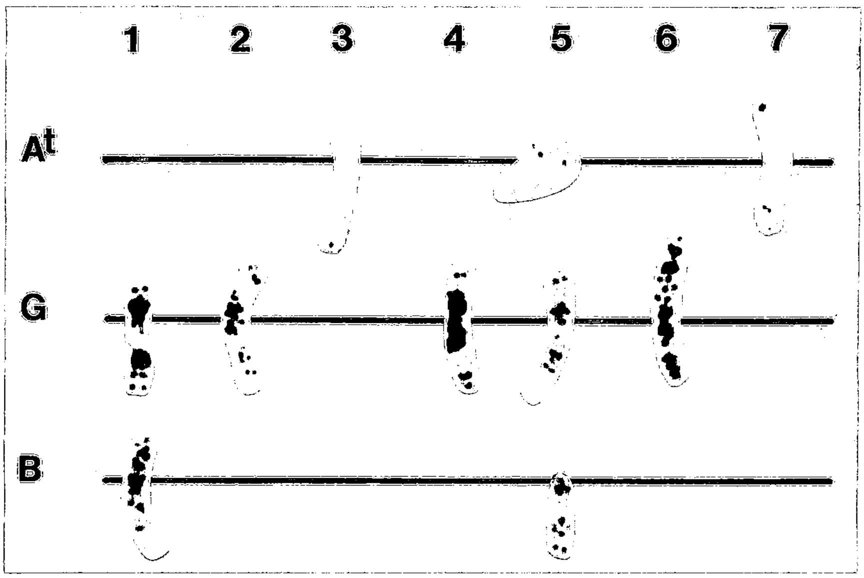
WHEAT INFORMATION SERVICE

ISSN 0510-3517



No.80

June, 1995

Kihara Memorial
Yokohama Foundation for
the Advancement of Life Sciences
Yokohama, Japan

WHEAT INFORMATION SERVICE

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Wheat Information Service
Number 80: 1 – 5 (1995)

I. Articles

Inheritance studies for yield and yield component traits in bread wheat over the environments

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Summary

The genetics of yield and yield component traits was studied in bread wheat (*Triticum aestivum* L.) by means of a 10 × 10 half-diallel progeny (F_2) over three environments. The components of variance analysis revealed that both additive (D) and non-additive (H_1 and H_2) components of variation were important for all the characters studied, except days to maturity, for which only non-additive component was important. The $(H_1/D)^{1/2}$ values revealed over-dominance for all the characters. The values of 'F' exhibited an excess of dominant alleles in the parents for days to heading, number of grains per spike, grain weight per spike, 1000 grain weight, harvest index and grain yield and directional dominance of the decreasing genes for plant height. Breeding methods such as bi-parental mating and/or recurrent selection by intermating the most desirable segregants, alternately with selection may be advantageous to combine the important yield component traits for more tangible advancement in bread wheat.

Introduction

The genetic research done on improvement in the recent past has revealed that grain yield in this crop is determined by component traits and it is a highly complex and variable character and the genes for yield per se do not exist (Grafius 1959). Therefore, the knowledge about the nature and magnitude of gene effects of such metric traits and the expression of gene involved over varied environment are of paramount importance for the wheat breeder in formulating an efficient breeding programme to achieve desired genetic improvement in this important cereal. In view of this, the present study aims to detect the genotype × environment interactions and obtain information regarding the component traits, by analyzing the performance of progeny from a 10 × 10 parental diallel over the three diverse environments.

Materials and methods

The studies were conducted on ten cultivars of bread wheat (*Triticum aestivum* L.) of diverse geographical origin, namely, Moncho, Pavon, Broohis, Chiroca, HD 2204, Raj 1482, WL 711, Raj

821, Durgapura 65 and Kharchia 65. The parents were crossed in all possible combinations, without reciprocals. The resulting 45 F_1's were grown to get F_2's seeds. All 45 F_2's and ten parents were grown in a randomized block design with three replications under early, normal and late sown environments at the experimental field of the Department of Plant Breeding. Each plot consisted of single 5 m row length of parent and 10 rows of F_2 with the spacing of 30 cm between rows and 15 cm between plants. Ten competitive plants in parents and twenty plants in F_2 progenies were selected randomly for recording observations for grain yield and its ten component characters (Table 1) under each environment, separately. Pooled analysis of variance over the environments was done according to Panse and Sukhatme (1967). The variance components analyses were done as suggested by Hayman (1954).

Results and discussion

The pooled analysis of variance over the environments for the experimental design (Table 1) showed highly significant differences amongst genotypes for all the traits studied. The genotype × environment interaction was also observed to be high for all the traits and is in agreement with those of Sharma and Singh (1982), Nanda et al. (1983), Sharma et al. (1986) and Dasgupta and Mondal (1988) who revealed the significant role of environments in the expression of yield and yield components in wheat.

As emphasized by Hayman (1954), the first important part of the analysis is testing the validity of the several assumptions underlying diallel analysis, vis: (1) diploid segregation, (2) homozygous parents, (3) no reciprocal differences, (4) no linkage, (5) no epistasis and (6) absence of multiple alleles. The absence of multiple allelism and independent distribution of genes are difficult to be established (Kempthrone 1956). Though diallel analysis has several limitations, the results obtained by many plant breeders do indicate that at least some insight could be made on the inheritance of relatively complex traits like yield even when only some of the assumptions are satisfied (Hayman 1954).

Table 1. Pooled analysis of variance over the environments for yield and yield components

Source	d.f	Days to heading	Days to maturity	Plant height	Flag leaf area	Peduncle length	Tiller number	No. of grain/ spike	Grain weight/ spike	1000 grain weight	Harvest Index	Grain yield
Environment (E)	2	4266.85**	27957.80**	1292.45**	24.89**	3261.05**	84.09**	3308.70**	53.50**	8922.76**	38569.15**	3331.99**
Genotype (G)	54	102.28**	6.13**	543.89**	10.86**	157.69**	10.36**	455.94**	0.77**	78.04**	240.46**	16.83**
G × E	108	13.54**	4.37**	26.38**	7.02**	31.80**	2.25**	67.60**	0.17**	19.34**	120.54**	3.77**
Error	324	1.53	2.79	7.57	2.06	4.40	0.92	8.63	0.07	2.19	17.16	1.90

** P=0.01

Significant deviation of 'b' from zero and the non-significant departure of regression coefficient from unity in respect of days to heading, peduncle length, number of grains per spike, grain weight per spike, 1000 grain weight and grain yield indicated that the aforesaid diallel assumptions were valid for these traits (Table 2). However, rest of the characters showed partial failure of the assumptions but estimates of the population parameters for that traits were still possible (Hayman 1954) though certainly the estimates for such a trait are less reliable than they would have been if all assumptions had been fulfilled. With the fulfillment of most of the assumptions of the diallel analysis fully or partially in the present study, the conclusions drawn are expected to be valid and should form a guideline for improvement in the genetic material studied.

The estimates of components of genetic variance (Table 2) exhibited that additive component (D) was highly significant for all the characters except days to maturity. The two measures of dominance H_1 (dominance effect) and H_2 (proportion of dominance due to positive and negative effect of genes) were also highly significant for all the traits studied. Thus, it is suggested that additive and non-additive gene effects were equally important for all the characters except days to maturity, for which only non-additive component was important. These findings confirm the results of Jatasra and Paroda (1980), Sharma and Singh (1982), Nanda et al. (1983), Sharma et al. (1986), Dasgupta and Mondal (1988), Solanki et al. (1993) and Singh et al. (1993) obtained through combining ability analysis for the same set of characters.

Table 2. Estimates of genetic components of variation for yield and yield components pooled over three environments

Components	Days to heading	Days to maturity	Plant height (cm)	Flag leaf area (cm^2)	Peduncle length (cm)	Tiller number	No. of grain/ spike	Grain weight/ spike (g)	1000 grain weight (g)	Harvest Index (%)	Grain yield (g)
D	22.38**	0.31	87.09**	1.13**	25.82**	1.29**	103.88**	0.18**	22.34**	31.39**	3.84**
	±0.97	±0.20	±2.46	±0.31	±1.15	±0.29	±7.77	±0.01	±1.58	±6.25	±0.31
H_1	34.79**	9.39**	119.50**	9.89**	59.98**	8.75**	274.60**	0.40**	73.69**	447.70**	14.09**
	±8.22	±1.72	±20.98	±2.60	±9.83	±2.40	±66.19	±0.05	±13.48	±53.20	±2.63
H_2	28.90**	7.50**	90.95**	8.69**	51.05**	7.71**	208.70**	0.28**	51.00**	338.40**	11.50**
	±6.98	±1.46	±17.83	±2.21	±8.35	±2.11	±56.25	±0.04	±11.46	±45.21	±2.24
F	10.34**	1.38	-41.17**	0.36	-2.49	0.34	94.85*	0.16**	39.29**	91.97**	4.98**
	±4.45	±0.93	±11.37	±1.41	±5.33	±1.34	±35.87	±0.03	±7.31	±28.83	±1.43
E	0.17	0.31**	0.84	0.23*	0.49	0.10	0.96	0.007**	0.24	1.95	0.21*
	±0.29	±0.06	±0.74	±0.09	±0.35	±0.07	±2.34	±0.002	±0.48	±1.88	±0.09
$(H_1/D)^{1/2}$	1.25	5.55	1.17	3.97	1.52	2.61	1.63	1.51	1.82	3.78	1.92
b-0/sb	3.07**	1.83	1.02	0.87	9.91**	0.43	4.73**	8.31**	2.88**	7.50**	12.29**
1-b/sb	0.38	6.50**	-0.01	5.80**	-0.82	2.08	-0.18	-0.62	0.96	5.00**	2.00

*P = 0.05

**P = 0.01

The estimates of 'F' value which indicated the relative frequency of dominant and recessive alleles in parents were found to be positive and highly significant for days to heading, number of grains per spike, grain weight per spike, 1000 grain weight, harvest index and grain yield indicating an excess of dominant alleles, while 'F' was significant and negative for plant height, which indicated the directional dominance of the decreasing genes. Positive but non-significant 'F' in days to maturity, flag lead area and tiller number gave some indications of the excess of dominant alleles in the parental lines. The environmental component (E) was significant for days to maturity, flag leaf area, grain weight per spike and grain yield. The proportion $(H_1/D)^{1/2}$ representing the degree of dominance was more than unity for all the characters indicating the existence of overdominance.

The present study revealed that both additive and non-additive components of genetic variances were involved in governing the inheritance of yield and yield components, although preponderance of non-additive genetic variance was noted. In such a situation, the most suitable breeding procedure would be one which mops up the additive genetic variance and at the same time maintains heterozygosity. Therefore, it is desirable to practice bi-parental mating and/or recurrent selection, intermating the most desirable segregants, alternately with selection. This would lead to an elevation of the genetic plateau, by accumulating favorable additive genes and simultaneously exploiting the dominance variance. Although it is difficult to produce enough seed in wheat by conventional methods, the 'obligate' cross-fertilization system using male sterility, as proposed by Athwal and Borlaug (1967) can bring about large-scale intermating among selected genotypes, as envisaged under the recurrent improvement programme.

Acknowledgement

The authors are thankful to the Director Research, Rajasthan Agricultural University for providing necessary facilities during the course of investigation.

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Wheat Information Service
Number 80: 6 – 11 (1995)

Genotype × environmental interactions in some Indian rainfed varieties of bread wheat under salt stress conditions.

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Summary

The objective of this study was to assess the genotype-environment interactions and the stability of fifteen Indian rainfed wheat varieties under varied salt stress environments, viz., two levels of salinity, and two levels of alkalinity along with a normal level. The results showed the existence of high linear interactions for grain yield, number of grains per ear, 1000 grain weight and number of ear-bearing tillers per plant. Varieties Hybrid 65 and PBW 65 proved to be high yielding and stable over the environments tested. Hybrid 65 also exhibited higher and stable performance for number of grains per ear and grain weight.

Introduction

Certain drought tolerant wheat cultivars are also known to show a high tolerance to salt stress (Mozafar and Goodin 1986). This is attributed to the fact that osmotic (physiological drought) effect and/or specific ion effect are among the mechanisms presently held responsible for the overall salt injury in plants. It is also known from the earlier studies that wheat genotypes respond differentially to varying salt stress (Rana 1978: Singh and Rana 1984). Thus it is necessary to identify high-yielding stable varieties under such conditions. Considering this, the present study was conducted to study the G × E interactions of some popular rainfed wheat varieties as well as to screen the stable genotypes under salt stress conditions.

Materials and methods

Fifteen rainfed wheat varieties (Table 2) were grown during the winter season of 1991-92. They were planted with two replications, each, in five diverse environments, viz., normal soil, two levels of saline water irrigation conditions (EC_{iw} 20 dSm^{-1} and 30 dSm^{-1}) and two levels of alkali soils (pH_2 9.2 and 9.4). These stress environments were settled to represent the actual field conditions wherein salinity and alkalinity as well as normal condition occur in patches. The experiment was laid out in a split plot design, with five edaphic environments in two replicated main plots and 15 rainfed wheat varieties in the subplots. Each variety was planted in single row of 80 cm with row distance of 23 cm. An effective row length of 50 cm was harvested for evaluating grain yield and number of ear-bearing tillers. Number of grains per ear and 1000 grain weight were evaluated for 10 randomly selected ear samples from the 50 cm row. Plot means were used for the stability analysis as proposed by Eberhart and Russell (1966).

Results and discussion

The analysis of variance separately conducted for each environment indicated significant differ-

Table 1. Analysis of variance for yield and its component traits of rainfed wheat varieties under edaphic stress conditions

Source	d.f.	Mean squares			
		Grain yield/row (g)	No. of grains/ear	1000 grain weight(g)	No. of ear-bearing tillers/row
Varieties	14	1070.324**	91.039**	95.674**	479.100**
Env.+ (Var. × Env.)	60	1581.789	85.671'	26.760	1106.883**
Env. (linear)	1	84935.176**	4471.956**	1282.809**	61497.290**
Var. × Env. (linear)	14	540.751**	28.312**	15.492**	222.935**
Pooled deviations	45	53.371	6.044	2.354	39.881
Pooled error	75	16.656	2.109	0.784	6.210

*, ** Significant at 0.05 and 0.01 level, respectively.

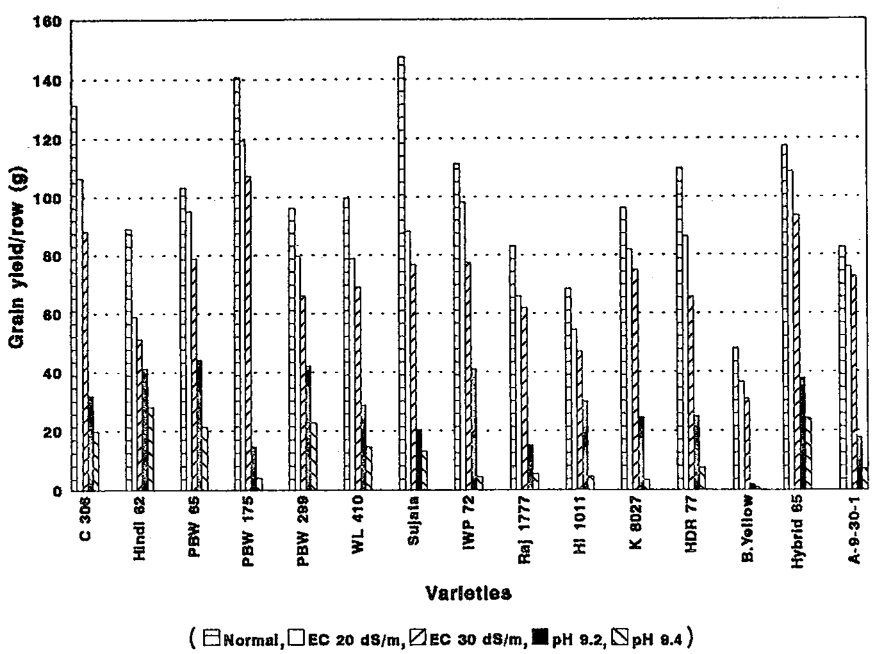

Fig. 1. Response of fifteen rainfed varieties to varying salt stress environments.

ences among the varieties for gain yield, number of grains per ear, 1000 grain weight and number of ear-bearing tillers. The pooled analysis (Table 1) based on Eberhart and Russell (1966) revealed significant differences among the varieties for all the characters. The linear effect of the environment was also highly significant for all the characters, indicating that salt stress widely influenced the performance of the varieties. The predictable linear variety × environment (salt stress) interaction component was also significant for all the characters.

The estimates of the three stability parameters μ (mean), b_i (linear regression coefficient) and S^2d_i (deviation from linear regression) for grain yield and its component characters for each variety are given in Table 2 and Table 3, respectively. The varieties were classified into the following groups (Table 4).

