

Associated Effects of Chromosome 1B/1R Translocation on Agronomic Traits in Hexaploid Wheat

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Summary

Two trials were conducted to determine the effect of 1B/1R chromosome translocation on selected agronomic characteristics of spring bread wheats (*Triticum aestivum* L.) developed at the International Maize and Wheat Improvement Center (CIMMYT). Five bread wheat genotypes with a chromosome 1B/1R translocation and five without representing a sample of high yielding germplasm were identified for the experiment. Non-limiting levels of fertility and moisture with a preventive pest and disease program were used. Plant height, days to heading, grain yield, above-ground biomass at maturity, harvest index, yield components and test weights were determined. Genotypes with the 1B/1R chromosome translocation had 2.2% higher above-ground biomass yield, 2.1% more spikes m^{-2} , 1.12 g higher 1,000-grain weight and 0.8 kg/ha^{-1} higher test weight. The non-1B/1R genotypes had 0.8% higher harvest index and 0.6 cm longer spikes. Cultivar comparisons indicated that the 1B/1R group headed 2.5 days later than the 1B group.

Key Words: *Triticum aestivum*, yield and yield components, 1B/1R translocation.

Introduction

The disease resistance potential of the short arm of rye (*Secale cereale* L.) chromosome 1R has been shown against the wheat pathogens leaf rust (*Puccinia recondita* Rob. et Desm. f.sp. *tritici*), stem rust (*Puccinia graminis* Pers. f.sp. *tritici* Brikss. et Henn.), stripe rust (*Puccinia striiformis* Westend f.sp. *tritici*) and powdery mildew (*Erysiphe graminis* Dc. f.sp. *tritici* Marchal) (Bartos and Bares 1971; Bartos *et al.* 1973; Zeller 1973; Mcintosh 1983; Heun and Fischbeck 1987). This rye segment has been successfully incorporated into many hexaploid wheat (*Triticum aestivum* L.) cultivars (Bartos *et al.* 1973; Cai and Liu 1989; Jahan 1990; Mcintosh 1983; Merker 1982; Mettin *et al.* 1973; Mujeeb-Kazi 1982, 1983; Zeller 1973) and to a limited extent in *T. turgidum* wheats (Friebe *et al.* 1987, 1989). Materials with chromosome 1B/1R translocation show a race specific resistance to leaf, stem and stripe rusts (*Lr26*, *Sr31*, *Yr9*), and to powdery mildew (*Pm8*) (Mcintosh 1983). Circumstantial evidence suggests that 1B/1R lines may

also possess resistance to *Septoria tritici* blotch, moderate tolerance to aluminum toxicity, with high yield potential, stability and wide adaptability (Rajaram *et al.* 1983).

The interchange segment from rye has been transmitted unconsciously by breeders from one wheat selection to another. Zeller (1973) mentioned that to follow the 1B/1R translocation in breeding programs, breeders only need to select for leaf disease resistance. This transfer was also identified by routine karyotype study and by Giemsa C-banding (Merker 1982).

Cytogenetic analyses of CIMMYT's 21st IBWSN (International Bread Wheat Screening Nursery) have shown that nearly 50 percent of the entries have the 1B/1R translocation. These lines were derived from crosses between Mexican spring semidwarfs and the 1B/1R winter wheat germplasm source from USA and USSR (Bartos *et al.* 1973; Merker 1982; Mettin *et al.* 1973; Zeller 1973). The breeding methodology employed to generate this germplasm has been described elsewhere (Dubin and Rajaram 1982; Rajaram *et al.* 1984).

The information on yield contribution of the 1B/1R chromosome translocation on wheat is very limited. Rajaram *et al.* (1983) reported on yield effects of this wheat-rye chromosome translocation in bread wheat, with additional information briefly provided in a recent study of Villareal *et al.* (1991). The present study is a follow-up with more detailed information in an attempt to measure the associated effects of the 1B/1R chromosome translocation on the yield potential of some selected spring wheat (*T. aestivum* L.) cultivars.

