BOOK OF ABSTRACTS

6. CONGRESS
OF THE SERBIAN GENETIC SOCIETY

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WELCOME TO VI CONGRESS OF THE SERBIAN GENETIC SOCIETY!

Dear colleagues,

Welcome to the 6th Congress of the Serbian Genetic Society. The Serbian Genetic Society (SGS) has been founded in 1968 and the first Congress organized by the SGS was held in 1994 in Vrnjacka Banja. Since then, the Congress of Serbian Genetic Society is held every five years. Over the past years, the Congress has grown from a national to an international meeting.

The experience of the past meetings motivated our efforts to continue with this series with a clear tendency to strengthen the scientific connections among researchers from different European countries.

The Congress will focus on the most recent advances in genetics and on wide range of topics organized in 9 sessions and two workshops. Many of the presentations will be in lecture-like settings, but we hope that there will also be ample opportunities for informal interaction outside the scheduled sessions.

The successful organization of the Congress has required the talents, dedication and time of many members of the Scientific and Organizing committees and strong support from our sponsors. I hope that you will find the Congress both pleasant and valuable, and also enjoy the cultural and natural beauty of Vrnjacka Banja.

Yours sincerely,

B. Vasiljević

Branka Vasiljevic
President of the Serbian Genetic Society

05 – 27 Poster

APPLICATION OF SSR MARKERS FOR ASSESSMENT OF GENETIC DIVERSITY OF THE HUNGARIAN OAK (*QUERCUS FRAINETTO* TEN) AT THE LEVEL OF THE SEED STAND RS-2-2-qfr-00-806

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Knowing the level of genetic diversity is of particular importance for the process of plant breeding and conservation of available gene pool. Knowing the level of genetic diversity of an individual seed stand is of great importance when choosing the source of reproductive material. The objective of this work was to analyze population structure and genetic diversity of *Quercus frainetto* RS-2-2-qfr-00-806 seed stands using SSR (Simple Sequence Repeat) markers. DNA was extracted from the buds of 20 test trees of the Hungarian oak which were sampled during the hibernation. The test trees were evenly distributed throughout seed stand and the distance between them was more than 50 m.

Seven SSR markers were analyzed and all were polymorphic. Total number of alleles revealed for all analyzed individuals were 23, ranging from two (QpZAG112, QpZAG36 and QpZAG15) to five (QpZAG9). Genetic similarities were calculated on binary data using Dice's coefficient by NTSYSpc2.1 program package. High genetic variation was observed among analyzed genotypes, as genetic similarity covered a larger range of values (0.23-0.93).

The obtained level of genetic variability of the seed stand RS-2-2-qfr-00-806 represent a good starting point for future experiments on breeding of the species. This is basic research for the improvement of mass production of quality reproductive material of Hungarian oak in Serbia.

HUNGARIAN OAK, SSR (SIMPLE SEQUENCE REPEAT) MARKERS, POPULATION, SEED STAND

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05 – 28 Poster

GENETIC RESOURCES EXPLOITATION IN WHEAT BREEDING AND IMPROVEMENT AT THE IFVCNS

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Modern agriculture depends on improved forms of crop plants, created by breeders from germplasm which provides the genetic information needed to increase yield and quality and add resistance to pests, diseases and adverse environmental factors. Genetic resources are maintained and evaluated in collections located worldwide and supported by national and international public funds. Institute of Field and Vegetable Crops, Novi Sad (IFVCNS) has its own collection of wheat genotypes that comprises around 2800 accessions originating from more than 30 countries, as well as 65 wheat ancestors and related species. For the maintenance purpose each year one third of the collection is sown and evaluated for some important characters, enabling us to refresh the seeds of the entire collection in three years. According to the evaluation results the genetic (core) collection with more than 850 entries is extracted from the world collection. From this collection the material for different projects and experiments was chosen and according to their objectives it was extensively evaluated for different agronomical, morphological, physiological and other traits in field and controlled conditions. It was also used for molecular diversity studies, association panels, and genome-wide association analyses. One of our international projects is dedicated to redesigning the exploitation of small grains genetic resources towards increased sustainability of grain-value chain (FAO project PR-166 - GRAINEFIT). The project addresses some of FAO sustainability goals, such as to end poverty, achieve food security and improved nutrition, promote sustainable agriculture, combat climate change and its impacts, halt biodiversity loss, promote inclusive societies and revitalize the global partnership for sustainable development.

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GENETIC RESOURCES, WHEAT GERMPLASM, MAINTENANCE, EVALUATION

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