(A) Absence of G × E interactions : This group comprises of varieties with non-significant b_i and S^2d_i, thereby suggesting their wide adaptability. However none of the varieties fell in this

Table 2. Grain yield/row (g) of fifteen rainfed wheat varieties under five environments and their stability parameters

Varieties	Grain yield/row under five environments					Overall mean	Response b_i	S^2d_i
	Normal	EC_{iw} 20 dSm^{-1}	EC_{iw} 30 dSm^{-1}	pH 9.2	pH 9.4			
C306	131.5	106.5	88.2	32.0	19.9	75.6	1.28#	-2.92
Hindi 62	89.1	59.0	51.4	41.4	28.1	53.8	0.56#	82.86**
PBW 65	103.4	95.1	78.8	44.6	21.3	68.6	0.92	11.67
PBW 175	140.7	119.4	107.1	14.6	4.2	77.2	1.66#	88.47**
PBW 299	96.1	79.6	66.1	42.2	22.8	61.4	0.77#	0.55
WL 410	99.6	78.8	68.9	28.8	14.6	58.1	0.94#	-15.38
Sujata	147.6	88.2	76.7	20.6	13.2	69.2	1.42	226.24**
IWP 72	111.3	98.1	77.4	41.1	4.4	66.4	1.14	57.72**
Raj 1777	83.1	66.0	61.9	15.1	5.5	46.3	0.90	-3.00
HI 1011	68.4	54.4	47.0	30.2	4.6	40.9	0.64#	26.30
K 8027	96.2	81.9	74.8	24.7	3.4	56.2	1.06	9.26
HDR 77	109.8	86.2	65.7	24.8	7.6	58.8	1.12	1.06
B. Yellow	48.1	36.5	30.7	2.1	1.0	23.7	0.56#	-6.44
Hybrid 65	117.2	108.5	93.6	37.8	24.2	76.2	1.12	21.69
A-9-30-1	82.5	75.9	72.6	17.8	7.2	51.2	0.93	52.65**
Grand mean	101.6	82.3	70.7	27.8	12.1	58.9		
S.E. (mean)	9.86	5.61	3.57	4.23	3.69	3.65		
Env. index	42.71	23.35	11.80	-31.08	-46.78			

#, ## Significant deviation of b_i from unity at the 0.05 and 0.01 level, respectively.

*, ** Significant at the 0.05 and 0.01 level, respectively.

group for any of the characters studied, thereby indicating the predominance of genotype × salt stress interactions.

(B) Presence of G×E interactions : In this group three types of varieties must be considered. (i) The major portion of G × E interactions was explained by the linear environmental change, i.e., a significant b_i and a non-significant S^2d_i. (ii) Along with a significant b_i the estimates of S^2d_i were also significant, suggesting a significant contribution of linear and non-linear components to the performance of the varieties. (iii) The major portion of G×E interactions was explained by the non-linear component, indicating high unpredicatability hence instability of the varieties.

Finlay and Wilkinson (1963) considered linear regression coefficient as a measure of stability, whereas Eberhart and Russell (1966) emphasized that both linear (b_i) and non-linear (S^2d_i) components of the interaction should be considered for judging the phenotypic stability of a genotype. Breese (1969) and Paroda and Hayes (1971) underlined that linear regression coefficient should simply be regarded as a measure of response of a particular genotype, whereas the deviation which could not be explained by the linear regression should be considered as a measure of stability; a genotype with the lowest deviation being the most stable and vice-versa. Keeping these in view the

Table 3. Stability parameters for component traits in rainfed wheat varieties under edaphic stress conditions

Varieties	No. of grains/ear			1000 grain wt. (g)			No. of ear-bearing tillers/row		
	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i
C 306	38.0	0.71##	-1.43	29.5	0.79	1.26	64.8	1.13#	-1.69
Hindi 62	32.9	0.89	41.84**	28.8	0.50##	-0.73	58.8	0.61##	26.43**
PBW 65	44.8	1.05	11.38**	29.6	0.88	0.25	48.0	0.90	19.29*
PBW 175	29.8	0.83	-0.40	37.4	2.14#	2.95**	56.6	1.36##	5.48
PBW 299	38.2	0.67#	-0.27	29.7	0.93	3.60**	51.0	0.63##	-2.11
WL 410	42.4	0.98	3.82*	26.4	1.07	4.11**	48.1	1.09	14.56*
Sujata	40.7	0.88	-0.62	31.6	0.83	1.07	46.1	1.00	13.67*
IWP 72	39.2	1.63#	3.35	24.4	0.76#	-0.63	49.5	1.32#	8.97
Raj 1777	36.2	1.44##	-0.78	21.2	1.84#	2.67*	42.0	1.01	2.40
HI 1011	30.8	1.00	2.06	24.8	0.71	-0.02	43.2	0.88	6.68
K 8027	38.0	1.01	-0.31	33.4	0.88	3.19**	40.3	0.87	30.53**
HDR 77	38.2	0.93	2.28	32.5	0.93	-0.14	44.1	1.08	186.28**
B. Yellow	33.9	1.49##	-0.88	23.5	0.89	5.41**	27.6	0.76#	0.95
Hybrid 65	39.1	0.97	-1.47	30.3	0.99	0.51	64.5	1.05	85.18**
A-9-30-1	32.4	0.52#	0.45	24.4	0.86	0.03	55.7	1.32	108.43**
Grand mean	37.0			28.4			29.4		
S.E. (mean)	1.23			0.77			3.16		

#, ## Significant deviation of b_i from unity at the 0.05 and 0.01 level, respectively.

*, ** Significant at the 0.05 and 0.01 level, respectively.

Table 4. Summary of the stability attributes of fifteen rainfed wheat varieties under salt stress conditions

Character	Group A Absence of G × E interaction	Group B Presence of G × E interactions		
		Linear[1]	Linear[2] & non-linear	Non-linear[3]
Grain yield/row	None	**Hybrid 65** **C 306#** **PBW 65** PBW 299# HDR 77 WL 410# K 8027 Raj 1777 HI 1011# Bijyaga Yellow#	**PBW 175#** **Sujata** **IWP 72** Hindi 62# A-9-30-1	None
No. of grains/ear	None	**Sujata** **IWP 72#** **Hybrid 65** PBW 299# HDR 77 K 8027 C 306## Bijyaga Yellow## Raj 1777## A-9-30-1# HI 1011 PBW 175	**PBW 65** **WL 410**	Hindi 62
1000 grain weight	None	**HDR77** **Sujata** **Hybrid 65** **PBW 65** C 306 Hindi 62## HI 1011 IWP 72# A-9-30-1	**PBW 175##** **K 8027** **PBW 299** WL 410 Raj 1777# Bijyaga Yellow	None
No. of ear-bearing tillers/row	None	C 306# PBW 175## PBW299## IWP 72# Raj 1777 HI 1011 Bijyaga Yellow#	**Hybrid 65** **Hindi 62##** **A-9-30-1** PBW 299 PBW 65 Sujata HDR 77 K 8027	None

#, ## Significant deviation of b_i from unity at the 0.05 and 0.01 level respectively. Varieties in bold are significantly better performers as compared to the overall mean.

1- Only b_i is significant. 2- Both bi and S^2d_i are significant. 3- Only S^2d_i is significant.

varieties classified to the first group are of more importance. Varietal classification given in Table 4 indicated that for a majority of varieties a significant portion of G × E interactions was explained by the linear environmental change, i.e., a significant b_i and a non-significant S^2d_i. In this group, varieties Hybrid 65 and PBW 65 showed significantly higher mean yield along with b_i nearly equal to unity. As shown in Table 2 and Fig. 1, varieties like Hybrid 65 and PBW 65 had high grain yield/row under normal environment and the reduction of yield was relatively small under salinity stress of EC_{iw} 20 and 30 dSm^{-1}. These varieties also gave moderately better yields under alkalinity stress of pH 9.2 and 9.4. Similar result was also seen in varieties Sujata and Hybrid 65 for number of grains per ear, and in varieties HDR 77, Sujata, Hybrid 65, PBW 65 and C 306 for 1000 grain yield, while no variety was stable for the number of ear-bearing tillers. It can be thus inferred that the variety Hybrid 65 was the most suitable variety under salt stress conditions.

The stability of grain yield and its component characters were also examined. The available evidence suggested the importance of component compensation in conferring homeostasis for a complex trait like grain yield (Grafius 1956; Allard and Bradshaw 1964; Bains and Gupta 1972). The results shown in Tables 2 and 3 suggested that any generalization regarding stability of a genotype for all the characters was very confusing as the genotypes studied did not exhibit uniform stability. Hybrid 65, a high yielding rainfed variety which was stable for grain yield, was stable in performance for number of grains per ear and 1000 grain weight, though unstable for the number of ear-bearing tillers, due to significant non-linear interactions. Similarly PBW 65 being stable for grain yield was stable for 1000 grain weight, but unstable for the number of grains per ear and the number of ear-bearing tillers. The number of ear-bearing tillers was in general the most unstable character under salt stress conditions. It was also observed that varieties unstable for grain yield were mostly unstable for its component characters. Bains and Gupta (1972) also observed highly buffered population for grain yield as poor or average in buffering ability for the component traits in wheat.

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Wheat Information Service
Number 80: 12 – 19 (1995)

Heterosis and combining ability estimates in diallel crosses of six cultivars of spring wheat

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Summary

The present research programme was conducted to study heterosis and combining ability for yield and its primary components in a 6 × 6 complete diallel cross involving six varieties of spring wheat. These genetic parameters were studied in F_1 generation for eight quantitative traits in a randomized block design during the year 1990-92. All the traits exhibited considerable level of relative heterosis (MP) and heterobeltiosis (BP). The extent of heterosis was appreciably influenced by the hybrid genotype, the direction of the cross and the trait concerned. Eight F_1's displayed heterotic values more than 60% for yield per plant. The analysis of combining ability indicated that a large portion of the total genetic variation for five out of eight traits was associated with genes which were additive in their effects, while nonadditive gene action was strong for single plant yield. The estimates of SCA were significant for four out of eight traits indicating the presence of epistasis and dominant gene effects in these traits. The parents, Z.A.77 and T.J.83 were good general combiner for grain yield. Magnitude of GCA variance was more pronounced than SCA variance for all the traits. Therefore, selection has been advocated on the basis of GCA's of hybrids and breeding method should be designed to exploit both additive and nonadditive gene action.

Introduction

One of the most important developments in plant breeding in recent years has been the use of heterosis particularly in allogamous crops (Baloch et al. 1991; Larik and Hussain 1990), and has also been observed in autogamous crops (Larik et al. 1992). Heterosis is the biological phenomenon and may be due to factors such as heterozygosity, allelic and non-allelic interaction, epistasis, dominance or overdominance. Breeding for yield includes genetical manipulation of the yield components which are polygenetically inherited exhibiting additive and non-additive genetic variation. On the contrary, combining ability analysis of cultivars is necessary to exploit the relevant type of gene action for a breeding programme. If SCA is predominant, it can be used in hybrid breeding programme.

In this context the present study was undertaken to study heterosis and combining ability in F_1 generation of wheat (*Triticum aestivum* L.).

Materials and methods

Six varieties of spring wheat (Table 1) were crossed in a 6×6 diallel system including reciprocals. The parents and their F_1's were grown during Rabi 1990-91 in the experimental field of Agriculture Research Sub-Station, Kot Deji, Khairpur, Sindh (Pakistan). The varieties had different parentages and wide ecogeographic diversity for their origin (Table 1).

Seeds were sown in a randomized block design with three replications in 10 feet long rows with 30 and 15 cms distance between rows and between plants respectively. Data on eight quantitative traits were collected from 10 sample plants selected randomly from each parent and their F_1 hybrids. Breeding value of the material was evaluated by analyzing the data on heterosis and combining ability for yield and yield components in F_1 generation. The method of analysis of variance of combining ability with model-2 of Griffing (1956) was used. Heterotic values were calculated by using the formula as reported earlier (Larik et al. 1992).

Table 1. Parentage of different varieties used in the present experiment

Symbol	Name of variety	Pedigree	Cross no. & selection	Year of release	Country
P_1	Veery(Vee's)	KVZ/BUHO's/KAL/BB	CM33027	1977	Mexico
P_2	Buck (Buc's)	BY/MAYA's'/4 BB	CM31678	1977	Mexico
P_3	Moncho(Monn's)	WE/GTO/KAL/BB	CM8288	1974	Mexico
P_4	Z.A-77.	(WOR67-7C)11	CM30367-IM	1977	Pakistan
P_5	T.J-83	Blue jay's'	CM5287-J-IY-2M-2Y-3M-OY.	1983	Pakistan
P_6	Blue Silver	M54-388/AN/3/YT54/NIOB/LR64.	CM8427	1983	Pakistan

Results and discussion

The degree and the direction of heterosis and combining ability in the F_1 hybrids of six cultivated spring wheat genotype crossed in a complete 6×6 diallel cross including reciprocals were investigated.

1. Heterosis

There was general decrease in plant height for most of the hybrids, indicating higher frequency of short statured plants which will resist lodging and give better response to higher fertilizer inputs (Table 2). It may be pointed out here that only certain genes in the heterozygous condition produce heterosis and that homozygosity due to selfing does not produce the desired effects. Out of 30 crosses, 8 crosses in F_1 generation produce mid parent (MP) heterosis. It can be concluded that increased height in case of these hybrids over MP may be due to the interaction of complementary growth genes for tallness and these hybrids could be exploited for developing varieties for Dobari, Bosi and rainfed areas where tall varieties appear to surpass weeds to some extent and produce more

Table 2. Heterosis(%) values over mid parent (M.P) and better parent (B.P) for eight quantitative traits in bread wheat (*Triticum aestivum* L.)

Cross	Plant height (cm)		Tillers/ plant		Spike length (cm)		Spikelets/ spike		Seeds/ spike		Yield/ spike (gm)		Seed index (gm)		Single plant yield (gm)	
Direct	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP
$P_1 \times P_2$	-5.8	-7.2	6.7	0.0	51.5	47.1	20.0	6.7	60.0	42.9	60.6	44.3	13.4	10.8	75.4	66.8
$P_1 \times P_3$	-3.2	-3.9	14.3	14.3	19.8	17.6	15.4	6.7	17.9	9.5	17.2	10.1	5.2	3.8	39.7	32.7
$P_1 \times P_4$	-6.5	-11.0	20.0	12.5	34.9	31.1	3.7	0.0	20.0	14.3	20.5	14.5	9.4	5.7	46.2	43.2
$P_1 \times P_5$	0.4	-3.1	13.3	6.3	35.4	33.0	3.7	0.0	13.4	11.9	17.5	13.2	10.6	8.1	39.6	31.4
$P_1 \times P_6$	4.0	0.3	7.1	7.1	16.6	13.3	4.0	-7.1	28.8	14.3	28.2	14.5	8.5	7.9	32.2	25.6
$P_2 \times P_3$	-3.6	-4.3	13.3	6.3	24.7	23.2	4.3	0.0	27.3	22.2	29.5	21.9	6.9	5.8	46.2	45.9
$P_2 \times P_4$	3.0	-3.3	12.5	12.5	21.2	14.1	25.0	15.4	35.2	26.3	35.8	26.4	4.0	2.7	54.9	42.7
$P_2 \times P_5$	-5.3	-7.2	12.5	12.5	31.0	25.0	16.1	7.7	27.8	18.0	28.9	18.3	9.7	5.3	48.6	33.5
$P_2 \times P_6$	-2.2	-4.4	13.3	6.3	41.0	25.0	18.2	18.2	45.5	45.5	45.6	45.6	7.2	4.5	62.2	57.2
$P_3 \times P_4$	-3.1	-8.4	6.7	0.1	15.1	16.0	12.0	7.7	8.1	5.3	8.6	5.6	3.0	0.7	17.6	9.5
$P_3 \times P_5$	3.0	-5.7	0.0	-6.3	20.0	15.9	4.0	0.0	28.0	23.1	28.2	22.2	8.5	5.1	23.5	10.9
$P_3 \times P_6$	-0.9	-3.7	28.6	28.6	27.9	22.2	13.0	8.3	39.1	33.3	35.1	21.2	9.7	7.7	36.0	32.1
$P_4 \times P_5$	9.0	2.9	18.8	18.8	43.3	41.7	20.0	15.4	68.2	64.1	60.3	58.1	15.8	9.8	41.5	37.7
$P_4 \times P_6$	-3.0	-10.8	20.0	12.5	25.6	25.6	16.7	7.7	35.2	26.3	35.8	26.4	7.1	3.2	64.7	49.3
$P_5 \times P_6$	-9.2	-9.0	20.0	12.5	29.2	27.8	18.3	0.0	3.3	23.1	33.8	23.0	5.1	3.5	57.4	57.7
Reciprocal																
$P_2 \times P_1$	9.4	-6.3	0.0	6.3	50.3	45.9	12.0	0.0	49.3	33.3	50.0	34.0	7.0	4.5	53.0	45.5
$P_3 \times P_1$	-6.5	-7.2	7.1	7.1	19.8	17.6	23.1	14.3	7.7	0.0	2.4	0.0	6.5	5.1	20.2	14.2
$P_4 \times P_1$	-7.2	-14.6	13.2	6.3	38.7	30.1	11.1	7.1	5.0	0.0	5.3	0.0	4.1	0.5	22.0	19.5
$P_5 \times P_1$	-3.9	-4.7	20.0	12.5	27.2	25.0	3.7	0.0	19.9	14.3	22.9	18.2	13.9	11.8	18.7	11.7
$P_6 \times P_1$	-2.4	-1.3	28.6	28.6	29.7	26.1	12.0	0.0	28.0	14.3	28.9	15.1	11.4	10.8	68.6	55.8
$P_3 \times P_2$	-5.0	-5.7	20.0	12.5	24.7	23.2	13.0	8.3	10.2	5.6	9.9	5.1	5.6	4.5	36.2	36.2
$P_4 \times P_2$	1.6	-4.6	25.0	25.0	27.1	20.0	16.7	7.7	29.6	21.1	30.6	21.5	2.0	0.7	67.1	58.2
$P_5 \times P_2$	-6.6	-8.6	0.0	0.0	27.4	21.6	16.7	7.7	33.3	23.1	33.8	23.0	10.8	6.3	33.9	20.3
$P_6 \times P_2$	-0.7	-2.9	20.0	12.5	38.8	31.1	9.1	9.1	27.3	27.3	27.2	27.2	8.5	5.8	55.7	50.9
$P_4 \times P_3$	-4.4	-9.7	0.0	-6.3	15.2	11.1	20.0	15.4	38.0	26.3	30.0	26.7	8.0	5.7	34.2	22.3
$P_5 \times P_3$	-4.5	-7.7	0.0	-6.3	21.2	17.0	4.0	0.0	22.7	17.9	23.2	18.2	5.8	2.6	38.9	28.7
$P_6 \times P_3$	3.0	3.0	21.4	21.4	30.0	30.0	21.7	16.7	6.2	3.6	37.4	31.4	12.1	10.0	70.2	65.3
$P_5 \times P_4$	26.2	10.4	19.8	18.8	46.1	44.4	15.4	15.4	24.7	23.1	27.2	27.2	16.8	11.1	66.2	46.0
$P_6 \times P_4$	-1.8	-9.7	26.7	18.8	22.2	22.2	25.0	15.4	40.8	31.6	29.5	27.7	4.6	0.7	80.2	63.4
$P_6 \times P_5$	-7.5	-7.6	26.7	18.8	23.6	22.2	16.7	7.7	33.3	23.1	33.8	23.0	7.8	6.1	66.8	55.8

