

STUDY OF SPIKE FERTILITY IN DURUM WHEAT GENOTYPES

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Triticum turgidum, *Triticum dicoccum*, Spike fertility

Wheat spike fertility is a complex trait strictly related to grain weight, number of kernels and fertile florets. Fertility traits play a key role, in the identification of new genotypes with high yield. For these reasons, it is really important to identify the genes and the molecular mechanisms involved in the expression of this complex trait.

The main goal of this study was to characterize a 257 Recombinant Inbred Lines (RIL), obtained with a interspecific cross between, cv Meridiano, a durum wheat productive cultivar, and *dicoccum* Lucanica, a emmer landrace, with nutritional qualities, for different phenotypic and qualitative traits. In particular, the population was characterized for spike related traits, such as spike lengths, spike weights, shapes, total and not-fertile spikelet numbers, total and not-fertile floret numbers, and qualitative traits, such as protein, color and kernel index. All the traits had the typical quantitative distribution.

Spikes length had a mean value about 8.50 cm, weight of 2.50 gr, while spikes had about 22 spikelets of which 2 spikelets not-fertile, and 6-7 florets, of which 2-3 not-fertile. For the qualitative traits the population showed a mean Kernel Index value of 4%, protein content of 15%, yellow index of 13%, shine of 70%, brown and red index of 25% and 2%, respectively.

Positive correlations were detected between spike length and spike weight, spike length and total spikelet numbers, between Kernel index and spike weight and between red and brown index. In addition, negative correlations

were identify between weight and spikelet not-fertile numbers, spikelet not-fertile numbers and Kernel index and between shine and red and brown index.

The RIL population was also genotyped using DArT markers for the genetic map construction and QTL identification. The analysis underlined the presence of 28,187 markers of which 8,419 were polymorphic. Of these, 3,358 markers were located on A genome and 3,512 on B genome. The results obtained from genotyping characterization will be used for linkage mapping analyzes to identify QTL and candidate genes associated with fertility, quality and productivity.