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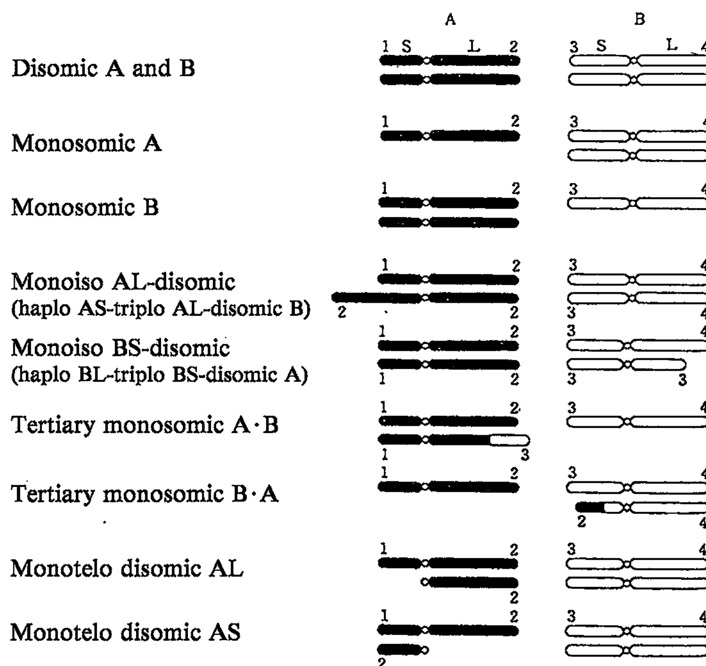

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WHEAT INFORMATION SERVICE

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Review

A guide to the wheat aneuploids

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Thanks to the late Dr. E. R. Sears, the various aneuploid series have been available in common wheat, which are indispensable for cytogenetic studies. To avoid confusion, Sears (1975) defined aneuploids as "individuals with a changed number of chromosomes, chromosome arms, or centromeres, or with arms so arranged that normal pairing and disjunction can not occur at meiosis".

1. Types of aneuploids

Monosomics and trisomics were primarily isolated in offspring of haploid Chinese Spring wheat, from which nullisomics and tetrasomics were subsequently derived, respectively. General description and breeding behavior of these complete series of aneuploids and some other aberrations were summarized by Sears (1954). By means of several backcrosses of a certain common wheat cultivar to Chinese Spring monosomics, the monosomics of that cultivar have been developed. Worland (1988) compiled the catalogue of monosomic series. Using monosomics, nullisomics and tetrasomic, Sears was successful in obtaining 42 possible nullisomic-tetrasomic compensating combinations and several non-compensating ones in variety Chinese Spring, and reported their origin and characteristics (Sears 1966).

So called secondary aneuploids, telocentrics and isochromosomes are also available in the variety Chinese Spring. Sears and Sears (1978) reported telocentrics; their origin, designations, cytological behavior, fertility, morphology, uses and so on. Representative monosomics and deletion aneuploids were illustrated in Figs 1 and 2.

Much effort has been successfully devoted to develop the alien chromosome lines, alien chromosome additions and substitutions. Shepherd and Islam (1988) compiled the compendium of wheat-alien chromosome lines.

Various types of aneuploids in tetraploid wheat are also available (Joppa 1987).

2. Use of aneuploids

Wheat aneuploids have been used not only for genetic analyses but for developing the new aneuploids. There are several references in which methods and procedures of using wheat aneuploids in cytogenetic studies are demonstrated (Sears 1953, 1969, 1972, Kimber and Sears 1980, Law and Snape 1987, McIntosh 1987).

	A	B	Chromosome configuration in common wheat
Disomic A and B			$2n=42$ $21''$
Monosomic A			$2n=41$ $20''+1'$
Monosomic B			$2n=41$ $20''+1'$
Monoiso AL-disomic (haplo AS-triplo AL-disomic B)			$2n=41+i^{L}$ $20''+i^{L}1''$
Monoiso BS-disomic (haplo BL-triplo BS-disomic A)			$2n=41+i^{S}$ $20''+i^{S}1''$
Tertiary monosomic A·B			$2n=40+1^{tr}$ $20''+1'$
Tertiary monosomic B·A			$2n=40+1^{tr}$ $20''+1'$
Monotelo disomic AL			$2n=41+t^{l}$ $20''+t^{L}1''$
Monotelo disomic AS			$2n=41+t^{s}$ $20''+t^{S}1''$

Fig. 1. Types of primary and tertiary monosomics concerning A and B chromosomes.

	A	B	Chromosome configuration in common wheat
Disomic A and B			$2n=42$ $21''$
Nullisomic A			$2n=40$ $20''$
Ditelosomic AS			$2n=40+2t^{S}$ $20''+t^{S''}$
Ditelosomic AL			$2n=40+2t^{L}$ $20''+t^{L''}$
Monotelosomic AS			$2n=40+t^{S}$ $20''+t^{S'}$
Monoisosomic AS			$2n=40+i^{S}$ $20''+i^{S''}$
Monoisosomic AL			$2n=40+i^{S}$ $20''+i^{L''}$
Di-isosomic AL			$2n=40+i^{L}$ $20''+i^{L''}$
Monoiso-ditelotrisomic AS			$2n=40+i^{S}+2t^{S}$ $20''+i^{S}2t^{S'''}$

Fig. 2. Types of deletion aneuploids concerning A and B chromosomes.

3. Nomenclature

Kimber and Sears (1968) proposed the rules for describing aneuploid conditions and pairing status, chromosome and chromosome arm designation, and chromosome substitutions. Table of descriptive terms and symbols in their proposal would be very instructive.

4. References

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Selective resistance of short arm of chromosome 4E of *Agropyron elongatum* to *Erysiphe graminis* f. sp. *tritici* isolates

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To-date, several alien addition lines of wheat have been developed in different parts of the world (Evans and Jenkins 1960, Islam et al 1978, Dvorak 1980, Morris et al 1990). Some of them have been successfully used as donors of disease resistance to wheat cultivars (Sears 1956, Riley et al 1968, Cauderon et al 1973).

Wheat-rye and wheat-barley addition lines tested against *Erysiphe graminis* f. sp. *tritici* from Punjab, India proved susceptible though barley and rye parents of these lines were resistant (Dhaliwal et al 1987).

In this investigation, a set of eight wheat-*Agropyron elongatum* disomic and ditelo addition lines obtained from Dr B. S. Gill of Kansas State University, Kansas, USA, was studied during 1990 and 1991.

Different lines were evaluated against an isolate of *E. graminis* f. sp. *tritici* of known virulence, using the detached leaf technique (Dhaliwal et al 1987) in the laboratory where temperature ranged from 18 to 22°C. Conidial germination and appressoria formation in vivo were studied, using the "Cello-tape" method. Additionally, the leaf surface was examined directly under the microscope to confirm the above observations.

Conidia germinated and the resulting germ tubes formed appressoria on different lines (Table 1). Subsequent development of *E. graminis* f. sp. *tritici* as visible powdery mildew colonies did not, however, occur on all lines. The line having disomic addition 4E was free from visible colonies of *E. graminis* f. sp. *tritici*. The ditelo addition 4EL, however, developed powdery mildew colonies.

