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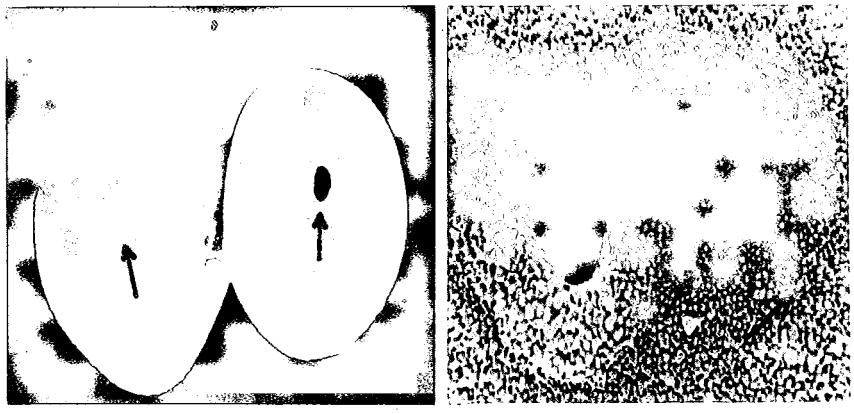

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Contents

I. Research Notes

Male fertility restoration against various alien cytoplasms. II. Genetical analysis of R-17127

D.K. GOTSOVA*, I. PANAYOTOV and K. GOTSOV

Institute for Wheat and Sunflower,
Tolbuhin, Bulgaria

The male fertility restorer line R-17127 was produced in the Institute for Wheat and Sunflower, Tolbuhin, Bulgaria, by one of the authors (K. Gotsov). It had been selected from the cross MS (*timopheevi*)-Aurora × R-255-2 (USA) with Rf-genes originating from *T. timopheevi.* This line possesses the cytoplasm of *T. timopheevi* but is highly self-fertile and exhibits all the characteristics of a contemporary true-bred cultivar, namely, high yield potential, short stem, very strong resistance to stem, leaf and stripe rusts and strong resistance to powdery mildew. Its vegetative period is 3 to 4 days shorter than that of the Bulgarian standard Sadovo 1, while its grain shows very good qualitative indices, i.e. high 1000-kernel weight, gluten content up to 40% and excellent bread-making qualities.

Our previous study (Panayotov *et al.* 1987) showed that line R-17127 restores high levels of male fertility in CMS-lines not only with the cytoplasm of *T. timopheevi* but also with the cytoplasms of *T. dicoccoides* var. *spontaneovillosum, Ae. speltoides* and *Ae. triuncialis.* Its ability to restore male fertility against *T. timopheevi* cytoplasm had been tested in the International Wheat Restorer Germplasm Screening Nursery (IWRGSN) in 1980 and proved to be both highly effective and very stable i.e., it occupied second place after R-line Zg 41 on the mean of eight trials in different countries.

In the present study we attempted to determine the number of the Rf-gene(s) of R-17127 as well as their chromosomal location.

Materials and Methods

In order to determine the number of the male fertility restoring genes of R-17127 it was crossed as pollen parent to the male sterile (MS) lines of two common wheat cultivars, Aurora and Roussalka, with the cytoplasms of *T. timopheevi, T. dicoccoides* var. *spontaneovillosum* and *Ae. speltoides.* The F_1 and F_2 generations were grown in the field and 2 to 3 spikes per plant were bagged before anthesis. The selfed seed fertilities of the hybrids were determined as percentage of the seeds set in the 1st and 2nd florets of each spikelet.

Simultaneously, monosomic analysis was carried out in order to determine the chromosomal location of the Rf-gene(s). First, at least three monosomic plants were identified from each line of

* Present address: Institute of Genetics, 1113 Sofia, Bulgaria

the monosomic series of Chinese Spring (Sears 1954). They were pollinated by R-17127 and, after a standard chromosome checking procedure, the monosomic F_1 plants were crossed as pollen parents to MS (*timopheevi*)-Siete Cerros 66 and the selfed seed fertilities of the hybrids were determined using 2-3 bagged spikes per plant.

In the present study all plants were classified according to their self seed fertilities into two groups, fertile and sterile, the sterile group being comprised of the plants that did not set any seeds in the bagged spikes.

Table 1. Segregation in the F_2 generation of hybrids between MS lines of Aurora and Roussalka as females and R-17127

Hybrid	No. of F_2 plants			Segregation ratio tested	x^2 – value
	Fertile	Sterile	Total		
(*timoph*) – Aurora x R-1727	71	20	91	3:1	0.44
(*dicoc*) – Aurora x R-17127	85	32	117	3:1	0.34
(*spelt*) – Aurora x R-17127	73	30	103	3:1	0.93
(*timoph*) – Roussalka x R-17127	85	14	99	54:10	0.16
(*dicoc*) – Roussalka x R-17127	84	18	102	54:10	0.31

Results and Discussion

The number of the fertile and sterile plants, that were studied in the F_2 hybrids between R-17127 and MS Aurora and MS Roussalka with the cytoplasms of *T. timopheevi, T. dicoccoides* var. *spontaneovillosum* and *Ae. speltoides* are presented in Table 1 together with the proposed segregation ratios. The results show that the male fertility restoration in the hybrids between R-17127 and the MS lines of Aurora is governed by one dominant gene. However, the segregation ratios between the fertile and the male sterile plants in the F_2 generation of the cross between R-17127 and the MS lines of Roussalka correspond to 54:10. This result suggests that three Rf-genes function in these hybrids and the complementary action of at least two of them is necessary in order to achieve even slightly lower levels of male fertility in the MS lines of Roussalka in comparison to MS Aurora (ref. Table 2 in Panayotov *et al.* 1987). Common wheat cultivars differ in their ease of restoration, that is, significant variation has been reported in the level of the restored male fertility when MS lines of different cultivars were pollinated by the same R-line (Wilson 1976; Mihaljev 1976; Jost & Milohnich 1976; Gotsov 1981). In general, this

Table 2. Segregation ratios of sterile vs. fertile plants in the disomic and monosomic lines of the hybrids, (*timopheevi*) – Siete Cerros 66×(CS monosomics × R-17127) F1

Line	No. of plants			% Fertile plants	x^2- value (15:1)
	Fertile	Sterile	Total		
Disomic	123	11	134	91.8	0.87
Mono-1A	77	0	77	100.0	5.13*
Mono-2A	73	4	77	94.8	0.15
Mono-3A	19	6	25	76.0	13.44**
Mono-4A	98	9	107	91.6	0.85
Mono-5A	60	3	63	95.2	0.24
Mono-6A	82	7	89	92.1	0.49
Mono-7A	46	3	49	93.9	0.00
Mono-1B	59	2	61	96.7	0.92
Mono-2B	39	9	48	81.3	12.80**
Mono-3B	52	4	56	92.9	0.08
Mono-4B	46	4	50	92.0	0.26
Mono-5B	335	0	35	100.0	2.33
Mono-6B	81	1	82	98.8	3.54*
Mono-7B	–	–	–	–	–
Mono-1D	60	2	62	96.8	0.97
Mono-2D	77	5	82	93.9	0.00
Mono-3D	58	9	67	86.6	5.89**
Mono-4D	42	1	43	97.7	1.13
Mono-5D	79	3	82	96.3	0.94
Mono-6D	77	7	84	91.7	0.62
Mono-7D	46	4	50	92.0	0.26

* and **: Significantly different for a 15:1 ratio at the 5% and 1% level, respectively.

phenomenon had been explained with the presence of weak fertility restoring genes in the genetic background of some wheat cultivars and their interaction with the Rf-genes of the restorer lines.

The data from the monosomic analysis presented an additional evidence in proof of the complex genetic basis of male fertility restoration by R-17127 (Table 2). The segregation between the fertile and sterile plants in the disomic test-cross fitted a 15:1 ratio. Moreover, about seventy percent of the plants belonging to the fertile class showed self seed fertility above 75% (Fig. 1). This fact suggests that four dominant Rf-genes might be involved in the control of male fertility restoration by R-17127. Two of them are located on chromosomes 1A and 6B of R-17127 because test-crosses with mono-1A and -6B showed significantly higher proportion of the fertile class in comparison to the disomic line. From previous studies (Yen *et al.* 1969; Bahl & Maan 1973) it is known that four genes, Rf1, Rf2, Rf4 and Rf5, all of which originate from *T. timopheevi,* are located on chromosomes 1A, 7D, 6B and 6D, respectively. R-17127 seems to possess two of them, i.e. Rf1 and Rf4, while its chromosome 5B may carry another Rf-gene. The present results also suggest that three Rf-genes are located on chromosomes 3A, 2B and 3D

of Chinese Spring. Their interaction with the fertility restoring genes of R-17127 to give a 15:1 ratio in the disomic line must be a subject of future investigations.

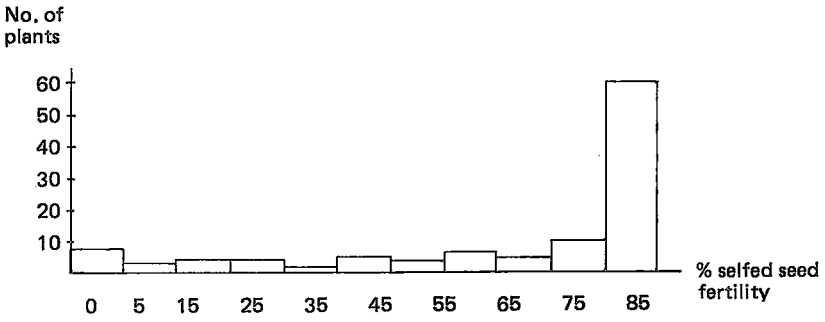

Fig. 1. Distribution into 11 classes of self seed fertility of the plants produced by the cross (*timopheevi*) – Siete Cerros 66 x (CS monosomics x R-17127) F1

Conclusions

Line R-17127 possesses a complex genetic system for male fertility restoration against the CMS-inducing cytoplasms of G plasma type. This system probably includes four Rf-genes, two of which were found to locate on chromosomes 1A and 6B. However, their penetrance and expressivity can be modified depending on the genetic background of the MS line. Further studies are necessary for the chromosomal location of the other two Rf-genes of R-17127 and for complete understanding of the interactions that determine the conditions for their full expression.

Acknowledgement

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Mutagenic efficiency of individual and combined treatments of Sodium Azide and Hydrazine Hydrate in bread wheat

A. S. LARIK

Department of Agronomy and Range Science, Gassim College of Agriculture, King Sand University
Saudi Arabia

Induction of useful mutations in bread wheat (*Triticum aestivum* L.) has gained tremendous interest in the last two decades owing to an increasing awareness of the potential of this method for creating genetic variability. In addition to physical mutagens, attempts have been made by the research workers (AUGUSTINE *et al.* 1975; AWAN *et al.* 1980; KHAN, 1981; KONZAK *et al.* 1975; NILAN *et al.* 1976) to determine the most effective and efficient chemical mutagen for the induction of desirable traits in crop plants. As a result, an extensive array of highly effective mutagenic agents are now available.

The present work on the effects of sodium azide (NaN_3) and hydrazine hydrate (HZ) in two hexaploid wheat genotypes has been undertaken with a view to study the mutagenic-sensitivity in respect of seed germination and survival, pollen and seed fertility.

Materials and Methods

About fifty seeds per treatment of two hexaploid wheat varieties viz., Al-Samma and Hinta Madina were presoaked in distilled water for about 16 hours at 20 ± 1°C prior to treatment with different concentrations of sodium azide and hydrazine hydrate (Table 1). The concentrations of azide and HZ were prepared using standard potassium phosphate (KH_2PO_4) buffer pH-7. Presoaked seeds were placed in freshly prepared azide and HZ solution of each concentration for 3 hours at a constant temperature of 20 ± 1°C. During the treatment the flasks containing the solution and the seeds were frequently shaken to ensure sufficient aeration. In combination treatments, the seeds were soaked first in sodium azide for 3 hours and after being thoroughly washed in water, were immersed in HZ solution for 3 hours. For control only buffer solution without azide and HZ was used.

After completion of treatment the treated seeds were washed for one hour in running tap water and sown in 12 inches pots along with control in a randomized design in three replicates in the greenhouse of the Department of Agronomy and Range Science, Gassim College of Agriculture, King Saud University, Saudi Arabia.

The M_1 generation was studied for the following parameters to determine the relative effects of individual and combined treatments on (1) Germination and seedling height on 10th day (2) Survival of seedling at maturity (3) Pollen and seed fertility. The mean values of 20 plants randomly selected from each treatment were considered for seedling growth. Germination and seedling height was determined according to the methods described by MYHILL & KONZAK (1967). Pollen fertility (stainability) was determined by staining pollen grains in a solution introduced by ALEXANDER (1969) and the seed fertility was calculated on the total population basis for each treatment.

