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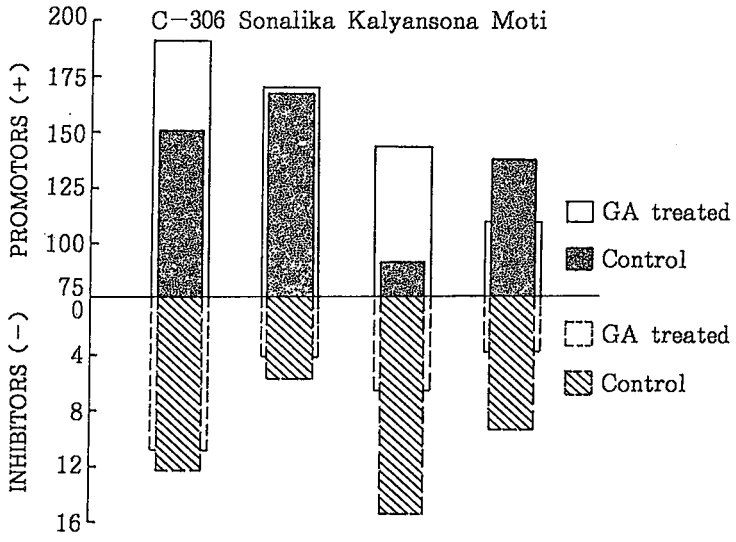
WHEAT INFORMATION SERVICE



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Kihara Institute for Biological Research

Yokohama, Japan

Contents

Dr. Kosuke YAMASHITA
(1909 – 1988)

It is our great regret to announce that Dr. Kosuke Yamashita, the former Managing Editor of Wheat Information Service, passed away on April 30, 1988.

He was a cheerful but sincere scientist, and made a great contribution to wheat genetics. Among many research works he engaged in, the micrograph of the ring-of-fourteen chromosome of *Triticum monococuum,* especially, impressed many people, which was in part of his studies on chromosome translocation and gene mapping of Einkorn. He was one of pioneers in the field of genetic resources of plants. He was the person who actually collected the accessions of *Aegilops squarrosa,* during the Karakorum and Hindukus Science Expedition organized by the late Dr. H. Kihara in 1955. He organized several science expeditions for cereal resources to Middle East, Mediteranian region and nothern Africa. He worked to establish and manage the international organizations for plant genetic resources including FAO and IBPGR.

As the managing editor of Wheat Information Service since its establishment in 1957, he organized and proposed the international communication and cooparation in the field of wheat reserches.

His hummane personality and scientific contributions will be alive in many wheat people.

M. Tanaka

Masatake Tanaka
Managing Editor

I. Research Notes

An analysis of induced homoeologous pairing in hybrids between *ph* mutant of *Triticum aestivum* and tetraploid wheat species *T. timopheevii* and *T. militinae*

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Triticum timopheevii Zhuk. (AAGG, 2n=28) is a tetraploid wheat species first found in Central Transcaucasia (Western area of Georgia, U.S.S.R.) by academician P.M. ZHUKOVSKI (1928). *Triticum militinae* Zhuk. et Migush. (AAGG, 2n = 28) was isolated as a spontaneous mutant from experimental plots of *T. timopheevii* by P.M. ZHUKOVSKI in 1950 and it differed from the latter by naked grains and black awns. Both of these species have attracted interest of wheat breeders and geneticists on account of their exceptionally high immunity to diseases. Therefore they have frequently been included as parental material in wheat breeding programs. However, a typical characteristic of these species is that their F_1 hybrids with other wheat species have irregular meiosis and they are highly sterile.

For a long period wheat breeders endeavoured to solve the problems of sterility in F_1 hybrids, since a deeper knowledge of the basic genetical structure and function of the genetic system in *T. timopheevii* and *T. militinae* is not only of fundamental but also of practical importance. SACHS (1953) and FELDMAN (1966) assumed that poor chromosome pairing in hybrids F_1 between tetraploid wheat species involving *T. timopheevii* was due to criptic structural differences. This conclusion was supported also by SEARS (1956) and RILEY *et al.* (1958). However, WAGENAAR (1961, 1963, 1966) suggested that irregular meiosis in F_1 hybrids was due to genetic system with some asynaptic genes which affected chromosome pairing and chiasma formation.

In our crosses we used a mutant *ph1* and nulli-tetrasomic line cv. Chinese Spring for the purpose of inducing alien chromosomes of hexaploid and tetraploid wheat to pair. It is known that homoeologous pairing in wide hybrids F_1 is limited by the *Ph1* gene located on chromosome 5B in common wheat. The use of mutant *ph1* with deletion of *Ph1* locus gives a possibility to transfer genetic material from alien species to common wheat varieties (SEARS 1976, 1980).

In this paper we present cytological analysis of meiosis in F_1 hybrids between hexaploid and tetraploid wheat species using mutant *ph1* and nulli-tetra compensation line.

Materials and Methods

Triticum aestivum cv. Chinese Spring (CS), the CS mutant *ph1* and CS nulli-5B-tetra-5A line (AABBDD, 2n = 42) were used as the female parent in crosses with tetraploid wheat species *T. timopheevii* and *T. militinae* (AAGG, 2 n = 28). Spikes of hybrid F_1 plants were fixed in Newcomer's fluid and anthers were squashed in 2% acetocarmine. PMCs were scored for the presence of uni-, bi- and multivalents.

Results and Discussion

The cytological data obtained from meiotic studies of F_1 hybrids CS x *T. timopheevii* and CS x *T. militinae* showed that both of these hybrids exhibited substantially the same degree of meiotic irregularities with the mean number of bivalents 7.2 and 6.4, and multivalents, 0.63 and 0.25, respectively, per cell (Table 1). It is supposed that the chromosomes of the A genome of *T. aestivum* as well as of *T. timopheevii* and *T. militinae* took part in bivalent formation whereas the chromosomes of the B genome and the D genome of *T. aestivum* and the G genome of *T. timopheevii* and *T. militinae* remained in univalent condition or partially included in multivalents associations.

When mutant *ph1* and CS nulli-5B-tetra-5A line were used in the crosses the rate of homoeologous pairing in F_1 hybrids increased significantly.

Table 1. Meiotic chromosome pairing in F_1s from crosses involving *T. aestivum* and two tetraploid wheat species

Hybrids	No. cells examined	Mean number per cell			
		bivalents	univalents	multivalents	chiasmata
CS x *T. timopheevii*	130	7.2±0.1	18.3±0.3	0.63±0.07	12.0±0.2
CS mutant *ph1* x *T. timopheevii*	243	8.3±0.1***	14.7±0.3***	1.1±0.05***	15.4±0.2***
CS x *T. militinae*	32	6.4±0.3	21.5±0.5	0.25±0.07	9.5±0.4
CS nulli-5B-tetra-5A x *T. militinae*	184	8.4±0.1***	16.0±0.2***	0.68±0.05***	13.3±0.2***
CS mutant *ph1* x *T. militinae*	313	8.7±0.1***	14.7±0.2***	0.85±0.04***	13.2±0.2***

*** ; $p < 0.001$

Table 2. Mean rate of univalents, bivalents, multivalents and chiasmata in interspecific hybrids F_1 of wheat

Hybrids	Range of observed				Percent of PMCs with multivalents (from 1 to 4 multivalents per cell)				
	univalents	bivalents	multivalents	chiasmata	1	2	3	4	Total
CS x *T. timopheevii*	3-12	11-29	1-2	4-19	41.5	12.3	0	0	53.8
CS mutant *ph1* x *T. timopheevii*	3-14	4-27	1-4	5-26	40.2	23.2	5.7	1.6	70.7
CS x *T. militinae*	3-11	13-29	1	3-14	25.0	0	0	0	25.0
CS nulli-5B-tetra-5A x *T. milit.*	5-14	6-23	1-3	6-23	39.1	10.3	2.2	0.5	52.1
CS mutant *ph1* x *T. militinae*	2-14	5-27	1-4	6-22	40.9	15.3	4.5	0.6	61.3

In F_1 hybrid plants CS mutant *ph1* x *T. timopheevii* the mean numbers of bivalents and multivalents per cell were 8.3 and 1.1, respectively, and the percentage of PMCs with multivalents (tri-, quadri- and pentavalents) was rather high, 70.7 (Table 2). In F_1 hybrids CS nulli-5B-tetra-5A x *T. militinae* and CS mutant *ph1* x *T. militinae* the mean numbers of bivalents per cell were 8.4 and 8.7, multivalents, 0.68 and 0.85, and chiasmata, 13.3 and 13.2, respectively (Table 1). The percentage of PMCs with multivalents in these hybrids was equal to 52 and 61. It must be noted that in hybrids where CS nulli-5B-tetra-5A line and CS mutant *ph1* were used as female parents the average number of bivalents in some PMCs reached 14 (Table 2). This fact suggested a possibility of pairing the homoeologous chromosomes of the G genome of tetraploids and the B genome of common wheat.

The data of FELDMAN (1966) who found that all the telocentric chromosomes of genome B of Chinese Spring tested paired to some extent with the corresponding chromosomes of *T. timopheevii*, suggested that the second genome of *T. timopheevii* (G) was closely related to the B genome of *T. aestivum* and could have differentiated from the B genome as a result of exchanges of the homoeologous chromosomal segments with other genomes. LILIENFELD & KIHARA (1934) were the first who specified by genome analysis that *T. timopheevii* should be considered a species distinct from other tetraploid wheat belonging to the emmer group and proposed for this species the genomic formula AAGG.

In our experiments the absence of chromosome 5B or locus *Ph1* in hybrids from crosses between *T. aestivum* and tetraploid wheat species showed significant increase in the homoeologous pairing in wheat chromosomes. From the data of the present studies a conclusion may be drawn that the use of nulli-5B-tetra-5A line and mutant *ph1* is an effective way to increase the rate of recombinations of genetic material and induce of homoeologous pairing of chromosomes not only in the wheat x rye hybrids, as it was shown by our experiments (SHNAIDER & PRIILINN 1984), but also in interspecific hybrids between *T. aestivum* and tetraploids *T. timopheevii* and *T. militinae*.

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Induced polygenic mutations in wheat (*Triticum aestivum* L.)

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Bread wheat being a polyploid, offers many opportunities of exploitation of mutations, recombinations and of increasing genetic variability in quantitatively inherited characters (LARIK 1975). From the work already reported by several authors on this crop (BHATIA & SWAMINATHAN 1962, BOROJEVIC 1969, BOROJEVIC & BOROJEVIC 1972, LARIK 1979, LARIK *et al.* 1980, CHOWDHARY 1982), it is now quite clear that polygenic mutation results in the release of considerable variability in irradiated populations. However, informations are scanty about the influence of chemical mutagens on quantitative characters particularly in wheat, compared to that of irradiations. It is quite likely that chemical mutagens may provide a better understanding since they induce a much higher mutation rate and causes less chromosomal disturbances than do radiations (JANA & ROY 1973). In view of above considerations, the present investigation has been carried out to induce mutations by EMS in four quantitative characters of wheat variety, Bansi.

Materials and Method

Dry seeds of a variety of wheat, Bansi were pre-soaked in distilled water for 9 h. and then treated with 0.1 to 0.4% ethyl methane sulfonate (EMS) for 6 h. at a constant room temperature of 20 ± 1°C. The treated seeds were washed thoroughly in running tap water for half an hour and sown in the field in randomized complete block design with three replications. In each replication, five lines of ten seeds each were allotted for each treatment and control with a inter-row distance of 1 ft. and inter-plant distance of 15 cm. The data on four quantitative characters i.e. no. of fillers, spike length, spikelets per spike and total plant yield were collected from each individual plant separately.