E. graminis f. sp. *tritici* is a variable pathogen having several distinct pathological races (Prabhu and Prasada 1963, Sharma et al 1990). The simultaneous handling of more than one race was not possible at Gurdaspur because of limited laboratory facilities. Alternatively, therefore, the lines were field evaluated at Keylong in Himachal Pradesh. *E. graminis* f. sp. *tritici* is believed to over summer in hilly areas of Himachal Pradesh (Mehta 1930). It was found that addition 4E of *A. elongatum* was susceptible to race(s) prevalent in Himachal Pradesh as no addition line was powdery mildew free. Thus, addition line exhibiting resistance against *E. graminis* f. sp. *tritici* from Punjab, proved susceptible to race(s) prevalent in Himachal Pradesh.

The powdery mildew resistance of 4E was, thus, race specific and it appears to be

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associated with short arm of the chromosome as the ditelo addition 4EL was susceptible to *E. graminis* f. sp. *tritici* from Punjab.

Table 1. Response of wheat-*Agropyron* addition lines to *Erysiphe graminis* f. sp. *tritici* under artificial inoculation.

Genotype	Conidial germination*	Appressoria formation**	Presence of visible colonies***
Chinese Spring/*Agropyron elongatum*			
Ditelo addition 1ES	+	+	+
Disomic addition 2E	+	+	+
Disomic addition 3E	+	+	+
Disomic addition 4E	+	+	−
Ditelo addition 4EL	+	+	+
Disomic addition 6E	+	+	+
Ditelo addition 6ES	+	+	+
Ditelo addition 7EL	+	+	+
Chinese Spring	+	+	+

* Lower side of detached leaves were inoculated

** 48 hours after inoculation

*** A week after inoculation

\+ Present − Absent

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Exploitaion of AAGG genomes of *Triticum timopheevi* (Zhuk.) Zhuk.

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Introduction

Indian durums (*T. turgidum* L. var. *durum*) have very narrow genetic base for yield and its attributes. Attempts are being made to improve the domestic varieties of durums by incorporating desirable traits from its related tetraploid species. *Triticum timopheevi* (Zhuk.) Zhuk. (AAGG) is one of them.

Materials and Methods

Two tall durum cultivars, NI 146 and MACS 9 were crossed as female parents with *T. timopheevi* strain. The F_1 hybrids of these crosses were backcrossed to their tall parents, and then the B_1 F_1 plants were crossed with semidwarf *durum* cultivars, Raj 1555 and DWL 5023, respectively. The second backcross plants were raised in the field and plants with desirable traits were selected. After eight generations of selfing and selection several homozygous timopheevi derivatives (possessing several desirable agronomic traits) were selected. These lines possess good plant types in addition ot their high yielding ability.

After ninth generation, derivatives were evaluated for agronomic traits like seedling height, coleoptile length, seminal root number, plant height, heading date, grain yield, 1000 kernel weight and lodging tolerance.

From the test entries two sister lines B 138 and B 139 drived from the cross *T. timopheevi* × NI 146^2 // Raj 1555 and the other two sister lines B 174 and B 180 derivatives of *T. timopheevi* × MACS 9^2 // DWL 5023 were compared with the best semidwarf durum cultivar PBW 34. For yield evalution, the derivatives were tested in two separately conducted (one for each set of cross) good fertility trials in which each entry was replicated three times, having a plot size of 1.38 × 6.0 m each.

To assess seedling height, coleoptile length and seminal root number, seeds of the lines B 138, B 139, B 174, B 180, *T. timopheevi* and PBW 34 (durum control) were germinated in the petridishes. Data were recorded after 8 or 9 days of imbibition on 20 seedlings in each case.

Results and Discussion

Mean values (Table 1) for various traits showed that the derivatives of *T. timopheevi* were shorter in seedling height than the control varieties. Plant height at maturtity in the field conditions maintained similar pattern in the derivatives. A good relationship between

Table 1. Averages of traits seedling height, coleoptile length, root number, plant height, heading days, lodging, grain yield and 1000 kernel weight of timopheevi derivatives and control varieties.

Derivatives/ control vareities	Seedling heitht (cm)	Coleoptile length (cm)	Root number	Plant height (cm)	Heading days	lodging (%)	Grain yeild (q/ha)	1000 kirnel weight (gm)
B 138	12.6	2.8	5.5	80.2	77.3	–	63.0	50.4
B 139	9.6	2.7	5.9	75.1	79.2	–	57.2	50.8
PBW 34 (C)	13.1	3.2	5.5	85.4	83.5	60	50.0	49.2
CD	–	–	–	–	–	–	6.7	–
B 174	11.0	3.0	4.9	83.5	83.4	–	46.6	62.8
B 180	10.5	3.4	5.0	85.3	83.4	–	43.1	63.2
PBW 34 (C)	13.1	3.2	5.5	84.9	83.3	40	46.4	50.0
T. timopheevi (C)	15.0	3.1	5.1	–	–	–	–	–
CD	3.0	NS	0.5	4.3	–	–	6.9	–

(C) = Control varieties; CD = Critical Difference; NS = Non significant.
Correlation between seedling height and plant height: $r = 0.55$

seedling height and plant height of B 139 suggests the possibility of selection of shorter seedlings possessing good root system from the petridishes. This way fairly a large material can be screened which otherwise may be difficult and time consuming task in the field conditions.

In the field conditions derivatives B 138 and B 139 produced 26% and 14.4% more grain yield than the control PBW 34, respectively. This increase in grain yield can be attrituted to the traits like shortening in the plant height, higher kernel weight, lodging tolerance and reduction in the heading days of these derivatives compared to control variety PBW 34 (Table 1).

Higher root number with reduced culm length in B 138 and B 139 appeared to be responsible for very strong straw in these devIratives resulting in high lodging tolerance even when the irrigation was povided during heavy winds in the season.

T. timopheevi line used in this programme was variety Viticulosum obtained from USSR. Looking into the encouraging results of derivatives, eleven *timopheevi* accessions received from different sources like U. K., USA, USSR and Israel are being used as donor to diversify the Indian durums.

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Effect of photosynth "Mixtalol" on grain improvement and yield in triticale

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Plant breeders produce high yielding varieties by having genotypes possessing combinations of efficient physiological processes capable of producing higher yields. An enormous amount of information has been collected on the effect of mineral nutrition, water relations, growth regulators and herbicides on various physiological processes for increasing crop productivity. However, specific attention to photosynthesis in plants as means of increasing crop productivity has not been sufficiently stressed in agriculture.

