Botanica SERBICA Vol. 42 (supplement 1) 7BBC Book of abstracts

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

x ssp. *americana* hybrids was reported in several European countries where ranges of two subspecies overlap. In Croatia, the disease was first recorded in Slavonia in 1929 and since then it is considered to be the most significant cause of the decline of elms in Croatian forests, especially affecting *Ulmus minor*. Recent investigation indicated that *O. novo-ulmi* is the only causal agent of DED in Croatia, while *O. ulmi* has probably completely disappeared. This study was conducted in order to determine distribution of *O. novo-ulmi* subspecies and estimate incidence of their hybrids in *U. minor* populations in Croatia. A total of 31 isolates of *O. novo-ulmi*, previously obtained from infected *U. minor* samples from three sites across Croatia (Nova Kapela, Đurđevac 1 Jastrebarsko), were analyzed by PCR-RFLP of cerato-ulmin (*cu*) and the colony type (*col1*) gene regions. Presence of both *O. novo-ulmi* subspecies was proven, but with significantly higher incidence of ssp. *novo-ulmi* at investigated sites. A twenty-one isolate was assigned to *O. novo-ulmi* ssp. *novo-ulmi* and only three isolates were assigned to ssp. *americana*. Seven isolates were shown to be subspecies hybrids. *O. novo-ulmi* ssp. *novo-ulmi* as well as hybrid isolates, were present at all three investigated sites, while *O. novo-ulmi* ssp. *americana* was detected only in Nova Kapela and Đurđevac. Results of this study represent significant contribution to understanding of the structure of DED pathogen populations affecting *U. minor* in Croatia.

KEYWORDS: *Ophiostoma novo-ulmi*, hybridization, subspecies hybrids, PCR-RFLP

Poster presentation 08 07 23

MOLECULAR CHARACTERIZATION OF *CHRYPHONECTRIA HYPOVIRUS* 1 FROM SLOVENIA

Ljiljana Krstin[1], Zorana Katanić[1], Jelena Repar[2], Marin Ježić[3], Ana Kobaš[1] & Mirna Ćurković Perica[2]*

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The pathogenic fungus *Cryphonectria parasitica* Murrill Barr has been responsible for the decline of European chestnut. This aggressive ascomycete causes chestnut blight, a serious disease that destroys chestnut trees by causing bark cankers that progressively enlarge, girdle and kill branches and trunks of infected trees. This disease in Europe is successfully controlled with naturally-occurring Cryphonectria hypovirus 1 (CHV1), a double-stranded RNA (dsRNA) virus that reduces the virulence, sporulation and pigmentation of fungus and can therefore be used as a biocontrol agent of the chestnut blight. CHV1 was probably introduced together with its fungal host to Europe from Asia and then naturally spread throughout C. parasitica populations. In Slovenia, the disease was first recorded in 1950 and has been reported to date in all investigated chestnut populations. C. parasitica in those chestnut populations has a high diversity of vegetative compatibility (vc) types that can limit the spread of CHV1. It is known that CHV1 easily spreads between C. parasitica strains of the same vc type, but between strains of different vc types it spreads less frequently. Despite a high diversity of vc types, CHV1 is widespread in Slovenian C. parasitica populations. In order to gain a better insight into the genetic diversity of CHV1, we have analysed CHV1 infected C. parasitica isolates from Slovenia. Molecular characterization of CHV1 included hypoviral dsRNA extraction, complementary DNA synthesis, PCR amplification and partial sequencing of CHV1 genome. The obtained nucleotide sequences were assembled and the number of nucleotide differences and genetic distance between them were determined. Phylogenetic analysis grouped CHV1 sequences from Slovenia to the Italian subtype of CHV1, the only subtype found so far in Slovenia. Among sequenced CHV1 isolates a large number of different haplotypes were detected which indicates a high genetic diversity of CHV1 in Slovenia. High genetic diversity is not a consequence of recombination events, but is probably the result of numerous point mutations.

KEYWORDS: biological control, chestnut blight, genetic diversity, hypovirulence

Poster presentation 09 07 13

ROOT PHENOTYING OF NS SUNFLOWER

Aleksandra Dimitrijević[1]*, Anna Galinski[1], Dragana Miladinović[1], Sandra Cvejić[1], Siniša B. Jocić[1], Šreten Terzić[1], Kerstin A. Nagel[2] & Fabio Fiorani[2]