For studying the polygenic variability in M_2 and M_3 generations, a random seed sample of 300 seeds was sown in randomized complete block design in three replications with the same distance as kept in M_1 generation. Data on individual plant of these four quantitative characters were collected and analysed statistically. The genetic parameters were calculated to estimate the extent of genetic variability in the treated populations. The expected genetic advance (Gs) with 5% selection intensity was calculated according to the modified formula (KHAN 1983),

$$Gs = k.\delta_p.h^2$$

where δ_p = phenotypic standard deviation of the mean performance of treated population, h^2 = broad-sense heritability and k = 2.06 constant for selection differential.

Table 1. Estimates of means values ($\bar{X}$), coefficient of variation (phenotypic and genotypic), heritability (h^2) and expected genetic advance (Gs) in the M_2 generation

Treatments	Mean $\bar{X}$	cv(p) %	cv(g) %	h^2 %	Gs % of $\bar{X}$
		Spike length (cm)			
Control	9.16	9.04	–	–	–
0.1% EMS	11.67**	10.12	12.14	44.20	16.10
0.2% EMS	11.22**	11.12	13.12	48.10	17.12
0.3% EMS	10.16**	12.10	12.22	37.20	21.00
0.4% EMS	10.42**	10.00	11.20	39.42	20.00
		Tillers/plant			
Control	10.10	12.12	–	–	–
0.1% EMS	12.12**	14.22	11.12	75.40	20.11
0.2% EMS	11.10**	14.00	13.11	66.40	22.12
0.3% EMS	11.00*	13.22	14.11	61.60	24.11
0.4% EMS	10.90*	12.24	13.11	72.00	23.12
		Spikelets/spike			
Control	16.67	12.34	–	–	–
0.1% EMS	18.00**	15.94	10.16	50.10	16.40
0.2% EMS	17.33*	15.22	9.22	52.10	15.20
0.3% EMS	17.80*	14.11	10.14	49.10	17.10
0.4% EMS	15.90	12.60	12.32	52.64	17.00
		Plant yield (g)			
Control	12.10	12.64	–	–	–
0.1% EMS	12.64*	13.23	14.12	42.10	21.00
0.2% EMS	14.62**	14.14	13.12	49.40	19.24
0.3% EMS	10.12**	15.82	11.00	56.20	16.12
0.4% EMS	15.18**	12.86	12.92	54.44	12.00

* = Significant at 5% level of probability.

** = Significant at 1% level of probability.

cv (p) = Phenotypic coefficient of variation.

cv (g) = Genotypic coefficient of variation.

Table 2. Estimates of mean values ($\bar{X}$), coefficient of variation (phenotypic and genotypic), heritability (h^2) and expected genetic advance (Gs) in the M_3 generation

Treatments	Mean $\bar{X}$	cv(p) %	cv(g) %	h^2 %	Gs % of $\bar{X}$
		Spike length (cm)			
Control	10.10	11.12	–	–	–
0.1% EMS	12.10**	12.64	11.11	70.00	19.11
0.2% EMS	12.40**	14.12	12.20	72.11	13.14
0.3% EMS	11.20**	13.11	12.00	65.40	14.16
0.4% EMS	12.64**	12.12	10.26	66.20	15.26
		Tillers/plant			
Control	10.94	14.16	–	–	–
0.1% EMS	11.11*	15.12	12.24	40.40	20.12
0.2% EMS	12.14**	14.96	14.10	37.16	19.11
0.3% EMS	12.13**	16.11	11.13	42.26	16.20
0.4% EMS	12.12**	15.26	12.16	40.00	11.26
		Spikelets/spike			
Control	20.10	18.11	–	–	–
0.1% EMS	21.44*	19.20	14.90	60.70	20.69
0.2% EMS	22.42**	18.12	16.20	70.10	19.20
0.3% EMS	20.94*	18.44	16.00	76.70	21.20
0.4% EMS	19.20	19.22	17.19	71.15	23.11
		Plant yield (g)			
Control	13.80	14.12	–	–	–
0.1% EMS	17.20**	16.11	14.02	42.10	21.00
0.2% EMS	16.10**	16.12	13.12	49.10	19.24
0.3% EMS	15.20**	15.12	11.00	56.20	16.11
0.4% EMS	14.64	15.00	12.92	56.10	12.00

* = Significant at 5% level of probability.

** = Significant at 1% level of probability.

cv(p) = Phenotypic coefficient of variation.

cv(g) = Genotypic coefficient of variation.

Results and Discussion

The present studies were carried out to measure the amount of induced variability in different quantitatively inherited characters and to recognize the potential of EMS treatment. Spike length and spikelets per spike are the most important yield components as they determine the ultimate crop yield (LARIK 1979). Spike length increased in both M_2 and M_3 generations. Mean values of spikelets per spike also increased significantly with the exception noticed at 0.4% of EMS in both the generations. The increase in the number of spikelets may be ascribed to the increased frequency of supernumery spikelets (MACKEY 1954, SCOSSIROLI & PALENZONA 1961). On the other hand, number of tillers increased significantly. Yield is a dependent character, and is the result of all the biological processes going on during the growth and development of plant (SCARASCIA-MUGNOZZA 1964). The general trend of reduced yield among the mutagenic treated material could be due to pleiotropic effects (GAUL 1977) on other characters. However, in the present study, yield per plant increased almost in all the treatments except 0.3% in M_2 generation. The increase was more in the M_3 as compared to M_2, may be due to the increased recombination and elimination of cytological variants.

As might be expected, the induced variability in the mutanized populations was higher than the control populations for almost all the characters measured. This is in agreement with the observations of other workers (MATSUO & ONOZAWA 1961, YAMAGATA 1964). However, there were differences for different traits in both the generations. This differential response has also been reported by GOUD (1967).

The estimates of heritability and expected genetic advance increased for all the characters in the treated populations. Number of tillers showed high values of heritability and genetic advance in the M_2 generation as compared to M_3, indicating that the selection for this character will be more effective if it is applied in early generations. On the other hand, spike length, spikelets per spike and yield per plant showed high estimates of heritability and genetic advance in the M_3 generation indicating that these characters can be transmitted to future generations and significant gain could possibly be achieved if selection is made at M_3 generation because of stabilization. The present studies have provided an evidence on the induction of genetic variability for yield and yield components of this crop. It might be possible to concentrate on the exploitation of the variability for these characters for the improvement of yield.

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Evaluation and utilisation of diploid species of wheat

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Diploid progenitors of wheat have successfully been exploited for incorporating resistance to rusts into common wheat. To find out the effectiveness of resistance available in the diploid wheats, 98 accessions belonging to *Triticum monococcum, T. urartu, T. boeoticum, T. speltoides* (*Aegilops speltoides*), *T. longissimum, T. bicorne, Ae. sharonensis* and *T. tauschii* (*Ae. squarrosa*) were evaluated for resistance under natural incidence of stem, leaf and stripe rusts infection over a period of four seasons at Wellington (Nilgiri Hills), a 'hot spot' location for wheat diseases in south India. Most of the accessions of *T. speltoides, T. longissimum* and *Ae. aucheri* exhibited a high degree of resistance to all the three rusts whilst the majority of *T. tauschii* strains did not possess adequate resistance to any of the three rusts. However, more forms were found resistant to leaf rust than to stem and stripe rusts. The einkorn wheats: *T. monococcum, T. urartu* and *T. boeoticum* were found to carry a high degree of resistance to leaf and stripe rusts.

A number of specific genes such as *Lr9, Lr21, Lr22a, Lr28* for leaf rust, *Sr33, Sr34* and *Sr35* for stem rust and *Yr8* for stripe rust have been transferred by various wheat workers from diploid wheats to common wheat. These specific genes conferring resistance to rusts were also screened against rusts under natural incidenee of stem, leaf and stripe rust infection over a period of six seasons at same location. The genes *Lr21* and *Lr22a* conferred moderate degree of adult plant resistance to leaf rust races existing in the Nilgiris, however, theses genes have been reported ineffective to most of the Indian races in seedling stage (SAWHNEY *et al.* 1977). Except the gene *Sr*34, all the genes were found to confer effective resistance to the rust-race-flora prevailing in the Nilgiri hills. Thus, diploid wheats are potentially useful and offer an excellent source of resistance to wheat rusts.

A programme of transference of resistance to rust from *T. speltoides* into common wheat was initiated in the year 1982. A tetraploid wheat variety of *T. durum* was crossed to a strain of *T. speltoides.* The F_1 triploid hybrid (2n=21) exhibited complete resistance to all the three rusts under field conditions. The two triploid hybrid plants were crossed to *T. aestivum* variety Sonalika. To ensure good seed set the florets were pollinated twice. Seven seeds were obtained out of which only three survived when planted. The cytological analysis made at first meiotic metaphase stage revealed that the hybrid progenies varied in chromosome constitution (Table 1).

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Table 1. Chromosome constitution of the hybrids between *T. durum* / *T. speltoides* // *T. aestivum* at first meiotic metaphase

Sl. No.	2n number	No. of cells scored	Average chromosome configuration				
			Univalents	Bivalents		Total bivalents	Trivalents
				rod	ring		
1	35	20	14.50 (9-12)	5.20 (3-4)	3.50 (5-7)	8.50	0.85 (0-2)
2	37	30	19.00 (17-21)	5.85 (4-7)	3.15 (3-5)	9.00	–
3	39	32	19.81 (18-23)	4.55 (4-7)	4.85 (1-7)	9.40	0.12 (0-1)

Range in parenthesis.

All the three plants were vigorous and produced 58, 64 and 41 ear bearing tillers respectively and showed excellent field resistance to stem, leaf and stripe rusts. There were no distinct morphological differences among these hybrids. The hybrid plants were dwarf and had thin stem with prominent nodes and narrow leaves like *T. speltoides*. Spikes were lax having 1-4 florets per spikelet. The plants were medium late in maturity. Most of the spikes were backcrossed to Sonalika and the florets were pollinated twice. Seed set in different spikes was poor ranging from 0.75% to 6.52%.

II backcroos generation. In the case of 2n = 35 plant a total of 42 seeds were obtained in the crosses but only 35 seeds germinated. The segregants were vigorous in growth, short statured with narrow leaves and thin stem. 80% progenies showed a high degree of adult plant resistance to leaf rust (*Puccinia recondita*) and high to moderate resistance to stem rust (*Puccinia graminis tritici*); however, the progenies were found susceptible to stripe rust (*Puccinia striiformis*). Comparatively seed setting on the hybrid plant 2n = 37 when backcrossed to Sonalika was poor than that obtained in 2n = 35 plant. In this case too, the segregants showed remarkable degree of mature plant resistance to stem and leaf rusts. Similarly, 2n = 39 hybrid plant yielded less number of seeds upon backcrossing, although 2n = 35 plant recorded a high frequency of trivalent formation (0.85/cell) than that of 2n = 39 plant which showed only 0.12 trivalents/cell. However, the type of resistance observed among the progenies of 2n = 39 x Sonalika was as good as observed in other two cases. The progenies were grown under natural infection of all the three rusts obtaining at Wellington. The chromosome constitution of the segregants has not been determined. Further backcrossing and selection work is under progress.