While increasing crop productivity by use of nutrients alone seems to have reached a plateau, there is an enormous scope of improving the yields through the photosynthetic route. The upper limit for maximum photosynthetic efficiency for terrestrial plants has been calculated to be of the order of 6.6% (Basshan 1977), but most crop plants achieve photosynthetic efficiencies only of the order of 0.15–0.2% (Boardman 1980), suggesting a possibility of increasing the rate many folds more and, consequently, yields. A study on the effects of "Mixtalol" which is a mixture of aliphatic alcohols, on improvement in grain shrivelling, yield contributing characters and yield is reported here. Mixtalol at the optimum dilution is absorbed throuth leaves as well as through roots and acts rapidly in the plant system (Menon and Srivastava 1984). It increases photosynthesis, CO_2 uptake, nutrient uptake and decreases photorespiration. It improves plant stature, flowering, rooting and tillering and general plant vigour. Some constituents seems to have an effect which simultaneously helps the growth of a deeper and better root system.

Materials and Methods

The experimental material used in the present study comprised of five strains of hexaploid triticale namely UPT 72142, UPT 78268, UPT 79245, UPT 79339 and UPT 79347. Plants were grown in four row plots, following a split plot design, with four replications and treated with Mixtalol, which is a mixture of a spectrum of aliphatic alcohols with chain lengths C-24 to C-34 (Menon and Srivastava 1984). Mixtalol has the following composition (%): C-24 Tetracosanol: 7–10; C-26 Hexacosanol: 12–16; C-28 Octacosanol: 15–20; C-30 Triacontanol: 24–30; C-32 Dotriacontanol: 11–14; and C-34 Tetratriacontanol: 4–5. Mixtalol treated and control plants were allotted to main plots and five strains were taken as sub-plots. Each strain was sown in four rows with a row-to-row distance of 23 cm and each row was 2.5 m long. 4.5 ml of Mixtalol was mixed in 1.5 litres of water and sprayed in about 9.2 square meters area. Spraying was done after 31 and 65 days of sowing. Ten plants were randomly selected from each replication and data was recorded on heading date, maturity

Table 1. Effect of Mixtalol spray on yield and yield contributing characters in triticale

Treatment	Days to 75% heading	Days to 75% maturity	Plant height (cm)	No. of tillers per plant	Spike length (cm)	100 seed weight (g)	Yield per hectare (g)
Control	91.2	134.8	94.9	6.5	10.5	4.1	40.9
Mixtalol spray	92.0	135.4	99.7	7.1	11.3	4.2	44.3
Varieties							
UPT 72142	88.0	132.9	88.4	7.9	10.6	31.3	40.8
UPT 78268	92.9	135.4	92.7	6.3	10.7	32.2	43.3
UPT 79245	91.8	132.0	94.9	6.6	10.2	33.0	42.6
UPT 79339	96.1	139.3	111.8	6.7	12.0	35.2	40.9
UPT 79347	89.0	135.0	98.7	6.4	10.9	35.7	44.1

Table 2. Analysis of variance showing mean squares for yield and yield contributing characters in triticale.

Source of Variation	d.f.	Days to 75% heading	Days to 75% maturity	Plant height (cm)	No. of tillers per plant	Spike length (cm)	100 seed weight (g)	Yield per hectare (g)
Replication	3	0.83	0.50	67.5	0.61	0.22	0.43	4.8
Main plot (control and Mixtalol spray)	1	6.00	7.00	235.91*	4.01*	6.70*	0.77*	114.6**
Error (a)	3	0.60	1.10	15.7	0.15	0.54	0.02	0.6
Sub-plot (varieties)	4	80.16**	62.31**	637.3**	3.25**	3.63*	0.45**	12.9**
Main plot × Sub-plot	4	0.34	0.81	28.6	0.52	0.30	0.01	0.7
Error (b)	24	0.98	0.64	13.7	0.71	0.99	0.10	2.6
Total	39							

*Significant at P=0.05

**Significant at P=0.01

date, plant height, number of tillers per plant, spike length, 100-seed weight and yield per hectare.

Results and Discussion

Table 1 shows the effect of Mixtalol spray on various characters. The analysis of variance is given in Table 2. Mixtalol treatment did not show any significant effect on days to 75 per cent heading and maturity, though it increased plant height significantly as compared to control. This increase may be due to an increased dry matter in the treated plants as a result of increased mitotic activity imparted either directly or possibly through a change in endogenous levels of auxins/cytokinins. The number of tillers per plant increased significantly after Mixtalol treatment as compared to control. Menon and Srivastava (1984) found an increase in the number of tillers per plant in rice, which is indicative of initial vigour due to Mixtalol application. Hundred grain weight and yield per hectare also increased significantly due to Mixtalol treatment. Menon and Srivastava (1984) attributed this to an increase in the rate of photosynthesis and a decrease in photorespiration rate. Grain type showed improvement which may have resulted because of an improvement in mitotic activity during grain formation and also improved photosynthesis. Extensive field trials with Mixtalol have shown yield increases of 14–27% in paddy, 13–27% in wheat, 33% in maize, 21–29% in potatoes and 48% in sorghum (Menon and Srivastava 1984). Mixtalol may prove to be very useful in increasing plant productivity by improved photosynthesis.

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Monosomic analysis of some quantitative characters in wheat, *Triticum aestivum* L. cv. "Chinese Spring".

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Monosomics occur spontaneously and can be recognized by phenotypic observations and cytogenetic analysis. These can be used to determine gene linkage groups, especially in polyploid plants, for identification of genes on particular chromosomes and for transference of genes from one chromosome to the others. Monosomic series in hexaploid wheat, *Triticum aestivum* cv. "Chinese Spring" was developed by Sears (1954).

Leaf size has a positive effect on biomass and yield of plants. In wheat, the flag leaf makes important contribution of photosynthates. This contribution is greatest during the stage of grain filling. Days to heading in wheat depends upon many factors such as temperature, sowing dates, length of days and latitude. It is a complex character controlled by many genes. Spike length is controlled by the additive gene action of different minor genes. The genes affecting spike length may thus be located on many chromosomes.

In the present study, observations were taken to locate genes governing some quantitative characters to specific chromosomes in cv. "Chinese Spring" of common wheat through monosomic analysis. The characters studied were: days to heading, length and width of flag lesf and spike length.

Materials and Methods

The material for the present study comprised of 17 monosomic lines of common wheat cv. "Chinese Spring" which germinated and could be maintained at the Department of Genetics, University of Karachi. The seeds were kindly provided by Prof. E. R. Sears of the University of Columbia, Missouri, U. S. A.

Chromosomes of every seedling were counted by the general procedure of Jahan and Vahidy (1989). The seeds were first sown in Petri dishes and placed at 20°C. After 3 days the root tips were harvested for the cytological confirmation of the monosomics and the seeds were transplanted individually in small pots and kept at 20°C. Root tips were pretreated in a mixture of 0.05% colchicine, 0.025% 8 hydroxyquinoline, and 25 drops DMSO in 100 ml distilled water for 3 hours. They were then transferred into 1.8% aceto-orcein. The root tips were heated to just boiling point on the spirit lamp and then squashed in 45% acetic acid. The slides were made permanent in liquid nitrogen and mounted in euparal. Cytologically confirmed seedlings were transferred into large pots and kept in the screen house under natural conditions.

Days to heading was considered as the average day the spike emerged from the boot leaf

counting from the day of sowing. Observations were also recorded on the spike length, flag leaf length, and flag leaf width at maturity. Observations on disomics were included to make comparisons.