Materials and Methods

The *Triticum aestivum* L. cultivars and advanced lines represent CIMMYT's highest yielding genotypes to date. The parentage of these materials are indicated in Table 1. Those genotypes with chromosome 1B/1R translocation were all derived from the Russian cultivar 'Kavkaz' while the non-1B/1R group was composed of high yielding cultivars from diverse genetic background well adapted to the growing conditions at Sonora, Mexico.

Cytological study for 1B/1R detection: Laboratory

Fifteen seeds of each genotype were germinated in Petri dishes lined with moist filter paper. Upon ger-

mination, root tips were collected from 10 seedlings and identified. The root-tips were pre-treated for 3.5 hours in a 8-hydroxyquinoline + colchicine + dimethyl-sulfoxide solution according to the procedure of Mujeeb-Kazi and Miranda (1985).

The root-tips were fixed after pretreatment in 0.1% aceto-carmine for 48 hours, squashed in 45% acetic acid and the cover-glass was removed by processing on dry ice. The slides were air-dried for 4 hours, treated in absolute alcohol (ethanol) for 2 hours and dried overnight. The treatments in barium hydroxide and SSC (Sodium citrate 0.03M + Sodium chloride 0.3M) were similar to those described by Bennett *et al.* (1977). The slides were then stained for 6 to 8 minutes with a 2% Giemsa stain (Sigma, G-4507) pH 6.8 and checked for the C-banded sites of chromosome 1B or 1B/1R.

Yield component investigations: Field

Ten genotypes of spring wheat (Table 1) were grown in randomized complete blocks of four replications at the Mexican Institute of Forestry, Agriculture and Livestock (INIFAP), Campo Agrícola Experimental Valle del Yaqui (CAEVY), research station (27° 20'N, 105° 55'W, elevation 40 m above sea level) in the Yaqui Valley, Sonora, Mexico, during the 1988-89 and 1989-90 wheat production seasons. Each plot consisted of eight rows, 5 m long and 20 cm apart. In each year, experiments were sown during the last week of November at approximately 120 kg ha⁻¹.

Table 1. Parentage of certain *Triticum aestivum* L. cultivars with and without 1B/1R chromosome translocation

Cultivar advanced line	Parentage
Bagula*	Teeter/Junco
Kauz*	Jupateco/Bluejay//Ures
Seri 82*	Kavkaz/Buho//Kalyansona/Bluebird
Parula/Veery #6*	Parula/Veery #6
Veery 10*	Kavkaz/Buho//Kalyansona/Bluebird
Ciano 79**	Bucky/Maya/4/Bluebird//HD832.5.5/ Olesen/3/Ciano 67/Penjamo
Opata 85**	Bluejay/Jupateco
Esmeralda 86**	Buckbuck/Bluejay
Yecora 70**	Ciano/Sonora 64//Klein Rendidor/3 /8156
Oasis 86**	Agatha/3* Yecora

* Cultivars /advanced lines with 1B/1R translocation.

** Cultivars without 1B/1R translocation.

Prior to seeding, fertilizers were applied at the rate of 150 kg N ha⁻¹ (in ammonium sulfate) and 40 kg P ha⁻¹ (in tri-superphosphate). Trials were surface irrigated just after planting and as required until the latest maturing genotype reached physiological maturity. During growth, the crop was sprayed with a selective weed-killer (Puma=Fenoxaprop-Ethyl=Ethyl (R) -2-[4 [(6-chloro-2-benzoxazolyl) oxy] phenoxy] propanoate; 2.5 liters/ha) and a fungicide (Folicur=Tebuconazole=Alfaterteriari-butyl-alfa-(p-chorofenetil)-1H-1, 2, 4-triazole-1 ethanol; 0.5 liters/ha) to control leaf and stem rusts.