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Studies on the physiology of dwarfism in wheat (*T. aestivum* L.)
VII. Endogenous and GA_3 induced IAA-like substances

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Dwarf mutants of several plant species have often been regarded deficient in some aspect of growth hormones. Since the classical work of VAN OVERBEEK (1935) who observed that the dwarf maize mutants either destroyed more IAA or produced less of it, a number of workers have emphasised the importance of auxins in dwarf plants (NAKAYAMA 1941). Discovery of gibberellin proved to be a turning point and several workers proposed that GA_3 controls plants growth via auxin metabolism (PALEG 1965). In fact, increased auxin levels in GA treated tissues of tall as well as dwarf plants have been reported by KOGL & ELEMA (1960) and several others.

Auxin-like content have been found to be higher in tall cultivar of wheat in comparison to their dwarf counter parts (BHARDWAJ & DUA 1974). The authors reported higher gibberellin -like substances in certain dwarf varieties of wheat (KUMAR & BAIJAL 1986) and therefore it was imperative for us to examine endogenous IAA-like substances as also to understand whether the action of GA_3 is mediated through IAA in these varieties. Further in view of the different GA responsiveness of these varieties to oxidative enzymes (KUMAR *et al.* 1981), plumule growth (KUMAR *et al.* 1982) and protein metabolism (KUMAR & BAIJAL 1985), GA_3 induced changes in IAA-like substances were investigated for their possible implication in the dwarfism.

Materials and Methods

Sterilized seeds of four wheat varieties viz C-306 (tall), Sonalika (single dwarf), Kalyansona (double dwarf) and Moti (Triple dwarf) were soaked in distilled water with or without GA_3 (1 mg/L) for 24 hours and grown according to the method of KUMAR *et al.* (1982). Random samples were collected at 0, 48, 96 hours and processed in duplicate for the estimation of auxin-like substances as follows.

Extraction and purification: Weighted samples were ground to a paste and extracted with 80% methanol at 0°C for 24 hrs. The supernatent was decanted. Extraction was repeated twice for 5 hrs and 1 hr with fresh methanol. The supernatents were pooled and filtered through a double layer muscline cloth.

The methanol extract was evaporated at room temperature under infra-red light. The aqueous phase was utilized for further extraction and purification of auxins, adopting the technique of NITSCH (1956). The purified acidic and neutral fractions of auxin-like compounds were subjected to chromatography.

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Chromatography: The two fractions were concentrated to a few drops and loaded on a Watman No. 1 filter paper strip (40 x 5 cm) and run ascendingly to a distance of about 25 cm at 20 ± 2°C using Isopropanol : Ammonia : water (10:1:1) as solvent. The chromatograms were air dried and cut into 10 equal parts each representing 0.1 RF and as such utilized for bioassy of auxin like substances.

Bioassay: Estimation of auxin activity were carried out adopting wheat coleoptile straight growth test as described by MER *et al.* (1962). Sections of coleoptile stumps were grown in sucrose-phosphate buffer (pH 4.5) with or without the elute of chromatogram. The percent increase (+) or decrease (-) in the length of section with elute over that without it were expressed as promotors and inhibitors, respectively.

Results

A chromatographic survey of IAA-like substances (Fig. 1 & 2) revealed that at the onset of germination as well as on an average the amount of promotors was highest in the tall variety C-306. Intergroup comparison reflected that the single dwarf Sonalika possessed maximum amount of promotors followed by triple dwarf Moti and double dwarf Kalyansona (Table 1). Frequent interconversions within different group of auxin-like substances were quite evident during the 96 hrs of seedling growth.

Like the promotors the IAA-like inhibitors were also observed to be highest in C-306. But amongst dwarfs, the Kalyansona which possessed minimum amount of promotors had maximum amount of inhibitors; against this, the Sonalika exhibited lowest level of inhibitors (Table 1). A look at the chromatograms (Fig. 1 & 2) revealed that the inhibitors in C-306 were present between RF 0.8 – 0.9 and/or 0.5 – 0.6 and in Sonalika between 0.5 – 0.6 and 0.0 – 0.1. In Kalyansona and Moti, the picture was not so clear yet the inhibitory substances remained more or less around these RFs.

The level of IAA-like promotors reached to the peak in 48 hrs old seedlings while the level of inhibitors was minimum at that time.

Gibberellin (GA_3) treatment lowered IAA-like inhibitors and enhanced IAA-like promotors (Table 1). However certain deviations were recorded at varietal level especially in the promotors (Fig. 3). The C-306 and Kalyansona registered a considerable increase in endogenous IAA-like promotors but Sonalika displayed only a marginal increase in the same. On the contrary, the triple dwarf Moti showed a sharp decline in promotors level due to GA_3 treatment. In contravention to promotors, all the four varieties exhibited reduction of various magnitude in IAA-like inhibitors as a result of GA_3 application.

Discussion

The results of the present study corraborate the classical finding of VAN OVERBEEK (1935).

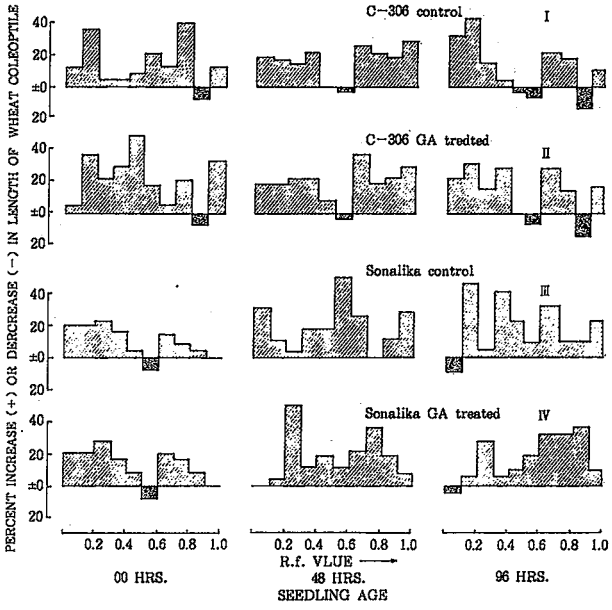

Fig. 1 Level (%) of promotors (+) and inhibitors (-) in the auxin bioassay test in untreated (control) and treated (GA_3 1 mg/L) wheat during seedling growth

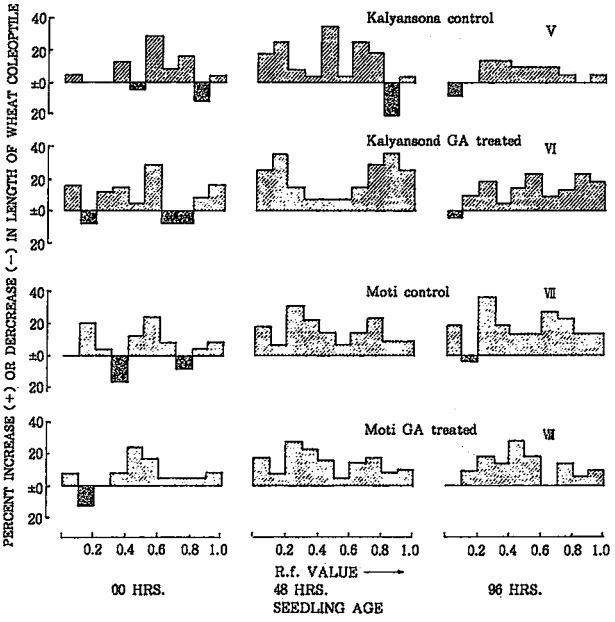

Fig. 2 Level (%) of promotors (+) and inhibitors (-) in the auxin bioassay test in untreated (control) and treated (GA_3 1 mg/L) wheat during seedling growth

Table 1. Average amount (%) of IAA-like promotors (+) and inhibitors (−) present in the untreated (control) and treated (GA_3 1 mg/L) wheat during seedling growth

Variety	Promotors (+)	Inhibitors (−)
G-306	168.8	11.6
Sonalika	166.5	5.6
Kalyansona	117.2	11.2
Moti	122.9	6.8
Treatment		
Control	136.4	10.8
GA_3	151.3	6.5
Seedling age		
00 hr	115.7	12.5
48 hr	172.5	3.6
96 hr	142.2	10.1

(values are mean of sums)

Thus the tall variety C-306 possessed more IAA-like promotors than the three dwarfs. BHARDWAJ & DUA (1974) also reported similar results.

The overall changes in IAA-like promoting or inhibiting substances did not commensurate with growth pattern. A similar report was published by MURAKAMI (1961). It is not necessary also that growth changes should correlate with hormonal changes, since altered tissue response might have resulted in the presence of other growth substances, inhibitors, physiological age of tissue etc. (MCCOMB & MCCOMB 1970). That may probably be how, the varieties exhibited different GA responsiveness.

Effect of gibberellic acid on IAA-like promotors indicated a considerable enhancement in C-306 and Kalyansona, a mild increase in Sonalika and an adverse effect in Moti the triple dwarf variety. The present study thus confirms the earlier report of KEFFORD & GOLDACRE (1961), if the former three varieties are considered. In certain instances gibberellic acid has been reported not to affect endogenous IAA content (CLELAND 1969) but the results of Moti do not fall in line with this either.

It became amply clear from this investigation that GA induced growth in wheat is auxin mediated, contrary to earlier conviction (RIZVI & SIROHI 1974). However, the way the gibberellin control auxin level is a controversial one. The most accepted view is that gibberellin influence oxidative or proxidative enzyme activity resulting a decrease in IAA degradation or an increase in IAA synthesis (PALEG 1965). The authors have reported GA_3 induced decrease in polyphenol

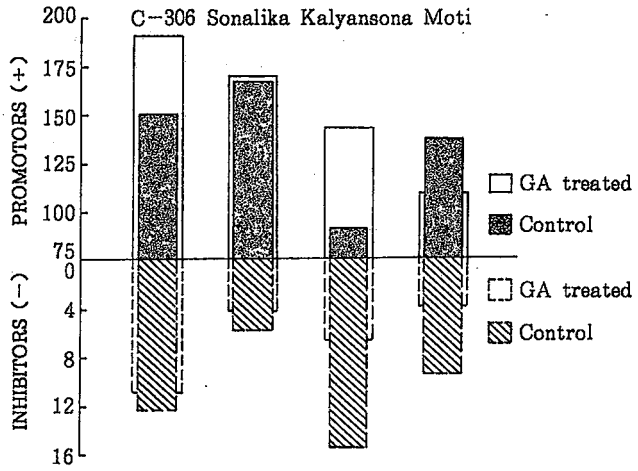

Fig. 3 Total amount (%) of auxin like promotors (+) and inhibitors (-) in untreated (control) and treated (GA_3 1 mg/L) wheat seedlings (based on bioassay test)

oxidase activity in the varieties presently undertaken (KUMAR *et al.* 1981) which probably could account for the increase in IAA level in C-306, Sonalika and Kalyansona but not in Moti.

It may further be noted that IAA content increased in those varieties which showed GA induced protease activity (KUMAR *et al.* 1982) and catalase activity (KUMAR *et al.* 1981). This could reflect a relationship of IAA synthesis from tryptophane. The later being made available as a result of proteolysis and the catalase indicating the interconversions in amino acids (BALDWIN 1963) either of which was not observed in Moti. KUMAR & BAIJAL (1984) opined that some proteinaceous inhibitor/antagonist might be involved in triple dwarf Moti which checks the expression of GA induced activity of several enzymes and consequent metabolic pathways including probably that of IAA too.

