

The effect of chromosome 1AL/1RS translocation on agronomic performance of 85 F₂-derived F₆ lines from three *Triticum aestivum* L. crosses

R.L. Villareal, E. del Toro, S. Rajaram & A. Mujeeb-Kazi

International Wheat and Maize Improvement Center (CIMMYT), Lisboa 27, Apdo. Postal 6-641, Deleg. Cuauhtemoc 06600, Mexico, D.F., Mexico

Received 29 August 1994; accepted 20 November 1995

Key words: *Secale cereale*, *Triticum aestivum*, yield components, 1AL/1RS translocation, wheat

Summary

The effect of the 1AL/1RS chromosome translocation on grain yield and other agronomic characteristics of 85 random F₂-derived F₆ bulks from three 1AL 1RS × 1A bread wheat crosses was determined under optimum and reduced irrigation conditions at CIANO, Yaqui Valley, Sonora, Mexico, during the 1991–1992 and 1992–1993 crop production cycles. Harvest plots of 5.0 m² were arranged in an alpha lattice design with three replications. The 1AL/1RS translocation increased grain yield, above-ground biomass, spikes/m², and test weight under both irrigated and dryland conditions. Homozygous chromosome 1A lines, on the other hand, possessed longer spikes with more grains. The 1AL/1RS cultivars had an advantage in 1000-grain weight, which was detected only under optimum irrigation. The translocation lines showed later maturity and longer grainfilling period than the 1A genotypes under one irrigation treatment. A significant relationship between grain yield and test weight was detected only among the 1AL/1RS genotypes, indicating that they possess heavier and plumper grains than the 1A genotypes. These results encourage the continued use of the 1AL/1RS translocation in wheat improvement.

Introduction

The rye genus *Secale* has great potential for increasing genetic variability that can be used in bread wheat (*Triticum aestivum* L.; 2n = 6x = 42; AABBDD) improvement. Translocation of the short arm of rye chromosome 1R to wheat is of particular interest to breeding. This rye segment has been successfully incorporated into many hexaploid wheat cultivars, either by translocating the short arm of rye chromosome 1R onto the long arm of wheat chromosomes 1A or 1B, which results in the 1AL/1RS or 1BL/1RS translocations, respectively. The importance of 1BL/1RS wheats has long been known, and they are widely distributed (Bartos et al. 1973; Cai & Liu 1989; Lukaszewski 1990; Mettin et al. 1973; Rajaram et al. 1990; Zeller 1973; Zeller & Hsam 1984). There is some concern regarding the translocations' adverse effect on bread making quality and the disease vulnerability that is associated with the 1RS segment. The

1RS segment in all 1BL/1RS wheats has a common origin: *Secale cereale* L. cv. Petkus (Jahan et al. 1990).

The winter wheat (*Triticum aestivum* L.; 2n = 6x = 42; AABBDD) Amigo was the first 1AL/1RS wheat-rye translocation cultivar released (Sebesta & Wood 1978). Amigo resulted from a cross between Gaucho, an octoploid triticales (Chinese Spring × Insave rye), and advanced wheat breeding lines exposed to mutagenic X-ray treatment (Wood et al. 1974). Amigo carries genes for resistance to greenbug (*Schizaphis graminum* Rond.), wheat curl mite (*Aceria tulipae* Keifer), powdery mildew (*Erysiphe graminis* Dc. f.sp. *tritici* Marchal), stem rust (*Puccinia graminis* Pers. f.sp. *tritici* Erikss. et Henn) and leaf rust (*Puccinia recondita* Rob. et Desm. f.sp. *tritici*) (Hollenhorst & Joppa 1983; Lowe 1981; Lowry et al. 1984; Sebesta & Wood 1978; Zeller & Hsam 1984). It is assumed that all these resistance genes are located on the short arm of rye chromosome 1R. Some of the Amigo 1AL/1RS translocation cultivars known today

are TAM 107, TAM 200 and Century (Knackstedt et al. 1994; Lukaszewski 1990).