Table 3. Mean squares of wheat genotype (varieties/F_1) for different quantitative characters

Character	Degres of freedom	Mean square	F-values	Significance
Plant height	35	84.39	42.40	***
No. of fertile tillers/plant	35	7.56	1.21	n s
Spike length	35	4.80	3.69	**
Spikelets per spike	35	3.83	0.44	n s
Seeds per spike	35	120.99	122.21	***
Yield per spike	35	0.16	0.51	n s
Seed index	35	0.09	0.06	n s
Single plant yield	35	72.24	23.30	***

***=Significant at 0.01% level
**= Significant at 0.1% level
ns=Non-significant.

straw that can be fed to cattle and used for other purposes. The expression of positive heterosis in these hybrids, indicates the preponderance of additive gene action for this trait (Liu et al. 1989). Significant mean squares for this trait also indicates the presence of additive and non-additive gene action (Table 3).

MP heterosis and heterobeltiosis (BP) in F_1 for tillers per plant, spike length, spikelets per spike, seeds per spike, yield per spike, seed index and single plant yield were significantly positive (Table 2). Among the crosses $P_1 \times P_2$ and $P_6 \times P_4$ each had more than 75.4% to 80.2% MP heterosis and 63.4% to 66.8% heterobeltiosis for yield per plant (Table 2), indicating that parents of these crosses are genetically more diverse than the parents of other crosses.

Grain yield is a total sum of the genetic expression of all the yield components, being polygenic (Larik 1978, 1979; Larik et al. 1978) and is greatly influenced by environmental factors (Kheradnan and Nikhejad 1974). The overall performance of a hybrid, therefore, may vary due to changes in environment. The selection of population simply on the basis of yield may not be beneficial and may lead to incorrect conclusions. In F_1 generation, heterosis for tiller per plant ranged from 6.3% to 28.6%. The range of heterosis for other quantitative traits were 10.0% to 51.0% for spike length, 7.1% to 25.0% for spikelets per spike, 0% to 65.2% for seeds per spike, 0% to 60.5% for yield per spike, 0.5% to 16.8% for seed index (Table 2).

According to the data presented in Table 2, low yielding parent Buc's and Blue Silver combine well to exhibit better parent heterosis, which indicated the preponderance of additive gene action. The hybrids $P_1 \times P_2$ and $P_4 \times P_1$ are likely to produce high yielding progenies in early generations due to better specific combining ability (Table 4), this indicates that yield per plant is the expression of additive and dominant genes. This is confirmed by the findings of Lupton (1961), who found that certain crosses with large standard deviation but low mean yield displayed greater promise than

Table 4. Estimation of specific combining ability (SCA) effects in F_1 generation for various quantitative traits in bread wheat

Cross	Plant height (cm)	Tillers/ plant	Spike length (cm)	Spikelets/ spike	Seeds/ spike	Yield/ spike (gm)	Seed index (gm)	Single plant yield (gm)
Direct								
$P_1 \times P_2$	-1.5	-0.9	1.1	0.8	9.3	0.3	0.1	3.1
$P_1 \times P_3$	0.4	0.2	-0.3	0.1	-1.1	-0.0	-0.1	0.7
$P_1 \times P_4$	-4.9	0.4	0.3	-0.6	-4.5	-0.2	-0.1	-1.6
$P_1 \times P_5$	1.1	0.7	-0.2	0.0	-3.1	-0.1	0.1	-1.4
$P_1 \times P_6$	4.8	-0.4	0.8	-0.3	-0.6	-0.0	0.0	-0.8
$P_2 \times P_3$	1.5	1.2	-0.1	-0.6	-3.0	-0.1	0.0	0.0
$P_2 \times P_4$	1.6	0.9	-0.8	1.3	-1.4	-0.1	-0.1	1.3
$P_2 \times P_5$	-3.0	-0.1	-0.6	0.3	-2.5	-0.1	-0.1	-1.7
$P_2 \times P_6$	1.4	-0.4	0.5	-1.0	-2.5	-0.1	0.0	-2.7
$P_3 \times P_4$	-2.8	-1.5	-0.4	-0.5	-0.7	-0.0	-0.0	-2.2
$P_3 \times P_5$	-1.4	-0.7	-0.2	-0.4	1.2	0.0	-0.1	0.7
$P_3 \times P_6$	2.2	0.7	1.0	1.4	3.7	0.1	0.2	1.0
$P_4 \times P_5$	8.8	0.5	1.3	0.4	5.8	0.2	0.2	1.1
$P_4 \times P_6$	-2.9	-0.2	-0.4	0.1	0.8	0.0	0.0	1.5
$P_5 \times P_6$	-5.6	0.2	-0.4	-0.3	-1.4	-0.1	-0.2	1.3
S.E.	0.60	0.10	0.46	1.21	0.40	0.24	0.45	0.59
Reciprocal								
$P_2 \times P_1$	1.5	0.5	0.1	0.5	2.0	0.1	0.1	2.3
$P_3 \times P_1$	1.2	0.5	0.0	1.5	2.0	0.1	-0.5	2.0
$P_4 \times P_1$	0.3	0.5	0.1	0.0	3.0	0.1	0.1	2.4
$P_5 \times P_1$	0.6	-0.5	0.4	0.0	-0.5	-0.0	0.0	2.4
$P_6 \times P_1$	0.6	-1.5	-0.6	-0.5	0.0	0.2	-0.1	-3.2
$P_3 \times P_2$	1.5	-0.5	0.0	0.5	3.0	0.1	0.0	1.0
$P_4 \times P_2$	0.6	0.0	-0.3	0.0	1.0	0.0	0.0	1.3
$P_5 \times P_2$	0.5	0.0	0.2	0.0	-1.0	-0.0	-0.0	1.3
$P_6 \times P_2$	-0.5	-0.5	0.1	0.5	3.0	0.0	-0.3	-0.7
$P_4 \times P_3$	0.6	0.5	-0.1	0.5	-4.0	-0.2	-0.0	-1.4
$P_5 \times P_3$	0.6	0.0	-0.1	0.0	1.0	0.0	0.5	-1.7
$P_6 \times P_3$	-0.3	0.5	-0.4	0.5	0.5	-0.0	-0.0	-3.2
$P_5 \times P_4$	-3.2	0.0	-0.1	0.0	8.0	0.2	-0.0	0.0
$P_6 \times P_4$	-0.5	-0.5	0.2	-0.5	-1.0	-0.0	0.1	1.6
$P_6 \times P_5$	-0.5	-0.5	0.3	-0.5	0.0	0.0	-0.1	1.0
S.E.	0.73	1.26	0.57	1.48	0.50	0.29	0.55	0.73

those with high yield. According to East (1936), hybrid vigour may also be due to accumulation and fixation of favourable genes, the maximum number of which is brought together in the F_1 hybrids, but the intensity of action of certain genes which manifest heterosis may be very low as a result of inbreeding.

Heterosis for these yield components has an important relationship with heterosis for grain yield. The crosses expressing significant and positive heterosis for yield per plant had significant and positive heterosis for some yield components. In F_1 generation significant and positive heterosis, particularly for spike length, spikelets per spike, seeds per spike, yield per spike and seed index was most frequently associated with significant and positive heterosis for yield per plant (Table 2). Similar positive relationship between heterosis for yield per plant and heterosis for yield components was reported by Larik et al. (1988, 1992).

When the heterosis for the crosses was compared with their SCA effects, it was observed that both were positively related. The crosses $P_1 \times P_2$, $P_2 \times P_4$, $P_4 \times P_6$, $P_5 \times P_6$, $P_2 \times P_1$, $P_3 \times P_1$, $P_4 \times P_1$ and $P_5 \times P_1$ had significant estimates of both SCA effects and heterosis for yield per plant (Table 4). Significant estimates of both heterosis and SCA effects suggest predominance of non-additive gene action for yield per plant in these crosses. Selection through conventional breeding methods would not be effective in these crosses, alternatively development of hybrid variety might be a good choice.

2. Combining ability

The analysis of variance for general combining ability (GCA), specific combining ability (SCA), and reciprocal effects (RE) are presented in Table 5. Both GCA and SCA variances were highly ($P<0.01$) significant for plant height, spike length, seeds per spike and single plant yield, whereas GCA was only significant ($P<0.05$) for fertile tillers per plant. RE were highly significant ($P<0.01$) for plant height, seeds per spike and single plant yield. GCA variance contains additive and additive × additive epistasis while SCA variance contains dominance and additive × dominance, dominance × dominance epistasis (Griffing 1956; Baker 1978), so the significant estimates of GCA and SCA variances suggest that both additive and non-additive gene actions were involved in controlling these characters in the present materials. The variance for GCA were larger than those of SCA for

Table 5. Analysis of variance (mean squares) for combining ability in F_1 generation

Source of variation	d.f.	Plant height	Fertile tillers/ plant	Spike length	Spikelets/ spike	Seeds/ spike	Yield/ spike	Seed index	Single plant yield
GCA	5	102.45**	5.08*	1.82**	1.38	29.60**	0.04	0.02	34.97**
SCA	9	39.87**	1.82	1.41**	1.19	42.46**	0.05	0.04	8.38**
Recip.	15	2.46**	1.03	0.10	0.56	15.93**	0.01	0.01	7.28**
Error	70	0.73	2.12	0.44	2.94	0.34	0.12	0.49	0.72
GCA: SCA		2.56:1	2.79:1	1.29:1	1.15:1	0.69:1	0.80:1	0.45:1	4.17:1

*, ** Significant at 5% and 1% level of probability, respectively.

all the traits, which suggest that the major portion of genetic variability in the base population was additive in nature. Higher estimates of non-additive genetic variance were noticed only for seeds per spike (Table 5). These results suggest that the yield components were predominantly controlled by additive gene action. But seeds per spike were mainly controlled by non-additive gene action.

Mean squares due to reciprocal effects were non-significant for tillers per plant, spike length, spikelets per spike, yield per spike and seeds index indicating the presence of reciprocal differences among the hybrids studied. The preponderance of additive genetic variation for five traits in F_1 generation indicated that the parents involved in these crosses may be selected out on the basis of their GCA. The importance of additive and non-additive gene action for these quantitative traits in hexaploid wheat has also been reported by Larik et al. (1992) and Sharma and Singh (1986).

3. GCA effects of the parents

Estimates of GCA effects of the parents are shown in Table 6. It is evident that parents Z.A.77 and T.J. 83 were good general combiners for single plant yield and other yield components. The parents Z.A.77 had significant GCA for all yield components and single plant yield. T.J.83 displayed similar results except plant height. The parents Mon's and Z.A.77 had significant effects for tallness and were good general combiner for this trait, while parents Blue Silver showed the highest GCA effects for dwarfness and can be exploited for breeding dwarf genotypes. Parent Vee's was good general combiner for spike length and seeds per spike (Table 6). It was observed that the significant GCA effects of the parents, Z.A.77 and T.J.83 for single plant yield were associated with the significant GCA effects for some of the yield components. Such positive association of GCA effects for yield components with GCA effects for single plant yield of spring wheat was also reported by Liu et al. (1989). This suggests that assessment on GCA effects for yield components has considerable importance in selecting parents for yield improvement.

4. SCA effects of the crosses

Estimates of SCA effects of the crosses (Table 4) showed that there were a good number of crosses having significant and positive SCA effects for single plant yield. The crosses were $P_1 \times P_2$, $P_2 \times P_4$, $P_4 \times P_6$, $P_5 \times P_6$, $P_2 \times P_1$, $P_3 \times P_1$, $P_4 \times P_1$, $P_5 \times P_1$, $P_4 \times P_2$ and $P_5 \times P_2$. These crosses showed also

Table 6. Estimation of general combining ability (GCA) effects in F_1 generation for various quantitative traits in bread wheat

Parents	Plant height	Tillers/ plant	Spike length	Spikelets/ spike	Seeds/ spike	Yield/ spike	Seed index	Single plant yield
P1 Vee's	-0.88	-0.88	0.20	0.08	1.12	0.05	0.01	-0.86
P2 Buc's	-1.66	0.08	0.08	-0.16	0.00	0.00	0.01	0.66
P3 Mon's	1.26	-1.04	-0.96	-0.54	-3.62	-0.14	-0.03	-3.88
P4 Z.A-77	6.64	0.83	0.18	0.70	0.75	0.02	0.06	1.53
P5 T.J-83	-0.70	0.45	0.26	0.08	1.87	0.07	0.01	1.24
P6 Blue Silver	-2.07	0.58	0.22	-0.16	-0.12	0.01	-0.06	1.30
S.E.	0.42	0.72	0.33	0.85	0.28	0.17	0.32	0.42

significant and positive SCA effects for some of the yield components. Seeds per spike showed significant SCA effects in 12 out of 30 crosses. There were differences among the arrays of parents from SCA effects of the cross. When all the characters were considered, the arrays of Mon's, Vee's and Z.A.77 had maximum number of estimates of significant SCA effects.

The crosses with significant SCA effects indicate presence of non-additive (dominance and epistasis) gene action in them. The combining ability studies indicate the existence of both additive and non-additive gene actions in the present material. Additive gene action was more prominent for yield components, while non-additive gene action was strong for single plant yield. Therefore, breeding method should be designed to exploit both additive and non-additive gene actions. Diallel selective mating of Jensen (1970) has suggested usefulness of such situation. But the method involves many crosses among diverse parents and intermating in F_1 populations, which makes it difficult for practical utilization. However, the crosses which have shown significant SCA effects for single plant yield may be used in the development of hybrid variety. Another possibility of these crosses is that the non-additive genes of the crosses would give wider transgressive segregation. Careful selection of the potential transgressive segregants through family selection would be worth while for yield improvement

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Wheat Information Service
Number 80: 20 – 25 (1995)

Transfer of rye chromosomes carrying Karnal bunt resistance to *Triticum aestivum* cv. WL711.

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Summary

The disomic addition lines of chromosomes 4R and 6R of *Secale cereale* cv. Imperial rye in *Triticum aestivum* cv. Chinese Spring were completely free from Karnal bunt disease of wheat under artificial inoculation. The rye chromosomes 4R and 6R were transferred into a high yielding but Karnal bunt susceptible bread wheat variety WL711 through backcrossing. The monosomic and disomic addition lines of 4R and 6R in WL711 also maintained resistance against a particular isolate of Karnal bunt during backcrossing whereas their euploid segregants were as susceptible as the recurrent parent. The 4R and 6R addition lines, however, were susceptible to a new isolate of *Neovossia indica* virulent on triticale. The work to substitute the rye chromosomes for their B and D wheat genome homoeologues is in progress.

