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ADAPTIVE ADVANTAGE TO 6R CHROMOSOME OF RYE IN THE GENOMIC BACKGROUND OF BREAD WHEAT

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Summary

The segregating populations of 20 crosses, resulting from hexaploid triticale X bread wheat hybridization, were advanced following pedigree selection on the basis of phenotypic superiority (without considering rye traits) under rainfed and moderately acidic soil conditions. Of the 100 single-plant progenies isolated on the basis of some identifiable rye traits in the F_6/F_7 generation, 35 were earlier studied for the nature of rye chromatin present in them following chromosome homology analysis in their F_1s with 3 bread wheats. Of the 21 lines found to have single substituting chromosomes of rye, 12 had the substitution of 6R chromosome, whereas 3, 2 and 2 lines had the substitution of 7R, 3R and 1R chromosome, respectiely. The segregating generations of 45 of these crosses (20 of which involved the derivatives as the female parent) were also advanced upto F_8 generation following pedigree selection for phenotypic superiority. It was found that the crosses involving the parental derivatives exhibiting no evidence of rye chromatin threw the highest number of superior progenies. When the parental derivatives involved substitutions, the highest number of superior progenies was observed when the chromosome involved in the substitution was 6R. This further indicated an adaptive advantage to the 6R chromosome of rye in the background of bread wheat under moderately acidic soil and rainfed conditions.

Key words: Triticale, X _Triticosecale_, rye, _Secale cereale_, wheat, _Triticum aestivum_, wide hybridization, chromosome substitutions

Introduction

Rye (_Secale cereale_ L.) offers a number of desirable genes, transfer of which in the background of the bread wheat (_Triticum aestivum_ L. em. Thell) can further improve its productivity and quality. The addition of complete genome of rye into wheat and synthesizing triticale (X _Triticosecale_ Wittmack) produces some reproductive disorders in the amphidiploid, e.g., meiotic instability, aneuploidy, partial sterility, grain shrivelling, etc., solutions for which are being sought (Müntzing, 1979; Gupta and Priyadarshan, 1982). However, triticales act as a bridge to transfer limited genetic material of rye into bread wheat. The hexaploid triticale X bread wheat hybridization results in the transfer of rye chromatin into bread wheat as substitution, translocation, and probably due to intergenomic recombination. Substitutions are perhaps the most common of all the transfers. In triticale X wheat hybrids, there is preferential transmission of those rye chromosomes, through male gametes, which cause the minimum meiotic disturbances and are compatible with the wheat genome. Selection advantage to different chromosomes is also expected to depend upon the natural/artificial selection pressure exerted. From an ongoing project on triticale X wheat hybridization, the segregating generations were studied to establish the selection advantage to specific rye chromosome(s) under rainfed and moderately acidic soil conditions.

Materials and methods

Ten diverse genotypes of hexaploid triticale, viz., TL 68, TL 161, UPT 72142, UPT 7440, UPT 74303, UPT 76001, DTS 138, JNIT 230, JNIT 231 and Rahum, were reciprocally crossed with 5 improved bread wheats, viz., Sonalika, Shailaja, Girija, HS 74 and VL 421. The F_1s of the crosses in which triticales were used as the female parent could attain maturity, and were partially fertile. The F_2 and subsequent segregating generations were handled following pedigree selection for agronomically superior phenotypes irrespective of the rye trait(s), under rainfed and slightly acidic soil (pH=5.5-5.8) conditions at Palampur. Single plant selections were made in the F_6/F_7 generations and 100 true-breeding lines were isolated. These lines were screened for the presence of probable phenotypically identifiable rye traits, like hairy neck, dark-green leaves, long spike, long anthers, red grains, presence of hairy tuft on the grains, etc. Thirty five lines having such traits were hybridized with 3 improved bread wheats, HB 618, CPAN 1922 and HD 2323, to know the nature of rye chromatin in these lines and to generate material for starting the second cycle of breeding. The breeding material was also handled in a similar fasion as described above. The number of superior progenies in the F_4, F_5, F_6 and F_7 generations was recorded to establish the selection advantage to specific chromosomes of rye in the genetic background of bread wheat.

Eight true-breeding lines derived from hybridizing triticale X wheat derivatives (RL accessions having 6R chromosome of rye) with bread wheats, HB 618 and CPAN 1922, were evaluated along with wheat check, CPAN 1796 under the above defined and short-day conditiions in a randomized block design with 3 replications. Data on days to heading, days to maturity and grain yield were recorded on plot basis.