Insect control was not required. The number of days from crop emergence to 50% heading was noted for all plots. After heading, plant height was measured from the ground to the tip of the terminal spikelet (excluding awns) for all test materials. Similarly, spike length was measured from the base of the spike to the tip of the highest spikelet (awns not included) for all the plots of the yield experiments.

At maturity, the crop from the central portion (3.75 m²) of each plot was hand harvested by cutting at ground level. The outer row and a 0.5 m border at each end of a plot were excluded from the samples. Harvesting was done early in the morning to minimize harvest losses. To obtain grain yield and its components, a subsample of 100 spike-bearing tillers was taken from the plot bundle immediately after harvest, weighed, placed in a cloth bag, and put in an over to dry at 75°C for 48 hours. The weight of the plot bundle was then taken. The subsample was used to estimate the moisture content of the plot bundle at harvest. After drying in the sun for seven days, the plot bundle was threshed using a stationary thresher, the grain cleaned and weighed. Just after weighing, a 40 gram grain sample was taken, weighed, oven-dried at 100°C for 48 hours and then reweighed to determine grain moisture content. This moisture content derived from the 40 g sample was used to adjust all reported grain yields to a 12% moisture basis. Two dried samples of 250 grains from each plot were used to determine thousand grain weights. Values of yield components (above-ground biomass, harvest index, spikes m⁻², grains m⁻², and grains per spike) were estimated from the data as described above. Test weights were recorded using an electronic hectoliter balance for each entry in both years.

A separate analysis of variance for each year produced similar error values. Consequently all variables measured on each genotype were used in a combined analysis of variance for the two trials. The general means of the 1B/1R and non-1B/1R cultivars were subjected to orthogonal contrast comparisons. Pearson correlation coefficients were also calculated on the mean value of each variable measured on every entry in the yield trials (SAS Institute 1985).

Results and Discussion

We evaluated a range of bread wheats adapted to north-west Mexico, including the latest genotypes ('Bagula', 'Kauz', and 'Parula/Veery # 6') which are being considered for varietal release in the area (Table 1). 'Yecora 70' 'Ciano 79' and 'Seri 82' are cultivars of the area released earlier in the area, but subsequently discontinued because of susceptibility to leaf rust (*Puccinia recondita* Rob. *et* Desm. f.sp. *tritici*). More recent releases like 'Opata 85', 'Oasis 86' and 'Esmeralda 86' occupied 36.5%, 14.6% and 0.1% of the wheat area respectively (Anonymous 1990). These cultivars represent the highest yielding cultivars available for this re-

gion and in the absence of randomly derived or near isogenic lines of 1B/1R wheats are unequivocally the ideal test materials that are globally available to further the findings of Villareal *et al.* (1991).

Cytological determination of 1B/1R translocation lines

Routine somatic cytology and observations of the secondary constriction sites was the diagnostic test for translocation lines which have two satellited chromosome (6B) rather than 4 (1B, 6B) in euploid *Triticum aestivum* (Jahan *et al.* 1990; Mujeeb-Kzai and Miranda 1985). Occasionally the satellites of chromosome 5D are resolved and uniquely characterized due to their extremely small satellites (Fig. 1). Chromosome banding however, precludes any erroneous interpretation and has logistical advantages. Using this analytical check, the 1B/1R translocated chromosome was characterized by prominent banding sites on the terminal end of the long-arm, at the centromeric region, terminal and sub-terminal sites on the short-arm, and a fainter interstitial banded sites on the long-arm. Based upon this diagnosis the 1B/1R lines were identified as 'Bagula',

