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Research article

Development of near-isogenic sets of derivatives with T1BL.1RS or 1B chromosome substitutions in bread wheat.

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Summary

Seventeen bread wheat (*Triticum aestivum* L.) cultivars homozygous for chromosome 1B or T1BL. 1RS were pollinated by diverse bread wheat cultivars to produce chromosome 1B,T1BL.1RS F_1 heterozygotes. Each F_1 combination was then pollinated by its respective bread wheat parent (maternal) to yield the first backcross (BC_1) derivatives. Heterozygous 1B,T1BL.1RS plants were identified by a combination of electrophoresis and Giemsa C-banding. These BC_1F_1 heterozygotes were backcrossed further to their respective maternal bread wheat parents to yield BC_2 derivatives, which were similarly advanced to BC_7 and then self-pollinated. From the selfed progeny, plants homozygous for chromosome 1B and T1BL.1RS were identified biochemically and cytologically. We discuss here the utility of these germplasms and their uniqueness.

Key words: Bread wheat, T1BL.1RS translocation, Isogenic lines

Introduction

Bread wheats (*Triticum aestivum* L.) with the T1BL.1RS translocation have been of interest over the past two decades, and are globally utilized in bread wheat breeding programs (Lukaszewski 1990). The 1RS chromosome arm possesses four race-specific biotic stress resistant genes (McIntosh 1983), contributing to the crops wide adaptation and yield potential (Rajaram et al. 1983; Villareal et al. 1994). Approximately 55 percent of our bread wheat germplasm possesses the T1BL.1RS translocation, and global cultivation of such wheats exceeds five million hectares.

The superior agronomic performance of T1BL.1RS wheats in comparison with 1B wheats has been an active study area, and has utilized various germplasm groups for experimentation. One such group comprised of several lines with the T1BL.1RS translocation or instead, with chromosome 1B. This set of germplasms developed by Mujeeb-Kazi et al. (1996) facilitated a stringent testing of the rye contribution in a near-isogenic cv. Seri M82 (Villareal et al. 1998). The need to evaluate the 1RS effect across several bread wheat genotypes led to our producing

the presently reported near-isogenic germplasms for seventeen bread wheat cultivars in which chromosomes 1B or T1BL.1RS were replaced by T1BL.1RS or 1B respectively by a series of backcrosses.

Materials and methods

Seventeen bread wheat cultivars homozygous for chromosome 1B or T1BL.1RS, the germplasms utilized in this study:

a) Parental wheats homozygous for chromosome 1B

Ten cultivars (Yecora, Agatha/6*Yecora, Yaco, Ciano T79, Mrl/Buc, Pfau, Opata, Ocoroni, Esmeralda, Buc//Maya/Mon) were crossed with either Glennson M81 or Seri M82 (T1BL.1RS homozygous) to generate 1B,T1BL.1RS heterozygote F_1 hybrids (Table 1). Each F_1 was backcrossed by its 1B parental cultivar to obtain 1B/1B or 1B, T1BL.1RS seed progeny. Endosperm halves of BC_1 of each cross were subjected to A-Page analysis and 1B homozygous progeny was discarded since they lacked the rye secalin bands which were present only in the 1B,T1BL.1RS heterozygotes. BC_1 heterozygote seeds were germinated and cytologically tested for the presence of one T1BL.1RS chromosome. Two seedlings were advanced/combination and used to generate the BC_2 generation as done for BC_1 production. The A-Page and cytological diagnostic protocols (Bushuk and Zillman 1978; Mujeeb-Kazi et al. 1996) were followed up to BC_7. Selfing the BC_7 heterozygote plants yielded a mixture of seed that were: (i) homozygous 1B and called "extracted", (ii) homozygous T1BL.1RS and (iii) the 1B,T1BL.1RS heterozygote, which were all identified by biochemical procedures. Endosperm halves from the BC_7 selfed seed were subjected to glucose phosphate

Table 1. Development of some bread wheat cultivars homozygous for chromosome 1B or T1BL.1RS and their near-isogenic BC_7 selfed derivatives possessing T1BL.1RS or 1B respectively. The donor cultivars of the T1BL.1RS or 1B chromosome in the 17 F_1 combinations are identified.