The means and standard errors of the four variables were calculated. Each monosomic line was compared with the disomic for each variable utilizing the statistical package SPSS/PC+. The contrast used in the analysis was "SIMPLE" as described by Norusis (1988). This allows the comparison of a particular variable, in this case, disomics with the rest, the monosomics. This comparison is non orthogonal in nature.

Results and Discussion

Days to heading in wheat seems to be a quantitative character. Such characters are controlled by a number of major and minor genes separately and collectively. These genes are different in their nature and action. Observations recorded on days to heading revealed the involvement of monosomics 2B, 3B, 5B, 3D and 6D. Of these, monosomics 2B, 3B, and 6D were late while 5B was early as compared to the disomic at the $p<0.01$. Monosomic 3D, when compared to the disomics, was late at the $p<0.05$ (Table 1). All of these chromosomes except 5B have been reported by previous workers to be involved in influencing heading time. According to Yoshida and Kawaguchi (1984), who worked on the monosomics of "Chinese Spring", monosomics 2B, 3B, 6B, 7B, 3D and 6D were involved in days to heading. Of these only 3D was early while the rest were late. Bhat and Goud (1979) worked on the monosomic lines of cv. "Pb. C591" and "UP. 301" and found the effect of chromosomes 5A, 7A, 3D and 7D on heading time. Of these monosomics 7A, 3D and 7D were early while 5A was late. Results reported by Goud and Sridevi (1988) showed that monosomics 1A, 4A, 5A, 6A, 3B, 2D and 7D carry the genes for days to heading in the cultivar "DWR. 39". Of these 6A and 7D were early while the others were late. They, in another report, (Sridevi and Goud, 1988) found the influence of chromosomes 4A, 5A, 2B and 6B in the trisomics of *Triticum durum* cv. HD. 4502. All of these trisomics were late. Thus the results reported by us are in confirmation with those reported by earlier workers except for monosomic 5B which is being reported here to be involved in heading time.

The mean flag leaf lengths of the monosomics were compared to that of disomics. In the monosomics 1A, 2A, 5A, 6A, 2B, 3B, 4B, 5B, and 6D, the deviations were found to be statistically different as compared to the disomics. Monosomics 5A, 3B and 5B were different at $p<0.05$ as compared to the disomic while the rest were different at $p<0.01$. The length of the flag leaf was increased in monosomics 1A, 2A, 5A, 6A, 2B, 3B and 4B while in the remaining two monosomics, i. e., 5B and 6D, it was reduced. Out of the above reported chromosomes, 2A, 2B, 3B and 5B have also been reported to influence the length of flag leaf by Sridevi et al (1989).

As far as the width of flag leaf is concerned, monosomics 1A, 2A, 3A, 3B, 4B, 6D, and 7D were found to affect this character. Of these the width of the flag leaf was decreased in

monosomics 6D and 7D while in the others it was increased (Table 1). The involvement of monosomics 2A and 3A was also reported by Sridevi et al (1989). Besides these two chromosomes, they found the effect of 6A, 1B, 2B, 7B, 1D, and 5D on the width of flag leaf. According to them, the flag leaf width was decreased in 5D while in the others it was increased. Chromosomes 1A, 2A, 3B, 4B, and 6D were involved both in flag leaf length and width and thus show greater contribution to flag leaf size. Some differences have thus been observed between our results and those of Sridevi et al (1989) as far as flag leaf size is concerned. Out of the eleven chromosomes shown by us to effect this chracter, six, viz., 1A, 5A, 6A, 4B, 6D and 7D have not been reported by them, although the homoelogues of 1A (1B and 1D), 5A (5B and 5D) and 7D (7B) have been shown by them to influence this character. The reason for this discrepancy could be due to the different cultivars used.

Spike length is under the control of many genes. According to our analysis, monosomics 1A, 2A, 5A, 3D and 7D affect the length of the spike. When the mean length of the

Table 1. Means and standard errors of four variables in the monosomic and disomic populations in *T. aestivum* cv. "Chinese Spring".

Monosomic lines	Flag Leaf				Spike			
	Length		Width		Days to heading		Length	
	Mean	S. E.	Mean	S. E.	Mean	S. E.	Mean	S. E.
1A	260.143	7.379	14.714	0.606	86.714	1.409	104.714	4.725
2A	244.611	10.771	14.500	0.572	87.944	1.480	90.389	3.358
3A	205.790	7.364	13.369	0.453	88.210	1.283	77.263	2.890
5A	215.193	9.578	11.580	0.392	88.161	0.900	97.064	2.131
6A	233.913	7.571	11.880	0.281	86.966	0.804	81.500	1.538
7A	203.343	8.708	11.375	0.369	86.438	0.862	83.093	1.803
1B	204.722	6.681	11.417	0.307	88.222	1.220	85.222	2.485
2B	231.320	8.612	12.320	0.325	92.040	1.315	87.000	2.482
3B	213.171	8.056	13.314	0.285	90.229	0.983	78.829	1.930
4B	229.400	9.170	13.000	0.468	86.267	1.364	88.067	3.390
5B	153.750	7.321	11.625	0.597	80.125	1.140	91.625	3.670
6B	208.000	0.210	11.333	0.210	83.167	1.990	82.167	4.743
7B	182.500	6.419	11.200	0.326	85.200	1.218	83.900	3.103
3D	212.889	13.599	12.556	0.690	91.778	1.891	72.444	3.473
5D	182.263	9.480	10.894	0.483	89.000	1.172	79.474	2.124
6D	156.917	8.166	9.250	0.446	92.417	1.305	77.583	3.700
7D	203.833	12.020	9.889	0.478	88.222	1.198	72.444	3.525
Disomics	192.071	5.142	11.642	0.336	86.892	0.768	82.929	1.725

spikes of these monosomics was compared to that of the disomics, it was found that the spike length was increased in monosomics 1A, 2A and 5A and decreased in monosomics 3D and 7D (Table 1). Of these, monosomics 1A, 5A and 7D were found to be different at the $p<0.01$ and monosomics 2A and 3D at $p<0.05$ as compared to the disomics (Table 2). All these chromosomes except 1A and 2A have been reported to affect spike length by previous workers. Yoshida and Kawaguchi (1984) reported that chromosome 5A was involved in spike length. According to them, monosomic 5A had longer spike length (speltoidy). The involvement of chromosomes 3A, 1B, 2B, 3B, 4B, 5B, 3D and 7D in influencing spike length was reported by Bhat and Goud (1979). According to them monosomic populations 2B and 4B had increased spike lengths whereas the others showed reduced spike lengths. Goud and Sridevi (1988) reported that chromosomes 4A, 5A, 6A, 7A, 3B, 4B, 6B and 7D decreased the spike lenght while 1B increased it. They in another publication (Sridevi and Goud, 1988) found the influence of chromosomes 4A, 5A, 2B and 7B on this chracter. Of

Table 2. Mean squares and F-values of the four variables in the monosomic as compared to the disomic populations in *T. aestivum* cv. "Chinese Spring".

