



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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Sessions:

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
- Sessions 2. Plant Taxonomy and Systematics
- Sessions 3. Plant Molecular Biology and Genetics
- Sessions 4. Floristics, Vegetation and Phytogeography
- 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

the Shannon diversity index was 0.77 indicating high level of morphological diversity in the collection. The lowest diversity (0.07) was found for CCT and the highest individual descriptor diversity was found for GC (0.68). The results indicated that morphological characterization with higher number of analysed traits can be used to improve description of wheat germplasm in addition to molecular and agronomical evaluations.

KEYWORDS: variability, morphological characters, Shannon index, *Triticum sp.*

Poster presentation 12 07 20

ENVIRONMENTAL MODELING OF INTERACTION VARIANCE FOR GRAIN YIELD OF MIDDLE-LATE MAIZE HYBRIDS

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The phenomenon of genotype by environment interaction (GEI) represents permanent interest for breeders and biometricians along with practical and theoretical aspects. We investigated GEI for grain yield of middle-late maize (*Zea mays* L.) hybrids from the official variety trial network by the Department of Protection and Recognition of Varieties of Republic Serbia that includes 25 experimental maize hybrids in the year of 2004, and 15 in the year of 2005, on eight sites over two years, using factorial regression model that captures additional environmental variables - maximum temperature (mxT), minimum temperature (mnt), mean temperature (mt), precipitation (pr), relative humidity (rh), insolation hours (in) and environmental index (EI). Environmental variables in the best of the tested models explained 76% and 76.2% of the GEI variation for two consecutive years, respectively. Factorial regression combined with stepwise procedure revealed the 5-variable model that includes variables pr7 (explaining 29.1% of the variation), EI (19.1%), mnt9 (14.5%), mxT4 (13.3%), in 2004 and the two-variable model: mnt6 (60.2%), mT9 (16.0%) in 2005 as the most explanatory models in the region of Vojvodina for these two consecutive years. These results provide a solid base for further research in GEI and stability analysis, and are a useful tool in characterizing the sub-regions of maize growing area and extending the existing results to new sites.

KEYWORDS: genotype by environment interaction, maize, yield, environmental variables

Poster presentation 13 07 24

EVALUATION OF THE BALKAN PHASEOLUS COCCINEUS L. GENETIC RESOURCES

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In the last decade several thousand accessions were collected in different parts of Europe and are stored in national gene banks; at present the Phaseolus Database as part of the EURISCO Web catalogue contains over 46000 records. Main objective of the study (ECPGR SMARTLEG project) was proper phenotypic and genetic evaluation of European *Phaseolus* accessions with emphasis to *Phaseolus coccineus* germplasm providing new data to EURISCO and AEGIS. During the project, we provided three different types of datasets including morpho-agronomic traits of plants, morphometric seed characteristics and genetic profiles of *P. coccineus* accessions from eight European geographic origins: Slovenia, Romania, Bosnia and Herzegovina, Serbia, Italy, Slovakia, Macedonia and Austria. Before sowing, the morphometric characterization of *P. coccineus* seeds was performed according to adopted Community Plant Variety Office-Technical Protocol and Phaselion/AIS descriptors observing 14 different seed characteristics. The morphological evaluations were performed upon adjusted descriptors for *Phaseolus* (ECPGR PhasChar from Austria) under field conditions in Slovenia, Romania, Serbia, Macedonia and Bosnia and Herzegovina. A set of 12 already proven and reliably cross-species amplified nSSR markers among *Ph. vulgaris* and *P. coccineus* genomes was applied to evaluate genetic structure of *P. coccineus* genotypes. Morpho-agronomic evaluation shows differentiation between *P. coccineus* accessions even for standard varieties under geographically distinct field conditions. Global principal component analysis extracted four components which cumulatively explains 74.6 % of morphometric variability of *P. coccineus* seeds. Analysis of molecular variability on the basis of allelic patterns reflects 3 % of the molecular variability among *P. coccineus* germplasm from eight different geographic origins which means that 97 % of germplasm is common to all accessions ($p > 0.01$). Regarding to genetic structure of the *P. coccineus* germplasm from eight geographically distinct collections, three genetic clusters were formatted; the average genetic distance between genotypes in each cluster varies between 0.592 and 0.816. Overall results indicate common geo-

graphic origin of *P. coccineus* accessions from different collections within the Balkan.

