WHEAT INFORMATION SERVICE

No. 54

March, 1982

Contents

I. Research Notes

Simulation of univalent distribution in a pentaploid
wheat hybrid

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The transmission of univalent D-genome chromosomes from a pentaploid hybrid ($2n = 5x = 35$) between common and emmer wheats has been studied by several workers (Kihara & Wakakuwa 1935, Alston & Jones 1965, Makino 1974, Tsuji & Maan 1981, and others). Kihara (1924) reported that seven univalents divided equationally at anaphase I (AI) and the chromatids were distributed at random at AII. As a consequence, the pentaploid produced gametes with different chromosome numbers ranging from 0 to 7 D-genome chromosomes. The data obtained by Kihara & Wakakuwa (1935) and by Makino (1974) are given in Table 1 in which the relative frequencies of eight kinds of the gametes transmitted from pentaploid hybrids are shown. Sears (1953) reported from his study of Chinese Spring monosomics that about 75% of the female gametes had only 20 chromosomes. This indicated that about 50% of the univalent chromosomes were lost or eliminated during meiosis. Supposing that random distribution and 50% elimination of each univalent take place in meiosis II of the pentaploid gametogenesis, we can calculate the theoretical frequencies of female gametes with 0 to 7 D-genome chromosomes by the expansion of the binomial $(0.75+0.25)^7$ (Table 1). When compared, however, it is clear that the actual distributions are flatter than the theoretical one. Thus, Kihara (1975) suggested that the unexpected flatness of the curve might be due to non-random distribution of the univalents in meiosis II, so that seven univalents might go frequently in a mass to one pole. If this is the case, then we can assume that the frequency distribution pattern of female gametes with 0 to 7 D-genome chromosomes is determined mainly by two factors, that is, non-randomness in univalent segregation and certain degrees of elimination of individual univalents. On the basis of this assumption, the computer simulation

Table 1. Observed and expected frequencies of female gametes with 0 to 7 D-genome chromosomes transmitted from the pentaploid wheat hybrids

	No. of gametes examined	% transmitted D-genome chromosomes							
		0	1	2	3	4	5	6	7
Observed									
KIHARA & WAKAKUWA (1935)[1]	482	7.01	14.11	20.13	20.54	18.05	13.69	5.19	1.24
MAKINO (1974)[2]	389	11.31	18.25	31.34	17.22	15.68	9.77	5.40	1.02
Expected from $(0.75+0.25)^7$	—	13.35	31.15	31.15	17.30	5.77	1.15	0.13	0.01

[1] Estimated from the crosses, (*T. spelta* × *T. polonicum*) F_1 × *T. spelta* and *T. polonicum*.

[2] Estimated from the cross, (*T. spelta* × *T. durum*) F_1 × *T. durum*.
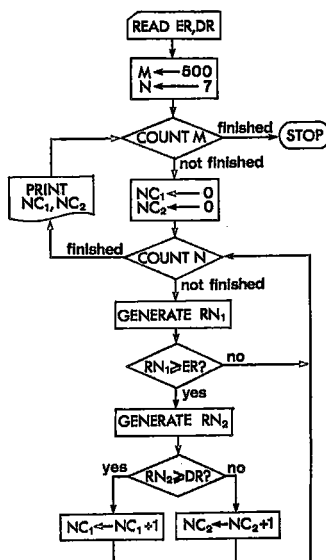
Fig. 1. Flow diagram for simulation of univalent elimination and distribution in meiosis II of the female gametogenesis in the pentaploid wheat hybrid (See text for description).

of univalent behavior in meiosis II was conducted. The result will be presented in this report.

A simplified flow diagram for the written computer program is illustrated in Fig. 1. It is assumed here that meiosis I give all cells with the exactly same chromosome constitution because of equational division of the univalents, although SEARS (1952) showed 96% univalent division in meiosis I in mono–5A of Chinese Spring. In this program, the fate of each univalent in meiosis II will be determined by two parameters ER (elimination rate) and DR (distribution rate), and 500 sets of two female gametes having different numbers of transmitted univalents will be produced as a result of meiosis II. The female gametes thus produced will be treated as a population of the gametes ready to fertilization, while in the real situation only one of the four cells formed in a female organ contributes to fertilization.

The first operation will be to input values of two parameters ER and DR. Counters M and N will be set to 500 and 7, respectively. The first of these is the number of meiotic events required, so 500 events of meiosis II will give a total of 1000 meiotic products. The second is the number of the univalent chromatids. The program will then enter a loop which will be repeated the required number of times ($=500$). Increment controls NC_1 and NC_2 will be both set to zero in order to count the numbers of univalents which will move to one pole and the other, respectively. Subsequently, the program will enter the inner loop which will simulate univalent elimination and distribution. It is now in a position that parameter ER will determine if a univalent is eliminated. If so, the program will return to the beginning of the second loop. If not, parameter DR will determine towards which pole the univalent migrates. The implementation by these two parameters is: If the elimination rate ER is x, and then random number (RN_1) between 0 and 1 is generated and a univalent is eliminated if this random number does not exceed x. Also, if the distribution rate DR is y, and then the other random number (RN_2) is generated and one gamete to be produced receives the un-eliminated univalent if this random number is greater than y; otherwise its counterpart receives it. For example, if $y=0.1$, the chance of one gamete receiving each un-eliminated univalent would be 90%, and that of its counterpart would be 10%. The univalents would distribute at random when $y=0.5$. After a cycle from 1 to 7 is completed, the number of univalents (NC_1 and NC_2) in a pair of the female gametes will be printed out, and then the program will return to the beginning of the first loop (meiosis cycle).

Simulation data were obtained from computer runs of a FORTRAN program. Comparisons were made between the estimated distributions by simulations at various
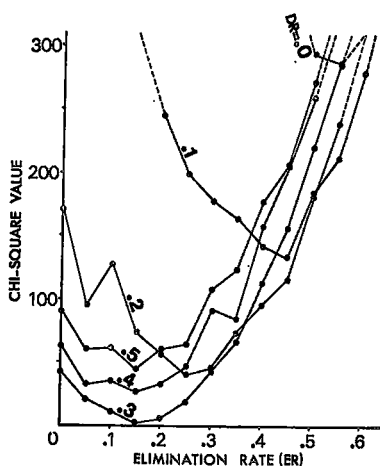
Fig. 2. Comparisons between the estimated distributions by simulations at various elimination rates (ER's) and distribution rates (DR's) and the actual distribution obtained by KIHARA & WAKAKUWA (1935). The smaller chi-square values are, the more the estimated and the actual distributions resemble.

elimination and distribution rates and the actual distributions. Statistical analyses were done by using 2×7 chi-square tests of independence, in which two types with 6 and 7 D-genome chromosomes were pooled because of small expected values in some cases. The estimated dsitributions were tested with the actual distribution obtained by KIHARA & WAKAKUWA (1935), and the change in chi-square value is presented in Fig. 2, from which it can be seen that chi-square values were very small and not statistically significant when ER was 0.15–0.20 and DR was 0.30. Similarly, there were satisfactory fits of the estimated distributions with the actual distribution obtained by MAKINO (1974) when ER was 0.15–0.20 and DR was 0.25–0.30. These simulation results indicated that 15–20% univalent elimination was a naturally occurring event in the pentaploid wheat hybrids investigated by those workers. In fact, NAKAMURA (1945) reported 12–19% elimination by observing micronuclei in quartets from several pentaploid hybrids. Both were comparable to each other. Our results also indicated that in actuality the univalent chromatids did not necessarily distribute at random (the 3:7 or 7:3 univalent segregation was the best estimate in the present work). Evidence has not yet been available for non-randomness in univalent distribution in wheat, and moreover it may not be an easy task to experimentally prove it. In higher plants other than wheat, however, there have been several reports on this subject. SMITH-WHITE (1948) has reported polarized univalent segregation during meiosis I in a *Leucopogon juniperinus* triploid. Therefore, we could postulate that there may be some mechanism to disturb random orientation of univalent chromatids in meiosis II of the pentaploid gametogenesis.

As shown above, our method seems to be useful to simulate univalent elimination and distribution, although it may not be a very good representation of reality. The present work has been preliminary, and further improvement of the algorithm and mathematical treatment, if possible, will be needed to have better understanding of univalent behavior during meiosis.

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Development of D genome monosomic addition lines
in durum wheat cv Bijaga Yellow*

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Durum wheat is commonly used for the production of pasta products such as spaghetti, macaroni and noodles. However, durum flour is generally considered unsuitable for bread production, because of its weak mixing characteristics, low loaf volume, poor texture and yellow colour. These properties suggest that the D-genome is primarily responsible for the strong mixing characteristics and bread making ability typical of the hexaploid wheat (JOPPA et al. 1975). But the durum wheat is drought and frost tolerant, resistant to rusts and can be grown even under poor management conditions. If the quality characters can be improved, this wheat could become more popular when compared to common wheat. For this purpose, careful manipulation of chromosomes, is needed to redesign this species and to improve not only quality, but also the nutritive value. Further, the nutritional potential of both tetraploid and hexaploid wheat proteins as would be improved if lysine, the first limiting amino acid, could be increased as percent of the total protein. For this purpose, it is essential to identify and locate the structural and/or regulatory genes controlling the synthesis of protein and lysine. The studies made by MATTERN et al. (1979), BHATIA et al. (1977), SADANANDA et al. (1977) and BHAT & GOUD (1978) indicated that the presence of genes responsible for protein and lysine content to be located on D-genome chromosomes. So, it is essential to produce D-genome addition lines in *durum* wheat, so that the effect of a particular D-genome chromosome can be studied and quality and technological characters could be improved without affecting fertility. The present investigation deals with the breeding behaviour of D-genome monosomic addition lines (haplosomics) in durum wheat or Bijaga Yellow.

Material and Methods

The last seven monosomic lines of hexaploid wheat variety Pb C 591 (monosomic for D-genome) was crossed as female parent with *T. durum*, or Bijaga Yellow. In F_1 generation the majority of the progenies were of two types. First being, plants with 34-chromosomes ($14''+6'$) which are nothing but monopentaploids. The second being the plants with 35–chromosomes ($14''+7'$) which are eupentaploids. In F_1 generation, the plants with 34–chromosomes were selected and back crossed to Bijaga Yellow. In first back cross generation,

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the plants with 14″+1′ were selected and others were discarded and such selected plants were again back crossed to Bijaga Yellow twice to study the breeding behaviour in each backcross generation.

Results and Discussion

Monosomic lines of Pb C 591 which were used as female parents in the present investigation would produce either 'n' or 'n–1' gametes in different proportions. As the transmission of monosomic condition from female side in hexaploid wheat is about 75 percent, 75 percent of the monopentaploid plants are expected when crossed with a tetraploid Bijaga Yellow. But in the present investigation only 52.51 percent of the plants were monopentaploids (Table 1). This may be due to reduced viability or inviability of n–1 spores or reduced viability of 2n–1 zygotes. Occurrence of the monopentaploid condition (81.82 percent) occurred in 5D and minimum was seen in line 2D. This may be due to differential transmission rate of monosomic condition to its progeny. BOZZINI & GIORGI (1971) also observed such variability in transmission rates of monosomic condition in different A and B genome lines.

ALSTON & JONES (1968) studied the breeding behaviour of monopentaploid plants when back crossed to *T. durum*. In the BC$_1$ progeny they observed 57 percent of the plants with 28 chromosomes and 23 percent of the plants with either 29 or 30 chromosomes.

Table 1.   Frequency of plants with different chromosome configurations at metaphase-I of meiosis in hybrids of crosses between D-genome monosomic lines of Pb C 591 and Bijaga Yellow

Populations	Number of plants analysed	Number of plants with 34 chromosomes	Number of plants with 35 chromosomes	Others
1D	12	8 (66.67)	3 (25.00)	1 (8.33)
2D	8	4 (50.00)	4 (50.00)	—
3D	10	6 (60.00)	3 (30.00)	1 (10.00)
4D	13	8 (61.54)	5 (38.46)	—
5D	11	9 (81.82)	2 (18.18)	—
6D	11	6 (54.55)	5 (45.45)	—
7D	7	4 (57.14)	2 (28.57)	1 (14.29)
Total	72	45 (62.51)	24 (33.33)	3 (4.16)
Disome	6	—	6 (100.00)	—

Figures in the parenthesis indicate the percentage.

