

BOOK OF ABSTRACTS



7th Conference on Cereal Biotechnology and Breeding
7-9 November 2023

18th EWAC
The European Cereals Genetics Co-operative Conference
6 November 2023

Wernigerode, Germany

Jointly organised with the Cereals Section of EUCARPIA

CBB7 2023
7th Conference on Cereal Biotechnology and Breeding

7–9 November 2023
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EWAC18 2023
18th EWAC – The European Cereals Genetics Co-operative Conference

6 November 2023
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Molecular characterization of local Serbian and Bulgarian wheat accessions for their contribution to sustainable agriculture

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The increasing pressure of climate change, reduction of genetic diversity on farms and constant decrease in arable land present the most challenging aspects for today's crop production. Reintroduction of diverse adapted local varieties and underutilised landraces of wheat, potentially tolerant to different biotic and abiotic stresses, could ensure stable yield under low-input agriculture. The uncharacterized local varieties and landraces of bread and durum wheat from Serbia and Bulgaria, were collected from small-scale farms and gene banks within a project funded by the Benefit-Sharing Fund of the International Treaty on Plant Genetic Resources for Food and Agriculture, aiming to evaluate their genetic diversity. As a part of this comprehensive project, the selected material was evaluated using different molecular marker techniques. The level of genetic diversity and relatedness of a set of 90 Serbian and Bulgarian local varieties and landraces of bread and durum wheat was assessed using microsatellite molecular markers and 25K wheat Infinium Array. The total of 141 alleles was detected at 20 microsatellite loci with an average number of 7.05 alleles per locus. The PIC value varied from 0.344 to 0.837. Markers of A genome were the most informative. The structure analysis revealed presence of three subpopulations, while principal coordinate analysis showed almost clear separation of durum wheat, Bulgarian and Serbian bread wheat accessions. For each group private alleles were detected. A total of 17,930 high-quality SNPs were retained after filtering and the highest number of SNPs was recorded for the B genome. The UPGMA analysis showed clear separation between Serbian and Bulgarian accessions. The obtained results indicate genetic richness of the collected material and contribute to better characterization and completion of the passport data. These results, together with the results of phenotypic evaluation, will build up to the knowledge required for utilization of local wheat genetic resources in breeding climate-resilient varieties suitable for sustainable farming.

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