Monosomic lines	Flag Leaf				Spike			
	Length		Width		Days to heading		Length	
	MS	F	MS	F	MS	F	MS	F
1A	28832.03	14.46**	58.70	14.15**	0.20	0.01	2953.17	19.39**
2A	37601.37	18.86**	111.20	26.80**	15.06	0.46	758.13	4.98*
3A	2669.71	1.34	42.24	10.18**	24.63	0.75	455.35	2.99
5A	10668.07	5.35*	0.00	0.02	32.10	0.98	3987.31	26.18**
6A	49881.97	25.02**	1.59	0.38	0.15	0.00	58.15	0.38
7A	2587.51	1.30	1.46	0.35	4.22	0.13	0.56	0.00
1B	3507.02	1.76	1.12	0.27	38.72	1.19	115.28	0.76
2B	26625.07	13.36**	7.93	1.91	457.91	14.02**	286.51	1.88
3B	9589.14	4.81*	60.17	14.50**	239.66	7.34**	362.06	2.38
4B	16485.56	8.27**	21.79	5.25*	4.64	0.14	312.34	2.05
5B	10279.72	5.16*	0.14	0.03	320.63	9.82**	529.40	3.48
6B	1375.00	0.69	0.52	0.13	72.25	2.30	3.15	0.02
7B	777.32	0.39	1.66	0.04	24.32	0.74	8.01	0.05
3D	3360.26	1.69	6.46	1.56	185.03	5.66*	852.28	5.60*
5D	1364.79	0.68	7.94	1.91	62.99	1.93	169.34	1.11
6D	12213.18	6.13**	56.58	13.64**	301.54	9.32**	282.35	1.85
7D	1884.45	0.95	41.91	10.10**	24.07	0.74	1497.25	9.83**

*, ** Significant at probability $<.05$ and $<.01$ respectively.

these, populations derived from trisomic 5A decreased the mean spike length while the rest increased it. Hence as far as length of spike is concerned except for 1A and 2A all the chromosomes reported by us are in confirmation with earlier reports. The homoeologues of 1A and 2A i. e. 1B and 2B have been reported instead by previous workers.

By comparing monosomic lines with disomics, the involvement of several chromosomes has been demonstrated for agronomic chracters like days to heading, flag leaf length and width and spike length. The discrepancies observed between our results and those of other workers could be due to three reasons. 1. The relative length of the day has been reported as a factor of prime importance in the growth and development of plants. Our plantation was done in Karachi during the period December 1988 to March 1989. The work done by previous workers quoted in this article was done in places with different photoperiods as compared to Karachi. 2. Among wheat genotypes high amount of variability exists for optimum temperature requirements. This variability is said to be related with post-spike differentiation phases (Singh and Behl, 1990). 3. Due to different cultivars used. We have worked with the monosomics of cv. "Chinese Spring", while, with the exception of Yoshida and Kawaguchi (1984), all previous workers quoted in this article have used other cultivars. It is evident that a number of genes exhibiting both positive and negative effects are involved for each of these characters. Due to homoeologous nature of chromosomes of wheat, the inheritance of characters is difficult to study, and interpret, nonetheless monosomics along with ditelosomics and nullisomic-tetrasomic lines have contributed greatly in understanding the pattern of inheritance in wheat.

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Radioprotective effect of gibberellic acid in triticale

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The damage caused by ionizing radiations has been reported to get reduced by pre-treatment with many chamicals. Thiourea and dimethly sulphoxide has been found to reduce chromosomal damage in various species of plants (Wolff 1954, Mikaslsen 1955, Riley 1957, Kaul 1969). Among the plant growth regulators gibberellic acid (GA_3) is known to reduce gamma radiation effects on plant growth in maize (Gaur and Notani 1960), wheat (Habar and Luipold 1960, Uppal and Maherchandani 1988), barley (Maharchandani and Vasudeva 1984), and *Avena fatua* (Maherchandani and Vasudeva 1985). Gibberellic acid has been reported to increase peroxidase activity (Jain et al 1980), due to which surviving paroxy radicals may be eliminated such that the resultant detectable damage is less (Alper 1979). Present study deals with the effects of a low concentration (10 ppm) of GA_3 on the seedling growth, cytological damage and peroxidase activity in the gamma-irradiated triticale seeds.

Materials and Methods

Seeds of triticale variety UPT 78268 with a moisture content of 10 ± 1 per cent were irradiated with 10–40 kR gamma rays. These were soaked either in water or in 10 ppm GA_3 soultion for 16 hours. The seeds were then removed from the solutions and germinated in petri-dishes on filter papers soaked with water or GA_3 soulution. There were three plates per treatment, each containing 25 seeds.

Root tips were fixed in acetic acid-ethanol (1:3) for cytological studies after 36 hours. After 24 hours in the fixative, these roots were transferred to 70 per cent alcohol and kept in a refrigerator. Root tips were hydrolysed in 1N HCl for 10 minutes, and stained and squashed in 1 per cent acetocarmine. Frequency of abnormal anaphases was estimated in each treatment from 500 anaphase cells scored from 5–6 slides from 10 root tips. Mitotic index was estimated from 1200–1900 cells. Seedling height was recorded on 5 day old seedlings. For peroxidase activity 0–6 days old seedlings were selected and dried with a blotting paper. One gram material was homogenized for 60 seconds in 5 ml of precooled 0.9 per cent NaCl, in a precooled mortar kept in an ice-bucket. The homogenate was centrifuged for 30 minutes at 12,000 rpm and the supernatant was collected. The crude enzyme extract (0.1 ml) was diluted in 5 ml of 50 mM Na_2CO_3-50 mM NaCl buffer having a pH of 6. The enzyme was assayed by the method of Karege et al (1982). Na-K phoshate buffer (40 mM), pH 6.1 containing 8 mM guaiacol and 2 mM H_2O_2 was added to the enzyme mixture. The increase in absorbance due to oxidation of guaiacol in the presence of H_2O_2 and enzyme was recorded at 470 nm after 2 min. Data was recorded on three replications.

Results and Discussion

Expermental results revealed that the frequency of cells with anaphase bridges as well as fragments increased with an increase in radiation dose (Table 1). The number of cells with bridges was more than those with fragments. Post treatment with GA_3 reduced the frequency of anaphase bridges as well as fragments. The difference between the control and GA_3 treated cells was more at higher radiation doses.

Mitotic index in the control decreased with an increase in the radiation dose, though at 10 kR there was some stimulatory effect resulting in an increase in the mitotic index (Table 2). This was also reported by Khanna (1990) in wheat. According to Simonis (1966), radiations are capable of considerably changing the type of information of certain DNA molecules. This may be the reason for the increase in mitotic index at lower doses and a decrease at higher doses. GA_3 increased the mitotic index, the increase being more in irradiated seeds.

Seedling height responded to GA_3 as well as to gamma radiation. It decreased with an increase in radiation except at 10 kR which stimulated seedling height. GA_3 also increased seedling height, the maximum increase being at 10 kR. Stimulation in seedling height may be due to faster cell division, change in auxin balance or enhancement in enzyme activity.

