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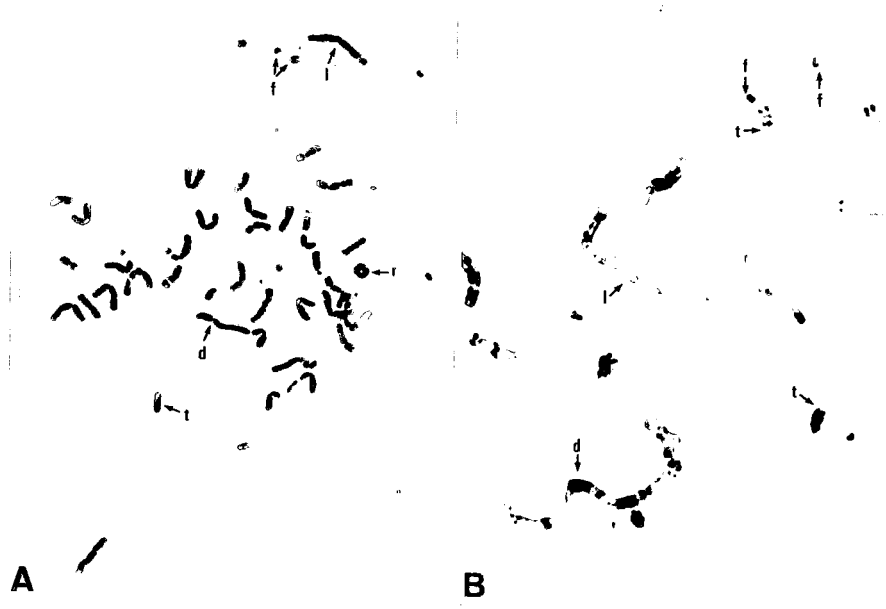

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Contents

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I. Research Notes

The meiotic analysis and morphological characters of the hybrid *Triticum aestivum* L. var. *delfii* Körn. × *Aegilops triaristata* Willd.

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A crossing program was organized to transfer genes for resistance to stripe rust (*Puccinia striiformis* West.) from *Aegilops triaristata* (2 n=28) to *Triticum aestivum* var. *delfii* (2 n=42). Crosses between these two species were made in the spring of 1980, under field

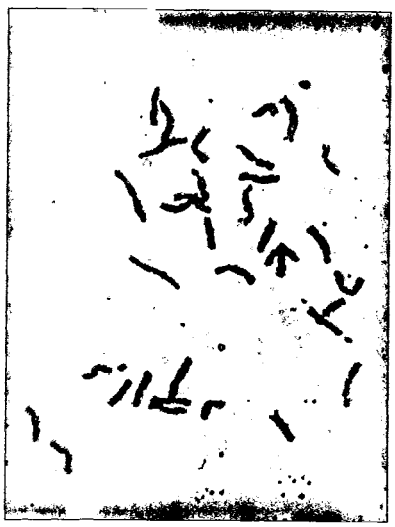

Fig. 1. Mitotic metaphase in a pentaploid hybrid between *T. aestivum* var. *delfii* × *Ae. triaristata* (×1670)

Fig. 2. Spikes of *T. aestivum* var. *delfii*, F_1 pentaploid hybrid and *Ae. triaristata* (from left to right)

Table 1. Some characters of *T. aestivum* var. *delfii*

	Awenduness	Rachis	Glume	Spike density[1)]
T. aestivum	Awnless	Tough	Hairy	14.93±0.32
Ae. triaristata	Awned	Weak	Hairy	11.92±0.31
F_1	Awned	Weak	Hairy	11.69±0.15

1) No. of spikelets/10 cm
2) S: Susceptible, R: Resistant

conditions.

In all, 712 florets from 28 spikes of *T. aestivum* var. *delfii* were pollinated with pollen of *Ae. triaristata*. Emasculating and crossing techniques were detailed in the previous study of ÖZGEN (1983a). 114 seeds were obtained from the crosses and chromosome numbers were determined by examining root tips under the microscope. Hybrids were found to be pentaploid (2n=35) (Fig. 1).

Only 86 of the 114 seeds germinated under laboratory condition. Seedlings were transplanted into the field and 57 F_1 plants were obtained. The F_1 plants were intermediate with respect to most of the morphological characters, but dominance was observed for some of the characters. The ears of the hybrid plants looked more like wheat than *Ae. triaristata* (Fig. 2). Some characteristics of the parents and hybrids are given in Table 1.

It has long been known that there are some genes which cause sterility by affecting meiosis or it's resulting gametes in the interspecific hybrids (STEBBINS 1958). The characteristics and numbers of chromosomes of parents may also be causes of sterility (KIHARA & YAMASHITA 1956). The hybrid plants had non dehiscent anthers. The seed-setting was rather poor: only 50 seeds were obtained from 2763 spikes of 57 plants, with free pollination.

Meiotic behaviour of the F_1 hybrids was analyzed at the first metaphase stage and chromosome pairing was observed (Table 2 and 3). This showed that the number of bivalents varied between zero and ten, and most of them were of the rod type (Fig. 3), but there also were some ring types.

Table 2. The mean and range of meiotic configurations in the F_1 hybrids *T. aestivum* var. *delfii* × *Ae. triaristata*.

I	II Rod	II Ring	II Total	III	IV	Number of cells
27.64	2.40	0.24	2.64	0.63	0.03	
10-35	0-9	0-2	0-10	0-5	0-2	91

Table 3. Meiotic configuration of F_1 PMC's at the first metaphase (%).

PMC's	0_{II}	1_{II}	2_{II}	3_{II}	4_{II}	5_{II}	6_{II}	7_{II}	8_{II}	9_{II}	Others
%	39.5	16.5	7.5	5.5	4.5	6.5	2.0	5.5	3.5	4.5	4.5

× *Ae. Triaristata* F_1 hybrids and their parents.

Lower internodes with/without (angle, knee)	Auricle		Growth habit	Resistance to stripe rust[2)]
	color	hairness		
Without	White	Glabrous	Erect	S
With	Red	Hairy	Prostrate	R
With	Red	Hairy	Prostrate	R

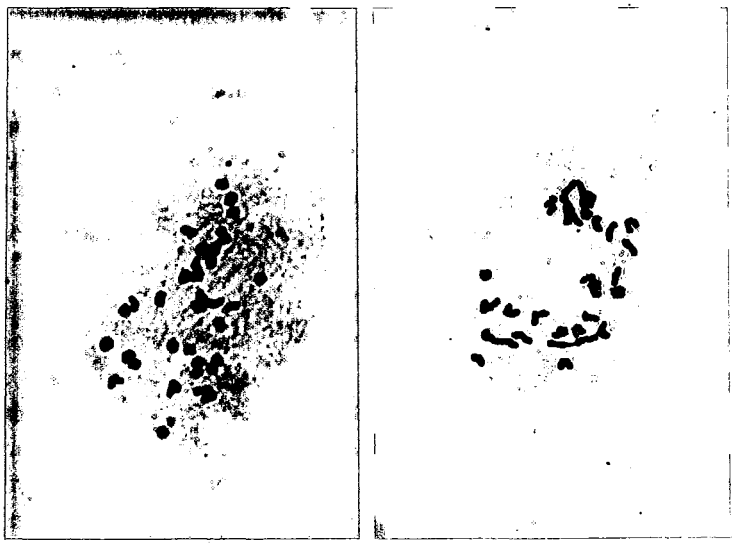

Fig. 3. Metaphase I chromosome associations in F_1tahybrids between *T. aestivum* var. *delfii* × *Ae. triaristata* (Left: ×455, Right: ×635)

As pointed out by DEWEY (1982), chromosome pairing shows the level of relationship between parents. Chromosome pairing in *T. aestivum* var. *erythroleucon* × *Ae. biuncialis* hybrids (ÖZGEN 1984), were similar to chromosome pairing in *T. aestivum* var. *delfii* × *Ae. triaristata* hybrids. Chromosome pairing in the F_1 hybrids of *T. aestivum* var. *delfii* × *Ae. triaristata* were found to be higher than for *T. durum* var. *hordeiforme* × *Ae. umbellulata*'s F_1 hybrids (ÖZGEN 1983b).

As indicated by this study, to transfer genes from *Ae. triaristata* to *T. aestivum* var. *delfii* is easier than to transfer genes from *Ae. umbellulata* to *T. durum* var. *hordeiforme*.

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EMS-induced meiotic anomalies in *Triticum aestivum*

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Triticum aestivum L. (2n=6x=42; AABBDD) offers some unique opportunities for the induction and exploitation of mutations of agronomic value. Though some earlier workers like STADLER (1930) were sceptical about the use of mutation breeding in grain crops, some interesing mutants have been induced in bread wheat (LARIK 1978 a, b, 1979; SIDDIQUI & ARAIN 1974). Chromosome anomalies such as translocations, deletions and duplications have been frequently observed in treated populations of several crop plants (LARIK 1975; LARIK *et al.* 1981, 1982). The present study reports meiotic anomalies and pollen sterility induced by EMS in three important hexaploid wheat varieties of Saudi Arabia and discusses their significance with reference to genetics and plant breeding.

Material and Methods

Homogeneous seeds of three bread wheat cultivars namely; Al-Samma, Maaya and Yocorojo were treated with different concentrations of ethyle methane sulphonate (EMS) with different durations in Rabi 1983. Treated seeds along with control were sown in pots in a complete randomized design in a greenhouse of the Department of Agronomy and Range Science, Gassim College of Agriculture, King Saud University, Saudi Arabia. EMS treatments are given as below:

Concentration	*Duration*
1. EMS 0.2 percent	i. 3 ½ hours
	ii. 7 hours
	iii. 9 hours
2. EMS 0.4 percent	i. 3 ½ hours
	ii. 7 hours
	iii. 9 hours
3. EMS 0.6 percent	i. 3 ½ hours
	ii. 7 hours
	iii. 9 hours
4. Control	

Immature spikes from treated and control plants were fixed in Carnoy's (6 : 3 : 1) solution (SNOW 1963). Analysis of different stages of meiosis were done at MI. Pollen fertility was determined by staining pollen grains in a solution introduced by ALEXANDER (1969). The data on seven meiotic parameters were analysed statistically using the General Linear Models (GLM) procedures of SAS (HELWIG & COUNCIL 1979). The least significant

difference (LSD) at the 0.05 probability level (LSD0.05) is reported for testing means of each parameter.

Results and Discussion

At metaphase I control plants regularly formed 21 bivalents characteristic of diploid-like pairing reported inthis species (RILEY 1974). Microsporocytes with ring bivalents were in greater frequency than rod bivalents in all the genotypes. Anaphase I in control plants revealed normal segregation of 21 : 21 chromosomes on both the poles.

The cytological data (Fig. 1) indicate that all the genotypes displayed a regular trend for the increase in the frequency of aberrations with every increase in the EMS dose. It is evident from Fig. 1 that EMS treatment of 0.6 percent at all the durations in all the genotypes produced maximum aberrations ranging from 4.52 percent (Al-Samma) to 13.81 percent (Maaya). Similar relationship between dose and chromoromal aberrations was reported by several workers (SEARS 1957; MATSUMURA 1961; LARIK 1975; LARIK *et al.* 1981, 1982). Multivalents ranged from trivalents to quadrivalents. Although not consistent there was a tendency for increased frequency of multivalents with increasing doses of EMS. A marked differences in the frequency of multivalents was apparent between treatments within the same genotype. A high incidence of ring bivalents in wheat may be attributed to the large size of the chromosomes; presumably large segments of chromosomes were involved in interchanges. The data have also suggested that there were genotypic differences in the frequency of occurrence of EMS-induced multivalents. Variety Maaya displayed maximum frequency of multivalents whereas, variety Al-Samma showed minimum frequency of multivalents. In few cases chromosomes at MI appeared to be clumped. This can be attributed to the straight and narrow nature of the spindle (LARIK *et al.* 1981).

