

## Abstract

Wheat (*Triticum aestivum* L.) is one of the most important cereals and is a major staple food in developing countries. Aluminum (Al) toxicity is one of the main factors limiting wheat growth and production in acid soils, which occur on up to 50% of the arable lands of the world especially in tropical and subtropical regions. Genetic improvement of aluminum (Al) tolerance is one of the cost-effective solutions to improve plant productivity in acidic soils around the world. This study was conducted to evaluate wheat traits and detecting QTLs of yield and phenological, morphological, agronomic, physiological and biochemical traits in SeriM82/Babax population. The parental lines, SeriM82 and Babax, and 167 derived recombinant inbred lines (RILs) were evaluated in an alpha-lattice design with two replications under two Al treatments (+Al, 800  $\mu$ M of Al; -Al, 0  $\mu$ M of Al) under field condition, in Darab Agricultural Research Station in 2014-15 and 2015-16 growing seasons. Results of REML analysis showed significant differences between the lines for the majority of tested traits, indicating the high phenotypic variation within the population for different traits. The RILs transgressively segregated for the most traits under contrasting conditions. The majority of tested traits were highly influenced by genotype  $\times$  environment interaction (GEI) suggesting complex and independent genetic control of aluminum tolerance. Grain yield had a positive correlation with days to germination, days to tillering, canopy temperature degradation at grain filling stage, plant height, total spikelet number per spike, grain number per spikelet, spike weight, diameter and length, grain width and length, grain number and weight per spike, thousand grain weight, relative water content, cell membrane stability, chlorophyll a and b, sodium and potassium amount, and protein. A number of 477 markers consisting of 121 SSR, 211 AFLP, 144 DArT, and an EST-SSR preformed in this study were used for map construction. All markers distributed over 29 linkage groups (LGs) that assigned to 20 chromosomes. No marker assigned to chromosome 3D. Based on single-locus analysis for phenological, morphological, agronomic, physiological and biochemical traits, 439 QTLs including 105 putative and 334 suggestive QTLs were identified for all studied traits. Individual QTLs explained 2.00%-25.31% of the phenotypic variance in different environments during both the crop seasons. These QTLs located unevenly throughout the wheat genome. Among them, 42.37%, 41.69%, and 15.94% were in the A, B, and D genomes, respectively. The highest number of putative QTLs was related to days to maturity. Based on two-locus analysis, 419 additive QTLs and 85 pairs of epistatic effects were detected, among which 217 additive and 54 pairs of epistatic QTLs showed significant QTL  $\times$  environment interactions. In general, the effect of epistasis



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