Table 1. Effect of single and combination treatments of sodium azide and hydrazine hydrate on various parameters in M1 generation of two hexaploid wheat genotypes

Variety/Treatment	Germination %	Root length (cm)	Injury %	Shoot length (cm)	Injury %	Survival %	Pollen fertility %	Seed fertility %
AL-SAMMA								
Buffer control	95.50	17.70	–	12.48	–	86.90	91.25	88.70
0.0001M NaN_3	95.82	17.88	–	12.60	–	88.75	92.38	88.90
0.001M NaN_3	95.40	16.46	7.00	12.10	3.04	87.72	82.37	77.17
0.005M NaN_3	90.18	15.90	10.17	11.88	4.81	84.89	75.75	70.59
0.01M NaN_3	60.16	12.00	32.20	10.00	19.87	30.95	58.68	55.85
0.1% HZ	80.71	16.20	8.47	11.80	5.44	80.10	85.47	77.45
0.2% HZ	80.00	14.80	16.38	10.78	13.62	78.25	80.57	76.94
0.4% HZ	60.58	10.85	38.70	8.94	28.36	50.25	75.77	71.35
0.6% HZ	40.35	8.50	51.97	6.58	47.27	25.00	50.80	46.58
0.0001M NaN_3 + 0.1% HZ	80.50	14.70	16.95	10.30	17.46	75.76	75.45	70.05
0.001M NaN_3 + 0.2% HZ	70.79	12.52	29.26	8.90	28.68	60.58	68.55	65.00
0.005M NaN_3 + 0.4% HZ	58.00	9.90	44.06	6.85	45.11	52.00	60.25	58.50
0.01M NaN_3 + 0.6% HZ	30.00	7.90	55.36	5.95	52.32	25.80	50.75	45.80
HINTA MADINA								
Buffer control	98.00	16.96	–	11.88	–	93.65	88.90	86.89
0.0001M NaN_3	93.80	15.98	5.77	11.65	1.93	89.00	88.00	87.13
0.001M NaN_3	90.75	13.98	17.57	11.20	5.72	88.08	87.50	85.65
0.005M NaN_3	90.00	14.00	17.45	10.50	11.61	82.87	83.38	80.20
0.01M NaN_3	70.50	11.80	30.42	8.77	26.11	66.00	60.67	59.25
0.1% HZ	92.00	15.90	6.25	11.50	3.19	88.87	87.50	86.70
0.2% HZ	89.87	15.08	11.08	11.00	7.40	85.38	85.60	84.10
0.4% HZ	85.31	12.13	28.47	10.38	12.62	80.90	80.00	79.25
0.6% HZ	60.00	8.98	47.05	6.90	41.91	55.76	60.70	58.90
0.0001M NaN_3 + 0.1% HZ	82.57	14.70	13.32	10.80	9.09	75.10	76.76	75.00
0.001M NaN_3 + 0.2% HZ	78.00	13.10	22.75	9.90	16.66	68.90	71.80	64.65
0.005M NaN_3 + 0.4% HZ	68.50	11.50	32.19	8.90	25.08	65.00	61.50	59.80
0.01M NaN_3 + 0.6% HZ	50.50	8.50	49.88	6.80	42.76	40.60	60.80	53.75

Results and Discussion

The effects of individual and combined treatments of sodium azide and hydrazine hydrate on different M1 parameters are depicted in Table 1. It was observed that individual and combined tratments of azide and HZ produced reduction in seed germination, seedling growth, pollen and seed fertility and survival at maturity in both genotypes except in variety Al-Samma where sodium azide 0.0001 molar concentration displayed some improvement in all the parameters studied. The reduction was found to be dose dependent; it increased consistently with increase in the concentration of the mutagen applied. Previous reports (SHARMA *et al.* 1979; SINGH *et al.* 1978) have also shown linear relationship between the dose of the mutagen applied and the

parameters studied. However, seed germination was adversely affected in combination treatments than in the individual treatment, thus indicating a negative synergistic effect by enhanced toxicity. It was noticed that HZ was relatively strong mutagen than the azide.

Genotypes displayed remarkable differences in their response to individual and combined treatments. The highest concentration apparently caused highest biological damage (Table 1), which indicate the efficiency of highest concentration. However, the efficiency of the mutagen is not only dependent on the concentration alone but also on other variables such as presoaking time, duration of the treatment and pH of the mutagen solution. Similar reduction in seed germination was reported by AWAN *et al.* (1980) in rice and NILAN *et al.* (1976) in barley and BHASHARAM and SWAMINATHAN (1961) in wheat and barley.

Since no cytological examination of primordial root tips were undertaken for these treated seeds, no precise interpretation, regarding the intrinsic events contributing this phenotypic manifestation, is possible. However, for this depreciated germination, one is allude to conclude that embryo which might have been disturbed by mutagen effects made slow recovery. Such plant injury effects may be due to physiological or chromosome mutations. According to GAUL (1977), physiological damage has probably both chromosomal and extra-chromosomal origin and the separation of these two causes is usually not possible.

It may be noted that in variety Al-Samma lower concentration (0.0001M NaN_3) has shown stimulatory effect in all the parameters and also in variety Hinta Madina lower concentration caused relatively less damage as compared to the higher concentration. This shows that the recovery after primary injury due to toxic effects of lower concentration was better, while the effects of higher concentration persisted up to the adult plant stage as was evident from the survival and seed fertility at maturity (Table 1).

Survival percentage displayed further decline. Here also both genotypes exhibited greater sensitivity. Variety Hinta Madina showed higher germination and better survival than variety Al-Samma. This probably is due to its genetic makeup and greater tolerance. The two genotypes under investigation do not show same degree of response to both mutagens. Al-Samma was found to be more sensitive than Hinta Madina. Already there exists much evidence that genetic differences even though they are as small as single gene difference, can produce significant changes in mutation expression (SMITH, 1958; NILAN, 1954) and will show different degree of response.

The seedling height decreased proportionally with increasing concentration of the mutagen used either individually or in combination. However, combined treatments produced maximum inhibitory effect in both genotypes. Adverse effects of both mutagens were much more pronounced on root growth than on shoot growth. The extent of the injury in seedling growth with increase in dose was not the same in the two genotypes, indicating differential genotypic response. Pollen and seed fertility also decreased with the increase in the concentration of the mutagen revealing a linear dependence of these traits on dose as reported earlier (SHARMA *et al.* 1979; NILAN *et al.* 1977). Low pollen and seed fertility at higher doses and in combination treatments could be due to translocations and other cytological anomalies induced by these treatments (LARIK 1975).

In combination treatments independent action of two mutagens leads to an additive effect. This effect gets modified depending upon the nature of interaction of mutagens in a combination

treatment. If one of the mutagens exposes previously protected sites or creates favourable condition to enhance the activity of other, more than additivity, a synergistic effect would result. If, on the contrary, two mutagens merely compete for the same site, the effect will be less than additivity (AASTVEIT 1968). Present results show negative synergism (less than additivity) which confirm the findings of AASTVEIT (1968). CHOPRA & SWAMINATHAN (1966) made analogous studies in common wheat suggested that "recovery, rather than induction appears to be the major obstacle for obtaining synergistic effects".

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Influence of combined treatments of N-Nitroso-N-Methylurea and Sodium Azide on physiological injury and the genetic effect in Triticale

JAN OIEJNICZAK and HENRYK PATYNA

Institute of Plant Genetics, Polish Academy of Sciences
Poznan 60-479, Strzeszynska 30/36. Poland

In recent years chemical mutagens have been used commonly in cereal plants to create genetic variability for desirable traits, as a source of new germ plasm material.

A mutagenic effect of N-nitroso-N-methylurea (MNUA) and sodium azide (SA) on higher plants have been known for many years. The frequency of mutations may be increased by combined treatments of MNUA with SA. There only few studies have been reported on the use of chemical mutagens in this new crop.

The subject of this study was the estimation of the effect of treatments of N-nitroso-N-methylurea, sodium azide and combined of their on physiological injury in M_1 generation and morphological frequency of traits in M_2 and M_3 generation.

Materials and Methods

Grains of hexaploid Triticale cultivar Grado and strain LT50/79 were presoaked in water for 12 hours at 25°C. The mutagen solution were freshly preparated in 0,025M phosphate buffer at pH-3 for sodium azide, whereas N-nitroso-N-methylurea was dissolved in distilled water at pH-5, 6. Grains were soaked in 2mM of SA and 1.5 mM of MNUA for 3 hours at 25°C. In combined treatments grains were expose to mutagens of SA and MNUA respectively for 3 hours at 25°C.

After treatments they were rinsed under running water. Grains were sown in the field at the space of 5 x 20 cm in three replication to obtain M_1, M_2 and M_3 generation. After harvesting of M_1 plants height of plant, length of spike, grains yield per spike, number grains per spike and 1000 grains weight were determined. The first three spikes of each M_1 plant were use to raise M_2 and M_3 generation. Grains from M_2 and M_3 generation were sown in the field at the space 5 x 20 cm.

The main pressure morphological selection in M_2 and M_3 generation was concerned on days to heading, plant height, spike length, resistance to diseases and leaft length.

Results from M_1 generation have been statistically calculated using a multivariate analyses of variance MANOVA and the other multivariate methods related.

Results

Height of plant was only slightly affected by sodium azide used in this experiment (Table 1). A significant difference in height of plant was found after treatments with MNUA and combined treatments of SA and MNUA. The date also indicate that height of plant was significantly reduced when MNUA was treated after application of SA. Azide applied after MNUA treatment caused

Table 1. Estimation of contrast between control (H_2O) and mutagens for phisiological injury in M_1 generation of Triticale

Contrast	Value of contrast				
	Height of plant cm	Length of spike	Grain yield per spike gram	Number grains per spike	1000 grains weight gram
GRADO - buffer	-1,97	-0,50	-0,42	1,55	-4,57
" - AS 2mM	1,50	-0,10	-0,07	4,05	-9,40
" - MNUA 1,5mM	13,97*	0,22	0,92	15,12*	-1,47
" - AS + MNUA	11,25*	-0,15	0,42	6,95	5,32
" - MNUA + AS	5,02	-0,37	-0,05	6,17	2,35
LT 50/-75 - buffer	-0,42	-0,40	0,22	-1,02	1,82
" - AS 2mM	3,40	-0,35	0,17	-2,70	5,90
" - MNUA-1,5mM	22,45*	0,35	1,35	10,05*	18,60
" - AS + MNUA	18,60*	0,27	1,12	4,60	18,90*
" - MNUA + AS	9,80*	0,17	0,85	3,32	8,27

* : significant contrast at α-0,05 level

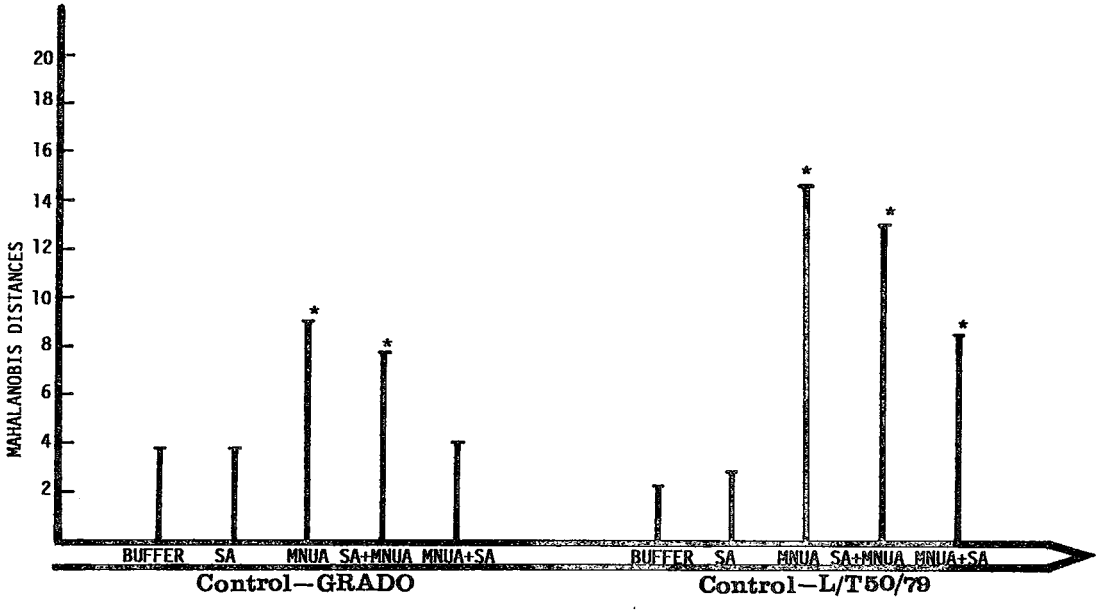
Table 2. Frequency of morphological mutants in M_2 and M_3 generation of Triticale induced by SA, MNUA and combined treatments

Treatments	Frequency in M_2 %	Frequency in M_3 %
GRADO		
Buffer	–	1,46
AS - 2mM	0,80	2,63
MNUA - 1,5mM	1,50	1,55
AS + MNUA	0,90	2,10
MNUA + AS	0,78	1,55
LT 50/79		
Buffer	–	–
AS - 2mM	0,25	0,80
MNUA - 1,5mM	0,66	1,20
AS + MNUA	0,41	0,55
MNUA + AS	0,28	0,64

less reduction of height plant as compared to the combination of SA and MNUA treatments.

In general the mutagen treatments has minor effect on yield components and there was no significant difference in the grain yield per spike, number grains per spike and 1000 grains weight. Although the difference from MNUA treatments in number grains per spike was noticed compared to the controls. It is very interesting pointed out (Fig. 1) that more response to the mutagen treatment was strain LT 50/79 than cultivar Grado.

The frequency of morphological mutants was different and depend on treatments (Table 2). More mutations were induced in SA and MNUA treatments. Combined treatments caused a degrease in mutation yield as compared to separate treatment. The frequency of morphological mutants in M_3 generation was much higher than in M_2 generation. In this study no chlorophyll mutations was observed in M_2 and M_3 generation. A great number of mutants were isolated from the M_2 and M_3 generation with different morphological characters e.g. early, plant height, spike length, leaft length and resistance to diseases.



* significant at 0.05 level

Figure 1. Mahalanobis distance for yield of phisiological injury between control (H_2O) and treatments for Triticale.

Discussion

Results obtained in the present study shown that SA and MNUA is powerful mutagens for Triticale. The most important is that azide induced higher mutation yield with very little influence on M_1 height of plant as compared to MNUA. These results are in confirm with Konzak *et al.* (1975) and Olejniczak Patyna (1981) who have observed similar effect after treatment with SA and MNUA. Although a slight mutagenic action of SA was found by Gichner and Weleminsky (1977) in Arabidopsis and Niknejad (1978) in chickpea.

In general separate treatment with mutagens had no influence on yield components in M_1 generation. In combined treatments when azide was used after MNUA decrease height of plant was observed, as compared to AS with MNUA treatment. The same effect was found by Konzak *et al.* (1975) in barley and Olejniczak (1986) in maize after combined treatments of MNUA with SA.