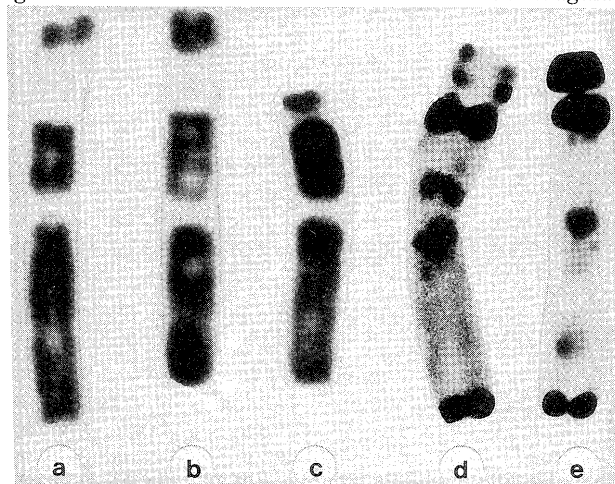


Fig. 1. Diagnostic somatic cytology details of some *Triticum aestivum* L. chromosome (left to right).

- Satellited chromosome 1B with a shorter short arm than chromosome 6B.
- Satellited chromosome 6B with a longer short arm than chromosome 1B.
- A heterobrachial chromosome 5D with a minute satellite.
- A C-banded 1B chromosome.
- A C-banded 1B/1R chromosome.

Table 2. Mean yield characteristics of ten *Triticum aestivum* L. genotypes during the 1988/89 and 1989/90 crop cycles

Test Genotype	Plant height	Heading days	Grain Yield	Above-ground biomass	Harvest Index	Spike m ⁻²	Grain m ⁻²	Grain no/spike	1000 grain weight	Spike length	Test weight
Bagula	101.7	92.4	7215.6	17.2	38.9	455.5	15095.4	35.5	43.0	10.5	82.0
Kauz	92.7	91.1	7769.1	16.5	43.1	513.2	19339.6	40.4	35.9	10.1	83.0
Seri 82	97.9	92.0	7382.0	16.3	43.5	403.3	16429.3	43.4	40.8	10.5	80.6
Parula/Veery #6	88.2	88.9	7006.2	15.6	41.2	496.1	16572.5	35.5	37.9	10.3	82.0
Veery 10	65.7	87.9	7031.2	14.9	43.9	411.5	15328.2	40.4	41.9	11.7	80.1
Ciano 79	94.0	88.4	7004.7	14.9	44.0	401.3	17218.6	42.4	36.7	11.0	80.7
Opata 84	100.6	91.7	6934.1	15.8	40.4	457.0	17872.7	38.5	34.5	10.8	82.0
Esmeralda 86	100.8	88.1	6816.9	15.8	40.5	358.4	15448.1	42.3	40.0	12.9	80.9
Yecora 70	76.3	83.5	7188.1	14.7	45.5	442.4	14553.5	33.6	44.0	10.9	80.9
Oasis 86	79.5	88.0	7855.2	16.0	44.3	525.8	17976.9	34.2	38.8	10.2	79.2

'Kauz', 'Seri 82', 'Parula/Veery # 6', and 'Veery 10' with the remaining 5 being homozygous 1B (Table 1, and Fig. 1).

Yield component investigations: Field

Plant height, days to heading, above-ground biomass, harvest index, grain yield, yield components and test weight means for all bread wheat genotypes represented in the experimental trails are presented in Table 2. Further, mean yield characteristics within 1B/1R genotypes and the non-1B/1R cultivars are also summarized (Table 3). The mean differences observed in comparing each character between the translocation groups are also presented, together with their respective coefficients of variation. Finally, the associations between all characters for each chromosome translocation group were measured (Table 4).

