



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).

Organizers:

University of Novi Sad, Faculty of Sciences, Department of Biology and Ecology, Novi Sad
Botanical Society „Andrea Wolny“, Novi Sad

Co-organizers:

Institute for Nature Conservation of Vojvodina Province, Novi Sad
Institute for Nature Conservation of Serbia, Belgrade
University of Belgrade, Faculty of Biology, Belgrade
University of Belgrade, Faculty of Forestry, Belgrade
University of Belgrade, Institute for Biological Research "Siniša Stanković", Belgrade
University of Novi Sad, Faculty of Medicine, Center for Medical-Pharmaceutical Research and Quality Control, Novi Sad
Natural History Museum in Belgrade, Belgrade

Support:

Republic of Serbia, Ministry of Education, Science and Technological Development
Republic of Serbia, Ministry of Environmental Protection
Republic of Serbia, Autonomous Province of the Vojvodina, Provincial Secretary for Higher Education and Scientific Research Activity
Republic of Serbia, Autonomous Province of the Vojvodina, Provincial Secretary for Urbanization and Environmental Protection
City of Novi Sad
PWMC "Vode Vojvodine", Novi Sad
PC "Vojvodinašume", Petrovaradin
PCC "Gradsko zelenilo", Novi Sad
PCC "Lisje", Novi Sad
Matica srpska, Novi Sad
Institute of Field and Vegetable Crops, Novi Sad
University of Novi Sad, Institute of Lowland Forestry and Environment, Novi Sad
University of Novi Sad, Institute of Food Technology in Novi Sad, Novi Sad
University of East Sarajevo, Faculty of Technology, Zvornik
Journal "Plant Systematics and Evolution"
World Wild Fund For Nature, Belgrade
IUCN ECARO, Belgrade
Vojvodina Environmental Movement, Novi Sad
Biology and Ecology Students' Scientific Research Society "Josif Pančić", Novi Sad
National Park "Pruška gora"
Nature Park "Rusanda"
SNR "Deliblato Sand"
SNR "Obediska bara"
SNR "Okanj bara"
SNR "Slano Kopovo"
SNR "Titelaki breg"
SNR "Zasavica"
Hungarian Natural History Museum, Budapest
Tourism Organization of Vojvodina
Tourist Organization of the City of Novi Sad, Novi Sad
PanaComp, Wonderland Travel, Novi Sad

Sponsors:

• Coca-Cola HBC, Belgrade
• Naftchem, Sremski Karlovi
• BioSPIN ltd, Novi Sad
• Mikronik ltd, Belgrade

• Nikon
• Pivnica "Gusan", Novi Sad
• Intercaffa ltd, Belgrade

Honorable Committee

Dr Ana Petrova, Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, Bulgaria
Dr Kit Tan, Department of Biology, Faculty of Science, University of Copenhagen, Denmark
Dr Arne Strid, Department of Biology, Faculty of Science, Lund University, Sweden
Dr Werner Greuter, Herbarium Mediterraneum, University of Palermo, Italy & Botanischer Garten und Botanisches Museum Berlin-Dahlem, Freie University of Berlin, Germany
Dr Branislava Butorac, Institute for Nature Conservation, Serbia
Dr Branka Stevanović, Faculty of Biology, University of Belgrade, Serbia
Dr Dušan Nikolić, Rector of University of Novi Sad, Serbia
Dr Jelena Blaženčić, Faculty of Biology, University of Belgrade, Serbia
Dr Milica Pavkov Hirvojević, Dean of Faculty of Sciences, University of Novi Sad, Serbia
Miloš Vučević, The Mayor of Novi Sad, Serbia
Dr Pal Boža, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad, Serbia
Dr Rudolf Kastori, Secretary General of the Department of Natural Sciences, Matica srpska, Serbia
Dr Vladimir Stevanović, Faculty of Biology, University of Belgrade & Serbian Academy of Sciences and Art, Serbia
Vladimir Gallé, Provincial Secretary for Urban Planning and Environmental Protection, Serbia
Dr Zoran Milošević, Provincial Secretary for Higher Education and Scientific Research, Serbia
Dr Karol Marhold, Plant Science and Biodiversity Centre, Slovak Academy of Sciences, Charles University, Prague, and Secretary-General of International Association for Plant Taxonomy, Slovak Republic & Czech Republic
Dr Tod Stuessy, Museum of Biological Diversity, The Ohio State University, United States of America