Introduction

Karnal bunt caused by *Neovossia indica* (Mitra) Mundkar (Syn. *Tilletia indica*) is a very serious disease of wheat. It was first reported in Karnal, a district in northern India, in 1930 (Mitra, 1931). It appears in epidemic proportion in the north-western states of India, Pakistan and Mexico (Munjal 1975; Goel et al. 1977). Karnal bunt not only causes appreciable losses in yield but also renders grains unfit for human consumption (Sekhon et al. 1981). Aujla et al. (1982) developed a technique for artificial epiphytotic of Karnal bunt which has been used for screening wheat and related species for resistance to the disease. Only a very small proportion of durum and bread wheat lines has been found to be resistant to Karnal bunt under artificial inoculations (Gill 1987).

However, the search for genetic sources of resistance to Karnal bunt in related species of wild wheat, *Aegilops* and cultivars of rye under artificial inoculation have met with some success. Dhaliwal et al. 1986; Warham et al. 1986; Pannu et al. 1994). Chromosomes 6 and 7 of *Secale cereale* cv. Imperial rye as wheat-rye addition lines in Chinese Spring were found to carry resistance to Karnal bunt under artificial inoculations (Dhaliwal et al. 1987).

The Chinese Spring being slightly late often escapes Karnal bunt incidence even under artificial conditions. The maintenance of resistance of the rye chromosomes in a high yielding but Karnal bunt susceptible commercial wheat variety needs to be investigated before efforts could be made to transfer the resistance from the rye chromosomes.

The present investigation was undertaken to transfer the rye chromosomes carrying gene(s) for resistance to Karnal bunt in WL711, a high yielding Karnal bunt susceptible variety through backcrossing.

Materials and methods

A complete set of disomic addition lines of *Secale cereale* cv. Imperial rye in *Triticum aestivum* cv. Chinese Spring used in this study, was received from Dr. S.M.Reader, PBI, Cambridge, UK. A high yielding but Karnal bunt susceptible commercial wheat variety WL711 developed by the Punjab Agricultural University, Ludhiana was used as the recurrent parent for the transfer of rye chromosomes.

The addition lines, recipient variety WL711, F_1's and subsequent backcrossed progenies were grown in the field during wheat crop seasons 1985-94 following standard agronomic practices. The presence of rye chromosomes in successive backcross generations was monitored cytologically by fixing spikes in Carnoy's solution and preparing squashes from PMCs in 2 per cent acetocarmine. Two to three spikes of the cytologically confirmed plants were inoculated by *Neovossia indica* isolates prevalent in north India at the boot stage for screening against Karnal bunt following the technique described by Aujla et al. (1982). The data on percent incidence of Karnal bunt was recorded by counting the total number of infected grains among the inoculated heads at maturity.

Table 1. Karnal bunt incidence in *Triticum aestivum* cv. Chinese Spring-Imperial rye disomic addition lines and their F_1's with *T. aestivum* cv. WL711 under artificial inoculation conditions during 1985-86 and 1986-87

Alien addition line	Disomic addition (2n=44, 21W''+1R'')		Monosomic addition F1 plants (2n=43, 21W''+1R')			
	No. of plants inoculated	%Karnal bunt incidence*	No. of plants inoculated	Free	Susceptible	%Karnal bunt incidence*
Addition-1R	4	7.2 (37/517)	10	0	10	17.7 (350/1978)
Addition-2R	5	7.3 (35/479)	12	2	10	14.8 (123/833)
Addition-3R	3	8.4 (39/463)	10	0	10	21.1 (167/791)
Addition-4R	6	0 (0/280)	12	12	0	0 (0/842)
Addition-5R	3	3.7 (9/242)	10	0	10	11.9 (161/1355)
Addition-6R	4	0 (0/184)	3	3	0	0 (0/275)
Addition-7R	2	1.4 (2/141)	15	0	15	17.6 (303/1724)

* Figures in parentheses indicate infected/total grains in inoculated spikes.

Results

The incidence of Karnal bunt under artificial inoculations of the isolate PBW 154 to seven disomic addition lines (2n = 44, 21W" + 1R") of rye and their F_1's with WL711 is given in Table 1. Disomic addition lines with rye chromosomes 1R, 2R, 3R, 5R and 7R in Chinese Spring background and their monosomic addition lines in F_1's with WL711 were susceptible to Karnal bunt. The percentage of infection ranged from 1.4 to 21.1 as compared to 12.3 percent in Chinese Spring.

Table 2. Karnal bunt incidence in 4R and 6R monosomic addition plants and their euploid segregants in successive backcross generations under artificial inoculation conditions

Backcross generation	No. of monosomic addition plants (2n=43 21W"+1R')	% Karnal bunt incidence*	No. of euploid segregants (2n=42, 21W")	% Karnal bunt incidence*
Addition-4R				
BC_1	7	0.0 (0/182)*	9	9.6 (49/508)
BC_2	5	0.0 (0/108)	12	9.2 (57/169)
BC_3	4	0.0 (0/23)	5	12.9 (26/201)
BC_4	2	0.0 (0/176)	15	14.8 (105/710)
BC_5	4	0.0 (0/259)	41	35.4 (841/2374)
Addition-6R				
BC_1	6	0.0 (0/212)	7	10.1 (37/367)
BC_2	6	0.0 (0/216)	17	10.6 (78/736)
BC_3	7	0.0 (0/146)	14	13.0 (73/560)
BC_4	7	0.0 (0/273)	18	9.3 (85/915)
BC_5	6	0.0 (0/676)	30	29.7 (714/2406)
T.aestivum cv. WL711	-		-	22.8

* Figures in parentheses indicate infected/total grains in the inoculated spikes.

Only two out of the 12 F_1 monosomic addition plants of 2R were free while the remaining plants had an average 14.8 percent incidence. The 4R and 6R disomic addition lines and their F_1's monosomic addition with WL711 were completely free from Karnal bunt infection indicating that the chromosomes 4R and 6R of rye carry gene(s) for resistance to Karnal bunt. Karnal bunt incidence in 4R and 6R monosomic addition plants (2n = 43) and the euploid derivatives (2n = 42) in various backcross generations is given in Table 2. The monosomic addition plants carrying 4R and 6R chromosomes in all the five backcross generations were free from Karnal bunt whereas the euploid segregants were susceptible with a range of incidence from 9.2-35.4 percent. The recurrent cultivar WL711 had 22.8 per cent mean infection with a range of 9.1 to 35.5 percent over five years of testing with a particular isolate (PBW 154) of *Neovossia indica.*

However, in BC_5F_2 both the 4R and 6R monosomic addition plants and their euploid segregants were found to be susceptible on inoculation with the mixture of the previous and a new isolate (C-21) found virulent on a Karnal bunt resistant triticale variety TL1210.

In 1993-94, the BC_5F_3 plants of both the monosomic addition chromosomes were inoculated with both the fungal isolates separately. The 4R and 6R monosomic addition plants remained free from the disease incidence on inoculation with the old isolate used upto BC_5 generation (PBW 154) but were susceptible to the new isolate (C-21) showing varying degrees of infection (Table 3).

Disomic addition lines of both 4R and 6R chromosomes have been isolated from the selfed progenies of BC_5 which are completely fertile and morphologically similar to the recipient parent WL711. These lines were free from the new isolate.

Table 3. Incidence of Karnal bunt in 4R and 6R euploid, monosomic and disomic addition segregants in BC_5F_3 generation under artificial conditions against two fungal isolates during 1993-94

No. of plant	Chromosome no.	Isolate	
		% Karnal bunt	
		PBW 154	C-21
Addition-4R			
7	42	38.0	25.2
6	43	0.0	17.2
3	44	0.0	0.0
Addition-6R			
12	42	80.0	20.2
8	43	0.0	30.0
1	44	0.0	0.0

Discussion

The chromosomes 4R and 6R *Secale cereale* cv. Imperial rye which had been received as disomic addition lines in Chinese Spring from Cambridge maintained resistance to Karnal bunt. The F_1's with a highly susceptible wheat variety WL711 and BC_1 to BC_5 and subsequent selfed generations also maintained resistance against a particular isolate. Using the same set of wheat-rye disomic addition lines received from Kansas State University, Dhaliwal et al. (1987), however, found the rye chromosome 6R and 7R conferring resistance to Karnal bunt. The discrepancy in the identification of different rye chromosomes, 4R and 7R, of the same set of wheat-rye addition lines in the present and previous screening might have been either due to misclassification or mislabelling of 4R and 7R addition lines from different sources as there is considerable controversy over the correct identification of the two rye chromosomes. This could also have been due to different fungal isolates used for artificial inoculations in the two investigations.

The 4R and 6R chromosomes of Imperial rye have been transferred into susceptible variety following five backcrosses. About 98.4 per cent genetic background of the recipient variety WL711 has been reconstituted. The maintenance of resistance in the 4R and 6R addition lines during continuous screening in the different backcross generations against an isolate (PWB 154) unequivocally confirms that both 4R and 6R Imperial rye chromosomes carry dominant gene(s) for resistance to Karnal bunt.

The 4R and 6R monosomic addition lines are, however, susceptible to an isolate (C-21) of *Neovossia indica* which had shown virulence on a Karnal bunt immune triticale variety TL1210. Sources of resistance against the new virulent isolate have also been identified in the related species of *Triticum* and *Aegilops* (Pannu et al. 1994).

Acknowledgements

The authors thankfully acknowledge the financial assistance from ICAR, New Delhi, India, Sanction No. 16.18/87/-FC.II/I which made the collections, evaluations, development and utilization of alien wheat addition lines possible.

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Wheat Information Service
Number 80: 26 – 31 (1995)

Spontaneous chromosome substitutions in hybrids of *Triticum aestivum* with *T. araraticum* detected by C-banding technique

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Abstract

One hundred thirty-one plants representing twenty-nine families of *Triticum aestivum* cv. Wichita × *T. araraticum* hybrids were analyzed by the C-banding technique. Transfer of genetic material involved whole chromosome(s) or chromosome arms. Nine different types of chromosome substitution were found. The mean number of substitutions per karyotype was 1.86 (range 1-3). Substitutions involving G genome chromosomes occurred more frequently than A^t genome chromosomes. Individual chromosomes also differed in the frequency of substitution. The most frequently substituted chromosome was 6G, while substitutions with $1A^t$, $2A^t$, $4A^t$, $6A^t$, $7A^t$, 3G, and 7G were not recovered. A recombinant (rec) $7AS\text{-}7A^tL$ chromosome was identified. The spectrum of substitutions was different from those in other *T. aestivum* × *T. timopheevii* hybrids, indicating that the genotype of the parental species determines the pattern of substitutions in their hybrids.

Introduction

Triticum araraticum Jakubz. is a wild tetraploid wheat with the genome formula A^tA^tGG. Morphologically similar to *T. dicoccoides*, *T. araraticum* differs from it in karyotype structure (Badaeva et al. 1986; Gill and Chen 1987; Jiang and Gill 1994). At present, there is no consensus opinion on the origin of these two wheat species. According to one hypothesis, *T. dicoccoides* and *T. araraticum* were derived from the common ancestor by introgressive hybridization with unknown diploid species (Gill and Chen 1987). On the other hand, there is much evidence that these species had independent origins (Jiang and Gill 1994).

Analysis of substitution types in common wheat × *T. araraticum* hybrids may provide an insight into genetic interrelationships between the A and B genomes of *T. dicoccoides* and the A^t and G genomes of *T. araraticum*. In addition, *T. araraticum* has agronomically valuable traits such as pest resistance and restorer genes for cytoplasmic male sterility and, as a consequence, may be used as a donor of these properties. The determination of chromosomal substitution patterns in the karyotypes of hybrids may be also useful in breeding work.

Materials and methods

Thirty families, consisting of one hundred thirty-six plants, were derived from two independent crosses of *Triticum aestivum* L. em Thell. cvs. Wichita (WI) and Newton (NWT) with *T. araraticum* (Fig. 1). The used accession of *T. araraticum.*, TA 39 from Iraq, is maintained at the Wheat Genetics Resource Center, Kansas State University, Manhattan, Kansas, USA. From two to 13 plants were analyzed in each family. A modified C-banding technique was used for karyotype analysis (Badaeva et al. 1994). Chromosomes of common wheat, *T. aestivum*, and *T. araraticum* were classified according to genetic nomenclature (Gill et al. 1991; Badaeva et al. 1991).

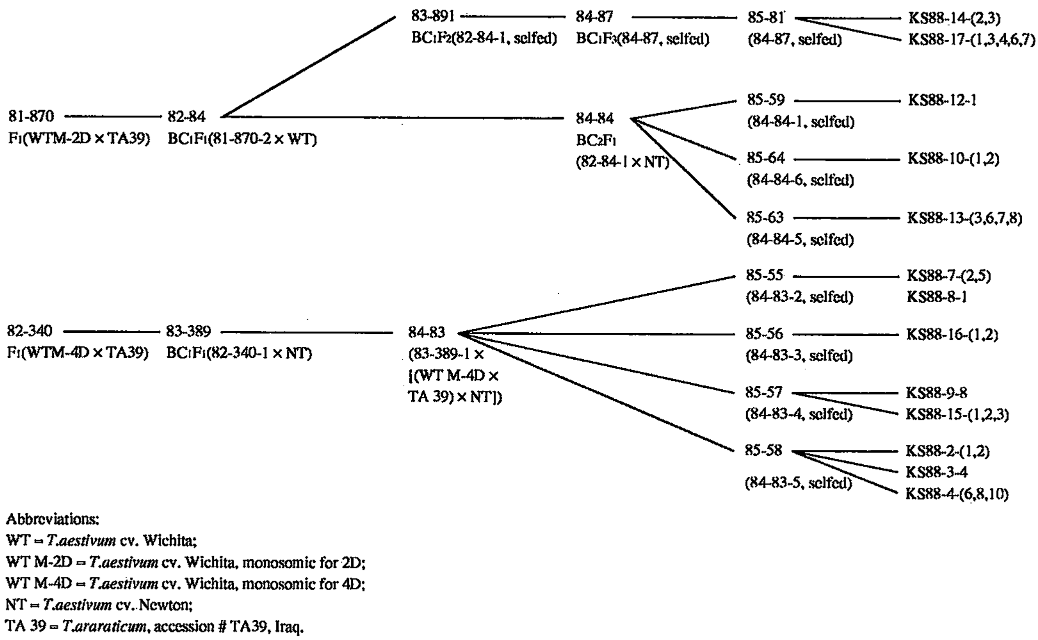

Fig. 1. A pedigree of the studied families.

Results and discussion

Cytogenetic analysis of hybrid lines showed that the majority of plants had a chromosome number of 2n=42 (Fig. 2a). Two plants were exceptional. Plant #4 of KS88-9-8 with 2n=43 had a 5G(5B) 6G(6B) double disomic substitution and 4G monosomic addition. Plant #3 of KS88-14-3 with 2n=41 was monosomic for 1G(1B) and had a double disomic $5A^t$(5A) 6G(6B) substitution.

Twenty-six plants from eight families shared the common chromosome rec 7AS-$7A^t$L. Two plants of KS88-16-2 had one 6B and one 6G chromosome. Telocentric 5BL chromosome in homozygous or heterozygous state was discovered in 11 plants of six families. Twenty-eight plants belonging to nine families had a terminal deletion of 1BL (Fig. 2b). The modified 1B chromosome was present in homozygous condition in all plants of KS88-17-1 and KS88-17-6, and was found in homozygous or heterozygous condition in a few plants of the other families. The number of substitutions per karyotype ranged from 0 to 3, and nine different substitution types were recovered (Table 1).

The first type was found only in the KS88-2-2 family, where six plants were homozygous and one plant was heterozygous for rec 7AS-7A^{t}L chromosome. This chromosome had telomeric and subtelomeric bands in the short and a faint proximal band near the centromere in the long arm which were typical of normal chromosome 7A. A large intercalary C-band in the distal half of the 7A^t long arm indicates that the cross-over site was probably located in the proximal part of the long arms of 7A and 7A^t. Two types of single disomic substitutions were found. Single 2G(2B) disomic substitutions were identified in five families. In four of these families the rec 7A-7A^t chromosome was also present. Single disomic 6G(6B) substitution was found in six families. In KS88-16-2, one plant was heterozygous for the rec 7A-7A^t chromosome.

There were two types of double disomic substitution. Double disomic substitution 3A^t(3A) 6G(6B) was found in all plants of KS88-7-2 family. One plant of KS88-14-3 and one plant of KS88-17-6 had a 1G(1D) 6G(6B) double disomic substitution.

