Available online at www.sciencedirect.com
SCIENCE DIRECT
Genomics 88 (2006) 74–87
GENOMICS
www.elsevier.com/locate/ygeno

High-density mapping and comparative analysis of agronomically important traits on wheat chromosome *3A*

Muharrem Dilbirligi [a,1,2], Mustafa Erayman [a,1,3], B. Todd Campbell [4], Harpinder S. Randhawa [a], P. Stephen Baenziger [b], Ismail Dweikat [b], Kulvinder S. Gill [a,*]

[a] *Crop and Soil Science Department, Washington State University, P.O. Box 646420, 277 Johnson Hall, Pullman, WA 99164, USA*
[b] *Department of Agronomy and Horticulture, University of Nebraska, Lincoln, NE 68583, USA*

Received 24 July 2005; accepted 5 February 2006
Available online 19 April 2006

Abstract

Bread wheat chromosome *3A* has been shown to contain genes/QTLs controlling grain yield and other agronomic traits. The objectives of this study were to generate high-density physical and genetic-linkage maps of wheat homoeologous group *3* chromosomes and reveal the physical locations of genes/QTLs controlling yield and its component traits, as well as agronomic traits, to obtain a precise estimate of recombination for the corresponding regions and to enrich the QTL-containing regions with markers. Physical mapping was accomplished by 179 DNA markers mostly representing expressed genes using 41 single-break deletion lines. Polymorphism survey of cultivars Cheyenne (CNN) and Wichita (WI), and a substitution line of CNN carrying chromosome *3A* from WI [CNN(WI3A)], with 142 RFLP probes and 55 SSR markers revealed that the extent of polymorphism is different among various group *3* chromosomal regions as well as among the homoeologs. A genetic-linkage map for chromosome *3A* was developed by mapping 17 QTLs for seven agronomic traits relative to 26 RFLP and 15 SSR chromosome *3A*-specific markers on 95 single-chromosome recombinant inbred lines. Comparison of the physical maps with the *3A* genetic-linkage map localized the QTLs to gene-containing regions and accounted for only about 36% of the chromosome. Two chromosomal regions containing 9 of the 17 QTLs encompassed less than 10% of chromosome *3A* but accounted for almost all of the arm recombination. To identify rice chromosomal regions corresponding to the particular QTL-containing wheat regions, 650 physically mapped wheat group *3* sequences were compared with rice genomic sequences. At an *E* value of $E \leq 10^{-5}$, 82% of the wheat group *3* sequences identified rice homologs, of which 54% were on rice chromosome 1. The rice chromosome 1 region collinear with the two wheat regions that contained 9 QTLs was about 6.5 Mb.
© 2006 Elsevier Inc. All rights reserved.

Keywords: Wheat chromosome *3A*; Grain yield; QTLs; Deletion mapping; Genetic-linkage mapping; RFLP; SSR; Wheat–rice comparison

Grain yield (GYLD) is perhaps the most commonly studied and poorly understood trait related to agronomic performance of wheat (*Triticum aestivum* L. em. Thell.). GYLD is controlled by a number of genes and is manifested via a complex relationship among the yield component traits such as 1000-kernel weight (TKWT), kernels per spike (KPS), spikes per square meter (SPSM), and kernels per square meter (KPSM) [1–4]. Some other agronomic traits, including anthesis date, plant height (PHT), and grain volume weight (GVWT), also have an effect on GYLD.

Detailed analysis of intervarietal chromosome substitution lines between the two winter wheat cultivars "Wichita" (WI) and "Cheyenne" (CNN) identified chromosome *3A* accounting for the major part of the yield advantage of WI over CNN [5–8]. Consistently detected across more than 15 different location-year environments, chromosome *3A* from WI, when presented in the CNN background, increased GYLD by 15–20% [1–4]. This effect of chromosome *3A* seems independent of the background, at least between these two cultivars, as the

* Corresponding author. Fax: +1 509 335 8674.
E-mail address: ksgill@wsu.edu (K.S. Gill).
[1] These authors have contributed equally to this work.
[2] Current address: Central Research Institute for Field Crops, P.O. Box 226, 0642 Ankara, Turkey.
[3] Current address: Department of Field Crops, Mustafa Kemal University, 31034 Hatay, Turkey.
[4] Current address: Coastal Plains Research Center, USDA-ARS, Florence, SC 29501, USA.

0888-7543/$ - see front matter © 2006 Elsevier Inc. All rights reserved.
doi:10.1016/j.ygeno.2006.02.001

reciprocal substitution line carrying CNN chromosome *3A* in the WI background showed a 15–20% decrease in GYLD. Detailed field and DNA marker analyses of 95 single-chromosome recombinant inbred lines (RICLs) involving chromosome *3A* of WI and CNN in the CNN background identified quantitative trait loci (QTLs) for GYLD, TKWT, KPS, SPSM, KPSM, PHT and GVWT [1–4]. The Physical locations of these QTLs and accurate estimates of kb/cM ratios for the harboring chromosomal regions are, however, not known.