In the present investigation, in the first back cross generation of monophentaploids x Bijaga Yellow, it was observed that the percentage of plants with 28, 29 and 30 chromosomes was 29.95, 5.88 and 27.81 respectively (Table 2). In all the D-genome lines, frequencies of plants with haplosomic condition $(14''+1')$ occurred in lesser frequency, the range being 3.23 percent to 9.25 percent. Same observations were made by ALSTON & JONES (1968). In the progenies of eupentaploids when back crossed to Bijaga Yellow, 40 percent of the plants were observed to be with 28 chromosomes, whereas only 5 percent of the plants had 29-chromosomes. Plants with 30 chromosomes were about 20 percent. ALSTON & JONES (1968) also observed the same frequencies. They noticed 49 percent of plants with 28-chromosomes and 28 percent with 29 or 30 chromosomes.

YAMASHITA (1947) and MATSUMURA (1952) isolated seven haplosomics representing each of the D-genome chromosomes from a *Triticum spelta* (2n=42) × *T. polonicum* (2n=28) pentaploid hybrid. MATSUMURA (1961) was able to maintain his lines as diplosomics (2n=30) selected from the progeny of each haplosomic line.

OPEKE (1961) studied the haplosomic lines from pentaploid hybrids of *T. aestivum* × *T. durum* and of *T. aestivum* × *T. dicoccum* but was not able to maintain them as diplosomics. However, he suggested that it might be possible to maintain them if the tetraploid complements were more homozygous.

In the present investigation, in the second back cross generation in general, plants with 29-chromosomes $(14''+1')$ were observed in less frequency (8.69 percent) compared to

Table 2. Frequency of plants with various chromosome configurations at metaphase-I of meiosis in BC $(14''+6' \times 14'')$ generation

Line	28	29	30	31	32	33	34	35	Total
1D	7.00 (29.17)	2 (8.33)	6 (25.00)	5 (20.83)	3 (12.50)	1 (4.17)	—	—	24
2D	6 (28.57)	1 (4.76)	6 (28.57)	4 (19.05)	3 (14.29)	1 (4.76)	—	—	21
3D	11 (35.48)	1 (3.23)	8 (25.80)	5 (16.13)	4 (12.90)	1 (3.23)	1 (3.23)	—	31
4D	6 (28.57)	2 (9.52)	6 (28.57)	4 (19.05)	2 (9.52)	1 (4.76)	—	—	21
5D	8 (34.79)	1 (4.35)	6 (26.08)	6 (26.08)	1 (4.35)	1 (4.35)	—	—	23
6D	8 (25.00)	2 (6.25)	9 (28.12)	7 (21.87)	4 (12.50)	1 (3.13)	1 (3.13)	—	32
7D	10 (28.57)	2 (5.71)	11 (31.43)	8 (22.86)	3 (8.57)	1 (2.86)	—	—	35
Total	56 (29.95)	11 (5.88)	52 (27.81)	39 (20.86)	20 (10.69)	7 (3.74)	2 (1.07)	—	187
Eupentaploid derivatives	8 (40.00)	1 (5.00)	4 (20.00)	1 (5.00)	2 (10.00)	2 (10.00)	1 (5.00)	1 (5.00)	20

Values in the parenthesis indicate the percentages.

Line	Plants with different chromosomes		Total No. of plants analysed
	28	29	
Monopentaploid derivative			
1D	38 (90.48)	4 (9.52)	42
2D	26 (92.86)	2 (7.14)	28
3D	39 (92.86)	3 (7.14)	42
4D	23 (85.19)	4 (14.81)	27
5D	39 (39.70)	4 (9.30)	43
6D	27 (90.00)	3 (10.00)	30
7D	35 (92.11)	3 (7.89)	38
Total	227 (90.80)	23 (9.20)	250
Eupentaploid derivative	21 (91.31)	2 (8.69)	23

Values in the parenthesis indicate the percentages.

disomics (91.31 percent) (Table 3). In third back cross generation (Table 4) also, the transmission frequency of haplosomic condition to its progeny was quite low (3.84 percent). The range was from 3.44 percent to 6.97 percent.

YASHVIR & KESAVAN (1979) also observed a low transmission rate. The frequency of monosomic addition plants in the progeny of double monosomic was only 8.4 percent. They could not recover monosomic addition palnts in the progeny of double monosomic addition lines. According to them, this is due to addition decay.

MATSUMURA (1952) produced three of the possible seven addition disomics from crosses of *T. spelta* and *T. polonicum*. Only one of them could be maintained without difficulty. The other two had low fertility, and one of them also had poor endosperm.

JOPPA & McNEAL (1972) could produce disomic addition lines in 1D, 2D, 3D, 4D, 5D and 7D. They were male sterile either partially or completely.

In the present study also, the fertility of haplosomic lines was reduced either partially or completely. The cause or causes of low fertility in the D-genome addition lines is unknown. Sterility in aneuploids such as trisomics has been attributed to chromosome imbalance. Differences in the genetic content of the A and B genomes of Pb C 591 may also contribute to the sterility encountered. The extracted tetraploids of KERBER (1964)

Table 4. Frequency of plants with D-genome haplosomic chromosome at metaphase-I of meiosis in third back cross generation i.e. $14'' + 1' \times 14''$

Line	Plants with different chromosome numbers		Total No. of plants analysed
	28	29	
1D	46 (95.83)	2 (4.17)	48
2D	37 (94.88)	2 (5.12)	39
3D	43 (95.13)	2 (4.87)	45
4D	27 (96.56)	1 (3.44)	29
5D	43 (93.34)	3 (6.66)	45
6D	35 (94.60)	2 (5.40)	37
7D	41 (93.03)	2 (6.97)	43
Total	272 (95.10)	14 (4.90)	286
Eupentaploid derivative	25 (96.16)	1 (3.84)	26

Values in the parenthesis indicate the percentages.

and KALTSIKES et al. (1968) were generally weak and low in fertility, thus demonstrating a lack of fitness for survival at the tetraploid level.

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Quantitative studies of the amphidiploid (*Aegilops sharonensis* × *Triticum monococcum*) and the origin of the B genome of wheat

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A number of lines of evidence have recently been advanced for *Ae. sharonensis* as putative donor of the B genome of wheat (KUSHNIR & HALLORAN 1981) using as evidence, cytoplasmic compatibility, chromosome pairing, plant morphology and karyomorphology. Additionally PARODA (1977) has found *Ae. sharonensis* to contain smaller divergences in DNA base sequences from tetraploid and hexaploid wheat than the other proposed B-genome donor species, *Ae. longissima* and *Ae. speltoides*. The aim of the present study was to investigate whether developmental and plant morphological characters in present day wild tetraploid wheat could have originated from hybridisation between *T. monococcum* and *Ae. sharonensis*.

Table 1. Developmental Responses of *Aegilops sharonensis*, *Triticum monococcum*, their hybrid A^{a}A^{a}B^{a}B^{a}S^{sh}S^{sh} grown under short (12

Species or hybrid	Days to floral initiation				Final	
	Short photo-period (12 h)	Long photoperiod (24 h)			Short photo-period (12 h)	Long
		No vernal-ization	30 days[+] vernal-ization	60 days[+] vernal-ization		No vernal-ization
Ae. sharonensis	98	76	18	12	18.12 ±0.44*	16.50 ±0.53
T. monococcum	50	11	14	9	10.87 ±0.22	6.00 ±0.00
Ae. sharonensis × *T. monococcum* A^{m}A^{m}S^{sh}S^{sh}	41	12	13	10	9.87 ±0.12	6.12 ±0.12
T. turgidum dicoccoides (cereal type)	42	26	25	15	10.37 ±0.18	9.00 ±0.18
T. turgidum dicoccodies ("grassy" type)	146	145	20	17	19.87 ±0.49	22.25 ±0.49
Ae. sharonensis × *T. turgidum dicoccodies* (cereal type) A^{a}A^{a}B^{a}B^{a}S^{sh}S^{sh}	46	19	15	15	11.00 ±0.26	7.12 ±0.12

+ From transplanting the vernalized seeds

The *Ae. sharonensis* line chosen for this study was collected by one of us (U.K.) from the coastal plain of Israel from an undisturbed habitat having no contact with *Ae. longissima* populations. The lines of *Triticum turgidum dicoccoides* were collected in Israel, the early type from Upper Galilee and the late type from the slopes of Mt. Hermon. The line of *T. monococcum* was collected in Turkey. The amphidiploid of (*Ae. sharonensis* × *T. monococcum*) and (*Ae. sharonensis* × *T. turgidum dicoccoides*) were produced by the application of 0.05% colchicine solution to the apices of seedlings of the respective hybrids at the 5 leaf stage for 5 hours. To quantify the influence of vernalization on rate of development and spikelet number two sets of the above plant material were vernalized, one for 30 days and the other for 60 days. Imbibed seed was placed in a cold room at 4°C under 8 hour photoperiod provided by low intensity (photoinductive) in candescent light. After the vernalization treatment eight vernalized and non-vernalized seedlings of each line were planted in two 18 cm diameter pots (four seedling per pot) containing a potting mix (1 part washed sand: 1 part Perlite: 1 part Derrimut red brown loam by volume). The non-vernalized lines were grown under two photoperiod regimes (short day-12 hours and long day-24 hours) and the vernalized material was grown under long photoperiod only. All plants grew under temperatures of 20°C (day) and 15°C (dark). The number of days from sowing to floral initiation was determined by the non-destructive method of AITKEN (1976). Observations were made of final leaf number, days to anthesis and spikelet number on the main shoot

$A^mA^mS^{sh}S^{sh}$, *Triticum turgidum dicoccoides* ($A^aA^aB^aB^a$) and its hybrid with *Ae. sharonensis* hours) and long photoperiod (24 hours)+

leaf number		Days to anthesis				Spikelet number			
photoperiod (24 h)		Short photoperiod (12 h)	Long photoperiod (24 h)			Short photoperiod (12 h)	Long photoperiod (24 h)		
30 days+ vernalization	60 days+ vernalization		No vernalization	30 days+ vernalization	60 days+ vernalization		No vernalization	30 days+ vernalization	60 days+ vernalization
6.37 ±0.18	6.85 ±0.13	159.00 ±3.89*	113.29 ±1.25	52.00 ±0.63	51.00 ±0.89	20.00 ±1.02*	17.00 ±0.73	7.75 ±0.25	6.12 ±0.48
6.00 ±0.00	6.00 ±0.00	123.00 ±1.91	46.75 ±0.45	49.29 ±0.27	53.12 ±2.06	47.71 ±2.29	10.87 ±0.35	10.86 ±0.43	10.25 ±0.16
5.12 ±0.12	5.71 ±2.29	123.25 ±2.29	49.86 ±0.77	49.62 ±1.73	48.86 ±1.20	25.62 ±1.01	12.43 ±0.29	9.50 ±0.60	8.29 ±0.27
7.75 ±0.16	7.00 ±0.00	87.62 ±1.29	64.00 ±1.29	56.12 ±2.07	56.43 ±1.79	15.25 ±0.25	12.75 ±0.16	10.37 ±0.26	7.71 ±0.44
6.75 ±0.16	6.12 ±0.12	237.28 ±8.68	195.16 ±2.31	52.62 ±0.80	50.25 ±1.23	12.00 ±0.41	11.00 ±0.22	7.12 ±0.29	6.12 ±0.40
6.25 ±0.16	6.12 ±0.12	106.71 ±2.20	52.75 ±1.22	48.25 ±0.70	46.75 ±0.96	18.14 ±0.88	9.12 ±0.35	7.50 ±0.19	6.00 ±0.00

* All figures are means±standard error

of each plant. Plant height, tiller no., grain number per spikelet, fertility (%) and kernel weight were measured for the main shoot of the unvernalized plants grown under the short day regime.

Results and Discussion

The (*Ae. sharonensis* × *T. monococcum*) amphidiploid exhibited similar developmental responses (days to floral initiation, final leaf number and days to anthesis) under both long and short photoperiod as *T. monococcum*, except spikelet number where it was significantly (p<.01) lower than *T. monococcum* under short photoperiod (Table 1). *Ae. sharonensis* possessed a strong vernalization response while *T. monococcum* possessed little or no response as indicated by its final leaf number (when vernalized and under long photoperiod) being close to the minimum for wheat. The (*Ae. sharonensis* × *T. monococcum*) amphidiploid was very similar to *T. monococcum* in vernalization response, indicating epistasis of *T. monococcum* over *Ae. sharonensis* genes for this character. The close similarity in developmental responses between the (*Ae. sharnonensis* × *T. turgidum dicoccoides* :cereal type) amphidiploid and those of *T. turgidum dicoccoides* is evidence for epistasis (A genome) or dominance (B genome) of genes for vernalization response in the amphidiploid over those in *Ae. sharonensis*.

