

Genome-Wide Association Studies of Agronomic and Quality Traits in Durum Wheat

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Durum wheat is used for products for human consumption, the quality of which depends on the content of protein and yellow pigments in the semolina. The challenges faced by modern breeding, related to population growth and climate change, imply improvement of both grain yields and quality in durum wheat germplasm well adapted to specific agro-climatic conditions. To address those challenges, a better understanding of the genetic architecture of agronomic and quality traits is needed. In the current study we used the Genome-Wide Association Study (GWAS) approach in a panel of Bulgarian and foreign genotypes to define loci controlling agronomic and quality traits in durum wheat. We mapped 26 marker traits associations (MTAs) for four of the six studied traits—grain yield, grain protein content, seed yellow color (CIELAB b*), and plant height. The greatest number of MTAs was detected for grain yield. Seven MTAs were detected for each grain protein content and seed color, and one MTA for plant height. Most of the reported associations had confidence intervals overlapping with already reported quantitative trait loci (QTLs). Two loci controlling grain yield were not reported previously. The most relevant putative candidate genes for grain yield were involved in stress response, growth, and development. Putative candidate genes for grain protein content were involved in nitrogen remobilization and transport, and for SC in biosynthesis and metabolism of terpenes. The MTAs detected in our study could be a good starting point for selecting genes potentially important for grain yield and quality in durum wheat for further functional analyses and validation.

Keywords: durum wheat; genome-wide association study (GWAS); grain yield; grain protein content; yellow pigments