Thus the complex interaction between exogenously applied GA, abnormal protein metabolism and IAA-like substances suggests that they are associated with GA insensitivity and dwarfism in wheat, albeit indirectly.

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Inheritance of leaf rust resistance in wheat

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Coevolution of host pathogen relationship (VAN DER PLANK 1968) and clossal losses which diseases like rusts can cause under epiphytotic conditions (JOSHI 1978) warrants for the identification of diverse sources of resistance. Moreover genotypes with diversified resistance be incorporated in breeding programme to avoid chances of narrow genetic base of resistant wheat cultivars.

In that context it would be imperative to know the nature and number of genes controlling the rust resistance in wheat. Present study deals with such an attempt.

Materials and Methods

Nine wheat genetic stocks were screened against three single spore cultures (IL004-162A, IL007-108 and IL009-11) of leaf rust (*Puccinia recondita* Rob. ex. Desm. f. sp. *tritici* Eriks) with known avirulence/virulence formulae (Table 1) at seedling stage and resistants were crossed with Agra local (a genotype devoid of any resistance gene). The F_1's and F_2's of these crosses were also screened against the same three cultures.

Twenty five plants of each parent and F_1 and about hundred plants of each F_2 were raised in earthen pots in a growth chamber maintained at a constant temperature of 20±2°C and 80-100% humidity. Normal procedures of seedling inoculations and green house maintainance were followed. Observations regarding reaction type (resistant or susceptible) as suggested by STAKMAN *et al.* (1962) were noted after 14 days of inoculations.

Results and Discussion

Among the nine genotypes screened against three cultures, only two (WC 313 and Fortylaya) were resistant to all the three cultures. On the contary Agra local was susceptible to these cultures. Remaining six genotypes were resistant to two cultures, IL004-162 A and IL007-108. (Table 1a).

In order to have an idea about nature and number of resistance genes the F_1 and F_2 populations of crosses of resistant parents with Agra local were analysed. The F_1 data (Table 1b) indicated that resistance was dominant in all the cases. The reaction of F_2 population against the three cultures indicated monogenic or digenic ratios of resistant/susceptible plants. (Table 2). This showed that either one or two genes are controlling the resistance against these cultures. In many cases two ratios (both monogenic or digenic) showed goodness of fit by X^2 test. This ambiguity for monogenic or digenic control for rust resistance in present case could be attributed to one of the following reasons:

Table 1-a. Seedling reactions of some genetic stocks and their F_1 progenies of crosses with Agra local, against three cultures of leaf rust

Sr. No.	Genetic stock	Rust reactions					
		IL004-162A		IL007-108		IL009-11	
		Parent	F_1	Parent	F_1	Parent	F_1
1.	WC 611	R	R	R	R	S	S
2.	CPAN 1409	R	R	R	R	S	S
3.	Kenya plume	R	R	R	R	S	S
4.	WC 313	R	R	R	R	R	R
5.	CPAN 1285	R	R	R	R	S	S
6.	K 227 M_4	R	R	R	R	S	S
7.	Fortylaya	R	R	R	R	R	R
8.	E 6840	R	R	R	R	S	S
9.	Agra local	S	–	S	–	S	–

R = Resistant, S = Susceptible.

Table 1-b. Avirulence Virulence formulae (GUPTA & SAINI 1981)

Culture IL004-162A

PLr1, PLr2, PLr2b, PLr2c, PLr3(bg), PLr3 (Ka), PLr3 (do), PLr9, PLr10, PLr11, PLr12, PLr13, PLr14a, PLr14b, PLr16, PLr16, PLr17, PLr18, PLr19, PLr21, PLr23, PLrEG, PLrB/pLr20.

Culture IL007-108

PLr3 (bg), PLr3 (Ka), PLr3 (do), PLr9, PLr15, PLr19/pLr1, pLr29, pL2b, pLr2c, pLr2d, pLr10, pLr11, pLr12, pLr13, pLr14a, pLr14b, pLr16, pLr17, pLr18, pLr20, pLr21, pLr22, pLr23, pLrEG, pLrB.

Culture IL-009

PLr1, PLr9, PLr11, PLr15, PLr20/pLr29, pLr2b, pLr2c, pLr2d, pLrx (bg), pLr3 (Ka), pLr3 (do), pLr10, pLr12, pLr13, pLr14a, pLr14b, pLr16, pLr17, pLr18, pLr21, pLr22, pLr23, pLrEG, pLrB.

Table 2. Seedling reactions of F_2 progenies of crosses of resistant genetic stock, with Agra local against three cultures of leaf rust

Crosses	IL004-162A			IL007-108			IL009-11		
	Mode of segration	X^2	P-Value	Mode of segration	X^2	P-Value	Mode of segration	X^2	P-Value
WC 11 x Agra local	11:5	0.13	0.90–0.70	–*	–	–	–	–	–
	3:1	0.88	0.50–0.30						
CPAN 1409 x Agra local	3:1	0.22	0.70–0.50	9.7	1.32	0.20–0.10	–	–	–
	13:3	1.01	0.50–0.30						
Kenya plume x Agra local	15:1	0.08	0.90–0.70	3:1	0.24	0.70–0.50	–	–	–
				13:3	0.35	0.70–0.50			
WC 313 x Agra local	9:7	0.43	0.70–0.50	3:1	3.05	0.10–0.05	3:1	0.20	0.30–0.20
				11:5	0.06	0.90–0.70	11:5	0.26	0.70–0.50
CPAN 1285 x Agra local	15:1	2.48	0.20–0.10	3:1	0.00	0.95–0.90	–	–	–
				13:3	1.56	0.30–0.20			
K 227 M_4 x Agra local	3:1	0.21	0.70–0.50	3:1	1.86	0.20–0.10	–	–	–
	11:5	0.84	0.50–0.30	13:3	0.09	0.90–0.70			
Fortylaya x Agra local	3:1	2.24	0.20–0.10	3:1	0.81	0.50–0.30	3:1	0.30	0.70–0.50
	9:7	1.37	0.30–0.20	11:5	0.09	0.90–0.70	13:3	0.57	0.50–0.30
E 6840 x Agra local	15:1	0.07	0.90–0.70	13:3	1.24	0.30–0.20	–	–	–

* not tested and both the parents and F_1 were susceptible.

1) Use of qualitative scale for monitoring rust resistant/susceptible genotypes.

2) Small population size.

This warrants for testing the F_3 progeny for rust resistance.

The digenic ratios viz 11:5, 13:3, 9:7, 15:1 suggested threshold effect, epistasis, complementary or duplicate gene action respectively. So, for breeding for resistance to rusts, such types of interactions must be kept in view.

According to avirulence/virulence formulae, the comperative study involving three cultures suggested the tentative presence of genes *Lr2, Lr3, Lr10, Lr12, Lr14, Lr15, Lr17, Lr18, Lr21, Lr23, LrB, LrEG* and *Lr20* in parent WC 313 and Fortylaya. Precise nature of genes involved in rust resistance can be worked out by crossing the parents possessing different sets of resistance genes. Such an information will enable a wheat breeder to evolve varieties with multigenic or monogenic back ground stable for their reaction against wheat rust.

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Combining ability analysis over environments in spring wheat

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Environmental fluctuations highly influence the phenotypic expression of quantitative traits. Genotypic x environment interaction, depending upon their nature and magnitude, leads to bias in the estimates of gene effects and combining ability for various characters sensitive to environmental modulations. Such traits are less amenable to be improved through selection. There are few reports available regarding the environmental effects on the estimates of gene effects and combining ability in wheat. The present investigation was, therefore, undertaken to drive information on the nature of gene effects and combining ability operative in the inheritance of different economic traits and also to detect the role of environmental components on the sensitivity of estimates of gene effects so as to ensure better prediction and gain under selection.

Materials and Methods

The eight genetically diverse lines, originating from different agro-climatic zones, included in the present investigation were HD 2285, WH 147, WH 291, WH 283, CPAN 1907, CPAN 1830, HD 2009 and HW 517. These lines were crossed in all possible combinations (excluding the reciprocals). The 36 genotypes (8 parents and 28 F_1s) were grown during the winter of 1984-85 in a randomized block design providing three replications in two environments i.e., normal (irrigated and timely sown) and stress (irrigated and late sown). The plant to plant and row to row spacings were kept at 15 and 30 cm, respectively, and the length of the row was 3 m. The data were collected on five randomly selected plants from each replication in each row for days to heading, plant height, tiller number, total biomass, number of grains/ear, 1000-grain weight, grain yield/plant and harvest index (ratio between the economic and biological yields). The combining ability analysis was carried out following GRIFFING (1956) and the combining ability in environment interaction effects were computed following SINGH (1973).

Results and Discussion

Analysis of variance over the environments showed highly significant differences due to environments for all the characters, indicating sufficient diversity among the measured environments. The genotypes and environment x genotypes were also significant for all the characters (Table 1).

The pooled analysis of variance for combining ability reflected that both the general combining ability (*gca*) and specific combining ability *(sca)* mean squares were significant. Thus both kinds of gene effects *i.e.*, additive and non-additive appeared to be important in controlling the inheri-

Table 1. Pooled analysis of variance

Source	d.f.	Mean squares							
		Days to heading	Plant height	Tiller number	Total biomass	No. of grains/ear	1000-grain weight	Grain yield/plant	Harvest index
Environments	1	2176.90**	69.50**	527.16**	642.87**	1037.44**	980.61**	392.10**	0.1730**
Genotypes	35	27.67**	45.56**	10.89**	538.53**	124.95**	52.17**	74.98**	0.0044**
G x E	35	4.50**	65.44**	7.27**	375.60**	151.69**	17.89**	65.56**	0.0042**
Error	140	1.32	3.01	1.14	34.49	15.03	8.78	6.24	0.0010
		Combining ability							
gca	7	60.63**	127.66**	4.88**	480.04**	330.82**	129.53**	56.27**	0.0213**
sca	28	3.88**	10.08**	3.32**	104.38**	25.61**	10.36**	17.18**	0.0017**
gca x environments	7	2.77**	52.20**	1.91**	85.70**	87.96**	2.20	28.76**	0.0012**
sca x environments	28	1.19**	14.22**	2.55**	135.07**	41.22**	6.91**	20.13**	0.0015**
Error	140	0.44	1.00	0.38	11.50	6.01	2.93	2.08	0.0003
$\hat{gca}/\hat{sca}$ ratio		1.75	1.39	0.15	0.50	1.66	1.71	0.36	1.50

** Significant at 1% level of probability.

tance of all the characters. This warrants some kind of population improvement approach as earlier suggested by JENSEN (1970). Both *gca* x environments as well as *sca* x environments interactions were significant for all the characters except *gca* x environments for 1000-grain weight, indicating thereby the sensitivity of both kinds of gene effects to the environmental variations except for 1000-grain weight for which only non-additive gene effects were sensitive. For the characters days to heading, plant height, number of grains/ear and grain yield/plant, there was higher magnitude of *gca* x environments interactions as compared to *sca* x environments interactions, suggesting a higher sensitivity of *gca* to environments than that of *sca* for these characters. Similar results were reported by PARODA & JOSHI 1970, PARODA & HAYS 1971, SHARMA & SINGH 1982 and SINGH *et al.* 1986. Perhaps the heterozygosity *per se* and physiological advantages attached hitherto by virtue of heterosis or enhanced metabolic rates (SINHA & KHANNA 1975) has contributed to lower sensitivity of *sca* to environmental fluctuations as compared to *gca*. While, rest of the characters i.e., tiller number, total biomass, 1000-grain weight and harvest index exhibited higher sensitivity of *sca* to environments than that of *gca*.

