

QTL analysis of germination heat sensitivity in winter wheat.

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Winter wheat is usually planted in early September in the southern Great Plains to increase forage production for the purpose of cattle grazing. As a negative consequence of early planting, wheat seed may exhibit secondary dormancy under the hotter soil conditions typically encountered in early September. Poor emergence and stand establishment of extremely sensitive cultivars may result in significant forage yield reduction of about 50%. This phenomenon is termed germination heat sensitivity (GHS) or thermodormancy. Evaluation of breeding material is difficult because of unpredictable weather conditions at planting and the continuous decrease in heat sensitivity during seed storage. The environment of the maternal plant in which seed production occurs also may confound differences in GHS. In this study, 94 recombinant inbred lines (RILs) derived from two local cultivars, Intrada (HW) and Cimarron (HRW), were used to map QTL controlling GHS. Seed samples were collected in years 2006 and 2007 from both the field and greenhouse and stored at room temperature until the end of August. Germination rates were investigated in growth chambers at two temperature regimes, 35/27°C day/night to test GHS, and constant 24°C as control. At 24°C, all RILs showed germination rates exceeding 90%, indicating that primary dormancy had been released at test time. Two major QTL were detected on chromosomes 3AS and 4AL. The locus *QGhs.osu-3A* was tightly linked with SSR marker BARC310, explaining 11–24% of the phenotypic variance. *QGhs.osu-4A* was located between *Xgwm637* and *Xwmc513*, accounting for 19–58% of the phenotypic variance. SNP marker BF474615 indicated that this locus was adjacent to the deletion bin 4AL13-0.59-0.66. There was significant epistatic interaction between the two QTL. Strong ‘QTL × environment’ interaction implied that the seed-storage condition and test time had large effects on expression of GHS. The coincidence of markers for GHS and preharvest sprouting tolerance suggested that they might share common points in their regulatory pathways, which might be reactivated by heat stress. In addition, phenotypic data and mapping results both confirmed that seed color had no association with GHS.

Association mapping of quantitative trait loci resistant to aluminum toxicity in U.S. winter wheat.

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Aluminum (Al) toxicity is a major constraint for wheat production in acid soils worldwide. To date, three QTL for Al resistance have been mapped through linkage mapping. To validate these mapped QTL and identify new QTL for Al resistance from U.S. wheat breeding lines, association mapping was conducted using 211 simple-sequence repeat (SSR) markers covering the 21 wheat chromosomes and 205 U.S. elite, winter wheat breeding lines, including 119 hard red winter wheat (HRWW), 21 hard white winter wheat (HWWW), and 65 soft red winter wheat (SRWW) from four U.S. wheat regional nurseries. On average, one SSR amplified 8.4 alleles across the 205 lines, ranging from 2 to 24. The 205 lines were divided into six subpopulations including four hard winter wheat (HWW) subpopulations and two soft winter wheat (SWW) subpopulations, on the basis of 1,770 alleles analyzed by the Structure2.0 software. Among the four HWW subpopulations, subpopulation 1, mainly from Oklahoma and Kansas, showed a higher level of Al tolerance than the other three subpopulations, with an average field score of 1.62 on a 0–5 scale. Two SWW subpopulations had a high level of Al tolerance with average field Al scores of 1.38 and 1.67. Genome-wide association analysis identified at least four significant regions that were associated with Al resistance, and three were reported previously by linkage mapping. Analysis of linkage disequilibrium indicated that markers in the 4DL major QTL region were closely linked and good markers for marker-assisted selection. Another major QTL on 3BL, identified from the Chinese landrace FSW in our lab, also showed a high association with Al tolerance ($P < 0.01$) in U.S. winter wheat lines. A minor QTL in the 2AS region also was validated in the association analysis, but an additional QTL with a large effect on Al resistance was identified in the association mapping study. In addition to the three mapped QTL, a new locus on 2DL also displayed a significant effect on Al resistance. Markers identified in this study will be useful for marker-assisted selection in U.S. winter wheat breeding programs.