

BOOK OF ABSTRACTS



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05 – 19 Poster

CHARACTERIZATION AND EVALUATION OF POTATO GENETIC RESOURCES IN MONTENEGRO

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Potato was introduced in Montenegro in the late 18th century. Over the course of more than 230 years of cultivation, potatoes in these areas have been differentiated into a large number of forms of different lengths of vegetation. The cultivation of local potato varieties lasted until the 1970s when massive introduction of new high-productive selections began. Right at that time, work on the conservation of these resources begins. The most important measures for their conservation were made in the period from 2008 to 2010, when 52 local populations of potatoes were collected from more than 150 sites.

In order to get a clear estimate of the value of this collection, but also to identify duplicates, a program of characterization and evaluation began in 2016. The morphological characterization of the sprout was made on the basis of the UPOV descriptor for the 11 characteristics of the sprout. Sixteen different phenotypes were identified. Morphological examination selected 23 samples for DNA analysis.

Molecular evaluation, using 12 microsatellite markers (SSR), confirmed the existence of 13 groups. Comparison of the DNA materials of Montenegrin populations with data base of over 8000 varieties at the SASA Institute in Scotland, found the existence of 5 unique genotypes, two of which were duplicates (genetic profile 1 - Ljubičasti šareni and Kromir rozi, genetic profile 2 - Koprivuš, genetic profile 3 - Maus and genetic profile 4 - Cvjetaš. All other Montenegrin populations were known varieties.

The characterization performed will significantly contribute to the reduction of the maintenance cost of the collection, but also raise the quality of its conservation to a significantly higher level.

POTATO, LOCAL POPULATIONS, CHARACTERIZATION, EVALUATION

05 – 20 Poster

GENETIC DIVERSITY OF SERBIAN ISOLATES OF *XANTHOMONAS CAMPESTRIS* PV. *CAMPESTRIS* ORIGINATED FROM WINTER OILSEED RAPE

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Oilseed rape (*Brassica napus* L.) is a hybrid species within Brassicaceae family, significant for its oil-rich seed, mainly used for vegetable oil and biodiesel production, but also for consumption as livestock feed. Yield of oilseed rape and other cruciferous crops can be reduced due to different plant pathogenic bacteria, fungi and pests. One of the most significant bacteria affecting crucifers is *Xanthomonas campestris* pv. *campestris* (Xcc) causing black rot disease. Xcc isolates from diseased winter oilseed rape plants showing bacterial blight symptom on leaves were collected in nine-year period (2010-2018), from different localities in Serbia, with the aim to examine their genetic features, through sequencing of housekeeping genes. DNA of the obtained isolates was therefore amplified with six primers (dnaK, fyuA, gapA, gyrB, lepA, rpoD) and sent for sequencing. The obtained sequences were checked for homology with strains available in NCBI database. Multilocus sequence analysis (MLSA) was then performed to determine relatedness among the tested isolates. Based on six genes, tested isolates were identified as Xcc using NCBI BLAST, showing 99-100% homology with the available data. Winter oilseed rape Xcc isolates were divided into five groups on Neighbour-joining tree, revealing intrapathovar diversity within isolates from this host. These results could be connected with pathogen adaptation to winter oilseed rape as a new host, providing completely distinct ecological niche from *B. oleracea* vegetable crops (broccoli, cabbage, cauliflower, etc.) which are common hosts for this bacteria. This observation on Serbian Xcc isolates gives a significant input on genetic variation and constitutes a highly informative sample of *X. campestris* diversity.

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OILSEED RAPE, *XANTHOMONAS*, BACTERIAL BLIGHT, MULTILOCUS SEQUENCE ANALYSIS (MLSA)