Poster 14. QTL validation for agronomic traits on chromosome 3A of hexaploid wheat using recombinant-inbred chromosome lines.

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A study of chromosome substitution lines between two hard red winter wheat cultivars Wichita (WI) and Cheyenne (CNN), showed that chromosome 3A from WI increased grain yield by 15 to 20% when placed in the CNN background, whereas the reciprocal substitution line with CNN chromosome 3A in a WI background decreased grain yield by 15 to 20%. Follow-up research was conducted to determine the trait variation caused by chromosome 3A by creating 98 recombinant inbred chromosome lines (RICLs) in the Cheyenne background where the RICLs involved chromosome 3A of both cultivars. In the CNN(RICL3A) population, QTL were detected for seven of the eight agronomic traits studied. A major, grain yield QTL detected in the combined analysis explained 28% of the phenotypic variance, and the substitution of the WI allele for a CNN allele increased grain yield by 66 kg/ha. The WI(RICL3A) population (the RICLs involve WI and CNN chromosome 3A in WI background) were used to validate the QTL detected in the CNN(RICL3A). Effectively, WI(RICL3A) are the mirror population to the previously studied CNN(RICL3A). The objectives of this study were to (1) identify and map QTL for eight agronomic traits on chromosome 3A in individual environments and combined across environments, (2) evaluate 'QTL x environment' interaction (QEI) by comparing the consistency of QTL detected in individual environments and, (3) compare the QTL detected in this study to those obtained in the CNN(RICL3A). A population of 90 WI(RICLs3A), developed through a doubled-haploid (DH) system from a cross between WI and chromosome substitution line WI(CNN3A), were used to investigate the QTL for grain yield and its components traits and were planted in Lincoln, Mead, and North Platte, NE, during the 2007–08 cropping season. QTL were detected for anthesis date, plant height, grain yield, grain volume weight, and 1,000-kernel weight. A grain yield QTL detected at Lincoln and in the combined analysis explained 17% of the phenotypic variance, and the substitution of a CNN allele for a WI allele decreased grain yield by 118 kg/ha. This grain yield QTL was the major grain yield QTL detected in the CNN(RICL3A) population and was at a similar position. In addition to grain yield, grain volume weight and 1,000-kernel weight QTL were detected in the combined analysis that explained 38% and 14% of the phenotypic variance, respectively. The first year results of this study indicated the possibility of detecting most of the major chromosome 3A QTL reported in the previous CNN(RICL3A) studies using a different background. The WI 3A alleles in a previous CNN(RICL3A) study showed an increased in grain yield and yield components traits and, as expected, the CNN 3A alleles in the this WI(RICL3A) study has a decreased effect on grain yield and yield components traits. The unique opportunity of using chromosome substitution lines provides a chance for examining the effects of QTL on a single chromosome. The use of RICLs from a reciprocal substitution also will avoid the limitation of a one-way chromosome substitution in determining the interactions between chromosomes.