Anaphase I and later stages were accompanied by various types of anomalies. Anaphase bridges appeared in various configurations, the most common being sticky bridges and bridges due to delayed separation of chromosomes. The occurrence of various forms of anaphase bridges suggest that their formation depends upon the event of crossing over, which occurs regularly at meiosis. The delayed separation of some chromosome associations was probably due to delayed chiasma terminalization. However, REES & THOMPSON (1955) and LEWIS & JOHN (1966) have shown that similar configuration could arise from spontaneous breakages.

The univalents accumulated in the equatorial region during MI become the lagging chromosomes at AI in PMC's. This was reported by several workers (KIHARA 1930; LARIK *et al.* 1981, 1982) and is also confirmed by the prresent study. In few cases at AI a 20 : 22 chromosome disjunction was observed. If the unbalanced gametes are functional as has been reported by SEARS (1954) in *Triticum aestivum* and LARIK (1978 a, b 1981) in *Avena sativa*, it may be possible to build up an array of aneuploids, which might be helpful in genetic study of our wheat cultivars.

Pollen fertility, as judged by stainability decrease with the increase of duration of EMS dose (Fig. 1). Similar results were reported by GAUL (1964). Low fertility may be ascribed

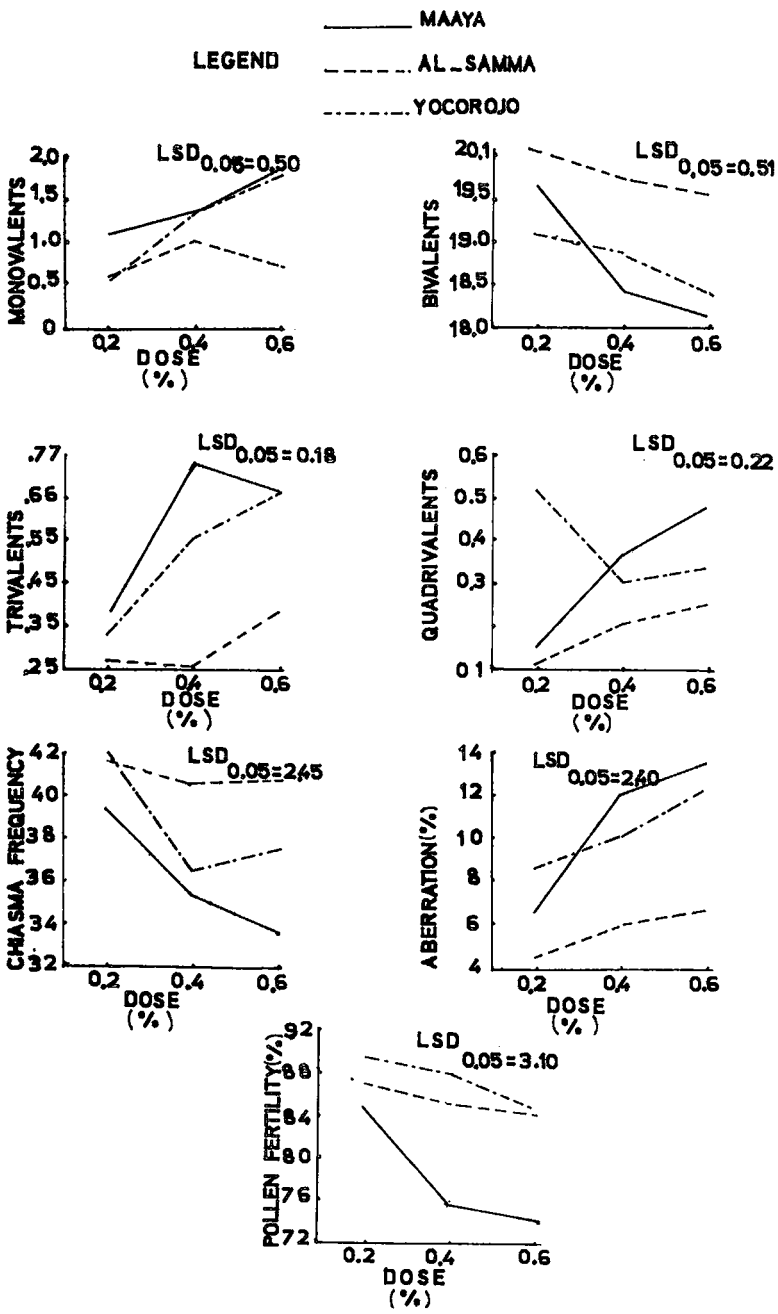

Fig. 1. Showing distribution of means of seven parameters at different doses of EMS.

Table 1. F-values of six meiotic parameters in three hexaploid wheat varieties using the General Linear Models (GLM) procedures of Statistical Analysis System (SAS)

Source	D.F.	Monovalents	Bivalents	Trivalents	Quadrivalents	Xt's/PMC	Aberration %
Variety (V)	2	14.15***	61.42***	17.52***	7.59***	116.64***	61.41***
Treatments (T)	3	30.57***	97.37***	26.98***	8.84***	204.98***	97.33***
Duration (D)	2	26.91***	41.79***	5.59**	3.71*	91.91***	41.80***
V×T	6	3.31**	5.84***	2.59*	3.93***	11.56***	5.84***
V×D	4	0.38ns	0.54ns	0.63ns	0.80ns	2.33*	0.54ns
T×D	4	1.75ns	0.55ns	0.13ns	0.21ns	3.60**	0.55ns
V×T×D	8	1.27ns	0.21ns	0.59ns	1.48ns	2.92**	0.21ns
Error	570						

*, **, *** Significant at 5%, 1% and 0.1% level of probability respectively.
ns = Non-significant.

at least partly due to irregular disjunction of chromosomes at anaphase resulting from the formation of interchange multivalents. On the contrary, the production of gametes with duplications and deficiencies for a certain chromosome sections add to pollen sterility. While recognising the role of meiotic anomalies in causing sterility, the role of genetic factors affecting meiosis cannot be ruled out in this polyploid. Orientation of chromosomes at MI is another factor influencing sterility (KUMAR & DAS 1973). Crossing over in the interstitial segments also affects sterility (RANA 1965).

The difference in chiasma frequency between varieties and interactions in treated populations were highly significant (Table 1). The continuous nature of the variation in chiasma frequency among genotypes, expressed by the Fig. 1, indicate that formation of chiasmata is controlled by polygenes and it has a profound effect on the distribution of the various chromosome configurations at meiosis (LARIK *et al.* 1982).

Statistical analysis in Table 1 reveal highly signifificant ($P>0.01$) differences between varieties, treatments and durations. This suggests that cultivars and treatments under study varied significantly for all the parameters and the treatments at different durations were effective in inducing meiotic anomalies in these meiotic parameters. Varieties × treatment interaction was also significant, indicating that varieties did not perform uniformly across different doses of EMS. On the other hand, all other interactions were not significant except chiasma frequency per PMC, which indicate a consistency in performance of each variety across different EMS treatments.

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Heterosis for important characters in hexaploid triticale

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With recent realization of the possibility of producing F_1 hybrid seed on a large scale, considerable emphasis has been given to exploitation of heterosis in self pollinated crops. Heterosis, the increased vigour of F_1 hybrid over mid and better parent performance is the result of allelic or non-allelic interaction of genes under the influence of a given environment (MACKEY 1976). Directed heterosis and its fixation, therefore, appears to be a distinct possibility. In that context, ample evidence of significant heterotic effects and availability of some economic means of producing hybrid seed are two basic considerations. Such information in triticale is scanty. Present study deals with hetetosis in triticale cross combinations involving parental genotypes selected on the basis of genetic divergence.

Materials and Methods

Based on genetic divergence, 22 hexaploid triticale genotypes were selected from germplasm collection. Each of the 18 lines namely, 1. T24., 2. T103., 3. T125., 4. T130., 5. T134., 6. Tc13., 7. T137., 8. T139., 9. T146., 10. T145., 11. UPT74364., 12. UPT74418., 13. UPT74460., 14. UPT74536., 15. Arm147., 16. Armadillo., 17. Koala., 18. Cinnamon were crossed to each of four testers viz., 1. St69-1., 2. 6TA204., 3. T122., 4. UPT74535 to yield 72 F_1 hybrids. Parents and hybrids were sown in randomized block design with three replications. Each genotype was accommodated in two rows, 3 meter long spaced 30 cm apart with intra-row distance among plants being 15 cm. Observations on randomly selected 5 plants were recorded for attributes related to plant morphology, grain yield and its components and physico-chemical qualities of grain. Percent heterosis measured as deviation of F_1 hybrid performance from the mid, better and best wheat check performance, designated as relative heterosis, heterobelteosis and standard heterosis, respectively.

Results and Discussion

Analysis of variance revealed significant differences among parents and hybrids for all the characters. Significant parents vs hybrid component indicated the presence of over all dominance and heterosis for most of the traits except days to spike emergence, number of tillers per plant, grain density and grain protein content.

Magnitude of heterosis varied from cross to cross and character to character (Table 1). Highest magnitude of relative heterosis and heterobelteosis was recorded for tillers per plant (80.5 & 72.3%) and grain crushing hardness (80.6 & 60.5%) followed by grain yield per plant (70.1 & 57.4%), 1000 grain weight (44.7 & 39.8%) and biological yield per plant (46.9 & 37.9%)

etc. Heterosis as a phenomenon was relatively more frequent for characters like 1000 grain weight, harvest index and biological as well as grain yield per plant. No cross revealed appreciable heterosis for floret fertility and invariably negative heterosis for this trait was evident which might be attributed to meiotic disturbances in inter varietal F_1 hybrids (GUPTA & PRIYDARSHAN 1982). No F_1 should, therefore, be rejected unless floret fertility is very low as continued selection for this character has been found to be effective. Only one cross, UPT74364×6TA204 manifested desirable and significant negative heterosis (−15.14) for plant height.

Most heterotic hybrids for grain yield also showed heterosis for harvest index or biological yield per plant, the latter being more frequent. Number of tillers per plant and 1000 grain weight also expressed more or less similar trend.

Heterosis in F_1 could be explained on the basis of dominance, overdominance, nonallelic interactions (MACKEY 1976), and pure additive gene action at individual loci coupled with favourable additive×additive interaction (ARUNACHALAM 1976). It will, therefore, be possible to recover homozygous lines as good as heterotic hybrids if the heterosis is caused by fixable gene action. However, our earlier studies, using these hybrids, revealed preponderance of nonadditive gene action for most of the characters including grain yield and overdominance being most possible reason could not be oversighted (BEHL & SINGH 1984). Thus, the chances of exploitation of heterosis at commercial level appear to be dim, at least in present case, because of moderate heterosis and its genetic control.