In the pooled analysis, the *gca/sca* ratio (based on equivalent component of mean squares) showed that *gca* effects were preponderant and played an important role than *sca* effects for the genetic control of days to heading, plant height, number of grains/ear, 1000-grain weight and harvest index, hence pedigree method of breeding can be used for the improvement of these characters. Contrary to it, characters like tiller number, total biomass and grain yield were mainly under the influence of non-additive gene effects, though these characters exhibited considerable amount of additive genetic variance. Therefore, the improvement of such characters warrants a breeding methodology which can exploit both additive as well as non-additive gene effects. Under such a situation biparental mating or recurrent selection may increase the frequency of desirable genes and hasten the rate of genetic improvement as also reported by SRIVASTAVA *et al.* 1980 and SINGH *et al.* 1986. Inclusion of F_1 hybrids showing stable *sca* and having parents with good *gca*, less altered by changes to environmental variations in multiple crosses, could also prove a worthwhile approach.

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Genetics of grain yield in relation to total biological yield in Triticale

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The utility of harvest index as a selection criterion for effective improvement of grain yield, particularly in cereals, has been emphasized (DONALD & HUMBLIN 1976). Combining ability analysis is useful for the selection of parents to be involved in hybridization programme aimed at recombining favourable gene constellations scattered over different genotypes. This has particular relevance to Triticale because of its narrow gene pool, low floret fertility and harvest index and high biological yield. Present study deals with combining ability analysis for productivity traits in hexaploid Triticale.

Materials and Methods

Hexaploid Triticale lines selected on the basis of genetic divergence were crossed in line x tester design. Parental strains included 18 lines viz., 1. T24, 2. T103, 3. T125, 4. T130, 5. T134, 6. Tcl. 3, 7. TL-37, 8. TL-39, 9. TL-46. 10. TL-56, 11. UPT74364, 12. UPT74418, 13. UPT74460, 14. UPT74536, 15. Arm-147, 16. Armadillo, 17. Koala and 18. Cinnamon and 4 testers, namely, 1. St69-1, 2. 6TA204, 3. TL-22 and 4. UPT73535. The parents and resultant 72 F_1 hybrids were sown in randomized block design with three replications. Inter and intra row distances between two plants were 30 cm and 10 cm, respectively. Five plants from each replication were selected for recording observation on number of grains per spike, floret fertility (%), 1000 grain weight (g), biological yield per plant (g) and grain yield per plant (g). Harvest index was expressed as ratio of grain yield to total biological yield per plant (excluding roots). Mean values for all the characters were subjected to analysis of variance for combining ability as suggested by KEMPTHORNE (1957).

Results and Discussion

Analysis of variance for combining ability revealed highly significant differences among hybrids for all the characters. Further partitioning of mean squares into orthogonal contrasts indicated that differences due to females, males and female x male interactions were also significant. (Table 1). Thus sufficient variation existed in the material.

Based on good *gca* effects and high *per se* performance (Table 2) few genotypes figured important. These were: Cinnamon and T130 for grain yield, harvest index, grains per spike and floret fertility; TL-39 and T134 for 1000 grain weight and biological yield; Armadillo and T125 for

Table 1. Analysis of variance for combining ability

Source of variation	d.f.	Mean sum of squares					
		No. of grains/ spike	Floret fertility(%)	1000 grain weight (g)	Biological yield per plant	Harvest index (%)	Grain yield (g)
Blocks	2	17.21	10.45	7.73	210.20	11.45	22.05*
Hybrids	71	94.18*	125.54**	39.17**	334.24**	30.86**	55.13**
Females	17	195.87**	171.16**	104.70**	754.85**	77.25**	138.36**
Males	3	163.53**	333.20**	19.14	163.56	44.73**	27.92**
Females x Males	51	56.21**	98.22**	18.50**	204.08**	14.57**	29.00**
Error	142	32.65	26.13	11.12	83.34	5.41	8.88
δ^2_F	–	3.72	1.92	5.05	37.55	4.97	7.44
δ^2_M	–	1.21	3.42	0.46	27.87	0.50	0.39
$\delta^2_{F \times M}$	–	7.85	24.00	2.26	40.25	3.05	6.71

*,** significant at 1% and 5%, respectively.

floret fertility and 1000 grain weight and UPT74535 for number of grains per spike, biological yield per plant and grain yield. Inclusion of such genotypes in population improvement programme following diallel selective mating (JENSEN 1970) or concurrent random mating and intermating in segregating generations followed by selection (JENSEN 1978) would maximize the chances of getting desirable recombinants for production attributes.

Being ephimeral in nature, normally non additive gene effects do not contribute tangibly in the improvement of self pollinated crops (ALLARD 1960). However, complimentary interaction is fixable and utilizable genetic variance. Parents with good *gca* and *per se* are expected to express such complimentary effects in crosses and advanced progeny generations. Though, the crosses with significantly high *sca* and *per se* in desirable direction mostly involved at least one parent with good *gca* effects, however, crosses viz. T125 x 6TA204 (3 x 2), T130 x 6TA204 (4 x 2), TL56 x ST 69-1 (10 x 1) and Cinnamon x UPT74535 (18 x 4) involved both parents with good *gca* and *per se* for grain yield and its components, notably, harvest index, number of grains per spike, floret fertility and biological yield. Cross T130 x 6TA204 (4 x 2), interestingly, was found good for most of the yield components. Inclusion of these crosses in multiple crosses would greatly enhance the chances of transgressive segregants for characters related to yield and harvest index. In this context, intermating in segregating generation followed by selection would be a worth while approach. The extent of variation obtained with in the progeny of biparental cross or intermating in F_2 could well depend, in general, on the genetic diversity in parental stocks (HABGOOD 1983). For that matter, parents involved in these five crosses showed desirable (moderate) magnitude of genetic

Table 2. *GCA* effects and *per se* performance of selected parental genotypes

Characters		Female					Male I	CD (*gca*) Female	CD Males
		1	2	3	4	5			
No. of grins/spike	*gca*	Cinnamon (6.3)	T130 (6.2)	T24 (5.0)	UPT74336 (3.6)	T103 (3.0)	UPT74535 (1.9)	3.4	1.8
	per se	T130 (75.6)	UPT74364 (67.6)	T103 (66.1)	T103 (67.2)	T134 (66.1)	UPT74535 (77.6)		
Floret fertility (%)	*gca*	Cinnamon (5.8)	T127 (5.7)	Armadillo (5.7)	TL39 (3.4)	T130 (2.62)	St69-1 (1.9)	2.8	1.5
	per se	Armadillo (84.9)	T125 (83.2)	UPT74460 (81.9)	T130 (81.9)	Cinnamon (80.9)	TL-22 (80.3)		
1000 grain weight(g)	*gca*	T134 (5.3)	Koala (3.8)	Armadillo (2.4)	T125 (2.4)	Arm 147 (2.0)	St69-1 (0.9)	3.1	1.1
	per se	T125 (47.2)	T134 (47.2)	T24 (46.9)	Armadillo (46.3)	TL39 (45.0)	TL-22 (49.7)		
Biological yield/ plant (g)	*gca*	Cinnamon (14.6)	T24 (12.6)	TL39 (10.0)	T134 (7.9)	T125 (5.6)	UPT74535 (1.4)	5.4	2.9
	per se	UPT74536 (90.1)	T134 (87.6)	TL39 (85.2)	T103 (84.8)	UPT74418 (84.3)	UPT74535 (99.4)		
Harvest index (%)	*gca*	Koala (4.0)	TL39 (3.6)	T125 (2.4)	T130 (2.1)	Cinnamon (1.9)	TL-22 (1.1)	1.4	0.7
	per se	Armadillo (35.2)	TL-56 (34.5)	TL37 (32.3)	Cinnamon (32.7)	T130 (32.3)	TL-22 (30.8)		
Grain yield/ plant (g)	*gca*	Cinnamon (6.3)	TL39 (5.4)	TL125 (3.9)	Cinnamon (3.4)	T130 (2.1)	TL-22 (0.8)	1.7	0.9
	per se	TL39 (26.8)	T130 (26.2)	Armadillo (25.9)	TL56 (25.5)	Cinnamon (25.4)	UPT74535 (27.4)		

Table 3. Specific combining ability effects and *per se* performance of seven best crosses

Characters		Crosses							
		1	2	3	4	5	6	7	CD(Sig)
No. of grains/spike	*sca*	13.75 (10x1)	13.58 (9x4)	11.81 (2x2)	10.49 (4x4)	9.46 (4x2)	9.08 (16x1)	8.92 (18x4)	5.51
	per se	79.88 (4x4)	78.42 (18x4)	77.05 (4x2)	76.28 (2x2)	73.26 (10x1)	72.58 (9x4)	72.19 (16x1)	9.31
Floret fertility	*sca*	13.29 (11x2)	10.26 (10x1)	9.39 (4x2)	8.83 (17x1)	8.82 (7x3)	8.13 (2x2)	7.90 (14x2)	4.63
	per se	82.96 (10x1)	82.01 (8x1)	81.95 (18x3)	81.36 (16x1)	80.95 (18x4)	80.88 (4x4)	80.87 (16x3)	8.51
1000 grain weight (g)	*sca*	6.86 (10x3)	6.83 (9x3)	6.26 (9x2)	5.42 (7x4)	4.63 (16x4)	4.56 (2x2)	4.35 (18x1)	3.22
	per se	56.56 (5x2)	55.59 (9x3)	55.23 (9x2)	54.45 (16x4)	54.24 (5x1)	54.13 (7x4)	53.63 (18x1)	5.30
Biological yield/ plant (g)	*sca*	20.05 (11x2)	15.32 (15x3)	13.88 (2x2)	13.69 (10x1)	12.95 (7x3)	12.66 (14x2)	11.87 (13x1)	8.84
	per se	109.52 (1x1)	107.81 (18x2)	105.27 (15x4)	105.92 (5x4)	105.62 (4x2)	104.13 (8x4)	102.86 (1x2)	15.05
Harvest index (%)	*sca*	4.87 (2x2)	4.38 (9x4)	3.23 (10x1)	3.13 (6x3)	2.91 (4x2)	2.76 (18x1)	2.74 (6x1)	2.25
	per se	37.12 (15x3)	35.91 (9x4)	35.49 (17x2)	35.48 (4x3)	35.07 (8x3)	34.71 (18x4)	34.23 (18x1)	4.06
Grain yield/plant (g)	*sca*	8.59 (4x2)	8.57 (2x2)	7.25 (10x1)	6.39 (15x4)	5.37 (9x4)	4.84 (14x2)	4.72 (7x3)	2.88
	per se	35.84 (4x2)	35.04 (18x3)	34.16 (8x3)	33.46 (8x4)	33.11 (2x2)	32.80 (18x1)	32.73 (10x1)	4.93

divergence (BEHL & SINGH, 1986). Positive association between *per se* and *sca* effects suggested that selection for crosses with high *sca* could be based on *per se* also.

Selection for high harvest index without change in biological yield may have value for improving grain yield of cereals (ROSILLEY & FREY 1975). This is particularly relevant in case of Triticale where grain yield improvement has been realised mainly by increasing biological yield. Invariably lower harvest index in recorded in Triticale lines as compared to wheat. Further, in intervarietal crosses of hexaploid Triticale quite often varying degree of sterility may be expressed (THOMAS & KALTSIKES 1976) which lowers the grain yield and harvest index and therefore, deserves consideration during selection. Both the floret fertility and harvest index are yield attributing traits. Selection based on these characters would therefore, offer promise in selecting desirable lines.