Three types of triple disomic substitution differed in their frequency of distribution. Triple disomic substitution 4G (4D) 5G(5B) 6G(6B) was only found in KS88-9-8. The 3A^t(3A) 2G(2B) 6G(6B) triple disomic substitution with rec 7A-7A^t chromosome was represented by two families. Triple disomic substitution 1G(1D) 5A^t(5A) 6G(6B) (Fig. 2a) was the most frequent, and was present in ten families (Table 1).

Table 1. Types of chromosome substitution in *T. aestivum* cv. Wichita × *T. araraticum* TA 39 hybrid families

Type of substitution	Families
rec 7A-7A^t	KS88-2-2
Single substitutions:	
2G(2B)	KS88-2-1, KS88-3-4, KS88-4-(6, 8, 10)
2G(2B) and rec 7A-7A^t	
6G(6B)	KS88-10-2, KS88-12-1, KS88-13-(3, 6, 7, 8), KS88-16-2
Double substitutions:	
3A^t(3A), 6G(6B)	KS88-7-2
1G(1D), 6G(6B)	KS88-14-3, plant #4; KS88-17-6, plant#3
Triple substitutions:	
4G(4D), 5G(5B), 6G(6B)	KS88-9-8
3A^t(3A), 2G(2B), 6G(6B) with rec 7A-7A^t	KS88-7-5, KS88-8-1
1G(1D), 5A^t(5A), 6G(6B)	KS88-14-(2, 3), KS88-15-(1, 2,3), KS88-17-(1, 3, 4, 6, 7)

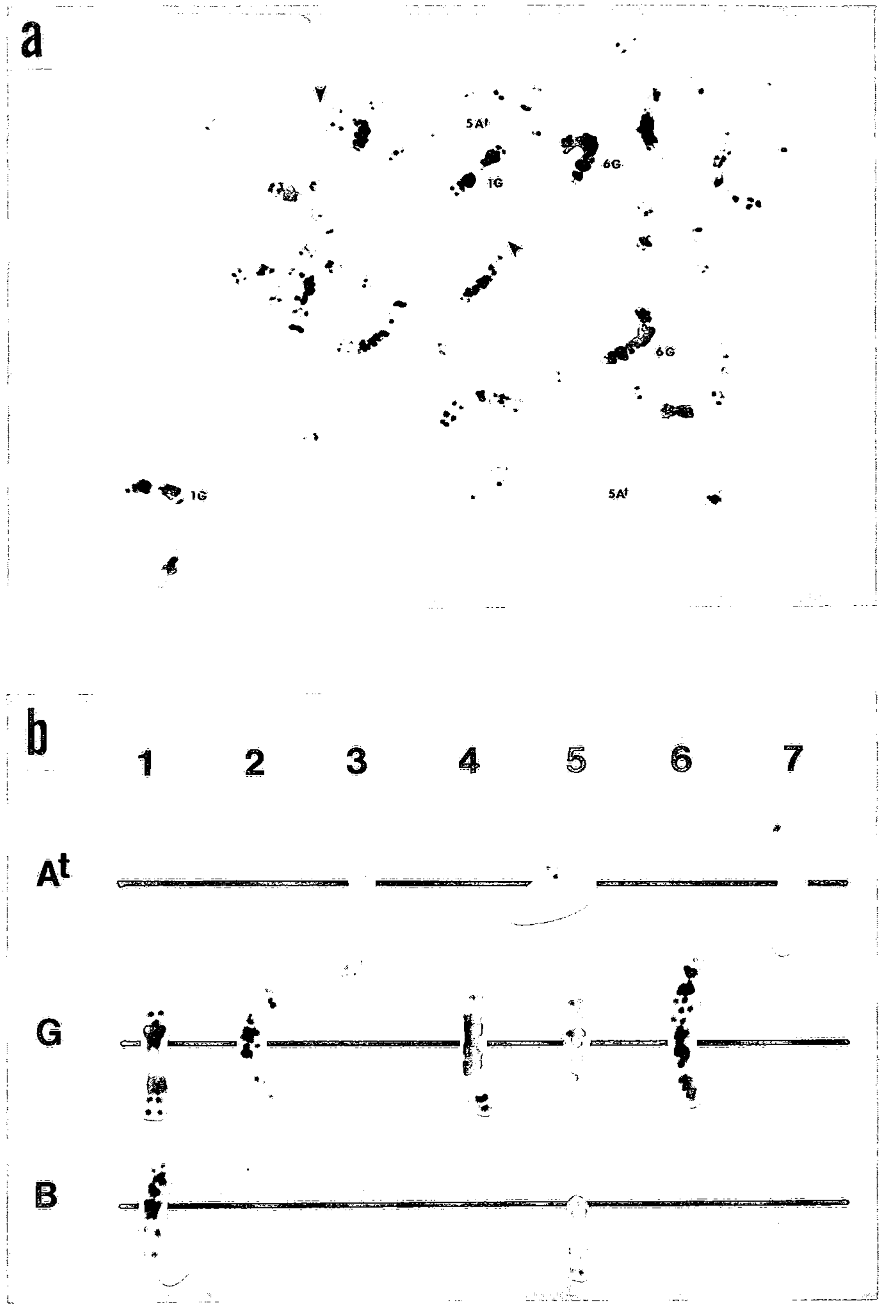

Fig. 2. a: A metaphase cell of KS88-17-6. Only the chromosomes of *T. araraticum* are indicated, and the 1B chromosomes with telomeric deletion are arrowed; b: The A^t- and G-genome chromosomes of *T. araraticum* and modified B-genome chromosomes of *T. aestivum*, which were present in different hybrid families.

Some of these substitution types were discovered in previous hybrid generations by Gill et al. (1988). However, they did not identify the rec 7A-7A^t chromosome, the 1G(1D) 6G(6B) double disomic substitution, and the 3A^t(3A) 2G(2B) 6G(6B) triple disomic substitution with rec 7A-7A^t chromosome. The substitution type 1G(1D) 5A^t(5A) 6G(6B) was described as ?G(5A) 6G(6B) in the previous study in which N-banding was used for chromosome identification. The N-banding technique does not permit differentiation between some A, A^t, and D genome chromosomes, including 1D and 5A^t.

The spectrum of substitutions of *T. aestivum* cv. Wichita × *T. araraticum* was different from those in hybrids derived from other cultivars (Badaeva et al. 1991). The genotypes of parental forms may have influenced the substitution pattern of their derivatives.

Individual *T. araraticum* chromosomes differed in the frequency of substitution. Chromosome 6G was the most frequently substituted (24 families). High frequencies of substitution were also found for chromosomes 1G and 5A^t (10 families each), 2G(7 families), and 3A^t (3 families). Substitutions of chromosomes 4G and 5G were present in one family, while substitutions involving other *T. araraticum* chromosomes were not recovered (Fig. 2b). Although rearrangements, involving A and A^t gemone chromosomes, were possible they could not be detected by cytological methods due to the absence of marker bands. These results are in agreement with data on substitutions in *T. aestivum* × *T. timopheevii* hybrids (Badaeva et al. 1991). The high frequency of substitutions involving 5A^t and 1G chromosomes in the present material is probably due to the common origin of families with this substitution type.

Based on the results of Badaeva et al. (1991) and present study, we found that some chromosomes have a high frequency of substitution while others are rarely involved in substitutions in different *T. aestivum* × *T. timopheevii* cross combinations. We compared these results with data on species-specific chromosomal rearrangements, which occurred during the speciation of the two tetraploid wheat species (Naranjo et al. 1987; Jiang et al. 1994). In durum wheat, the 4A-5A-7B cyclic translocation was discovered, while in Timopheevi wheat a species-specific cyclic translocation included chromosomes 6A^t, 1G and 4G. The chromosomes 4A^t, 5A^t, 6A^t, 1G, 4G, and 7G had a low frequency of substitution. A comparatively high number of 5A^t and 1G substitutions were found in only one cross combination, was due to the common origin of the lines. These data indicated that the frequency of substitutions between two homoeologous chromosomes correlates with the level of their genetic diversity. The *T. araraticum* accession TA 39 used in this study is characterized by high resistance to leaf rust (04C). Although the derivatives of the crosses with Wichita have not yet been evaluated, some of the lines may have inherited resistance from *T. araraticum* and they will be useful in breeding programs.

Acknowledgements

The authors thank to W.J. Raupp for critical reading of the manuscript. This investigation was supported by a special USDA grant to WGRC. Contribution no. 95-190-J from the Kansas Agricultural Experimental Station, Kansas State University, Manhattan.

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Wheat Information Service
Number 80: 32 – 36 (1995)

Partial amphiploids from *Triticum durum* × *Elytrigia intermedia* and *T.durum* × tetraploid *Elytrigia elongata*

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Summary

Stable hexaploid × *Trititrigia* lines were obtained from the derivatives of two crosses, i.e. (*Triticum durum* × *Elytrigia intermedia*) × *T.durum* and (*T.durum* × *E.elongata* 4x) × *T.durum*. The number of chromosomes in the root-tip cells was 42 and that of bivalents at metaphage I in PMC was 21. The hexaploid × *Trititrigia* from *E.intermedia* might involve three types of genomic constitution (AABBXX, $AABBE_1E_1$ and $AABBE_2E_2$), whereas that from tetraploid *E. elongata* might involve two types ($AABBE_1E_1$ and $AABBE_2E_2$).

Introduction

The wild relatives of wheat have been considered as a useful reservoir of agronomic genes in wheat breeding. One underutilized genetic source is the genus *Elytrigia* (Schulz-Schaeffer and Haller 1988).

Wild species of the genus *Elytrigia* is an important source for improving the agronomic characteristics of wheat. Among the possible genetic sources are for resistance to wheat streak mosaic virus and barley yellow dwarf virus, resistance to rust and tolerance to salt stress (Friebe et al. 1992). Agroromic characteristics of *Elytrigia* including cold, salt, drought, pest and disease resistance could be transferred into wheat. Amphiploids were obtained by chromosome doubling of F_1 hybrids. Another kind of amphiploid from wheat–*Elytrigia* crosses was recovered in the backcross derivatives (Sharma et al. 1987). Cauderon (1977) backcrossed *T.aestivum* × *E. intermedia* F_1 twice with wheat and, through the selection for fertility obtained a partial amphiploid with three genomes of common wheat and one genome of *E.intermedia*. In order to produce hexaploid × *Trititrigia*, we made crosses and backcrosses between *T.durum* and *E.intermedia* and between *T.durum* and tetraploid *E.elongata*. Chromosome pairings of the hybrids in F_1 and BC_1F_1 plants were studied. In this article, the new production of hexaploid × *Trititrigia* is reported.

Material and methods

Seeds of *Triticum durum* Desf. cultivars Italy363, Kekereiter, Yenminmai and *Elytrigia intermedia* (Host) Nevski (*Thinopyrum intermedium* (Host) Barkwath and Dewey) were obtained from Hei Long Jing Academy of Agricultural Sciences, Harbin, China. Tetraploid *Elytrigia elongata* (Host) Nevski (*Thinopyrum intermedium* (Host) Barkwath and Dewey) was obtained from Northwest

Institute of Botany, ShanXi province and Academia Sinica. The initial hybrids between *T.durum* and *E.intermedia* and tetraploid *E.elongata* were produced by Han et al. (1993) and Han and Li (1993), respectively. The BC_1F_1 plants were obtained by backcrossing of F_1 hybrids with *T.durum* as male parent. Embryo culture was used to hasten the generation cycle on MS medium. The chromosome numbers were determined from root tip squashes. For meiotic analysis, suitable spikes were fixed in Carnoy's fixative (6:3:1). Pollen mother cells were stained with iron-hematoxylin and squashed in 45% acetic acid.

Results and discussion

1. Production of hexaploid × *Trititrigia* from *Elytrigia intermedia.*

The seed sets in the crosses *T.durum* cv Italy363 × *E.intermedia* and *T.durum* cv Kekereiter × *E.intermedia* were 47.7% and 28.1%, respectively. Morphology of the F_1 hybrids was intermediate between parents and the hybrids were vigorous but self sterile. BC_1 seed set on the F_1 hybrids using Italy363, Kekereiter, Yenminmai pollen was much lower (0.5% - 2.3%) than the F_1 seed set, probably because only unreduced (complete or partial) gametes formed by rare restitution in the F_1 hybrids functioned. Chromosome number of 37 BC_1F_1 plants checked varied from 38 to 49. Twenty-five plants (67.6%) having 2n=49 were likely derived from unreduced gametes of the F_1

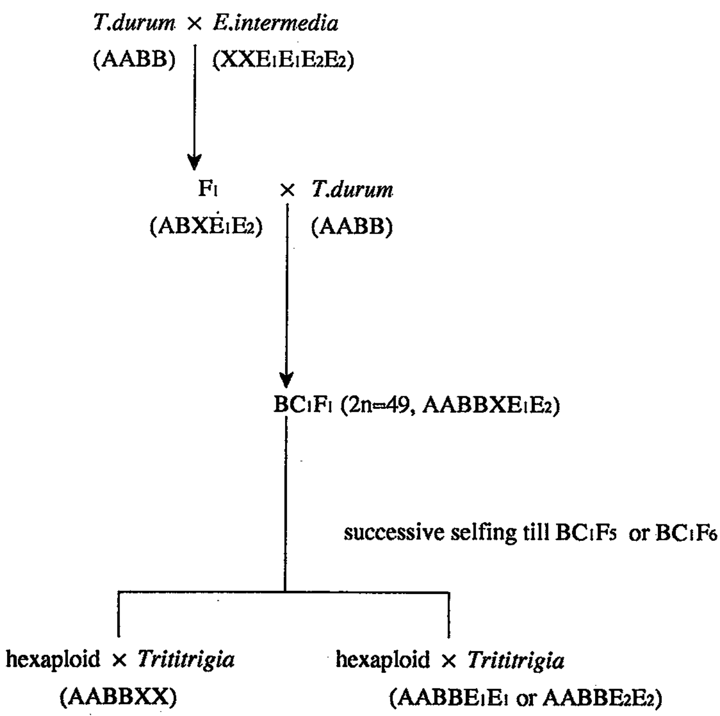

Fig. 1. Synthetic process of hexaploid × *Trititrigia* from *E.intermedia.*

hybrids. In the F_1 hybrids, chromosome pairing averaged $21.4_{I} + 5.6_{II} + 0.8_{III}$. In the BC_1F_1 plants (2n=49), chromosome pairing averaged $11.2_{I} + 17.9_{II} + 0.6_{III}$ (Han et al. 1993). The genomic constitution of the F_1 hybrid was $ABXE_1E_2$ and that of the BC_1F_1 was $AABBXE_1E_2$. The BC_1F_1 plants showed a low self fertility (6.3%). Progeny of the BC_1F_1 plants were successively selfed to F_5 or F_6 generations. The derivatives showed normal fertility and a high incidence of bivalents in meiosis of progeny of F_6 generation, from which a partial amphiploid was isolated. In the BC_1F_1, the genomes of AABB might have played an important role as pivotal genomes with cushioning action, which in turn produced progeny and hexaploid × *Trititrigia* were obtained by selection (Fig. 1). The production of the hexaploid × *Trititrigia* opened a new possibility of gene flowing from *E.intermedia* to wheat and of developing alien addition and substitution lines for useful characteristics.

2. Production of hexaploid × *Trititrigia* from *E.elongata* 4x.

The seed set in the crosses *T.durum* cv. Italy363 × tetraploid *E.elongata* was rather low (1.4%). Morphology of the F_1 hybrids was intermediate between parents and the hybrids were perennial but self sterile. Chromosome pairing in the F_1 hybrids averaged $13.8_{I} + 6.9_{II} + 0.2_{III}$. BC_1 seed set on the F_1 hybrids using Italy363, Kekereiter and Yenminmai pollen was low (11.2%). Chromo

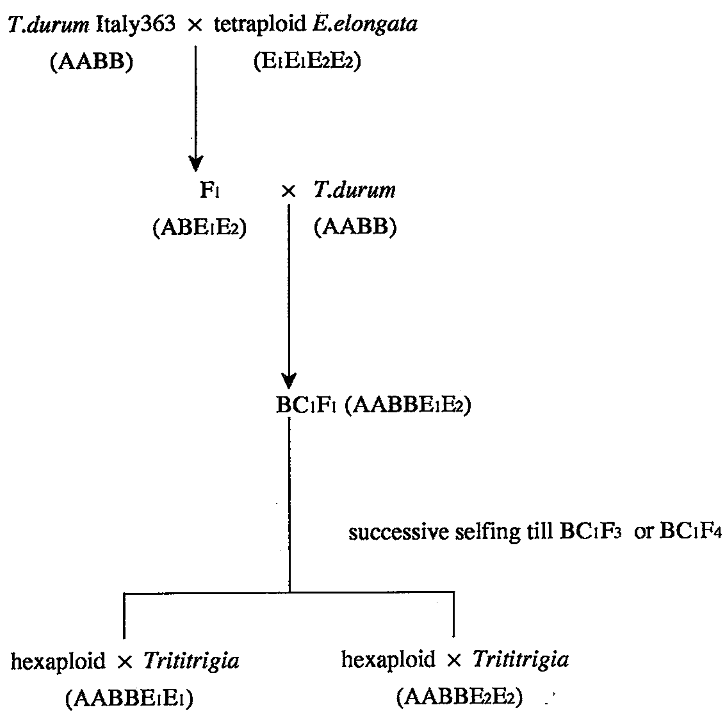

Fig. 2. Synthetic process of hexaploid × *Trititrigia* from tetraploid *E.elongata*.

some number was 42 in root tip cells of the BC_1F_1 plants and the chromosome pairing averaged $7.5_{I} + 17.1_{II} + 0.1_{III}$. The BC_1F_1 plants had a low self fertility (29.6%). One BC_1F_1 plant showed a high self fertility (71%). All of the BC_1F_2 plants derived from the self-fertilized BC_1F_1 plant had 2n=40–42. The derivatives obtained in the process of successive self-fertilization showed normal fertility and a high incidence of bivalents in meiosis. The BC_1F_1 plants in our study were apparently derived from the fusion of an unreduced gamete of the F_1 hybrid with a normal gamete of *T.durum*. Charpentier, Cauderon, Feldman (1988) proposed $E_1E_1E_2E_2$ as the genomic constitution for tetraploid *Elytrigia elongata*. The genomic constitution of the F_1 hybrids thus was ABE_1E_2 and that of the BC_1F_1 plants was $AABBE_1E_2$. The genomes of AABB might play a role as a pivotal genome in these plants. Its derivatives would be $AABBE_1E_1$ or $AABBE_2E_2$. These are, therefore, partial amphiploid, hexaploid × *Trititrigia* (Fig. 2).