The similar developmental responses of the (*Ae. sharonensis* × *T. monococcum*) amphidiploid with those of *T. monococcum* is compatible with the notion of the first tetraploid wheats occupying similar habitats as *T. monococcum*, but eventually replacing it through superior competitive ability.

The most significant changes in yield potential of the *Ae. sharonensis* × *T. monococcum* amphidiploid over *T. monococcum* were a substantial increase in both Kernel weight and grain number per spikelet (Table 2). Spikelet number per head was significantly (p<.01) decreased compared with *T. monococcum* but significantly (p<.01) higher than *Ae. sharonensis*. A previous report (SEARS 1941) has been made of increased grain size of synthetic tetraploid wheat over its diploid parents. This could have arisen as a consequence of favourable interaction between genes influencing grain size in the two parents and/or as a consequence of tetraploidy, more likely due mostly to the former. Previous studies of the genetic control of kernel weight in hexaploid wheat (HALLORAN 1976) revealed genes of major effect on its expression in both the A and B genomes. This observation is compatible with the knowledge that kernel weight appears to reach a maximum in tetraploid wheat with decreased weight accompanying the evolution of hexaploid wheat (HALLORAN & PENNELL 1981).

The fertility of the (*Ae. sharonensis* × *T. monococcum*) amphidiploid was similar to *T. monococcum*. This, together with the increase in kernel weight of the amphidiploid over the diploid parents indicates high combining ability between the A and B genomes. A previous report has been made of the comparatively high combining ability of the A and B genomes, as seen in advanced tetraploids of wheat, against the low level exhibited by the A and D genomes, in the *T. monococcum* × *Ae. squarrosa* hybrid (SHEBESKI 1958).

Table 2. Morphology and fertility of *Aegilops sharonensis*, *Triticum monococcum*, their hybrid A^{m}A^{m}S^{sh}S^{sh}, *Triticum turgidum dicoccoides* (early and late types).

Species or Hybrid	Plant height (cm)	Tiller no./ plant	Spikelt no. on main head	Grain no. per spikelet	Fertility (%)	Kernel weight (mg)
Ae. sharonensis	88.78±3.66*	22.86±2.72*	20.00±1.02*	1.83±0.09*	89.87±4.19*	6.05±0.21*
T. monococcum	60.12±0.91	26.87±3.41	47.71±2.20	1.06±0.09	67.25±3.67	10.62±1.40
Ae. sharonensis × *T. monococcum* A^{m}A^{m}S^{sh}S^{sh}	83.50±1.40	29.83±1.13	25.62±1.01	1.29±0.08	64.60±4.33	20.54±1.68
T. turgidum dicoccoides (cereal type)	107.75±3.69	9.25±1.03	15.25±0.25	1.60±0.08	79.87±4.20	36.70±1.68
T. turgidum dicoccoides ("grassy" type)	77.12±3.91	33.37±3.91	16.50±0.94	0.95±0.07	50.11±3.70	19.45±1.17

* All figures are means±standard error

The expressions of developmental and morphological characters of the (*Ae. sharonensis* × *T. monococcum*) amphidiploid were generally within the ranges of those in the cereal and "grassy" forms of *T. turgidum dicoccoides*. It is presumed that these two forms of *dicoccoides* represents a range from primitive ("grassy") to more advanced (cereal) genotypes and are some indication of genetic differentiation that has occurred within *dicoccoides* throughout its evolution. In accord with this postulation the "grassy" (primitive) form was similar in tiller number per plant and kernel weight to the (*Ae. shaornensis* × *T. monococcum*) amphidiploid. The cereal (advanced) form of *dicoccoides* had a much lower tiller number per plant than the amphidiploid and the "grassy" form, which accords with reports (BAMAKHRAMAH 1974, HALLORAN & PENNELL 1981a) on the reduction in tiller number from primitive to advanced forms in tetraploid wheat. Another possible source of genetic variation in *T. turgidum dicoccoides* is repeated hybridization between *T. monococcum* and *Ae. sharonensis* forms with intraspecific variation in morphological and developmental characters.

These observations on the (*Ae. sharonensis* × *T. monococcum*) amphidiploid further support *Ae. sharonensis* candidature as the donor of the B genome of wheat on the grounds of compatibilities in morphological and developmental characters of the amphidiploid with the range found in *T. turgidum dicoccoides*. The amphidiploid possessed a comparable fertility level with *T. monococcum* and a much larger kernel weight. The greatly increased kernel weight indicates that the first tetraploids of wheat most likely possessed superior competitive ability over *T. monococcum* during seedling growth (HALLORAN & PENNELL 1981b) and, hence, in population establishment. This may have been significant in the eventual preeminence of tetraploid over diploid wheat.

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Estimates of genetic variability in mutated population of triticale

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In various autogamous crops it has been now well established that radiations when applied to plants induce mutations in polygenic characters (Gaul 1977, Larik 1978). Attempts have also been made to indentify and evaluate radiation induced variations in quantitative characters and have estimated the progress that can be made by subsequent selection. Brock (1965) has put the hypothesis that random mutations are expected to increase the variance and shift the mean away from the direction of previous selection. Recently there has been a trend to apply mutation in already hybridized populations to find out whether or not variability could be extended.

The present study was designed to compare the relative effectiveness of X-rays and fast neutrons for inducing improvement in yield and yield components of triticale and wheat cultivars.

Materials and Methods

M_3 populations of Norwegian highest yielding spring wheat variety "Runar" and Canadian spring form triticale derived from irradiation treatments of X-rays (3KR, 5KR, 10KR) and fast neutrons (1.5 N) were critically examined for spikes per plant, spikelets per spike, kernels per spike and seed set. Data on individual M_3 plants randomly selected from each of M_3 families were analysed. The heritability estimates was obtained from the following equation.

$$V_t = V_g + V_e$$

Where V_t stands for total variation, while V_g and V_e denoted components due to genetic and environmental variation respectively.

Results and Discussion

Response to selection for quantitative characters (*i.e.* yield components) is directly proportional to the function of its heritability and its genetic variance. Heritability enables a plant breeder to recognise the genetic difference among strains and variance indicates the potential for the improvement of a population. Keeping in view these points, the estimates such as genotypic coefficient of variation and heritability were obtained separately from each quantitative character and are presented in Table 1.

Table 1. Ranges, means, different±standard error, variances, coefficient of variaton (c.v.) genetic variance (V_g) and broad sense heritabilities h^2 (b.s)

Treatment	No. of plants	Ranges	Means and differences from the control.	Variances	c.v.	V_g	h^2(b.s)
Spikes per plant							
Wheat control	35	2.1-3.8	2.8 ±0.25	0.44	23.64	0	0
1.5 N	100	1.2-6.2	0.9* ±0.33	2.23*	40.33	1.79	0.8
5 KR X-rays	100	2.1-5.7	0.36 ±0.22	0.97	30.9	0.53	0.55
10 KR X-rays	100	1.2-7.8	0.1 ±0.39	3.10**	60.75	2.66	0.86
Triticale control	40	2.3-3.8	3 ±0.18	0.27	17.3	0	0
1.5 N	55	1.1-6.9	−0.28 ±0.59	3.85**	72.17	3.58	0.9
3 KR X-rays	100	1.3-5.2	0.42 ±0.23	1.1*	30.71	0.83	0.75
5 KR X-rays	100	1.1-9.6	−0.5 ±0.5	5.16**	90.9	4.89	0.94
Florets per head							
Wheat control	35	40-58.6	48.23 ±2.66	49.46	14.6	0	0
1.5 N	100	26-59.6	−4.08 ±1.66	55.19	16.83	5.73	0.13
5 KR X-rays	100	32.2-67.4	2.45 ±2.22	99.05	19.64	49.59	0.5
10 KR X-rays	100	19.2-69.6	0.57 ±3.09	190.7*	28.29	141.24	0.74
Triticale control	40	44.4-78.4	63.87 ±3.9	124.66	17.48	0	0
1.5 N	55	22.4-101.0	−12.74 ±7.39	600.43**	47.92	475.77	0.79
3 KR X-rays	100	23.0-80.0	−3.59 ±3.76	283.44	27.93	158.78	0.56
5 KR X-rays	100	12-101.4	−8.12 ±5.25	551.46*	42.12	426.8	0.77
Kernels per head							
Wheat control	35	36.6-46.8	37.6 ±1.8	22.33	14.6	0	0
1.5 N	100	13.8-44.2	−9.61** ±1.64	54.14	26.29	31.81	0.59
5 KR X-rays	100	17.2-48.2	−1.91 ±2.01	80.54*	25.14	58.21	0.72
10 KR X-rays	100	3.8-50.8	−8.62 ±3.23	208.24**	49.79	185.91	0.89
Triticale control	40	38.2-46.6	41.75 ±0.94	7.03	6.35	0	0
1.5 N	55	3.2-58.6	−21.19** ±4.47	219.57**	72.07	212.54	0.96
3 KR X-rays	100	6.6-51.8	−13.1** ±2.92	170.19**	45.53	163.16	0.96
5 KR X-rays	100	2-65.8	−13.78** ±3.9	303.7**	62.31	296.67	0.97
Seed set							
Wheat control	35	67.5-96	78.7 ±3.96	109	13.3	0	0
1.5 N	100	38.97-79.45	−15.48** ±2.69	54.14	26.29	0	0
5 KR X-rays	100	26.79-88.19	−7.26* ±3.36	226.23	21.06	117.23	0.52
10 KR X-rays	100	9.05-93.3	−21.06 ±4.86	472.06*	37.86	363.06	0.77
Triticale control	40	51.8-90.54	67.05 ±4.16	138.23	17.53	0	0
1.5 N	55	13.77-66.85	−27.51** ±5.48	330.13	45.95	191.9	0.58
3 KR X-rays	100	16.48-63.1	−20.07** ±3.16	199.65	30.6	61.42	0.31
5 KR X-rays	100	4.88-89.1	−17.56* ±4.78	458.1*	43.25	319.87	0.70

Productive tillers, florets per spike, kernels per spike and seed set are important yield components and are considered reliable measure of yielding ability (Borojevic & Borojevic 1972), as the frequency of induced changes in subsequent generation depends on the number of seeds which transmit them (Larik 1978). Mean values for seeds per head and seed set characters (Table 1) were significantly (P≥0.05, 0.01) reduced in triticale after both the radiation sources, for florets and spikes (Table 1). The reduction was non-significant. Wheat displayed significant (P≥0.05) increase only for spikes per plant at 1.5 N and significant (P≥0.05, 0.01) decrease for seed set at 1.5 N and 5KR and for kernels per head at 1.5

N. The shift of mean values for these quantitative characters is mostly in negative direction in triticale and wheat gave plus as well as minus effects, it provides support for the hypothesis of GAUL & AASTVEIT (1966).

Heritability estimates for above quantitative characters showed considerable increase in genetic variation among the mutated populations indicating that the characters could be transmitted to further generation and significant gain could possibly be achieved through selection in early generation (LARIK 1978). The results showed decrease the mean values and increase in genotypic variance in mutant populations of triticale. Similar results were obtained by GAUL (1965), SIDDIQUI & GHAFOOR (1974) and LARIK (1975). These authors also observed a decrease in the mean values and increase in genotypic variance in mutant populations concomitant with a high frequency of plants having values on the negative side of the control mean.

Thus, the variation observed in the M_3 generation for all the characters in triticale due to the mutagenic treatment indicate the potential usefulness of mutation breeding for improvement of triticale. The investigation are preliminary in nature, and more extensive experiments are needed before definite conclusion can be drawn. Such studies are in progress in Sweden, and GUSTAFSSON and other have stated that mutation breeding which has produced useful strains in barley and other crop plants (MUNTZING 1972), would be used in triticale. RAMANATHA & JOSHI (1976) have also observed induced variation in triticale and recommended mutation as a method for improvement. The procedures should be aimed at increasing the genetic base that is also too narrow in the existing triticales. This should lead to an acceleration of the improvement in this new crop.

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Induced mutation of Saudi Arabian local variety of bread wheat. I. Yield and yield components

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Genetic variation is essential for the success of any plant breeding program. These variations can be created by either hybridization or treatment with mutagens. Limitation of variation would be highly influenced with diverse genetic backgrounds of the parental used in crossing.