Application of mutagens in present study did not induced chlorophyll mutations in M_2 and M_3 generation. This is in agreement with the result obtained by Sapra *et al.* (1975) in Triticale. The only explanation of this results in Triticale as an alloploid. Its seems necessary to point out that we have selected many morphological mutants with different characters. After treatment with MNUA of Triticale Grzesik (1980) and Olejniczak & Patyna (1984) have also detected Triticale mutants. It is very interesting to point out that induced morphological mutants have been used as materials for hybridization breeding programmes. Mutation breeding is only one of the current methods of Triticale improvement and can produce desirable results when combined with selection or with other methods of manipulating genetic variation.

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Characterization of pollen grains of some wheat cultivars– Scanning Electron Microscopy

M. A. KARIM[1], M. P. SINGH and S. L. MEHTA[2]

Indian Agricultural Research Institude
New Delhi-110012
India

With a view to ascertain minute structural differences of pollen grain surface, scanning through electron microscope was undertaken in four wheat cultivars (Chinese Spring, NP 880, HD 2009 and Mex. C.B. 116), which were having diverse genetic background and distinct contrasting morphological features. Mature pollen grains were collected from anthers prior to anthesis and the pollen grains were immediately boiled in a mixture of 9 parts acetic acid and one part concentrated H_2SO_4 for 6 minutes. The extracted pollen grains were rinsed in distilled water and subsequently fixed in the solution of 6.5% glutaraldehyde in cacodylate buffer (pH 7.2) for one hour at 8°C. The pollen grains after washing were transferred to solution of cacodylate buffered 2% Osmium tetraoxide and post fixed for one hour and then passed through series of graded alcohol for dehydration at room temperature. The dried samples of pollen grains were mounted on the aluminium slubs coated with a thin layer of gold having 200A° thickness and were examined on S4-10 Cambridge Stereoscan, Electron microscope at 10 Kv accelerating voltage.

Results and Discussion

Exine sculpturing of pollen grain as viewed under scanning showed two components, first indicating density process (the number of particulates /granulars/ protrusions per unit area) and the second pertains to frequency of group aggregations. The pollen grain of all the four varieties were oval in shape and their relative size was in descending order of NP 880, HD 2009, Mex. C.B. 116 and Chinese Spring. Many of the pollen grains showed single germ pore in the form of small hump on the surface and some of the germ pores had holes at the tip of the hump.

The surface projections were not sharp enough to be termed as spines, hence we thought it appropriate to use inter-changeable terminology of particulates and protrusions for the granular structures. The particulates were densely packed on the pollen surface of HD 2009 and Chinese spring. The protrusions of NP 880 and Mex C.B. 116 pollen, however revealed some minor gaps in between. The particulates of NP 880 and Chinese spring pollen were alike with comparatively smooth tips. Then average diameter of these particulates was 0.07 and 0.05μ and their height was of 0.1μ and 0.07μ respectively. The particulates of HD 2009 were slightly sharper, but these were blunt tipped in Mex C.B. 116. The average diameter of particulates of HD 2009 and Mex C.B. 116 was 0.09μ and 0.12μ and their heights 0.14μ and 0.18μ respectively. The average size of

1) Department of Botany, Bangladesh Agricultural University, Bangladesh.
2) Division of Biochemistry, Indian Agricultural Research Institute, New Delhi.

the particulate at the hump of the germpore in the Chinese Spring was more distinct and prominent when compared to that of surface protrusions (Fig. 1 and 2).

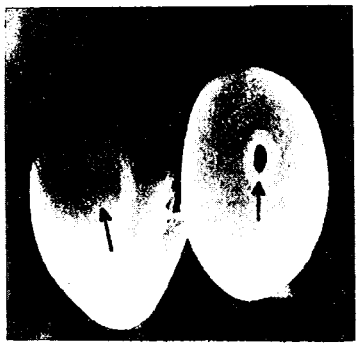

Fig. 1 Pollen grain depicting open germ pore (arrow) in one of them and depression surface in the other (arrow). x 3204.

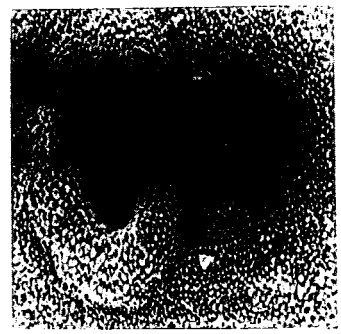

Fig. 2 Enlarged view of pollen surface near the germ pose. The germ pore particulates are slightly broader than the surface particulates. The particulates on pollen surface show distribution pattern of single, fusion and aggregation of many. x 18586.

From the grouping pattern of particulates on the surface of pollen, it became evident, that maximum groups occur in Chinese Spring. Frequency distribution data compiled in Table 1 would indicate that aggregation of 6-12 particulates were invariably present in NP 880. Maximum number of particles were single, but fusion of two particulates was quite frequent. Co-joining of three – six particulates was also noticed, but their frequency of occurrence was somewhat restricted. The distribution pattern of particulates showed mutual aggregation in all the pollen. On the basis of protrusions length, HD 2009 and Mex. C.B. 116 formed one group, whereas NP 880 and Chinese Spring were separately grouped. Chinese spring had small pollen grain size with collapsed surface, indicating hollow nature. It also manifested comparatively low seed wt. (100 grain wt. 2.2 gm.), maximum frequency of surface protrusions, complex aggregations, and reduced protrusion height and diameter. It may be mentioned that some of these distinct characteristics depicted at morphological and ultra-structural levels indicated a separate position of Chinese Spring. The sculpturing of pollen grain is generally considered a fairly constant character and an excellent means of recognition (Faegri & Iverson 1975). It has been suggested by Gornall, 1977 that aggregation pattern of particulates may be linked with the breeding system and in the course of selection it underwent rapid evolution. The adoptive significance of specific sculpturing type as manifested on pollen grain surface is not yet clearly known, but some ideas have been put forward on the basis of studies of pollen grain and spore walls (Heslop Harrison 1971). There is hardly

any report on scanning studies pertaining to pollen grain. Surface in wheat crop, therefore, the present investigation indicate the relevance of ultrastructural studies to understand evolutionary trends and taxonomic potentials for characterization and grouping of wheat cultivars.

Table 1. Frequency of pollen surface sculptures indicating grouping pattern of particulates

Pollen Source	1*	2	3	4	5	6	7	8	9	10	11	12*
NP880	9.6	7.3	4.0	4.3	4.6	2.0	0.3	0.0	0.3	0.0	0.3	0.3
HD 2009	14.6	19.0	13.0	9.3	2.0	0.3	0.3	0.3	0.0	0.0	0.3	0.0
Mex. C.B. 116	13.0	8.6	8.3	3.6	1.3	0.0	0.3	0.0	0.0	0.0	0.0	0.0
Chinese Spring	3.0	1.0	0.5	3.5	1.5	2.5	2.0	1.0	1.0	2.5	1.5	0.5

* 1-12 refers to number of particulates/protrusions in each group.

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Mapping of the complex *T. sphaerococcum* locus

Dalmir SINGH

Genetics Division, Indian Agricultural Research Institute
New Delhi – 110012, INDIA

Triticum sphaerococcum Perc. ($2n = 6x = 42$) is characterised by short culms, dense spikes and small spherical grains. *Sphaerococcum* phenotype is reported to be controlled by a single gene (Ellerton 1939; Singh 1946). Sears (1947) showed that *sphaerococcum* (*s*) gene was located on chromosome 3D (XVI) which in double dose produces the *sphaerococcum* effect but in single dose it is relatively ineffective. It was also suggested that chromosome 3D (XVI) of *T. aestivum* increases apike and culm length, particularly between the dosage 0 and 1. On the basis of mutation studies, Swaminathan *et al.* (1963) concluded that *sphaerococcum* factor was not a null (c.f. Ellerton) but a functional unit that can be broken up into small mutons. Koba & Tsunewaki (1978) mapped the gene *s* on the long arm of chromosome 3D with a genetic distance of 5.0% between the locus and the centromere. Prabhakara Rao (1971) reported that the *sphaerococcum* gene *s* is located either very close to centromere on 3Dα (long arm) or it is on 3Dβ (short arm) of chromosome 3D.

The long arm of chromosome 3D besides possessing the *sphaerococcum* gene also carries a dominant gene R_1 for red seed colour in wheat var. Chinese Spring (sears 1954). Prabhakara Rao (1973) reported that the R_1 gene was located distally. The present investigation was undertaken to resolve the intricacies related to the complex character of *sphaerococcum* and the location of red grain colour locus in *T. sphaerococcum.*

Materials and Methods

Monosomic 3D of var. Pb. C 591 (white seeded) and ditelocentric for 3D long arm (3D L) of var. Chinese Spring (red seeded) were crossed with a red seeded var. of *T. sphaerococcum.* All the F_1 plants were raised in the field.

Chromosome number and meiotic cofigurations were studied at first meiotic metaphase of all the F_1 plants and their morphological characters were recorded. Seeds were harvested from all the F_1 plants and sown separately in the field for raising F_2 generation. All the F_2 plants were pulled out from the field and data were recorded on morphological characters. Contrasting characters between *T. sphaerococcum* and *T. aestivum* were taken as follows:

T. aestivum	*T. sphaerococcum*
1. Long grain (*Lg Lg*)	Spherical grain (*lg lg*)
2. Long spike 6.0 cm (*Lsp Lsp*)	Short spike 3.5 cm (*lsp lsp*)
3. Long peduncle 37% (*Lpd Lpd*)	Short peduncle 25% (*lpd lpd*)
4. Red grain colour (R_1 R_1)	Red grain colour (R_1 R_1)

Results

From the cross involving monosomic 3D of var. Pb. C 591 and *T. sphaerococcum*, two types of F_1 plants were observed with chromosome configurations of 20″ + 1′ (monosomic) and 21″ (disomic) at first meiotic metaphase. F_1 plants of the cross involving ditelocentric 3DL of var. Chinese Spring and var. *T. sphaerococcum.* were found to have a meiotic chromosome configuration of 20″ + 1′ het. at first meiotic metaphase.

Morphologically all the F_1 plants resembled *T. aestivum,* except erectoid type of leaves, typical of *spaerococcum* leaf character. The F_1 plants produced only red seeds. Although the monosomic F_1 hybrids possessed one full 3D chromosome of *T. sphaerococcum.* (but in hemizygous state) still they did not show *T. sphaerococcum* characters, confirming the contention of Sears (1947) that *sphaerococcum* gene (*s*) in single dose (hemizygous) is ineffective. Appearance of erectoid leaves in the F_1 plants do not support the suggestion that this character might be the pleiotropic effect of sphaerococcum gene (*S*). From the observations on F_1 plants, it could not be determined whether *s* locus is simple or complex. To analyse this, F_2 population was raised.

F_2 Population obtained from both the types of F_1 plants of cross involving monosomic 3D of Var. Pb. C591 and *T. sphaerococcum.* was screened for seed colour to ascertain the location of gene governing red seed colour in *T. sphaerococcum.* It was found that monosomic F_1 hybrids ($2n$ = 41, 20″ + 1′) where chromosome 3D of *sphaerococcum* is present as a univalent produced plants with red seeds only in F_2 while the F_2 of disomic ($2n$ = 42, 21″) plants segregated for 3 red: 1 white seeded plants (Table 1). This observation confirmed that there is one dominant gene responsible for red colour grains in *sphaerococcum* and it is located on chromosome 3D.

Data were recorded on the F_2 population raised from the F_1 plants of cross involving telocentric 3DL of var. Chinese Spring and *T. sphaerococcum.*. Characters on which the data were

Table 1. Segregation of seed colour in the F_2 population obtained from F_1 hybrids of cross involving monosomic 3D of var. Pb. C 591 and *T. sphaerococcum.*

F_2 population of		Number of plants observed		X^2 value	"P" value
		Red	White		
Disomic F_1 hybrids ($2n$ = 42, 21″)	1.	145	51	0.10	
	2.	105	39	0.33	
	3.	137	49	0.17	
	4.	118	36	0.22	
	5.	127	45	0.12	
	6.	221	70	0.11	
				1.05	0.98–0.95
Monosomic F_1 hybrids ($2n$=41, 20″+1′)	1.	208	–		
	2.	171	–		
	3.	159	–		
	4.	183	–		

Table 2. The frequencies of parental and recombinant types obtained from the F2 population of F1 cross involving ditelocentric 3DL of var. Chinese Spring and *T. sphaerococcum*.

	Frequencies			
	Red seeds		White seeds	
Parental Type				
Long peduncle-long spike-long grain	466	812 (78.83%)	24	34 (3.3%)
Short peduncle-short spike-spherical grain	346		10	
Recombinant Types				
Long peduncle-short spike-spherical grain	52	101 (9.8%)	0	8 (0.78%)
Short peduncle-long spike-long grain	49		8	
Long peduncle-long spike-spherical grain	20	52 (5.05%)	0	4 (0.4%)
Short peduncle-short spike-long grain	32		4	
Long peduncle-short spike-long grain	14	17 (1.65%)	2	2 (0.19%)
Short peduncle-long spike-spherical grain	3			
Total 1030				

taken included grain shape (Long *vs* spherical), spike length (Long *vs* short), peduncle length (Long *vs* short) and grain colour (Red *vs* white) and the results are summarised in Table 2.

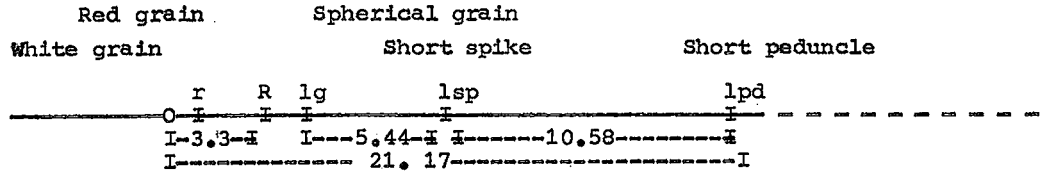
F2 segregating plants obtained were classified into two distinct classes, parental type (812 plants, morphologically *sphaerococcum* and *aestivum* types) and recombinant type (218 plants having hybrid characters of *sphaerococcum* and *aestivum*).