Lines homozygous for the 1AL/1RS translocation generally have superior performance under dryland conditions (Meeteren & Sears 1991). Unfortunately, this translocation has frequently shown unsatisfactory baking quality, specifically poor mixing tolerance and poor crumb grain, according to the baking industry (Peterson et al. 1990). Since the 1AS chromosome arm is replaced by 1RS in the 1AL/1RS translocated wheats, gluten proteins controlled at *Gli-A1* (omega and gamma-gliadins) and *Glu-B3* (low *Mr* glutenins) loci are lost because of their location on the 1AS arm. The 1RS chromosome arm leads to the introduction of rye proteins controlled at the *Sec-1a* (40-K gamma-secalins), *Sec-1b* (omega-secalins) and *Pr-3* (55-K secalin) loci. How these protein composition changes affect gluten functionality in the translocated wheats is as yet not well understood; but Dhaliwal & McRitchie (1990) have suggested a shift in the proportions of polymeric and monomeric proteins that may influence the adverse quality of the translocation wheat. On the other hand, Payne et al. (1987) demonstrated that the presence of 1RS is beneficial for biscuit-making quality. The overall frequency of 1AL/1RS entries in the major 1989 US wheat nurseries was 4.3% (Lukaszewski 1990).

Information on the effect of the Amigo translocation on agronomic performance of wheat is very limited and to our knowledge this was the first study performed on spring wheats. The objective of the study was to measure the associated effects of the 1AL/1RS chromosome translocation on the yield potential and other agronomic characteristics of 85 F₂-derived F₆ lines of spring hexaploid wheat.

Materials and methods

Plant materials. Three winter × spring wheat crosses, Tam 200/Turaco, Tam 200/Parula, and Tam 200/Trap, were used to develop recombinant inbred populations. Cultivar Tam 200, obtained from Texas A & M University at College Station, Texas, USA, was the 1AL/1RS donor cultivar. Cultivars Turaco, Parula and Trap are high yielding spring wheat cultivars developed by the Bread Wheat Breeding Program of the International Wheat and Maize Improvement Center (CIMMYT) in Mexico. The 500 F₂ plants per cross obtained from field-grown F₁ plants were planted about 0.1 m apart within the row, in 10-m rows spaced

0.3 m apart in the field at the Mexican National Institute of Forestry, Agriculture and Livestock, Agricultural Research Center for Northwest Region (CIANO; 27°20'N, 105°55'W, elevation 40 m above sea level), Sonora, Mexico, during the 1989–90 crop cycle. About 200 spikes were randomly selected from each F₂ population and advanced to the F₃, by field planting 10 seeds of each individual F₂ spike 0.1 m apart, in 1 m long rows with 0.25 m between rows. One spike per F₃ plot was harvested and advanced to F₄. A similar procedure was followed to advance the F₄ to F₅. A total of 422 F₅ lines from the three crosses were produced. Subsequently, these F₅s were grown at El Batan (another Mexico location) in 1991 in one double row, 2 m long, to produce sufficient seeds for the yield trials. One hundred eleven F₅ plots homogeneous for height and maturity were bulk harvested and subjected to 1AL/1RS determination using A-PAGE electrophoresis and C-banding analysis as described by Jahan et al. (1990). Based upon this diagnosis, 39 homozygous 1AL/1RS lines and 46 homozygous 1A lines from the three crosses were identified and subjected to yield testing. Twenty-six lines still segregating for the translocated chromosome were discarded.

Field experiments. Eighty-five individual random F₂-derived F₆ lines were evaluated in yield trials at CIANO during the 1991–92 and 1992–93 wheat production cycles to evaluate the effect of the 1AL/1RS chromosome translocation on their agronomic performance. Two types of experiments were designed: (i) optimum irrigation (OIYT), with five irrigations during the crop cycle and (ii) reduced irrigation (RIYT), with only one irrigation after germination.

The two trials were arranged in an alpha lattice design with three replications. Each plot consisted of 8 rows, 0.2 m apart and 5 m long, and was machine-sown at a seeding rate of 120 kg/ha. The trials were surface-irrigated just after seeding. Irrigation of OIYT was continued until the latest maturing entry reached physiological maturity. One hundred-fifty kg N/ha (in ammonium sulfate) and 40 kg P/ha (in tri-superphosphate) were applied prior to seeding of the trials. Weeds were chemically controlled by Puma (Fenoxaprop-Ethyl = Ethyl(R)-2-(4((6-chloro-2-benzoxazolyl)oxy)phenoxy) propanoate; 2.5 l/ha). A fungicide (Folicur = Tebuconazole = Alfa-tertiari-butyl-alfa-(p-chlorofenetil)-1H-1,2,4-triazole-1 ethanol; 0.5 l/ha) was used to control leaf and stem rust. Insect control was not required.