Scientific Committee**Presidents:**

Dr Goran Anačkov, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad, Serbia
Dr Lana Zorić, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad, Serbia

Members:

Dr Alfred Mullaj, Faculty of Natural Sciences, University of Tirana, Albania
Dr Lulëzim Shuka, Department of Biology, Faculty of Natural Sciences, University of Tirana, Albania
Dr Božo Frajman, Institute of Botany, University of Innsbruck, Austria
Dr Peter Schönschetter, Institute of Botany, University of Innsbruck, Austria
Dr Faruk Bogunić, Faculty of Forestry, University of Sarajevo, Bosnia and Herzegovina
Dr Senka Barudanovic, Faculty of Science, Bosnia and Herzegovina
Dr Siniša Škondrić, Department of Biology, Faculty of Sciences, University of Banja Luka, Bosnia and Herzegovina
Dr Rosen Tsonov, Faculty of Biology, Sofia University "St. Kliment Ohridski", Bulgaria
Dr Vladimir Vladimirov, Department of Plant and Fungal Diversity and Resources, Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, Bulgaria
Dr Antun Alegro, Department of Biology, Faculty of Science, University of Zagreb, Croatia
Dr Božijan Surina, Natural History Museum Rijeka, Croatia
Dr Sandro Bogdanović, Faculty of Agriculture, University of Zagreb, Croatia
Dr Sonja Šiljak Jakovljević, Ecologie Systématique Evolution, CNRS, AgroParisTech, Univ. Paris-Sud, Université Paris-Saclay, France
Dr Dimitris Tzanoudakis, Division of Plant Biology, Department of Biology, University of Patras, Greece
Dr Panayotis Dimopoulos, Institute of Botany, Division of Plant Biology, Department of Biology, University of Patras, Greece
Dr Theophanis Constantinidis, Department of Ecology and Systematics, Faculty of Biology, National and Kapodistrian University of Athens, Greece
Dr Károly Gergely, Institute of Silviculture and Forest Protection, University of Sopron, Hungary
Dr Zoltán Barina, Department of Botany, Hungarian Natural History Museum, Hungary
Dr Vlado Matevski, Institute of Biology, Faculty of Natural Sciences and Mathematics, Ss. Cyril and Methodius University and Macedonian Academy of Sciences and Arts, Macedonia
Dr Danka Caković, Faculty of Natural Sciences and Mathematics, University of Montenegro, Montenegro

