskei rozsa less represented in the assortment of apricot cultivars grown in Serbia. Being selected from the limited cultivation area, although differing in phenotypes, their genotypic characterization has not yet been performed. The goal of the research was to determine the genetic diversity among apricot genotypes selected at the Faculty of Agriculture Novi Sad and compare them with 13 other cultivars grown worldwide. Plant material consists of 7 apricot cultivars and selection from Faculty of Agriculture, University of Novi Sad breeding program (Novosadska kasnocvetna, Novosadska rodna, NS 4, NS 6, Buda, SK1 andSK3), as well as 13 cultivars from other worldwide breeding programs. Young, fully developed leaves were collected, and total genomic DNA was extracted using modified CTAB protocol. A set of 17 SSR primer, from which 8 was associated with QTL-s for ripening time, PPV resistance, Xanthomonas resistance and chilling requirement according to GDR (Genome Database for Rosaceae) was used. High genetic diversity level was observed between all analyzed genotypes. Using described set of markers we were able to distinguish all genotypes with exception of SK 3, NS 4 and Magyar kajszi. Cluster analysis grouped all cultivars from University of Novi Sad breeding program closely together while cultivar Buda was clustered away from this group. It can be concluded that all analyzed genotypes from Faculty of Agriculture, Novi Sad exhibited moderate level of genetic diversity assed by SSR markers. Regarding its phenotypic characteristics and genotype profile cultivar Buda is the most divergent from other genotypes arising from same breeding program.

KEYWORDS: breeding, diversity, molecular markers, SSR, microsatellites

MOLECULAR TOOLS FOR SUGAR BEET IMPROVEMENT IN INSTITUTE OF FIELDS AND VEGETABLE CROPS, NOVI SAD

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Sugar beet is one of the most important industrial crops. Beet sugar now accounts for almost all sugar production in the Europe and for about 20% of total world production. Crop improvement is important in order to enhance productivity, sugar content or other desirable traits, and molecular techniques can help to accelerate such efforts. One of our research interests is focused on to the development of new sugar beet lines and hybrids combining marker assisted selection with conventional breeding methods. DNA markers were used to assess the genetic diversity and distance among breeding lines and correlate them with hybrid performance, in order to define the heterotic groups and predict heterosis effect. Our activities also involve the investigation of different reaction of sugar beet genotypes to reduced water supply, as the major limiting environmental factor in sugar beet growing. Genotypes with different ability to maintain turgor in the unfavorable field conditions were analyzed in the greenhouse and *in vitro* for morphological and physiological parameters of water regime under conditions of water deficit. The obtained plant material was also studied for the expression of genes that are known to respond to osmotic stress. There are reasons to believe that fullerenol ability to form hydrogen bonds with water molecules makes this nanoparticle a potential intracellular water depot, which can be used if osmotic stress occurs. In collaboration with colleagues from the Faculty of Science, Novi Sad we have started to analyze the influence of fullerenol on sugar beet plants exposed to drought stress. Results indicate that application of fullerenol can modify intracellular water metabolism and enable adaptation of plants to drought stress. The activities as part of phytopathological studies consider the main sugar beet leaf and root pathogens such as *Cercospora beticola* and *Macrophomina phaseolina*. The research presented here are an attempt toward fulfilling the potential of molecular tools in an improvement of sugar beet crop to better tolerate biotic and abiotic stresses.

KEYWORDS: crop improvement, molecular research, sugar beet

FUNCTIONAL ENRICHMENT ANALYSIS OF MARKER EFFECTS FROM GENOMIC PREDICTION MODELS IN SOYBEAN

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Genomic selection is a promising tool that can increase the efficiency of crop breeding, being particularly useful for improvement of quantitative traits. This approach is based on prediction of plant performances by estimation of breeding values using simultaneously effects of molecular markers across the genome. Even though all available genome-wide markers are used for selection, it could be expected that markers located near genes responsible for particular biological function will have higher effects on final breeding value. This work aimed to estimate marker effects for soybean yield by developing prediction model and to perform functional annotation and enrichment in order to reveal the differences in marker effects related to different biological functions on yield prediction. Training population of 230 lines from the existing breeding program of Institute of Field and Vegetable Crops, was analysed using genotyping-by-sequencing and evaluated for yield in field trails over three growing seasons. Molecular, single nucleotide polymorphism (SNP) and phenotypic data were combined in prediction model, considering ridge-regression best linear unbiased prediction statistical method. Each SNP located inside predicted gene model was assigned with gene ontology (GO) terms for biological processes. The distribution of marker effects with particular GO term was compared with distribution of effects of all remaining markers by using Kolmogorov–Smirnov test. False discovery rate correction was performed, adjusting p<0.05 as significant. Functional enrichment identified 3471 unique GO terms, 1829 of which were related to biological processes. In total, it was identified 21333 SNPs associated with a biological processes GO terms, covering 10594 predicted gene models. GO terms were further clustered to 36 higher categories, including from 15 to 805 GO terms. Significant enrichment was observed for terms related to cell differentiation and cell death. Furthermore, cluster covering biosynthesis was also significant, including multiple terms related to protein, lipid, carbohydrate and nucleic acid metabolism, as well as secondary metabolism. This indicates that processes involving primary and secondary metabolites can be important for predicting yield breeding values. Preliminary data revealed associations with potential for elucidating biological processes relevant to yield, which should be deeply investigated.

KEYWORDS: soybean, genomic prediction, functional enrichment, gene ontology