The recombinant class (21.7%) consisted of plants with different *sphaerococcum* sub characters. These recombinants were classified into 4 main sub-classes –

1. Long peduncle-short spike-spherical grain and short peduncle-long spike-long grain. 10.58%
2. Long peduncle-long spike-spherical grain and short peduncle-short spike-long grain. 5.44%
3. Long peduncle-short spike-long grain and short peduncle-long spike-spherical grain. 1.84%
4. Long peduncle-long spike-long grain-white grain and short peduncle-short spike-spherical grain-white grain. 3.3%

The frequencies of recombinant subclasses clearly show that character *sphaerococcum* is not governed by a single gene but at least three closely linked independent genes are involved in controlling this character. These genes are located very close to the centromere on the long arm of chromosome 3D.

On the basis of recombination frequencies in relation to the centromere the placement of these genes is shown below –



All these genes are located in a gene order of Red grain colour (3.30) - Spherical grain (very closed to red grain) - Short spike (5.44) - and Short peduncle (10.58) within a map unit of 21.17 from the centromere.

Another significant finding observed in the present study was the occurrence of plants with white seeds in the F_2 population of these two red seeded varieties. Plants with white seeds are not expected if the gene (R_1) which controls the red seed colour in these varieties is at the same locus. Occurrence of plants with white seeds but with low frequency (3.3%) clearly shows that the genes which control red colour of seeds in vars. Chinese Spring and *T. sphaerococcum* are not situated at the same locus.

Acknowledgment

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Genetic architecture of characters related to lodging in wheat

O. P. LUTHRA

Department of Genetics,
Haryana Agricultural University,
Hisar, India

Informations on the genetic architecture of attributes related to lodging in wheat are very scanty. Therefore, the investigation was conducted to understand the nature of gene effects governing the inheritance of attributes related to lodging.

Materials and Method

Seven genotypes viz. Sonalika, WG377, WH147, WH157, UP368, HD2160 and C281 were crossed in all possible combinations to produce 21 crosses in diallel fashion excluding reciprocals. The genotypes were selected on the basis of visual observations for variation in lodging behaviour. The 28 progenies (21 F_1 crosses plus 7 parents) were grown in randomised block design with three replications. Observations were recorded on ten competitive plants from each genotype in each replication for plant height (cm), Mother-shoot weight (g), shoot weight (g), root weight (g), straw strength (g) and length of second internode (cm). Data were subjected to diallel cross analysis as outlined by Hayman (1954). Heritability in narrow sense was estimated by using the formulae of Crumpacker and Allard, 1962.

Results and Discussion

According to the analysis of variance for randomised block design, the differences among parents and crosses were statistically significant in respect of all the attributes related to lodging under study. Before carrying out the genetic analysis for diallel cross, however, it was considered advisable to test the validity of the hypothesis underlying diallel analysis. Using the formula which yields uniformity of Vr and Wr and testing the value of t^2 against the table value of F (4,5 d.f) showed that this estimate was not statistically significant for all the attributes except straw strength and length of second internode. As such it was assumed that hypotheses of diallel analysis were largely satisfied. Even when a trait exhibits partial failure of the assumptions, estimates of population parameters for that trait are still possible (Hayman 1954), though the results for such a trait are less reliable than what these would have been if all the assumptions are fulfilled.

The estimates of components of genetic variation according to Hayman (1954) and some derived parameters in respect of the different characters are presented in Table 1. The additive variance component D was significant and so was the dominance variance component H_1. The relative magnitude of the former was higher than the latter. The estimate of average degree of dominance $(H_1/D)^{1/2}$ was less than one which indicated partial dominance for all the traits. This suggested that as the inheritance of quantitative characters become more complex, the contribu-

Table 1. Estimates of components of genetic variance and certain derived estimates in a diallel cross of wheat

Component	Plant height	Mother shoot weight	Shoot weight	Root weight	Straw strength	Length of second internode
D	369.66* ±22.33	4.07* ±0.18	75.05* ±6.19	4.09* ±0.39	4736.27* ±848.35	4.32* ±0.04
H_1	183.12* ±53.82	2.56* ±0.44	63.44* ±14.89	2.76* ±0.94	2563.60* ±968.59	2.40* ±0.09
H_2	122.68* ±47.42	2.28* ±0.44	47.28* ±13.16	3.00* ±0.83	5891.28* ±872.50	6.80* ±0.27
h^2	1.09 ±2.18	0.11 ±0.25	7.06 ±8.82	0.01 ±0.52	1093.36* ±396.42	1.01* ±0.30
F	-263.84* ±53.66	-1.20* ±0.44	-48.80* ±14.89	-2.12* ±0.94	-2929.88* ±916.05	-0.56* ±0.02
E	2.13 ±7.88	0.01 ±0.06	1.82 ±2.17	0.01 ±0.13	625.32* ±29.97	0.11 ±0.00
$(H_1/D)^{1/2}$	0.49	0.62	0.84	0.67	0.54	0.55
K	0.04	0.20	0.59	0.49	0.06	0.59
Heritability	0.44	0.54	0.38	0.45	0.37	0.56
b(Vr, Wr)	0.7689 ±0.0840	0.8366 ±0.0858	0.7724 ±0.0506	0.7833 ±0.1401	0.5482 ±0.3496	1.0681 ±0.0117
t^2	4.87	2.73	0.01	1.13	11.60	11.63

* Significant at 5 percent level

tion of dominant gene effects to the inheritance becomes greater. Under such situation rapid improvement in component characters may be expected through standard selection procedure which may exploit the fixable genetic variance most effectively. Simultaneously care should be taken that dominance variance is not dissipated rather they should be concentrated. Heritability in narrow sense was high for length of second internode, mother shoot weight followed by root weight and plant height. Thus it was seen that out of the six traits studied for their genetic architecture, length of second internode, plant height and mother shoot weight appeared to be better attributes from the viewpoint of a practical plant breeder.

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Effect of Mn stress on the growth and yield parameters in wheat and triticale cultivars

Narinder P. KAUR and P. N. TAKKAR

Department of Soils, Punjab Agricultural University, Ludhiana, India

Nine promising cultivars of wheat and a triticale were found to be differentially susceptible to Mn deficiency stress when grown in the Mn deficient soil (DTPA Mn 0.8 mg Mn kg^{-1}) in pots. On the basis of severity of deficiency symptoms, the cultivars were categorised into:

i) highly susceptible (DWL 5023 and KSML 3),
ii) moderately susceptible (WL 1562, WL 711 and WL 410),
iii) slightly susceptible (WG 377, WG 357 and HD 2009) and
iv) tolerant (TL 419 and C 306).

The present paper is an attempt to study the association of tolerance to Mn deficiency, with some yield parameters especially in relation to straw and grain yield, harvest index, reduction in assimilate wastage as well as increase in sink size of different cultivars.

Materials and Methods

Nine promising wheat cultivars and a triticale were grown in Mn deficient soil in polyethylene lined earthen pots. pots. The physico-chemical characteristics of the soil were: pH 8.8; EC 0.3SS; organic carbon 0.21%; available P 7.5 kg/ha; K 210 kg/ha and DTPA extractable Mn 0.8 mg/kg. Three kg soil filled in each pot was supplied with 120 mg N/kg from urea; 60 mg P_2O_5/kg and 33 mg K_2O/kg from KH_2PO_4 and 5 mg Zn/kg from $ZnSO_4 \cdot 7H_2O$. Mn was supplied @ 0, 5.0, 10.0 and 20.0 mg/kg as $MnSO_4 \cdot 5H_2O$ and the soil was thoroughly mixed. Four replications were provided in a completely randomized design. Five uniform plants were grown in each pot. The deficiency symptoms were recorded at 15, 35 and 55 days of growth. The time of emergence of ears was recorded in various treatments. The number and length of tillers were recorded just before havesting. The number of spikes in each pot and the spike length were recorded and mean length in five plants was calculated.

After harvesting at maturity, the spikes were separated and grains taken out of these. The grains of 5 spikes (top most in each plant) were pooled together and counted. The wt. of one hundred grains (two replications from each pot) was recorded. Total grain yield per pot was calculated and straw yield data included the wt. of glumes and peduncles as well. The seeds were stored for six months and then allowed to germinate on moist filter paper in petridishes (6" dia). Number of seeds germinated (out of 50) were recorded after 3 days and percent seeds germinated were calculated to asses the seed viability.

Results and Discussion

The economic yield in grain crops can be limited due to one or more of the following factors:

1) low biological yield
2) low harvest index
3) low efficiency of allocating assimilates to grain
4) reduction in assimilate production
5) increased assimilate wastage
6) reduced sink capacity (sink strength)
   i) due to sink size (grain number/number of ears)
   ii) due to sink activity (grain size)

There is much evidence that increases in yield are due primarily to partitioning of a greater proportion of total assimilates to the useful part of plant (i.e. by a higher harvest index) rather than total dry matter production. Under mineral nutrient deficiencies, overall growth rate may still be sink limited (Wareing 1979).

Grain yield

Mn stress reduced the grain yield to nil in cultivars DWL 5023 and WL 1562 and very poor in cultivars WL 711, WG 377, KSML 3 and WG 357 (Table 1). Grain filling was not complete in WG 377. As the differences among these cultivars were non-significant these were susceptible to Mn deficiency. Grain yield response increased successively and significantly up to 20 mg Mn/kg rate in DWL 5023, upto 10 mg Mn/kg in KSML 3, WL 410 and TL 419 and upto 5 mg Mn/kg in WL 711, WG 377, WG 357, HD 2009 and C 306.

Straw yield

In control pots, the straw yield of DWL 5023, WL 711 and WL 1562 was very poor as compared to other cultivars (Table 1). The yield of TL 419 and HD 2009 increased significantly upto 5 mg Mn/kg^{-1} but of rest of cultivars upto 10 mg Mn kg^{-1}.

Harvest index

Harvest index was considerably reduced in highly and moderately susceptible cultivars which had higher index than tolerant cultivars when adequate Mn fertilization was supplied (Table 2). Optimum harvest index in most cultivars was obtained with 5-10 mg Mn kg^{-1} except in DWL 5023 where the response was upto 20 mg Mn kg^{-1} indicating a higher requirement of Mn for reaching the potential yield.

The previous studies also indicated that tolerant cultivars were not necessarily the highest yielders when adequate supply of plant nutrients was available (Wegrzyn *et al.* 1980).

Increased assimilate production and reduction in assimilate wastage

The cultivars which are able to reduce assimilate wastage and have higher efficiencies to allocate assimilates are likely to show higher harvest indices. Rate of photosynthesis as measured by POE has already been reported (Kaur *et al.* personal communication). The effect on Mn deficiency on the following parameters was studied:

Table 1. Grain and straw yield (g/pot) of cultivars in relation to susceptibility and rates of Mn application

Rating of susceptibility	Cultivar	Grain yield Rates of Mn (mg/kg) 0	5	10	20	Straw yield Rates of Mn (mg/kg) 0	5	10	20
Highly susceptible	DWL 5023	0.0	2.49	5.45	9.66	2.55	9.04	12.33	15.15
	KSML 3	1.54	5.67	9.69	9.95	6.19	10.23	15.78	18.12
Moderately susceptible	WL 1562	0.0	10.34	12.01	11.43	3.32	11.98	18.83	18.48
	WL 711	0.42	9.31	10.19	9.48	2.97	12.42	17.78	17.94
	WL 410	2.23	7.49	9.85	8.28	4.61	17.33	22.91	20.78
Slightly susceptible	WG 377	1.44	8.86	9.43	9.23	6.19	12.53	17.71	18.83
	WG 357	1.71	8.20	8.99	8.24	5.89	12.89	21.73	18.71
	HD 2009	3.71	7.59	7.96	7.99	6.09	18.35	20.35	20.48
Tolerant	C 306	2.41	6.71	6.91	8.92	8.88	13.65	19.69	21.58
	TL 419	3.05	8.02	11.77	8.52	9.09	19.63	22.94	22.21
	Mean	1.6	7.47	9.23	9.17	5.58	13.81	19.01	19.23

C.D. at 0.05 P

Cultivar means	0.94	2.31
Mn rates means	0.65	1.46
Cultivar x Mn rate means	1.88	4.63

Table 2. Harvest indices and number of infertile tillers (per five plants in a pot) in different cultivars as affected by rate of Mn application

Cultivar	Harvest Index [1] Rate of Mn (mg/kg) 0	5	10	20	No. of Infertile tillers Rate of Mn (mg/kg) 0	5	10	20
DWL 5023	0	21.6	30.6	38.9	0.3	4.0	4.0	9.4
KSML 3	19.9	35.7	38.0	35.4	2.0	2.3	5.6	9.7
WL 1562	0	46.3	38.9	38.2	1.3	4.0	4.3	5.3
WL 711	12.4	42.8	36.4	34.6	1.0	7.3	3.3	8.0
WL 410	32.5	30.2	30.1	28.5	0	4.6	5.3	5.3
WG 377	18.9	41.4	34.7	32.9	2.4	3.7	3.6	6.3
WG 357	22.5	38.9	29.3	30.6	2.0	4.0	7.4	6.4
HD 2009	34.2	29.2	28.1	28.1	1.7	5.0	6.4	6.1
C 306	21.3	33.0	26.0	29.0	4.3	2.3	0.7	3.0
TL 419	25.1	29.0	33.9	27.7	3.3	2.7	4.7	4.4

1) per aerial part of plant

Number of infertile tillers

The number of infertile tillers is indicative of assimilate wastage, its magnitude lowering the harvest index of the plant. In highly susceptible cultivars, the 20 mg Mn kg^{-1} application highly increased the number of infertile tillers (Table 2). Thus the applied Mn although contributed to increased assimilate production but also resulted in its wastage because of the failure of reproductive mechanism in the infertile tillers. On the contrary, the tolerant cultivars had more infertile tillers under Mn stress and its alliviation produced more fertile tillers, thus increasing the ratio of fertile/infertile tillers resulting in higher harvest index.