3. Morphology and agronomic characteristics of hexaploid × *Trititrigia*.

The hexaploid × *Trititrigia* lines had shorter spike internodes, larger spikelets than *E.intermedia* and tetraploid *E.elongata*. The hexaploid × *Trititrigia* from *E.intermedia* had an erect growth habit.

Table 1. Morphology and agronomic characteristics of hexaploid × *Trititrigia*

	E.intermedia			*E.elongata* 4x	
	8704-1-89*	363-1-21	8703-1-89	88001	88002
Plant height (cm)	88.5 ± 5.5	84.3 ± 2.9	95.1 ± 4.0	77.1 ± 3.0	73.6 ± 2.4
Number of ear per plant	32.2 ± 8.9	20.3 ± 6.9	27.6 ± 7.8	16.5 ± 2.6	15.6 ± 3.4
Flag leaf length (cm)	27.8 ± 4.7	19.4 ± 3.2	25.1 ± 5.3	14.5 ± 2.7	16.9 ± 2.5
Flag leaf width (cm)	1.9 ± 0.1	1.2 ± 0.2	1.6 ± 0.3	0.9 ± 0.1	1.1 ± 0.1
Ear length (cm)	19.8 ± 1.1	13.4 ± 1.9	17.6 ± 2.3	11.5 ± 1.5	13.7 ± 1.4
Number of spikelets/ear	18.6 ± 1.4	18.7 ± 1.3	17.0 ± 1.7	15.9 ± 2.1	16.9 ± 3.1
Spike internode length (cm)	1.0 ± 0.1	0.7 ± 0.1	1.1 ± 0.1	0.79± 0.1	0.9 ± 0.1
Spikelet length (cm)	1.9 ± 0.1	1.8 ± 0.1	2.0 ± 0.1	1.9 ± 0.1	1.8 ± 0.1
Selfed seed fertility (%)	75.3 ±10.4	76.4 ± 3.4	41.5 ±10.2	83.6 ± 0.3	86.5 ± 6.5
Awn type (cm)	7.5 ± 0.6	8.4 ± 0.3	8.6 ± 0.9	4.1 ± 0.2	None

* Blue grain

The line of 8704-1-89 survived for three years and exhibited strong heterosis, vigorous tillering, and flowering lasted for several weeks. The line of 363-1-21 showed strong resistance to powdery mildew. The hexaploid × *Trititrigia* from tetraploid *E.elongata* lacked an erect growth habit and had similar growth habit to Chinese Spring. During flowering, they had yellow and purple anthers. Their seeds showed a color similar to tetraploid *E.elongata.* The hexaploid × *Trititrigia* from *E.intermedia* and *E.elongata* 4x showed strong resistance to rust, barley yellow dwarf virus and good quality. They expressed high crossability with common wheat and octoploid × *Trititrigia.* The plant height, number of ears per plant, spikelet length, awn length and other agronomic characteristics are shown in Table 1.

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1993

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(         76)
ACCN:001285952    CTLN:3524874
ABSJ:G (Genetics Abstracts)
AUTH:Zaghmout, O.M.-F.;Trolinder, N.L.
AFFN:USDA-ARS, P.O. Box 215, Route #3, Lubbock, TX 79401, USA
TITL:Factors affecting transient gene expression in protoplasts isolated
     from very slowly growing embryogenic callus cultures of wheat
     (Triticum aestivum L.)
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 86, no. 6, pp. 721-730
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(         77)
ACCN:001286062    CTLN:3524984
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Chauvin, L.-P.;Houde, M.;Sarhan, F.*
AFFN:Dep. Sci. Biol., Univ. Quebec Montreal, C.P. 8888, Succ. 'A', Montreal,
     PQ H3C 3P8, Canada
TITL:A leaf-specific gene stimulated by light during wheat acclimation to
     low temperature
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1993
HCOL:vol. 23, no. 2, pp. 255-265
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(         78)
ACCN:001286070    CTLN:3524992
ABSJ:G (Genetics Abstracts)
AUTH:Takada, H.;Uchiyama, Y.
AFFN:Hokkaido Natl. Agric. Stn. Sapporo 062, Japan
TITL:Varietal difference of sterility induced by high temperature in wheat
HTIL:JAP. J. BREED.
HSSN:0536-3683
HYER:1993
HCOL:vol. 43, no. 1, pp. 107-112
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(         79)
ACCN:001286125    CTLN:3525047
ABSJ:G (Genetics Abstracts)
AUTH:Endo, S.;Okada, K.;Seko, H.
AFFN:Nisshin Flour Milling Co., Food Res. Cent., Ohi, Saitama 354, Japan
TITL:Comparison of structure of the kernel cross-section and gliadin
     components between registered Japanese and Australian wheat cultivars
HTIL:JAP. J. BREED.
HSSN:0536-3683
HYER:1993
HCOL:vol. 43, no. 1, pp. 29-40
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(         80)
ACCN:001286197    CTLN:3525119
ABSJ:G (Genetics Abstracts)
AUTH:Nakamura, T.;Yamamori, M.;Hirano, H.;Hidaka, S.
AFFN:Tohoku Natl. Agric. Exp. Stn., Akahira 4, Shimokuriyagawa, Morioka,
     Iwate 020-01, Japan
TITL:Identification of three Wx proteins in wheat (Triticum aestivum L.)
HTIL:BIOCHEM. GENET.
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HSSN:0006-2928
HYER:1993
HCOL:vol. 31, no. 1-2, pp. 75-86

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(81)
ACCN:001287018 CTLN:3526076
ABSJ:G (Genetics Abstracts)
AUTH:Bjoernstad, Aa.;Skinnes, H.;Uhlen, A.-K.;Marum, P.;Maroy, A.-G.
AFFN:Dep. Crop Sci., Agric. Univ. Norway, N-1432 As, Norway
TITL:Genetic marker segregations in doubled haploids in spring wheat crosses
HTIL:HEREDITAS
HSSN:0018-0661
HYER:1993
HCOL:vol. 118, no. 1, pp. 55-62

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(82)
ACCN:001287020 CTLN:3526078
ABSJ:G (Genetics Abstracts)
AUTH:Peltonen, J.;Salopelto, J.;Rita, H.
AFFN:Dep. Plant Prod., Univ. Helsinki, Viikki, SF-00710 Helsinki, Finland
TITL:The optimal combination of HMW glutenin subunits coded at gene loci Glu-A1 and Glu-B1 for bread-making quality in Scandinavian wheats
HTIL:HEREDITAS
HSSN:0018-0661
HYER:1993
HCOL:vol. 118, no. 1, pp. 71-78

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(83)
ACCN:001287023 CTLN:3526081
ABSJ:G (Genetics Abstracts)
AUTH:Winfield, M.;Davey, M.R.;Karp, A.*
AFFN:Dep. Agric. Sci., Univ. Bristol, AFRC Inst. Arable Crops Res., Long Ashton Res. Stn., Long Ashton, Bristol BS18 9AF, UK
TITL:A comparison of chromosome instability in cell suspensions of diploid, tetraploid and hexaploid wheats
HTIL:HEREDITY
HYER:1993
HCOL:vol. 70, no. 2, pp. 187-194

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(84)
ACCN:001295105 CTLN:3534927
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Szurmak, B.;Dobrzanska, M.*
AFFN:Inst. Biochem. and Biophys., Polish Acad. Sci., 36 Rakowiecka, 02-532 Warsaw, Poland
TITL:A large DNA repeat of the dispersion pattern common to wheat and rye genomes
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1993
HCOL:vol. 21, no. 5, pp. 919-921

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(85)
ACCN:001297194 CTLN:3537637
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Saini, R.G.;Shiwani;Preet, K.;Kaur, M.;Gupta, A.K.
AFFN:Dep. Genet., Punjab Agric. Univ., Ludhiana-141004, India
TITL:Genetic basis of resistance to leaf rust of wheat in the Indian sub-continent
HTIL:CROP IMPROV.
HSSN:0256-0933
HYER:1993
HCOL:vol. 20, no. 2, pp. 131-138

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(86)

ACCN:001301088   CTLN:3540869
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Mudgett, M.B.;Clarke, S.*
AFFN:Dep. Chem. and Biochem. and Mol. Biol. Inst., Univ. California, Los Angeles, CA 90024, USA
TITL:Characterization of plant L-isoaspartyl methyltransferases that may be involved in seed survival: Purification, cloning, and sequence analysis of the wheat germ enzyme
HTIL:BIOCHEMISTRY (WASH.)
HSSN:0006-2960
HYER:1993
HCOL:vol. 32, no. 41, pp. 11100-11111

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(87)
ACCN:001301090   CTLN:3540871
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Youssefian, S.;Nakamura, M.;Sano, H.
AFFN:Lab. Mol. Genet., Biotechnol. Inst., Akita Prefectural Coll. Agric., Ohgata 010-04, Akita, Japan
TITL:Tobacco plants transformed with the O-acetylserine (thiol) lyase gene of wheat are resistant to toxic levels of hydrogen sulphide gas
HTIL:PLANT J.
HSSN:0960-7412
HYER:1993
HCOL:vol. 4, no. 5, pp. 759-769

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(88)
ACCN:001301158   CTLN:3540939
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Metz, A.M.;Browning, K.S.*
AFFN:Dep. Chem. and Biochem., Univ. Texas, Austin, TX 78712, USA
TITL:Sequence of a cDNA encoding wheat eukaryotic protein synthesis initiation factor 4A
HTIL:GENE
HSSN:0378-1119
HYER:1993
HCOL:vol. 131, no. 2, pp. 299-300

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(89)
ACCN:001309623   CTLN:3549774
ABSJ:J (Microbiology Abstracts B: Bacteriology); A (Microbiology Abstracts A: Industrial & Applied Microbiology); W2(Agricultural and Environmental Biotechnology Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Pfender, W.F.;Kraus, J.;Loper, J.E.
AFFN:Dep. Plant Pathol., Kansas State Univ., Manhattan, KS 66506, USA
TITL:A genomic region from Pseudomonas fluorescens Pf-5 required for pyrrolnitrin production and inhibition of Pyrenophora tritici-repentis in wheat straw
HTIL:PHYTOPATHOLOGY
HSSN:0031-949X
HYER:1993
HCOL:vol. 83, no. 11, pp. 1223-1228

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(90)
ACCN:001310178   CTLN:3550431
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Futers, T.S.;Onde, S.;Turet, M.;Cuming, A.C.*
AFFN:Dep. Genet., Leeds Univ., Leeds LS2 9JT, UK
TITL:Sequence analysis of two tandemly linked Em genes from wheat
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1993
HCOL:vol. 23, no. 5, pp. 1067-1072

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(91)
ACCN:001313499   CTLN:3554354
ABSJ:G (Genetics Abstracts)

AUTH:Tohver, M.;Enno, T.
AFFN:Eesti Teaduste Akad. Eksperimentaalbiol. Inst., Inst. tee 11, EE-3051 Harku, Harjumaa, Estonia
TITL:Cytological and morphobiological analysis of unstable morphological wheat mutants induced by chemical mutagens.
OTIL:Keemiliste mutageenide poolt indutseeritud ebastabiilsete nisumutantide liinide morfoloogiline ja tsuetoloogiline analueues
HTIL:PROC. ESTON. ACAD. SCI. BIOL.
HSSN:0013-2144
HYER:1993
HCOL:vol. 42, no. 2, pp. 85-93

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ACCN:001314014 CTLN:3554949
ABSJ:G (Genetics Abstracts)
AUTH:Ahmad, S.D.;Narayan, R.K.J.
AFFN:Univ. Coll. Agric., Rawalakot, Poonch A.K., Pakistan
TITL:Ribosomal RNA gene spacer sequences in Lathyrus and their homology with wheat rDNA spacer sequences
HTIL:PAK. J. ZOOL.
HSSN:0030-9923
HYER:1993
HCOL:vol. 25, no. 1, pp. 79-81

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(93)
ACCN:001314200 CTLN:3555215
ABSJ:G (Genetics Abstracts); D (Ecology Abstracts)
AUTH:David, J.L.;Pham, J.-L.
AFFN:Stn. Genet. Veg., INRA-UPS, La Ferme du Moulon, 91190 Gif-sur-Yvette, France
TITL:Rapid changes in pollen production in experimental outcrossing populations of wheat
HTIL:J. EVOL. BIOL.
HSSN:1010-061X
HYER:1993
HCOL:vol. 6, no. 5, pp. 659-676

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ACCN:001319412 CTLN:3562244
ABSJ:G (Genetics Abstracts)
AUTH:Ahn, S.;Anderson, J.A.;Sorrells, M.E.;Tanksley, S.D.*
AFFN:Dep. Plant Breed. and Biomet., 252 Emerson Hall, Cornell Univ., Ithaca, NY 14853, USA
TITL:Homoeologous relationships of rice, wheat and maize chromosomes
HTIL:MOL. GEN. GENET.
HSSN:0026-8925
HYER:1993
HCOL:vol. 241, no. 5-6, pp. 483-490

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(95)
ACCN:001320372 CTLN:3563204
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Rosenberg, N.;Shimoni, Y.;Altschuler, Y.;Levanony, H.;Volokita, M.; Galili, G.*
AFFN:Dep. Plant Genet., Weizmann Inst. Sci., Rehovot 76100, Israel
TITL:Wheat (Triticum aestivum L.) gamma -gliadin accumulates in dense protein bodies within the endoplasmic reticulum of yeast
HTIL:PLANT PHYSIOL.
HSSN:0032-0889
HYER:1993
HCOL:vol. 102, no. 1, pp. 61-69

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(96)
ACCN:001333258 CTLN:3576874
ABSJ:G (Genetics Abstracts)
AUTH:Sethi, G.S.;Plaha, P.;Thakur, K.S.
AFFN:Dep. Plant Breed. and Genet., Himachal Pradesh Krishi Vishvavidyalaya,

Palampur-176 062, India
TITL:Breeding bread wheat for cold stress
HTIL:ANN. BIOL.
HSSN:0970-0153
HYER:1993
HCOL:vol. 9, no. 2, pp. 165-173

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(97)
ACCN:001333878 CTLN:3577495
ABSJ:V (Virology & AIDS Abstracts); G (Genetics Abstracts); A (Microbiology Abstracts A: Industrial & Applied Microbiology); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Singh, R.P.
AFFN:Int. Maize Wheat Improv. Cent. (CIMMYT), Lisboa 27, Apdo. Postal 6-641, 06600, Mexico, D.F.
TITL:Genetic association of gene Bdv1 for tolerance to barley yellow dwarf virus with genes Lr34 and Yr18 for adult plant resistance to rusts in bread wheat
HTIL:PLANT DIS.
HSSN:0191-2917
HYER:1993
HCOL:vol. 77, no. 11, pp. 1103-1106

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(98)
ACCN:001337455 CTLN:3580528
ABSJ:G (Genetics Abstracts)
AUTH:Bishnoi, O.P.;Behl, R.K.;Singh, K.P.
AFFN:Dep. Plant Breed., CCS Haryana Agric. Univ., Hisar-125 004, India
TITL:Character correlation and path analysis in wheat
HTIL:ANN. BIOL.
HSSN:0970-0153
HYER:1993
HCOL:vol. 9, no. 2, pp. 320-322

