

## VALIDATION OF GRAIN PROTEIN CONTENT IN DURUM WHEAT

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Marker assisted selection (MAS) is a powerful tool for traits like grain protein content (GPC) of durum wheat (*Triticum turgidum* L. convar *durum*), which exhibits high genotype-environment interaction leading to low heritability. In a previous work, undertaken to identify molecular markers associated with QTLs for GPC in durum wheat, Blanco et al. (2011) identified some QTLs in the RIL mapping population Svevo x Ciccio evaluated under different environmental conditions. In order to employ these QTLs in breeding programs, additional studies are necessary to validate them in different genetic backgrounds where the GPC loci should be expressed without penalties on grain yield. A good way is to verify the effects of the QTLs in a different mapping population. An alternative way is to obtain near isogenic lines (NILs) for the two alleles of the target QTL using the markers identified for that QTL.

Three QTLs, localized on chromosome arms 1AL, 2AS, and 4AL, respectively, were validated in a recombinant inbred line population developed by crossing the durum wheat cultivars Svevo and Duilio and evaluated in two environments for three years. Selection for the positive allele resulted in 0.12 to 0.22% increase in GPC. The molecular markers *Xgwm95* and *Xgwm339*, significantly associated with the grain protein content, showed little effect on yield in most environments.

Six NILs sets, each consisting of two homozygous genotypes, were developed starting from heterozygous lines at the marker associated with the grain protein QTL on chromosome arms 1AL, 2AS and 3BS from the RIL Svevo x Ciccio. The phenotypic analysis were performed on two genotypes of each NIL grown in two environments for two years and evaluated for grain protein content and grain yield per spike. The QTL for GPC located on 2AS, associated with *Xgwm339*, was validated in different environmental conditions and was not correlated with yield per spike. The Svevo allele at this marker showed an additive effect on GPC (0.25 to 0.40%). Given the consistent expression pattern in multiple populations and environments, *Xgwm339* can be used for marker-assisted selection for high GPC.