Induced mutations has already proved beneficial for tailoring better variaties of crop plants, especially in seed propagated ones. Significant amounts of induced genetic variations following treatments with chemical and physical mutagens were reported by many investigators (Hussein 1968, Gottschalk 1971, Ojomo & Chheda 1972, Hussein & Disouki 1976). Kassem et al. (1976) showed that the chemical mutagen EMS was more effective for creating genetic variability than was the physical; gamma rays.

The present investigation deals with the evaluation of the responses of chemical mutagen, viz Diethyl Sulfate (DS) on 6x local bread wheat variety (Hinta Madeni). Making use of the mutants gain advantages for breeding program orientation and gene fixation aim at improving the yield and yield components.

Material and Methods

The seeds of hexaploid local wheat variety (Hinta Madeni) obtained from Plant Production Department, Faculty of Agriculture, University of Riyadh, Saudi Arabia, were treated with different concentrations of diethyl sulfate (DS) at different times as follows:

$$0.26\% \quad DS+30 \, min$$
$$0.26\% \quad DS+ \, 1 \, h$$
$$0.008\% \quad DS+24 \, h$$
$$0.02\% \quad DS+24 \, h$$

A sample of 250 seeds in each treatment were soaked in DS dissolved in potassium acid phosphate-sodium hydroxide buffer solution, pH 7.4. The solution was changed every 90 minutes and agitated continually at 20°C. The chemically treated seeds after thorough washing were imbeded in jiffy pots for sometimes in the green house for obtaining M_1 generation, as well as untreated seeds. After complete germination, the seedlings were transplanted in the field experiment which was designed in a randomized complete block with four replications. Each replicate contains 50 single plants from each treatment sown

in two rows; 5 m long and 30 cm apart. The data of M_1 plants were collected on a single plant basis (main tiller) and the seeds were sown in the field for M_2 generation.

Selection had been made in M_2 generation for two types, namely (SS) spike length and number of spikelets per spike; and (GH) grain yield and harvest index, within each high, medium and low selection levels were taken to establish different genetic make up across the generation. The present investigation deals with variations induced by diethyl sulfate (DS) in yield and yield components of wheat. The experiments were carried out at the Agricultural Experiment Station (Olisha), University of Riyadh, Saudi Arabia during the year 1979–1980.

Results and Discussion

M_1-generation:

The effect of diethyl sulfate (DS) on mean performance of a pure line wheat cultivar (Hinta Madeni) for the grain yield and various yield components are presented in Table 1.

The results showed that the treatment with the highest concentration (0.26%) and least time (30 minutes) caused an enhancement effect on genes controlling traits which reflected an increase in population means for all the triats studied. To some extent, treatment with lowest concentration (0.008%) and longest time (24 hours) came up with similar trend for all traits except the number of spikes per plant. In contrast, treatments with highest concentrations and longest times, i.e. 0.26% DS+1 hour and 0.02% DS and 24 hours, resulted in a reduction in the mean values of most traits. This reduction in means may be due to detrimental mutations which occur more frequently than favourable ones. WILLIAMS & HANWAY (1961), BOROJEVIC (1966) and SIDDIQUI et al. (1981) found negative shifts in the population mean due to mutagen treatments. KASSEM et al. (1976) found that EMS resulted in significant reduction in the mean of grain yield, kernels/spike and kernel weight of Sonora 64 and means of kernel weight of Giza 150.

Table 1. Mean values for different traits in M_1-generation and control.

No.	Treatment	Grain yield/plant	No. of spikes/plant	No. of kernels/spike	100-Kernel weight	Harvest Index
(1)	0.26% DS+30 min.	5.90	17.60	34.36	1.76	0.211
(2)	0.26% DS+ 1 h.	3.43	15.96	28.04	1.47	0.121
(3)	0.008% DS+24 h.	4.33	14.99	32.52	1.57	0.161
(4)	0.02% DS+24 h.	3.83	12.59	29.66	1.64	0.184
(5)	Control	3.85	15.90	31.64	1.53	0.164

M_2-generation:

a. Analysis of variance:

Mean squares of different traits studied in M_2 generation are presented in Table 2. The results showed that M_2 lines under M_1selected categories, i.e. types of SS, GH and levels of high (H), medium (M) and low (L) activated or induced by diethyl sulfate (DS) showed

Table 2. ANOVA and partition mean squares for different traits in M_2 generation.

S.V.	d.f.	Grain yield/plant	No. of spikes/plant	No. of kernels/spike	100-kernel weight	Harvest index
Replications	3	4.31	52.31**	86.89	0.11*	0.002
M_2-lines	7	37.88**	23.03**	185.54**	0.25**	0.024**
Selection types (ST)	1	14.15*	52.89**	158.73	0.01	0.002
Control vs. (SS)	1	49.39**	45.86**	206.05*	0.23**	0.012*
Control vs. (GH)	1	2.81	0.41	6.82	0.15*	0.004
Among (SS)	2	77.79**	6.29	457.44**	0.25**	0.061**
Among (GH)	2	21.31**	24.73*	6.15	0.42**	0.017**
Error	21	1.81	5.26	44.22	0.03	0.002

(SS):   Selection type of spike length and number of spikelets.
(GH):   Selection type of grain yield and harvest index.
(ST):   Selection types according to (SS) and (GH).
*,**:   Significant at 5% and 1% levels respectively.

highly significant differences for all traits studied. In general, it can be concluded that the higher frequencies of positive and negative mutants were found to be distributed in the early M_1 generation. NAYAR & NINAN (1978) came up to similar conclusion in rice. On the other hand selection types i.e. (SS) spike length and spikelets per spike; and (GH) grain yield and harvest index, revealed significant differences for grain yield and number of spikes per plant while the other traits were insignificant. It can be concluded that selection levels within each type was more pronounce than selection of types itself. These results are in agreement with those obtained among (SS) and (GH) levels, hence highly significant differences were obtained for all traits except the number of spikes/plant (among SS) and number of kernels/spike (among GH). It can be concluded from these results that the effect of mutagen (DS) under two M_2 types and selection levels within both types, in positive and negative directions, was highly significant. Consequently, disruptive selection successed in distinguishing various levels in each type.

Comparing the selected type (SS) with the control showed highly significant differences (1% level) for grain yield, number of spikes/plant; and significant differences (5% level) for the remaining traits. While the other type (GH) vs. the control showed insignificant differences for all traits except the 100-kernel weight.

b. Mean performance:

Data means and percent deviations of selected levels (H, M and L) from the control in the two mutant types (SS and GH) are given for different traits in Tables 3 and 4. The situation in mutant selected from DS mutagenic treatment is remarkable. The high level (H) of (SS) type showed a highly significant increase compared with the control for all traits studied. Regarding the grain yield and harvest index, both showed the highest improvement percent than the mother cultivar with values of 237.40 and 125.61%, respectively. This is mainly due to the presence of higher frequencies of positive mutants as a result of mutagenic effect. HUSSEIN & ABDALLA (1981) in field bean found that M_2 plants selected for high yield showed a higher response to selection. The results of non-

Table 3. Mean values for different traits in M_2 generation involving SS (spike length & spikelets/spike) and GH (grain yield & harvest index).

M_2 generation		Grain yield/plant	No. of spikes/plant	No. of kernels/spike	100-wernel weight	Harvest index
SS	(H)	12.99	21.19	51.91	2.08	0.370
	(M)	5.13	19.48	36.51	1.61	0.156
	(L)	5.59	18.75	31.36	1.71	0.166
	(C)	3.85	15.90	31.64	1.53	0.164
GH	(H)	8.29	19.15	34.05	2.13	0.283
	(M)	5.27	15.52	33.38	1.61	0.183
	(L)	3.76	14.39	31.64	1.53	0.159
	(C)	4.80	15.98	34.53	1.53	0.173
LSD 5%		1.98	3.37	9.78	0.25	0.067
1%		2.69	4.58	13.30	0.34	0.091

Table 4. Deviation percentages of selection levels (H, M and L) of the two selection types (SS, GH) against the control in M_2 generation.

M_2 generation	Grain yield/plant	No. of spikes/plant	No. of kerenels/spike	100-kernel weight	Harvest index
SS (H)	237.40**	33.27**	64.06**	35.94**	125.61**
(M)	34.61	22.52*	15.39	8.00	−4.88
(L)	45.19	17.92	−0.88	11.76	1.22
GH (H)	72.71**	19.84	−1.39	39.22**	63.58**
(M)	9.79	−2.88	−3.33	5.23	5.78
(L)	−21.67	−9.95	−8.37	0.00	−8.09

*: Significant at 0.05 level.
**: Significant at 0.01 level.

selected traits, i.e. number of spikes/plant, number of kernels/spike and 100-kernel weight, relatively showed some improvement, consequently. On this ground, it could be said that these increases may be attributed to genetic correlation or the micromutation effects in the positive direction. The remainder levels (M and L) of the same mutant type (SS) showed irregular deviations (positive or negative) concerning the parent variety. In general, these deviations were insignificant with regard to all traits except the number of spikes/plant in the medium level (M).

Regarding the (GH) mutant type i.e. grain yield and harvest index, the higher selected level (H) showed a highly significant marked increase over the control in the two traits. The percent productivity were 72.71 and 63.58% respectively. 100-kernel weight showed indirect increase than the control, with a highly significant value (39.22%), while the remaining traits i.e. number of spikes/plant and number of kernels/spike failed to shift the population means significantly. KASSEM et al. (1976) reported that both chemical and physical mutagens failed to shift the population means of grain yield and number of kernels/spike. On the other hand, the yield and yield component traits in the lowest level (L) of (GH) mutant type did not even reach the level of the mother cultivar. Whereas, three

out of five traits, in the medium level (M), showed insignificant increase over the control; the other two revealed a reduction.

However it could be concluded that the response of yield and yield components to mutagenic treatment was more pronounce in positive (H) than in negative (L) direction, since selection intensity for higher traits could be attributed to the micromutations. KRULL & BORLAUG (1970) found that grain yield was improved at various levels through intensive selection. SIDDIQUI et al. (1981) obtained three wheat mutants that gave higher mean yield compared to the mother cultivar and one mutant with the lowest yielding genotype. HUSSEIN & ABDALLA (1981) in field bean experiments found that some induced mutants increased seed yield of more than 40%.

Heritability:

Heritability percentages for the DS derived populations from both M_2 mutant types (SS and GH) are presented, for yield and yield component traits, in Table 5. The results showed that the values tended to be higher for the selected traits, i.e. grain yield (83.91%) and harvest index (78.79%). It can be concluded that the DS mutagen increased heritability values of both selected traits. KASSEM et al. (1976) found that heritability percentage for grain yield (82%) was much higher in EMS derived population of Sonora 64 wheat cultivar. This clearly suggests that the environment has a little influence, and the mutagen has induced a wider variability. Consequently, improvement through DS mutagenic treatment is possible in these particular traits because it generally causes point mutations rather than chromosomal aberrations (SHARMA & SEARS 1964, WASHINGTON & SEARS 1970). If the induced variability is due to point mutation, it should be heritable and useful in a hybridization program (KRULL & FREY 1961).

Contradictory, the number of spikes per plant, number of kernels per spike and 100-kernel weight showed decreases in heritability with values of 35.96, 49.96 and 52.98% respectively for these traits. These results matches with those reported by KASSEM et al. (1976) in number of kernels per spike (54 to 60%) and kernel weight (38 to 46%). These results clearly shows that these traits selection might not be profitable in early generations, because of the higher environmental effect.

Table 5. Heritability percentage in broad sense for the
traits studied in M_2 selected lines.

Traits	Heritability %
Grain yield/plant	83.91
No. of spikes/plant	35.96
No. of kernels/spikes	49.96
100-kernel weight	52.98
Harvest index	73.03

Correlation Coefficient:

Adequate knowledge of interrelationship between factors related to complex characters,

Table 6. Genotypic (upper) and phenotypic (lower) correlation coefficient values between different traits in selection lines of M_2 generation.

	No. of Spikes/Plant.	No. of Kernels/Spike	100-Kernel weight	Harvest Index
Grain yield/ plant	0.837** 0.788**	0.961** 0.895**	0.935** 0.877**	0.986** 0.954**
No. of spikes/ plant		0.822** 0.690**	0.859** 0.764**	0.624** 0.588*
No. of kernels/ spike			0.757** 0.607*	0.852** 0.784**
100-kernel weight				0.930** 0.815**

*,**: Significant at 0.05 and 0.01 levels, respectively.

such as grain yield, is essential for designing successful wheat breeding programs. Estimates of genotypic and phenotypic correlations between all possible combinations of five traits, i.e., grain yield per plant, number of spikes per plant, number of kernels per spike, 100-kernel weight and harvest index in M_2 populations are presented in Table 6.