Peroxidase activity increased with seedling growth from 0–6 days of germination of the seed (Table 4). An increase in radiation doses decreased enzyme activity except at 10 kR where it was more than control. Kuzin (1980) suggested that irradiation at lowaer doses often induced the production of small quantities of radiotoxins with resulted in stimulation, on growth and development. Peroxidase activity was more in GA_3 treated seeds.

This study shows that post-treatment with very low concentrations of GA_3 decreased the frequancy of anaphase aberrations due to gamma irradiation in triticale. Similar protective effects of GA_3 could also be seen on seedling growth and mitotic index. Peroxidase activity also increased in GA_3 treated seeds.

Chemicals such as aminothiols, that are known to give protection against radiation damage, must be present at the time of irradiation and are effective only as pre-treatments. These may act either as free-radical scavengers or by causing anoxia in the system (Bacq and Alexander 1961, Alper 1979). Gibberellic acid enhances metabolic rate (Jones 1973) and increases peroxidase activity (Thakral 1979, Jain et al 1980). Our results also show that GA_3 enhanced peroxidase activity. Due to higher respiratory activity in GA_3 treated seeds, a local state of relative anoxia may be created in the cell so that there is low cell damage (Alper 1979) or due to enhanced peroxidase activity, surviving peroxy radicals may be eliminated such that the resultant detectable damage is less. Another possibility is that gamma radiation caused potential lesions (Bacq and Alexander 1961) which are normally converted to real cytological damage on imbibition of seed, and are eliminated due to a high metabolic rates of GA_3 treated seeds.

Table 1. Effect of GA_3 on the fequency of mitotic anaphase anomalies (%) in root tips of gamma irradiated triticale seeds

Dose kR**	Without GA_3			With GA_3			Difference
	Bridges	Fragments	Total	Bridges	Fragments	Total	
0	1.82	0.76	2.58±0.61*	1.12	0.71	1.83±0.24	−0.75
10	9.26	4.59	13.85±1.40	6.73	3.26	9.99±0.98	−3.86
20	17.75	8.21	25.96±1.82	11.85	6.11	17.96±1.63	−8.00
30	21.27	12.19	33.46±2.46	16.47	8.59	25.06±1.47	−8.40
40	29.43	18.64	48.07±2.28	23.26	14.24	37.50±1.84	−10.57

* S. E.

** 1 R=258 μC/kg

Table 2. Effect of GA_3 on mitotic index in root tips of gamma irradiated triticale seeds

Dose kR	Without GA_3		With GA_3		Difference
	No. of cells	Mitotic index	No. of cells	Mitotic indax	
0	1206	19.32±1.69*	1631	20.78±1.42	+1.46
10	1320	21.67±1.86	1423	25.26±2.02	+3.59
20	1240	16.25±1.44	1698	21.34±1.64	+5.09
30	1819	14.83±1.09	1876	18.12±1.46	+3.29
40	1417	9.62±1.04	1522	12.98±0.92	+3.36

* S. E.

Table 3. Effect of GA_3 on seedling height of gamma irradiated triticale seeds

Dose kR	Shoot length (cm)		
	Without GA_3	With GA_3	Difference
0	6.23±0.42*	7.93±0.58	+1.70
10	8.46±0.61	11.68±0.47	+3.22
20	5.41±0.38	7.22±0.32	+1.81
30	3.29±0.44	5.67±0.41	+2.36
40	1.67±0.24	4.41±0.29	+2.74

* S. E.

Table 4. Effect of GA_3 on the peroxidase activity in the germinating seedlings from gamma irradiated triticale seeds

Dose kR	Without GA_3				With GA_3			
	0 day	2 days	4 days	6 days	0 day	2 days	4 days	6 days
0	3.12±0.24*	3.47±0.40	7.26±0.32	10.81±0.44	3.27±0.22	3.98±0.32	9.46±0.37	12.24±0.46
10	4.27±0.31	4.59±0.24	9.31±0.41	13.41±0.61	4.42±0.27	6.04±0.28	11.44±0.52	16.17±0.48
20	3.01±0.26	3.84±0.31	7.47±0.36	9.62±0.34	3.76±0.21	4.62±0.24	10.21±0.33	12.21±0.32
30	2.25±0.20	3.06±0.39	5.23±0.68	8.04±0.29	2.84±0.19	3.91±0.36	7.73±0.21	11.08±0.18
40	1.68±0.14	1.92±0.22	2.88±0.21	4.28±0.33	2.23±0.22	2.87±0.19	4.01±0.27	5.66±0.26

* S. E.

The unit activity is defined as the amount of enzyme which causes an extinction increase of 0.1 after 2 minutes (Putter 1974).

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Hybrid necrosis in bread wheat. III.

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Hybrid necrosis is the pre-mature gradual death of leaves and leaf sheaths in certain crosses of wheat and is the major barrier in combining desirable traits into hybrid combinations. Based on the earlier studies, two complementary ganes, namely, *Ne1* and *Ne2* when brought together in hybrid combination, either in homo- or heterozygous form, cause necrosis (Hermsen 1963). The degree of necrosis in F_1 plants varies depending on the multiple alleles (s, m and w) of these two genes (*Ne1* and *Ne2).* Hermsen (1963) has given 0–9 grades of necrosis in F_1 hybrids depending on different combinations of the three alleles of *Ne1* and *Ne2* genes as:

0–3 Weak necrosis (Hybrids produce normal seeds)
3–6 Moderate necrosis (Hybrids produce pre-mature seeds)
6–9 Severe (No seed obtained from hybrids)

Indian varieties have been reported to be generally having *Ne1* gene, while Mexican varieties are supposed to have *Ne2* gene (Gill et al 1969, Anand et al 1969, Chowdhury 1981, 1983). Because of these reasons, many times it becomes cumbersome to combine desirable traits of Indian varieties with that of Mexico, if the genotypes in combination have *Ne1* and *Ne2* genes, respectively. This problem has already been experienced in case of variety C306, which is one of the top drought tolerant varieties and has good quality grains. Since it carries *Ne1* gene many of the crosses to Mexican varieties with *Ne2* gene fail, though some way-outs have been suggested to overcome the necrosis in F_1 generations of the crosses (Dhaliwal et al 1986).

While breeding of high yielding and drought and rust resistant varieties, we at Haryana Agricultural University are attempting a number of crosses in bread wheat every year and screening their hybrid generations. We came across many of the crosses showing necrotic behaviour in F_1 generation. We have already published two lists of such crosses (Chowdhury, 1981, 1983). Here we have compiled the third list of bread wheat crosses showing necrosis. Depending on the gene combination we have sorted out wheat genotypes having *Ne1* or *Ne2* genes. Other varieties have also been listed which have given indication of non-carrier of either *Ne1* or *Ne2* or both (Table 1). The data on morphological features like plant height and number of leaves (green as well as dry) per tiller of some of the necrotic F_1 hybrids have been given in Table 2.

The observations made on these necrotic F_1 hybrids showed that the yellowing of leaves started at 2–3 leaf stage and most of the hybrids died at the 5–6 leaf stage without producing ear, showing the characteristic of severe necrosis of grade 7 as described by Hermsen (1963).