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II. Genetic Stock

Germplasm resources in *durum* wheat: Extreme variants for some quantitative spike characters in the USDA world collection

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Most of the world collection of *durum* wheat (*Triticum turgidum* L. *durum* group) of the U.S. Department of Agriculture was systematically surveyed in a field planting at Tulelake, California in 1970. The variation observed for heading time was reported and a listing of the accessions having earliness and winter habit was reported (QUALSET & PURI - 1974a, b). In addition, the amount of variation in this collection was estimated using qualitative characters of the spike, such as glume and awn color, kernel color, and glume pubescence. The measure of diversity at local and regional levels provides useful information to germplasm conservationists and plant breeders (JAIN *et al.* 1975).

Data for some quantitative characters in the spike were collected at the same time. These were recently analyzed to illustrate how multivariate statistical analysis can be used to describe variation and patterns of variation among ecogeographic regions. The analysis provides a basis for plant breeders to select parental lines from a large collection. We have suggested that this multivariate approach be used to identify highly diverse genotypes to broaden the genetic base of *durum* wheat breeding programs (SPAGNOLETTI ZEULI & QUALSET 1986).

Genetic improvement in grain yielding potential is a major objective in *durum* wheat. This improvement must be expressed in one or more yield components, and since the spike contributes two of the three end-point yield components, there is obvious interest in identifying genetic resources for these characters. We present herein a list of entries of the USDA World Collection of *durum* wheat that have interesting spike characteristics that might be useful in breeding programs.

About 3500 *durum* wheat entries were planted at Tulelake, California (41°58′ N latitude, 121°28′ longitude; 1240 m elevation) in April 1970. The crop was mature about 10 September. A single 2-m row, with rows spaced 60 cm apart was grown for each entry. Sentry and Oviachic 65 *durum* cultivars were grown periodically throughout the planting for comparisons.

Those entries that failed to head because of strong vernalization requirements were not considered in this survey. At maturity five spikes were harvested at random from each row. These

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Table 1. *Durum* wheat entries of the USDA World Germplasm Collection with awn length 2.0 standard deviations longer than the whole collection mean

PI No.	Origin	mm
184531	Portugal	192
185744	"	230
185766	"	195
191654	Spain	196
191767	"	190
191773	"	192
191979	"	192
192334	"	190
192511	"	200
192654	"	190
136571	"	200
191145	"	190
191187	"	220
157981	Italy	192
166938	Turkey	195
211708	"	192
221492	Afghanistan	192
Mean		123
S.D.		33.4

spikes were then visually examined and one representative spike was chosen for measurement of awn length and number of spikelets per spike. Then all spikes were threshed *en masse* and the total kernel number and weight was determined for calculating kernels per spike and individual kernel weight. More details are given in SPAGNOLETTI ZEULI & QUALSET (1986).

For each character the entries with mean values at least 2.5 standard deviations (2.0 for awn length) higher than the world collection mean were identified. These entries are listed in Tables 1, 2, and 3 with their PI or CI number, their country of origin, and means and standard deviations for the whole collection.

It must be considered that these results were obtained only in one location and in one year, that the environmental conditions were exceptionally favorable with high radiation, and that no temperature, water or nutrient stress occurred during the growing season. We could comment that we have used several of the accessions with very heavy kernels in the California breeding program and found that size was highly heritable (unpublished results).

Table 2. *Durum* wheat entries in the USDA World Collection having spikelets/spike and kernels/spike greater than 2.5 standard deviations above the population mean

PI or CI No.	Spikelete/Spike		PI or CI No.	Kernels/Spike	
	Origin	Number		Origin	Number
204018	Portugal	24	185724	Portugal	60
191774	Spain	24	192625	Spain	60
191806	"	25	192822	"	69
191809	"	25	CI 3824	Tunisia	66
191909	"	24	60869	Morocco	69
192420	"	24	306660	France	62
192822	"	26	174645	"	61
42571	"	24	5645	USSR	62
CI 3824	Tunisia	24	41026	"	63
152440	Morocco	24	CI 5014	"	63
225305	Iraq	25	57538	"	62
166634	Turkey	24	57544	"	62
166691	"	25	57550	"	64
166854	"	24	57602	"	70
167537	"	24	57609	"	60
167566	"	26	61119	"	66
167628	"	25	61126	"	61
173414	"	25	61127	"	69
295015	Bulgaria	24	61131	"	68
295031	"	24	61139	"	61
295033	"	24	61157	"	63
295051	"	26	61169	"	66
193110	France	25	61173	"	61
57190	USSR	25	61189	"	63
61121	"	24	CI 7674	"	69
61126	"	24	CI 7675	"	67
61147	"	24	CI 7678	"	63
293918	"	25	67395	"	65
195090	Ethiopia	24	68103	"	62
195712	"	25	68238	"	63
125343	Afghanistan	26	68257	"	60
			92385	"	65
			CI 8383	USA	60
			CI 12068	"	61
			60613	Ethiopia	61
			195712	"	64
Mean		18.6	Mean		38.7
S.D.		2.1	S.D.		8.3

Table 3. *Durum* entries in the USDA World Collection having kernel weight/spike and kernel weight per kernel greater than 2.5 standard deviation above the population mean

PI or CI No.	Kernal Wt/Spike		PI or CI No.	Kernel Wt/Kernel	
	Origin	g		Origin	mg
134930	Portugal	3.8	274678	Poland	85
185724	"	4.3	134932	Portugal	76
192114	Spain	3.6	204047	"	78
192653	"	3.7	191654	Spain	81
192822	"	4.0	191979	"	80
47890	"	3.6	190999	"	76
136572	"	3.8	191445	"	78
191087	"	3.5	157969	Italy	83
191126	"	3.5	CI 3155	Tunisia	76
191145	"	3.5	60738	Egypt	79
191189	"	3.6	60739	"	76
157972	Italy	3.5	60866	Morocco	76
157974	"	3.5	211835	Iraq	78
264954	"	3.5	119343	Turkey	76
CI 3178	Tunisia	3.7	165189	"	76
60738	Egypt	3.6	166450	"	78
237631	Cyprus	3.6	166619	"	76
60865	Morocco	3.5	166857	"	75
60869	"	3.5	166894	"	75
60870	"	3.5	166943	"	75
304919	"	3.5	167436	"	81
268298	Iraq	3.5	211708	"	83
182699	Syria	3.7	223162	Jordan	87
119343	Turkey	3.7	113165	"	75
119367	"	4.1	51211	"	80
177912	"	3.5	94725	USSR	83
177937	"	3.7	220696	Afghanistan	81
223162	Jordan	3.9	221492	"	82
295035	Bulgaria	3.5			
5645	USSR	3.8			
37159	"	3.6			
61127	"	3.7			
61195	"	3.9			
CI 7674	"	3.8			
127098	Afghanistan	3.5			
Mean		2.1	Mean		53
S.D.		0.65	S.D.		7.9

Request for seed stocks of these entries should be made to the National Small Grains Germplasm Collection, USDA-ARS, Aberdeen, Idaho, USA.

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III. Record

Catalogue of gene symbols for wheat: 1988 supplement

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Chlorophyll Abnormalities

cn-D1		v :	CD3 (952)

Crossability with Rye and *Hordeum* spp

For list of wheat/rye crossabilities see 930.

Kr1 is the most potent gene in suppressing crossability, followed by *Kr2* and *Kr3*, respectively. Allelic variation in the potency of the dominant suppressor genes was reported in 940 and 941.

Hairy Leaf Sheath

Hs (948). *Hls* (949).		tv :	*T. dicoccoides* G25 (949).
		v :	Certain hexaploid derivatives of G25 produced in Israel (249).
hs		tv :	*T. dicoccoides* G7 (949).
		v :	Most hexaploid wheats (249).

Levy and Feldman (949) concluded that complementary genes determined hairy leaf sheath in *T. dicoccoides.*

Height.

Rht12	5A (938)	v :	Karcagi 522 M7K.

Hybrid Weakness

1. Hybrid necrosis

List of genotypes can be found in 946.

Male Sterility

Chromosomal

Ms2 – causes sterility when present in octaploid triticale (917).

Ms3 (934).	5AS (934).	i :	Chris derivative (934).

Megasporogenesis

Control of Megasporogenesis

msg (921).	7AS (921)	tv :	Langdon (921)

Meiotic Characters

2. Pairing homoeologous

ph1c (906)	tv: Cappelli ph1 - mutant (953, 906) deficient for a terminal portion of chromosome 5BL (953).

Proteins – Enzymes

2. Alcohol dehydrogenase

Adh-V1 (772).	4V (772).	ad :	CS/*D. villosum*
Combine former *Adh-E^{i}1* and *Adh-Ag^{i}1* entries:			
Adh-Ag^{i}1 [591] (774). [*Adh-X1*(735)].	4Aβ^{i}(591).	ad :	Vilmorin 27/*Ag.intermedium.*

3. Aminopeptidase

Amp-A1a.		v :	CS (796).
Amp-A1b.		v :	Vitka (796).
Amp-B1a.		v :	CS (796).
Amp-B1b.		v :	Iskra (796).
Amp-R1.	6R (767).	ad :	Holdfast/King II (767).

4. α-Amylase

α-*Amy-Ag^{i}1* (774).	6Ag^{i} (774).	ad :	Vilmorin 27/*Ag. intermedium.*
α-*Amy-Ag^{i}2* (774).	7Ag^{i} (774).	ad :	Vilmorin 27/*Ag. intermedium.*

A further set of α-amylase genes, designated α-*Amy-3* [α-*Amy 3*] is located in chromosomes 5A, 5B and 5D (768). Evidence for these genes, which are expressed in early development, derives from cross-hybridization with α-*Amy-1* and α-*Amy-2* probes. The protein(s) have not been identified.

5. β-Amylase

β-Amy-Ag^{i}1 [580] (774). Change 3rd column entry to 4Ag^{i} (580).

Replace the *β-Amy-A2* section with the following:

β-Amy-B1 [518] (794).	[*β-Amy-A2a* (518)].	5AL(518,579)	**v**: CS (518). **s**: CS/Federation (579).
β-Amy-B1a.	[*β-Amy-A2a* (518)].		**v**: CS.
β-Amy-B1b.	[*β-Amy-A2b* (518)].		**v**: Koga II.
β-Amy-B1c.	[*β-Amy-A2c* (518)].		**v**: *T. macha* Line 1.
β-Amy-B1d.	[*β-Amy-A2d* (518)].		**v**: Holdfast.
β-Amy-B1e.	[*β-Amy-A2e* (518)].		**v**: Bezostaya 1.

Delete *β-Amy-B2* entries and *β-Amy-R2* entry.

Add:

β-Amy-R1. [*β-Amy-R2* (723), *β-AmyrR1*].	5R (582,767) 5RL (581).	**ad**:	FEC 28/Petkus (582, 581); Holdfast/King II(581, 767).
		tr:	CS/Imperial 5BL/5RL(581).
β-Amy-U1. [*β-Amy-U2* (723)].	5U (723).	**su**:	CS/*Ae. umbellulata.*

A second set of loci with homology to *β-Amy-1* was identified in 2AS, 2BS and 2DS and designated the *β-Amy-2* set. Evidence for these genes derives from cross-hybridization with a *β-Amy-H1* cDNA probe (794). Further members of the same set have been identified in 2H (793) and 2R and 2U (794).