Dr Danijela Stešević, Faculty of Natural Sciences and Mathematics, University of Montenegro, Montenegro
 Dr Vesna Mažić, Institute of Marine Biology, University of Montenegro, Montenegro
 Dr Łucja Łukasz, Department of Botany, Institute of Applied Biotechnology and Basic Sciences, University of Rzeszów, Poland
 Dr László Bartha, Institute for Interdisciplinary Research in Bio-Nano Sciences Romania
 Dr Biljana Božin, Department of Pharmacy, Faculty of Medicine, University of Novi Sad, Serbia
 Dr Bojan Konstantinović, Department of Environmental and Plant Protection Faculty of Agriculture, University of Novi Sad, Serbia
 Dr Bojan Zlatković, Department of Biology and Ecology, Faculty of Science and Mathematics, University of Niš, Serbia
 Dr Branišlava Lakičić, Faculty of Pharmacy, University of Belgrade, Serbia
 Dr Dmitar Lakičić, Institute of Botany and Botanical Garden "Jevremovac", Faculty of Biology, University of Belgrade, Serbia
 Dr Dragana Miladinović, Institute of Field and Vegetable Crops, Serbia
 Dr Dragana Raničić, Faculty of Agriculture, University of Belgrade, Serbia
 Dr Dragana Vukov, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad, Serbia
 Dr Gordana Tomović, Institute of Botany and Botanical Garden "Jevremovac", Faculty of Biology, University of Belgrade, Serbia
 Dr Ivana Maksimović, Faculty of Agriculture, University of Novi Sad, Serbia
 Dr Ivana Marković, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad, Serbia
 Dr Maša Karaman, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad, Serbia
 Dr Marjan Niketić, Natural History Museum, Serbia
 Dr Marko Šabovljević, Institute of Botany and Botanical Garden "Jevremovac", Faculty of Biology, University of Belgrade, Serbia
 Dr Milijana Pan, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad, Serbia
 Dr Milan Stanković, Department of Biology and Ecology, Faculty of Sciences, University of Kragujevac, Serbia
 Dr Milen Veljić, Institute of Botany and Botanical Garden "Jevremovac", Faculty of Biology, University of Belgrade, Serbia
 Dr Mirjana Šijačić Nikolić, Faculty of Forestry, University of Belgrade, Serbia
 Dr Miroslava Mitrović, Institute for Biological Research "Siniša Stanković", University of Belgrade, Serbia
 Dr Nataša Nikolić, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad, Serbia
 Dr Neda Mimica Đukić, Department of Chemistry, Biochemistry and Environmental Protection, Faculty of Sciences, University of Novi Sad, Serbia
 Dr Pavle Pavlović, Institute for Biological Research "Siniša Stanković", University of Belgrade, Serbia
 Dr Peda Janacković, Institute of Botany and Botanical Garden "Jevremovac", Faculty of Biology, University of Belgrade, Serbia
 Dr Petar Marín, Institute of Botany and Botanical Garden "Jevremovac", Faculty of Biology, University of Belgrade, Serbia
 Dr Saša Orić, Institute of Lowland Forestry and Environment, University of Novi Sad, Serbia
 Dr Slobodan Jovanović, Institute of Botany and Botanical Garden "Jevremovac", Faculty of Biology, University of Belgrade, Serbia
 Dr Slobodanka Pjević, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad, Serbia
 Dr Snežana Radulović, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad, Serbia
 Dr Srđan Stojnić, Institute of Lowland Forestry and Environment and Faculty of Agriculture, University of Novi Sad, Serbia
 Dr Vladimir Radelović, Department of Biology and Ecology, Faculty of Science and Mathematics, University of Niš, Serbia
 Dr Andraž Čarni, "Jovan Hadži" Institute of Biology, Slovenia
 Dr Nejc Jogan, Biotechnical Faculty, University of Ljubljana, Slovenia
 Dr Neriman Özhataş, Department Of Pharmaceutical Botany, Faculty of Pharmacy, Istanbul University, Turkey

Organizing Committee

Presidents:

Dr Ružica Iglj, President of Botanical Society "Andreas Wolny", Novi Sad
 Dr Biljana Panjković, Head of Institute for Nature Conservation of the AP Vojvodina, Novi Sad

Secretaries:

Bojana Bokić, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad
 Milica Rat, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad

Members:

Dr Biljana Božin, Department of Pharmacy, Faculty of Medicine, University of Novi Sad
 Dr Dragana Vukov, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad
 Dr Dušana Cvijanović, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad
 Dr Goran Anačković, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad
 Dr Jadranka Luković, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad
 Dr Lana Zorić, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad
 Dr Ilijana Nikolić, Faculty of Agriculture, University of Novi Sad

Dr Milan Borišev, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad
 Dr Milan Župunski, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad
 Dr Nebojša Kladar, Department of Pharmacy, Faculty of Medicine, University of Novi Sad
 Dr Slobodanka Pjević, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad
 Ana Vestak, Botanical Society "Andreas Wolny", Novi Sad
 Boris Radak, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad
 Danijela Arsenov, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad
 Dragan Obradov, Botanical Society "Andreas Wolny", Novi Sad
 Dunja Karanović, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad
 Durdica Šimin, Botanical Society "Andreas Wolny", Novi Sad
 Goran Tmušić, Botanical Society "Andreas Wolny", Novi Sad
 Jelena Jocković, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad
 Jelena Knežević, Botanical Society "Andreas Wolny", Novi Sad
 Marija Kovački, Botanical Society "Andreas Wolny", Novi Sad
 Marko Ručando, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad
 Miloš Ilić, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad
 Mirjana Čuk, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad
 Ranko Perić, Institute for Nature Conservation of the AP Vojvodina
 Sara Pavkov, Institute for Nature Conservation of the AP Vojvodina
 Slobodan Bojčić, Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad

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 i 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

MOLECULAR CHARACTERIZATION OF CHRYSPHONECTRIA HYPOVIRUS 1 FROM SLOVENIA

Ljiljana Kustin¹, Zorana Katanić², Jelena Repar¹, Marin Ježić³, Ana Kobaš⁴ & Mirna Čurković Perica^{4*}