It is well established that Indian variety C306 carries *Ne1* gene. Therefore, the varieties

like IWP72, WH331, UP262, P488, Raj 939, CBS289, cm 58803, cm 59376, cm 66675, CBS102, PC89, WL410, Kalyansons, which have produced necrotic hybrids with C306, carry *Ne2* gene. Similarly, the variety GP104 which give normal plants with C306 but showed necrosis with above listed varieties must have *Ne1* gene. Other varieties like GP106, WH157 and AP105 also gave indication of having *Ne1* gene in their genotypic background. The crosses involving WH331 showed less necrosis, indicating that this variety may be having m or w allele of *Ne2* but it needs further confirmation. There were varieties like WH157, IWP72 and WL410 which were earlier reported to be non-carrier of necrotic genes, have now been identified having *Ne1* (WH157) and *Ne2* (WL410 and IWP72) genes. These information will be of importance to be wheat breeders and geneticists in their hybridization programme.

Table 1. List of carrier and non-carrier of necrotic gene in bread wheat

Ne1 carrier	*Ne2* carrier	Non-carrier of *Ne1*	Non-carrier of *Ne2*	Non-carrier of *Ne1* and *Ne2*
C306	cm 58803	K227-1	HS 33	HS 90
GP104	cm 59376	K227-7	HS 43	HS 74
GP106	cm 66675	WL 1562	NI 574	NI 5439
WH157	WH 331	Hindi 62	WH 129	HI 1011
AP105	P 48 B	Kharchia-65	DL 172	HD 2281
	Raj 939			
	CBS 102			
	PC 89			
	UP 262			
	WL 410			
	IWP 72			
	CBS 289			
	Kalyansona			

Table 2. Morphological characteristics of some of the F_1 hybrids showing necrotic behaviour in bread wheat.

Cross		Necrotic behaviour	Plant height (cm)*	No. of leaves/tiller		
				Green	Dry	Total
CBS 102	× C 306	Severe	12.67	1	4	5
	× WH331	Normal	36.67	5	0	5
	× WL410	Normal	32.00	4	1	5
	× IWP72	Normal	29.33	5	0	5
GP 104	× C 306	Normal	63.00	5	1	6
	× WH331	Weak	45.00	1	5	6
	× WL410	Severe	35.00	1	4	5
	× IWP72	Severe	40.00	1	4	5
C 306	× IWP72	Severe	58.00	1	4	5
	× WH331	Weak	46.00	0	5	5
	× UP262	Severe	—	1	4	5
	× P 488	Severe	—	0	5	5
	× Raj939	Severe	45.00	1	4	5
	× CBS289	Severe	30.00	1	5	6
WH 157	× WH331	Weak	76.00	2	4	6
cm 58803	× C306	Severe	10.00	0	5	5
cm 59376	× C306	Severe	8.0	1	5	6
cm 66675	× C306	Severe	24.00	0	5	5
Raj 939	× C 306	Severe	45.00	0	5	5

* —: Not observed

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A note on drought resistance in wheat

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Breeding major food crops for stable yields under drought and rainfed stress environments has become a subject of major interest (Fischer et al 1982). Various mechanisms imparting drought resistance like escape, endurance, avoidance and tolerance etc have been put forward by various workers. However, still plant breeders are largely guided by the grain yield response in selecting for drought resistance due to lack of well defined informations on the above mechanisms. The black box approach, ie, testing of performace of genotypes under stress situation is a very useful step in breeding programmes mainly because it allows a direct estimate of drought resistance of susceptibility of individual genotypes.

Although stricking increases have been achieved in the wheat yields all over the world with the development of modern high yielding and high input responsive varieties after the introduction of dwarfing genes of Norin 10, however, yields under drought and rainfed conditions are still low and stagnant. The rainfed wheats accounts for about 35 per cent of the total acreage of wheat in India, therefore, it would be desirable to screen the genotypes under rainfed conditions so that the best or better genotypes could be identified and utilized in future breeding programmes.

Having this in mind, a total of 115 genotypes of wheat including aestivum and durum mostly taken from "National Drought Screening Nursery" were screened for their yield performance at Haryana Agricultural University, Regional Research Station, Bawal for three years; 1979–80, 1980–81 and 1981–82 to identify variations best suited under drought/rainfed conditions. Bawal is situated in South-Western part of Haryana State. The climate in this zone is semi-arid with very erratic rainfed. The soil is loamy sand, weakly alkaline (pH 7.8), bulk density 1.45 g/cm^3 having 84.6% sand, 6.7% silt and 8.7% clay. The data were recorded on grain yield/m row length (g) and total dry matter produced, ie, biological yield/m row length (g). The harvest index (%) was calculated by dividing grain yield with total biological yield.

Genotypic differences were found highly significant for all the three characters studied in the present study (grain yield, biological yield and harvest index) indicating, thereby, that sufficient genotypic variability existed in the material. Based on the results of three years on grain yield, 15 varieties have been identified which yielded consistantly good. Their data are presented in Table 1. These varieties appeared to be the most drought tolerant or can give good yields under drought/rainfed conditions particularly South-Western part of Haryana State. Many of these varieties have been recommended for commercial cultivation under drought/rainfed conditions in various states in India like, C306, NI 5439, Narbada 4, WL 410 etc and also have been identified better under drought by Chowdhury and

Table 1. Mean performance of 15 best varieties of wheat under rainfed conditions over three years.

	Variety	Mean grain yield / m row length during:		
		1979–80	1980–81	1981–82
1.	MP157	107	103	120
2.	MP823A	105	117	85
3.	Narbada112	100	140	100
4.	HP1258	110	105	110
5.	MP195	115	83	115
6.	HY-11	95	112	110
7.	C306	105	82	130
8.	NI5439	125	84	130
9.	K-7527	120	80	130
10.	N-7231	85	110	115
11.	HI 617	100	73	115
12.	HS82	85	127	90
13.	WL-410	95	124	125
14.	Narbada 4	85	119	105
15.	HD-2037	130	69	120

coworkers while studying 60 wheat genotypes under six varying levels of irrigations under Bawal conditions. Chowdhury et al (1985) reported C306, Narbada 112, N 7231 and HI 617 as the outstanding varieties under zero irrigation. While studying stability parameters, Chowdhury et al (1985) indentified varieties Narbada 112 and N 7231 suitable for poor environment. Variety C306 appeared to be the stable over wide range of environments. Chowdhury et al (1986) also, reported low/moderate drought susceptibility indices($\bar{s}$) for some of these varieties. Those having $\bar{s}$ below 0.7 as least drought susceptible or most drought tolerant ones were NI 5749, HS32, MP 823 A and HD 2037 while moderately drought tolerant ie having $\bar{s}$ value between 0.7 to 1.0 were NI 5439, K7527, HP1258, N7231, Narbada 112 and MP195. Based on drought susceptibility index and productivity under drought environment varieties Narbada 4, and HS 82 were found to be best for drought conditions. There were varieties like C306, Narbada112, N7231, HI617 and NI5749, which had $\bar{s}$ value on higher side, but gave higher yields under drought conditions and thus were best for drought environment. The drought susceptibility index of variety C306 was also reported between 0.91 to 1.08 by Fischer and Maurer (1978).