6. Endopeptidase

Delete current entries and substitute:

Ep-A1 (133).	7AL (133).	**v**: CS.
Ep-A1a (785).		**v**: CS.
Ep-A1b (785).		**v**: Capelle-Desprez.
Ep-A1c (785).		**v**: Synthetic.
Ep-B1 (133). [*Ep1* (133)].	7BL (133).	**v**: CS.
Ep-B1a (785).		**v**: CS.
Ep-B1b (785).		**v**: Capelle-Desprez.
Ep-B1c (785).		**v**: Ciano 67.
Ep-B1d (785).		**v**: Bersee.
Ep-B1e (785).		**v**: Synthetic.

Ep-D1 (133).	7DL (133).	**v** : CS.
Ep-D1a (785).		**v** : CS.
Ep-D1b. [*Ep-V1* (736)].		**v** : VPM1(736),Rendezvous(785).
Ep-D1c (785).		**v** : Synthetic.
Ep-E1 (520).	7EL (520).	**ad** : CS/*E. elongata.*
Ep-H1 (562).	7HL (562).	**ad** : CS/Betzes.
Ep-H^{ch}1 (785).	7H$^{ch}\alpha$(785).	**su** : CS/*H. chilense.*
Ep-R1 (785).	7RL (785).	**ad** : CS/Imperial; CS/King II

An *Ep* locus was located in 4RS in King II (767), using Holdfast/King II addition lines.

Ep-S^{b}1 (785).	7S^{b} (785).	**su** : Holdfast/*Ae. bicornis.*
Ep-S^{l}1 (786).	7S^{l} (786).	**ad** : CS/*Ae. longissima.*
Ep-U1 (785).	7U (785).	**su** : CS/*Ae. umbellulata.*
Ep-V1 (785).	7V (785).	**ad** : CS/*H. villosum.*

7. Esterases

Est-Ag^{i}5 (774).	3Ag^{i}(774).	**ad** : Vilmorin 27/*Ag. intermedium.*

Est-R5. Add (767) as a reference to both 6R and 6RL in column 3 and to Holdfast/King II in column 4.

8. Glucosephosphate isomerase

Gpi-Ag^{i}1 [735] (774).	[*Gpi-X1* (735)].	1Ag^{i}(735).	**ad**: Vilmorin 27/*Ag. intermedium.*
Gpi-V1 (772).		1V (772).	**ad**: CS/*D. villosum.*

9. Glumatic oxaloacetic transaminase

Got-R2 In the 3rd column, add "6RL (767)," and change the 4th column to, "**ad**: CS/Imperial 6R (437), Holdfast/King II 6RL (767)."

Got-V2 (772).	6V (772).	**ad** : CS/*D. villosum.*

Got-Ag3. Add superscript "e" to Ag in all columns, i.e. "Ag^{e}."

Got-H^{ch}3 (788).	3H^{ch} (788).	**ad** : MA/*H. chilense.*

11. Lipoxygenase

Lpx-A1a.	**v** : CS (796).
Lpx-A1b.	**v** : Bosanka (796).

12. Malate dehydrogenase

Mdh-H^{ch}1 (787).	1H^{ch} (787).	**ad :**	MA/*H. chilense.*

13. Peroxidases

Retain all *Per-1* entries and delete all other *Per* entries.

Add:

Per-B2 (775).	2BS (775).	**v :**	CS.
Per-D2 (775).	2DS(775).	**v :**	CS.
Per-H2 (775).	2H(775).	**ad :**	CS/Betzes.
Per-R2 (775).	2RS(775).	**ad :**	CS/Imperial, Kharkov/Dakold.
Per-A3 (776).	3AL (776).	**v :**	CS.
Per-B3 [585] (776). *(Per4).*	3BL (585, 776).	**v :**	CS.
Per-D3 [585] (776). *(Per5).*	3DL (585, 776).	**v :**	CS.
Per-A4 [573] (776). *(Per 3).*	7A(573), 7AS(574, 585, 776).	**v :**	CS.
Per-B4 [573] (776). *(Per 2).*	4B(573), 4BL(574, 585, 776).	**v :**	CS.
Per-D4 [573] (776). *(Per 1).*	7D(573), 7DS(574, 585, 776).	**v :**	CS.
Per-Ag^{e}4.	7Ag^{e}S (574)	**tr :**	certain CS 7D/Ag^{e} lines
Per-Ag^{i}4. [*Per-Ag^{i}3* (774)].	7Ag^{i} (580)	**ad :**	Vilmorin 27/*Ag. intermedium.*

15. Phosphogluconate dehydrogenase

Replace the note with:

'Loci have also been identified in 1RL (*Pgd2*)(775), 1H^{ch} (787) and 1HL (*pgd*)(792).

16. Phosphoglucomutase

Pgm-Ag^{i}1 [735] (774).	Change the 3rd and 4th column entries to, "4Ag^{i}(735)", and "**ad**: Vilmorin 27/*Ag. intermedium.*"		
Pgm-H^{ch}1 (788)	4H^{ch}(788).	**ad :**	MA/*H. chilense*

17. Shikimate dehydrogenase

Skdh-H1 (765).	5H (765).	**ad :**	CS/Betzes.
Skdh-R1.	In the 3rd column, add "5R (765)." and in the 4th column, in the **ad** section, add, "CS/King II and Kharkov/Dakold 5R (765)."		
Skdh-S^{1} (765).	5S^{1}S (765).	**ad :**	CS/*Ae. longissima.*
Skdh-V1 (765).	5V (765).	**ad :**	CS/*D. villosum.*

18. Superoxide dismutase

Sod-V2 (772).	2V (772).	**ad** : CS/*D. villosum.*

19. Triosephosphate isomerase

Tpi-Ag^{i}2 (774).	5Ag^{i} (774).	**ad** : Vilmorin 27/*Ag. intermedium.*

20. Aromatic alcohol dehydrogenase

Aadh-B1a.		**v** : CS (796).
Aadh-B1b.		**v** : Drina (796).
Aadh-R1.	5RL (767).	**ad** : Holdfast/King II.
Aadh-A2, -B2, and -D2.	In the 3rd and 4th columns, delete (553) and insert (766).	
Aadh-R2.	6RL (767).	**ad** : Holdfast/King II.

21. Aconitase

Aco-A1 (764).	6AL (764).	**v** : CS.
Aco-A1a.		**v** : CS (796).
Aco-A1b.		**v** : Dubravka (796).
Aco-B1 (764).	6BL (764).	**v** : CS.
Aco-B1a.		**v** : CS (796).
Aco-B1b.		**v** : Dubravka (796).
Aco-B1c.		**v** : Slavonka (796).
Aco-D1 (764).	6DL (764).	**v** : CS.
Aco-E1 (764).	6Eβ (764).	**ad** : CS/*E. elongata.*
Aco-H1 [763] (764).	[*Aco-1* (763)].	6H (763), 6HL (764).
		ad : CS/Betzes.
Aco-R1 (764).	6RL (764).	**ad** : Sturdy/PI 252003
Aco-S^{1}1 (764).	6S1(764).	**ad** : CS/*Ae. longissima.*
Aco-U1 (764).	CSU-31 (764).	**ad** : CS/*Ae. umbellulata.*
Aco-A2 (764).	5AL (764).	**v** : CS.
Aco-B2 (764).	5BL (764).	**v** : CS.
Aco-D2 (764).	5DL (764).	**v** : CS.
Aco-E2 (764).	4EL (764).	**ad** : CS/*E. elongata.*
Aco-R2 (764).	5RL (764).	**ad** : CS/King II 5R, Holdfast/King II 5RL.

22. NADH dehydrogenase

Ndh-A1 (766).	4Aα(766).	v : CS.
Ndh-B1 (766).	4BL(766).	v : CS.
Ndh-B1a.		v : CS (796).
Ndh-B1b.		v : Sutjeska (796).
Ndh-B1c.		v : Fruskogorka (796).
Ndh-D1 (766).	4DS (766).	v : CS.
Ndh-H1 [763] (766).	[*Nadhd-1* (763)]. 4H(763).	ad : CS/Betzes.

23. Dipeptidase

Dip-A1 [769] (770).	[*Pept-A1* (796)]. 6AL (769, 770)	v : CS.
Dip-A1a (770).		v : CS.
Dip-A1b (770).		v : Cheyenne.
Dip-B1 [769] (770).	[*Pept-B1* (769)]. 6BL (769, 770)	v : CS.
Dip-B1a (770).		v : CS.
Dip-B1b (770).		v : Capelle-Deprez.
Dip-D1 (770).	6DL (770).	v : CS
Dip-H1 [763] (770).	[*Pept-1* (763), *Dip 1* (771)]. 6H (763, 771, 770).	
		ad : CS/Betzes.
Dip-J1 (770).	6J (770).	ad : CS/*Ag. junceum.*
Dip-V1 (770).	6V (770).	ad : CS/*D. villosum.*

Proteins-Endosperm Storage Proteins

1. Glutenins

Modify the 3rd paragraph of the preamble to, 'No'Y-type' proteins from the *Glu-A1* locus were demonstrated in hexaploid wheat (738), although they were found in diploid wheats (791, 782, and sequencing . . . . .

Glu-A1d (791).		v : V74, Spain (783).
Glu-A1e (791).		v : 132c, Poland (783).
Glu-A1f (791).		v : 112-29, Sudan (783).
Glu-A1g (791).		v : Landrace 1600.
Glu-A1h.	[*Glu-A1-I* (795)].	v : PI 94683.
Glu-A1j.	[*Glu-A1-II*(795)].	v : CI 12213.
Glu-A1j.	[*Glu-A1-III*(795)].	v : PI 352359.

Add to the note following *Glu-A1*, 'A number of alleles in *T. turgidum* var. *dicoccoides* populations were described, 12 at *Glu-A1-1* and 3 at *Glu-A1-2* (782),'

and add,

Glu-B1m.	[*Glu-B1-I* (795)].	**v**: PI 94640.
Glu-B1n.	[*Glu-B1-II*(795)].	**v**: PI 355505.
Glu-B1o.	[*Glu-B1-III* (795)].	**v**: PI 352354.
Glu-B1p.	[*Glu-B1-IV* (795)].	**v**: PI 94665.
Glu-B1q.	[*Glu-B1-V* (795)].	**v**: 94633.
Glu-B1r.	[*Glu-B1-VI* (795)].	**v**: PI 94669.

Add to the note following *Glu-B1*, 'Eight alleles at *Glu-B1-1* and 10 alleles at *Glu-B1-2* were described in *T. turgidum* var.*dicoccoides* populations (782).

Also add,

Glu-Ag^{i}1 (774).	1Ag^{i} (774).	**ad**: Vilmorin 27/*Ag. intermedium.*
Glu-H^{ch}1.	1H^{ch} (789).	**ad**: CS/*H. chilense.*
Glu-V1 (772).	1V (772).	**ad**: CS/*D. villosum.*

New entries after the *Glu-1* section:

'The symbol *Glu-2,* formerly used to identify a prolamin locus in 1BS (599), is now obsolete (781).

The *Glu-3* loci are now defined as the cluster of LMW glutenin genes previously considered a component of the compound *Gli-1* loci. Only *Glu-B3* has been shown to recombine with the gliadin genes (1.7%)(666).

Glu-A3 (784).	1AS (784).	**v**: CS.
Glu-B3 (784).	1BS (784).	**v**: CS.
Glu-D3 (784, 799).	1DS (784, 799).	**v**: CS.