All trials were seeded in late November, which is considered the optimal seeding time for wheat in the State of Sonora, and reached maturity during April. Traits measured on each plot were: (i) days to flowering, number of days from crop emergence until 50% anthesis; (ii) plant height (cm), using three measurements in the plot from the ground to the tip of the spike excluding awns; (iii) spike length (cm), using three measurements from the base of the spike to the tip of the highest spikelet (awns excluded); (iv) days to physiological maturity, recorded when the green color was completely lost from 50% of the spikes in the plot, (v) grain yield (kg/ha), grain weight from a 5.0 m² plot excluding border rows and 0.5 m of all rows at each plot end; (vi) test weight (kg/hl), recorded using an electronic hectoliter balance for each entry; and (vii) 1000-grain weight (g), determined from two dried samples of 250 grains from each plot.

One week after physiological maturity, a random sample of 50 culms was harvested at ground level from each plot. The spike number, grain and total weights were determined on this sample so that calculations could give the harvest index (%) and grains/spike. Using the total plot grain yield, biomass (t/ha), spikes/m², and grains/m² were calculated. For example, spikes/m² was estimated by dividing plot grain yield by grains/spike multiplied by grain weight.

Mean air temperatures during the 1991–92 and 1992–93 wheat seasons were comparable (18.5 °C vs. 18.9 °C) but slightly higher than the long-term average temperature of 17.1 °C at CIANO. Minimum lodging was observed only during 1991–92. Production management was optimum for weed, disease and bird control and at no time during either cropping season were these factors a yield constraint.

Data analysis. Analysis of variance was conducted on a total of 85 lines derived from three 1AL/1RS × 1A crosses across two irrigation treatments and two wheat production cycles. The effects of the entries and their interactions with environments were partitioned. The key partitions were among chromosome groups (1AL/1RS vs. 1A), to test if the chromosome translocation affects a trait, lines within each chromosome class, to find out if variability exists within each group, and chromosome group interaction with environment e.g. year (YR) × chromosome group, irrigation treatment (IT) × chromosome group, etc. This would indicate whether the 1A responded differently from the 1AL/1RS in YR or IT. The years, replications, and lines within a chromosome class were considered

random effects, while irrigation treatment and chromosome class were considered fixed effects. The data were also analyzed separately for each cross. Average performance in a specific irrigation environment was of greater interest than across environments; therefore, the data for each irrigation treatment were analyzed separately. The general means of the 1AL/1RS and 1A lines were subjected to orthogonal contrast comparisons. Mean comparisons utilized the Least Significant Difference (LSD) estimates. Tables 1 and 2 summarize the mean comparisons between the two chromosome groups under full and reduced irrigation treatments, respectively. Correlation coefficients were calculated between grain yield and other variables measured for all lines within the chromosome classes averaged over irrigation environments and years of experiment to determine whether the grain yield correlations in one chromosome class are different from the grain yield correlations in the other chromosome class (SAS Institute 1988).

Results

The information generated by A-PAGE electrophoresis and C-banding was useful in classifying the test materials into 1AL/1RS and 1A chromosome groups. Total inbreds scored per genetic background were as follows: 35 lines (17 1AL/1RS vs. 18 1A) in TAM200/Turaco cross, 28 lines (11 1AL/1RS vs. 17 1A) in TAM200/Parula cross, and 22 lines (11 1AL/1RS vs. 11 1A) in TAM200/Trap cross.

Combined analysis of variance (analysis not shown) showed significant variation between years, irrigation treatment, and lines (genotypes) for all traits except on the effect of irrigation treatment on harvest index, grains/spike and days to flowering. The year × genotype, irrigation treatment × genotype, and year × irrigation treatment × genotype interactions were also significant for all traits with the exception of irrigation treatment × genotype interaction on spike length and test weight. The year × among chromosome-class interaction was significant for spike length and days to flowering. Moreover, interactions between irrigation treatment and chromosome group were significant for test weight, spike length and grainfilling period. Year × irrigation treatment × chromosome group interactions were significant for test weight and spike length. These interactions were mainly due to changes in magnitude and a few reversals in order. Genotypes within the 1AL/1RS and 1A chromosome classes showed sig-

Table 1. Yield characteristics of 85 F₂-derived F₆ lines classified according to presence or absence of 1AL/1RS translocation from three 1AL/1RS × 1A bread wheat crosses under optimum irrigated condition (OIYT) during the 1991–92 and 1992–93 crop cycles

