

Abstract

In order to identify genomic locations controlling terminal heat tolerance related traits in wheat, an experiment was conducted at Research Farm of Agricultural and Natural Resources Research Center of Zabol in 2015 and 2016 cropping cycles. The experiment was carried out using four alpha lattice designs with two replications under non-stress and terminal heat stress conditions. Plant materials were 167 recombinant inbred lines and their parents (SeriM82 and Babax). In this study 28 phenological, physiological and morphological traits were measured. Wheat molecular marker linkage map comprised of 211 AFLP marker, 120 SSR marker and 144 DArT markers with 1864 cM length and 4.4 cM mean distance. QTL analysis was separately conducted by composite interval mapping (CIM) and Mixed-Model based composite interval mapping (MCIM) methods. Results of Analysis of variance showed significant difference among the recombinant inbred lines for most of the traits. Based on combined analysis, there were significant differences among genotypes for most of the traits and transgressive segregations in both directions were also observed. Simple correlation coefficient analysis indicated a significant positive association between grain yield with biological yield, harvest index, Fv/Fm and 1000 grain weight for both normal and stress conditions in two cropping cycles. Using composite interval mapping, a total of 120 QTLs with an additive effect for all under studied traits were identified. Phenotypic variances explained by these QTLs varied from 5.29% for number of grains per spike to 22.31% for days to germination. The highest LOD score was obtained for flag leaf sheet length on chromosome 1D. Using Mixed-Model based composite interval mapping, a total of 165 main-effect QTLs for all traits on various chromosomes were detected. QEs interaction was significant in 30 main-effect QTLs and R^2_{ae} ranged from 0.02 to 6.09% for each trait. Twelve digenic interactions involving 24 loci were detected for the twenty eight traits, and one pair of epistatic QTLs were involved in QQEs. Results of the current research showed that QTLs of biological yield and WSC with that of grain yield were co-located. In addition, a common QTL for days to heading and days to maturity on chromosome 3B was identified. Most of mapped QTLs For studied traits were stable. Therefore, after complementary experiments can be used in marker-assisted selection (MAS) in order to produce heat tolerant and high performance wheat varieties.

Key words: QTL, Heat stress, recombinant inbred line, wheat



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**Mapping genomic regions of
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