

# 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**

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<https://akcongress.com/comec/>

**Please be aware that certain changes introduced in the Conference programme after editing has been closed may not be included in this Book of Abstracts due to the publishing deadline.**

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E-mail: [ak@akademiai.hu](mailto:ak@akademiai.hu)  
[www.akjournals.com](http://www.akjournals.com) / [www.akademiai.hu](http://www.akademiai.hu)  
ISBN 978-963-454-987-1

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## Application of SSR-markers in local Ukrainian winter wheat breeding program

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**Keywords:** SSR-markers, alleles, polymorphic information content, clusters, *Triticum aestivum* L.

The simple sequence repeats (SSR) markers are widely used for genetic analysis in plant breeding enabling investigation of the genetic divergence and similarity, identification of the unique alleles and determination of the genetic diversity level. Selection based on markers allows selecting a genotype with the necessary combination of genes, significantly increasing the efficiency of breeding programs. Ukraine has a rich history of wheat breeding spanning over 100 years, which has led to the development of specific allele combinations in Ukrainian cultivars.

The aim of this study is to assess the genetic diversity among the genotypes presented in a local Ukrainian breeding program and to differentiate closely related material using highly informative SSR markers compare with Ukrainian and foreign winter wheat varieties.

The first stage of the our study has been considered assessment of 42 wheat genotypes from the local breeding program of Poltava State Agrarian University by 11 SSR markers (Xgwm 11, Xgwm 44, Xgwm 46, Xgwm 135, Xgwm 174, Xgwm 186, Xgwm 194, Xgwm 219, Xgwm 312, Xgwm 372, Xgwm 389). A total of 80 alleles were identified for the studied 11 loci. Among them, a total of 25 unique alleles were found, which were each allele only occurring in one genotype. The polymorphism information criterion (PIC) values ranged from 0.48 to 0.84. Five major clusters were identified with varying numbers of genotypes within each. The newly developed lines and recently released cultivars did not have any unique alleles according to the investigated markers.

The next stage of the study has been carried out on 82 samples of different geographic origin. A total of 15 SSR markers (Xgwm 003, Xgwm 005, Xgwm 011, Xgwm 044, Xgwm 046, Xgwm 120, Xgwm 160, Xgwm 174, Xgwm 194, Xgwm 219, Xgwm 234, Xgwm 251, Xgwm 325, Xgwm 427, Xgwm 539) distributed throughout the wheat genome were used. A total of 104 alleles have been detected with an average of 6.93 alleles per locus. The PIC values ranged from from 0.16 to 0.79.

The obtained results reveal the genetic similarity among the studied genotypes and can be used as a significant factor in the final breeding decision. The allelic profiles can be used not only to compare with profiles of lines at advanced breeding stages, but also to choose parental pairs for the future crosses, and to identify unique genotypes valuable for breeding.

Hybridization and selection across generations within a given pool with the constant involvement of new sources create a valuable set of alleles for adaptation under certain environmental conditions. The long-term involvement in the hybridization of an extensive ge-

netic material of various origin allows the concentration of valuable alleles that can provide a high level of adaptivity to environmental conditions.

This study has been carried out due to a collaboration of Poltava State Agrarian University with High School of Province Hainaut CONDORCET and Centre for Agricultural research CARAH during 2005-2020 years.