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Sunflower breeding, in the past decades, had lead to significant improvements in sunflower yield, pest resistance, and altered oil composition; however breeding is oriented towards analysis and improvement of above-ground parts, while root development has been significantly neglected. Future breeding efforts that would be aimed at modifying root traits can result in improved crops regarding stress-tolerance and ultimately increased yields by optimizing the capacity of the plant for soil exploration (water and nutrient acquisition). Development of novel phenotyping platforms for non-invasive root analysis facilitates characterization of root architecture and investigation of developmental dynamics and root growth. Up to our knowledge, this is the first report of sunflower root phenotyping using modern phenotyping platforms. In this preliminary study, one cultivated and one wild sunflower genotype were examined by use of the automated phenotyping platform, *GROWSCREEN-Rhizo*. Imaging of the rhizotron grown plants had been performed twice per week and the following traits were quantified using the image processing software GrowScreen-Root: total root length, primary and lateral root length, rooting depth, root system width, and area covered by the root system. At the end of the experiment, fresh and dry shoot weight were measured. After harvest, sunflower roots were used for determining total root length and root diameter by utilizing the WinRhizo system. During plant development and imaging of the roots, it had been observed that cultivated sunflower developed faster comparing to the wild relative. Preliminary analysis of total root length after washing and the one obtained by imaging showed that approx. 1/3 of the whole root system is visible at the transparent surface of the rhizotrons.

ACKNOWLEDGEMENTS: This study was supported COST Action FA 1306: The quest for tolerant varieties -Phenotyping at plant and cellular level (STSM); by Provincial Secretariat for Higher Education and Science of Vojvodina, project 114-451-2126/2016-03; by Ministry of Education, Science and Technological Development of Republic of Serbia, project TR31025.

KEYWORDS: *H. annuus* L., root architecture, rhizotrons

Poster presentation 10 07 06

COMBINED APPROACH FOR IDENTIFICATION OF PHENOTYPIC AND -OMICS MARKERS THAT COULD BE INCLUDED IN SUNFLOWER BREEDING PROGRAMS

Dragana Miladinović*, Šreten Terzić, Jelena Ovuka, Aleksandra Dimitrijević, Milan Jocković, Sandra Cvejić, Siniša B. Jocić, Nada Hladni, Ana Marjanović Jeromela & Vladimir Miklič

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Diversity in plant genetic resources provides an opportunity for plant breeders to develop new and improved cultivars with altered quality traits, resistant to diseases and unfavourable environment. Novel approaches in genotyping and phenotyping enabled more efficient data collection for identification of quantitative characters and to explain the genetic basis of agriculturally important traits. The flip side of these new approaches is the risk of drowning in the massive amounts of data. That is why it is essential to develop proper approaches for data management and integrated analysis of differently collected data. Within the framework of ongoing projects, we have started to perform comparative phenotypic, metabolic and molecular analyses of 7 annual and 21 perennial wild sunflower (*Helianthus* spp.) species, as well as 19 genotypes of cultivated sunflower. The material consists of annual and perennial wild sunflower species (http://www.nsseme.com/about/inc/oilcrops/wild.php), interspecific hybrids, varieties, lines and hybrids, chosen from the IFVCNS collection, which is one of the largest sunflower germplasm collections. Data are collected for 48 morphological and respective metabolic parameters. This is further complemented by molecular analyses for identification of molecular markers and QTLs correlated to parameters studied. The aim of this combined approach is to identify desirable traits and genotypes that could be further included in sunflower breeding programs for development of highly productive, stress resistant hybrids. A long-term goal is creation of ideotypes specific for certain agro-ecological conditions. Special attention is paid to the integration of phenotypic and -omics data in order to identify traits and markers of real practical value for the breeders, avoid massive collection of redundant data and render the process more efficient.

ACKNOWLEDGEMENTS: This study was supported by Ministry of Education, Science and Technological Development of Republic of Serbia, project TR31025, Provincial Secretariat for Higher Education and Science of Vojvodina, project No. 114-451-2126/2016-03, Serbian-German bilateral cooperation project No. 451-03-01732/2017-09/3 and COST Action CA 16212.

KEYWORDS: *Helianthus* sp., phenotyping, genotyping, breeding

Poster presentation 11 07 19

DIVERISTY OF WHEAT GENOTYPES BASED ON MORPHOLOGICAL MARKERS

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Phenotypic, biochemical and molecular evaluations of wheat collections are of a great importance to increase the knowledge of genetic diversity as the basic prerequisite for crop improvement in different breeding programs. Large scale genotyping by molecular markers as well as phenotyping of agronomical important traits generated a lot of valuable information for wheat researchers during the last few decades. However, some morphological traits are almost forgotten and very rarely used in evaluating diversity of wheat germplasm. The aim of this study was to analyse the morphological diversity in a collection of 450 wheat accessions originating from all over the world. The genotypes were chosen from the wheat genetic collection of the Small Grains Department and sown at the experimental field of the Institute of Field and Vegetable Crops, location of Rimski Šančevi (45°20`N, 19°51`E). Five morphological traits were analysed and used as markers for distinctness of wheat genotypes: auricle colour (AC), coleoptile colour (CC), leaf colour (LC), colour at tillering time (CTT) and grain colour (GC). The Shannon diversity index (H) was estimated as a measure of morphological diversity. The results have shown that the most of the genotypes had white auricle colour (87%), white coleoptile colour (81%), dark green colour at tillering time (96%), green leaf colour (61%) and light red grain colour (43%). The average value for

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