In general, the genotypic and phenotypic correlation coefficient values matched closely in each case. Grain yield was significantly positive correlated with all traits. Apparently, it appeared that during selection for increasing grain yield in populations resulting after mutagenic treatment the other traits will increase directly at the same time. SIDDIGQUI et al. (1981) found that grain yield was positively correlated with the number of tillers per plant and number of grains per spike in mutants derived from C 591 and Nayab bread wheat. BHATT (1973) concluded that the direct effect of kernel weight on yield was quite high. Likewise, the other traits expressed strong positive correlations with each other. It could be said that the direct effect of selection on one trait in segregating populations from mutagenic treatment resulted in significant increases in other traits.

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Induced quantitative variation in wheat

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Experimental modification of genotype was unknown until the work of Muller (1927) and Stadler (1928). Since then extensive work on artificial production of mutations, through various mutagenic agents, has been carried out in various crop plants. Mike (1975) has given a list of crop cultivars bred through induced mutagenesis. The induced mutations have also rendered a significant contribution to the present day knowledge of genetic mechanism particularly in understanding the structure and function of genetic material. The primary aim of mutation breeding are to enlarge the mutation frequency and spectrum of mutations, increase the percentage of viable mutations and to gain some degree of control and precision over mutation process, ultimately leading to directed mutagenesis. This paper reports the preliminary results on the effect of gamma rays on different quantitative traits of wheat in M_1 and M_2 generations.

Materials and Method

Dry seeds of six well adapted varieties of wheat (*Triticum aestivum* L.) namely; C 306, S 308, WH 147, WH 157, K 227 and HD 2009 were irradiated with gamma rays (Cobalt 60 source) using 10, 20, 30 and 40 KR doses. Counted seeds from each dose (100) and control (50) were sown in randomised block design at the research farm of Regional Research Station, Bawal during 1979–80. The M_2 generation alongwith their controls were grown in family block design during 1980–81. The data were recorded from normal looking plants for plant height, tillers per plant, ear length, spikelets per ear and grain yield per plant in each dose and control in M_1 and M_2 generations.

Results and Discussion

Gaul (1964) described plant breeding as the controlled evolution. By mutations, plants can genetically be improved. However, future importance of mutation breeding depends on whether it succeeds in securing better control of the whole complicated process of "obtaining mutants" starting with mutation induction to selection. It is still a matter of debate whether radiation induced mutations of polygenes occur towards positive or negative direction. Gregory (1968) emphasized that mutants with very small phenotypic effects occur with high frequency and will have an equal chance of being positive or negative in their phenotypic effect. Oka *et al.* (1958) found no change in rice for plant height and heading date. Rowlings *et al.* (1958) reported increase in seed weight of soybean

after irradiation and no change in plant height and maturity. While GREGORY (1961) noticed that the yield of dry peanut pods decreased by irradiation. BROCK (1971) emphasized that the induced mutations are expected to increase the variance and shift the mean away from the direction of previous cycle.

In the present material, the mean values for different traits in treated material did not show any change/shift compared to their control values except in few cases in M_1 generation. On the other hand, the coefficients of variations were increased in treated populations compared to their controls in almost all the cases (Table 1). Also, there was increase in variance with the increase in radiation dose, however, the relationship between variance and dose was not linear.

The range for different traits has been given in Table 2. This table clearly supports the increase in variance, as the range was also enlarged in almost all the doses. Thus, by using mutagenic treatments, we can increase variability. However, ultimately the

Table 1. Coefficients of variation for different doses in M_1 and M_2 generations

Variety		Plant height		Tillers/plant		Ear length		Spikelets/ear		Grain yield/plant	
		M_1	M_2	M_1	M_2	M_1	M_2	M_1	M_2	M_1	M_2
C 306	Control	7.76	8.52	36.66	36.63	6.67	10.40	17.21	12.66	33.80	46.58
	10 KR	8.11	8.80	30.98	35.80	16.33	12.29	17.00	14.79	40.27	51.74
	20 KR	6.49	12.70	36.46	42.60	18.93	13.06	23.58	17.47	49.54	48.92
	30 KR	9.78	8.40	48.71	44.00	24.24	13.25	27.26	14.45	65.78	47.99
	40 KR	17.32	17.20	50.47	45.50	26.03	16.14	19.85	15.95	64.58	59.89
S 308	Control	7.29	8.24	23.18	32.62	17.19	11.38	13.91	10.69	33.09	47.87
	10 KR	7.15	7.40	29.38	34.30	19.06	13.05	15.99	13.31	45.50	54.70
	20 KR	10.01	16.23	33.01	37.29	20.41	15.27	15.92	14.71	45.60	58.79
	30 KR	10.54	12.40	31.18	43.79	21.56	18.57	16.57	15.67	54.05	62.84
	40 KR	12.22	9.50	35.23	43.74	19.09	21.59	19.57	15.34	47.13	52.86
WH 147	Control	6.52	6.87	25.38	29.88	17.48	12.87	16.78	14.75	31.30	41.71
	10 KR	6.34	8.61	28.60	40.14	18.06	16.38	16.64	14.98	34.54	54.05
	20 KR	7.78	11.96	37.25	39.03	18.57	20.36	16.53	17.59	41.17	57.65
	30 KR	7.63	13.85	47.67	49.32	17.25	17.58	18.81	18.16	50.42	68.17
	40 KR	9.46	10.75	49.33	42.09	16.35	20.69	18.04	19.20	42.62	60.60
WK 157	Control	8.43	6.13	33.69	35.98	12.28	9.92	14.84	12.91	46.09	48.81
	10 KR	9.97	8.00	35.14	48.18	16.63	12.62	17.17	14.51	48.91	50.23
	20 KR	8.47	6.65	39.99	39.03	16.76	17.27	17.05	14.06	63.18	54.74
	30 KR	8.68	6.93	43.94	37.22	18.81	13.35	19.03	16.13	65.07	79.60
	40 KR	10.59	6.82	37.77	37.15	18.04	13.47	19.47	18.94	69.53	60.30
K 227	Control	5.19	7.14	28.24	27.87	11.80	10.79	11.31	9.85	36.02	42.80
	10 KR	8.46	7.10	28.91	37.54	14.75	12.53	12.58	13.34	39.69	60.52
	20 KR	6.54	11.64	29.03	36.25	12.72	14.15	13.63	15.33	46.59	56.21
	30 KR	5.59	11.03	38.59	42.10	16.85	16.27	14.09	17.44	37.92	52.66
	40 KR	6.40	12.90	59.53	43.29	15.24	14.59	20.21	14.33	56.48	52.83
HD 2009	Control	10.97	9.00	30.04	32.14	13.73	11.22	15.08	14.58	46.71	39.20
	10 KR	13.27	9.30	35.96	37.37	16.30	12.88	18.61	15.97	47.54	56.24
	20 KR	10.75	12.25	32.02	43.80	18.25	15.30	19.08	19.18	55.32	45.41
	30 KR	11.48	10.25	44.99	53.69	14.36	12.96	17.80	24.73	40.72	54.37
	40 KR	8.98	11.73	45.77	45.11	13.49	12.14	22.76	20.82	52.88	62.24

Table 2. Range for different traits in M_1 and M_2 generations

Variety		Plant height (cm)		Tiller/plant		Ear length (cm)		Spikelets/ear		Grain yield/plant (g)	
		M_1	M_2	M_1	M_2	M_1	M_2	M_1	M_2	M_1	M_2
C 306	Control	70-91	80-130	4-10	4-20	6.0-11.0	5.0-12.5	11-21	13-21	4.5-26.0	5.0-28.0
	10 KR	70-92	85-133	3-12	3-18	5.0-11.0	6.0-12.5	11-23	13-22	3.5-19.0	4.0-31.0
	20 KR	65-84	64-135	3-16	4-25	5.0-10.0	5.0-13.0	9-23	11-22	1.0-10.5	6.0-36.0
	30 KR	56-88	80-145	2-11	3-32	6.0-12.0	6.5-14.5	9-25	13-23	0.5-14.5	2.0-34.0
	40 KR	35-94	73-125	1-10	3-31	6.0-12.0	5.0-12.5	9-23	11-21	0.5-13.5	2.0-46.0
S 308	Control	60-74	60-93	3-8	5-21	7.0-13.0	7.0-13.5	11-17	11-21	2.0-11.5	5.0-30.0
	10 KR	52-72	68-108	2-10	4-21	6.0-12.0	8.0-16.0	9-19	11-21	2.0-10.5	2.0-31.0
	20 KR	50-76	37-105	4-11	3-21	5.0-14.0	5.0-16.0	7-19	11-21	1.0-13.5	2.0-39.0
	30 KR	45-73	45-100	2-9	3-19	6.0-14.0	5.0-15.0	7-19	11-21	0.5-12.0	4.0-44.0
	40 KR	40-68	50-96	2-11	3-21	3.6-12.0	5.0-14.0	9-17	7-19	0.5-13.5	1.0-43.0
WH 147	Control	46-65	54-82	3-7	3-22	4.5-9.5	6.0-12.0	7-19	9-19	1.5-16.0	2.0-38.0
	10 KR	51-60	48-84	3-6	3-17	4.2-9.0	4.0-12.0	7-17	7-23	3.0-11.0	2.0-31.0
	20 KR	45-61	47-92	3-11	3-21	5.5-10.0	5.0-13.0	7-17	5-20	1.0-20.5	3.0-37.0
	30 KR	41-58	44-88	2-8	5-24	4.0-10.0	5.0-14.0	7-17	7-22	1.0-10.0	1.0-44.0
	40 KR	43-62	49-84	2-6	3-24	5.0-11.5	4.0-12.5	9-19	9-25	1.5-13.0	2.0-39.0
WH 157	Control	51-71	70-100	3-6	4-14	7.0-12.0	8.0-14.5	13-21	13-22	2.0-15.0	4.0-26.0
	10 KR	47-75	65-98	3-7	3-18	5.0-11.0	6.0-15.0	9-23	11-22	1.0-12.0	2.0-22.0
	20 KR	53-76	73-100	2-10	3-25	6.0-12.0	9.0-16.0	9-21	9-22	1.5-20.0	3.0-37.0
	30 KR	55-77	70-100	3-10	3-15	5.0-11.0	8.0-14.0	7-23	13-22	1.5-16.5	1.0-23.0
	40 KR	42-74	63-93	3-11	3-14	5.0-12.0	8.0-14.5	9-23	11-22	1.0-25.5	5.0-25.0
K 227	Control	54-72	61-89	2-12	3-15	7.0-12.0	6.0-14.5	15-25	9-22	2.0-10.5	4.0-30.0
	10 KR	49-71	65-98	2-7	3-15	4.0-13.0	8.0-14.5	13-23	11-22	2.0-12.5	3.0-34.0
	20 KR	56-76	59-102	2-10	4-14	7.0-13.0	5.0-14.5	15-23	11-23	2.0-13.5	2.5-30.0
	30 KR	55-71	55-97	2-9	3-19	4.5-13.0	6.5-14.0	11-23	13-22	2.5-9.5	2.0-27.0
	40 KR	55-74	60-96	1-14	4-19	5.0-14.0	7.0-15.0	11-25	11-23	0.5-11.5	2.0-47.0
HD 2009	Control	41-65	63-90	3-10	3-22	6.0-13.0	7.0-13.5	9-21	9-21	2.5-15.5	3.0-24.0
	10 KR	40-65	55-81	3-13	3-16	6.5-13.0	5.0-14.0	9-21	9-21	1.0-17.5	3.0-32.0
	20 KR	46-60	56-88	2-9	3-22	5.5-13.0	6.0-13.0	9-25	9-25	1.0-12.5	3.0-32.0
	30 KR	44-76	52-82	2-11	3-16	6.0-12.0	8.0-14.0	7-23	7-23	2.5-10.0	2.0-28.0
	40 KR	45-62	46-78	1-9	4-19	4.5-12.0	7.0-13.5	11-25	11-25	0.5-9.0	4.0-24.0

breeder will be interested in the variability which is in the desired direction.   For example, reduced plant height will be desirable to overcome lodging problem particularly in varieties like WH–147.   Similarly for other traits studied, the increase in mutation spectrum on positive side is desirable which is required for higher production.   This type of variability particularly in M_2 generation can be utilized for breeding better types.   We have isolated a number of plants having desirable traits from M_2 generation and will be tested for their purity in successive generations.   Dwarf mutants isolated during this study particularly in variety WH–147 deserve special mention since some of them simultaneously had other desirable traits also like more number of tillers, high grain yield etc.

