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Abstract – SY27

VALIDATION OF TWO GRAIN PROTEIN CONTENT QTL BY CANDIDATE GENES NEAR ISOGENIC LINES DEVELOPMENT

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Among the Mediterranean Basin's countries, Italy is the major durum wheat (*Triticum turgidum* var. *durum* Desf.) producer, with an average of almost 4.0 MMT year. Several grain quality characteristics determine semolina's high end-use quality, a parameter extremely required by pasta factories. Among them, grain protein content (GPC), a quantitative trait regulated by a complex genetic system and affected by environmental factors, is directly related to both final products' nutritional and technological values. The improvement of both GPC and yield could be pursued by considering a candidate gene approach. The glutamine synthetase (GS)/glutamate synthase (GOGAT) cycle represents a bottleneck in the first step of nitrogen assimilation, as these two enzymes work synergistically to incorporate the up-taken ammonium into organic molecules. QTL for GPC have been located on all chromosomes, and several major ones have been reported on 2A and 2B chromosomes, where GS2 and Fd-GOGAT genes have been mapped. QTL validation is of primary importance for further breeding programs development or cloning. 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. NILs are indeed lines segregating only at target QTL but homozygous at the rest of the genome. Here we present the development of two distinct set of heterogeneous inbred family (HIF)- based NILs segregating for GS2 and Fd-GOGAT genes from heterozygous lines at those loci previously identified in a RIL population, along with their genotypic and phenotypic characterizations, aimed to validate the previously identified GPC QTL on 2A and 2B chromosomes, along with the role of these key genes in GPC control.