Recurrent bread wheat cultivars	Parental chromosome status	Cultivar used to produce F_1	BC_7 selfed status	
			Homozygous near-isolines	Homozygous "Extracted"
Yecora F70, Agatha/6*Yecora, Mrl/Buc, Pfau, Buc//Maya/Mon	1B	Seri M82	T1BL.1RS	1B
Yaco, Ciano T79, Opata M85, Ocoroni F86, Esmeralda M86	1B	Glennson M81	T1BL.1RS	1B
Glennson M81, Bagula, Bobwhite	T1BL.1RS	Ciano T79	1B	T1BL.1RS
Spinebill, Fink, Kauz, Veery 10	T1BL.1RS	Pavon 76	1B	T1BL.1RS

isomerase (GPI) analyses (Chojecki and Gale 1982) which separated the T1BL.1RS homozygotes. The remaining endosperm halves after the GPI assay were subjected to A-Page analyses which separated the 1B homozygotes (were saved), and 1B,T1BL.1RS heterozygotes that were discarded. Embryo portions corresponding to endosperm data for T1BL.1RS or 1B homozygotes were germinated and served for increasing seed of each combination.

b) Parental cultivars homozygous for chromosome T1BL.1RS.
Seven cultivars (Glennson M81, Spinebill, Bagula, Fink, Kauz, Bobwhite, Veery 10) were crossed with either Ciano T79 or Pavon 76 (1B homozygous) to produce heterozygote T1BL.1RS,1B F_1's. The protocols for the advance up to BC_7, selfing, identifying T1BL.1RS homozygotes (extracted), 1B homozygotes, and T1BL.1RS,1B heterozygotes to be discarded were similar to those described for the germplasm in (a).

After the seed increase, one plant per combination was analyzed by fluorescent *in situ* hybridization (Islam-Faridi and Mujeeb-Kazi 1995), seed increased if validated and serve as the cultivars genetic stock. For each of the seventeen cultivars, three groups of germplasm form a tester set. Each cultivar set will comprise of:
1) The original breeders line,
2) The line selected after BC_7 selfing possessing the same chromosomal 1B or T1BL.1RS composition as present in the breeders line and designated as "extracted" (Table 1), and
3) The line resembling the original breeders line but differing in having that cultivars 1B or T1BL.1RS chromosome replaced (substituted) by T1BL.1RS or 1B.

Results and discussion

For each of the 17 bread wheats chromosome 1B in 10 cultivars (Yecora, Agatha/6*Yecora, Yaco, Ciano T79, Mrl/Buc, Pfau, Opata, Ocoroni, Esmeralda, Buc//Mayo/Mon) was substituted by T1BL.1RS, and chromosome T1BL.1RS in seven cultivars (Glennson M81, Spinebill, Bagula, Fink, Kauz, Bobwhite, Veery 10) was substituted by 1B (Table 1). The seven bread wheat cultivars involved allowed the end products of each cultivar to yield near-isogenic lines. For each cultivar three sets have been formulated to stringently evaluate the 1RS contributions in this diverse set of wheat cultivars. To exemplify further, in the three sets of each cultivar the first entry is the breeders original cultivar. If this cultivar was T1BL.1RS (e.g. Glennson M81, Table 1) then the second entry would be a near-isogenic Glennson M81 with the lB chromosome substitution. The third entry would be a T1BL.1RS line selected after selfing of the backcross 7 heterozygotes. This entry is called "extracted". Though it is a T1BL.1RS type phenotypically like the parent cultivar (Glennson M81), genetically it may differ from it due to several allelic variations on 40 chromosomes, and the 1BL arms, but not for the 1RS arm. These variations occur due to the recombination event that may happen when Glennson M81 is crossed by Ciano T79 to generate the F_1 heterozygote (T1BL.1RS,1B). Subsequent backcrosses to Glennson M81 give a Glennson M81 phenotype. Genetic differences however, will exist since 20 chromosomes of Glennson M81 and 20 of Ciano T79 are involved in recombination after the F_1 is produced and advanced up to BC_7. Only the 1RS arm remains similar, since it does not associate at meiosis remaining as the unpaired arm of the T1BL.1RS/1B rod bivalent.

Each of the cultivars which are T1BL.1RS homozygotes possess biotic stress resistance genes

Lr26, *Sr31*, *Yr9*, and *Pm8* located on the rye chromosome arm 1RS (McIntosh 1983). Agronomic differences amongst wheat cultivars have been attributed to the presence of the T1BL.1RS chromosome. These translocation genotypes give superior grain yield, aerial biomass, kernel weight, and spikelet fertility (Moreno-Sevilla et al. 1995; Carver and Rayburn 1994; Schlegel and Meinel 1994). Plant height reduction and delayed heading was observed by McKendry et al. (1996). T1BL.1RS associated positive effects for above-ground biomass at maturity, spikes m^{-2}, 1000-kernel weight, and test weight, were reported by Villareal et al. (1991, 1994) when diverse spring wheat cultivars were evaluated. Villareal et al. (1995) further reported a performance advantage of T1BL.1RS derivatives from random F_2-derived F_6 lines of the Nacozari (1B)/Seri M82 (T1BL.1RS) cross for higher grain yield, above-ground biomass, kernels $spike^{-1}$, 1000-kernel weight, and test weight. Considering these contributions from the above investigation we feel that the presently reported germplasm using the backcross protocol and having the "extracted" entry inclusion will be an asset to further evaluate the T1BL.1RS contributions more stringently.

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