Heterosis, being deviation of F_1 from mid or better parent value, can be high or low depending on the average performance of the parents. Therefore, heterosis coupled with high *per se* performance should be considered while selecting cross combinations for population improvement work. Though, none of the cross, as expected, manifested heterosis for all the component attributes of grain yield and quality, yet few crosses expressed high heterosis for two to five characters. In that context, crosses viz., T24×St69-1 for tillers per plant, biological yield and grain yield per plant, T134×6TA204 for grain density, biological yield and harvest index ; UPT74364×6TA204 for days to spike emergence, plant height, 1000 grain weight, grain density and biological yield ; Arm147×6TA204 for grain weight, grain crushing hardness and grain protein content ; Koala×T122 for harvest index and grain yield ; Cinnamon×T122 for number of grains per spike, biological yield and grain yield per plant ; T134×UPT74535 for tillers per plant, and grain protein content ; T103×6TA204 for grain crushing hardness and grain yield per plant ; UPT74536×St69-1 for floret fertility and UPT74418×UPT74535 for number of spikelets per spike figured important. Pairwise or multiple crosses involving these hybrids offer some promise to facilitate synthesis of dynamic population and to recover better homozygous lines in progeny generations with improved plant type, grain yield and better nutritional and end use grain quality as parents involved in their synthesis were genetically divergent and either good or average general combiner (BEHL & SINGH 1984). Our results are in partial confirmity with that of SRIVASTAVA & ARUNACHALAM (1977), ANSINGKAR *et al.*, (1978) and ROSENKOVA & MASTENPOVA (1981). However, for physico-chemical characters such as grain density, grain crushing hardness and grain protein

Table 1. Seven best crosses on the basis of

S. No.	Days to ear emergence		No. of spikelets/spike		Floret fertility (%)	
	M.P.	B.P.	M.P.	B.P.	M.P.	B.P.
1.	−9.5* (11×2)	−9.2* (11×2)	34.6* (15×3)	33.9* (15×3)	8.5* (14×1)	6.8* (17×1)
2.	−5.6* (6×3)	−0.7 (6×3)	22.1* (14×3)	19.9* (2×3)	7.6* (8×1)	6.5* (8×1)
3.	−5.1* (8×1)	1.5 (8×1)	20.0* (2×3)	13.9* (16×1)	7.4* (17×1)	6.4 (14×1)
4.	−4.7* (1×1)	2.6 (1×1)	15.0 (16×1)	13.8* (4×1)	7.3* (14×2)	5.2 (14×2)
5.	−4.6* (1×3)	−2.0 (1×3)	15.0* (2×1)	12.5* (2×1)	6.8* (10×1)	5.2 (2×2)
6.	13.7* (4×1)	19.8* (15×1)	14.4* (4×1)	8.1* (14×3)	6.2 (2×2)	4.0 (10×1)
7.	13.3* (15×1)	18.2* (4×1)	9.3* (1×3)	6.8 (12×4)	4.4 (11×1)	3.9 (11×1)
C.D. 5%	3.6	5.1	1.9	2.7	3.4	8.5
Range	−9.5 to 13.6	−9.2 to 21.9	−32.5 to 34.6	−35.1 to 33.9	−26.3 to 8.5	−29.2 to 6.8
No. of heterotic hybrids						
+ve	14	31	21	24	40	32
−ve	5	1	6	17	35	30

Table 1. contd.

S. No.	Harvest index (%)		Tiller number			No. of
	M.P.	B.P.	M.P.	B.P.	W.C.	M.P.
1.	33.2* (2×2)	30.8* (2×2)	80.5* (1×1)	72.3* (1×1)	26.1* (1×1)	16.4* (16×1)
2.	29.0* (17×2)	18.7* (17×3)	54.2* (15×1)	50.0* (15×1)	19.4* (15×1)	14.6* (12×3)
3.	27.0* (3×2)	13.9* (3×2)	48.9* (15×4)	41.1* (15×4)	19.1 (15×4)	14.4* (18×3)
4.	19.6* (17×3)	13.5* (17×2)	47.6* (4×2)	40.9* (4×2)	18.5 (4×2)	14.3* (10×1)
5.	15.8* (12×1)	13.1* (12×1)	42.2* (5×4)	37.8* (5×4)	15.3 (5×4)	11.7* (18×4)
6.	20.0* (9×4)	12.2 (2×1)	40.0* (5×3)	37.6* (5×3)	15.1 (5×3)	10.6* (12×2)
7.	18.8* (2×1)	11.3 (9×4)	40.1* (6×4)	34.0* (6×4)	15.0 (6×4)	10.0* (14×1)
C.D. 5%	2.9	4.1	2.5	3.5	3.5	6.5
Range	−12.2 to 33.2	−17.5 to 30.8	−28.5 to 80.5	−44.2 to 72.3	−21.8 to 26.4	−24.9 to 16.4
No. of heterotic hybrids						
+ve	32	15	13	11	5	28
−ve	3	7	1	2	3	20

percent heterosis over mid and better parent

Grain crushing hardness		Grain density g/cc		Protein content (%)		Biological yield/plant (g)	
M.P.	B.P.	M.P.	B.P.	M.P.	B.P.	M.P.	B.P.
80.6* (15×2)	60.5* (15×2)	22.6* (5×2)	22.2* (5×2)	16.0* (15×2)	14.5* (15×2)	46.9* (1×1)	37.9* (1×1)
52.5* (12×2)	37.6* (2×2)	19.4* (11×2)	17.5* (11×2)	14.8* (5×4)	13.6* (5×1)	41.0* (18×2)	37.8* (18×2)
42.5* (2×2)	35.4* (12×2)	13.7* (16×4)	12.4* (16×4)	14.5* (5×1)	13.0* (13×1)	39.3* (13×1)	35.9* (11×2)
31.9* (11×1)	21.8* (11×1)	13.6* (10×4)	7.9* (10×4)	14.0* (13×1)	12.4* (17×1)	36.9* (11×2)	30.8* (10×1)
31.3* (13×4)	19.8* (13×4)	13.7* (12×1)	5.9* (2×1)	13.0* (17×1)	11.0* (11×3)	34.7* (10×1)	30.3* (4×2)
33.9* (4×1)	18.3* (11×4)	10.9* (5×3)	4.6* (9×2)	12.3 (9×3)	8.8 (5×4)	33.7* (4×2)	29.6* (1×2)
29.9* (11×4)	18.0 (4×1)	10.8* (6×4)	4.2* (12×1)	12.2 (11×3)	7.0 (9×3)	33.5* (1×2)	28.6 (18×3)
1.4	2.0	0.1	0.2	1.0	1.5	10.6	15.1
−26.6 to 80.6	−30.1 to 60.5	−20.3 to 22.6	−22.7 to 22.2	−14.9 to 16.0	−17.7 to 14.5	−19.3 to 46.9	−23.1 to 37.9
17	8	15	6	25	14	34	24
3	3	7	4	8	8	4	6

grains per spike		1000-grain weight (g)			Grain yield/plant (g)		
B.P.	W.C.	M.P.	B.P.	W.C.	M.P.	B.P.	W.C.
16.0* (16×1)	41.3* (12×3)	44.7* (9×2)	39.8* (7×4)	24.1* (5×2)	70.1* (12×2)	57.4* (4×2)	44.9* (4×2)
11.0* (10×1)	36.6* (18×4)	44.2* (7×4)	33.1* (9×2)	19.5* (16×4)	63.2* (4×2)	54.6* (2×1)	41.7* (18×4)
9.7 (18×4)	36.1* (4×2)	37.9* (5×2)	27.8* (11×4)	19.4* (5×1)	60.2* (2×1)	40.3* (17×3)	38.1* (8×2)
6.9 (8×1)	34.7* (2×2)	32.7* (15×4)	22.8* (15×4)	18.8* (7×4)	51.7* (17×3)	38.3* (17×2)	35.3* (8×4)
6.9 (12×3)	27.9* (9×4)	31.7* (16×4)	20.4* (18×2)	18.5* (9×3)	49.9* (1×3)	36.8* (2×2)	33.9* (17×2)
—	27.6* (10×1)	31.7* (11×4)	19.8* (5×2)	17.7* (9×2)	49.1* (17×2)	34.3* (17×1)	32.6* (2×2)
—	27.2* (16×1)	29.8* (17×2)	19.7* (18×1)	17.7* (18×1)	47.8* (3×2)	33.5* (3×1)	32.3* (10×1)
9.3	9.3	3.7	5.3	5.3	3.5	4.9	4.9
−28.1 to 16.0	−16.8 to 41.3	−14.8 to 44.7	−20.6 to 39.8	−13.5 to 24.1	−26.6 to 70.1	−33.5 to 57.4	−31.7 to 44.9
30	23	45	21	18	47	30	28
27	2	2	3	3	4	6	7

content available information is scanty.

Since triticale has to compete with wheat, it would be logical to emphasize heterosis over best wheat checks. Highest standard heterosis for grain yield was recorded for T130×6TA204, followed by Cinnamon×UPT74535, T139×T122, T139×UPT74535 and Koala×T122 etc. while crosses viz., T24×6TA204, T103×6TA204 and Koala×T122 depicted considerable standard heterosis for biological yield per plant and harvest index. Inclusion of these crosses for breeding better triticale lines might be fruitful.

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Evaluation of wheat cultivars under different cultural regimes

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Among the plant characters associated with lodging and nitrogen responsiveness, height is predominant factor affecting loging resistance (SCARASCIA-MUGNOZZA 1970) and characters such as straw architecture exert an influence on polygenic trait like grain yield (LARIK *et al.* 1980). It is therefore necessary to take into consideration all the related plant attributes in any meaningful genetic evaluation of wheat mutants. The present investigation was therefore, initiate to study the effectiveness of different fertilizer levels in enhancing grain yield in winter wheats.

Materials and Methods

The material originated from different doses of gamma rays (25 and 35 kR) of varieties Indus and Nayab of bread wheat received through the courtesy of Head Plant Genetics Division, Atomic Energy, Agricultural Research Centre, Tandojam. *Triticum aestivum* L., Phenotypically stable mutants and Pak-70 were evaluated for straw and yield characteristics under different fertilizer levels of nitrogen, phosphorous and their combination.

The details of treatments are given as under:

Treatment	Nitrogen	P_2O_5
F_1	179.37 kg/ha.	89.68 kg/ha.
F_2	156.95 kg/ha.	78.47 kg/ha.
F_3	134.53 kg/ha.	67.26 kg/ha.
F_4	112.10 kg/ha.	56.05 kg/ha.
F_5	89.68 kg/ha.	44.84 kg/ha.

The combinations of these treatments were as follows.

	N kg/ha.	P_2O_5 kg/ha.
T_1 = Mutant-5	179.37	89.68
T_2 = 〃	156.95	78.47
T_3 = 〃	134.53	67.26
T_4 = 〃	112.10	56.05
T_5 = 〃	89.68	44.84

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	N kg/ha.	P_2O_5 kg/ha.
T_6 =Pak-70	179.37	89.68
T_7 = 〃	156.95	78.47
T_8 = 〃	134.53	67.26
T_9 = 〃	112.10	56.05
T_{10}= 〃	89.68	44.84
T_{11}=Mutant-35	179.37	89.68
T_{12}= 〃	156.37	78.47
T_{13}= 〃	134.53	67.26
T_{14}= 〃	112.10	56.05
T_{15}= 〃	89.68	44.84

Fertilization

Nitrogen and phosphorous were used in the form of D.A.P. and Urea. The entire quantity of phosphorous were applied at the sowing time in form of D.A.P. Remaining dose of Nitrogen fertilizer was given in the form of Urea with first irrigation. Fertilization was applied via broadcast.

Experiment and Method of Sowing

The experiment was conducted during Rabi 1979-80 at the Experimental form of the Department of Agronomy in Factorial Randomized Block Design with four replications. The sowing was done by hand drill in rows 25 cms apart. The soil was clay loam.

Observations

Data on 10 randomly selected mutant and Pak-70 plants in each replication were recorded for eleven material traits viz., plant height, first, second, third and fourth inter node length, spike length, spikelets per spike, grains per spike, yield per plot, biological yield and harvest index. Thus 40 plants were selected from each mutant and Pak-70 genotype. The data was analysed and subjected to analysis of variance.

Results and Discussion

Straw Characters

Analysis of variance for straw characters indicate that cultivars differ significantly for all the straw characters. The data reveal highly significant differences among the average varietal effects and few significant differences among fertilizer levels. The non-significant interaction indicates that the fertilizer levels have not much different effects for each cultivar (Table 3). From the comparison of means of Pak-70 and Mutants, it can be concluded that cultivar, having longer first internode length, possess shorter second, third and fourth inter node length (Table 1). Fertilizer effects on straw characters were non-significant displaying

Table 1. Modification of straw characteristics under different cultural regimes.