Differential effectiveness of radiation dose and response of varieties in producing variability were observed in this study.   The average coefficients of variation for different varieties pooled over doses for different traits has been given in Table 3.   The results indicate that the maximum variance was observed for grain yield per plant followed by tillers per plant both in M_1 and M_2 generations.   Though, there were differences in variatal response with regard to different traits, however, on overall basis variety WH–147 appeared to be the most radiosensitive followed by S 308 and HD 2009.

Similarly, the coefficients of variation were pooled over varieties for different doses of different traits (Table 4).   Here also, there were differences for different traits like the maximum variation for tillers, spikelets and grain yield was observed in 30 KR while 20 KR gave maximum variation for plant height.   From overall picture, we can conclude that the maximum variability was generated in 30 KR treatment.   In 40 KR, either it was constant or reduced.   Further, it can be confirmed that there was increase in variation with the increase in dose, however, the increase in variance did not have linear relationship with the increase in dose.

Table 3.   Coefficients of variation for different varieties (pooled over doses)

Variety	Plant height		Tillers/plant		Ear length		Spikelets/ear		Grain yield/plant	
	M_1	M_2	M_1	M_2	M_1	M_2	M_1	M_2	M_1	M_2
C 306	10.425 (34.34)	11.775 (38.85)	41.640 (13.58)	41.975 (14.58)	21.380 (28.25)	13.685 (31.55)	21.923 (27.39)	15.665 (23.74)	55.043 (6.36)	52.135 (11.933)
S 308	9.980 (36.90)	11.383 (38.81)	32.200 (38.91)	39.780 (21.95)	20.030 (16.52)	17.120 (50.44)	17.013 (22.23)	14.758 (38.12)	48.060 (33.17)	58.630 (22.48)
WH 147	7.803 (19.68)	11.293 (64.50)	40.700 (60.36)	42.645 (42.72)	17.533 (0.30)	18.753 (45.77)	17.505 (7.53)	17.483 (18.53)	42.190 (34.79)	60.120 (44.14)
WH 157	9.428 (11.84)	7.100 (15.77)	42.340 (25.67)	40.400 (12.27)	17.560 (42.99)	14.408 (45.24)	18.180 (22.51)	15.910 (23.24)	61.650 (33.76)	61.220 (25.44)
K 227	6.748 (30.02)	10.818 (51.15)	39.015 (38.16)	39.795 (42.81)	14.890 (26.18)	14.385 (33.38)	15.128 (33.76)	15.110 (53.40)	45.170 (25.40)	55.560 (29.82)
HD 2009	11.120 (1.37)	10.883 (20.92)	39.680 (32.11)	44.993 (40.12)	15.600 (13.62)	13.320 (18.72)	19.563 (29.73)	20.180 (38.41)	49.120 (5.15)	54.570 (39.05)

Values given in parenthesis are percent increase over their control C.V.

Table 4. Coefficient of variation for different doses (pooled for all varieties)

Dose	Plant height		Tillers/plant		Ear/length		Spikelets/ear		Grain yield/plant	
	M_1	M_2	M_1	M_2	M_1	M_2	M_1	M_2	M_1	M_2
Control	7.693	7.650	29.530	32.524	14.858	11.100	14.272	12.739	37.840	44.500
10 KR	8.872 (15.32)	8.300 (8.50)	31.490 (6.63)	38.888 (19.57)	16.855 (13.44)	13.290 (19.73)	16.332 (14.44)	14.483 (13.69)	42.740 (12.95)	54.580 (22.65)
20 KR	8.340 (8.41)	11.905 (55.62)	34.627 (17.26)	39.667 (21.96)	17.600 (19.00)	15.902 (43.26)	17.632 (23.54)	16.390 (28.66)	50.233 (32.75)	53.620 (20.49)
30 KR	8.950 (16.34)	10.477 (36.95)	42.510 (43.96)	45.033 (38.46)	18.845 (26.83)	15.330 (38.11)	18.927 (32.62)	17.763 (39.44)	52.327 (38.28)	60.888 (36.83)
40 KR	10.828 (40.75)	11.480 (50.07)	46.350 (56.96)	42.810 (31.63)	18.023 (21.30)	16.437 (48.08)	19.983 (40.01)	17.430 (36.82)	53.870 (42.36)	58.120 (30.61)

Values given in parenthesis are percent increase over the control.

It would, therefore, appear that gamma irradiation particularly 30 and 40 KR doses have induced significant amount of variability particularly in M_2 generations compared to their controls, confirming the results of earlier workers (OKA *et al.* 1958, BHATIA & SWAMINATHAN 1962, CLAYTON 1964). The release of variability has been interpreted as due to increased recombinations (LAWRENCE 1961). However, it can not be decided from the present study whether the entire variability is due to release of hidden variability or due to mutations or both. Whatever may be the nature of induced variability, it should be possible to exploit it for the production of better genotypes.

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Improved grain mutant in the wheat, variety Arjun (HD 2009)

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Experimental evidence has shown that induced mutagenesis technique is a very useful component of plant breeding methodology particularly when the objective of the exercise is limited and well defined and the character aimed to be improved or rectified is under simple genetic control. In this latter category are seed characteristics of cereals like grain colour, boldness and lusture. In this communication we report the development of a mutant line in the wheat variety, Arjun. Arjun is an improved, high yielding wheat variety officially released in 1973. The variety is characterized by a very high yield potential, wide adaptability and high degree of resistance to the fungal rust diseases. A short-coming in this variety is the tendency of its grain to mottle, some times heavily. This defect of grain mottling renders the grains of the variety to pricing disadvantage in the market.

With the objective of removing the defect of grain mottling, we mutagenized seeds of Arjun with 0.02% Nitrosomethyl urea. In a population of about 30,000 plants in M_2, vigorous selection was exercised for non-mottled grains. The plants with non-mottled grains produce improved average kernal weight, compared to the parental variety, Arjun. Fig. 1 shows comparison of the grains of the mutant culture and Arjun. The progenies of three mutant plants isolated in M_2 were observed to segregate for the grain mottling

Fig. 1. Seeds of the wheat variety Arjun. Control (left) and induced mutant (right).

characteristic for a few generations. Selection for grain non-mottled was therefore exercised over successive generations till three lines viz., M 354, M 360, and M 361, each derived from different M_2 plants, were found fixed for non-mottled and improved grain weight. Care was taken that the selected grain mutants were phenotypically not distinguishable from the parent variety and had maintained their rust resistance so as not to unfavourably influence the varietal acceptability.

The mutants were tested extensively for their yielding ability in comparison with both the parental variety and subsequently released varieties bred specifically for yield through conventional recombination breeding during the crop years 1977–78 and 1978–79 on experimental plots and on farmer's fields. Tables 1, 2 and 3 summarize data from these trials. It is seen that the mutant (M 354) compares well not only with the parent, HD 2009 but also with the three best checks (Table 1) in trials on farmer's fields in four Delhi villages. Similarly, the mutant M 360 has given yield performance comparable to HD 2009 and the recommended local check HD 2122 at eight locations in two Delhi villages (Table 2). Table 3 compares the yield of mutant cultures M 360 and M 361 at the Indian Agricultural Research Institute, New Delhi and at the Agricultural University's farm at Pantnagar in the state of Uttar Pradesh. The yield tests over locations and over years have convinced

Table 1. Yield performance of HD 2009 mutant relative to that of the parental line and other high yielding checks in Minikit trials at Delhi villages (1977–78)

Variety	Yield (g/ha)				
	Ghoga		Sanoth	Holumbi	Bowana
	Location				
	I	II			
HD 2122	47.5	49.6	49.8	49.8	—
HD 2177	50.6	52.5	—	44.6	—
HD 2204	51.0	—	53.6	51.3	—
Mutant M 354	50.5	54.2	56.8	52.0	60.0
Arjun	49.0	53.0	55.9	50.6	55.0

Table 2. Yield performance of HD 2009 mutant relative to that of the parental variety and HD 2122 (the best check) in Minikit trials at Delhi villages (1978–79)

Variety	Village Pochanpur					Village Bhartal			Average of 8 demonstrations
	Yield (g/ha) at locations					Yield (g/ha) at Locations			
	1	2	3	4	5	1	2	3	
Mutant M 360	52.5	49.0	49.5	53.5	55.0	51.0	51.5	54.0	52.00
HD 2122	55.0	48.5	48.0	49.0	50.5	55.0	56.0	—	51.70
Arjun (HD 2009)								49.5	49.50

Table 3. Performance of HD 2009 mutant lines in comparison to the parental line (1978-79)

Variety	Yield (g/ha)		Rust reactions in rust test plot (Delhi)		
	Delhi	Pantnagar	Black	Brown	Yellow
Mutant M 361	43.65	44.22	F	TR	F
Mutant M 360	—	47.08	F	TR	F
HD 2009	42.30	45.83	F	TR	F
C.D. at 5%	8.69	9.43			

us that the better grain mutant cultures have retained the yield adoptability and rust resistant characteristics of the parental variety.

Wheat mutants with acceptable grain colour have been previously reported from the mutation programme at the Indian Agricultural Research Institute (VERGHESE & SWAMINATHAN 1966, SAWHNEY et al. 1971, 1977). The present communication establishes that other grain characteristics like uniform grain development are equally amenable to the induced mutation technique. Our results also suggest that yield loss is not an inescapable consequence of improvement achieved through mutagenesis. That is particularly so in situations where intensive breeding efforts have elevated the yield levels of varieties to a plateau.

We are grateful to Dr. H.K. JAIN, Director, IARI, for his interest and advice and Shri M.D. NANDKEOLYAR, Shri Braham SINGH and staff of the extension unit in the Division of Genetics for their help in organizing trials in Delhi villages.

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Biometrical association of yield and yield components in durum and bread wheat

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Grain yield is a complex phenomenon, resulting from various contributory characters, highly influenced by environmental fluctuations. However, yield could easily be estimated on the basis of the performance of yield components and other closely associated characters of the plants (LARIK et al. 1980). Correlation coefficient has been used to identify the grain yield components (LARIK 1978) but the technique of path coefficient analysis (DEWEY & LU 1959 JAIN et al. 1975, LARIK 1979) has been found more useful as it differenciates specific forces acting directly and indirectly to produce a particular association which can be successfully employed in formulating efficient selection programme for synthesis of new wheat ideotypes with improved yield and yield components.

Materials and Methods

Two durum (66T12, Red 5132) and three hexaploid wheat cultivars (Tosun 22, 66T 1435, Bezosteya 1) were grown during the year 1978–79 in a randomized block design with four replications at the Agronomic Research Area of the Faculty of Agriculture, University of Ankara, Turkey. Homogeneous seeds of these cultivars were drilled in rows each 300 cm long with 30 cm interrow distance. Observations were recorded on plants in one meter row length selected randomly. Following characters were measured: X_1=plants/m², X_2=spikes/m², X_3=seeds/m², X_4=days to heading, X_5=harvest index, Y=yield/m² (dependent character). Correlations and path coefficients were calculated by the technique out lined by DEWEY & LU (1959) in which the end product:

$$Y = \sum_{i}^{N} P_i X_i$$

Components of correlation $r_{x_i y} = P_i + \sum_{i=j}^{N} p_j \, r_{ij}$ which indicate direct as well as indirect effects of one variable through another one on the end product. Multiple correlations and partial regressions were calculated by using the formulae suggested by STEEL & TORRIE (1960).

Results and Discussion

Simple Correlation Coefficient:

The estimates of phenotypic correlation coefficients (Table 1) reveal that plant productivity was most strictly affected by seeds/m² and harvest index followed by spikes/m². These characters ie. X_3, X_5 and X_2 participated in the variability of yield/m² from 78 to 89%. This component ranking agrees well with the results reported by LARIK (1979) and SMOCEK (1977). On the contrary association of yield/m² with days to heading was negative (–.7614). Negative significant association between yield/m² and days to heading is desirable one, which suggests that early maturing genotypes with higher yield potential may be obtained in the present material. SANDHA et al. (1980) also observed similar association between days to heading and grain yield. Plants/m² though have contributed to yield/m² but its contribution is of second order.

