

BOOK OF ABSTRACTS

3rd International Conference on Plant Biology (22nd SPSS Meeting)



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Serbian Plant Physiology Society

Institute for Biological Research "Siniša Stanković", University of Belgrade

Faculty of Biology, University of Belgrade

**3rd International Conference
on Plant Biology
(22nd SPPS Meeting)**



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SECTION 3

**Biodiversity,
Conservation and
Evolution of Plants**

On average, the samples in natural habitat Rudnik 3 are the tallest, while the shortest are samples from urban population in Belgrade. Trees in Belgrade have the smallest breast diameter, while the biggest ones are detected in Rudnik 2 population. The tree of the biggest biometric characteristics is in natural habitat Rudnik 2 and the one with the smallest biometric characteristics is in urban population in Belgrade. Individuals superior in size are in populations Rudnik 2 and Rudnik 3, while the trees of the best vitality are in Rudnik 1. Trees in urban population are of a good vitality and decorative values and close to Rudnik 1 population in their morphological and phenotypic characteristics. Therefore, good adaptability of Norway maple to challenging environmental conditions in urban areas is confirmed. Selected genotypes are the good basis for collecting seeds and production of planting materials as well as for further research.

Phenotypic variations are transmitted further in sexual and asexual ways, and deviations in Norway maple morphology in different environments allow survival of the species in different habitats. According to the results of the study, Norway maple is promising for various uses and favorable for survival under changed environmental conditions.

Keywords: Norway maple, superior specimens, variability, phenotype, climate change

Molecular tools for the study of genetic diversity in Faba bean

PP3-7

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Faba bean (*Vicia faba* L.) is an important food and feed legume used mainly in eastern and northern Africa and western Asia but having a sound prospect to become one of the eight priority grain legumes for reducing poverty, hunger and malnutrition in mankind. Renewed interest in faba bean breeding and cultivation has led to the enrichment of *ex situ* seed collections worldwide and to the intensification of efforts on their phenotypic and genotypic characterization. Nuclear microsatellites are still markers of choice for genotyping at various scales. However, selection of reliable and informative nuclear microsatellites may be a tedious task. At present, more than 600 microsatellite loci for genotyping in faba bean are available. We report our efforts on assessing performance of both genomic and genic nuclear microsatellites for genotyping in faba bean.

Keywords: faba bean, legumes, nuclear microsatellites

Variation in the amount of Hsp70 among different floral organs in three alternative color phenotypes of *Iris pumila*

PP3-8

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The 70kD heat shock proteins (Hsp70s) are highly conserved molecular chaperones that play essential roles in numerous cellular processes, including the folding of newly synthesized and stress-denatured proteins, the translocation of proteins across membranes, as well as the degra-

dition of aggregated proteins. Here we examined the variation in the abundance of Hsp70s in different floral organs of the three distinctive color morphs in *Iris pumila*. Flowers of twenty seven genotypes raised in a common-garden and belonging to three colour classes: yellow, dark blue and dark violet, were collected (9 per each class) for an immunoblot analysis. The content of Hsp70 was quantified in four floral organs: falls, standards, stamens and style arms. The immunoblot analysis revealed that the expression of Hsp70s was floral organ-specific. While only one Hsp70 isoform was expressed in the standards and falls, the stamens and style arms expressed two isoforms. The relative abundance of Hsp70 varied among differed flower organs as well. The lowest value was recorded in the standards and the highest in the stamens, whereas its abundance in the falls and style arms appeared to be intermediate. Such variation pattern was detected exclusively in the dark violet colour morphs. In the yellow flowers, however, the amount of Hsp70 tended to be lower compared to the dark blue or dark violet colour morphs. This study provides original evidence for organ-specific Hsp70 expression in flowers of *I. pumila* plants, likely due to the differential metabolic activities occurring in the cells of these functionally distinctive floral structures.

Keywords: Hsp70, floral organs, *Iris pumila*, flower colour

Genetic diversity of *Nepeta rtanjensis* based on RAPD data

PP3-9

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Nepeta rtanjensis Diklić et Milojević (*Lamiaceae*) is an endemic, herbaceous plant, found only in a very small area of Mount Rtanj in Southeast Serbia. The whole species is represented by several hundred specimens distributed within three known populations: Greda, Mirčin del and Javor. Like many species of the genus *Nepeta*, *N. rtanjensis* is also famous for its secondary metabolite production (mainly nepetalactones and phenolics) and it is well known that these compounds show antibacterial, antifungal, cytotoxic, phytotoxic and antioxidant activities. Because of its limited distribution and the status of critically endangered species, it is important to find as much as possible information about the population genetic structure of this species. Therefore, we performed randomly amplified polymorphic DNA (RAPD) analysis to get an insight into the genetic diversity and variation of this species within and between the populations. DNA material used in this process was isolated from leaves collected from plants in their natural habitats. To our knowledge, this is the first employment of RAPD markers in the assessment of the *N. rtanjensis* genetic structure. Genetic variability between populations was not detected, but only small variations between individual plants from the same populations were recorded. These preliminary data give us a good base for further studies towards elucidating the genetic structure of this rare species using more reliable *EST-SSR* markers, designed based on *N. rtanjensis* transcriptome.

Keywords: *Nepeta rtanjensis*, DNA, RAPD, population genetics

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