

Genetic diversity and population structure of Bulgarian bread wheat varieties

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Determining the genetic diversity and population structure of the modern hexaploid wheat varieties currently grown in Bulgaria is fundamental for selection of genotypes with desirable traits resilient under climatic fluctuations and development of successful crop improvement programs. In this study, simple sequence repeat (SSR) markers were used to characterize a population of 117 modern wheat varieties (*Triticum aestivum* L.) from Bulgaria and several Western, Central and Eastern European countries. The genetic diversity was higher in the Western and Central European varieties than in the Bulgarian and the remaining Eastern European ones. Model-based population structure analysis defined 2 sub-populations ($K=2$) dividing the Central and Western European varieties from the Bulgarian ones. Subsequent genetic structure analysis at $K=3$ revealed an additional separation of the Bulgarian varieties in two distinct sub-populations. The phenotypic diversity among the varieties was evaluated in the fields of Dobrudzha Agricultural Institute, G. Toshevo in North-Eastern Bulgaria for three consecutive years. The distribution of the varieties in the biplot analysis in terms of grain yield and its components revealed differences in their adaptation to the agro-climatic conditions of North Bulgaria according to their geographical origin. These results and the prevalence of specific SSR alleles in the sub-populations suggest distinct adaptive mechanisms to specific agro-ecological regions. The data will be of interest for both breeders and farmers and could serve as a basis for wheat improvement programs and further association mapping for important agronomic traits expressed under different environmental conditions.

Reference

Stefan Tsonev, Nikolai Kirilov Christov, Gallina Mihova, Anna Dimitrova & Elena Georgieva Todorovska (2021) Genetic diversity and population structure of bread wheat varieties grown in Bulgaria based on microsatellite and phenotypic analyses, *Biotechnology & Biotechnological Equipment*, 35:1, 1520-1533, <https://doi.org/10.1080/13102818.2021.1996274>