Fertilizer treatments	Plant height (cm)	First internode length (cm)	Second internode length (cm)	Third internode length (cm)	Fourth internode length (cm)
T_1 M-5	84.05	35.02	16.85	11.05	7.03
T_2 M-5	89.22	34.35	17.55	12.72	5.97
T_3 M-5	88.01	36.85	17.92	12.92	6.95
T_4 M-5	82.07	33.05	17.47	12.05	9.05
T_5 M-5	81.03	34.05	16.09	10.77	6.62
T_6 Pak-70	101.32	34.97	23.07	14.07	10.85
T_7 Pak-70	96.01	36.05	21.22	13.27	10.03
T_8 Pak-70	98.75	37.47	20.09	13.52	9.02
T_9 Pap-70	92.82	36.27	21.32	13.57	10.15
T_{10} Pak-70	94.07	32.75	19.52	12.47	9.27
T_{11} M-35	92.47	39.05	20.75	12.77	8.67
T_{12} M-35	92.62	40.52	20.87	11.07	6.05
T_{13} M-35	96.52	39.77	22.22	12.05	7.95
T_{14} M-35	89.87	39.15	20.05	12.27	7.47
T_{15} M-35	82.87	38.00	19.95	11.22	6.62
S.E. for (CV × V) fertilizer interaction.	2.96	2.60	0.718	0.630	1.005
Cdi	7.03	6.175	1.705	1.496	2.386
Cdii	10.126	8.89	2.456	2.155	3.438

that fertilizers were not able to induced significant changes in straw characters. Maximum height was recorded at F_3 (134.53 NKg/ha+67.26P_2O_5 Kg/ha). This might be due to longer second and third internode length at the same fertilizer level.

Ear-head Characters

Spike length, spikelets per spike, 100 grain weight and grains per spike are important yield components and are considered a reliable measure of yielding ability (BOROJEVIC & BOROJEVIC 1972) as the frequency of induced changes in next generation depends on the number of seeds which transmit than (LARIK 1978). The best criteria for the evaluation of superior genotypes is a comparison of its 100 grain weight with its monther cultivar (GUSATFFSON *et al.* 1971). The mean performance of the mutants and Pak-70 is presented in Table 2. Data reveal significant changes in all the ear characters due to fertilizer input. Mutant-35 possesses highest spike length but lowest number of grain per spike compared to other character. This shows that spike produced in this mutant were Lax type. On the contrary, Mutant-5 displayed shortest spike length but higher number of grains per spike, which indicate that spike produced in this mutants were compact types leading to higher number of grains. Ear characters did not show any significant differences with the alteration in fertilizer levels. However, more number of spikeletes and grains per spike were recorded

Table 2. Perfaorance of wheat cultivars for yield and yield components under different clutural regimes.

Fertilizer treatment	Number of tillers per plant	Spike length (cm)	Spikelets per spike	Grains per spike	Yield per plot (Kg)	Biological yield (Kg)	Harvest index (Kg)
T_1 M-5	5.55	7.92	23.35	43.08	5.05	12.01	42.14
T_2 M-5	6.05	6.62	20.65	42.25	4.32	10.72	40.43
T_3 M-5	4.08	7.01	16.06	41.25	4.03	11.15	38.39
T_4 M-5	7.02	6.47	18.45	38.08	5.67	11.05	48.47
T_5 M-5	7.35	6.08	17.01	35.03	4.27	9.05	44.27
T_6 Pak-70	4.85	8.05	18.03	38.45	4.85	11.08	41.24
T_7 Pak-70	7.07	7.09	18.05	37.09	5.42	13.12	41.19
T_8 Pak-70	6.07	7.08	20.35	37.55	4.57	12.05	42.33
T_9 Pak-70	5.07	8.05	23.07	49.25	3.75	11.62	39.45
T_{10} Pak-70	5.25	7.17	20.02	35.05	3.07	9.52	39.37
T_{11} M-35	5.09	8.62	18.01	37.06	3.32	11.57	26.24
T_{12} M-35	7.05	8.52	17.45	36.00	4.02	12.52	30.14
T_{13} M-35	8.03	9.05	19.25	39.05	4.67	13.87	29.58
T_{14} M-35	6.45	8.37	21.75	44.05	3.32	11.72	39.38
T_{15} M-35	7.15	7.09	16.15	31.02	3.68	10.97	31.98
S.E. for (CV × Fertilizer) interaction.	1.330	0.384	0.748	2.424	0.545	0.913	5.077
Cdi	—	0.912	1.776	5.757	1.294	2.170	12.05
Cdii	—	1.313	2.558	8.292	1.864	3.124	17.368

Table 3a. Mean squares for difference quantitative traits of hexaploid wheat cultivar.

Seurce of variation	D.F.	Plant height	First internode length	Second internode length	Third internode length	Fourth internode length	Tillers per plant	Spike length	Spikelete perskike	Grains per spike
Replication	3	143.28	9.94	8.43	0.74	1.12	14.25	2.34	6.85	45.27
Cultivars (C)	2	684.45**	121.04*	89.78**	12.02**	47.43**	14.25^{ns}	11.42**	12.55	66.08
Fertilizer (F)	4	142.26^{ns}	9.05^{ns}	4.61^{ns}	3.43^{ns}	5.83^{ns}	3.88^{ns}	1.45^{ns}	21.72	175.55**
C×V interaction	8	27.59^{ns}	4.06^{ns}	2.28^{ns}	1.32^{ns}	2.48^{ns}	4.69^{ns}	2.23*	23.85	61.29*
Error	42	35.03	27.14	2.06	1.58	4.05	7.09	0.06	0.02	23.52
Total	59									

*,**=Denote significance at 5% and 1% level.
ns=Non-sinificant.

Table 3b. Mean squares for difference quantative traits of hexaploid wheat cultivar.

Seurce of variation	D.F.	1000-kernel weight	Yield per plot	Biological yield	Harvest index
Replication	3	3.13	2.09	16.57	32.57
Cultivars (C)	2	108.04**	7.35**	4.30^{ns}	703.89**
Fertilizer (F)	4	21.96^{ns}	2.19**	11.13*	68.07^{ns}
C×V interaction	8	7.23^{ns}	1.38^{ns}	3.13^{ns}	43.11^{ns}
Error	42	13.09	1.19	3.34	103.12
Total	59				

*,**=Denote significance at 5% and 1% level.
ns=Non-significant.

at F_4 (112.10 NKg/ha+56.04 P_2O_5 Kg/ha).

Tillers per Plant

Tillers per plant have evolutionary significance (LARIK 1978) and is important from breeders point of view because of its direct influence on crop yield (SHUKLA 1974). Application of nitrogenous fertilizers results in increased number of tillers per plant.

Analysis of variance (Table 3) for this character did not exhibit any significant difference for cultivar and fertilizer level. Hence all the cultivars had a similar tendency of producing tillers at all fertilizer levels. Maximum tillers per plant were recorded at F_2 (156.95 nkg/ha+78.47 P_2O_5 kg/ha) Table 2. Similar results were reported by RAJPUT (1968) who observed that fertilizer applications do not necessarily enhance the number of tiller in wheat.

Yield Characters

Analysis of variance for grain yield per plot, biological yield and harvest index show that highly significant differences were present in cultivars for the grain yield and harvest index and non-significant differences for biological yield. However, Mutant-5 gave medium grain yield and higher harvest index whereas, M-35 gave lowest harvest index, grain yield and highest biological yield. However, at F_4 (112.10 nkg/ha+56.05 P_2O_5 kg/ha) highest grain yield, biological yield and harvest index (Table 2) were obtained. At maximum input of fertilizers decline in grain yield was noted. Such decrease at higher input has already been noted by RAJPUT (1968).

It is concluded that fertilizer dose with 112.10 nkg/ha+56.05 P_2O_5 kg/ha should be recommended for getting maximum economic and biological yield in winter wheat cultivars under other optimum cultural requirements.

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Genetics of kernel weight in wheat under different environments

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Grain yield is a complex character governed by many genes and it is dependent on the sum total of contribution made by its direct components. Kernel weight is one of the most important component of yield in wheat. GRAFIUS (1956) has suggested the possibility of improving yield components than yield itself. Since then "component breeding" rather than direct selection on yield has commonly been practised. To improve the desirable attribute like kernel weight, the breeder has to adopt suitable breeding methodology. Obviously, knowledge of genetics of attribute will help in planning a strategy to achieve the objective. In the present paper genetical studies on kernal weight under different environments over the years using various biometrical approaches have been made.

Materials and Methods

Eight wheat varieties namely Kharchia 65, WH 157, HD 2009, WL 711, WG 357, K 68, IWP 72 and Narmada 4 having different height groups and seed size were crossed in all possible combinations excluding reciprocals. Both parents and F_1's were grown vnder irrigated (EI), rainfed (EII) and saline (EIII) conditions at Hisar, Bawal and Karnal locations respectively during 1979-80 and 1980-81. Sowings were done in 3 m long rows spaced 25 cm apart with a plant to plant distance of 15 cm. 500 seeds were counted out of the bulk seed of the 10 competitive plants per replication and weighed. Weight of 1000 grain was obtained by doubling this weight of 500 seeds.

Results and Discussion

Significant differences were observed among genotypes in all the three environments over the years (Table 1). The mean squares due to gca and sca for kernel weight were highly significant under all the environments revealing thereby that both additive and non-additive type of gene effects were involved in the inheritance of this trait. The $\hat{sca}/\hat{gca}$ ratio was more than one except in EIII (saline) during first year suggesting predominance of non-additive gene effects. The present findings are in close agreements with the earlier reports

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Table 1. Analysis of variance for kernel weight under three distinct environments for two years.

Source of variations	d.f.	Mean sum of squares					
		Normal environment		Stress environment			
		Irrigated (EI)		Rainfed (EII)		Saline (EIII)	
		1979-80	1980-81	1979-80	1980-81	1979-80	1980-81
Replications	2	0.72	4.14	0.02	0.01	1.77	0.91
Genotypes	35	47.71**	55.15**	67.97**	47.10**	73.52**	42.27**
Error	70	1.08	1.30	1.17	1.21	0.15	0.46
GCA	7	35.88**	24.37**	77.02**	60.32**	62.57**	35.11**
SCA	28	10.91**	16.89**	9.07**	4.55**	14.99**	8.84**
Error	70	0.36	0.43	0.39	0.40	0.05	0.15
$\hat{S}CA/\hat{G}CA$		2.69	6.89	1.13	0.69	2.39	2.48
CV		2.06	2.30	2.15	3.00	0.93	1.33

Table 2. Estimates of general combining ability effects of kernel weight under three distinct environmental conditions for two years.

Parent	Irrigated (EI)		Rainfed (EII)		Saline (EIII)	
	1979-80	1980-81	1979-80	1980-81	1979-80	1980-81
Kharchia 65	−1.32**	0.44*	0.55**	0.53**	−2.13**	0.86**
WH 157	3.34**	3.07**	2.87**	2.06**	3.00**	2.29**
HD 2009	−1.09**	−1.83**	−3.64**	−3.84**	−1.18**	−2.63**
WL 711	−0.66**	−1.72**	−3.35**	−1.59**	−0.69**	−0.76**
WG 357	0.64**	0.22	2.75**	−1.58**	−2.52	0.12
K 68	1.87**	1.41**	2.35**	2.45**	1.88**	1.96**
IWP 72	−2.57**	−1.72**	−2.57**	−1.24**	−2.10**	−2.59**
Narbada-4	−0.20	1.13**	1.04**	3.21**	3.75**	0.74**
S.E. (gi)	0.18	0.19	0.18	0.19	0.06	0.11
S.E. (gi-gj)	0.27	0.29	0.28	0.28	0.10	0.17

* Significant at 5% level
** Significant at 1% level

Table 3. Superior crosses selected on the basis of sca effects and *per se* performance under irrigated, rainfed and saline environments over years.

Character	Environments			
	Irrigated (EI)	Rainfed (EII)	Saline (EIII)	Overall the environments
1000 kernels weight	Kharchia 65 (A) ×WH 157 (G)	WH 157 (G) ×WL 711 (P)	WH 157 (G) ×Narbada 4 (G)	WH 157 (G) ×Narbada 4 (G)
	WH 157 (G) ×Narbada 4 (G)	WH 157 (G) ×Narbada 4 (G)		
	K 68 (G) ×IWP 72 (P)			

(MULLAR *et al.* 1971 ; SRIVASTAVA *et al.* 1981).