Total number of tillers

The number of tillers formed were significantly less in Mn stressed plants of DWL 5023, WL 1562 and WL 711 (Table 3) possibly reducing assimilate production . Application of even 5 mg Mn kg^{-1} significantly increased the tiller number to the level of more tolerant cultivars. The tiller number had a significant positive relationship in control plants with straw yield ($r = 0.90^{**}$) and grain yield ($r = 0.72^{**}$). The increased tiller number obviously increased assimilate production capacity of the plant.

Average Height of tillers

Tiller height increased significantly with Mn application especially 10 mg Mn kg^{-1} rate. The tiller height was minimum in DWL 5023 especially under Mn stress. It was significantly related to grain yield in control and 5 mg Mn kg^{-1} supplied plants ($r = 0.81^{**}$ and 0.72^{**} respectively) and straw yield in control and 10 mg Mn kg^{-1} supplied plants ($r = 0.71^{**}$ and 0.84^{**} respectively).

Average height of top tiller (Plant height)

Plant height was depressed in Mn deficient plants and removal of stress increased it significantly (Table 3). The maximum height was obtained in taller cultivars HD 2009 and C 306. Thus potential tallness appeared to be related to Mn stress tolerance in wheat. Effect of Mn was more pronouned on the growth of the top tiller in comparison to younger tillers. However in different Mn rates, the differences were insignificant except in highly susceptible cultivars DWL 5023 and KSML 3 which had significant increase even with 20 mg Mn kg^{-1}. The plant height was positively related to grain and straw yields ($r = 0.84^{**}$ and 0.80^{**} respectively).

The height of tillers, likely to contiribute towards increased assimilate production for grain, seemed to have acted as a secondary sink for assimilates, contributing more towards straw yields.

Sink capacity

If the assimilates are not limiting the sink capacity determines the ultimate grain yield. The sink capacity comprised of the interaction of the following factors:

Number of spikes (ears)

The spike number (number of fertile tillers) was very low in control plants of DWL 5023 – the only spike produced was devoid of grains (Table 4). The spike number was poorly related

Table 3. Total number of tillers (a total of 5 plants in a pot), average height of tillers and height of top tillers as affected by cultivars and Mn application

Cultivar	No. of tillers				Average height of tillers				Height of top tiller			
	Rates of Mn (mg/kg)											
	0	5	10	20	0	5	10	20	0	5	10	20
DWL 5023	1.3	11.3	11.7	16.7	18.0	37.8	42.3	49.9	19.0	39.9	47.7	58.0
KSML 3	8.3	8.0	13.3	15.7	37.4	49.7	54.1	61.2	38.8	49.7	58.1	70.5
WL 1562	5.0	9.3	13.7	15.3	30.4	56.6	53.9	53.8	31.0	58.3	62.1	64.3
WL 711	4.3	14.0	11.3	16.0	33.7	64.3	70.7	66.4	33.5	70.2	77.8	74.2
WL 410	6.3	10.3	13.0	11.3	40.7	64.5	71.0	62.3	41.5	67.3	77.3	73.1
WG 377	8.7	9.7	11.3	14.3	43.3	54.3	64.8	63.2	42.6	68.5	73.8	69.5
WG 357	5.7	11.7	15.7	14.7	41.3	63.5	69.5	66.7	45.3	66.1	73.4	70.3
HD 2009	7.0	13.7	14.7	14.3	43.5	61.2	66.5	72.6	45.0	70.6	71.1	77.9
C 306	10.7	10.0	10.7	15.0	39.6	62.8	61.9	64.1	45.0	74.7	74.2	77.8
TL 419	9.0	8.7	10.7	12.7	43.0	60.4	70.9	57.3	46.7	65.6	72.5	66.4
Mean	6.6	10.7	12.6	14.6	37.1	57.5	62.5	61.7	38.8	63.1	68.8	70.2
C.D. at 0.05 P												
Cultivar means			1.8				5.5				4.7	
Mn rate means			1.1				3.52				2.9	
Cultivar x Mn rate means			3.5				11.16				9.3	

Table 4. Number of spikes (Total of 5 plants in a pot) and mean spike length affected by cultivar and Mn application

Cultivar	Number of spikes				Mean spike length			
	Rates of Mn (mg/kg)							
	0	5	10	20	0	5	10	20
DWL 5023	1.0	7.3	7.7	7.3	2.8	6.6	6.6	7.1
KSML 3	6.3	5.7	7.7	6.0	7.6	10.0	11.3	12.3
WL 1562	3.7	5.3	8.0	10.0	5.8	11.2	11.6	11.3
WL 711	3.3	6.7	8.0	8.0	7.1	12.3	11.9	12.1
WL 410	6.3	5.7	7.7	6.0	6.7	11.0	11.5	11.1
WG 377	6.3	6.0	7.7	8.0	8.5	11.0	11.2	11.4
WG 357	3.7	9.0	9.7	9.0	6.8	9.1	9.8	9.7
HD 2009	5.3	8.7	8.3	8.3	8.4	11.5	11.3	11.2
C 306	6.3	7.7	10.0	12.0	7.8	9.0	9.2	9.0
TL 419	5.7	6.0	6.0	8.3	8.8	10.4	10.7	10.3
Mean	4.8	6.8	8.1	8.3	7.0	10.2	10.5	10.6
C.D. at 0.05 P								
	Cultivar means			1.1		0.7		
	Mn rate means			0.7		0.4		
	Cultivar x Mn rate means			2.2		1.4		

to straw and grain yields and thus did not serve as a good indicator of grain yield as the size of the spike and grain number in each differed widely.

Average spike length

Under Mn stress the spike length was very small in DWL 5023 but increased significantly with 5 mg Mn/kg application, but the differences between Mn rates were non-significant (Table 4). The grain yield was poorly related to spike length in control, implying possibilities of both impaired grain development as well as grain filling. However, in 5 and 10 mg Mn kg^{-1} supplied plants the grain yield was related to average spike length.

Number of grains in the top spike (Number of flowers fertilized)

The average number of grains was very significantly decreased with Mn stress, and these strikingly and significantly increased when Mn stress was removed (Table 5). All the cultivars produced maximum number of grains at 10 mg kg^{-1} Mn rate of application except DWL 5023, KSML 3 and C 306 which gave maximum grain number at 20 mg kg^{-1} Mn rate. The average grain number was highest in cultivar WG 377 followed by WL 711, WL 410, HD 2009, TL 419, WL 1562, C 306, KSML 3, WG 357 and DWL 5023 in decreasing order.

Table 5. Number of grains per five spikes (topmost of each plant) and average 100 grain weight as influenced by cultivars and rates of Mn application

Cultivar	Number of grains [1]				100 grain weight [2]			
	Rates of Mn (mg/kg)							
	0	5	10	20	0	5	10	20
DWL 5023	0	55	132	200	0.0	4.89	3.85	4.38
KSML 3	31	133	246	252	2.97	4.27	3.97	4.05
WL 1562	0	254	278	242	0.0	4.13	4.65	4.82
WL 711	32	267	275	253	1.20	3.44	3.72	3.66
WL 410	63	226	307	212	3.54	3.59	3.74	3.89
WG 377	84	291	295	276	2.66	3.05	3.42	3.41
WG 357	48	197	216	196	3.55	4.17	4.16	4.28
HD 2009	106	232	230	228	3.01	3.73	3.46	3.44
C 306	85	192	193	211	2.79	3.35	3.48	4.63
TL 419	96	215	271	210	2.68	3.88	3.94	3.98
Mean	56	206	244	228	2.24	3.85	3.84	4.05
LSD at 0.05 P								
	Cultivar means			27		0.47		
	Mn rate means			17		0.29		
	Cultivar x Mn rate means			54		0.93		

1) average of three pots
2) average of 6 replicates

The highly susceptible DWL 5023 and moderately susceptible WL 1562 did not produce any grains under Mn stress. Failure to set grains in these cultivars could be ascribed to a single or a combination of the following factors:

a) Interruption of sink capacity
b) Improper translocation mechanism
c) Scarcity of leaf photosynthates
d) Infertile pollen/nondehiscence of anthers
e) Non-receptive stigmas
f) Absence of fertilization
g) Non-viability of embryos
h) Deficiency of growth regulators/ accumulation of inhibitors of cell division.

Most of the anthers were found dorsally attached to the mature grains in cultivars DWL 5023, WL 1562, WL 711, WG 377 and TL 419 (Fig. 1). Most likely, these anthers were not fully mature to attain normal versatile attachment. These did not dehisce probably due to incomplete maturation or water imbalance in the anther/anther walls, thus affecting pollination and fertilization in these cultivars.

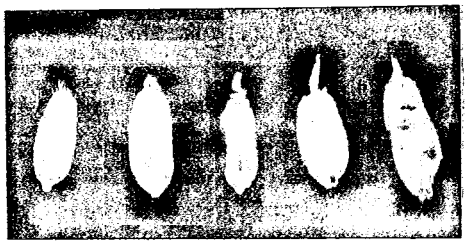

Fig. 1. Dorsally attached anthers to the mature grains (From left to right; DWL 5023, WL 1562, WL 711, WG 377 and TL 419)

The number of grains produced could be a useful indicator of the number of flowers fertilized as well as conditions required for setting and filling of grains. However, in this study the number of grains was not indicative of total grain yield, as in cultivars WL 711, WG 357, KSML 3 and WL 410, the grain filling was incomplete. Even in dried ears, the grains were only at half seed stage and appeared to be dry. The inhibited translocation did not appear to be the only reason for this effect because in that case, shrivelled but complete grains were likely to be produced. Thus, in addition to interrupted translocation, the grain development was also incomplete. Thus cultivars TL 419, HD 2009, C 306 and WG 377 appeared to be relatively tolerant to Mn stress implying that process of fertilization and grain development were not much harmed by Mn stress. This would indicate preferential utilization of Mn or capacity of the cultivars to manage with limited supply of Mn.

Average wt. of 100 grains (Translocation of assimilates to the developing grains)

The average 100 grain wt. of cultivars increased significantly with Mn application, but the differences among 5, 10 and 20 mg Mn/kg soil, were non-significant except C 306 at 20 mg Mn/kg rate (Table 5). Under Mn stress condition, the maximum 100 grain wt. was in cultivars WG 357 (low susceptible) and WL 410 (moderately susceptible).

Thus in tolerant cultivars, the number of grains formed were more (showing efficiency of fertilization) but the grain weight was not correspondingly increased. This indicated lesser availability of photosynthates than the sink requirement in these cultivars. In less susceptible cultivars (WG 357, WL 410) the number of grains formed was low, the limited amount of photosynthates distributed among lesser grains resulted in increase in grain weight.

Wardlaw (1968) and Bremner (1972) emphasized on the ability of the individual grain to grow and precipitate carbohydrates rather than the translocation as the major determinent of seed growth. Asana (1974) advocated that during the early stages of grain ontogeny when the assimilates were not limiting, some inherent factor(s) must be controlling the growth of grains which differed within same ear as well as variety. Dua & Bhardwaj (1979) have shown that variations among varieties with regard to 100 grain wt were traceable to endogenous auxin and cytokinin production of the variety vis.a vis that of the ear. It is imperative to study the varietal differences in content of endogenous growth regulators in the flag leaf, flowers/ears.

Fresh wt. of flaf leaf

Fresh wt. per flag leaf was significantly lower in Mn stressed plants except in KSML 3 (Table 6). The growth of flag leaf was not much depressed except in DWL 5023 and WG 357. This implied that although the deficiency symptoms were abundantly present on other highly and moderately susceptible cultivars, the flag leaf growth was not affected. Alternatively, at later growth stage, the mobilization of Mn upwards increased following sufficient root growth. In cultivars WL 1562 and WG 377, the flag leaf wt. was highest although grain formation in these cultivars was nil (WG 1562) or partially inhibited (small triangular grains in WG 377). Thus photosynthesis of the flag leaf did not appear to be the major contributing factor for ultimate grain yield as advocated previously by Evans and Dunstone (1970) and Jatimliansky *et al.* (1982). Probably, the other limiting factors like lack/or imbalance of growth regulators, infertility of pollen(stigma and) or inviability of embryos might be responsible for this effect.

Table 6. Fresh weight (mg) per flag leaf and percent seeds germinated as affected by cultivars and Mn application

Cultivar	Fresh weight of flag leaf			Percent seeds germinated			
	Rates of applied Mn (mg/kg)						
	0	20	% increase	0	5	10	20
DWL 5023	155	290	87	–	75	75	70
KSML 3	457	484	6	100	27	34	87
WL 1562	447	517	16	–	40	63	76
WL 711	340	446	31	35	39	67	80
WL 410	360	580	61	83	66	64	86
WG 377	457	650	42	36	61	72	79
WG 357	178	264	48	92	41	40	87
HD 2009	X	X	–	87	73	64	86
C 306	X	X	–	70	74	67	85
TL 419	391	722	85	72	76	62	86
Mean				48	49	60	82

t value significant at 0.01 P

X = Not done

CD at 0.05 P

Cultivar means	3.7
Mn rate means	2.3
Cultivar x Mn rate means	7.4

Viability of seeds

The Table 6 shows that the germination of seeds was not affected in Mn-deficient plants, although the number of germinated seeds was less in WL 711 and also in WG 377, but in the latter, the ungerminated seeds were the underdeveloped half seed structures. Thus there appeared to

be no deficiency of starch in the developing grain. The main processes that were affected were the pollination and fertilization and not the grain filling.

It can be concluded that triticale TL 419 and C 306 were Mn efficient and thus could be grown on marginally deficient soils. It remains to be established whether the mechanism of enhanced Mn utilization is linked with the morphology of root system in these cultivars.