2. Gliadins

New gliadin preamble:

After descriptive statement (. . . without quatemary structure.) Insert, 'The *Gli-1* loci are compound and are now considered to comprise the omega-gliadin and gamma-gliadin (749,661) multigene families (746), which may in some circumstances be further divided into *Gli-1-1* and *Gli-1-2,* respectively. The LMW glutenin multigene families which are closely linked to the *Gli-1* loci are now listed separately as the *Glu-3* set (784). Recombination (1.7%) has been shown between *Glu-B3* and *Glu-B1* (666). The gene order on the short arms of group 1 chromosomes is not known. There is evidence that a few of the omega-gliadin genes are separated from the main omega-gliadin gene cluster (798).

Delete the paragraph beginning 'In hexaploid wheat, the *Gli-1* loci . . . . .
In the following paragraph, replace 649 with 543 and delete the last sentence.

Gli-Ag^{i}1 In the 3rd column, change L3 to 1Ag^{i}.

Gli-V1 (772). 1V (772). **ad :** CS/*D. villosum.*

In the barley paragraph, replace 'is partly equivalent to *Gli-1* (526)' with 'is equivalent to the omega-gliadins (*Gli-1-1*) in *Gli-1* (526).'

Gli-Ag^{i}2 (774). 6Ag^{i}(774). **ad :** Vilmorin 27/*Ag. intermedium.*

After the *Gli-2* section add,

'A further set of gliadin loci *Gli-3*, coding for omega-type gliadins, are present in the short arms of group 1 chromosomes between 22 and 31 mu proximal to *Gli-1* (593, 664, 599).

Gli-A3 [664] (781). [*Gld-2-1A* (760)]. 1AS (664) **v :** Bezostaya 1.
Gli-B3 [593] (781). [*Gld-B6* (593), *Glu-B2* (599)]. 1BS (593, 599).
s : CS/Thatcher (593) **v :** Sicco (599).

Delete entirely the section called, "2. Other" located at the end of the endosperm protein section in the 1987 update and add,

3. Other endosperm storage proteins

Triplet proteins

Disulphide-linked proteins with a subunit composition similar to 11 - 12S globulins of oats and legumes (762).

Tri-A1 [762] (790). 1AS (762). **v :** CS.
Tri-D1 [762] (799, 790) 1DS (762). **v :** CS.

Allelic variation has been observed at both loci (762).

Protease Inhibition

Delete the current entries and substitute the following:

Ti-H1. 3R (759). **ad :** CS/Imperial.
Ti-R1. [*Iti 1* (753)]. 3H (753). **ad :** CS/Betzes.

Ti-A2(773). 5AL (773). **v :** CS.
Ti-B2 (773). 5BL (773). **v :** CS.
Ti-D2(773). 5DL (773). **v :** CS.

Ti-D2a (773).		v :	CS.
Ti-D2b (773).		v :	Champlein.
Ti-D2c (773).		v :	Synthetic.
Ti-Ag^{i}2 (773).	5Ag^{i} (773).	ad :	Vilmorin 27/*Ag. intermedium.*
Ti-R2 (773).	5RL (773).	ad :	CS/Imperial. su : CS/King II.
Ti-Mt2 (773).	5Mt (773).	ad :	CS/*Ae. mutica.*
Ti-S^{l}2 (773).	5S^{1}L (773).	ad :	CS/*Ae. sharonenis.*
Ti-U2 (773).	1U (773).	ad :	CS/*Ae. umbellulata.*

In barley, in addition to *Ti-H1*, other genes encoding inhibitors were located in chromosomes using the CS/Betzes addition lines and other aneuploids as follows:

Ica1 (Ica 1) and *Ica2 (Ica 2).*	1HL (753).	– encode inhibitors of chymotrypsin and bacterial and fungal alkaline proteases.
Isa1 (Isa 1).	2H (753).	– encodes inhibitors of bacterial protease subtilisin and endogenous α-amylase (752).

Genes encoding inhibitors immunochemically related to the above barley inhibitors were located in 1R and 2R, respectively, using CS/Imperial and Holdfast/King II addition lines (759).

Response to Vernalization

Vrn1 s: Kharkov 22MC*?/Rescue 5A (951);
Winalta*8/Rescue 5A (951). v: Hope *Vrn5* (939).

Vrn4. Stelmakh (939) doubted the existence of *Vrn4* and attributed misinterpretation to mixed genotypes and other causes.

Vrn5 v: Hope *Vrn1* (939)
References to additional studies given in 939.

Tiller Inhibition

tin (954). 1AS (954). v : Israel Uniculm 494 (954).
Restricted tiller number is a recessive character (954).

Reaction to *Erysiphe graminis*

Pm2 v: Galahad (943); Longbow (943). Brimstone *Pm6* (943); Gawain *Pm6* (943); Heiduck *Pm6* (944). Hornet *Pm8* (943).
Rendezvous *Pm4b Pm6* (943). Apollo *Pm4b Pm8* (924, 944).

Parade *Pm6 Mli* (943).

Pm4b v: Sorbas *Pm6* (924). Kronjewel *Pm8* (924, 944). Boxer *Mli* (924); Mission *Mli* (943). Rendezvous *Pm2 Pm6* (943). Apollo *Pm2 Pm8* (924, 944).

Pm5 v: Granada *Pm8* (924); Sensor *Pm8* (924).

Pm6 v: Brimstone *Pm2* (943); Gawain *Pm2* (943); Heiduck *Pm2* (924, 944). Sorbas *Pm4b* (924). Rendezvous *Pm2 Pm4b* (943). Parade *Pm2 Mli* (943).

Pm8 v: Ambassador (943); Corinthian (943); Dauntless (943); Disponent (924, 944); Götz (924); Kormoran (944); Merker (924); Nicklas* (924); Odilo (924). Hornet *Pm2* (943). Kronjewel *Pm4b* (924, 944). Sensor *Pm5* (924). Kristall (924). Apollo *Pm2 Pm4b* (924).

Pm10 (928). 1D (928). v: Norin 4 (928); Norin 26 (928) Norin 29 (928); Penjamo 62 (928); Shin-chunaga (928). *Pm10* was detected using a culture derived from a hybrid of *E.g. tritici* and *E.g. agropyri.*

Pm11 (945). 6BS (945). v: Chinese Spring (945); Salmon (945). *T. compactum* No. 44 (945). *T. spelta duhamelianum Pm 10* (945). *Pm11* was detected using a culture derived from a hybrid of *E.g. tritici* and *E.g. agropyri.*

Pm 12 (931). 6A (931) v: Wembley Derivative (931). al: *Ae speltoides* (931).

mli v: Aquila (924); Carimulti (924); Cariplus (924); Dolomit (924); Falke (924); Kormoran (924); Kraka (924); Markant (924); Mercia (943); Milan (924); Reiher (924); Rektor (924); Severin (924); Sperber (924); Tukan (924); Urban (924); Wattines (924), Boxer *Pm-4b* (924); Mission *Pm-4b* (924, 943). Bert *Pm6* (924). Kristall *Pm8* (924). Parade *Pm2 Pm6* (943).

Reaction in *Mayetiola destructor*

H3 v: Clara Fay H6 (932).
H5 1AS (927).
H6 v: Clara Fay H3 (932).
H11 1A (927).
H14 (913). 5A (913). tv: IN8455 Seln. (913). ELS6404-160 *H15* (913).

H15 (913). 5A (913). tv: IN81602 Seln. (913). ELS6404-160 *H14* (913).
H16 (914). tv: IN80164 Seln. PI 94587 *H6 H11* (914).
H17(915). 5A (915) tv: PI 428435 (915).
H18 (915). tv: Marquillo (929).
H19 (936). tv: PI 422297 (936). This wheat possesses a second gene which is allelic or closely linked with *H16.* (936).

Reaction to *Puccinia graminis*

Sr5 v: Dong-Fang-Hong 2 (922); Dong-Fang-Hong 6 (922); Feng-Kong 13 (923); Ke-Fang 1 (922). An-Hewi II *Sr8a* (922). Jing-Hong *Sr17* (922); Jing-Hong 2 *Sr17* (922). Dong-Xie 3 *Sr31* (923); Dong-Xie 4 *Sr31* (923). Beijing 10 *Sr Tmp* (922). Qing-Chung 5 *Sr6 Sr11* (922).

Sr6 v: Qing-Chung 5 *Sr5 Sr 11* (922)
Sr8a v: An Hewi II *Sr5* (922). E-Gan-Zao *Sr17* (922).
Sr10 v: Geneva (950)
Sr11 v: Qing-Chung 5 *Sr5 Sr6* (922).
Sr12 3B (947) v: Marquillo (947).
Sr17 v: Jing-Hong 1 *Sr5* (922); Jing-Hong 2 *Sr5* (922); E-Gan-Zeo *Sr8a* (922).
Sr31 v: Feng-Kang 2 (923); Feng-Kang 8 (923); Jing-Dan 106 (923); Lu-Mai 1 (923); Jan 7770-4 (923); Yi 78-4078 (923); Dong-Xie 3 *Sr5* (923); Dong-Xie 4 *Sr5* (923).

Sr Tmp v: Bai-Yu-Bao (922); Beijing 9 (922); Beijing 11 (922); Fertodi 293 (926); Martonvasari 5 (926); Nung-Ta 139 (922); Parker (926); Yen-An 15 (922); Xuzhou 14 (922). Beijing 10 *Sr5* (922).

Sr25 7AL (933) v: Sears' Translocation #12 (933).

Reaction to *Puccinia recondita*

Lr19 7AL (933) v: Sears' Translocation #12 (933).

Reaction to *Puccinia striiformis*

Yr2 v: Heines Kolben *Yr6* (919).
Yr6 v: Heines Kolben *Yr2* (919).

Reaction to *Tilletia carries* (D.C.) Tul., *T. foetida* (Wallr.) Liro, *T. controversa*

Bt2	v: Selection PS60-1-1075 (942).
Bt5	v: Selection R60.3432 (942).
Bt7	v: Selection 5077 (942).
Bt9	v: Selection M69-2073 (942).
Bt10	v: Selection M69-2094 (942).

Genetic Linkages

Chromosome 1A

1AS	tv:*Gli-A1 - Bg (Bla 1)*	< 2.33%	(955).
	tv:*Bg (Bla 1) - Hg*	1.17±1.40%	(955).
		1.52±1.88%	(955).
		1.32±1.15%	(955).
	tv:*Gli-A1 - Hg*	3.06±1.40%	(955).
		2.97±1.64%	(955).
		2.31±1.31%	(955).
		2.97±0.84%	(955).
	tin: - *Hg*	10 ± 3cM	(954).
	H5 - H11	4.4 ± 1.8 cM	(422, 927).

Chromosome 1B

1BS	tv:*Rg-Gli-B1*	6.44±1.71%	(955).

Chromosome 4D

4DS	*Ms2 - Rht10*	0.005% (937).

Chromosome 5A

5AS	*Ms3* - centromere	3.1% (934).
5A	*H9 - H15*	Close linkage (913).
	H10 - H14	Loose linkage or independent (913).

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IV. Editorial Remarks

Announcement for Future Issues

WIS No. 69 will be planned for publication in September, 1989, Manuscripts for this issue are most welcome and accepted any time, not later than July 31, 1989.

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Explanation of the Figure on the Cover

Receponces of GA_3 (1 mg/ℓ) to seedling growth of dwarf mutants of common wheat. See the detail informations described in the article of this volume by KUMAR and BAIJAL.

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