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GENETIC DISSECTION OF COMPLEX TRAITS IN DURUM WHEAT USING MULTI-LOCUS GWAS

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Since the establishment of the mixed linear model (MLM) method for genome-wide association studies (GWAS), a series of new MLM-based methods have been proposed. Most of the methods require Bonferroni correction, which often is too conservative. As a result, most of the small effects associated with complex traits, especially those with low heritability, are still not captured by these GWAS methods. To address this concern, here, we tested six different multi-locus models (mrMLM, FASTmrMLM, FASTmrEMMA, pLARmEB, pKWmEB, and ISIS EM-BLASSO) using the SNP-effect as a random factor and adopting a modified Bonferroni correction to calculate the threshold value for significance. To show the effectiveness of these models, we analyzed more than 40 phenotypic traits with high and low heritability in two different wheat panels, including wild and domesticated *Triticum turgidum* spp. accessions, and modern durum wheat cultivars. For the traits with high heritability (*i.e.*, plant height, PH), two reliable QTNs (detected by more than two different methods) were localized on chromosome 4B, ~ 9kb far from the main *Rht-1* gene controlling PH. Similarly, three reliable QTNs on chromosomes 2A, 3A and 7B coincided with the physical regions of known QTLs for the same trait, demonstrating the effectiveness of multi-locus GWAS methods. Interestingly, a reliable QTN, previously not reported in the literature on chromosome 1A (Excalibur_c6255_1119), had the highest LOD value (LOD = 17; log10(P) = 19.77). This marker was found nearby the *Receptor-like kinase* (*RLK*) gene, which could represent a good candidate gene, as it plays an important role during wheat growth and development.
For low heritability traits, the multi-locus approach identified genomic regions that the classic single-locus models failed to detect. For example, one reliable QTN was found associated with the grain protein content (GPC) on chromosome 6B, in the genomic regions previously identified in several studies. This leads us to argue that, the mrMLM approach provides a robust alternative for GWAS applications, especially for complex traits regulated by many small-effect loci.