The estimates of gca effects are presented in Table 2. Cultivars WH 157, K68 and Narmada 4 were identified as good general combiners for kernel weight under all the three environments under study, whereas HD2009, WL711 and IWP72 were poor combiners for this trait. Kharchia 65 was good under rainfed but average under normal and saline conditions. WG357 was good, average and poor combiner under normal, rainfed and saline environments respectively. The rank correlation between parental per se and gca effects was observed as significant.

Crosses selected on the basis of sca effects and per se performance in different environments over years are presented in Table 3. The only cross WH157×Narbada 4 was found desirable under all the environments which involved both parents as good general combiner under all the environments. This cross may be exploited through conventional breeding methods which make use of only additive and additive×additive type of gene effects. The cross combinations Kharchia 65×WH157, WH157×Narbada 4, K68×IWP72 under irrigated, WH157×WL711 and WH157×Narbada 4 under rainfed and WH157×Narbada 4 under saline environments were found desirable for this trait. These crosses involved at least one parent having good general combining ability. Therefore, such combinations could through up desirable transgressive segregants if the additive genetic system present in the good combiner and complementary epistatic effects act in the same direction to maximize the desirable plant attribute.

The estimates of the components of genetic variation $\hat{D}$, $\hat{H}_1$, $\hat{H}_2$, $\hat{F}$ alongwith their ratios are presented in Table 4. The $\hat{D}$ and $\hat{H}_1$ were found significant in all the three environments over years. This indicated the role of both additive and non-additive components of variation. The magnitude of $\hat{H}_1$ was higher than $\hat{D}$. The estimated degree of dominance was more than one except EII during 1980-81, suggesting over dominance and thus predominance of non-additive type of gene effects. These results support the results obtained through combining ability analysis.

Significant and positive value of $\hat{F}$ estimate revealed that the frequency of dominant alleles was higher than that of recessive alleles in EII and EIII during 1980-81. In rest of the environments $\hat{F}$ values were non-significant. The ratio $\hat{H}_2/4\hat{H}_1$ indicated slight deviation from symmetrical distribution of genes with positive and negative effects in EI and EIII during 1979-80, while in rest of the cases asymmetrical distribution was observed. The ratio $\hat{h}_2/\hat{H}_2$ indicated that at least one or two dominant genes or gene groups were responsible for controlling this character under different environments over the years. The narrow sense heritability of this character was low under normal ; low to high under saline and moderate to high under rainfed environments.

From the foregoing discussion it is now clear that both additive and non-additive types of gene effects were responsible for 1000 kernel weight in wheat. The breeding plan such as recurrent selection which can exploit both the fixable as well as non-fixable components of genetic variation is suggested. In this situation biparental mating may increase the frequency of desirable recombinants and hasten the rate of genetic improvement. SHARMA &

Table 4. Estimates of components of genetic variance and ratio for kernel weight under three distinct environmental conditions for two years.

Components of variation	Normal environment (non-stress)		Stress environment			
	Irrigated (EI)		Rainfed (EII)		Saline (EIII)	
	1979-80	1980-81	1979-80	1980-81	1979-80	1980-81
$\hat{D}$	15.19±3.34**	13.05± 6.07**	24.37±2.20**	29.98±1.91**	20.70± 5.17**	26.19±2.12**
$\hat{H}_1$	37.29±7.93**	65.58±13.95**	36.01±5.06**	22.67±4.39**	55.39±11.88**	38.14±4.87**
$\hat{H}_2$	35.06±6.90**	50.62±12.14**	25.69±4.40**	13.65±3.82**	53.62±10.34**	29.68±4.24**
$\hat{h}^2$	53.88±4.63**	78.20± 8.14**	43.59±2.95**	−0.17±2.56	43.52± 6.93**	15.12±2.84
$\hat{F}$	2.96±8.15	16.25±14.34	0.35±5.20	14.42±4.52**	−3.96±12.22	22.01±5.01**
$\hat{E}$	0.36±1.15	0.43± 2.02	0.39±0.73	0.40±0.64	0.05± 1.72	0.15±0.71
$(\hat{H}/\hat{D})^{0.5}$	1.57	2.24	1.21	0.87	1.63	1.21
$\hat{H}_2/4H_1$	0.23	0.19	0.18	0.15	0.24	0.19
KD/KR	1.13	1.77	1.01	1.77	0.89	2.07
$\hat{h}^2/\hat{H}_2$	1.54	1.54	1.70	−0.01	0.81	0.51
Heritability	29.82	20.35	39.56	75.11	25.80	60.99
t^2	1.31	0.33	6.49*	0.03	0.11	0.63
r	−0.87	−0.64	−0.22	0.46	0.13	−0.56
bi±S.E. bi	0.50±0.21	0.29± 0.31	0.65±0.10	0.80±0.22	0.46± 0.42	1.03±0.22

* Significant at 5% level.

** Significant at 1% level.

SINGH (1976) and SHARMA *et al.* (1977) also suggested population breeding in the form of biparental mating between selected recombinants to exploit the additive and non-additive gene effects in wheat.

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Effect of cytozyme on yield and yield components in wheat (*Triticum aestivum* L.)

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The Plant growth regulators are playing an important role in agriculture since last 50 years. Plant growth regulators like Indole acetic acid, Naphthalene acetic acid, Gibberellic acid, 2, 4-Dichloro phenoxy—acetic acid etc. are used to bring about changes in the physiological process of the plant. Recently however, cytozyme has been added to the list of plant growth regulators. There are different formulations of this biologically derived active enzyme compound, e.g. Cytozyyme seed$^+$, Cytozyme soil$^+$ and Cytozyme crop$^+$ which also augment nutritional support for plant.

According to SILVA & STUTTE (1980) cytozyme is a plant biostimulant bacterial enzyme+cytokinin+auxin and micronutrient. They observed that, application of cytozyme increased grain yield of rice from 9.2 to 17.0 percent over control. Present study has been carried out keeping in view the potential of cytozyme for taking the maximum crop yields with advantage.

Cytozyme is used on many crops e.g. wheat, rice, cotton, corn, forage, potatoes, vegetables and fruits, for increased emergence rate, seeding vigour through improved plant support, improved crop quality and greater yield (METCALF 1970; ASGHAR *et al.* 1981).

Materials and Methods

The studies were under taken to observe the effect of different formulations of cytozyme on wheat cultivar P94. The experimental material was sown in split plot design with four replications. The 12 sub-plots of each replication with three different formulations of cytozyme were applied on each of four sub-plots, that is:

A_1 Seed$^+$: seed was soaked in cytozyme seed$^+$ solution for 2 hours before sowing.

A_2 Soil$^+$: It was sprayed on soil surface after final seed bed preparation and before sowing.

A_3 Crop$^+$: The formulation was sprayed on the crop when it was at pre-booting stage.

Four doses of each formulation including control were used. The doses of seed$^+$ formulation were 0.125, 0.250 and 0.375 litres per hectare and for soil$^+$ and crop$^+$ were 0.425, 0.850 and 1.275 litres per hectare for D_1, D_2 and D_3 respectively, compared to control (D_0). The soil was loamy in texture with pH value of 7.4 having very low organic matter. The data was recorded on spike number, spikelet number, floret number, grain number, seed index and grain yield per plot.

Results and Discussions

Average number of spikes per plant is given in Table 1, It shows that higest average number of 2.55 spikes per plant was observed from untreated crop. The next high number 2.4 was produced by Crop$^+$ formulation at D_3 level and lowest number of 2.20 spike per plant was provided by seed$^+$formulation at D_2 level. However, all these differences were found to be non-significant.

Although differences in spikelet number (Table 1) of three formulations at all doses were non-significant, yet it was observed that all the treatments increased spikelets per spike over that of control. Meximum spikelets were recorded from crop$^+$ formulation at higher dose and the lowest spikelet number was provided by seed$^+$ formulation.

Similar increase in floret number (Table 1) was recorded for all the doses of each formulation but increase in floret number at dose levels found to be non-significant. The differences among formulations for floret number were found to be significant. Maximum floret number of 46.9 were recorded for crop$^+$ formulation at the dose of 1.275 litre and significant low number of 44.9 florets per spike was recorded for seed$^+$ formulation at the dose of 0.125 litres. The observstions, revealed that crop$^+$ formulation was more effective for increasing floret number in wheat crop.

The grains per spike (Table 1) are increased due to increasing rate at each formulation. Maximum grains of 28.9 per spike were obtained from crop$^+$ formulation as compared to control which produced 27.9 grains per spike. The minimum grain number of 27.8 was

Table 1. Effect of different formulations of cytozyme and their doses on yield and yield components of wheat

Formulations	Doses	Number of spikes per plant	Spikelets per spike	Florets per spike	Grains per spile	Seed index	Grain yield per plot in kg
Soil$^+$ A^1	D0	2.325	14.937	45.300	27.838	3.995	3.815
	D1	2.100	14.897	44.970	27.895	3.961	3.570
	D2	2.225	14.867	45.232	28.165	4.194	3.715
	D3	2.300	15.032	45.468	28.00	4.040	3.725
Seed$^+$ A^2	D0	2.400	14.962	46.085	27.972	3.665	3.630
	D1	2.225	15.03	45.745	28.4	3.916	3.740
	D2	2.250	14.952	45.995	28.185	3.870	3.630
	D3	2.450	15.025	45.96	27.882	4.000	3.695
Crop$^+$ A^3	D0	2.550	15.012	45.495	27.928	4.044	3.560
	D1	2.450	15.002	46.528	28.027	3.968	3.655
	D2	2.170	15.012	46.747	28.045	3.416	3.710
	D3	2.525	15.175	46.905	28.978	4.137	4.050
LSD	C.V.	9.59	0.667	2.07	1.862	5.51	7.629
	S.E.	0.065	0.029	0.274	0.023	0.063	0.021
	(P≥. 0.5)	0.1127	NS.	0.681	NS.	NS.	NS.

recorded for untreated crop (Table 1).

Increase in seed index (Table 1) was recorded for seed$^+$ and soil$^+$ formulation at different doses whereas crop$^+$ formulation responded to lower extent. Data on seed index was found to be significant.

Crop$^+$ formulation at higher dose of 1.275 litre per hectare provided maximum average grain yield of 2.337 tons per hectare as compared to 2.292 tons per hectare obtained in case of untreated crop. Thus an increase of 4.1 percent in grain yield over control was obtained. Seed$^+$ and soil$^+$ formulation at all the doses, on an average, provided lower grain yield.

Although differences among different formulations at various doses were non-significant, yet observations of this study revealed that application of crop$^+$ formulation at higher dose was beneficial for the crop. The results are in co-operation with those of METCALF (1978) and COTHREN & COTTENMAN (1980), who have shown that cytozyme crop$^+$ foliar spray increased yield of maize and cotton respectively. Similar findings have been reported by SILVA & STUTTE (1980) in rice. ASGHAR *et al.* (1981) have also reported 5.14% increase in grain yield of wheat with application of crop$^+$ cytozyme, which also confirm present findings.

Present study has suggested that application of cytozyme on wheat crop has some benificial effects on yield. Crop$^+$ formulation was found to be more effective at higher dose, but most of the results were non-significant. Therefore, further investigations are suggested before generalization.

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II. Record

Proceedings of the 18th Wheat Genetics Symposium of Japan

The 18th Wheat Genetics Symposium of Japan was held at Tottori Mycological Institute, Tottori, Japan on Oct. 14 and 15, 1984. The followings are the abstructs of the contributed presentation. In addition to these constribution, a film demonstration was presented by the Institute.

