

Genetic diversity and population structure of Bulgarian and foreign durum wheat

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The genetic variation and population structure of a panel of 90 durum wheat (*Triticum durum* desf.) consisting of 62 varieties and breeding lines originating from two agro-ecological zones in Bulgaria (Northern and Southern Bulgaria) and 28 introduced varieties from South-western, Central and Eastern Europe, and the USA were determined by 34 microsatellite markers (SSR). The genetic diversity in the modern durum wheat was 0.5612 with 6.88 alleles per locus. The genetic structure of the collection was analyzed with a model-based approach implemented in the STRUCTURE software. This identified two sub-populations ($K=2$) separating the South Bulgarian varieties (SP1) from all others (SP2), including South-Western, Central-Eastern European and North Bulgarian ones. Subsequent genetic structure analysis at $K=4$ revealed an additional division of each sub-population into two (SP1-2, SP1-4, SP2-1, SP2-3). Phylogenetic trees were constructed with Unweighted Pair Group Method with Arithmetic mean (UPGMA) and clusters of genetically related individuals identified with Discriminant Analysis of Principal Components (DAPC) based on SSR data. The results were in excellent agreement with the Subpopulations defined by STRUCTURE analysis. The Principal Component Analysis (PCA) revealed that among the 5 agronomically important traits studied, the correlation between grain yield and plant height was the highest and distinguished 10 varieties and advanced breeding lines from Southern Bulgaria (SP1-2 and SP1-4) as most promising in regard to yield stability. This study showed a good relationship between the genetic and phenotypic population structures according to the division of the genotypes by their agro-geographical origin. It will be useful for both breeders and farmers and could serve as a fundament for durum wheat improvement programs under drought prone environmental conditions.

Reference:

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