

APPROACHING THE IDENTIFICATION OF GRAIN YIELD COMPONENTS CONTROLLING GENES IN DURUM WHEAT

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Grain yield in cereals is a complex trait whose main components are: spikes number per plant, grain number per spike and grain weight which in turn is positively correlated with grain size. Grain number is strongly linked to spike morphology and development; in wheat, the inflorescence meristem (IM) forms a determined number of lateral spikelet meristems (SMs), and each SM is indeterminate and genetic variability is observed in the number of fertile florets that can develop within a single spikelet, thus influencing the final yield.

On the other hand, grain size is a well studied trait in model species and more than 40 genes, controlling this trait, have been identified and characterized to date in rice and Arabidopsis. The recent release of durum wheat genome sequence (cv. Svevo) and the availability of diverse genetic resources pave the way to develop different approaches to identify and characterize genes controlling grain yield components. In this work we report on two different strategies to identify genes controlling yield components in durum wheat with the long term goal of obtaining durum wheat lines improved for such traits.

The first strategy is to exploit the variation in florets number per spikelet that arose during durum wheat domestication process: strictly 2 in *T. turgidum* ssp *dicoccum* and 3 to 6 in *T. turgidum* ssp *durum*. The aim is to dissect, from both a morphological and a molecular point of view, spike development in a *T. turgidum* ssp *durum* (Latino) and a *T. turgidum* ssp *dicoccum* (MG5323) to get insights into the genetic mechanisms controlling the final florets number. A RIL population (F8; Latino x MG5323) already developed and genotyped producing a high-density genetic map (~11000 markers), has been phenotyped for different fertility traits, to identify QTL contributing to florets number determination. QTL data and molecular analyses of parental lines and most divergent RILs will be integrated to identify key genes on which to perform functional analyses. The second strategy is a translational biology approach in which knowledge acquired in model species are transferred in durum wheat. Orthologs of rice negative regulators of seed size (*FUWA*) and seed number (*OsCKX2*) have been identified and a *genome editing* experiment is undergoing to functionally characterize the role of these genes in durum wheat. Preliminary results are reported.