Plant characteristic	Wheat lines (no. of lines)		Pr > F	Cv (%)
	1A/1R	1A		
	(39)	(46)		
Grain yield (kg/ha)	5585	5348	***	8.9
Above-ground biomass (t/ha)	14.8	14.3	**	9.3
Harvest index (%)	36.6	36.5	ns	10.5
Spikes/m ²	474	441	***	12.3
Grains/m ²	14341	14310	ns	10.9
Grains/spike	31.4	33.6	***	11.5
1000-grain weight (g)	40.2	38.5	***	4.5
Test weight (kg/hl)	80.8	79.5	***	2.2
Plant height (cm)	90.5	90.8	ns	8.1
Spike length (cm)	9.2	9.5	***	5.1
Days to flowering	83.0	83.1	ns	7.5
Physiological maturity	130.4	129.8	ns	4.0
Grainfilling period (day)	47.3	46.7	ns	9.9

ns Not significant.

, * Significant at the 0.01 and 0.001 levels of probability, respectively.

nificant variation for all traits. Hence, genetic diversity exists among the lines within both chromosome groups. Individual analysis of crosses showed consistent response of chromosome groups on yield and yield characteristics. Pooled analysis of all genotypes within chromosome classes across the three crosses was then performed.

OIYT experiment. The combined analysis across years revealed non-significant year × chromosome group interaction for grain yield. Satisfactory experimental precision was inferred from an 8.9% coefficient of variation. Larger plots allowed edge trimming to minimize errors due to edge effects. The 1AL/1RS cultivars had 4.4% more grain yield than the 1A lines (Table 1). The highest (6636 kg/ha) and the lowest (3870 kg/ha) yielding entries were both 1A genotypes (data not shown). Overall mean grain yield of the entries across two years was 5466 kg/ha.

Above-ground biomass yield at maturity of the 1AL/1RS cultivars was 3.5% higher than the 1A lines and also had more spike-bearing tillers. Biomass yield of all genotypes ranges from 11.2 t/ha to 17.3 t/ha (data not shown). Test weight and 1000-grain weight

Table 2. Yield characteristics of 85 F₂-derived F₆ lines classified according to presence or absence of 1AL/1RS translocation from three 1AL/1RS × 1A bread wheat crosses under reduced irrigated conditions (RIYT) during the 1991–92 and 1992–93 crop cycles

Plant characteristic	Wheat lines (no. of lines)		Pr > F	Cv (%)
	1A/1R	1A		
	(39)	(46)		
Grain yield (kg/ha)	4388	4282	*	9.8
Above-ground biomass (t/ha)	11.6	11.2	*	10.4
Harvest index (%)	36.6	37.3	ns	11.8
Spikes/m ²	414	389	***	12.7
Grains/m ²	12884	12576	*	10.7
Grains/spike	31.7	32.9	*	12.0
1000-grain weight (g)	34.3	33.9	ns	5.1
Test weight (kg/hl)	80.2	79.4	***	2.3
Plant height (cm)	89.1	88.4	ns	9.4
Spike length (cm)	9.2	9.4	*	6.7
Days to flowering	82.9	83.0	ns	5.7
Physiological maturity	122.1	121.0	*	4.7
Grainfilling period (day)	39.2	38.0	***	9.9

ns Not significant.

*, *** Significant at the 0.05 and 0.001 levels of probability, respectively.

comparisons indicated that the 1AL/1RS lines possessed plumper and heavier grains. In contrast, the 1A lines had longer spikes with more grains, compared to the 1AL/1RS materials. Combined analyses across two cycles of testing showed non-significant year × translocation class category interaction for the above characters. Very good coefficients of variation were calculated in all cases.

Observed differences between the chromosome translocation groups in harvest index, grains/m², plant height, days to flowering, physiological maturity and grainfilling period were insignificant. There was significant year × translocation group interaction only for harvest index.