An *Aegilops longissima* chromosome causing chromosome aberrations in common wheat

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A chromosome of *Aegilops longissima,* (2n=14, S^lS^l), which was spontaneously substituted for wheat chromosome 4A in a common wheat (*Triticum aestivum,* 2n=42, AABBDD) cultivar 'Selkirk', was found to render the wheat gametes without it functionless, thus being exclusively transmitted to the offspring (Maan 1976). In order to produce the *longissima* chromosome substitution line in another common wheat cultivar 'Chinese Spring', 'Chinese Spring' monosomic 4A was crossed as female with the monosomic *longissima* chromosome addition line of 'Chinese Spring'. The somatic chromosome constitution in root-tip cells of the offspring was examined by a chromosome banding technique, N-banding which could identify 16 of 21 'Chinese Spring' chromosomes and the *longissima* chromosome. Unexpectedly, obvious chromosome aberrations, such as deletion, translocation, and ring chromosome, were found in many of the effspring; nineteen out of 34 plants examined had one or more of such aberrations.

The same addition line was crossed as male to euploid 'Chinese Spring', and a part of the offspring (four out of 12 examined) showed at least one chromosome aberration. However, no chromosome aberration was detected in any of the offspring (19 plants were examined) from the self-pollination of the disomic substitution line of 'Chinese Spring', in which a pair of 4A chromosomes were substituted with a pair of the *longissima* chromosomes. It was hardly suspected that the chromosome aberrations had occurred in the gametogenesis of the monosomic addition line because its pollen meioses had been perfectly normal. From these facts, it was suggested that the *longissima* chromosome in the monosomic condition itself caused the chromosome aberrations in common wheat, though the genetic background might affect the frequency of the occurrence of the aberrations.

The aberrations seemed to occurr in any chromosome, including the *longissima* chromosome, and in any chromosome region, and were demonstrated to last to meiosis, though only a few plants were examined with the pollen mother cells. A few plants showed clear karyotype mosaics; different roots from the same seedling had different chromosome aberrations. This fact implied that the aberrations had occurred in early embryogenesis.

Besides *Ae. longissima, Ae. sharonensis* (2n=14, S^lS^l) and *Ae. speltoides* 2n=14, SS) were so far proved to have a chromosome causing chromosome aberrations like the *longissima* chromosome. Such chromosomes might not be rare in *Triticum* and *Aegilops* and at least partly responsible for the karyotype differentiation in those genera.

Chromosomal aberrations induced by *Agropyron* chromosome in common wheat

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Four alloplasmic monosomic addition lines for the *Agropyron* chromosome were crossed with other common wheat cultivars, Chinese Spring and Salmon. The F_1 seeds had poor germination. Some had slow germination and short roots, but the others were inviable. Mitotic cells from these short roots exhibited an extensive chromosomal aberrations, such as chromosomal fragments, telocentric, dicentric and ring chromosomes, translocations and chromosome mosaic (Fig. A). From Giemsa N-banding patterns of metaphase cells showing aberrations, breakage occurred in both eu- and heterochromatic regions, and break points on the chromosomes seem to be random (Fig. B). On the other hand, in metaphase cells from roots of the plants 60 days after germination, most had normal chromosome constitution and did not show any chromosomal aberrations,

Cytological results also indicate that chromosomal aberrations occur in embryos and seedlings, and cells with aberrations tend to be selected in the successive nuclear divisions during young plants. Mitotic chromosome pairing data show that the used plants retained one *Agropyron* chromosome. Therefore, it can be concluded that at least aberrations were induced by gene(s) on the *Agropyron* chromosome. The chromosome rearrangement gene(s) may be useful for the induction of translocations between non-homologous chromosomes.

This work was supported in part by a Grant-in-Aid (No. 59740307) from the Ministry of Education, Science and Culture, Japan.

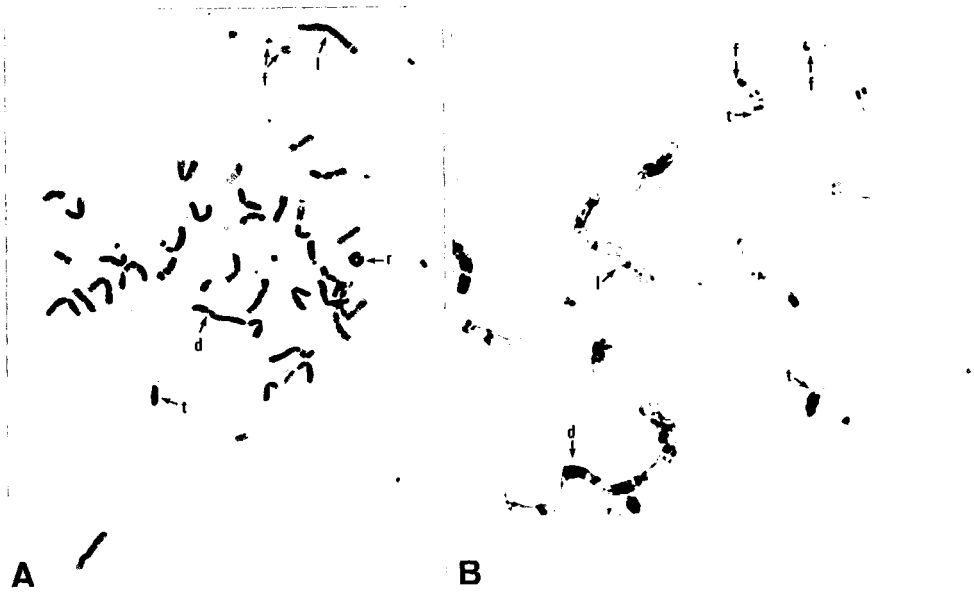

Fig. Mitotic metaphase in monosomic *Agropyron intermedium* chrosome addition line of common wheat, sheat, showing chromosomal aberrations. Arrows indicate chromosomal fragments (f), telocentric (t), dicentric (d) and ring (r) chromosomes and translocations (1). A: Acetocarmine staining, B: Giemsa N-band staining.

The relationships of the M and M^u genomes of *Aegilops*

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The genome constitutions of the 2x species of *Aegilops comosa* (incl. *heldreichii*) and *Ae. uniaristata* were established as MM and M^uM^u, respectively, by KIHARA (1937). Recently, KIMBER *et al.* (1983) have proposed the genome symbol of *Ae. uniaristata* for Un, namely the genome of *Ae. uniaristata* is comletely different from that of *Ae. comosa* from the results of meitotic chromosome pairing configurations in triploid, tetraploid and pentaploid hybrids involoving M and M^u genome species.

However, we have cytological and morphological evidences for their relationships. The high frequencies of pairing have been observed in F_1 and BF_1 hybrids between *Ae. comosa, heldreichii* and *uniaristata* by KIHARA & YAMADA (1942) and YAMADA & SUZUKI (1941), as shown in Table 1. From the data obtained, it can be said that in the F_1 plant (MM^u) with *comosa* plasma, gamete with M^u genome is lethal. On the basis of the morphological analysis, these species are regarded as the collectives as shown in Table 2.

Accordingly, it can be concluded that the M and M^u genomes were derived from a common genome constitution.

Table 1. Chromosome pairing in F_1 and BF_1 hybrids between *Ae. comosa, heldreichii* and *uniaristata*

Cross combination	No. of PMC's observed	Average bivalents per cell	Typical pairing type (frequency)	P.f.*	S.f.*
como. ×uni.[1)]	233	5.39	$1_{III}+5_{II}+1_I$ (36.5%)	0.9%	0.0%
F_1 ×uni.	104	5.75	$1_{III}+5_{II}+1_I$ (36.5%)	—	0.0
F_1 ×como.	120	6.95	7_{II} (95.0%)	91.6	92.9
held. ×uni.[1)]	100	5.48	$1_{III}+5_{II}+1_I$ (42.0%)	1.5	0.0
F_1 ×uni.	77	5.81	$1_{III}+5_{II}+1_I$ —	1.3	0.0
como. ×held.[2)]	1093	6.85	$1_{IV}+5_{II}$ (89.2%)	74.1	83.0

[1)] Kihara & Yamada, 1942 (Seiken Ziho 1), [2)] Yamada & Suzuki, 1941 (Jap. J. Genet. 17).

* P.f.: pollen fertility S.f.: seed fertility

Table 2. The morphological difference between the three species, namely *Ae. comosa, heldreichii* and *uniaristata*

	comosa	*heldreichii*	*uniaristata*
Ear	spindle	narrow conical	
Empty glume of apical spikelets	both glumes are 3 awns, or 3 awns and 1 awn, or both glumes are single awn		both glumes are single awn
Upper margin of empty glume in the lateral spikelets	bi-dentat, two teeth, one of them broader		bi-dentat, a strong awn and a broadly triangular tooth

Variation of chromosome pairing in hexaploid wheat 7. A model and simulation for the chromosome arrangement in premeiotic nucleus

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In hexaploid wheat, anyone of those three factors, extra dosage of 5BL, colchicine and high temperature treatments, reduced the degree of homologous pairing and in the same PMCs it induced homoeologous pairing (Feldman 1966; Driscoll *et al.* 1967; Kato and Yamagata 1980). This peculiar pairing behavior can reasonably be explained by a hypothesis that a chromosome is situated closely to its homologous chromosome but is separated from its homoeologous ones in premeiotic nucleus (Feldman 1966). In premeiotic nucleus, however, direct observation on the chromosome condition was very difficult and did not contribute enough information to the precise analysis on this problem.

The present study was undertaken to analyse the chromosome arrangement in premeiotic nucleus from other lines of approach. First, topographical model was applied to the chromosome arrangement and its variation. Then, the simulation which was based on

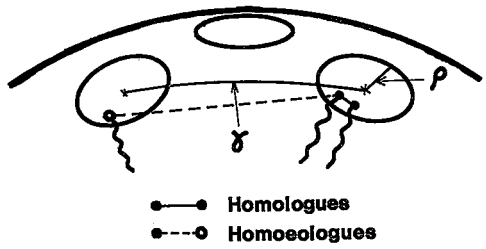

Fig. 1. A model for the chromosome arrangement in premeiotic nucleus. See text for the details.

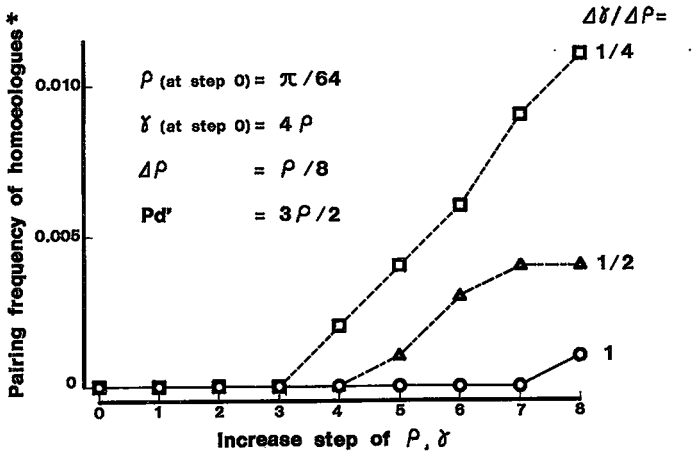

Fig. 2. Simulated occurrence of homoeologous pairing with increasing ρ and γ.
* Freguency of the case when the distance between homoeologues is less than pd'.

the model was carried out to examine whether it could reproduce the peculiar pairing behavior as described above.

The details of the model were as follows (see Fig. 1); 1) The premeiotic nucleus is spherical in shape. 2) On the nuclear envelop (spherical surface), there exist three circular regions. Each region corresponds to the individual genome. This region has a radius, ρ and is separated from other regions by a distance, γ. 3) Every chromosome belonging to the same genome attaches its one particular part to the corresponding region. The chromosome part attached to that region is unique point from where synapsis starts. 4) When the distance between homoeologues (between attached sites) is less than the constant, Pd', such homoeologues can form synapsis at zygotene stage, otherwise they do not succeed in pairing. The other constant, Pd, is provided for the case of homologues. 5) The above three factors causing the peculiar pairing affect the chromosome arrangement with increasing ρ and γ.

After setting adequate values in parameters (see Fig. 2), ρ and γ were increased by $\Delta\rho$ and $\Delta\gamma$, respectively. In each increase step, chromosomes (attached sites) were scattered randomly 1000 times within the region, and the distances between homeologues or homologues were measured and compared with Pd' or Pd, respectively.

