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ASSOCIATION MAPPING FOR QUALITY TRAITS IN A DURUM WHEAT COLLECTION

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Grain protein content and gluten strength are major targets in durum wheat breeding programs (*Triticum turgidum* L. var. *durum*). Six experiments were conducted in the south of the province of Buenos Aires (Argentina) using a world-wide durum wheat germplasm collection (170 entries) in order to analyze grain protein content, thousand kernel weight and gluten strength. This collection was genotyped with the Breeders' 35K Axiom[®] array and four major genes markers. The population structure was assessed by using a subset of 1,000 SNPs in low linkage disequilibrium and association mapping (AM) was performed for all the phenotypic traits using 3,745 markers. It was possible to find associations between the three phenotypic traits and the molecular markers used, confirming previously reported chromosomal regions and in some cases, detecting novel QTLs. Seven SNPs on 2A, 2B, 3B and 7B chromosomes were associated with thousand kernel weight in three environments, some of them were previously reported in similar genome regions in bread and durum wheat panels. Six markers located on chromosomes 2B and 4A were associated with grain protein content in two environments. Additional marker-trait associations (MTA) for protein content were considered unsatisfactory showing low environmental stability. Several MTA were detected on 1B (7.46 - 36.42 cM) for gluten strength. AM was effective to detect several of the QTLs previously reported on the same chromosomal regions through biparental mapping. These results suggest that AM is a suitable tool to identify genomic regions for traits that are routinely measured in wheat breeding programs.

ABSTRACT