

# Identification and mapping of quantitative trait loci for kernel-related traits in a durum wheat x *T. dicoccum* segregating population

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## Introduction

Durum wheat breeding relies on grain yield improvement in order to meet its upcoming demand while coping with climate change. Kernel size and shape have a determinant role in thousand kernel weight (TKW), a key component of grain yield, and it is through understanding the genetic control behind these traits that progress can be achieved. The present study aimed to dissect the genetic bases responsible for kernel size components (length, width, perimeter and area) and kernel shape (width-length ratio and form coefficient) and their relationships with kernel weight, plant height (PH) and heading date (HD). Diversity of the wheat domesticated ancestor of durum wheat, that is emmer (*T. turgidum* ssp. *dicoccum*), was exploited through QTL mapping on a durum x emmer RIL population.

## Methods

Segregating population of 110 RIL, derived from a cross between MG5323 x Latino (Fig. 1), evaluated in 4 different environments in Italy.

High throughput phenotyping of kernels by image analysis (WinSEEDLETM).

QTL mapping using a high-density genetic map  
QTL clusters identification as co-locating loci for different traits.

QTL clusters projection to the consensus map and the *T. durum* reference genome sequence cv. Svevo to hypothesize candidate genes by inspecting the functional annotations within physical positions.

Comparison of the QTL identified with previous genetic knowledge to highlight stable and novel QTL regions for the mentioned traits.

**Figure 1.** Kernel morphology of parental lines (*T. dicoccum* accession MG5323 and *T. durum* cultivar Latino).

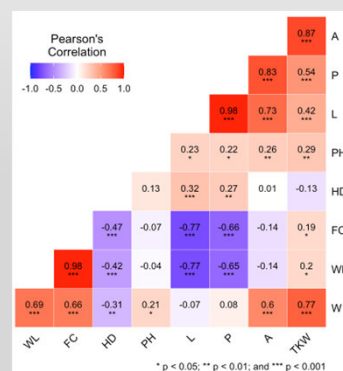


## Results

As depicted in **Fig. 2**, the frequency distribution of phenotypic values in all the environments suggests the contribution of several loci controlling the phenotypic variation for each trait. Additionally, the high transgressive segregation observed implies the presence of superior alleles from both parental lines. The analysis of variance across the 4 environments suggested that the genetic factors contribute largely to the phenotypic variability. Interestingly, TKW showed a significant and highly positive correlation to A ( $r \approx 0.9$ ) and W ( $r \approx 0.8$ ) and moderate positive correlation to L ( $r \approx 0.4$ ) and P ( $r \approx 0.5$ ) for all environments and across them (**Fig. 3**).

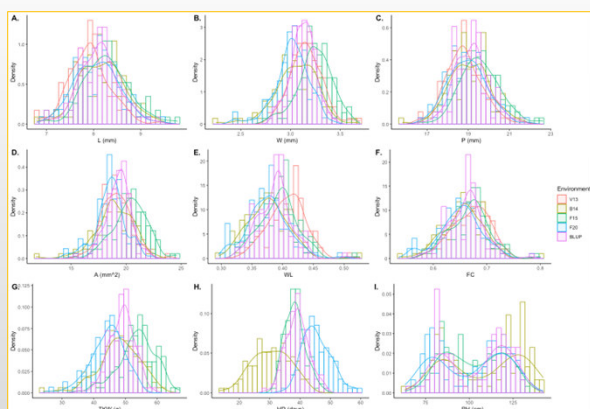
Overall, 83 of the 100 total detected loci were found relevant to more than one trait, meaning they were co-locating loci. Hence, these QTL were grouped in 9 clusters on chromosomes 2A, 2B (2 clusters), 3A, 3B, 4B (two clusters), 6B and 7A. A QTL cluster on 4B chromosome was found explaining from 9.6 to 12.7% of the kernel weight variance and up to 22% of the kernel size traits (length, perimeter and area) variation. The parental MG5323 contributed the favourable allele for this cluster. Validation of the cluster was performed by previously QTL found related to area and TKW from different genetic backgrounds, however, suggesting that this cluster is likely to be new for the relationships detected in a *T. dicoccum* derived population.

**Figure 3** Pearson's correlation for the 9 traits from BLUP values.

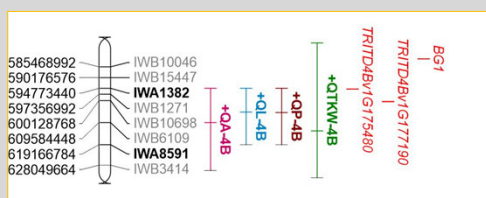


The physical positions of the cluster, spanning from 595 to 619 Mbp (**Fig. 4**), overlapped with the rice gene BIG GRAIN PROTEIN 1, described as a positive auxin regulator involved in grain development

**Figure 2** Frequency distribution of the 9 traits in the 4 environments and across environments (BLUP dataset).



**Figure 4.** Physical representation of cluster 7 on chromosome. 4B.



## Conclusions and perspectives

- This study validated QTL previously detected and incremented the traits associated to each of the 9 clusters of co-locating QTL, contributing on understanding the genetic basis on the relationships between kernel-related traits.
- A major and stable loci was detected on chromosome 4B related to kernel size traits and kernel weight, being the superior allele donated by the *T. dicoccum* line, supporting its use as a valuable genetic resource to improve durum wheat germplasm.
- Further validation as with fine mapping is needed to refine the position of the QTL detected here.

## References

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