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Diallel analysis for combining ability over environments in wheat

Iqbal SINGH, R. S. PARODA[1] and R. K. BEHL

Department of Plant Breeding
Haryana Agricultural University, Hisar, India

Phenotypic expression of quantitative characters is highly influenced by environmental fluctuations. Genotype 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 selection. It is, therefore, necessary to assess the sensitivity of estimates of gene effects under variable environmental conditions so as to ensure better prediction and gain under selection. Present study deals with such an endeavours.

Materials and Methods

The experimental material consisted of parental and F_1 generations of a 9 x 9 diallel set (excluding reciprocals) of spring wheat (*Triticum aestivum* L. em. Thell). The experimental material was laid out in a randomized block design with three replications in two environments, namely, normal (irrigated) and stress (rainfed). The nine parents included were WL 711, NP 846, WG 377, HD 1981, UP 262, HD 1925, HD 2122, Raj 821 and Sonalika. Single seeds were sown in 3m long rows and at 30 x 15 cm row to row and plant to plant distance, respectively. From each entry (parent and F_1) five competitive plants were randomly selected from each replication in both the environments for recording observations on characters days to heading, plant height, tiller number, total biomass, number of grains/ear, 1000-grain weight and grain yield/plant. Pooled analysis for combining ability was carried out following Method 2, Model 1 of Griffing (1956) as extended by Singh (1973).

Results and Discussion

Pooled analysis of variance over the environments (Table 1) revealed highly significant differences amongst them. So was true for genotype x environment interactions.

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 figured important in controlling inheritance of all the characters studied. Both gca x environments as well as sca x environments interactions were significant for all the characters except sca x environments for days to heading, indicating thereby the sensitivity of both kinds of gene effects to the environmental variations. However, relatively higher magnitude of gca x environments interactions as compared to sca x environments interactions suggested a

1) Present address: Director, National Bureau of Plant Genetic Resources, New Delhi-110012, India.

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
					Layout			
Environments	1	32148.30**	155395.10**	3583.22**	236823.66**	2270.03**	660.21**	7047.10**
Genotypes	44	182.74**	780.40**	5.44**	308.52**	198.38**	95.88**	26.01**
Genotypes × environments	44	9.80**	99.14**	3.66**	231.83**	54.90**	11.59**	19.82**
Error	176	3.88	6.74	0.38	27.20	8.39	2.66	1.94
					Combining Ability			
gca	8	305.40**	1326.66**	3.62**	272.43**	307.30**	148.84**	12.04**
sca	36	6.59**	23.14**	1.41**	65.16**	12.54**	5.99**	7.92**
gca × environments	8	9.78**	132.99**	1.45**	85.29**	33.15**	8.88**	9.06**
sca × environments	36	1.83	10.85**	1.17**	75.50**	15.01**	2.75**	6.06**
Error	176	1.29	2.25	0.29	9.07	2.80	0.89	0.65
gĉa / sĉa ratio		5.22	5.76	0.27	0.43	2.84	2.64	0.14

** Significant at 1% level of probability.

higher sensitivity of gca to environments than that of sca. Similar results were obtained by Paroda and Joshi, 1970a, b; Paroda and Hays, 1971 and Sharma and Singh, 1982. Perhaps the heterozygosity *per se* and physiological advantages attached hitherto by virtue of heterosis or enhanced metabolic rates (Sinha & Khanna, 1975) have contributed to lower sensitivity of sca to environmental fluctuations as compared to gca.

The $\hat{g}ca/\hat{s}ca$ ratio (based on equivalent component of mean squares) in the pooled analysis indicated that gca effects were predominant and played a more important role than the sca effects in exercising genetic control for days to heading, plant height, number of grains/ear and 1000-grain weight, hence pedigree method of selection 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 control of non-additive gene action, though they also showed considerable amount of additive genetic variance. Improvements of such characters warrants for a breeding methodology which can capitalize additive as well as non-additive genetic variance. In this situation biparental mating offers good promise to increase the frequency of genetic recombination and hasten the rate of genetic improvement (Gill *et al.* 1972; Srivastava *et al.* 1980). Inclusion of F_1 hybrids showing stable sca and having parents with good gca, less altered by changes to environmental variations into multiple crosses, could also prove a worthwhile approach.

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A diallel cross analysis of grain number and grain weight under different environments in wheat

P. N. NARULA

I. A. R. I., Regional Station, Pusa, Bihar, India

Plant breeders are unanimous over the fact that yield is a very complex character and gains by selection on the basis of yield alone are difficult to achieve. This point has been further emphasized by the classical work of Grafius (1956) who put forward the geometrical logic for working on the basis of yield components. Extensive studies carried out by Mc Neal (1960), Kronstad & Foote (1964), Sharma & Knott (1964), Paroda and Joshi (1970) and Randhawa and Gill (1978) have shown that grain weight and grain number/ear can effectively be used for component breeding. The precise knowledge of the genetic parameters governing various component characters is useful in making decisions with regards to appropriate breeding system to be adopted to achieve the objectives. The present paper embodies results of genetical studies on grain number and grain weight under three experimental conditions under which wheat is commonly grown in India.

Materials and Methods

Nine wheat variaties of Indian and Mexican origin, namely NP 4, NP 852, NP 884, E 4845, E 5477, Sonora 64, Kalyansona, Safed Lerma and Sonalika having many contrasting characters, were crossed in all possible combinations excluding reciprocals. Both parents and their 36 F_1's were grown under timely sown high fertility (E_1), timely sown low fertility (E_2) and late sown, moderate fertility (E_3) levels at I.A.R.I., Regional Station, Pusa. Sowing was done in a randomized block design with three replications by dibbling the seeds 15 cms apart in rows 2.5 m long and 30 cms apart. Two rows were alloted to each parent and F_1 per replication. Five plants per row were selected at random for recording data. Grain number per ear was recorded from the main tiller where-as 250 seeds were counted out of the bulk seed of the ten selected plants/replication. The analysis of variance for combining ability and estimation of various effects was done following the technique of Griffing (1956) for system 2, Model 1 and the genetic parameters were estimated as described by Hayman (1954).

Results and Discussion

Analysis of variance (Table 1) indicated highly significant differences due to progenies for the two measured traits under all the three environments. The variation among parents, F_1 hybrids and parents vs hybrids comparison, were highly significant, showing thereby that considerable genetic diversity was present in the experimental material.

Table 1. ANOVA for grain number and 250 grain weight under the three test environments

Source	d.f.	Mean squares					
		Grain number / ear			250 grain weight		
		E_1	E_2	E_3	E_1	E_2	E_3
Progenies	44	143.12**	164.89**	165.30**	4.31**	3.80**	3.11*
Parents	8	164.64**	241.70**	227.00**	5.66**	4.84**	4.91**
Hybrids	35	137.31**	150.91**	150.31**	2.89**	2.44**	2.57**
P. vs Hyb.	1	174.53**	39.50**	195.36**	43.18**	43.23**	7.37**
Error	88	4.85	6.32	4.92	0.07	0.13	0.10
GCA	8	200.320**	269.546**	250.510**	4.661**	4.032**	4.347**
SCA	35	14.054**	7.175**	11.578**	0.720**	0.651**	0.299**
Error	88	1.618	2.105	1.639	0.023	0.043	0.033
GCA / SCA		14.25	37.59	21.45	6.47	6.20	14.50

* Significant at 5 percent ** Significant at 1 percent

Grain number/ear

Kalyansona, in general recorded the maximum (74-61) grain number/ear and was followed by Safed Lerma, Sonora 64 and E 4845. NP 4 had the minimum (45-35) grains/ear under all the environments. Rest of the parents were intermediate. Amongst the F_1's, there were only two crosses in E_1, none under E_2 and as many as four in E_3 which were significantly superior to the best parent. The analysis of combining ability revealed that both gca and sca mean squares were highly significant under all the three experimental conditions, indicating the importance of both additive and non-additive gene effects in the control of grain number/ear. The present results are in close agreement with those of Singh *et al.* (1969), Paroda & Joshi (1970), Rehman (1979), and Thombre *et al.* (1983).

The estimates of gca effects and mean value of the parents under the three environments are presented in Table 2. Cultivars, Kalyansona, Sonora 64, Safed Lerma and E 4845, in that order, were the best general combiners over environments, whereas all other varieties showed negative gca effects. It is to be noted that the value of the parents *per se* was in fairly close agreement with the one obtained by gca estimates. Thus the selection of the parents based on parental values, which has been the common practice is reasonably good.

There were 10, 6 and 11 crosses under E_1, E_2 and E_3, respectively which had shown high positive and significant sca effects. The top four crosses under each of the three environments are presented in Table 3. The cross Kalyansona x Safed Lerma was the unique combination which had manifested high sca effects under all the three conditions. Both the parents involved in this cross are good general combiners and thus is expected to release desirable segregants in subsequent generations since it involved additive and additive x additive interactions. The two other promising crosses, NP 884 x E 4845, E 5477 x Kalyansona which had also shown high sca effects under two of the three conditions, involved at least one parent having good general combining ability. Therefore, such combinations are likely to throw transgressive segregates if the additive genetic system present in the good combiner and complementary epistatic effects act in the same direction to maximize the desirable effect.

The estimates of components of genetic variation are presented in Table 4. The component $\hat{D}$ and $\hat{H}_1$ were found to be highly significant under all the three situations. This further supports the role of both additive and non-additive effects in the inheritance of grain number. The estimated degree of dominance which was less than one under two of the three environments (E_2 and E_3), denoting partial dominance and thereby, preponderance of additive gene effects. Further, significant and negative value of the component $\hat{F}$ under all the three environments reaffirms the results obtained through combining ability analysis. The ratio $\hat{H}_2/4\hat{H}_1$ indicated deviation from symmetrical distribution of genes with positive and negative effects. The ratio $\hat{h}_2/\hat{H}_2$ showed that at least two to three dominant genes or gene groups were responsible for the control of grain number/ear under all three environments.

250-Grain weight

As expected, the grain weight was higher under timely sown experiments E_1 and E_2, whereas it was badly reduced under late sowing (E_3). The parental range was 10.87 to 6.87 gms/250 grains

Table 2. Estimates of General combining ability effects and mean values of parents under three environments

Parents	Number of grains/ear			250 grain weight		
	E_1	E_2	E_3	E_1	E_2	E_3
1. NP 4	−7.24** (46.40)	−7.27** (46.13)	−8.27** (35.73)	0.02 (7.27)	0.15** (8.07)	0.06 (6.5)
2. NP 852	−3.12** (52.97)	−3.88** (47.87)	−4.01** (41.80)	0.44** (9.40)	0.42** (8.67)	0.68** (7.37)
3. NP 884	−0.05 (56.13)	−0.71 (54.80)	−1.94** (50.14)	0.47** (9.40)	0.53** (8.70)	0.94** (7.20)
4. E 4845	0.37 (63.03)	1.09* (59.93)	2.14** (53.00)	−0.81** (6.77)	−0.77** (6.43)	−0.81** (6.00)
5. E 5477	−1.80** (56.53)	−2.24** (53.27)	−1.27** (42.27)	−0.25** (7.87)	0.38** (7.17)	−0.52** (5.33)
6. Sonora 64	3.54** (65.87)	2.46** (57.63)	5.22** (61.80)	−0.03 (8.27)	−0.17** (8.13)	−0.09 (6.17)
7. Kalyansona	7.36** (70.53)	9.14** (74.53)	6.88** (60.60)	−0.91** (6.57)	−0.55** (6.43)	−0.62** (5.50)
8. Safed Lerma	2.99** (63.41)	4.61** (65.47)	3.09** (50.33)	−0.10 (8.53)	−0.34** (6.90)	−0.26** (5.67)
9. Sonalika	−2.04** (57.87)	−3.18** (50.93)	−1.83** (45.13)	1.17** (10.87)	1.11** (10.63)	0.62** (8.27)

(Mean values of parents are presented in parenthesis)

under E_1, 10.63 to 6.49 gms under E_2 and 8.27 to 4.0 gms under E_3. Sonalika had the highest and E 4845 the lowest grain weight under all the three conditions. The corresponding range for F_1 hybrids was 11.67 to 7.83, 11.73 to 7.10 and 8.57 to 4.97 gms/250 grains under E_1, E_2 and E_3 conditions, respectively. In general, the F_1 fell in between the parental limits and none except one, NP 884 x Sonalika under E_2 could transgress the parental limit significantly.

Mean squares for general combining ability were highly significant under all the three environments. While the specific combining ability mean squares were also of statistical significance, the magnitude of the effect was considerably less than that of general combining ability effect for this trait. This suggests that the major portion of the total genetic variability is the result of additive gene action. These results are in conformity with those of Singh *et al.* (1969), Paroda and Joshi (1970), Knott & Talukdar (1971), Sharma *et al.* (1978), Schmidt *et al.* (1978) and Singh *et al.* (1985). The gca effects showed that Sonalika, NP 884 and NP 852 were the good general combiners and all the remaining parants were poor in their combining ability.

A number of crosses exhibited significant sca effects. Most prodigious cross combinations

Table 3. Crosses showing high sca effects for grain number and grain weight under the three environments

Character	Environments		
	E_1	E_2	E_3
Grain number/ear	NP 884 x E 4845 (L x H)	NP 852 x Kalyansona (L x H)	E 4845 x Kalyansona (H x H)
	Kalyansona x Safed Lerma (H x H)	NP 884 x E 4845 (L x H)	E 5477 x Safed Lerma (L x H)
	NP 884 x Sonalika (L x L)	Safed Lerma x Sonalika (H x L)	Kalyansona x Safed Lerma (H x H)
	E 5477 x Kalyansona (L x H)	Kalyansona x Safed Lerma (H x H)	E 5477 x Kalyansona (L x H)
250 Grain weight	NP 4 x E 4845 (M x L)	NP 884 x Kalyansona (H x L)	NP 884 x E 5477 (H x L)
	NP 852 x E 4845 (H x L)	NP 852 x E 4845 (H x L)	NP 4 x E 4845 (M x L)
	NO 4 x E 5477 (M x L)	NP 884 x Sonalike (H x H)	NP 852 x E 4845 (H x L)
	NP 884 x Kalyansona (H x L)	NP 4 x E 4845 (M x L)	NP 884 x Kalyansona (H x L)

(H, M and L denote High, Medium and Low general combining ability of the parents)

under each of the environment are presented in Table 3. It would be seen that the three crosses, namely NP 884 x Kalyansona, NP 852 x E 4845 and NP 4 x E 4845 had shown high sca effects under all the three conditions. Two of these crosses involved at least one parent having good general combining ability whereas the 3rd cross was between Average x Poor combiners. In general, the crosses between two good combiners did not exhibit sca effects in the desired direction. This suggests epistatic interactions resulting in internal cancellation of components of heterosis. (Murty 1965).