It is critical to know the physical locations of genes and QTLs, particularly in wheat, because the distribution of both genes and recombination is highly uneven on chromosomes [9–15]. More than 85% of the wheat genes are present in 48 gene-rich regions (GRRs) with varying sizes and densities, encompassing less than 29% of the wheat genome [10]. The remaining 71% of the genome is very gene-poor, consisting of large blocks of repeated DNA interspersed with very few genes. Recombination occurs mainly in the GRRs but various GRRs differ as much as 140-fold in recombination rate [10]. Of the 252 phenotypically characterized useful wheat genes, 241 were physically localized in GRRs [10,16]. Twenty-one of these genes were located on wheat homoeologous group *3* chromosomes.

Genomic information from model systems has been used for isolation of genes from larger genomes via comparative analysis [17–26]. For wheat, the rice (*Oryza sativa*) genome is of particular interest as rice and wheat belong to the same family, Poaceae. Based on comparisons of common markers on genetic linkage maps, wheat and rice genomes were reported to be very collinear, but detailed analyses at the micro level show many exceptions [19,27–31]. Comparison of 4485 physically mapped wheat ESTs with the rice genomic sequence confirmed that the wheat–rice collinearity is frequently interrupted by segments from the other chromosomes [30,32,33]. Wheat homoeologous group *3* chromosomes are collinear with rice chromosome 1 and this is perhaps the best among all chromosomes of wheat–rice comparisons [30,32]. Conserved blocks are present on syntenic chromosomes; however, several rearrangements are also apparent, particularly around the centromeric region [32]. Along with many discontinuities, the exact size, order, and distribution of the rice segments orthologous to gene-containing regions on wheat group *3* chromosomes are, however, not known. The objectives of this study, therefore, are to reveal the precise genetic as well as physical location of genes controlling agronomic traits such as yield and yield component traits relative to DNA markers and to enrich the corresponding regions with additional markers by using the available genomic resources of both wheat and rice.

Results

Physical mapping

Gel-blot analysis results for 179 DNA probes on wheat group *3* nullisomic–tetrasomic (NT) and chromosome deletion lines are given in Table 1. Except for 6, all probes identified wheat group *3*-specific bands. The probes TAM32, TAM63, and KSUG59 detected a smear pattern, and none of the fragment bands detected by the probes BCD1802, CDO1396, and CDO389 were missing in group *3* NT lines. The 173 probes detected 924 fragment bands, of which 520 (56%) mapped to group *3* chromosomes. The remaining 402 (44%) fragment bands were either not resolved by the restriction enzyme used or specific for other wheat chromosomes. The 520 group *3*-specific bands corresponded to 415 unique loci, of which 141 mapped on *3A*, 142 on *3B*, and 132 on chromosome *3D* (Fig. 1). About 55% (94/172) of the probes detected loci on all three homoeologs, 27% on two, and 18% on only one of the homoeologs (Table 1; Fig. 1). On average, each probe detected 2.4 loci. Seven of the probes detected paralogous loci, as the fragment bands for probes FBB271, FBA133, KSUE2, KSUH7, UNL130, BE444148, and BE483203 showed more than one location on each of the group *3* chromosomes (Fig. 1).

Consensus physical map

Physical mapping data from the three homoeologs were combined to generate a consensus map (Fig. 2). There were 43 breakpoints on the consensus map corresponding to the 41 group *3* deletion lines. The consensus map contains 170 loci corresponding to 167 of the 173 physically mapped markers (Fig. 2, left). The remaining 6 markers were not placed on the consensus map because their location either was inconsistent among homoeologs (*XksuG62*) or had insufficient mapping data (*Xbcd1127, Xbe497524, Xbe637850, Xfbb366*, and *XksuF34*). Location of markers *Xbcd1380, Xpsr56, Xunl150, Xbe500083*, and *Xbe607045* was not considered discrepant among the homoeologs and thus they were placed between fraction length (FL) 0.3 bracketed by deletion lines 3DL-1 (0.23) and 3BL-9 (0.38) on the consensus map (Fig. 2, left). These markers were present between FL 0.28 and 0.42 on *3A*, between 0.07 and 0.22 on *3B*, and between 0.23 and 0.27 on *3D* (Figs. 1 and 2). This difference among homoeologs was within the range of a 5% error rate that is observed for the FL value estimations [45].

Distribution of the markers was highly uneven on the consensus map. Forty-three breakpoints on the homoeologous group *3* chromosomes resulted in 14 chromosomal regions on the consensus map. Of these regions, 7 contained about 91% of the mapped loci but physically spanned only about 36% of the chromosomes. The remaining 9% of the loci were present in marker-poor regions containing markers *Xbcd102, XksuI32, Xbcd127*, and *Xpsr909* on the short arm and markers *Xbcd134, Xcdo920, XksuE2.2, XksuH7.2, Xpsr394, Xtag609*, and *Xwg222* on the long arm (Fig. 2).

The seven marker-rich regions differed significantly in their size and marker density. Of the seven marker-rich regions three were present on the short arm and four on the long arm. The size of these regions ranged from 1.5 (3L0.8) to 8.5% (3S0.9) of the chromosome and their number of loci ranged from 13

Download English Version:

https://daneshyari.com/en/article/2821423

Download Persian Version:

https://daneshyari.com/article/2821423

Daneshyari.com