



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

Oral presentation 09 02 18

ALYSSUM MONTANUM-A. REPENS GROUP (BRASSICACEAE) IN THE BALKANS, GENETIC AND MORPHOLOGICAL PATTERNS AND REVISED TAXONOMIC TREATMENT

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The high genetic, karyological and morphological complexity of the *Alyssum montanum*-*A. repens* species group (Brassicaceae) in the Balkans makes it a challenging study subject for exploring different speciation mechanisms and their taxonomic consequences. Ploidy level, genetic (AFLPs and chloroplast DNA sequences) and morphometric data were examined and confronted with recent taxonomic concepts. Remarkable genetic and morphological variation, which is often geographically structured, and high incidence of polyploids suggest a very complex evolutionary history in this area, involving allopatric differentiation and past hybridisation and polyploidisation events. A new taxonomic treatment, differing substantially from recent concepts, is suggested. Several Balkan taxa are clearly morphologically differentiated, namely *A. handelii*, *A. moellendorffianum*, *A. piranicum*, *A. rostratum* and *A. wierzbickii*. Other species, *A. bosniacum*, *A. montenegrinum*, *A. reiseri* and *A. vernale*, exhibit overlaps in values of the most differentiating characters, but can all be steadily distinguished. *Alyssum repens*, which is not genetically compact, is still morphologically recognizable from other Balkan taxa. Two species, *A. austrodalmaticum* and *A. gmelinii*, despite having clear genetic differences and an allopatric distribution, only have minor morphological differences. Phylogenetic relationships among populations from the central Balkans and Greece are partly blurred apparently due to more extensive reticulations, and they are treated here under the tentative name *A. spruneri*.

KEYWORDS: *Alyssum*, Balkan Peninsula, Carpathians, molecular systematics, morphometrics, polyploidy

Oral presentation 10 02 27

INSIGHTS INTO POLYPLOID EVOLUTION, RAPID RADIATION AND EXTENSIVE GENE FLOW IN DINARIC TAXA OF THE GENUS KNAUTIA (CAPRIFOLIACEAE)

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In recent years several phylogenetic and phylogeographic studies of different plant groups from southeastern Europe have revealed complex patterns in geographic distribution of genetic diversity, and have challenged traditional taxonomic concepts. *Knautia* section *Trichera*, which consists of mostly European perennial species with highest diversity in southern and southeastern Europe – especially the Alps and the Balkan Peninsula – presents a well-suited model to study evolutionary history and biogeographic patterns in the region. Recent research within the genus *Knautia* revealed a shallow genetic structure with mostly low resolution and only partial congruence between plastid and nuclear datasets possibly due to recent rapid diversification and ongoing hybridisation among different taxa. One of the revealed groups is an assemblage of several closely related taxa with distribution area restricted to Croatia and Bosnia and Herzegovina. The members of this group were previously assigned to the *K. dalmatica* and *K. velutina* groups. The *K. dalmatica* group is characterised by shortened internodes towards the stem base and regularly divided leaves with several linear to narrowly lanceolate lobes. It includes *K. adriatica*, *K. clementii*, *K. dalmatica*, *K. pectinata* and *K. travnicensis* from the Dinaric Mountains, all growing in (sub)mediterranean meadows and pastures. The *K. velutina* group is characterized by not or only weakly divided leaves with one to three pairs of lobes and a dense lanuginose to tomentose indumentum and – apart from the Apennine taxa – it includes *K. velebitica* from the Velebit Mts. All these taxa are morphologically very similar and difficult to differentiate. The aim of our study was to elucidate the relationships between the mentioned taxa as well as to answer the question, which taxa do really occur in the Dinaric Mountains. Ploidy-level screening of all investigated taxa revealed multiple cytotypes (di-, tetra- and/or hexaploids) within most of the taxa as well as similarity of genome sizes across different taxa belonging to the same ploidy level, with the exception of a few populations with divergent genome size. Preliminary morphological analyses confirmed the challenging differentiation based on leaf shapes and indumentum, while AFLP data revealed that most species do not form tight clusters.

KEYWORDS: *Knautia*, Dinaric mountains, AFLP, genome size, phylogeography

Oral presentation 11 02 58

HOW COMPLICATED ACTUALLY IS GENUS ORNITHOGALUM?