The estimated components of genetic variation (Table 4) showed that both $\hat{D}$ and $\hat{H}_1$ were found to be highly significant. This indicated the role of both additive and non-additive components in the control of grain weight. The magnitude of the component $\hat{H}_1$ was slightly higher than the $\hat{D}$ component under E_1 and E_2 whereas reverse was true under late sown E_3. Similarly the estimated degree of dominance was more than unity except in E_3, suggesting over dominance and thus greater role of non-additive gene effects. The ratio $\hat{H}_2/4\hat{H}_1$ indicated slight deviation from symmetrical distribution of genes with positive and negative effects in E_1 and E_2, while in E_3 symmetrical distribution was observed. The ratio $\hat{h}_2/\hat{H}_2$ indicated that a large number of

Table 4. Estimates of genetic components of variation for grain number and 250 grain weight under three environments

Component of variation	Grain number/ear			250 grain weight		
	E1	E2	E3	E1	E2	E3
$\hat{D}$	121.86**	179.04**	168.58**	4.22**	3.58**	3.65**
	±10.99	±4.68	±12.64	±0.41	±0.24	±0.16
$\hat{H}_1$	127.19**	67.05**	116.57**	5.22**	4.32**	2.92**
	±24.25	±10.33	±27.88	±0.91	±0.54	±0.34
$\hat{H}_2$	109.49**	53.55**	80.96**	4.61**	4.08**	2.01**
	±20.87	±8.89	±23.99	±0.79	±0.46	±0.29
$\hat{h}_2$	244.42	35.95**	256.58**	56.85**	56.92**	9.70**
	±13.98	±5.95	±16.07	±0.53	±0.31	±0.20
$\hat{F}$	-36.39	-38.97**	-14.78	1.01	0.57	0.86*
	±25.56	±10.89	±29.38	±0.96	±0.56	±0.36
$\hat{E}$	1.62	2.24	1.74	0.02	0.04	0.03
	±3.48	±1.48	±3.99	±0.13	±0.08	±0.05
$(\hat{H}_1/\hat{D})^{0.5}$	1.02	0.61	0.83	1.11	1.10	0.96
$\hat{H}_2/4\hat{H}_1$	0.21	0.20	0.17	0.22	0.24	0.17
$\hat{h}_2/\hat{H}_2$	2.23	0.67	3.17	12.33	13.96	4.82

dominant genes or gene groups were governing this character.

The estimates of gca effects pointed out that none of the parents were the good general combiners for both grain number and grain weight. This is evidently so because of the fact that grain number and grain weight are negatively correlated. (Sikka & Jain, 1958; Gandhi *et al.* 1964; Paroda & Joshi, 1970). In fact, many plant breeders have believed that breaking of this negative correlation offers one of the most important means to bring about further spurt in the yield productivity of wheat. In the present study also, although substantial heterosis for both grain weight and grain number/ear was simultaneously obtained in certain cross combinations, none of the promising F_1 hybrids combined the high grain weight of Sonalika and grain number of Kalyansona.

In a situation, where additive and non-additive genetic variations are significant, the most suitable breeding procedure would be one which mops up the additive genetic variance and at the same time maintains certain degree of heterozygosity. Therefore, it is desirable to practice recurrent selection, by intermating the most desirable segregants, alternately with selection, as suggested by Dwivedi & Singh (1980).

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Path analysis in wheat under different sowing dates

B. K. JADAV and B. S. JADON

Gujarat Agricultural University
Junagadh, Gujarat, India

With the improvement in the production technology in agriculture, different crop rotations are being advocated in order to increase cropping intensity and thereby total agriculture production. Varieties wih specific characteristics are needed for a particular crop rotation which can yield more under given set of production conditions. The knowledge of genetic association between grain yield and its components under different production conditions will improve the efficiency of breeding programme by preparing appropriate selection indices for developing suitable varieties. Though, studies on path coefficient in wheat have been made but such studies under different sowing times are scanty. The present study was, therefore, planned to achieve a clear picture of the inter-relationship with grain yield of various components and developmental traits under early, timely and late sowing. The direct and indirect effects were worked out using path analysis at genotypic level.

Materials and Methods

One hundred diverse wheat varieties selected from different wheat growing zones of the country including exotics and lines from CIMMYT were grown in randomized block design with three replications on 5 October (early), 15 November (timely) and 15 December (late). 3.5 meter long row plot was randomly assigned to each variety. Distances between row to row was 30 cm and plant to plant within row being 10 cm. Recommended cultural practices were followed uniformly to raise the good crop. Five random comptitive plants were selected from each plot for observations on days to flowering, days to maturity, peduncle length, plant height, tillers/plant, grains/spike, grain weight/spike, 1000 grain weight, grain yield/plant and harvest index. Genotypic and phenotypic correlation coefficients were calculated using the formula suggested by Miller *et al.* (1958). Direct and indirect effects of component characters on grain yield were worked out using path coefficient analysis (Dewey / Lu, 1959).

Results and Discussion

The analysis of variance in early, normal and late sowing revealed significant differences amongst genotypes for all the characters. The phenotypic and genotypic correlation coefficients between grain yield an its components were computed for early, timely and late sowing. All the characters under study showed significant positive correlation with grain yield except harvest index under normal and plant height under late sowing. The direct and indirect effect of each character on grain yield are presented in Table 1.

The path analysis in early sowing indicated that tillers/plant and grain weight/spike had high

Table 1. Correlation coefficients alongwith direct and indirect influences of different characters on grain yield of wheat in early, timely and late sowing

	1	2	3	4	5	6	7	8	9	rph	rg
						Early sowing					
1. Days of flowering	*0.03*	−0.19	−0.17	0.22	0.56	−0.05	0.46	−0.06	−0.02	0.74*	0.76
2. Days of maturity	0.03	*−0.20*	−0.20	0.24	0.60	−0.06	0.52	−0.07	−0.03	0.80*	0.82
3. Peduncle length	0.02	−0.15	*−0.27*	0.26	0.54	−0.07	0.56	0.07	−0.03	0.55*	0.80
4. Plant height	0.02	−0.17	−0.26	*0.28*	−0.07	0.60	0.59	−0.07	−0.03	0.88*	0.90
5. Tillers/plant	0.02	−0.17	−0.21	0.23	*0.72*	−0.07	0.47	−0.05	−0.02	0.92*	0.93
6. 1000 grain weight	0.02	−0.13	−0.17	0.19	0.52	*−0.10*	0.58	−0.05	−0.03	0.15*	0.83
7. Grain weight/spike	0.02	−0.15	−0.22	0.24	0.49	−0.08	*0.69*	−0.08	−0.03	0.54*	0.87
8. Grains/spike	0.02	−0.15	−0.20	0.22	0.44	−0.06	0.62	*−0.09*	−0.03	0.76*	0.78
9. Harvest index	0.02	−0.14	−0.18	0.19	0.43	0.08	0.55	−0.08	*−0.04*	0.66*	0.68
Residual effect	0.018										
						Timely sowing					
1. Days to flowering	*−0.11*	0.15	−0.01	0.04	0.43	−0.16	−0.12	−0.11	−0.01	0.08	0.10
2. Days to maturity	−0.10	*0.16*	−0.01	0.05	0.52	−0.11	−0.01	−0.11	−0.02	0.23*	0.29
3. Peduncle length	−0.02	0.04	*−0.05*	0.07	0.32	−0.10	0.04	−0.00	−0.01	0.37*	0.49
4. Plant height	−0.06	0.10	−0.05	*0.08*	0.05	0.46	0.02	−0.01	−0.01	0.45*	0.57
5. Tillers/plant	−0.06	0.10	−0.02	0.05	*0.81*	0.02	−0.08	−0.17	−0.01	0.73*	0.63
6. 1000 grain weight	0.05	−0.05	−0.01	0.01	0.04	*0.35*	0.14	−0.03	0.00	0.39*	0.50
7. Grain weight/spike	0.05	−0.06	−0.01	0.01	−0.26	0.20	*0.26*	0.32	0.01	0.48*	0.51
8. Grains/spike	0.03	−0.04	−0.00	−0.00	−0.34	−0.02	0.20	*0.41*	0.01	0.30*	0.24
9. Harvest index	0.10	−0.14	0.02	−0.05	−0.46	0.11	0.15	0.20	*0.01*	−0.01	−0.05
Residual effect	0.024										
						Late sowing					
1. Days to flowering	*0.13*	0.03	−0.03	0.01	−0.12	−0.07	−0.11	−0.25	−0.34	−0.65*	−0.73
2. Days to maturity	0.13	*0.03*	−0.01	0.02	0.12	−0.05	−0.10	−0.22	−0.34	−0.55*	−0.66
3. Peduncle length	−0.04	−0.01	*0.08*	0.03	0.04	0.05	0.05	0.10	0.04	0.32*	0.33
4. Plant height	0.04	0.02	0.06	*0.04*	0.02	−0.02	−0.00	−0.03	−0.16	−0.00	−0.03
5. Tillers/plant	−0.04	−0.01	0.01	−0.00	*0.35*	0.05	0.03	0.13	0.18	0.69*	0.69
6. 1000 grain weight	−0.07	−0.01	0.03	0.01	0.11	*0.13*	0.11	0.13	0.19	0.58*	0.66
7. Grain weight/spike	−0.10	−0.02	0.03	−0.00	0.08	0.10	*0.14*	0.29	0.32	0.42*	0.82
8. Grains/spike	−0.10	−0.02	0.02	−0.01	0.13	0.05	0.12	*0.33*	0.32	0.74*	0.86
9. Harvest index	−0.12	−0.03	0.01	−0.01	0.16	0.07	0.11	0.28	*0.38*	0.78*	0.84
Residual effect	0.053										

* Significant at 0.01 probability

rph = Phenotypic Correlation Coefficients

rg = Genotypic Correlation Coefficients

positive direct effect on grain yield/plant. The indirect effect of all characters on grain yield via tillers/plant and grain weight/spike was also of high positive magnitude. The plant height had positive direct and indirect effect of moderate magnitude. Whereas, Days to maturity, peduncle length and 1000 grain weight had negative direct and indirect effects except indirect effect of 1000 grain weight through plant height. The magnitude of positive direct effect of days to flowering and negative direct effect of grains/spike and harvest index was low.

In timely sowing, tillers/plant, grains/spike, 1000 grain weight, grain weight/spike and days to maturity had directly contributed to increased yield. Of these tillers/plant and grains/spike had higher values. However, the indirect effect of grains/spike, grain weight/spike and harvest index through tillers/plant was negative. Grains/spike, 1000 grain weight and grain weight/spike contributed positively through each other except grains/spike via 1000 grain weight. Days to flowering had negative direct effect.

The partitioning of direct and indirect effects in late sown conditions evinced that harvest index, grains/spike and tillers/plant had high positive direct effect. The indirect effect of tillers/plant was of low magnitude. However, grains/spike, harvest index, grain weight/spike and 1000 grain weight contributed positively towards yield through each other. Days to flowering and days to maturity had significant negative correlation with grain yield but their direct effect of low magnitude was positive.

The present study thus revealed that tillers/plant and grain weight/spike were the most important yield contributing characters under the three dates of sowing. These results are in agreement with those of obtained by Paroda & Joshi (1970), Das (1976), Sharm & Ahmed (1978), Shrivastave *et al.* (1980). Paroda & Joshi (1970) reported that high positive correlation of 1000 grain weight and grains/spike with grain yield/plant was the result of high positive indirect effect of grain weight/spike. Grains/spike and 1000 grain weight in timely and late sowing and plant height in early sowing also showed high positive direct effect on grain yield in the present study. The indirect effect of tillers/plant in early sowing was of positive high magnitude whereas in late sowing it was of very low magnitude. Upadhyaya *et al.* (1979) while screening the varieties for thermoinsensitivity found that those varieties which did not flower quickly under the temperature influence but continue to tiller and take long time to flower give better yield under early sown conditions. The positive association between days to flowering and grain yield in early sowing and negative association in late sowing indicated that it could be possible to breed late flowering high yielding varieties for early sowing and vice verse for late sowing.

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II. Record

Catalogue of Gene Symbols for Wheat: 1986 Supplement

R. A. MCINTOSH

The University of Syndney, Plant Breeding Institude,
P.O. Box 180, Castle Hill, N.S.W., Australia, 2154

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Anthocyanin Pigmentation

2. Red Auricles
   For review see (619).

Hairy Leaf

Hl	4Aβ (621).	**v** : Saratovskaya 29 (621).

Hybrid Weakness

1. Hybrid Necrosis
   Unknown *Nel* allele — **tv** : HW75 (616); HW178 (616).

   Rye apparently possesses a gene giving progressive necrosis when crossed with wheat cv. Siesta I (617). Assuming that Siesta I (CS/Tobari 66) possesses *Ne2m* (249) then the gene in rye simulates *Nel*. A gene, Ne_r, was identified in a triticale with known parents. This rye-derived gene simulated *Ne2* (618).

2. Hybrid chlorosis
   Ch1 — **tv** : 36 *T.dicoccum* cultivars (616).

   Different alleles for the *Ch2* gene in C306 (strong) and Sonalika (medium) were suggested (616).