RIYT experiment. Results of the reduced irrigated trials revealed the superiority of the 1AL/1RS cultivars over 1A homozygous lines for grain yield, biomass yield at maturity, spikes/m², grains/m² and test weight (Table 2). The 1AL/1RS lines yielded 2.5% higher than the 1A lines. The highest (5114 kg/ha) and the lowest (3229 kg/ha) yielding genotypes both possess normal 1A chromosomes (data not shown). Moreover, the analyses detected 3.6% more biomass

Table 3. Characteristic correlation associations for groups of 1AL/1RS and 1A F₂-derived F₆ lines from three crosses of *Triticum aestivum* L. cultivars, under two irrigation treatments during the 1991–92 and 1992–93 crop cycles

	GY	BIO	SPM	GPM	GPS	TGW	TW	PH	PM
GY	–	0.72**	0.48**	0.61**	–0.01	0.52**	0.31**	–0.02	0.41**
BIO	0.73**	–	0.58**	0.69**	–0.04	0.13	–0.12	0.29*	0.59**
SPM	0.26*	0.51**	–	0.41**	–0.65**	0.12	0.19*	–0.08	0.24*
GPM	0.72**	0.70**	0.37**	–	0.35**	–0.31**	–0.17	0.34**	0.48**
GPS	0.30*	0.07	–0.61**	0.44**	–	–0.37**	–0.33**	0.38**	0.17
TGW	0.45**	0.14	–0.08	–0.24*	–0.14	–	0.53**	–0.42**	–0.02
TW	0.15	–0.23*	–0.13	–0.20*	–0.04	0.41**	–	–0.40**	–0.23*
PH	0.06	0.32**	0.01	0.25*	0.24*	–0.27	–0.26*	–	0.47**
PM	0.42**	0.57**	0.15	0.44**	0.28*	0.06	–0.38**	0.39**	–

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

Abbreviations: GY, grain yield; BIO, above-ground biomass at maturity; SPM, spikes/m²; GPM, grains/m²; TGW, 1000-grain weight; TW, test weight; PH, plant height; and PM, physiological maturity.

Note: The triangular matrix of correlation coefficients on the top right is obtained from the 1AL/1RS lines while that on the bottom side was from the 1A lines.

yield at maturity, 6.4% more spikes/m², 2.4% more grains/m² and better formed, plump grains (80.2 kg/hl vs. 79.4 kg/hl) for the 1AL/1RS lines. The translocation lines also took longer to mature physiologically (122.1 days vs. 121.0 days) and required a longer grainfilling period (39.2 days vs. 38.0 days). On the other hand, the homozygous 1A lines produced longer spikes (9.4 cm vs. 9.2 cm) with more grains (32.9 vs. 31.7). No significant differences were observed for harvest index, 1000-grain weight, plant height and days to flowering. Pooled analyses across tests for the above characters (except spikes/m²) revealed non-significant year × chromosome translocation class interaction. Coefficients of variation for all these characters were satisfactory and ranged from 2.3% to 12.7%.

Phenotypic correlations. Character correlations within the 1A and within the 1AL/1RS classes across the irrigation treatments and two years of experiments are summarized in Table 3. Data on harvest index, spike length, days to flowering and grainfilling period were also analyzed but not included in the table. Grain yield was strongly associated to above-ground biomass yield at maturity, spikes/m², grains/m², 1000-grain weight and physiological maturity in both chromosome groups. A significant relationship between grain yield and test weight was only detected within the 1AL/1RS group. Other significant associations found only within the 1AL/1RS chromosome class were between spikes/m² and test weight; spikes/m² and physiological maturity; grains/spike and 1000-grain weight; and grains/spike and test weight. The following charac-

ter relationships were found to be significant within the 1A group only: grain yield and grains/spike; test weight and biomass yield; test weight and grains/m²; and grains/spike and physiological maturity.

Discussion

Performance of genotypes having the chromosome translocation was determined under two contrasting irrigation treatments that simulated the well-watered and dryland environments where most CIMMYT breeding materials (about 70%) are cultivated. Eighty-five individual random F₂-derived F₆ lines from three 1AL/1RS × 1A crosses were used to avoid confusing the effects of the chromosome translocation with those of the cultivar background. Comparison of the translocation groups suggested that the 1AL/1RS chromosome translocation improves agronomic performance under both optimum and reduced irrigation conditions. This advantage was attributed to high grain yield, above-ground biomass yield at maturity, spikes/m² and test weight. These partially conform with the earlier findings of Meeteren & Sears (1991) using winter wheat lines. The superiority of the translocation group on 1000-grain weight was only expressed under optimum irrigation. Similarly, more grains/m², longer grainfilling period and physiological maturity were observed only under limited irrigation. The 1A genotypes, however, produced longer spikes with more grains under both irrigation treatments. Correlation between grain yield and test weight was detected

only within the 1AL/1RS genotypes, indicating they possess heavier, better formed and plumper grains than the 1A genotypes. This is probably a major component contributing to differences among chromosome classes for grain yield.

