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IDENTIFICATION OF THE QUANTITATIVE TRAIT LOCI CONTROLLING SPIKE-RELATED TRAITS IN DURUM WHEAT

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Wheat grain yield is a complex trait influenced by a variety of genetic and environmental factors. The number of grains per spike, one of the three major components that determine yield, is closely related to the number of fertile spikelets and fertile florets per spikelet. A population of recombinant inbred lines (RILs) resulting from the cross of a *Triticum durum* cultivar (Latino) and a *Triticum dicoccum* (MG5323) provides a useful tool for studying this trait because genetic variability in the number of florets per spikelet and spike morphology varies widely across the domestication history of durum wheat. In the present study, spike morphology and florets-related traits were investigated in two environments for three consecutive seasons. The Pearson correlation matrix showed a highly significant and positive correlation between the traits spike weight, total floret number (FRT), net floret (NFRT), total spikelet number (SPK), and net spikelet number (NSPK). There was also a positive and highly significant correlation between the trait spike length and NSPK, SPK, and spike weight. On the other hand, a negative and significant correlation was found between heading date and florets traits. A total of seventy-nine QTL were detected along all chromosomes using the high-density genetic map. We identified several genomic regions with QTL associated with spike morphology and florets, explaining a portion of the phenotypic variance ranging from 6.5% to 29.5%. QTL regions were detected for SPK and NSPK on chromosomes 2A, 5A, 5B, 7A, 7B, with stable QTL on chromosomes 2A, 5A, and 7A and detected consistently in almost all test environments. In addition, QTL regions for FRT and NFRT were identified on chromosomes 1B, 2A, 3A, 3B,

4A, 4B, and 6A. Notably, the FRT and NFRT QTL identified on chromosome 2A were consistently and stably detected under all tested environments. The SPK and FRT QTL identified in this study were distinct and non-overlapping. Finally, the release of the reference genome sequence of T. durum allowed us to define the physical interval of our QTL and hypothesize new candidate genes by examining the gene content of the genomic regions associated with the target traits. Known genes involved in inflorescence meristem development and spike morphology, such as *FUL2*, *FUL3*, *PPD -1*, *FT2*, *VRN-B1*, and *Q-5A*, are colocalized in our QTL regions and were investigated by qRT-PCR in the parental lines of the RIL population.