Nuceolus Organiser Regions/Ribosomal RNA

1. (18S-5.85-26S rRna genes)

Nor-A1	[*Nor 1*(543)].	1AS	(711, 712, 720, 727).	**v** : *T. spelta.*
Nor-B1		1BS	(710, 711, 712, 720).	**v** : CS.
Nor-R1		1RS	(713).	**ad** : CS/Imperial.
Nor-S1		1SS	(714).	**al** : *Ae. speltoides.*
Nor-U1		1U	(717).	**su** : CS/ *Ae. umbellulata.*
Nor-B2				
Nor-B2	[*Nor 2*(543)].	6BS	(710, 711, 712, 734).	**v** : CS.
Nor-E2		6ES	(714).	**ad** : CS/ *E. elongata.*
Nor-G2		6G	(726).	**al** : *T. timopheevi* PBI no. 1.
Nor-H2		6H	(728, 713).	**v** : Clipper (713).
Nor-S2		6SS	(714).	**al** : *Ae. speltoides.*
Nor-A3		5AS	(715).	**al** : *T. urartu* PBI Acc. A.
Nor-D3		5DS	(711, 712).	**v** : CS.
Nor-E3		5ES	(714).	**ad** : CS/ *E.elongata.*
Nor-H3		5H	(728, 713).	**v** : Clipper (713).
Nor-U3		5U	(717).	**ad su**: CS/ *Ae. umbellulata.*

NORs have been observed as secondary constrictions associated with nucleoli on satellited chromosomes (e.g. 711), by hybridisation *in situ* to chromosome preparations of 18S-5.8S-26S DNA (rDNA) probes (718), and by hybridisation of rDNA probes to endonuclease-treated DNA on Southern blots (720, 719). The latter method allows detection of 'allelic' variation at NOR loci. Variation has been demonstrated at *Nor-B1* and *Nor-B2* (721, 543). Intervarietal 'allelic' variation in gene number has been demonstrated by variation in density of *in situ* label at all wheat NOR genes and at *Nor-R1* (727).

2. 5S rRNA genes

5S-rRNA-B1	1BS	(713).	**cv** : CS.
5S-rRNA-R1	1RS	(713).	**al** : *S. cereale.*

A single 5S rRNA hybridisation site was observed in barley. The chromosome involved was not 5H or 6H, identified by the presence of secondary constrictions (713).

Proteins

Enzymes

2. Alcohol dehydrogenase (Aliphatic)

Adh-R1 **ad** : FEC28/Petkus (581).

Three *Adh-1* genes have been identified in *Hordeum vulgare* and *H. spontaneum* (562, 704, 705, 706). Two of these are tightly linked at the *Adh-H1* locus (704). The third gene was tentatively located in 5H (706). The gene series formerly designated *Adh-2* and *Adh-3* now appear under Aromatic alcohol dehydrogenase.

4. α-Amylase

α-Amy-B1		Change, 6AL to 6BL.		
α-Amy-B1f	Change *Amy4* to $Amy4^{m}$ and $Amy6B1^{4}$ to $Amy6B1^{4'}$.			
α-Amy-B1h				**v** : Change, *T. macha* to *T.macha* Line 1 (576).
α-Amy-H1	[*α-Amy1*(578)].	6H	(578, 716).	
α-Amy-H2	[*α-Amy2*(578)].	7H	(578, 716).	
α-Amy-E1 (723).		6E	(723).	**ad** : CS/ *E. elongata.*
α-Amy-R1 (723).		6RL	(723).	**su ad** : CS/Imperial;CS/King II; Holdfast/King II.
α-*Amy-R*^{m}*1* (723).		$6R^{m}L$	(723).	**ad** : CS/ *S. montanum.*
α-Amy-E2 (723).		7E	(723).	**ad** : CS/ *E. elongata.*
α-*Amy-H*^{ch}*2* (724).		$7H^{ch}\beta$	(724).	**su ad** : H. *chilense.*
α-Amy-R2 (723).		7RL	(723).	**su ad** : CS/Imperial;CS/King II; Holdfast/King II.
α-Amy-U2 (723).		7U	(723).	**ad** : CS/ *Ae. umbellulata.*

5. *β-Amylase*

β-Amy-A2c				**v** : *T. macha* Line.
β-Amy-R2	[*β-AmyR1*]	5R	(581).	**ad** : FEC28/Petkus 5R; Holdfast/ King II 5R.
				tr : CS/Imperial 5BL/5RL (581).

7. Esterase

Est-B5
First three alleles should appear as *Est-B5a, Est-B5b* and *Est-B5c.*

Est-D5d **v** : Change to *T. macha* Linel.

In *S. cereale,* in addition to *Est-R1,* genes encoding leaf esterases have been located in three chromosomes (701). These include a gene designated *Est8* in 6R in cvs. Imperial and King II, a gene designated *Est2* and two genes, designated *Est6* and *Est7,* which are part of a separate compound locus (722), in 5RL in Imperial, and a gene designated *Est10* in 4R of King II and 4RL of Imperial. In *Hordeum vulgare,* genes encoding leaf esterases have been located in 3H (707, see also 708, 562), and 7H (562).

Est-H5 (725).	3H (725).	**ad** :	CS/Betzes.
Est-H^{ch}5 (725).	3H^{ch} (725).	**ad** :	CS/ *H. chilense.*
Est-R5 (725).	6R (581), 6RL (725).	**ad** :	CS/Imperial (581, 725); Kharkov/Dakold (581); CS/King II (725); Holdfast/King II (581).
Est-R^{m}5 (725).	6R^{m} (725).	**ad** :	CS/ *S. montanum.*
Est-S^{b}5 (725).	3S^{b} (725).	**su ad** :	CS/ *Ae. bicornis.*
Est-S^{l}5 (725).	3S^{l} (725).	**ad** :	CS/ *Ae. longissima.*

9. Glutamic oxaloacetate transaminase

Got-R2	6RL (709).	**ad** :	CS/Imperial 6R(437, 709); Kharkov/Dakold 6R(709); Holdfast/King II 6RL (709).
Got-H3 [*Got-B3*(703)].	3H (703).	**ad** :	CS/Betzes.
Got-R3		**ad** :	CS/Imperial (437); Holdfast/ King II (709); Kharkov/Dakold (709).

12. Malate dehydrogenase

Mdh-R1 [*Mdh2-1*(702)].	1RL (702).	**ad** :	CS/Imperial 1R; Kharkov/ Dakold 1R; Holdfast/King II 1RL.
Mdh-H2 [*Mdh2-b2*(703)].	3H (703).	**ad** :	CS/Betzes.
Mdh-R2 [*Mdh2-2*(702)].	3R (702).	**ad** :	CS/Imperial.

13. Peroxidase

Per-R1 (572).	[*Prx*(701)].	1RS	(572, 701).	**ad** : CS/King II (572); Holdfast/King II(701) **tr** : Veery 'S' (572).

16. Phosphoglucomutase

Pgm-H1	[*Pgm-b1*(703)].	4H	(703).	**ad** : CS/Betzes.
Pgm-R1		4RS	(701, 709).	**ad** : CS/Imperial 4R (701, 709); Kharkov/Dakold 4R (709); Holdfast/King II 4RS (701, 709).

18. Superoxide dismutase

Sod-R1 (588).	[*Sod-3*(589)].	2R	(588).	**ad** : CS/Imperial.

20. Aromatic alcohol dehydrogenase

Aadh-A1	[*Adh-A2*(521)].	5AL	(521)	**v** : CS.
Aadh-A1a				**v** : CS; 133 other accessions (521).
Aadh-A1b				**v** : *T. spelta;* K-24696; 11 other accessions (521).
Aadh-B1	[*Adh-B2*(521)].	5BL	(521).	**v** : CS.
Aadh-D1	[*Adh-D2*(521)].	5DL	(521).	**v** : CS.
Aadh-E1	[*Adh-E2*(520)].	5EL	(520).	**ad** : CS/*E. elongata.*
Aadh-A2	[*Adh-A3*(553)].	6A 6AL	(590), (553, 758).	**v** : CS(553); Carola (590).
Aadh-B2	[*Adh-B3*(553)].	6B 6BL	(590), (553).	**v** : CS(553); Carola (590).
Aadh-D2	[*Adh-D3*(553)].	6D 6DL	(590), (553).	**v** : CS(553); Carola (590).
Aadh-E2	[*Adh-E3*(520)].	6Eβ	(520).	**ad** : CS/ *E. elongata.*

The *Aadh-1* and *Aadh-2* loci have been designated with the synonyms *Adh-2* and *Adh-3,* respectively, in a number of publications in addition to 520, 521 and 553; these include 561, 588, 729, 730, 731, 732, 733.

Endosperm Storage Proteins

Glutenin

Glu-A1c		v : Add (599).
Glu-B1c		v : Sicco (599).
Glu-Ble		v : V538 (599).
Glu-B2 (599, 600).	1BS (599).	
Glu-B2a		v : CS (599); V538 (599).
Glu-B2b		v : Sicco (599).
Glu-D2 (601).		

Response to Photoperiod

Ppd2	v : Spica (620).

Response to Vernalisation

Vrn1	s : Rescue*/Cadet 5A *Vrn3* *Vrn4* (628).
	v : Cadet (628).
Vrn2	v : Bersee (620); Spica (620).
Vrn3	s : Rescue*/Cadet 5A *Vrn1* *Vrn4* (628).
	v : Rescue *Vrn4*.
Vrn4	s : Rescue*/Cadet 5A *Vrn1* *Vrn3* (628).
	v : Cypress (628); Rescue *Vrn3* (628).

Uniculm Stunt

US1 and *US2* located in chromosomes 4B and 5B (623).

Reaction to *Puccinia recondita*

Lr1	v : Newton (624, 625); Plainsman V *Lr3* (624).
Lr3	v : Bennett (624); Gage (624); Homestead (624); Lancota (624); Plainsman V *Lr1* (624).

Lr10		v : Centurk (624); Centurk 78 (624); Rocky (624); TAW W-105 (624).
Lr11		v : Hart (624).

Resistance to *Puccinia striiformis*

Yr11	R11(602). Adult-plant resistance.	v : Joss Cambier (608).
Yr12	R12(602). Adult-plant resistance.	v : Fleurus(609);Frontier (610); Armada *Yr3a Yr4a*(629); Mega *Yr3a Yr4a*(602); Pride (602); Waggoner *Yr3a Yr4a Yr6*(609).

Yr13 R13(602). Adult-plant resistance. v : Copain *Yr3a Yr4a*(609); Professor Marchal *Yr2 Yr3a Yr4a*(611). Bounty *Yr1 Yr3a Yr4a*(612); Sportsman *Yr1 Yr3a Yr4a*(612); Virtue *Yr1 Yr3a Yr4a*(609, 612, 603). Mardler *Yr1 Yr2 Yr3a Yr4a* (612); Marksman *Yr1* (Seg.) *Yr2 Yr3a Yr4a*(612). Hustler *Yr1 Yr2 Yr3a Yr4a*(612, 603). Gawain *Yr2 Yr3a Yr4a Yr14*(629); Guardian *Yr2* (613); Maris Nimrod *Yr2 Yr3a Yr4a* (611, 612, 602). Pageant *Yr2 Yr3a Yr4a* (613); Maris Huntsman *Yr3a Yr4a* (612, 603). Kinsman *Yr3a Yr4a Yr6* (612). Brigand *Yr2 Yr3a Yr4a Yr14* (614).

Yr14 R14 (602). Adult-plant resistance. v : Avalon *Yr3b Yr4b* (612); Kador (609); Maris Bilbo *Yr3a Yr4a* (602, 612); Score (602); Wembley (631); Galahad *Yr1 Yr2* (Seg.) *Yr3a Yr4a* (603, 612). Gawain *Yr2 Yr3a Yr4a Yr13* (629). Rapier *Yr2 Yr3b Yr4b* (603); Wizard *Yr2* (seg.) *Yr3b Yr4b* (612, 603). Brigand *Yr2 Yr3a Yr4a Yr13* (612, 603, 614). Hobbit *Yr3a Yr4a* (612, 602). Avalon *Yr4* (603). Moulin *Yr6* (630).

Yr15 (604).		v : Hexaploid derivatives of *T. dicoccoides* G-25 (604, 605). tv : *T. dicoccoides* G-25 (604, 606).
Yr16 (607).	2D (607). Adult-plant resistance.	v : Capelle-Desprez (607).

Reaction to *Mayetiola destructor* (Say) - Hessian fly

H3	v : Roland (627).
H6	v : Compton (622); Fillmore (626).

Resistance to Colonization by *Eriophyes tulipae (Aceria tulipae)* - Wheat curl mite

Eriophyes tulipae is the vector of wheat streak mosaic virus (MSMV) and the wheat spot mosaic agent (WSpM).

Cmc - curl mite colonization — v : *Ae. squarrosa* C14/Novamichurinka AC PGR 16635 (615).

Cmc1 (615).

Genetic Linkages

Chromosome 1B

1BS	*Glu-B1*	–	*Glu-B2*	16.7 + 5.2 cM (599).
	Glu-B2	–	*Gli-B1*	22.4 + 6.3 cM (599).
	Glu-B1	–	*Gli-B1*	39.1 cM (599).
Probable gene order:	*Glu-B1*	–	*Glu-B2* – *Nor-B1* (599).	

Chromosome 2D

Rht8	–	*Ppd1*	0.17 + 0.04 (607).
Rht8	–	*Yr16*	0.44 + 0.05 (607).
Rht8	–	*D4*	Independent (607).
Ppd1	–	*Yr16*	0.36 + 0.05 (607).
Ppd1	–	*D4*	Independent (607).
Yr16	–	*D4*	0.25 + 0.01 (607).
			0.26 + 0.08 (607).
D4	–	*Su-D*	Independent (607).

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III. Editorial Remarks

Announcement for Future Issues

WIS No. 65 will be planned for publication in September, 1987, Manuscripts for this issue are most welcome and accepted any time, not later than July 31, 1987.

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:

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The Managing Editor

Explanation of the Figure on the Cover

SEM micrograms of pollen grains in *Triticum aestivum.* See the text article by KARIM *et. al.* for the details.

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