Furthermore, this study supports the positive effect of the 1RS segment on agronomic performance of wheat, as demonstrated particularly by increased above-ground biomass, spikes/m², seed weight and test weight, all of which have been attributed to the utilization of 1BL/1RS translocated wheats (Moreno-Sevilla et al. 1995; Carver & Rayburn 1994; Schlegel & Meinel 1994; Villareal et al. 1991). Unfortunately, the disease-resistance genes located on the 1RS segment are not effective against new races of leaf rust and powdery mildew in Europe (Zeller & Hsam 1984; Bennett 1984) and Mexico (Rajaram personal communication), and may be breaking down in other areas as well. Genetic vulnerability caused principally by wide cultivation of 1BL/1RS cultivars, which have a narrow genetic base contributed by the 1RS chromosome arm from Petkus rye, could be improved through the use of 1AL/1RS cultivars, which offer another source of variability (Insave rye).

The authors are working on evaluating the effects of the 1AL/1RS chromosome translocation on industrial quality aspects because adverse bread-making quality has been associated with the presence of the alien 1RS segment. Peña et al. (1990) have provided contradictory evidence and concluded that dough stickiness is not associated exclusively with 1BL/1RS translocated wheats but appears to be a function of the genetic background interlinked with the growing environment. A study comparing quality characters of 1BL/1RS and 1AL/1RS wheat-rye translocation lines showed that SDS sedimentation volumes and mixograph tolerance scores were higher among the 1AL/1RS lines than among 1BL/1RS sister lines (Graybosch et al. 1991). These results encourage further use of the 1AL/1RS translocation to improve agronomic and quality traits of wheat.

Acknowledgements

The authors gratefully acknowledge the contributions of CIMMYT's bread wheat and wide crosses program field staff to the field experiments. They also thank Mr. Oscar Bañuelos for doing the statistical analysis and Ms. Martha Larios for typing the manuscript.

References

- Bartos, P., J. Valkoun, J. Kosner & U. Skovencikova, 1973. Rust resistance of some European wheat cultivars derived from rye. In: E.R. Sears & L.M.S. Sears (Eds). Proc. 4th Int. Wheat Genet. Symp., Aug. 6–11, 1973, pp. 145–146. Agric. Expt. Stn., College of Agric. Univ. of Missouri, Columbia, Missouri.
- Bennett, F.G.A., 1984. Resistance to powdery mildew in wheat: A review of its use in agriculture and breeding programs. Plant Pathol. 33: 279–300.
- Cai, X. & D. Liu, 1989. Identification of a 1B/1R wheat-rye chromosome translocation. Theor. Appl. Genet. 77: 81–83.
- Carver, B.F. & A.L. Rayburn, 1994. Comparison of related wheat stocks possessing 1B or 1RS.1BL chromosomes: Agronomic performance. Crop Sci. 34: 1505–1510.
- Dhaliwal, A.S. & F. MacRitchie, 1990. Contributions of protein fractions to dough handling properties of wheat-rye translocation cultivars. J. Cereal Sci. 12: 145–149.
- Graybosch, R.A., C.J. Peterson, D. Worrall, D. Shelton & A. Lukaszewski, 1991. Comparative quality characteristics of 1BL/1RS and 1AL/1RS wheat-rye translocation lines. Agron. Abstr., American Society of Agronomy, Madison, Wisconsin. p. 96.
- Hollenhorst, M.M. & L.R. Joppa, 1983. Chromosomal location of the genes for resistance to greenbug in 'Lago' and 'Amigo' wheats. Crop Sci. 23: 91–93.
- Jahan, Q., N. Ter-Kuile, N. Hashmi, M. Aslam, A.A. Vahidy & A. Mujeeb-Kazi, 1990. The status of the 1B/1R translocation chromosome in some recent varietal releases and in the 1989 national uniform wheat yield trials (NUWYT) in Pakistan. Pak. J. Bot. 22: 1–10.
- Knackstedt, M.A., R.G. Sears, D.E. Rogers & G.L. Lookhart, 1994. Effects of T2BS.2RL wheat-rye translocation on breadmaking quality in wheat. Crop Sci. 34: 1066–1070.
- Lowe, H.J.B., 1981. Resistance and susceptibility to colour forms of the aphid *Sitobion avenae* in spring and winter wheats (*Triticum aestivum*). Ann. Appl. Biol. 99: 87–98.
- Lowry, J.R., D.J. Sammons, P.S. Baenziger & J.G. Moseman, 1984. Identification and characterization of gene conditioning powdery mildew resistance in 'Amigo' wheat. Crop Sci. 24: 129–132.
- Lukaszewski, A.J., 1990. Frequency of 1RS/1AL and 1RS/1BL translocations in United States. Crop Sci. 30: 1151–1153.
- Meeteren, Van N. & R.G. Sears, 1991. Effect of 1AL/1RS wheat-rye chromosome translocation on yield of wheat. Agro. Abstr., American Society of Agronomy, Madison, Wisconsin. p. 119.
- Metlin, D., W.D. Bluthner & G. Schlegel, 1973. Additional evidence on spontaneous 1B/1R wheat rye substitutions and translocations. In: E.R. Sears & L.M.S. Sears (Eds). Proc. 4th Int. Wheat Genet. Symp., Aug. 6–11, 1973, pp. 179–184. Agric. Expt. Stn., College of Agric. University of Missouri, Missouri, Columbia, Missouri.
- Moreno-Sevilla B., P.S. Baenziger, C.J. Peterson, R.A. Graybosch & D.V. McVey, 1995. The 1BL/1RS translocation: Agronomic performance of F₃-derived lines from a winter wheat cross. Crop Sci. 35: 1051–1055.
- Payne, P.I., M.A. Nightingale, A.F. Krattiger & L.M. Holt, 1987. The relationship between HMW glutenin subunit composition and the bread-making quality of British-grown wheat varieties. J. Sci. Food Agric. 40: 51–65.
- Peña, R.J., A. Amaya, S. Rajaram & A. Mujeeb-Kazi, 1990. Variation in quality characteristics associated with some spring 1B/1R translocation wheats. J. Cereal Sci. 12: 105–112.
- Peterson, C.J., R.A. Graybosch, S. Niaz & A.W. Grombacher, 1990. Influence of genotype and environment on quality of hard red