Results and discussion

Results obtained from the meiotic analysis of the F_1s of 35 triticale x wheat derivatives with bread wheat (Sethi and Plaha, 1988; Sethi et al., unpub.) revealed the presence of a single substituting rye chromosome in 21 derivatives. Twelve of these had the substitution of 6R chromosome of rye, whereas 7R, 3R and 1R chromosome substitutions were present in 3, 2 and 2 derivatives respectively. Thus, about 55 per cent of the substitutions had 6R chromosome of rye. The high frequency of substitutions carrying 6R chromosome might be due to an adaptive advantage to this chromosome in the genetic background of bread wheat under rainfed and soil-acidity conditions. It is pertinent to mention that the triticale x wheat derivatives under study were selected for their agronomic superiority i.e. good tillering, impressive spike, and good grain appearance under the defined conditions with low pressure of wheat rusts and powdery mildew in the segregating generations. Therefore, the substitution of only those chromosomes of rye would have been favoured, which had high affinity for the wheat genome and did not disturb its genetic balance markedly. This gets support from the findings of Merker (1975), who showed that all rye chromosomes, but 6R, were frequently replaced by the wheat homoeologues when selection was practised for agronomic traits in some secondary triticales. Gustafson and Zillinsky (1978) from the analysis of 30 F_4 triticale x wheat derivatives, reported that 2R (the longest rye chromosome) was lost in all but one plant, whereas 1R (the smallest) was present in all the plants studied. Further, under natural selection, chromosomes 3R, 4R, 5R, 6R and 7R were present in 70, 77, 60, 73 and 50 per cent of the plants respectively. The stability of 1R and 6R chromosomes of rye in the genetic background of wheat was also reported by Gustafson and Bennett (1976) and Gupta and Priyadarshan (1982). Taketa et al. (1988), however, reported the lowest rate of transmission for 6R chromosome and the highest for 1R. Such differential frequencies of substitution of different rye chromosomes in the bread wheat's genetic background might be due to different selection pressure exerted while advancing the generation.

Forty five crosses (20 of which involved triticale x wheat derivatives as the female parent) of the parental derivatives with 3 bread wheats, viz., CPAN 1922, HB 618 and HD 2323, were also advanced under the rainfed and soil acidity conditions following pedigree selection for the same traits as mentioned earlier. The number of desirable progenies of 26 crosses in the F_4, F_5, F_6 and F_7 generations involving different substitutions in the parental derivatives is presented in Table 1, which evinces that the maximum number of desirable segregants was observed in those crosses, whose parental derivatives showed no evidence of rye chromatin. However, when the parental derivatives involved substitutions,

Table 1. Number of superior progenies in different generations and mode of rye chromatin introgressed in the parental triticale X wheat derivatives (RL accessions)

Cross	Rye chromatin introgressed in RL accessions	Generations			
		F_4	F_5	F_6	F_7
CPAN 1922 x RL 1	Substitution (7R)	43	11	11	2
HB 618 x RL 1	Substitution (7R)	14	6	4	1
HD 2323 x RL 1	Substitution (7R)	5	1	1	0
CPAN 1922 x RL 2	NE	2	1	0	0
RL 3 x CPAN 1922	NE	6	1	0	0
RL 3 x HD 2323	NE	10	3	4	5
HB 618 x RL 5	NE	32	16	6	7
HD 2323 x RL 6	NE	24	14	12	4
HB 618 x RL 8	Substitution (6R)	6	3	2	0
CPAN 1922 x RL 14	NE	10	11	8	6
CPAN 1922 x RL 16	Substitution (6R)	26	3	3	4
HB 618 x RL 18	NC	2	2	1	0
HB 618 x RL 21	Substitution (6R)	5	5	1	0
HB 618 x RL 22	Substitution (6R)	22	12	6	7
RL 22 x CPAN 1922	Substitution (6R)	4	2	1	2
CPAN 1922 x RL 24	Substitution (6R)	2	1	7	6
CPAN 1922 x RL 25	Translocation ?	16	5	1	1
HD 2323 x RL 29	NE	22	1	1	0
HB 618 x RL 30	NE	16	7	2	1
RL 30 x HB 618	NE	13	8	1	1
HB 618 x RL 31	Substitution (6R)	67	12	2	1
HB 618 x RL 34	Substitution (6R)	21	10	2	3
HB 618 x RL 35	Substitution (6R)	3	3	1	2
HB 618 x RL 36	Substitution (6R)	9	3	0	0
HB 618 x RL 68	NE	20	19	4	2
RL 68 x HB 618	NE	20	0	0	0

NE: No evidence of rye chromatin
NC: Substituting chromosome not confirmed
*(Sethi and Plaha, 1988; Sethi et al., unpub.)

the maximum number of agronomically superior progenies was isolated in crosses which involved 6R chromosome of rye, followed by 7R chromosome. The true-breeding lines are being analysed for the presence of 6R chromosome or Robertsonian/translocations involving this chromosome.