Grain Yield

There was no significant genotype \times year interaction for grain yield. The mean grain yield of the five 1B/1R genotypes was 7,281 kg ha⁻¹ as compared to 1B genotype yields of 7,160 kg ha⁻¹ across the two trials; a difference that was non-significant ($P > 0.05$). Grain yield in these experiments was not limited by nitrogen, water, weeds or disease. No incidence of lodging nor mineral element deficiency was observed during the experiment. The overall grain yield mean of these test materials was 7,220 kg ha⁻¹. Grain yield was most strongly associated with higher biomass, harvest index, number of grains m⁻², grains per spike, 1,000-grain weight, and test weight for the two groups of materials (Table 4). The correlation between grain yield and biomass at maturity deserves little attention since grain yield is a part of the biomass trait. However, this result supports the idea that increased biomass could be a selection index for increased yield potential. The experimental precision was reasonable with a 4.6% coefficient of variation (Table 3).

Biomass and Harvest Index

Significant above-ground biomass differences were detected between the 1B/1R and non-1B/1R cultivars.

Table 3. The effect of 1B/1R chromosome translocation on yield characteristics of ten *Triticum aestivum* L. cultivars during the 1988/89 and 1989/90 crop cycles

Plant Characteristic	With 1B/1R	Without 1B/1R	Difference Mean	C. V. (%)
Plant height (cm)	89.2	90.2	1.1 ^{ns}	2.6
Heading days	90.4	87.9	2.5**	1.5
Grain yield (kg ha ⁻¹)	7281.0	7160.0	121.0 ^{ns}	4.6
Aboveground biomass (t ha ⁻¹)	16.1	15.4	0.7**	5.4
Harvest index (%)	42.1	42.9	0.8*	5.4
Grain m ⁻²	16553.0	16614.0	61.0 ^{ns}	5.8
Spike m ⁻²	456.0	437.0	19.0*	6.6
Grain no/spike	39.0	38.2	0.8 ^{ns}	7.6
1000-grain weight (g)	39.9	38.8	1.1**	2.9
Spike length (cm)	10.6	11.2	0.6**	5.8
Test weight (kg hl ⁻¹)	81.5	80.7	0.8**	0.5

^{ns} = not significant; *, ** Significant at the 0.05 and 0.01 level of probability, respectively.

The mean biomass for the 1B/1R lines (16.1 t ha⁻¹) was superior ($P < 0.01$) to that of the non-1B/1R cultivars (15.4 t ha⁻¹). In contrast, the harvest index of the non-1B/1R group (42.9%) was significantly higher ($P < 0.05$) than that of the 1B/1R group (42.1%). There was genotype \times year interaction for harvest index but none for biomass. Highly significant correlations were observed between harvest, above-ground biomass, grain number m⁻², grain number per spike, 1,000-grain weight and test weight for both groups of materials.

Yield Components and Test Weight

Cultivar comparisons on primary yield components indicated that 1B/1R lines had more spike bearing tillers (456) than the non-1B/1R (437) lines ($P < 0.05$). Similarly, the 1,000-grain weight was higher for the 1B/1R

lines (39.9 g) than the non-1B/1R lines (38.8 g) ($P < 0.01$). Test weight comparisons also indicated that 1B/1R lines possessed better formed grains (81.5 kg/ha⁻¹ vs. 80.7 kg/ha⁻¹) at 0.01 level of probability. In contrast, the non-1B/1R lines had longer spikes (11.2 cm) compared to the 1B/1R (10.6 cm) materials ($P < 0.01$). However, when grain number was compared on an area (m²) and spikes basis, no significant difference was observed ($P > 0.05$). Significant negative associations were found between the number of spikes m⁻² and grain number per spike for both groups.

Other Characteristics

Comparison between the 1B/1R translocation and 1B groups showed no significant difference in plant height ($P > 0.05$). The 1B/1R translocation material headed 2.5 days later than the 1B material ($P < 0.01$). There was a strong association of plant height with characters such as heading and test weight (Table 4). Contrasting results were observed between the two groups when relationships between plant height and spike length were examined. The genotypes possessing the chromosome 1B/1R translocation manifested a highly significant negative correlation between plant height and spike length while those cultivars without the translocation showed a positive relationship. Coefficients of variation were 2.6% for plant height and 1.5% for heading days (Table 3).