Figure 2 shows a typical result from the simulation. In this figure, it is clearly found that the pairing frequency of homoeologues increased with ρ and γ. Figure 2 indicates also that the decrease of $\Delta\gamma/\Delta\rho$ made homoeologous pairing occur at earlier increase step of ρ. The increase of ρ obviously resulted in the decrease of the pairing frequency of homologues. Hence, this result means that when $\Delta\gamma$ is sufficiently small compared with $\Delta\rho$, homoeologous pairing can be induced even in the PMCs showing higher degree of homologous pairing. This situation may correspond to the actual result from high temperature treatment.

Influence of alien cytoplasms on callus proliferation and streptomycin resistance in common wheat

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It is important to know the alloplasmic effects for the manifestation of characters both at cellular and whole plant levels.

The seeds of eighteen kinds of allo- or euplasmic lines were provided by the courtesy of Dr. Tsunewaki and used for this investigation. These lines have a common nuclear genotype of 'Chinese Spring' (abbereviated as CS). Murashige and Skoog (MS) medium containing 2 mg of 2, 4-D (2, 4-dichlorophenoxy acetic acid) per liter was used for the seed callus initiation and tissue cultures. Callus culture bioassays were performed by transferring small callus pieces, each weighing approximately 50 mg, onto MS medium with the addition of 0, 125, 250 or 500 ppm of streptomycin sulfate. Callus cultures were incubated in darkness at 26℃ for 74 days before measuring callus for fresh weight and the resistance index was exhibited as the percentage of the weight measured after the treatment to those of control calli grown in the absence of streptomycin. In correspondence to the examination at callus level, the germinating ability and streptomycin resistance at seedlings were evaluated using the same materials.

Although there was no marked difference as to the callus initiation and the morphological characteristics of callus irrespective of allo- or euplasmic lines, the growth rates were remarkably reduced in seed calli of several alloplasmic lines. It is probable that the reduction of callus growth may arise from the physiological nature of the specific alloplasmic lines and the cytoplasmic factors may insert their effects on the ability of callus proliferation in co-operation with the genotype of CS. It is also noted that the proliferation of the seed calli has some relation with the initial growth of radicle in the germination. In both cases, euplasmic line indicated the best growth. The delay of growth in (*crassa*) CS and (*ovata*) CS were conspicuous in both characters. It is recognized that (*ovata*) CS shows slow growth in the spring and delayed heading at plant level.

Streptomycin resistance can be used as a marker for selection of somatic hybrids in culture. In this experiment, a considerable increase of streptomycin resistance was observed in (*ovata*) CS both at cellular and plant levels. In addition, several alloplasmic lines showed a high resistance though the growth rate of calli was relatively low. This is deduced from the fact that streptomycin will prevent active cell divisions as its effect. It is concluded that the cytoplasmic factors from the alien species are deeply related to the physiological nature such as callus growth and streptomycin resistance. Thus, cytoplasmic genes may insert their various effects both at cellular and plant levels in co-operation with nuclear genes.

Mitochondrial DNA diversity among *Triticum* and *Aegilops* species

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In order to characterize mitochondrial(mt) geonomes in *Triticum* and *Aegilops*, mtDNAs are isolated from cytoplasms of 20 species (27 accessions in total) as listed in Table 1, and their restriction fragment patterns with five enzymes (*Bam*HI, *Hin*dIII, *Pst*I, *Pvu*II and *Xho*I) are analyzed. In paticular, cytoplasms of five Sitopsis species are included in order to reveal the cytoplasm donor of polyploid wheats. Different sources of cytoplasms for each of type 1b, 3 and 4 chloroplast(ct) genomes are also included because of some differences observed in their phenotypic effects on wheat characters. Intact mitochondria are isolated from etiolated seedlings by a modified method of Bonen and Gray (1980), and mtDNAs are purified by CsCl equilibrium centrifugation. Figure 1 shows *Hin*dIII restriction fragment patterns of mtDNAs from B, G, S, S^b, S^l, S^v plasma types. MtDNA of *Ae. longissima*(11) gives identical restriction pattern with those of *T. dicoccum*(22) and *T. aestivum*(52a), whereas mtDNA of *Ae. aucheri*(09) shows identical pattern with those of *T. timopheevi*(25) and *T. zhukovskyi*(51). These facts prove that *Ae. longissima* and *Ae. aucheri* have provided their mitochondrial genomes, and consequently their cytoplasms, to the Emmer Dinkel and Timopheevi groups of wheat, respectively. Mt DNA variations are observed among some cytoplasms having the identical ctDNAs. For example, mtDNAs of *T. dicoccoides*(21) and *T. spelta*(52b) are distinguishable from those of *Ae. longissima* group by two *Hin*dIII fragments, although, at least, 36 fragments are found in common. MtDNAs of *T. araraticum*(23, 24) are distinguished from those of *Ae. aucheri* group by five of 69 *Hin*dIII fragments in total. Six cytoplasms having type 1b chloroplast genome are classified into four types (i, j, k and l) from their mtDNA restriction pattern. The i, j, k and l types have three, two, three and three unique *Hin*dIII fragments, respectively, in additon to 42 commom fragments. MtDNA of *Ae. bicornis*(12) and those of *Ae. kotschyi*(33) and *Ae. variabilis*(34) have nine and eight unique *Hin*dIII fragments, respectively, besides 113 common fragments. MtDNAs of two *Ae. mutica* lines (13, 14) differ from each other by eight and 11 unique *Hin*dIII fragments though 36 fragments are the same between them. Results of the restriction endonuclease analyses with *Hin*dIII and four other enzymes are summarized in Table 1. Mitochondrial genome

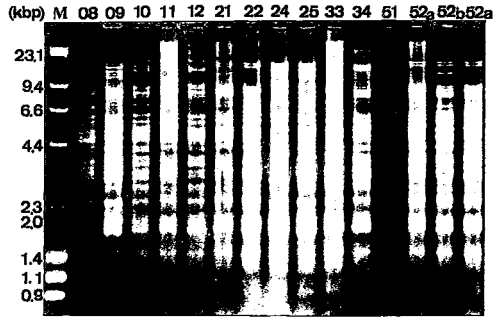

Fig. 1. Hin*Hinb*III restriction fragment patterns of mtDNAs.

Table 1. Sources of the cytoplasm used for mtDNA extraction

Code no.	Species	Plasma type	Ct genome type	Mt genome type[2)]
08	*Ae. speltoides*	S_1	8	a
10	*Ae. sharonensis*	S_b	1c	b
12	*Ae. bicornis*	S_v	1b	c
33	*Ae. kotschyi*	S^v	1b	d
34	*Ae. variabilis*	S^v	1b	d
09	*Ae. aucheri*	G	5	e
25	*T. timopheevi*	G	5	e
51	*T. zhukovskyi*	G	5	e
23	*T. araraticum* K	G	5	f
24	*T. araraticum* M	G	5	f
11	*Ae. longissima*	B	7	g
22	*T. dicoccum*	B	7	g
52 a	*T. aestivum*	B	7	g
21	*T. dicoccoides*	B	7	h
52 b	*T. spelta*[1)]	B	7	h
03	*Ae. umbellulata*	C^u	3	i
26	*Ae. triuncialis*	C^u	3	j
29	*Ae. biuncialis*	C^u	3	j
30	*Ae. columnaris*	C^u	3	k
32	*Ae. triaristata* 4x	C^u	3	l
54	*Ae. triaristata* 6x	C^u	3	l
13	*Ae. mutica* M	Mt	4	m
14	*Ae. mutica* P	Mt^2	4	n

[1)] Euplasmic line is used. (All others are alloplasmic lines of common wheat)

[2)] Tentative designation.

designation given in it is tentative. The results clearly indicate that the mitochondrial genome shows higher variability than the chloroplast genome in *Triticum* and *Aegilops*. Thus, the mtDNA variability can be useful objective in the studies of interspecific relationship and intraspecific variation of the cytoplasm.

Leaf photosynthesis in reconstituted tetraploid wheat

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Three cultivars of bread wheat and their reconstituted teraploid (AABB) wheat were used as shown in Table 1. The discs were prepared from fully expanded leaf blades of two developmental stages of each strain. Seedling stages: for each strain, five seeds were sown in acrylic tubes filled with 0.7% agar, from which seedlings were grown at 25℃ in a growth chamber. The first leaves of seedlings fully expanded were used for the preparation of leaf discs. Flowering stages: these strains were grown in clay pots in a green house. When fully flowered, the discs of flag leaf were prepared. The reaction system for measuring photosynthesis with an oxygen electrode (Rank Brothers Inc., England) consisting of 3 ml of 50 mM HEPES buffer (pH 7.2) with 50 pieces of 3 mm diameter leaf discs at 25℃. The photosynthetic reaction was started by adding 100 μl of 0.625 M $NaHCO_3$ under illumination with a halogen lamp of 300 W. The chlorophyll content was measured according to ARNON (1949) using leaf discs taken from the same leaves after exygen evolution measurements.

The photosynthetic rate was determined for six strains. Although the growth of reconstituted tetraploid wheat was not so vigorous as compared with genuine hexaploid wheat, the photosynthetic rate of reconstitutedd tetraploid wheat was higher than that of hexaploid wheat. The chlorophyll content was not significantly different between hexaploid and tetraploid wheats. In the first leaf, the tetraploid/hexaploid ratio of photosynthesis rate was 1.80 in Chinese Spring, 1.53 in Thatcher and 1.48 in Prelude. In the flag leaf, the ratio of photosynthesis rate was 1.02 in Chinese Spring, 1.19 in Thatcher and 1.69 in Prelude. These differences were found under a unit leaf area. The first leaf is less complex than the flag leaf. Its growth is influenced by grain reserves. The growth of the flag leaf is influenced by all previous leaves and grain filling.

Nuclear ploidy levels in plant species are frequently correlated with changes in several cellular features, the number of cells found under a unit leaf area and the number of chloroplasts per cell. In wheat, the interpretation of the effect of cell size on photosynthesis is complicated by the effect of ploidy. When comparisons are made under a unit number of cells or chloroplasts, the ploidy effects are more informative because these were compared from a view point of function of cells and chloroplasts.

Table 1. Photosynthetic rate in leaves of reconstituted tetraploid wheat

Strains	Photosynthesis (μmol O_2-evolved/dm²/hr)		Chlorophyll (a+b) (mg/dm²)	
	first leaf	flag leaf	first leaf	flag leaf
Hexaploid wheat (AABBOO)				
Chinese Spring	88.4	44.5	3.43	3.98
Thatcher	98.4	70.9	3.19	4.01
Prelude	88.2	38.9	3.41	4.46
Tetraploid wheat (AABB)				
Tetra Chinese Spring	159.4	45.5	3.66	2.90
Tetra Thatcher	150.4	84.8	3.33	4.19
Tetra Prelude	130.4	65.9	3.36	4.09
L.S.D. (0.05) d.f.=12	48.1	27.3	0.92	0.85

New types of *Cs* chlorosis found in hybrids between the Emmer and the Timopheevi group of the tetraploid wheats

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Intra- and interspecific hybrids of wheat often show various types of hybrid weakness. Of these, necrosis and chlorosis are most commonly observed. In hybrids between the Emmer and the Timopheevi group, chlorosis is reported by TSUNEWAKI & HAMADA (1968) and by TSUNEWAKI & NAKAI (1973). It is caused by two complementary genes; *Cs1* carried by the Emmer group and *Cs2* of the Timopheevi group. In the present study, a *Cs1* tester strain was crossed to 11 strains of the Timopheevi wheats and three types of chlorosis differing with the time of appearance were recognized in the hybrids. Of these, two types were not described in the earlier reports.

