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RESEARCH ARTICLE

A genetic evidence of chromosomal fragment from bridge parent existing in substitution lines between two common wheat varieties

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Abstract

Locating of important agronomic genes onto chromosome is helpful for efficient development of new wheat varieties. Wheat chromosome substitution lines between two varieties have been widely used for locating genes because of their distinctive advantages in genetic analysis, compared with the aneuploid genetic materials. Apart from the substituted chromosome, the other chromosomes between the substitution lines and their recipient parent should be identical, which eases the gene locating practice. In this study, a set of chromosome substitution lines with *cv*. Wichita (WI) as the recipient parent and *cv*. Cheyenne (CNN) as the donor parent were studied for the composition of high molecular weight glutenin subunits (HMW-GS) as well as a range of agronomic important traits. Results revealed that the substitution lines of WI(CNN5D), WI(CNN6A) and WI(CNN7B) had higher plant heights than the two parents of WI and CNN, and WI(CNN3D) had later maturity than the parents. By sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS) analysis, a substitution line WI(CNN5B) was found to contain different HMW-GS patterns from its two parents, in which 1By9 was replaced by 1By8 on chromosome 1BL. Simple sequence repeat (SSR) analysis confirmed that the variation on 1BL in WI(CNN5B) was originated from Chinese Spring (CS). It is concluded that chromosomal fragments from bridge material and donor parent were quite often retained in intracultivaral chromosome substitution lines except the substituting chromosomes.

Keywords: wheat, intracultivaral chromosome substitution lines, agronomic traits, high molecular weight glutenin subunits (HMW-GS), molecular markers

1. Introduction

Wheat is an economical valued crop in the globe, and its genetic improvement contributes to its stable increase of grain production greatly (Shewry 2009). Gene locating onto chromosome would help to accelerate the development of new wheat varieties (Law *et al.* 1987). Chromosome substitution lines between two varieties have been used for more than half century for the primary screening and chromosomal locating of some interesting genes controlling important agronomic and physiological traits in wheat (Kuspria and Unrau 1957). Compared with other genetic germplasm used for gene locating in wheat such as nullisomic and ditelosomic lines, substitution lines have no negative effect on plant growth and development (Yen

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and Baenziger 1992). Thereby, using substitution lines to locate genes is a more appropriate way.

By using Chinese Spring (CS) ditelosomics, nullisomic-tetrasomics and CS-Cheyenne disomic substitution lines, four allelic genes of puroindoline b (Pinb) *Pinb-2v1*, *Pinb-2v2*, *Pinb-2v3*, and *Pinb-2v4* were mapped on chromosomes 7DL, 7BL, 7B, and 7AL, respectively (Chen *et al.* 2010). Previously, by employing two substitution lines CS(Cheyenne 5A) and CS(*T. Spelta* 5A) the synthesis synthase gene of glutathione and hydroxymethylglutathione in wheat during heat stress was located on chromosome 5A (Kocsy *et al.* 2004). Zemetra *et al.* (1986) developed a complete set of intracultivaral substitution lines between two winter wheat cultivars, Cheyenne (CNN) and Wichita (WI), in which CNN was used as the recipient and WI was the donor cultivar. This substitution set has been extensively used in wheat genetic analysis. By using the substitution lines, a gene affecting winterhardness and vernalization was located on chromosome 3B (Zemetra and Morris 1988), and two genes controlling the activities of two DNA-degrading enzymes of 24.0 and 27.0 kDa were mapped onto chromosome 2D (Yen and Baenziger 1994). To understand grain yield in winter wheat, the reciprocal set of chromosome substitution lines in duplicate between CNN and WI were used, and it was found that chromosomes 3A, 6A, 2B, and 3D greatly affected grain yield and yield components such as culms m^{-2}, seed weight and seeds per culm (Berke *et al.* 1992a, b). Chromosome 3A also affected plant height and anthesis date (Shah *et al.* 1999a, b). Further study demonstrated that the quantitative trait loci (QTLs) for the above main agronomic traits were generally localized to three regions of chromosome 3A, in which the major QTLs for kernels m^{-2} and grain yield were associated within a 5-centimorgan (cM) interval (Campbell *et al.* 2003). Substitution lines of CNN(WI3A) and CNN(WI6A) had 15–20% higher grain yield than CNN, whereas WI(CNN3A) and WI(CNN6A) had 15–20% lower grain yield than WI (Baenziger *et al.* 2011). By using another complete set of chromosome substitution lines between CS and Synthetic 6x, it was proved that the genes inhibiting spikelet differentiation are located on chromosomes 2B and 7D, the genes related to drought tolerance on chromosome 2D (Bai *et al.* 2007), the genes regulating chlorophyll fluorescence parameters including F_o, F_m, F_v/F_m, and F_v/F_o on chromosomes 5B, 3A, 4D, and 7A (Bai *et al.* 2011), and the genes associated with tolerance to low phosphorus stress on chromosome 2A (Zheng *et al.* 2013).

In addition to above mentioned material, other intracultivaral substitution lines were also used in locating genes in wheat. For examples, employing CS (recipient)/Cappelle Desprez (donor) substitution lines, the genes controlling argine accumulation in wheat plants under osmotic stress were assigned on chromosomes 5A and 7A (Galiba *et al.* 1993), and the genes controlling relative water content, excised leaf water loss rate, and drought susceptibility index on chromosomes 1A, 5A, 7A, 4B, 5B, 1D, and 5D (Farshadfar *et al.* 1995). Investigation applying CS (recipient)/Hope (donor) substitutions under drought conditions indicated that chromosomes 4B, 5A and 5D carry proline accumulation associated genes, while chromosomes 6B and 6D contain proline biosynthesis inhibiting related genes (Yang *et al.* 1998).

All wheat intracultivaral substitution lines were developed using the corresponding mono-telocentric lines of CS as starting material. For the substitution lines with background of CS, mono-telocentric lines of CS were used as the recurrent parents to be crossed with a donor variety. For the substitution lines with background of other wheat cultivar, mono-telocentric lines of CS were used to develop mono-telocentric lines of other cultivars first by crossing and backcrossing. In each hybrid generation, selection was made for monosomic individuals for use as pollen parents in the next backcrossing cycle with the mono-telocentric recipient lines. After a minimum of six backcrosses, the monosomics were self-pollinated and plants with 42 chromosomes were selected in which the targeted chromosome pairs were derived from the donor variety (Law *et al.* 1987; Yen and Baenziger 1992; Kocsy *et al.* 2004). Because of frequent chromosome crossover in the crossing and backcrossing hybrids, chromosome fragments from donor or bridge parent are expected to be retained in the final background of recipient parent. By applying wheat intracultivaral substitution lines to locate some target genes on chromosomes, the substitution lines should be the complete same to their recipient cultivar in genetics except the replacement chromosome in each line. In this case, some important genes can be located onto chromosome correctly, and wheat breeding program can be accelerated. Otherwise, the mapping of some wheat genes is not precised and convinced by this strategy. Therefore, it is very important to confirm wheat substitution lines between two varieties, especially the quite often used intracultivaral substitution lines of WI and CNN, by proteomics and genetics methods. In order to detect if chromosome fragments of CS are present in the intracultivaral substitution lines, the WI and CNN substitution lines were tested by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE), matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS) and simple sequence repeat (SSR) markers in this study. The obtaining results will provide useful information for the correct use of the wheat substitution lines between the two varieties and convinced locations of some important genes in common wheat.