- winter wheat. In: 1990 Fall Cereal Conf., July 30–31, 1990, pp. 51–56. Kansas Agric. Exp. Stn., Kansas University, Manhattan.
- Rajaram, S., R. Villareal & A. Mujeeb-Kazi, 1990. The global impact of 1B/1R spring wheats. *Agronomy Abstr.*, American Society of Agronomy, Madison, Wisconsin. p. 106.
- SAS Institute, 1988. SAS/STAT users guide. Release 6.03 ed. SAS Institute, Inc., Cary, North Carolina.
- Schlegel, R. & A. Meinel, 1994. A quantitative trait locus (QTL) on chromosome arm 1RS of rye and its effect on yield performance of hexaploid wheat. *Cereal Res. Commun.* 22: 7–13.
- Sebesta, E.E. & E.A. Wood, 1978. Transfer of greenbug resistance from rye to wheat with X-rays. *Agron. Abstr.*, American Society of Agronomy, Madison, Wisconsin. pp. 61–62.
- Villareal, R.L., S. Rajaram, A. Mujeeb-Kazi & E. del Toro, 1991. The effect of chromosome 1B/1R translocation on the yield potential of certain spring wheats (*Triticum aestivum* L.). *Plant Breed.* 106: 77–81.
- Wood, E.A. Jr., E.E. Sebesta & K.J. Starks, 1974. Resistance of 'Gauche' triticale to *Schizaphis graminum*. *Env. Entom.* 3 (4): 720–721.
- Zeller, F.J., 1973. 1B/1R substitutions and translocations. In: E.R. Sears & L.M.S. Sears (Eds). *Proc. 4th Int. Wheat Genet. Symp.*, Aug. 6–11, 1973, pp. 209–221. Agric. Expt. Stn., College of Agric., University of Missouri, Columbia, Missouri.
- Zeller, F.J. & S.L.K. Hsam, 1984. Broadening the genetic variability of cultivated wheat by utilizing rye chromatin. In: S. Sakamoto (Ed). *Proc. 6th Int. Wheat Genet. Symp.*, Nov. 28–Dec. 3, 1983, pp. 161–173. Plant Germ-Plasm Inst., Fac. of Agric., Kyoto University, Kyoto.