KEYWORDS: morpho-agronomic traits, morphometric characterization, genetic structure, ECPGR SMARTLEG project, EURISCO

Poster presentation 14 07 05

WILD FRUIT CROPS: PRESERVATIONS AND UTILIZATION

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Due to specific phyto-geographic relations, specific climatic, orographic and edaphic conditions forest phytocoenoses in Vojvodina (North Serbia) are very diverse. Significant and completely unused parts of this biodiversity are autochthonous wild fruit species. Due to the unique variability of the species, the Balkan peninsula can be considered as the secondary center of genetic diversity of several species and genera, such as: *Malus × domestica*, *M. sylvestris*, *Pyrus communis*, *Prunus cerasifera*, *P. mahaleb*, *P. fruticosa*, *P. tenella*, *Morus spp.*, *Corylus colurna*, *Castanea sativa*, *Fragaria vesca*, *Olea europaea*, *Cornus mas*, *Sambucus nigra*, *Sorbus spp.*, *Rosa spp.* These wild and underutilized species produce fruits of unique quality and high nutritional value, which are used in human nutrition, food and pharmaceutical industries. Elderberry (*Sambucus spp. L.*), one of the most common and widespread species, can be considered as a source of natural antioxidants with promoting effect on human health. Eight divergent genotypes of elderberry were selected from natural populations of Central Serbia and Vojvodina with high antioxidant capacity and high content of vitamin C. Within genus *Morus* three species were analyzed and underwent selection. Selections of *Morus nigra* and *Morus rubra* were distinguished by high content of vitamin C. Genotypes with dark colored fruits contained high amount of anthocyanins and total phenols. Cornelian cherry (*Cornus mas L.*) holds great biological and economic potential, and it is rich source of material for further breeding. Within natural populations in whole Serbia high diversity considering fruit weight was observed. Five genotypes with large fruits and high soluble solids content were selected. *Sorbus domestica* exhibited high diversity level in Vojvodina, and on account of that selection of superior genotypes is currently in progress.

KEYWORDS: biodiversity, variability, selection, Balkan peninsula

Poster presentation 15 07 17

EXPLORING AND GATHERING THE SERBIAN AND CZECH CROP WILD RELATIVES FOR INCREASING CROP DIVERSITY IN AGRICULTURE

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Conservation of plant genetic resources for food and agriculture is a very important task from the strategic and economic points of view almost in the whole world. Collecting expeditions and gathering of crop wild relatives, such as meadow (field and vegetable crops), aromatic, medicinal plants and some threatened species, are important parts of plant genetic resources activities which enrich gene bank storage composition. Common collecting missions have been organized annually in both countries since 2011. Seven of them took place in Serbia and seven in the Czech Republic. In total, 228 localities have been visited and 1202 seed samples of crop wild relatives have been collected. In the Czech Republic it was 107 localities and 659 seed samples, while in Serbia it was 121 localities and 543 seed samples. The numbers present large source of biodiversity, which can be utilized in breeding and within *in situ* conservation activities. All the samples are stored in the working collections of both institutes, after regeneration and multiplication process the seeds are stored in both national gene banks. These collecting missions provided new information concerning the distribution of crop wild relatives and traditional farming practices still present in some regions, especially in Serbia. Our preliminary results indicated that the wild seed lots are an important source of valuable genetic variability for utilization in breeding programs. In the paper detailed survey of collected material and its utilization is presented.

KEYWORDS: genetic resources, collecting missions, Serbia, Czech Republic, gene banks, conservation, evaluation

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