¹Department of Biology, Josip Juraj Strossmayer University of Osijek, HR-31000 Osijek, Croatia, ²Division of Molecular Biology, Ruđer Bošković Institute, HR-10000 Zagreb, Croatia, ³Department of Biology, Faculty of Science, University of Zagreb, HR-10000 Zagreb, Croatia

*Corresponding author: mirna.curkovic-perica@biol.pmf.hr

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

ROOT PHENOTYPING OF NS SUNFLOWER

Aleksandra Dimitrijević^{1*}, Anna Galinski², Dragana Miladinović³, Sandra Cvejić⁴, Siniša B. Jocić⁵, Sreten Terzić⁶, Kerstin A. Nagel⁷ & Fabio Fiorani⁸

¹Institute of Field and Vegetable Crops, Maksima Gorko 30, 21000 Novi Sad, Serbia, ²IBG-2: Plant Sciences, Forschungszentrum Jülich GmbH, 52425 Jülich, Germany

*Corresponding author: aleksandra.dimitrijevic@ifvcns.na.ac.rs

Sunflower breeding. In the past decades, had led 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 (SISIM); by Provincial Secretariat for Higher Education and Science of Vojvodina, project No. 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

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

Dragana Miladinović¹, Sreten Terzić², Jelena Ovuka, Aleksandra Dimitrijević, Milan Jocković, Sandra Cvejić, Siniša B. Jocić, Nada Hladni, Ana Marjanović Jeromec & Vladimir Mikić

¹Institute of Field and Vegetable Crops, Novi Sad, Serbia (IFVCNS)

*Corresponding author: dragana.miladinovic@ifvcns.na.ac.rs

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.nsemc.com/about/inc/olcrops/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

DIVERSITY OF WHEAT GENOTYPES BASED ON MORPHOLOGICAL MARKERS

Ankica Kondić-Špika^{1*}, Sanja Mikić², Dragana Trkulja³, Ana Marjanović Jeromec⁴, Srđislav Denčić⁵ & Borislav Kobiljkić⁶

¹Institute of Field and Vegetable Crops, Novi Sad, Serbia, ²Biogramac, Novi Sad, Serbia

*Corresponding author: ankica.spika@nsemc.com

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: awicle 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 awicle 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

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.*

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

Bojan Mitrović*, Milica Perišić, Dušan Stanisavljević, Petar Čanak, Sanja Mikić & Miroslav Zorić

Institute of Field and Vegetable Crops, Maksima Gorkog 30, Novi Sad, Serbia

*Corresponding author: bojan.mitrovic@niseem.com

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%), mnt9 (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

EVALUATION OF THE BALKAN PHASEOLUS COCCINEUS L. GENETIC RESOURCES

Barbara Pipen¹, Jelka Šuštar-Vozlić², Vida Todorović^{2*}, Marina Antić³, Brezeanu Creola⁴, Sonja Ivanovska⁴, Mirjana Jankulovska⁴, Aleksandra Savić⁵, Mirjana Vasić^{6*} & Vladimir Meglič¹

¹Agricultural Institute of Slovenia, Crop Science Department, Slovenia, ²University of Banja Luka Faculty of Agriculture, ³Genetic Resources Institute, Bosnia and Herzegovina, ⁴University of Agricultural Sciences and Veterinary Medicine, Vegetable Research and Development Station Bacau, Romania, ⁵Ss. Cyril and Methodius University of Skopje, Faculty of Agricultural Sciences and Food, Republic of Macedonia, ⁶Institute of Field and Vegetable Crops, Vegetable Crops Department, Serbia

*Corresponding author: vasicika00@gmail.com

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

WILD FRUIT CROPS: PRESERVATIONS AND UTILIZATION

Goran Barać¹, Vladislav Ognjanov, Jovana Dulčić, Maja Miodragović, Tijana Narandžić & Mirjana Ljubojević

University of Novi Sad, Faculty of Agriculture, Tig Dastjeva Obradovića 8, 21000 Novi Sad, Serbia

*Corresponding author: goranb@polj.uns.ac.rs

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

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

Tomáš Vymyslický^{1*}, Dejan Sokolović², Daniela Knotová¹ & Vladimír Zornič²

¹Agricultural Research, Ltd., Zahradní 1, 664 41, Troubsko, Czech Republic, ²Institute for Forage Crops, Ltd., Globoder, Kruševac, Serbia