Path Coefficient Analysis:

Path coefficient analysis of different attributes (Table 1) revealed that harvest index exerted maximum positive direct effect (70.56%) on yield/m² followed by spikes/m² (48.33%). On the contrary plants/m² had the maximum negative influence on yield/m². However, the major effect of plants/m² on yield/m² was through the path of spikes/m² and harvest index. The negative effect of plants/m² on yield/m² may be attributed to interplant competition for nutrients, water, light and limited supply of photosynthates to all the developing sinks created with increased tillers/m². With the increasing number of tillers/m² ear potential decreased which consequently affect yield/m². However, the issue needs further probing before such a relationship could be established.

The direct effect of spikes/m² is 48.33% however, its effect via seeds/m² and harvest index was substantial. The effect of spikes/m² on yield/m² is diminished because of its negative effects through plants/m² and days to heading. The direct effect of seeds/m² on yield/m² is 14.71%, the major effects were through harvest index (53.62%) and spikes/m² (36.14%) whereas its effect via plants/m² and days to heading is negative. The direct effect of days to heading on yield/m² is very low (0.30%) but its major effects were through spikes/m² (–45.20%) and harvest index (–43.68%). Thus it appeared that the most desirable traits for improving yield are harvest index and spikes/m² followed by seeds/m². Some attention therefore must be devoted on plants/m² to improve yielding ability of wheat cultivars under study.

Multiple Correlation and Partial Regression Coefficient:

The cummulative effect of different quantitative traits measured on unit area basis (m² basis) on m² yield has been investigated taking yield/m² as dependent variable and other metrical traits as independent variables. Multiple correlation coefficient between yield/m² and these characters was 0.956 (Table 1). This means that 95% variation in yield/m² can be attributed to these characters. The significance of partial regression coefficients were

Table 1. Estimates of multiple correlation, partial regression and path-coefficient analyses between yield/m² and different quantitative traits in durum and bread wheat.

Characters correlated	Mean	Standard deviation	Phenotypic correlation	Path coefficients					Partial regression	F-value
				X_1	X_2	X_3	X_4	X_5		
X_1 Plants/m²	262.0496	211.1508	0.7280**	-.0573 (-7.87%)	.2313 (31.77%)	.0866 (11.90%)	-.0011 (-.15%)	.4685 (64.35%)	-.0173±.0155	-730.36***
X_2 Spikes/m²	585.2904	209.7776	0.7834**	-.0350 (-4.46%)	.3786 (48.33%)	.1115 (14.23%)	-.0021 (-.27%)	.3304 (42.17%)	.1151±.0253	252.19***
X_3 Seeds/m²	15518.4240	4232.9514	0.8909***	-.0378 (-4.25%)	.3220 (36.14%)	.1311 (14.71%)	-.0020 (-.23%)	.4777 (53.62%)	.0020±.0012	159.59***
X_4 Days to heading	26.7600	2.3440	-0.7614**	.0265 (3.48%)	-.3442 (-45.2%)	-.1134 (-14.9%)	.0023 (.30%)	-.3326 (-43.68%)	.0600±2.248	0.89 ns
X_5 Harvest index	28.0560	2.8805	0.8779***	-.0433 (-4.93%)	.2020 (23.0%)	.1011 (11.51%)	-.0012 (-.14%)	.6194 (70.56%)	13.73±1.274	116.05***
Y Yield/m² (dependent variable)	424.0648	63.8360	—	—	—	—	—	—	—	—

Point of intersection on Y axis=-56.1229
Multiple correlation coefficient =0.9558
Estimated Standard Error   =19.1486

$$Y=-56.1229-0.0173X_1+0.1151X_2+0.0020X_3+0.9600X_4+13.7228X_5$$

D.F=119
**=Significant at 1% level of probability
***=F-value at 0.1%=5.78
n.s=Non significant

tested through F-value which revealed that the contribution of plants/m² was significantly negative and days to heading was not significant, while the other three parameters (spikes/m², seeds/m² and harvest index) contributed significantly towards yield/m². This trend is also confirmed by path-coefficient analysis in which plants/m² have shown highest direct negative effect on yield/m² (Table 1). These results are in good agreement with the results obtained by SINGH et al. (1979) in *Triticum aestivum* L.

From the path-coefficient and partial regression analyses carried out in the present study, it may be inferred that yield/m² depends primarily on harvest index and spikes/m² followed by seeds/m² rather than on plants/m².

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Screening and utilization of wild-wheat germplasm
for rust resistance

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Wild wheats are distributed very widely in the Mideast from the Balkan Peninsula to Transcaucasia and in both arcs of the Fertile Crescent to the Persian Gulf on the east and the Dead Sea on the west (JOHNSON & DHALIWAL 1976). *Triticum boeoticum* extends from Transcaucasia to Greece across Anatolia. *T. urartu* is distributed in Transcaucasia, eastern Anatolia and the entire fertile crescent including Syrio-Palestinian area. *T. dicoccoides* is endemic to the western arc of the Fertile Crescent but is also distributed sporadically in Iran, Iraq and south eastern Anatolia whereas *T. araraticum* is restricted to eastern arc of the Fertile Crescent. Due to their wide adaptation to diverse eco-geographic regions wild wheats are expected to vary genetically with respect to cold and drought tolerance, resistant to insect-pests and diseases and in seed protein content and quality (JOHNSON & WAINES 1977).

Our cultivated wheats, bread wheat (*Triticum aesitivum* L. em Thell, 2n=42) and durum wheat (*T. durum* Desf. 2n=28) combine the genetic complement of three and two diploid species, respectively. The cultivated emmer tetraploid *Triticum durum* was domesticated from its wild progenitor *T. dicoccoides* Körn Schweinf, which evolved from an amphiploid involving two diploid wheat species, *T. boeoticum* Boiss and *T. urartu* Tum. (JOHNSON & DHALIWAL 1978). Another wild tetraploid wheat *T. araraticum* Jakubz. ancestral to the cultivated *timopheevii* tetraploid wheats was also derived from the same parentage as that of *T. dicoccoides*. Bread wheat originated from chromosome doubling in a hybrid between the cultivated emmer tetraploid and the wild diploid Goat grass, *Aegilops squarrosa* L. (McFADDEN & SEARS 1946). At each step of hybridization and chromosome doubling only one or a few accessions of the diploids or tetraploid were involved and the resultant polyploid got reproductively isolated immediately from its parent species as a result of which the tetraploids and hexaploid wheats received only a minor fraction of the gene pool existing in their wild and primitive germplasm. It is, therefore, very important to screen the wild germ for its usefulness in the improvement and enrichment of cultivated germplasm.

The importance of the wild and cultivated germplasm in the improvement and sustained production of our crop plants and the need to preserve and conserve it has been

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universally recognized. Several institutes throughout the world are engaged in the collection maintenance, screening and utilization of germplasm of wheat. The University of California at Riverside is maintaining a comprehensive collection of Wild wheats and *Aegilops* spp. and primitive wheats. JOHNSON & WAINES (1977) have reported screening of wild wheats for protein content, essential amino acids, lysine and threonine, resistance to a nematode (*Pratylenchus thornei*) and "take all" disease of wheat.

A representative sample (Table 1) of the wild and primitive wheat collection at the University of California at Riverside was obtained through the kind courtesy of Dr. B.L. JOHNSON. The accessions were grown at Gurdaspur in *Rabi* 1980–81 for screening against yellow and brown rusts. The plot consisted of single one metre row. A row of infector line containing a mixture of Agra Local and Kalayansona varieties was provided all around the field.

A majority of the collections were found to be very poorly adapted probably because of their higher vernalization and longer photoperiod requirements. None of the *T. urartu* lines flowered at Gurdaspur. Most of the *T. boeoticum*, *T. monococcum* and *T. araraticum* collections flowered very late in the season in the middle of April. There was either a very poor seed set or the grains shrivelled in the early stages of development. All *T. dicoccoides* and a few *T. araraticum* and *T. monococcum* collections flowered timely. Artificial vernalization at 4°C for 6–8 weeks and longer photoperiod (12–16 h) might help the wild wheats to flower timely for good seed set and for crossing them with spring and durum wheats.

Well spread rains and suitable temperature in the season at Gurdaspur favoured maximum development of yellow and brown rusts of wheat. The rust data was recorded at the time of maximum appearance of each rust. The accessions with immune to traces of rust reactions were designated as resistant (R) while with reactions from traces to 100S were

Table 1. Incidence of yellow rust (*Puccinia striiformis*) in different species of wild and primitive wheats

Species	Rust reaction and no. of accessions form country of origin/collection																					Total
	Turkey			Iraq			Iran			Lebanon			Israel			USSR			others*			
	R	S	X	R	S	X	R	S	X	R	S	X	R	S	X	R	S	X	R	S	X	
T. boeoticum	12	2	-	13	-	3	6	-	-	-	-	-	-	-	-	1	-	-	4	-	-	42
T. urartu	1	-	2	-	-	-	-	-	-	14	4	3	-	-	-	-	-	-	-	-	-	24
T. monococcum	15	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	1	27	4	-	48
T. araraticum	2	-	-	62	1	3	2	1	-	-	-	-	-	-	-	3	1	-	-	-	-	75
T. dicoccoides	-	36	-	-	2	-	-	1	-	4	2	1	5	14	-	-	-	-	4	4	-	72
T. timopheevi																1	-	-	-	-	-	1
T. zhukovskyi																1	-	-	-	-	-	1
T. aestivum							-	1	-										1	1	-	3
Country Total	71			84			11			27			19			9			45			266

* U.S.A., Sweden, Hungary, Greece, Romania, Germany, Syria. X; lines died.

marked as susceptible (S). Stem or black rust appeared only in traces, and hence the data was not recorded.

Yellow rust

A majority of the accessions of wild diploid wheats *T. boeoticum* from Turkey, Iraq and Iran were resistant to yellow rust (Table 1). Out of 18 accessions of *T. urartu* from Lebanon 14 were resistant. Cultivated diploid wheat, *T. monococcum* from Turkey, USSR and various other countries showed excellent resistance. Accessions of wild tetraploid wheat *T. araraticum* from Iraq were also free from yellow rust. *T. dicoccoides* from Turkey, Iraq and Israel were highly susceptible and succumbed to yellow rust before the boot stage. Only a few accessions of *T. dicoccoides* from Lebanon and Israel were found to be resistant. The only accessions of *T. timopheevi* and *T. zhukovskyi* were free from rust.

Brown rust

Only a few accessions of *T. boeoticum* from Turkey, Iraq and Iran were susceptible to grown rust while others were resistant (Table 2). Among *T. urartu* collections from Lebanon, about 50% were resistant to brown rust. Again *T. monococcum* lines from Turkey and other countries were immune to brown rust. *Triticum araraticum* collections were both resistant and susceptible. Out of 72 collections of *T. dicoccoides* from Turkey, Iraq, Iran, Lebanon, Israel and other countries, 66 were susceptible while only two were resistant. *T. timopheevii* and *T. Zhukovskyi* were again resistant. Primitive wheats accessions of G 524 and G 1569 (*T. aestivum* spp. *spetla*) and G 532 (*T. aestivum* spp. *macha.*) were also susceptible to brown rust.

Table 2. Incidence of brown rust (*Puccinia recondita*) in different species of wild and primitive wheats

Species	Rust reaction and no. of accessions from country of origin/collection																					Total
	Turkey			Iraq			Iran			Lebanon			Israel			USSR			Others*			
	R	S	X	R	S	X	R	S	X	R	S	X	R	S	X	R	S	X	R	S	X	
T. boeoticum	12	3	–	9	4	3	4	2	–	–	–	–	–	–	–	–	1	–	4	–	–	42
T. urartu	–	1	2	–	–	–	–	–	–	10	8	3	–	–	–	–	–	–	–	–	–	24
T. monococcum	15	–	–	–	–	–	–	–	–	–	–	–	–	–	–	1	–	1	31	–	–	48
T. araraticum	1	1	–	35	28	3	–	3	–	–	–	–	–	–	–	1	3	–	–	–	–	75
T. dicoccoides	–	36	–	–	2	–	–	1	–	–	6	–	–	19	–	–	–	–	2	6	–	72
T. timopheevi																1	–	–	–	–	–	1
T. zhukovskyi																1	–	–	–	–	–	1
T. aestivum							–	1	–							–	–	–	–	2	–	3
Country total	71			84			11			27			19			9			45			266

* U.S.A., Sweden, Hungary, Greece, Romania, Germany and Syria. X; lines died.