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In most of the studies, genus *Ornithogalum* is characterized as „complicated“, and species are defined as conspecific. This is common in large sections such as sect. *Heliocharmos*, *Albuca*, *Dipcadi*, which have more than 30 species within them. The issue is evident if different identification keys are compared. Even species that have specific characteristics, i.e. *O. oligophyllum*, *O. refractum*, can easily be misidentified. In the same time, some investigations simplify genus diversity, aiming to describe most of infrageneric taxa as monophyletic. In that sense, from *Ornithogalum sensu lato*, 19 genera are recognized as monophyletic groups, with claim that they are easily recognized at morphological level as well. Other studies suggest that cytotype evolution went beyond phenotypic evolution. This is one of the explanations why cytotype diversity is above species diversity. All these „complications“ and inconsistencies in *Ornithogalum* taxonomy caused the need to change the problem focus. *Ornithogalum* s.l. is distinguished with simple morphology. In general, genus and its representatives can be described with few informative characteristics. Problem arises after 19th and 20th century, when more than 150 species were described only in sect. *Heliocharmos*. Based on that, in this study we try to find out which morphological characteristics are taxonomically important, and can be interpreted efficiently in identification key. We focused on sect. *Heliocharmos*, distributed in Mediterranean region, and far on the east, north and west of Asia and Europe. Material used for analysis is from Balkan Peninsula, Pannonia plain and neighboring regions. Overall, 26 species, 72 quantitative and 18 qualitative morphological and micromorphological characteristics are analyzed on fresh and pressed herbarium material. For analyses were used Multiple Correspondence Analysis, Principal Component Analysis, and Discriminant Function Analysis, all performed in Statistica ver. 13.3. Taxonomically important characters for morphological recognitions of sect. *Heliocharmos* and its species are presented, followed by combinations of characters that are useful for description of series or aggregates. In addition, characters that are too variable for quality interpretation, or cannot be recognized in dry specimens and in every phenophase are highlighted, as insufficiently descriptive. At the end, general identification key for sect. *Heliocharmos* is presented.

KEYWORDS: *Ornithogalum*, Hyacinthaceae, Ornithogaloideae, identification key

Oral presentation 12 02 17

TAXONOMIC AND PHYLOGENETIC RELATIONS OF ALLIUM CHAMAESPATHEM BOISS., A REMARKABLE SPECIES OF BALKAN FLORA

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Based on recent systematic and phylogenetic researches, the genus *Allium* L. currently includes 920 species arranged in 15 subgenera and 15 sections. Among these groups, subgen. *Allium* is the largest one with over 300 species, 130 of which belong to the sect. *Allium*, well supported as monophyletic. Within this section, *Allium chamaespauthum* Boiss. stands out as the only autumn-flowering species, considered a Tertiary wild relative of a potential gene donor to many *Allium* crops, including *A. cepa*, *A. fistulosum*, *A. porrum*, *A. sativum* and *A. schoenoprasum*. It represents a typical Balkan element, occurring in several localities of Albania, mainland Greece, Peloponnese, Evvia, Crete, Ionian and Aegean islands, extending to South Italy, and growing in rocky places, usually garrigues and grasslands, rarely open woodlands and dunes. This species is very rare, with restricted populations. Literature data, herbaria examination, and new field surveys throughout its distribution area revealed a significant morphological variation among populations which suggested more detailed bio-systematic investigations. To clarify the taxonomic position of this peculiar *Allium*, and assess the variability range of its populations, living plants from several sites were analysed. Qualitative and quantitative morphological features were measured under stereomicroscope (6–66×) from both fresh and herbarium materials; karyotypes were obtained and characterized from somatic mitotic plates of root meristematic cells, through traditional karyotyping methods; leaf anatomy was studied on leaf cross sections from leaf blades of maximum size and optimal vegetative development; seed coat microsculpturing was assessed by SEM technique; for phylogenetic investigations, DNA extractions by CTAB2× and PCR amplifications of *nr*- and *cp*-DNA sequences using specific protocols were performed. Obtained sequences for ITS, *trnL-trnF* and *trnH-psbA* genes were assembled to generate MP, ML, and BI phylogenetic trees, and TCS haplotype networks. Though all populations share the same chromosome count $2n=16$ and the typical karyotype structure of sect. *Allium*, with chromosomes having long linear satellites, relevant macro- and micro-morphological features, different ecological requirements, and significant genetic diversity, suggest that *A. chamaespauthum* should be treated as a complex species, with