Interestingly, more than 85 per cent of the superior combinations in all the generations studied had the hexaploid (6x) cytoplasm of bread wheat. Out of the 20 crosses which involved the triticale x wheat derivatives as the female parent, only 4 could be selected upto the F_4 generation and 3 of these could cope with the selection pressure upto the F_7 generation. Ostensibly, this delineates superiority of the 6x cytoplasm of wheat over the 4x one as earlier reported by Plaha and Sethi (1989). Of the 3 wheats used to generate the second cycle derivatives, the highest number of superior progenies in the different generations studied was obtained in crosses with bread wheat cultivar HB 618, followed by CPAN 1922 and HD 2323 (Table 2). This is perhaps due to good general combining ability of HB 618 with the derivatives.

All the derivatives, except RL 22-2-1, were at par with wheat check, CPAN 1796, for days to flowering (Table 3). The exceptional line was not only late in flowering but was also the last to mature. However, 4 derivatives, *viz.*, RL 22-2-2, RL 35-2-1, RL 24-1-2 and RL 24-1-1, were early in maturity and were at par with the check, CPAN 1796. For grain yield, all the derivatives were at par with CPAN 1796, except RL 24-1-2 and RL 22-2-2, which were significantly superior. It is pertinent to mention here that none of the parental derivatives was superior to this check in an earlier evaluation.

The most useful alien transfer in commercial wheat has been the one that involved either the substitution of rye chromosome 1R for the wheat chromosome 1B or a translocation involving 1RS and 1BL chromosomes. This is because the short arm to 1R chromosome carries genes conferring resistance of leaf, stem and stripe rusts, and powdery mildew, described as *LR26*, *Sr31*, *Yr9* and *Pm8*, respectively (McIntosh, 1988). It has been advocated that 1RS. 1BL translocation and 1R (1B) substitution have a significant yield advantage due to an unknown gene complex on the short arm of 1R, which also confers disease resistance (Gustafson, 1988). From the results of the present study this can be visualised that 6R chromosome of rye also offers yield advantage to wheat, at least under rainfed and acidic soil conditions (having low availability of P). Perhaps, the 6R chromosome contains gene(s) responsible for drought tolerance and increased P-uptake efficiency, thereby leading to yield advantage under such conditions. The chromosome has been reported to carry genes for powdery mildew (Heun and Friebe,

Table 2. Number of superior progenies in different generations involving the 3 wheat cultivars

Wheat cultivars	No. of superior progenies in			
	F_4	F_5	F_6	F_7
CPAN 1922	109(25.92)	35(21.88)	32(39.51)	21(38.19)
HB 618	250(59.52)	106(66.24)	31(38.27)	25(45.45)
HD 2323	61(14.56)	19(11.88)	18(22.22)	9(16.36)

Corresponding percentages are given in the parentheses

Table 3. Performance of some true-breeding lines derived from the crosses of triticale x wheat derivatives with bread wheats

Designation	Parentage	Days to heading	Days to maturity	Grain yield (q/ha)
RL 24-1-1	CPAN 1922 x RL 24	107.00	168.00	33.10
RL 24-1-2	CPAN 1922 x RL 24	120.50	166.50	41.42
RL 34-2-1	HB 618 x RL 34	130.00	171.50	26.85
RL 22-2-1	HB 618 x RL 22	150.50	175.00	18.70
RL 35-2-1	HB 618 x RL 35	128.00	167.00	29.86
RL 24-1-3	CPAN 1922 x RL 24	122.00	170.00	39.09
RL 22-2-2	HB 618 x RL 22	115.00	168.00	53.50
RL 22-2-3	HB 618 x RL 22	119.00	170.00	28.21
	CPAN 1796 (check)	117.00	164.50	21.89
	CD at 5%	22.12	3.33	12.17

1990), Karnal bunt resistance (Sethi et al., 1988), cereal cyst nematode resistance (Asiedu et al., 1990) and Al-tolerance (Aniol and Gustafson, 1984). The importance of 6R. 6B translocations has also been emphasized by Rai (1978). Thus, the commercial exploitation of the 6R chromosome or its segments, may be in conjunction with the 1RS, will be very rewarding to increase the productivity of bread wheat.

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