Identification of the quantitative trait loci controlling spike-related traits in durum wheat

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BACKGROUND

Grain yield is a complex trait influenced by genetic and environmental factors. The number of grains per spike is determined by the number of fertile spikelets per spike and fertile florets per spikelet. In the picture, we can see that the durum wheat cultivar Latino has 3-5 fertile grains, while the *T. dicoccum* accession MG5323 has only 2 fertile grains. This difference is due to the evolutionary events that occurred during the domestication process, but the genetic determinants are not yet identified.

OBJECTIVES

- ✓ To decipher quantitative trait loci associated with floret and spikelet number traits in the RIL population (Latino x MG5323).
- ✓ To dissect the developmental process of the inflorescence meristem in the parental lines, to understand if the different number of fertile grains is due to differences in meristems number, meristem development or degree of floret fertility/abortion.
- ✓ To study the expression profile of genes known to be involved in spike morphology during the developmental stages of the inflorescence meristem.

RESULTS

A high-density genetic map of the RIL population (110 RILs Latino x MG5323) was developed with iSelect 90K wheat SNP BeadChip array and 10,840 SNP markers were mapped. Four environments (3 years, 2 locations) and BLUP values of phenotypic data (listed in Table 1) were used for QTL analysis.

A. Phenotypic data analysis: Frequency distribution and correlation among traists of interest

- The RIL population reveals continuous variation and a normal distribution for most traits across 4 environments and BLUP values, indicating polygenic inheritance and Environment x Genotype interactions (GxE) as shown in Figure 1.
- Positive and significant correlations were observed among floret number and spike weight, spikelet number with spike weight, spike length and spike density (Figure 2). Interestingly, a significant and negative correlation was observed between the heading date and the number of florets, which reveals that the longer the heading date is, the fewer florets are formed.

Table 1. List of traits used in phenotyping

Acronym	Trait name
HD	Heading date
SD	Seed density
SPW	Spike weight
SPL	Spike length
FRT	Total Floret number
NFRT	Net floret number
SPK	Total spikelet number
NSPK	Net spikelet number

Figure 1. Distribution frequency of inflorescence development related traits across environments

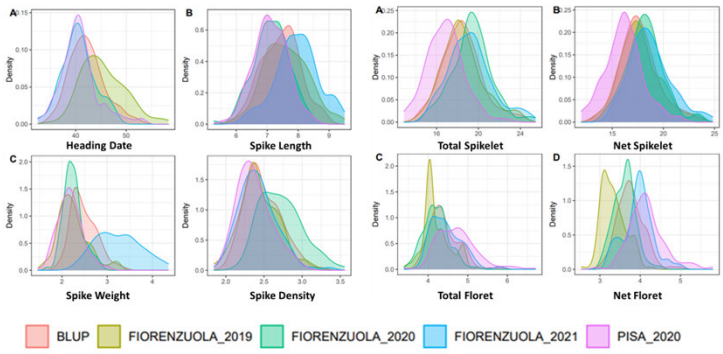
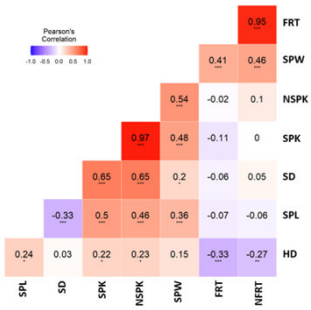