*Corresponding author: vymyslicky@vuplt.cz

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

Uysal, A. 147, 154

V

Vagff, A. 95, 96
 Valcheva, M. 112
 Valkova, N. 171
 Vardar, R. 24
 Varga, F. 181
 Varga, G. 173
 Varga, M. 22, 32
 Varga, N. 198
 Vasić, M. 166
 Vasiljev, K. 72, 98
 Veštag, E. 160
 Vechtu, E. 178
 Velev, N. 72, 98
 Velzi, M. 28
 Vejić, M. 199
 Venkova, D. 107, 175
 Venturilla, G. 197
 Vesic, A. 82, 203
 Vestek, A. 48, 54
 Vidaković, D. 202, 203, 204
 Vidic, D. 131, 132
 Vilović, T. 174, 182, 190
 Vlasović Kostić, I. 185
 Vladimirov, V. 35, 106, 120
 Vladović, D. 177
 Vlainić, I. 24
 Vlika, A. 84
 Vogel-Mikulić, K. 12
 Vollmann, J. 183
 Vrahnakis, M. 72
 Vraneš, M. 169
 Vrbničanin, S. 162
 Vujčić, V. 146, 159
 Vujčić, M. 194
 Vujčić, V. 24
 Vukaković, N. 82
 Vukelić, J. 73
 Vučko, E. 119
 Vučkojević, J. 154
 Vučkojević, N. 195, 196
 Vučkojević, S. 97
 Vučković, D. 78, 81, 82, 100, 158, 185, 191
 Vučković, A. 28, 29
 Vučković, N. 108, 182, 192
 Vučković, R. 28, 29
 Vuksanović, S. 71, 84
 Vymyslický, T. 167

W

Weidinger, M. 192
 Weiss-Schneeweiss, H. 54
 Willner, W. 78

Y

Yaman, B. 87, 161, 182
 Yankova-Isvetkova, E. 15, 21, 22, 23, 156
 Yaprak, A.E. 51, 98, 113, 114
 Yildirim, M. 114
 Yıldızatugay, E. 29, 30, 31, 32, 147
 Yilmaz Cengiz, I. 124
 Yilmaz Ozer, O. 154

Z

Zaklan, J. 158
 Zambonelli, A. 197
 Zaro, G. 46
 Závada, E. 41, 71
 Zayova, E. 20
 Zbiljić, M. 50, 133
 Zebec, M. 163
 Zelnik, I. 72
 Zengins, G. 147, 154
 Zhelev, P. 49, 144
 Zheljazkov, V.D. 15, 21, 127
 Zikos, A. 91
 Zlatić, A. 155
 Zlatković, B. 14, 16, 39, 53, 130, 134, 141, 142
 Zorić, L. 16, 17, 18, 20
 Zorić, M. 166
 Zornić, V. 167
 Zovko, I. 174
 Zozomová-Lihová, J. 41, 42, 56, 61

Ž

Ždero Pavlović, R. 143, 162
 Žikić, V. 44
 Žilić, D. 151
 Živanić, J. 119
 Živanović, M. 203
 Živković, I. 23
 Živković, M. 82, 109
 Župnik, M. 26

Contents

Plenary Lectures	7
Session 1.	
Plant Anatomy and Physiology	
Introductory lectures	11
Oral presentations	12
Poster presentations	14
Session 2.	
Plant Taxonomy and Systematics	
Introductory lectures	38
Oral presentations	40
Poster presentations	47
Session 3.	
Plant Molecular Biology and Genetics	
Poster presentations	65
Session 4.	
Floristics, Vegetation and Phytogeography	
Introductory lectures	71
Oral presentations	73
Poster presentations	83
Session 5.	
Conservation Botany and Plant Invasion	
Introductory lectures	106
Oral presentations	107
Poster presentations	110
Session 6.	
Phytochemistry and Plant Resources	
Introductory lectures	126
Oral presentations	127
Poster presentations	129
Session 7.	
Agronomy and Forestry	
Introductory lectures	161
Oral presentations	161
Poster presentations	163
Session 8.	
Botanical Collections and History	
Introductory lectures	173
Oral presentations	173
Poster presentations	175
Session 9.	
Ethnobotany	
Introductory lectures	181
Oral presentations	181
Poster presentations	183
Session 10.	
Cryptogam Biology	
Introductory lectures	189
Oral presentations	190
Poster presentations	193
Index	205