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Poster Communication Abstract – 3.19

DIFFERENT GENOMIC REGIONS DEFINE FLORETS NUMBER AND SPIKE-RELATED TRAITS IN T DURUM SSP.

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Wheat grain yield is a complex trait that can be further dissected into different components such as the number of grains per spike, the grain size/weight and the number of spike per plant, and each of these factors is in turn composed by several sub-components. These traits have been subjected to strong selection during the domestication history of Triticeae and are still the main target of modern breeding.

In this study we focused on yield in terms of grains per spike, considering the number of fertile spikelets per spike and fertile florets per spikelet as main traits.

With the aim of identifying genetic components of these traits, we deployed a segregant population, resulting from the cross of a durum wheat cultivar (Latino) and a cultivated emmer accession (MG5323) that show a wide variability in the number of grain per spike.

Before performing a classic QTL mapping approach, we dissected at the stereomicroscope the developing spikes of the parental lines to determine the morphological traits responsible for a different number of grains per spike. The analysis revealed that a different number of floret meristem, set during spike development, and a different developmental timing, is at the basis of the observed differences.

For the QTL mapping analysis, the RIL population was phenotyped for spike morphology and florets-related traits in four environments. A total of 94 QTLs were detected along all chromosomes, grouped in 17 regions, based on their physical position. Five QTL groups were identified for floret number and eight for spikelet number/spike morphology. The QTL regions identified for spikelet and floret number are distinct and non-overlapping suggesting that these traits are under different genetic control. Finally, the physical interval of our QTL was defined, and candidate genes were proposed. Known genes involved in inflorescence meristem development and spike morphology, such as FUL2, FUL3, PPD -1, VRN-A1, and Q-5A, are colocalized in our QTL regions and were investigated by qRT-PCR in the parental lines of the segregant population.

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