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(99)
ACCN:001339875 CTLN:3583273
ABSJ:G (Genetics Abstracts)
AUTH:Serebryanyi, A.M.;Zoz, N.N.
AFFN:N.N. Semenov Inst. Chem. Phys., Russian Acad. Sci., Moscow, Russia
TITL:Antioxidants increase the adaptive response of seeds during radiation mutagenesis of wheat plants
HTIL:RADIOBIOLOGIYA
HSSN:0033-8192
HYER:1993
HCOL:vol. 33, no. 1, pp. 81-87

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(100)
ACCN:001340089 CTLN:3583487
ABSJ:G (Genetics Abstracts)
AUTH:Nematullah;Jha, P.B.
AFFN:Dep. Plant Breed., Rajendra Agric. Univ., Bihar, Pusa - 848125
TITL:Effect of biparental mating in wheat
HTIL:CROP IMPROV.
HSSN:0256-0933
HYER:1993
HCOL:vol. 20, no. 2, pp. 173-178

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(101)
ACCN:001340090 CTLN:3583488
ABSJ:G (Genetics Abstracts)
AUTH:Sharma, D.L.;Guleria, S.K.;Sharma, T.R.
AFFN:HPKV Reg. Res. Stn., Bajaura, Kullu (H.P.)175 125
TITL:Studies on shade tolerance for grain yield in wheat
HTIL:CROP IMPROV.
HSSN:0256-0933
HYER:1993
HCOL:vol. 20, no. 2, pp. 169-172

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(102)
ACCN:001347533 CTLN:3591835
ABSJ:G (Genetics Abstracts)
AUTH:Miura, H.;Tanii, S.
AFFN:Dep. Crop Sci., Obihiro Univ. Agric. and Vet. Med., Obihiro, 080, Japan
TITL:Endosperm starch properties in several wheat cultivars preferred for Japanese noodles
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993-94
HCOL:vol. 72, no. 3, pp. 171-175

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(103)
ACCN:001347536 CTLN:3591838
ABSJ:G (Genetics Abstracts)
AUTH:Ahokas, H.
AFFN:Dep. Genet., P.O. Box 17 (Arkadiankatu 7), FIN-00014 Univ. Helsinki, Finland
TITL:Searching for DNA introgressed from wheat and for wheat-like grain proteins in a rice x wheat hybridization derivative
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993-94
HCOL:vol. 72, no. 3, pp. 177-182

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(104)
ACCN:001347538 CTLN:3591840
ABSJ:G (Genetics Abstracts)
AUTH:Zhong-hu, He;Rajaram, S.
AFFN:Int. Maize and Wheat Improvement Cent. IMMYT, Lisboa 27, 06600 Mexico, D.F. Mexico
TITL:Differential responses of bread wheat characters to high temperature
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993-94
HCOL:vol. 72, no. 3, pp. 197-203

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(105)
ACCN:001347643 CTLN:3591945
ABSJ:G (Genetics Abstracts)
AUTH:Gotor, C.;Romero, L.C.;Inouye, K.;Lam, E.*
AFFN:AgBiotech. Cent., Waksman Inst. Microbiol., Rutgers State Univ., Piscataway, NJ 08855, USA
TITL:Analysis of three tissue-specific elements from the wheat Cab-1 enhancer
HTIL:PLANT J.
HSSN:0960-7412
HYER:1993
HCOL:vol. 3, no. 4, pp. 509-518

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(106)
ACCN:001347765 CTLN:3592067
ABSJ:G (Genetics Abstracts)
AUTH:Elings, A.
AFFN:Genet. Resour. Unit, Int. Cent. Agric. Res. in the Dry Areas (ICARDA), P.O. Box 5466, Aleppo, Syria
TITL:Durum wheat landraces from Syria. III. Agronomic performance in relation to collection regions and landrace groups
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993
HCOL:vol. 70, no. 1-2, pp. 85-96

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(107)
ACCN:001347778 CTLN:3592080
ABSJ:G (Genetics Abstracts)
AUTH:Romani, M.;Borghi, B.;Alberici, R.;Delogu, G.;Hesselbach, J.;Salamini,

F.
AFFN:Ist. Sper. colt. Foraggere, Via Piacenza 27, 20075 Lodi, Italy
TITL:Intergenotypic competition and border effect in bread wheat and barley
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993
HCOL:vol. 69, no. 1-2, pp. 19-31

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(108)
ACCN:001347786 CTLN:3592088
ABSJ:G (Genetics Abstracts)
AUTH:Luo, M.C.;Yen, C.;Yang, J.L.
AFFN:Triticeae Res. Inst., Sichuan Agric. Univ., Dujiangyan City, Sichuan 611830, China, People's Rep.
TITL:Crossability percentages of bread wheat collections from Tibet, China with rye
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993
HCOL:vol. 70, no. 1-2, pp. 127-129

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(109)
ACCN:001347800 CTLN:3592102
ABSJ:G (Genetics Abstracts)
AUTH:Sharma, R.C.
AFFN:Dep. Agron., Inst. Agric. and Anim. Sci., Rampur, Chitwan, Nepal
TITL:Selection for biomass yield in wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993
HCOL:vol. 70, no. 1-2, pp. 35-42

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(110)
ACCN:001347801 CTLN:3592103
ABSJ:G (Genetics Abstracts)
AUTH:Shroyer, J.P.;Cox, T.S.
AFFN:Dep. Agron. Kansas State Univ., Manhattan, KS, 66502, USA
TITL:Productivity and adaptive capacity of winter wheat landraces and modern cultivars grown under low-fertility conditions
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993
HCOL:vol. 70, no. 1-2, pp. 27-33

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(111)
ACCN:001347808 CTLN:3592110
ABSJ:G (Genetics Abstracts)
AUTH:Knezevic, D.;Surlan-Momirovic, G.;Ciric, D.
AFFN:Inst. Small Grains "Kragujevac", Kragujevac, Serbia, Yugoslavia
TITL:Allelic variation at Glu-1 loci in some Yugoslav wheat cultivars
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993
HCOL:vol. 69, no. 1-2, pp. 89-94

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(112)
ACCN:001347820 CTLN:3592122
ABSJ:G (Genetics Abstracts)
AUTH:Belay, G.;Tesemma, T.;Becker, H.C.;Merker, A.
AFFN:Debre Zeit Agric. Res. Cent., Alemaya Univ. Agric., P.O. Box 32, Debre Zeit, Ethiopia
TITL:Variation and interrelationships of agronomic traits in Ethiopian tetraploid wheat landraces
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993
HCOL:vol. 71, no. 3, pp. 181-188

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(113)
ACCN:001347823 CTLN:3592125
ABSJ:G (Genetics Abstracts)
AUTH:Simane, B.;Struik, P.C.;Nachit, M.M.;Peacock, J.M.
AFFN:Dep. Agron., Wageningen Agric. Univ., Haarweg 333, 6709 RZ Wageningen, Netherlands
TITL:Ontogenetic analysis of yield components and yield stability of durum wheat in water-limited environments
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993
HCOL:vol. 71, no. 3, pp. 211-219

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(114)
ACCN:001347825 CTLN:3592127
ABSJ:G (Genetics Abstracts)
AUTH:Tesemma, T.;Becker, H.C.;Belay, G.;Mitiku, D.;Bechere, E.;Tsegaye, S.
AFFN:Alemaya Univ. Agric., Debre Zeit Agric. Res. Cent., P.O. Box 32, Debre Zeit, Ethiopia
TITL:Performance of Ethiopian tetraploid wheat landraces at their collection sites
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993
HCOL:vol. 71, no. 3, pp. 221-230

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(115)
ACCN:001353219 CTLN:3597451
ABSJ:G (Genetics Abstracts)
AUTH:Nirmal, S.C.;Sharma, S.K.*;Singh, K.P.;Kumar, J.;Tripathi, I.D.
AFFN:Dep. Genet., Haryana Agric. Univ., Hisar-125 004, India
TITL:Combining ability analysis of some high grain weight and high grain number genotypes of wheat (T. aestivum)
HTIL:ANN. BIOL.
HSSN:0970-0153
HYER:1993
HCOL:vol. 9, no. 2, pp. 224-229

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(116)
ACCN:001356970 CTLN:3602270
ABSJ:G (Genetics Abstracts)
AUTH:Wang, G.;Ji, J.;Wang, Y.-B.;Hu, H.;King, I.P.;Snape, J.W.*
AFFN:Cambridge Lab., JI Cent. Plant Sci. Res., Colney Lane, Norwich NR4 7UJ, UK
TITL:The genetic characterisation of novel multi-addition doubled haploid lines derived from triticale x wheat hybrids
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 87, no. 5, pp. 531-536

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(117)
ACCN:001356980 CTLN:3602280
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Delibes, A.;Romero, D.;Aguaded, S.;Duce, A.;Mena, M.;Lopez-Brana, I.; Andres, M.-F.;Martin-Sanchez, J.-A.;Garcia-Olmedo, F.*
AFFN:Lab. Bioquim. y Biol. Mol., ETS Ingenieros Agron.-UPM. E-28040 Madrid, Spain
TITL:Resistance to the cereal cyst nematode (Heterodera avenae Woll.) transferred from the wild grass Aegilops ventricosa to hexaploid wheat by a "stepping-stone" procedure
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 87, no. 3, pp. 402-408

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(118)

ACCN:001356986 CTLN:3602286
ABSJ:G (Genetics Abstracts)
AUTH:Ruiz, M.;Carrillo, J.M.
AFFN:Dep. Genet., E.T.S.I. Agron., Univ. Politecnica de Madrid, 28040 Madrid, Spain
TITL:Linkage relationships between prolamin genes on chromosomes 1A and 1B of durum wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 87, no. 3, pp. 353-360

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(119)
ACCN:001356994 CTLN:3602294
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Zeuli, P.L.S.;Qualset, C.O.*
AFFN:Dep. Agron. and Range Sci., Univ. California, Davis, CA 95616, USA
TITL:Evaluation of five strategies for obtaining a core subset from a large genetic resource collection of durum wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 87, no. 3, pp. 295-304

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(120)
ACCN:001357055 CTLN:3602355
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Boubaker, M.;Yahyaoui, A.;Kurauchi, N.;Yamada, T.
AFFN:Plant Breed Dep., Ecole Super. d'Agric. Kef, 7119, Le Kef, Tunisia
TITL:Variability in germplasm of wheat introduced to Tunisia for reaction to yellow rust
HTIL:JAP. J. BREED.
HSSN:0356-3683
HYER:1993
HCOL:vol. 43, no. 2, pp. 299-305

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(121)
ACCN:001376520 CTLN:3623354
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Denissen, C.J.M.
AFFN:Cent. Plant Breed. and Reprod. Res., CPRO-DLO, P.O. Box 16, NL-6700 AA Wageningen, Netherlands
TITL:Components of adult plant resistance to leaf rust in wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993
HCOL:vol. 70, no. 1-2, pp. 131-140

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(122)
ACCN:001376524 CTLN:3623358
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Chen, Xianming;Line, R.F.
AFFN:Dep. Plant Pathol., Washington State Univ. and USDA-ARS, Pullman, WA 99164-6430, USA
TITL:Inheritance of stripe rust (yellow rust) resistance in the wheat cultivar Carstens V
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993
HCOL:vol. 71, no. 1-2, pp. 107-113

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(123)
ACCN:001376528 CTLN:3623362
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology,

Mycology & Protozoology)
AUTH:Danial, D.L.;Broers, L.H.M.;Parlevliet, J.E.
AFFN:Plant Breed. Dep., Agric. Univ., P.O. Box 386, 6700 AJ Wageningen, The Netherlands
TITL:Does interplot interference affect the screening of wheat for yellow rust resistance?
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993
HCOL:vol. 70, no. 3, pp. 217-224

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(124)
ACCN:001376529 CTLN:3623363
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Arseniuk, E.;Goral, T.;Czembor, H.J.
AFFN:Dep. Plant Pathol., Plant Breed. and Acclimatization Inst., Radzikow, 05-870 Blonie, Poland
TITL:Reaction of triticale, wheat and rye accessions to graminaceous Fusarium spp. infection at the seedling and adult plant growth stages
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993
HCOL:vol. 70, no. 3, pp. 175-183

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(125)
ACCN:001381298 CTLN:3628729
ABSJ:G (Genetics Abstracts)
AUTH:Kumar, J.;Luthra, O.P.;Nirmal, S.C.
AFFN:Dep. Genet., CCS Haryana Agric. Univ., Hisar-125 004, India
TITL:Gene effects of some physiological characters in wheat (Triticum aestivum L.)
HTIL:ANN. BIOL.
HSSN:0970-0153
HYER:1993
HCOL:vol. 9, no. 1, pp. 48-51

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(126)
ACCN:001398689 CTLN:3648728
ABSJ:G (Genetics Abstracts)
AUTH:Thomas, J.B.;Schaalje, G.B.;Grant, M.N.
AFFN:Res. Stn., Agric. Canada, Lethbridge, AB T1J 4B1, Canada
TITL:Height, competition and yield potential in winter wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993-1994
HCOL:vol. 74, no. 1-2, pp. 9-17

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(127)
ACCN:001398697 CTLN:3648736
ABSJ:G (Genetics Abstracts)
AUTH:Winzeler, H.;Schmid, J.E.;Winzeler, M.
AFFN:Swiss Fed. Res. Stn. Agron. (FAP), Dep. Plant Breed., CH-8046 Zuerich, Switzerland
TITL:Analysis of the yield potential and yield components of F sub(1) and F sub(2) hybrids of crosses between wheat (Triticum aestivum L.) and spelt (Triticum spelta L.)
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993-1994
HCOL:vol. 74, no. 3, pp. 211-218

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(128)
ACCN:001398698 CTLN:3648737
ABSJ:G (Genetics Abstracts)
AUTH:Morgunov, A.;Montoya, J.;Rajaram, S.
AFFN:Int. Wheat and Maize Improvement Cent. (CIMMYT), Lisboa 27, Apdo Postal 6-641, Col. Juarez, 06600, Mexico D.F.

TITL:Genetic analysis of resistance to Karnal bunt (Tilletia indica (Mitra)) in bread wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993-1994
HCOL:vol. 74, no. 1-2, pp. 41-46

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(129)
ACCN:001399614 CTLN:3649708
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Pretorius, Z.A.;Kloppers, F.J.;Drijepondt, S.C.
AFFN:Dep. Plant Pathol., Univ. Orange Free State, Bloemfontein 9300, South Africa
TITL:Effects of inoculum density and temperature on three components of leaf rust resistance controlled by Lr34 in wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993-1994
HCOL:vol. 74, no. 1-2, pp. 91-96

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(130)
ACCN:001399615 CTLN:3649709
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Zwer, P.K.;Qualset, C.O.
AFFN:Oregon State Univ., Columbia Basin Agric. Res. Cent., P.O. Box 370, Pendleton, OR 97801, USA
TITL:Genes for resistance to stripe rust in four spring wheat varieties. 2. Adult plant responses
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993-1994
HCOL:vol. 74, no. 1-2, pp. 109-115

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(131)
ACCN:001402309 CTLN:3652527
ABSJ:G (Genetics Abstracts)
AUTH:Xie, D.X.;Devos, K.M.;Moore, G.;Gale, M.D.*
AFFN:Cambridge Lab., Colney Lane, Norwich NR4 7UJ, UK
TITL:RFLP-based genetic maps of the homoeologous group 5 chromosomes of bread wheat (Triticum aestivum L.)
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 87, no. 1-2, pp. 70-74

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(132)
ACCN:001402311 CTLN:3652529
ABSJ:G (Genetics Abstracts)
AUTH:Shu, G.;Muthukrishnan, S.;Liang, G.H.;Paulsen, G.M.
AFFN:Genet. Program, Kansas State Univ., Manhattan, KS 66506-5501, USA
TITL:Restriction fragment patterns of chloroplast and mitochondrial DNA of Dasypyrum villosum (L.) candargy and wheats
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 87, no. 1-2, pp. 44-48

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(133)
ACCN:001402731 CTLN:3652999
ABSJ:G (Genetics Abstracts); Z (Entomology Abstracts)
AUTH:Schroeder-Teeter, S.;Zemetra, R.S.;Schotzko, D.J.;Smith, C.M.;Rafi, M.
AFFN:Dep. Plant, Soil and Entomol. Sci., Univ. Idaho, Moscow, Idaho 83844, USA
TITL:Monosomic analysis of Russian wheat aphid (Diuraphis noxia) resistance in Triticum aestivum line PI137739
HTIL:EUPHYTICA

HSSN:0014-2336
HYER:1993-1994
HCOL:vol. 74, no. 1-2, pp. 117-120

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(134)
ACCN:001416629 CTLN:3666939
ABSJ:G (Genetics Abstracts)
AUTH:Kolster, P.;Krechting, C.F.;Van Gelder, W.M.J.
AFFN:Agrotechnol. Res. Inst. (ATO-DLO), P.O. Box 17, NL-6700 AA Wageningen, Netherlands
TITL:Expression of individual HMW glutenin subunit genes of wheat (Triticum aestivum L.) in relation to differences in the number and type of homoeologous subunits and differences in genetic background
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 87, no. 1-2, pp. 209-216