Leaf Pubescence

It is generally believed that leaf pubescence provides protection to the plants against insect-pest attack but its role in protection against rusts is not reported anywhere.

Collections of *T. boeoticum, T. araraticum*, and *T. dicoccoides* had pubescent as well as glabrous leaves and leaf sheaths while *T. monococcum* and *T. urartu* had only glabrous leaves and sheaths. Accessions with and without pubescence were equally susceptible to both rusts indicating that pubescence afforded little or no protection against rusts.

Transfer of rust resistance

Excellent resistance to yellow and brown rusts exhibited by all. *T. monococcum* and some lines of *T. boeoticum, T. urartu* and *T. araraticum* can be transferred to both bread and durum wheats through interspecific crosses. The resistance can be readily transferred to the A genome as the chromosomes of *T. monococcum, T. boeoticum* and *T. urartu* are capable of perfect pairing with those of the A genome of wheat but not with the B or D genomes (Chapman *et al.* 1976). The chromosomes of the B and D genomes can also be induced to pair with those of the diploid wheats in the absence of chromosome 5B of bread and durum wheats or in the presence of the ph mutant (SEARS, 1976). The information on genetic control of rust resistance in the wild diploid and tetraploid wheats whether dominant or recessive is, however, a prerequisite before initiating a programme for the transfer of resistance. If the resistance is dominant its transfer in the A genome only should serve the purpose. But if it is recessive it will have to be transferred in all the genomes of wheat and durum for its full expression for practical utilization. It will be necessary to culture the young embryos for crossing the bread wheat with the diploid wheats successfully. *T. monococcum* and *T. boeoticum* are readily crossable with durum in either direction but *T. urartu* can be crossed only as the male parent (JOHNSON & DHALIWAL, 1976). *Aegilops squarrosa* and other *Aegilops* spp. of *Sitopsis* section such as *Aegilops spelotides, Aegilops bicornis* and *Aegilops longissima* etc. should also be screened for resistance to rusts as it would not be difficult to transfer the resistance from the *Aegilops* spp. into wheat and durum.

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Gene action effects in wheat under different soil fertility levels

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Grain yield and most of the yield components are complex characters and are polygenic (BHATT 1973, SINGH 1978, RAO 1977), and manifestation of these characters is greatly determined by interaction of genotype and the environment complex in which these develop (ANTOUN 1977, KUMAR 1979). As such, various studies on the nature of gene action have invariably reported a preponderance of additive effects for yield and the components of yield, although non-additive effects were also important in several cases (BHULLAR et al. 1979, ALI & EL-HADDAD 1978, JAIN & SINGH 1976). ALLARD (1956) and TSIL'KE et al. (1979) emphasised the usefulness of diallel crosses for investigating the effect of environment on the component of genetic variation. These components were shown as environments, dominance, array, environment × dominance, environment × array, and dominance × array and that significance of first five parameters was of great use in such studies. Furthermore the technique provides information right in early generation on the genetic mechanism controlling the phenotypic expression of plant characters.

The present studies, therefore elucidates information on the gene action mechanism controlling the differential response of various wheat varieties to higher doses of Nitrogen application

Materials and Methods

A 4×4 diallel cross on wheat under two nitrogen fertilizer levels, 90 lbs. and 180 lbs. N per acre was conducted in the department of Plant Breeding and Genetics, Agricultural University Faisalabad.

The data for F_1 and F_2 and parents was recorded on the following characters.
KERNELS PER SPIKE: Kernels per spike were determined by actual counting of the seeds per spike.
100 KERNEL WEIGHT: 100- Kernel weight in grams was measured with Mettler's balance upto two dicimal places from three 100- grain samples at random from the bulk produce of each plot.
GRAIN YIELD: Grain yield per plant in grams was estimated by dividing the total weight of grains from each plot by the number of harvested plants in the plot.

The analysis of gene action for the diallel crossing system was done using the

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technique developed by HAYMAN (1954) and JINKS (1954, 1955, 1956) and used by WHITEHOUSE *et al.* (1958) for genetic analysis.

Results and Discussion

As for kernels per spike, in low nitrogen level in F_1., (Fig. 1a) indicated the full dominance type of gene action, as the regression line passes the Wr/axis through the origin. As the line deviates significantly from a unit slope it signifies some kind of gene interaction. The position of array points on the line suggested that LU75 carried most of the dominant genes while Ch70 being away from the origin had most of the recessinve alleles. For F_2, (Fig. 1b) shows additive gene action with partial dominance. The b value (0.5519±0.3213) reveals interallelic gene interaction. C273 lying nearest to the origin possessed most dominant genes, while reverse was true for Mexipak 65.

As for higher nitrogen dose, in F_1 (Fig. 1c) and for F_2 (Fig. 1d), the regression line cuts the Wr/axis above the origin, indicating additive gene action with partial dominance. Mexipak 65, being nearest to the origin possessed maximum dominant genes while Chenab 70 farthest away from the origin had most of the recessive alleles, and in F_2, LU75 possessed
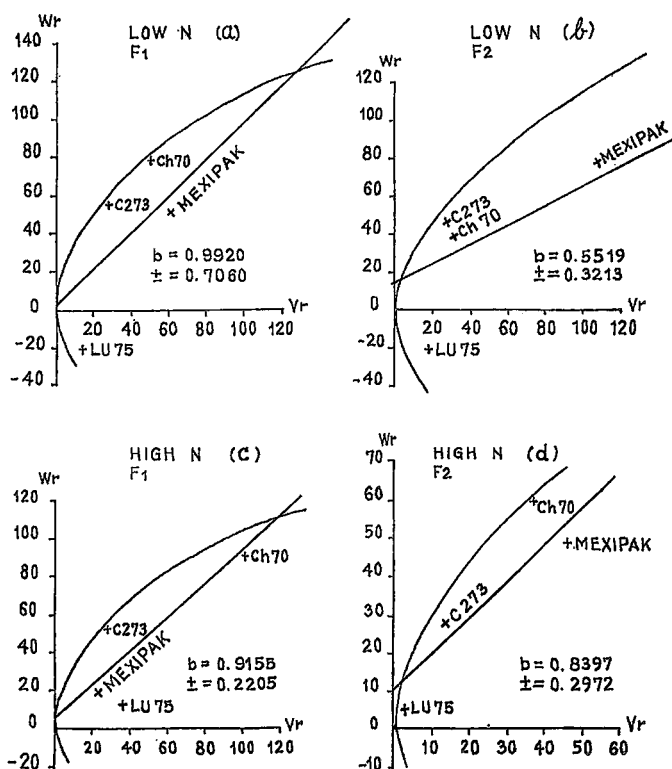
Fig. 1. Number of kernels per spike
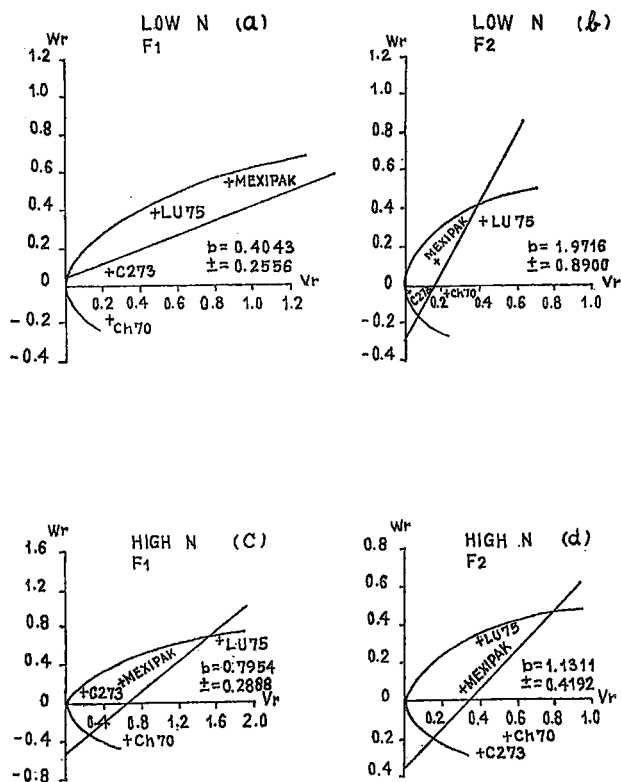
Fig. 2. 100-kernel weight

most dominant genes while Mexipak 65 was shown to have most recessive alleles. Kronstad & Foote (1964), Brown *et al.* (1966), Gyawali *et al.* (1968), made observation about the relative importance of additive effects for kernels per spike and other wheat characters.

As for 100-kernel weight in F_1, under low nitrogen, additive type of gene action coupled with partial dominance was evident from Fig. 2a, Array point position on regression line suggested that Chenab 70 possessed most dominant genes while reverse was true of Mexipak 65 which had most of the recessive alleles. For F_2 (Fig. 2b) overdominance type of gene action with epistatic gene interaction was indicated. C273 carried most dominant genes while LU75 had maximum recessive alleles.

As it is seen from Fig. 2c and 2d, under high nitrogen, the regression line cuts the Wr/ axis below the origin revealing overdominance with interallelic interaction in F_1 and F_2. Array point position showed that C273 and Mexipak 65 possessed, most dominant genes respectively and LU75 had preponderance of the recessive alleles. Similar results have been presented by Jhonson & Aksel (1964), Hsu & Walton (1970), and Walton (1971a) they found major part of the variability for yield and 100-kernel weight due to overdominance and some degree of additive genetic effects.
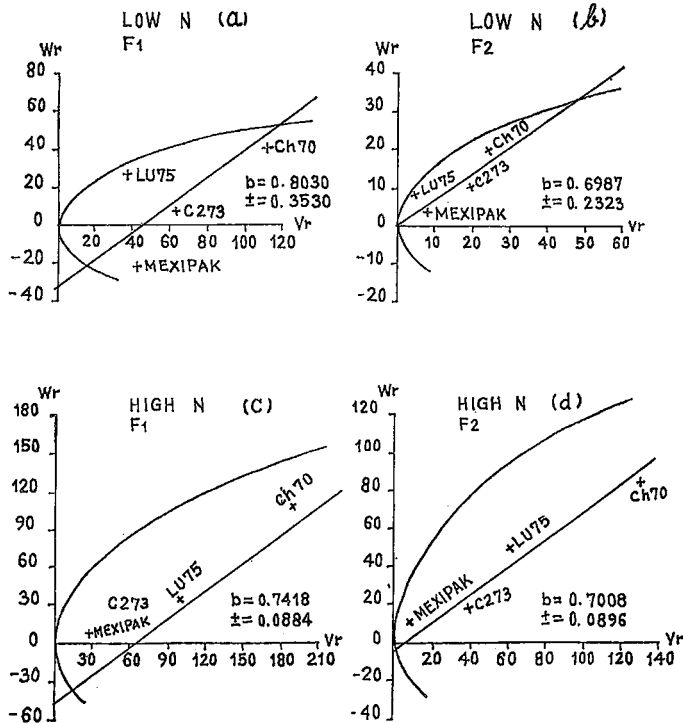
Fig. 3. Grain yield per plant

A reference to (Fig. 3a and 3b) for F_1 and F_2 under low nitrogen shows overdominance with interallelic interaction and complete dominance type of gene action respectively. The position of array points on the regression line showed that Mexipak 65 was nearest to the origin and thus contained most of the dominant genes while most recessive alleles were present in Chenab 70.

Figures 3c and 3d revealed that the regression line intercepted the Wr/axis below the origin, indicating overdominance. Mexipak 65 possessed most dominant genes while Chenab70 had most recessive alleles.

A perusal of foregoing findings would indicate the presence of overdominance in F_1 and complete dominance in F_2 suggesting that non-additive gene effects played a significant role in the expression of grain yield. Identical results have been reported by several workers including for example, WHITEHOUSE et al. (1958) who attributed a large part of the total genetic variability for yield and its components to overdominance with significant environmental influence.

To conclude, it may be stated on the basis of the various parameters discussed heretofore that the gene action changed with a change in the environment, suggesting environment × genotype interaction. Although the present inferences drawn from the

space planted data might have considerable relavance to solid plantings, caution must be exercised in relating results to generalised situation.

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II. Editorial Remarks

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Acknowledgement

Explanation of the Figure on the Cover

Flow diagram for simulation of univalent elimination and distribution in meiosis
II of the female gametogenesis in the pentaploid wheat hybrid. See the article
by TSUJI & NAGASAWA on page 2 for the details.