

NITROGEN USE EFFICIENCY CANDIDATE GENES AND RELATIONSHIP WITH GRAIN PROTEIN CONTENT IN DURUM WHEAT

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durum wheat, Grain Protein Content, Nitrogen Use Efficiency, Near Isogenic lines, GS/GOGAT cycle

Durum wheat (*Triticum turgidum* L. ssp. *durum*) is grown on about 17 million hectares of land worldwide. Several grain quality characteristics determine semolina's high end-use quality. Among them, grain protein content (GPC), is directly related to both final products' nutritional and technological values. The development of new varieties with high GPC has been a priority of the last decades breeding, although it has been difficult to select genotypes for protein content since, as a quantitative trait, it is regulated by a complex genetic system and affected by environmental factors, and furthermore, it is affected by a strong negative correlation with grain yield, which makes the simultaneous increase of both traits challenging to achieve. Several studies have taken into account GPC and grain yield components simultaneously assessed on the same population to identify GPC loci without pleiotropic effects and/or not closely linked to gene for low yield-related traits, and some interesting results were reported both for 2A and 2B chromosomes. The improvement of GPC could be then pursued by considering a candidate gene approach. Several authors have focused on deciphering GPC and NUE QTL, and genetic diversity at candidate genes have recently been considered for this purpose. The glutamine synthetase (GS)/glutamate synthase (GOGAT) cycle represents a bottleneck in the first step of nitrogen assimilation. In our previous studies we identified both genes as good candidates in GPC study in the SxC RIL population. A useful and efficient method to validate a putative QTL is the constitution of near-isogenic lines (NILs) for the two alleles of the target QTL by using the marker found to be associated to that QTL. So far, we developed two distinct set of heterogeneous inbred family (HIF)- based NILs segregating for *GS2* and *Fd-GOGAT* genes from heterozygous lines at those loci, to validate the previously identified GPC QTL on 2A and 2B chromosomes. The near-isogenic lines we developed at both *GS2* and *Fd-GOGAT* loci showed that despite having significant differences in GPC, no significant differences were observed in GYS. This could be either explained with both *GS2* and *Fd-GOGAT* having no negative pleiotropic effects on yield components, or that a potential effect is actually masked by environment. Furthermore, for both HIF-NIL families, the one derived from parental line Svevo showed higher and statistically significant different GPC values compared with the ones developed from cv Ciccio confirming that the allele from Svevo increases the GPC trait. Our results showed that the genomic region surrounding *GS2* and *Fd-GOGAT* genes and their promoter regions are involved in grain protein accumulation, and the identification of new useful alleles for marker-assisted selection is valuable for breeding wheat varieties with improved agronomic performance and N-use efficiency.