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(135)
ACCN:001418900 CTLN:3669334
ABSJ:G (Genetics Abstracts)
AUTH:Singh, A.K.
AFFN:Cereals Sect., Agric. Res. Inst., Patna 800001, India
TITL:Study on efficiency of rope method of pollination in wheat (Triticum aestivum L.)
HTIL:INDIAN J. GENET. PLANT BREED.
HYER:1993
HCOL:vol. 53, no. 1, pp. 101-102

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(136)
ACCN:001432734 CTLN:3683293
ABSJ:G (Genetics Abstracts)
AUTH:Pogna, N.E.;Metakovsky, E.V.;Redaelli, R.;Raineri, F.;Dachkevitch, T.
AFFN:Ist. Spe. Cerealicolt., Sec. Appl. Genet., via Cassia 176, 00191 Roma, Italy
TITL:Recombination mapping of Gli-5, a new gliadin-coding locus on chromosomes 1A and 1B in common wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 87, no. 1-2, pp. 113-121

1994

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(1)
ACCN:001310126 CTLN:3550379
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Elborough, K.M.;Simon, J.W.;Swinhoe, R.;Ashton, A.R.;Slabas, A.R.
AFFN:Lipid Mol. Biol. Group, Biol. Sci. Dep., Univ. Durham, South Rd., Durham, DH1 3LE, UK
TITL:Studies on wheat acetyl CoA carboxylase and the cloning of a partial cDNA
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1994
HCOL:vol. 24, no. 1, pp. 21-34

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(2)
ACCN:001312790 CTLN:3553592
ABSJ:J (Microbiology Abstracts B: Bacteriology); A (Microbiology Abstracts A: Industrial & Applied Microbiology); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:De Leij, F.A.A.M.;Sutton, E.J.;Whipps, J.M.;Lynch, J.M.
AFFN:Microbiol. Crop Prot. Dep., Hortic. Res. Int., Worthing Rd., Littlehampton, W. Sussex, BN17 6LP, UK
TITL:Effect of a genetically modified Pseudomonas aureofaciens on indigenous microbial populations of wheat

HTIL:FEMS MICROBIOL. ECOL.
HSSN:0168-6496
HYER:1994
HCOL:vol. 13, no. 4, pp. 249-258

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(3)
ACCN:001316979 CTLN:3559376
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts); G3(Human Genome Abstracts)
AUTH:Dever, T.E.;Wei, Chia-Lin;Benkowski, L.A.;Browning, K.;Merrick, W.C.; Hershey, J.W.B.
AFFN:Dep. Biochem., Case Western Reserve Univ. Sch. Med., Cleveland, OH 44106-4935, USA
TITL:Determination of the amino acid sequence of rabbit, human, and wheat germ protein synthesis factor eIF-4C by cloning and chemical sequencing
HTIL:J. BIOL. CHEM.
HSSN:0021-9258
HYER:1994
HCOL:vol. 269, no. 5, pp. 3212-3218

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(4)
ACCN:001317850 CTLN:3560320
ABSJ:G (Genetics Abstracts)
AUTH:King, I.P.;Reader, S.M.;Purdie, K.A.;Orford, S.E.;Miller, T.E.*
AFFN:Cambridge Lab., JI Cent., Colney Lane, Norwich NR4 7UJ, UK
TITL:A study of the effect of a homoeologous pairing promoter on chromosome pairing in wheat/rye hybrids using genomic in situ hybridization
HTIL:HEREDITY
HSSN:0018-067X
HYER:1994
HCOL:vol. 72, no. 3, pp. 318-321

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(5)
ACCN:001323608 CTLN:3565804
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Sano, H.;Youssefian, S.
AFFN:Biotechnol. Inst., Akita Prefect. Coll. Agricul., Ohgata, Akita 010-04, Japan
TITL:Light and nutritional regulation of transcripts encoding a wheat protein kinase homolog is mediated by cytokinins
HTIL:PROC. NATL. ACAD. SCI. USA
HSSN:0027-8424
HYER:1994
HCOL:vol. 91, no. 7, pp. 2582-2586

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(6)
ACCN:001331027 CTLN:3574053
ABSJ:G (Genetics Abstracts)
AUTH:Beharav, A.;Cahaner, A.*;Pinthus, M.J.
AFFN:Hebrew Univ. Jerusalem, Fac. Agric., Rehovot 76100, Israel
TITL:Mixed model for estimating the effects of the Rht1 dwarfing allele, background genes, CCC and their interaction on culm and leaf elongation of Triticum aestivum L., spring wheat
HTIL:HEREDITY
HSSN:0018-067X
HYER:1994
HCOL:vol. 72, no. 3, pp. 237-241

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(7)
ACCN:001334328 CTLN:3578054
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Penner, G.A.;Bezte, L.J.
AFFN:Agric. Canada Winnipeg Res. Stn., 195 Dafoe Rd., Winnipeg, MB R3T 2M9, Canada
TITL:Increased detection of polymorphism among randomly amplified wheat DNA fragments using a modified temperature sweep gel electrophoresis (TSGE)

technique
HTIL:NUCLEIC ACIDS RES.
HSSN:0305-1048
HYER:1994
HCOL:vol. 22, no. 9, pp. 1780-1781

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(8)
ACCN:001337500 CTLN:3580577
ABSJ:G (Genetics Abstracts)
AUTH:Suzuki, T.;Nakamura, C.*;Mori, N.;Iwasa, Y.;Kaneda, C.
AFFN:Lab. Plant Genet., Fac. Agric., Kobe Univ., 1 Rokkodai-cho, Nada-ku, Kobe 657, Japan
TITL:Homoeologous group 1 chromosomes of Agropyron restore nucleus-cytoplasmic compatibility in alloplasmic common wheat with Agropyron cytoplasms
HTIL:JAP. J. GENET.
HSSN:0021-504X
HYER:1994
HCOL:vol. 69, no. 1, pp. 41-51

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(9)
ACCN:001340185 CTLN:3583583
ABSJ:G (Genetics Abstracts)
AUTH:Shani, N.;Rosenberg, N.;Kasarda, D.D.;Galili, G.*
AFFN:Dep. Plant Genet., Weizmann Inst. Sci., Rehovot, 76100, Israel
TITL:Mechanisms of assembly of wheat high molecular weight glutenins inferred from expression of wild-type and mutant subunits in transgenic tobacco
HTIL:J. BIOL. CHEM.
HSSN:0021-9258
HYER:1994
HCOL:vol. 269, no. 12, pp. 8924-8930

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(10)
ACCN:001347619 CTLN:3591921
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Mikami, K.;Sakamoto, A.;Iwabuchi, M.*
AFFN:Dep. Bot., Fac. Sci., Kyoto Univ., Kyoto 606-01, Japan
TITL:The HBP-1 family of wheat basic/leucine zipper proteins interacts with overlapping cis-acting hexamer motifs of plant histone genes
HTIL:J. BIOL. CHEM.
HSSN:0021-9258
HYER:1994
HCOL:vol. 269, no. 13, pp. 9974-9985

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(11)
ACCN:001352293 CTLN:3596481
ABSJ:G (Genetics Abstracts)
AUTH:Yadava, R.K.;Maherchandani, N.;Singh, M.
AFFN:Dep. Genet., CCS, Haryana Agric. Univ., Hisar 125004, India
TITL:Genotype x macro- and micro-environment interactions in two bread wheat populations
HTIL:ENVIRON. ECOL.
HSSN:0970-0420
HYER:1994
HCOL:vol. 12, no. 1, pp. 110-115

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(12)
ACCN:001356950 CTLN:3602250
ABSJ:G (Genetics Abstracts)
AUTH:Hartmann, C.;Recipon, H.;Jubier, M.-F.;Valon, C.;Delcher-Besin, E.; Henry, Y.;De Buyser, J.;Lejeune, B.;Rode, A.
AFFN:Lab. Biol. Mol. Vegetale, URA CNRS 1128, Batim. 430, Universite de Paris Sud, F-91405 Orsay, France
TITL:Mitochondrial DNA variability detected in a single wheat regenerant involves a rare recombination event across a short repeat
HTIL:CURR. GENET.
HSSN:0172-8083

HYER:1994
HCOL:vol. 25, no. 5, pp. 456-464

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(13)
ACCN:001366480 CTLN:3612356
ABSJ:G (Genetics Abstracts)
AUTH:Ji, Liang-Hui;Langridge, P.*
AFFN:Dep. Plant Sci., Waite Inst., Univ. Adelaide, Glen Osmond, S.A. 5064, Australia
TITL:An early meiosis cDNA clone from wheat
HTIL:MOL. GEN. GENET.
HSSN:0026-8925
HYER:1994
HCOL:vol. 243, no. 1, pp. 17-23

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(14)
ACCN:001366511 CTLN:3612387
ABSJ:G (Genetics Abstracts)
AUTH:Sullivan, M.L.;Carpenter, T.B.;Vierstra, R.D.*
AFFN:Dep. Horticult., Univ. Wisconsin, 1575 Linden Dr., Madison, WI 53706, USA
TITL:Homologues of wheat ubiquitin-conjugating enzymes - TaUBC1 and TaUBC4 are encoded by small multigene families in Arabidopsis thaliana
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1994
HCOL:vol. 24, no. 4, pp. 651-661

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(15)
ACCN:001372439 CTLN:3619954
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology); A (Microbiology Abstracts A: Industrial & Applied Microbiology); G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Das, M.K.;Griffey, C.A.
AFFN:Dep. Crop and Soil Environ. Sci., Virginia Polytech. Inst. and State Univ., Blacksburg, VA 24061, USA
TITL:Heritability and number of genes governing adult-plant resistance to powdery mildew in houser and redcoat winter wheats
HTIL:PHYTOPATHOLOGY
HSSN:0331-949X
HYER:1994
HCOL:vol. 84, no. 4, pp. 406-409

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(16)
ACCN:001378620 CTLN:3625652
ABSJ:G (Genetics Abstracts)
AUTH:Ashraf, M.
AFFN:Coll. Agric., Dep. Plant Sci., Univ. Arizona, Tucson, AZ 85721, USA
TITL:Genetic variation for salinity tolerance in spring wheat
HTIL:HEREDITAS
HSSN:0018-0661
HYER:1994
HCOL:vol. 120, no. 2, pp. 99-104

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(17)
ACCN:001381108 CTLN:3628539
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Jia, Ji-Zeng;Miller, T.E.;Reader, S.M.;Gale, M.D.
AFFN:Inst. Crop Germplasm Resour., CAAS, Beijing 100081, PRC
TITL:RFLP tagging of a gene Pm12 for powdery mildew resistance in wheat (Triticum aestivum L.)
HTIL:SCI. CHINA SER. B
HSSN:1001-652X
HYER:1994
HCOL:vol. 37, no. 5, pp. 531-537

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(18)
ACCN:001389720 CTLN:3639730
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology);
W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Zhang, L.;Mitra, A.;French, R.C.;Langenberg, W.G.
AFFN:Dep. Plant Pathol., Univ. Nebraska, Lincoln, NE 68583, USA
TITL:Fungal zoospore-mediated delivery of a foreign gene to wheat roots
HTIL:PHYTOPATHOLOGY
HSSN:0331-949X
HYER:1994
HCOL:vol. 84, no. 7, pp. 684-687

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(19)
ACCN:001397489 CTLN:3647423
ABSJ:G (Genetics Abstracts)
AUTH:Enno, T.
AFFN:Eesti Teaduste Akad. Eksperimentaalbiol. Inst., Instituudi tee 11, EE-
3051 Harku, Harjumaa, Estonia
TITL:Cytogenetical analysis of wheat-aegilops hybrids
HTIL:PROC. ESTON. ACAD. SCI., BIOL.
HSSN:0013-2144
HYER:1994
HCOL:vol. 43, no. 1, pp. 1-11

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(20)
ACCN:001398689 CTLN:3648728
ABSJ:G (Genetics Abstracts)
AUTH:Thomas, J.B.;Schaalje, G.B.;Grant, M.N.
AFFN:Res. Stn., Agric. Canada, Lethbridge, AB T1J 4B1, Canada
TITL:Height, competition and yield potential in winter wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993-1994
HCOL:vol. 74, no. 1-2, pp. 9-17

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(21)
ACCN:001398697 CTLN:3648736
ABSJ:G (Genetics Abstracts)
AUTH:Winzeler, H.;Schmid, J.E.;Winzeler, M.
AFFN:Swiss Fed. Res. Stn. Agron. (FAP), Dep. Plant Breed., CH-8046 Zuerich,
Switzerland
TITL:Analysis of the yield potential and yield components of F sub(1) and F
sub(2) hybrids of crosses between wheat (Triticum aestivum L.) and
spelt (Triticum spelta L.)
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993-1994
HCOL:vol. 74, no. 3, pp. 211-218

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(22)
ACCN:001398698 CTLN:3648737
ABSJ:G (Genetics Abstracts)
AUTH:Morgunov, A.;Montoya, J.;Rajaram, S.
AFFN:Int. Wheat and Maize Improvement Cent. (CIMMYT), Lisboa 27, Apdo
Postal 6-641, Col. Juarez, 06600, Mexico D.F.
TITL:Genetic analysis of resistance to Karnal bunt (Tilletia indica (Mitra))
in bread wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993-1994
HCOL:vol. 74, no. 1-2, pp. 41-46

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(23)
ACCN:001399212 CTLN:3649306
ABSJ:D (Ecology Abstracts); K (Microbiology Abstracts C: Algology, Mycology
& Protozoology); A (Microbiology Abstracts A: Industrial & Applied
Microbiology); W2(Agricultural and Environmental Biotechnology

Abstracts)
AUTH:Legard, D.E.;McQuilken, M.P.;Whipps, J.M.*;Fenlon, J.S.;Fermor, T.R.;
Thompson, I.P.;Bailey, M.J.;Lynch, J.M.
AFFN:Hortic. Res. Int., Littlehampton BN17 6LP, UK
TITL:Studies of seasonal changes in the microbial populations on the phyllosphere of spring wheat as a prelude to the release of a genetically modified microorganism
HTIL:AGRIC. ECOSYST. ENVIRON.
HSSN:0167-8809
HYER:1994
HCOL:vol. 50, no. 2, pp. 87-101

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(24)
ACCN:001399344 CTLN:3649438
ABSJ:G (Genetics Abstracts)
AUTH:Sharma, H.C.;Waines, J.G.
AFFN:Dep. Agron., Purdue Univ., West Lafayette, IN 47907, USA
TITL:Inheritance of leaf pubescence in diploid wheat
HTIL:J. HERED.
HSSN:0022-1503
HYER:1994
HCOL:vol. 85, no. 4, pp. 286-288

III. Editorial Remarks

During this period, many subscribers and friends wrote valuable suggestions to office about improvement of Wheat Information Service. Also, some organizations like SIMMYT proposed cooperative projects to develop world-wide reputation of this journal, especially in the developing countries, where important genetic resources and practical problems are unrevealed because of lack of international information systems. Editorial office would like to express thanks for these cooperations.

From the next issue, we are going to accept some model changes of the journal as followed. New regulation is seen in the attached sheet, and in detail in the next issue No. 81.

(1) Name of Journal

Some proposed changing the name of the journal to adapt for competitive world of modern science, and some wanted to keep this traditional title. Conclusively, we decided to use Wheat Information Service with subtitle of The International Journal of Wheat Genetics and Breeding.

(2) Contents

As already started in this or previous issues, WIS include Research Information, informal information, methods and ideas for research progress, in addition to Articles, which are scientific research reports with reviewing system by authorities. Also, List of Genetic Resources, Bibliography on wheat research, and Review Articles are continuously included.

(3) Donation System

For last 5 years, WIS has been financially supported 100% by Kihara Memorial Foundation. But this is not fare, and has some limitation. Therefore, voluntary donation system will be introduced from next year, in which subscribers will be asked to contribute donation about ¥2000 (US$25) per year. But at the same time, we should accept the point that there are some wheat researchers in the world who have economical or social difficulties for payment. Donation system is based on the idea of mutual development.

In the present issue, we are glad to have informative articles, and several manuscripts have already been sent to reviewers. Thanks for your cooperation.

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Explanation of the picture on the cover

C-banding pattern of metaphase chromosome of KS88-17, a Wichita-*ararticum* substitution line. See the article by Badaeva and Gill for details.

WIS No.80

編集 国際小麦研究連絡会議
西　川　浩　三

発行所 木原記念 横浜生命科学振興財団
〒244 横浜市戸塚区舞岡町641-12
TEL. 045-825-3487, FAX. 045-825-3307

発行日 1995年6月30日

印刷 株式会社 野 毛 印 刷
Tel.(045) 252-2511

Wheat Information Service No. 80

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