The results of crosses of ten strains of *Triticum araraticum* Jakubz. and one of *T. timopheevi* Zhuk. with a *Cs1* tester strain of *T. dicoccum* Schübl. KU-123 are shown in Table 1. Hybrids were grouped into four types: 1) Normal. 2) Weakly chlorotic. Chlorosis began to appear in early tillering stage. Chlorotic plants tillered and headed normally but were less vigorous than normal ones with lower plant height and fewer tillers. 3) Moderately chlorotic. Chlorosis gegan to appear in early winter when the seedlings had 2 or 3 leaves. These plants showed stunted growth and mostly died in winter. Few survived plants were very weak and produced only a few tillers in spring. This would be the same type of chlorosis as that reported earlier. 4) Severely chlorotic. Most of the seedlings died without extending the leaves. Several plants produced 1 or 2 yellow leaves indicating chlorosis but they also died soon after.

In order to study the genes responsible to chlorosis, four strains of the Timopheevi wheats were crossed with F_1 hybrid between *T. dicoccum* KU-114(*cs1*) and KU-123. In these four hybrid combinations, segregation of normal and chlorotic plants fitted well to 1 : 1 ratio (Table 2). This confirmed that *T. dicoccum* KU-123 carries a single chlorosis gene which

Table 1. Result of crosses between *T. araraticum* or *T. timopheevi* and Csl tester strain, *T. dicoccum* 123

Cross combination*	Phenotype
196-1 ×123	Normal
8821 B ×123	Normal
8940 ×123	Normal
107-1 ×123	Weakly chlorotic
8947 ×123	Weakly chlorotic
196-2 ×123	Moderately chlorotic
1911 ×123	Moderately chlorotic
1913 ×123	Moderately chlorotic
1914 ×123	Moderately chlorotic
1908 A ×123	Severely chlorotic
1909 A ×123	Severely chlorotic

* 107-1: *T. timopheevi*, other female parents: *T. araraticum*.

Table 2. Segregation of normal and chlorotic plants in the cross, *T. araraticum* or *T. timopheevi* × (*T. dicoccum* 114 × *T. dicoccum* 123) F_1

Cross combination	No. of seedlings	No. of plants	χ^2 value (1 : 1)	Plant height (cm)	No. of tillers
107-1 × (114 × 123)	67 N*	66 { 33 N	0.00	105.2	7.3
		33 WC		86.2	4.9
1911 × (114 × 123)	24 N ⟶	24 N	0.020	108.5	8.0
	25 MC⟶	0			
1914 × (114 × 123)	27 N ⟶	27 N	0.158	110.0	7.9
	30 MC⟶	9 MC		39.5	3.8
1908 A × (114 × 123)	21 N ⟶	21 N	1.00	103.1	8.3
	28**SC ⟶	0			

* N : Normal, WC : Weakly Chlorotic, MC : Moderately Chlorotic, SC : Severely Chlorotic.

** Because seeds were sown in soil, it was difficult to distinguish chlorotic seedlines from those which died without appearing above ground due to other causes (fungi etc.) Therefore, all the unappeared seedlings and ungerminated seeds were included in this category.

interacts with the gene of the Timopheevi wheats. Further, it may be assumed that the gene carried by the Timopheevi wheats consists of four alleles instead of the two reported earlier.

Seed shriveling caused by a gametocidal gene, Gc1

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A gametocidal gene kills its non-carrier female and male gametes which are produced by the hetero- or hemizygous plants for it. Such genes are known in several species of *Aegilops* having C, S or S^1 genome. We introduced a gametocidal gene, *Gc1*, of *Ae. speltoides* into a common wheat, *Triticum aestivum* cv. Chinese Spring (CS), by backcross method (TSUJIMOTO & TSUNEWAKI 1984). The isogenic line of CS for *Gc1* gene is not different in morphology from normal CS. This line, however, causes seed shriveling when it is crossed as male to some common wheat cultivars. No shriveled seeds are produced by the reciprocal cross, the isogenic line (♀)×those cultivars (Fig. 1), or the cross between those cultivars and a carrier of other gametocidal genes as male. Occurrence of seed shriveling is greatly affected by the temperature about eight hours after the pollination. When temperature is lower than 17℃, more than 75% of the seeds become shriveled, whereas it is higher than 22℃, no seed shriveling occurs. Although most shriveled seeds do not germinate, some of them do germinate, giving rise to mutants with speltoid or half-awned spikes, or showing chlorosis in their leaves. Frequency of the mutants is higher in the F_1 lines which show lower germination rate (Table 1). No chimeric plants which havd different types of spikes are obtained except a single plant. This fact indicates that the mutation occurs before the first zygotic cell division. Seed shriveling and mutation observed in the F_1 plants are two symptoms of "hybrid dysgenesis" caused by the gametocidal gene in wheat.

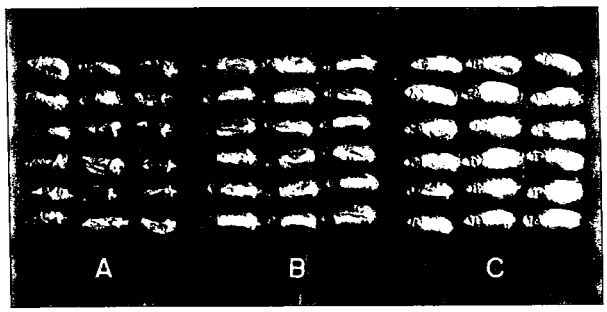

Fig. 1. Seeds produced from the cross, Norin 16 (♀)×CS carrying *Gc1* gene (A), its reciprocal cross (B) and Norin 26 (♀)×normal CS (C).

Table 1. Germination and mutation rate of the F_1 plants between CS carrying *Gg* 1 gene as male and common wheat cultivars

Germination rate (%)	No. of F_1 lines	No. of seeds sown	No. of seeds germinated	No. of mutants	Mutation rate (%)
100-75	17	192	185	6	3.2
75-25	8	98	47	3	6.4
25- 0	30	607	35	4	11.4
Total	55	897	267	13	4.9

Wheat breeding for scab resistance

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More than three thousands wheat varieties and strains collected from home and abroad so far were screened for scab resistance. However, no vareity was immune or highly resistant under optimum conditions for the pathogen. Wheat group from Asia and Japan were recognized to contain many varieties resistant to the disease, comparing with those from Oceania, South America, Africa, Mediterenean countries and Europe. In home grown wheat varieties, Nobeokabozukomugi showed highest resistance to scab. This variety is a local variety in Miyazaki Prefecture in Kyushu region where the disease causes most severe damage. Some of relatives of Einkornreihe and Emmerreihe and some of strains of *Aegilopus* and *Agropyron*, which were tested, were not contained immune or highly resistant strains.

Judging from the results of genetical analysis on F_1, F_2, B_1, B_2 and F_3 hybrids, wheat scab resistance seemes to be conditioned by polygene.

Favorable genetic correlation between scab resistance and other agronomic characters was not found.

The selection for scab resistance by generation of hybrid population showed that line selection in later generation is more effective than individual selection in early generation.

For the purpose of increasing genetic variation of scab resistance in hybrid population, seeds of three varieties, Norin 61, Sumai 3 and Nobeokabozu-komugi, were irradiated with 20k rad from the ^{60}Co source, and M_4 and M_5 generation were screened to select more resistant line than unirradiated parent. Only one resistant line was selected from the population Nobeokabozu-komugi irrdiated. However, the degree of the resistance of the selected line was not so high compared with that of original parent, whereas it was statistically significant. Up to now, little success have been obtained in breeding of comercial vareity resistant to scab at regional agricultural experiment station under juridiction of the Agriculture, Forestry and Fitheries Research Council, MAFF.

The scab resistance selection experiment was carried out to get more resistant line from the crosses among relatively high resistant varieties. In the results, no more resistant line than parent varieties was selected but some selected lines were recognized to have the same resistance as that of higher resistant parent.

Major causes not selected scab resistance line with desirable agronomic characters, seemed to be that most of the resistant varieties have some inferior agronomic characters such as long stem and late maturity, and that scab resistance is governed by polygenes which are separated in succeeding generation after cross.

Therefore, most effective method for scab resistance breeding would be ones containing cycles of selection intercrossing, which woule allow greater chance for recombination between favorable genes.

In a case where two varieties, deriving from different genealogy, have medium scab resistance but many superior agronomic characters, the crossing between these varieties might be expected to induce transgression that accumulated genes for scab resistance of the parent.

Current status of wheat breeding in Japan

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Wheat production has been increased to 232 thousand hectares in 1984, with the yield of 3.2 ton/ha, since the bottom of 75 thousand hectares of 1973. The present production is 740 thousand tons which are supplied to the domestic demand at the self-sufficiency of only 12%. Wheat breeding programmes in Japan are conducted at the seven agricultural research stations, including the NARC. The main breeding objectives are early maturity, high yield and good quality for nuddle. The additional objectives are dependent on the climate conditions where wheat is cultivated.

The recently bred cultivars (Table 1) show early maturity, short statue and high yield. The genetical control of earliness depends on the insensitivity to daylength and vernalization . Attempts for accumulating the physiological factors with respect to earliness are under investigation. The lodging resistance due to semi-dwarfness realizes the cultural improvement of yield performance under the heavy-fertilized and dense-sowing conditions. There is also the breeding objective emphasized as flour quality. Wheat grains harvested at the rainy season suffer from sprouting, deterioration and high α-amylase activity, resulting in worse flour quality. The genetical and physio-chemical survey on the wheat flour and the nuddle are carried out for a rapid selection of breeding lines.

Breeding for disease resistance to leaf rust, yellow mosaic virus, scab, and powdery mildew are important for developing cultivars. Leaf rust resistant genes derived from T. timopheevi and rye were successfully transferred to wheat breeding lines, 'Sabikei 40' and 'Sabikei 43', respectively, which were registered from the Tohoku Nat. Agr. Exp. Sat. in 1984. The selection for resistant plants to yellow mosaic virus is progressed, as the infected plants can be easily distinguished by using ELISA method. The breeding of cultivars with scab resistance has been discussed by Gocho in the ealier paper.

Finally, genealogical consideration on pedigrees of Japanese wheat cultivars (FUKUNAGA & INAGAKI 1985) indicates that most clutivars released in the southern part of Japan have been derived from progenies of crosses between only local varieties. Transfer of alien genetic sources from other relative species is positively attempted for future improvement of wheat cultivars. Saving the time required for cultivar development may be accomplished by using doubled-haploid method. MAFF has recently intensified the research activities on genetic resources and biotechnology of crops, which will be studied at the National Institute of Agro-biological Resources.

Table 1. New wheat cultivars and their agronomic characters

Cultivar	Released in	Pedigree	Major characteristics	Growth habit
Fukuwasekomugi	1983	Chukei 3989/ Chukei 4010	Very early maturity	Spring
Nishikazekomugi	1984	Shiroganekomugi/ Ushiokomugi	Early maturity YMV resistance High yield	Spring

III. Editorial Remarks

Announcement for Future Issues

WIS No. 61 will be planned for publication in September, 1985, Manuscripts for this issue are most welcome and accepted any time, not later than July 31, 1985.

WIS is open to all contributions regarding methods, materials and stocks, ideas and research results related to genetics, breeding and cytology of *Triticum, Aegilops, Seeale, Haynaldia* and related genera. Manuscripts should be typewritten (double-space) in English, and submitted with duplicates. One article should not exceed five printed pages, including two textfigures (smaller than 7×7 cm^2). Lists of stocks are exempted from this page limit. Authors receive 50 reprints of their contributions free of charge. Extra copies are printed by order at cost price. Communications regarding editorial matters should be addressed to :

Wheat Information Service,
c/o Kihara Institute for Biological Research,
Mutsukawa 3-122, Minami-ku,
Yokohama 232, Japan

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The Managing Editor

Explanation of the Figure on the Cover

Mtotic metaphase plates of root-tip cells in monosomic *Agropyron intermedium* chromosome addiion line of common wheat, showing chromosomal aberrations. Arrows indicate chromosomal fraglents (f), telocentric (t), dicentric (d) and ring (r) chromosomes and translocations (l). A: Acetocrmine staining, B: Giemsa N-band staining. See the text article by MUKAI for the details.

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