Among the different characters studied, genotypes with the 1B/1R chromosome translocation possessed increased above-ground biomass yield, number of spikes m⁻², 1,000-grain weight and test weight. The slight advantages observed in the translocation lines for grain yield and grain number per spike were inconclusive and not significant. However, the 1B group recorded a high-

Table 4. Character correlations within *Triticum aestivum* L. genotypes homozygous for the 1B/1R chromosome translocation or for chromosome 1B averaged over 2 years of yield trial

	Plant height	Heading days	Grain yield	Above-ground biomass	Harvest Index	Spike m ⁻²	Grain m ⁻²	Grain no/spike	1000 grain weight	Spike length	Test weight
plant height	-	0.691**	-0.007	0.272	-0.286	-0.508**	0.272	0.539**	-0.339*	0.431**	0.434**
Heading days	0.702**	-	0.195	0.441**	-0.171	0.018	0.503**	0.379*	-0.376*	0.046	0.337*
Grain yield	0.156	0.476**	-	0.856**	0.783**	0.001	0.876**	0.711**	0.620**	0.044	0.662**
Aboveground biomass	0.396*	0.603**	0.852**	-	0.353**	0.007	0.809**	0.629**	0.442**	0.156	0.642**
Harvest Index	-0.147	0.220	0.833**	0.428**	-	-0.077	0.611**	0.581**	0.613**	-0.045	0.473**
Spike m ⁻²	0.174	-0.167	-0.258	-0.096	-0.431**	-	0.075	-0.577**	-0.261	-0.506**	-0.453**
Grain m ⁻²	0.160	0.436**	0.943**	0.774**	0.793**	-0.048	-	0.758**	0.177	0.023	0.598
Grain no/spike	0.037	0.447**	0.914**	0.685**	0.884**	-0.541**	0.858**	-	0.321*	0.384*	0.755**
1000 grain weight	-0.018	0.259	0.540**	0.520**	0.449**	-0.686**	0.235	0.529**	-	0.131	0.493**
Spike length	-0.447**	0.003	0.389*	0.279	0.418**	-0.483**	0.250	0.433**	0.562**	-	0.178
Test weight	0.422**	0.418**	0.758**	0.716**	0.508**	0.205	0.803**	0.574**	0.167	-0.077	-

*, ** significant at 0.05 and 0.01 levels of probability respectively.

Note: The triangular matrix of correlation on the top right is obtained between five genotypes without 1B/1R chromosome translocation, and that below on the left side is between cultivars with 1B/1R chromosome translocation.

er harvest index and longer spikes. These results require wider validation, in particular with other genetic backgrounds now currently used in our bread wheat breeding program. Since the study has only involved materials with 1B/1R chromosome derived from 'Kavkaz', other sources (like 'Weique Redmace') also need to be investigated. It is doubtful however, if the IRS segment will make much difference since it goes back in each case to Petkus rye. The recombination effects for the 1BL chromosome arm could prove to be a contributing factor.

Unequivocal data to astutely answer the yield/agronomic effects of 1B/1R *T. aestivum* cultivars as compared to 1B wheats cannot be obtained from any other stringent selection emanating from the global wheat germplasm. A possibility however, of coming close to better understanding the 1B/1R contributions does exist by comparing near isogenic lines; development of such germplasm requires several cycles of backcrossing (often up to BC₈) and requires at least four to five years before yield tests can be undertaken (Ter-Kuile *et al.* 1990). The case is equally strong for the examination of other environmental interactions, especially now that the 1B/1R germplasm is being used increasingly in various national wheat research programs (Jahan *et al.* 1990; Ter-Kuile *et al.* 1991). It is probable that after delineating the "adaptive" influence of the IRS segment in the 1B/1R lines a search for interactions with other major "adaptation" genes may prove equally beneficial in developing breeding strategies to optimize exploitation of this genetic component.

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