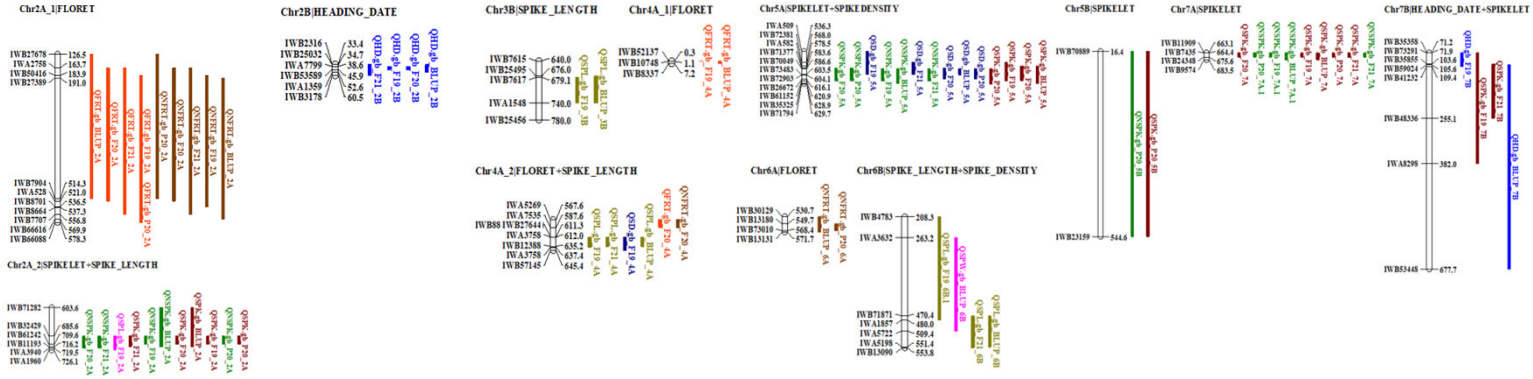
Figure 2. Pearson's correlation among all phenotypic traits



B. Quantitative genetic analysis

- Quantitative genetic analysis detected a total of **51 QTLs** among which 42 are stable across the tested environments. Overall, the highest phenotypic variance was explained by QTL for floret number (24%) and spikelet number (29%) on chromosome 2A in the Pisa_2020 environment.
- As reported in Figure 3, QTLs for spikelet and floret numbers were detected separately in different positions of the chromosomes (QTL for spikelet number identified at 2A,5B,7A and 7B; QTL for floret number located at chromosomes 2A, 4A and 6A), meaning that the chromosomal regions (and genes) associated to traits are distinct.
- 158 QTLs associated with yield components , previously identified in tetraploid wheat and summarized in Maccaferri et al. (2019), have an overlapping position with all loci detected in this study, except for a region in the short arm of chromosome 4A that is unique to this study.
- Some genes, known from the literatures and characterized as inflorescence meristem development regulators, are also overlapped in the regions of QTL detected in this study. In particular, *FUL1* and *FUL2* in chromosome 2A, *Ppd-B1* in chromosome 2B, and *VRN-B1* and *Q* in chromosome 5A.

Figure 3. Map for QTLs detected in the Latino x MG5323 RILs for floret and spikelet related traits along with their physical map positions (Mbp)



C. Meristem microdissection and expression assay

To follow the inflorescence meristem development, plants of both parental lines were grown in controlled conditions and sampled every two days using a stereomicroscope. The time span of inflorescence meristem development after double ridge formation is very rapid in Latino (2 weeks) and resulted in the formation of 6 to 8 floral meristems, while MG5323 required 26 days and produced only up to 4 floret meristems (Figure 4).

The *FUL1A* and *FUL1B* genes, which are homologous to vernalization gene 1, are frequently expressed in leaves and spike primordia, and their expression is thought to prolong heading time, which in our study resulted in a slight up-regulation in MG5323 at lemma primordium stage. On the other hand, *GNI1B*, known in the literature as a regulator of floret fertility and involved in distal flower suppression in wild emmer, shows a relatively higher expression fold in MG5323 than in Latino, suggesting that perhaps both genes, *FUL1* and *GNI1*, play a role in prolonging flowering time and forming less fertile grains in MG5323 (Figure 5).

Figure 4. Microdissection of inflorescence meristem developmental phases of the parental lines

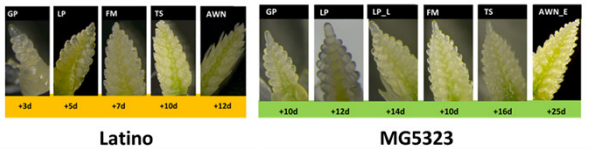


Figure 5. Real time expression of target genes involved in inflorescence meristem developmental phases