The results of the present study also showed that the grain yield was contributed mainly by the total biological yield in most of the varieties. Chowdhury et al (1985) also reported that grain yield was mainly contributed by total biological yield. The studies also showed

the correlation of grain yield with plant height, total biological yield and harvest index.

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Studies on pollen germination, pollen tube growth and seed set in reciprocal wheat-barley crosses

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Hordeum species have a number of agronomic traits those are useful for improvement of wheat, such as wide geographic adaptation, salinity tolerance, high lysine content and others. However, the intergeneric hybrids between barley and wheat are difficult to obtain due to disturbances in the processes of fertilization, impaired development of hybrid embryos and endosperm degeneration (Bannicova 1975). The cross wheat × barley has been reported to be more difficult than its reciprocal cross (Fedak 1980, Islam et al 1981).

It is well known that two dominant genes, *Kr1* and *Kr2* located on wheat chromosomes 5B and 5A, respectively, inhibit crossability of wheat with rye (Riley and Chapman 1967). The dominant alleles at these crossability loci actively inhibit the production of intergeneric hybrids of wheat (Lange and Wojciechowska 1976). These factors are known to be implicated in the crossabilities of wheat with *H. bulbosum* (Snape et al 1979) and with barley (Fedak and Jui 1982). Similar crossability genes are reported in barley (Elbern 1981).

In wheat-rye crosses, the growth of the pollen tubes in the poorly crossable types of wheat was found to be either slower (Singh and Khanna 1988) or not retarded at all (Tozu 1966). Furthermore, pollen tube inflation and bursting has also been shown to occur in incompatible hybridizations between wheat and rye (Tozu 1966, Zeven and Heemert 1970, Jalani and Moss 1980, Singh and Khanna 1988), and barley and wheat (Fedak and Jui 1982). Similarly, growth of pollen tubes were inhibited before penetration into embryo-sacs of non-crossable wheats pollinated with *H. bulbosum* (Snape et al 1980).

Present paper deals with pollen germination and pollen tube behaviour with the aim to determine the factors which reduce crossability in the reciprocal crosses between wheat and barley. The effect of hormones on crossability is also reported.

Materials and Methods

One variety of common wheat, *Triticum aestivum*, UP 2121, one variety of durum wheat, *T. durum*, PBW 34 and two varieties of diploid huskless barley, *Hordeum vulgare*, Karan 4 and Karan 265 were used in the present study.

The seeds of the varieties were sown in the field on 25th of Nov. and 2nd of Dec., 1989. The crosses were made reciprocally in all possible combinations in February and March, 1990.

The styles along with the stigmas were detached from the top of the pollinated flowers with forceps with the intervals of 5min, 30min, 60min, 4h and 24h after pollination. They

were kept in 1:2 lacto-alcohol solution for 48h. Five styles were chosen at random from each spike and all the pollen grains on the stigma were observed for pollen germination. For pollen tube growth, the lengths of the three longest pollen tubes in each style were recorded. These pistils were washed in distilled water and stained with cotton blue solution (D'Souza 1972). The pollen grains and the pollen tubes were stained deep blue whereas the stylar tissue was either colorless or very lightly stained. The data on pollen germination, pollen tube growth and abnormal pollen tubes were taken from spikes without treatment of hormones.

In order to clarify the effect of hormones on crossability between wheat and barley, each of three growth hormones namely, Gibberellic acid (GA_3), Indole acetic acid (IAA), and Kinetin (KIN) were sprayed on the floweres with the concentration of 75ppm, respectively, after 24h of pollination.

Results and Discussion

The onset of pollen germination was variable among the cross combinations (Table 1). There was only one cross which showed germination of pollen grains after 5min, whereas pollen in six crosses started germination after 30min, and in the other five after 60min. There was no correlation between pollen germination and seed set. Some crosses with comparatively high pollen germination showed a poor seed set, while others in which pollen germination were poor showed a high seed set. Therefore, a good pollen germination may not ensure a good seed set.

The emergence of pollen tubes on the bifurcated hairy stigma and style could be observed at different timings in different crosses. When pollen tube grew faster, there was a good seed set and vice-versa, except in common wheat × barley, ie, UP 2121 × Karan 265, UP 2121 × Karan 4 and UP 2121 × UP 2121 (Table 1). Pollen tube growth was very slow (99 μm at 30min after pollination) in durum wheat × barley and the seed set was also very poor (4%). When common wheat was crossed with barley, no such correlation was observed. In this case less seed set may be due to comparatively higher abnormal pollen tubes. Sudha (1991) reported a highly significant and positive correlation between pollen tube growth and seed set in wheat × barley crosses.

A study was made on the development of pollen tubes in different crosses to find out whether the disturbance of pollen tube growth was due to the abnormal development of pollen tubes. A striking aberration was swelling of pollen tube tips filled with densely stained cytoplasm. The degree of the swellings was variable. Other aberrations observed were wrong direction of pollen tubes/growth, swelling of the pollen tube tips and coiling of pollen tubes. The ratios of the abnormalities recorded after 24h of pollination were much higher in intergeneric crosses than in selfings (Table 1). There was no direct correlation between pollen tube abnormalities and seed set. Pollen tube inflation and bursting have also been shown in incompatible hybridizations of wheat × rye (Tozu 1966 Zeven and Heemert

Table 1. Pollen germination (upper, %), pollen tube growth (lower, μm) and frequency of pollen abnormalities in reciprocal wheat-barley crosses.

Cross	Duration after pollination					No. pollen/ stigma	Abnormal pollen tubes (%)	Seed set (%)
	5 min	30 min	60 min	4 h	24 h			
Self								
common wheat (UP 2121)	0	6.2	13.5	14.3	20.0	60	1.0	46.5
	0	71.5	82.5	88.0	95.0			
durum wheat (PBW 34)	0	0	3.6	10.7	25.0	42	0	38.3
	0	0	220.0	258.5	280.5			
barley (Karan 4)	0	2.9	3.7	3.8	4.5	114	0 .33	83.9
	0	55.0	99.0	115.5	148.5			
barley (Karan 265)	0	3.4	4.0	4.0	4.3	51	0	63.6
	0	60.5	60.5	126.5	148.5			
Wheat × barley								
UP 2121 × Karan 4	2.9	12.9	28.6	33.3	57.1	23	3.3	6.7
	16.5	38.5	60.5	137.5	148.5			
UP 2121 × Karan 265	0	5.2	9.6	11.5	52.9			
	0	55.0	247.5	522.5	544.5			
PBW 34 × Karan 4	0	0	4.0	5.3	14.3	16	0	4.0
	0	0	11.0	16.5	27.5			
PBW 34 × Karan 265	0	0	2.3	2.6	3.1	25	0 .8	4.0
	0	0	49.5	60.5	99.0			
Barley × wheat								
Karan 4 × UP 2121	0	3.3	4.0	4.7	9.7	107	1.2	55.5
	0	115.5	159.5	220.0	236.5			
Karan 4 × PBW 34	0	0	23.5	23.8	24.1	32	5.2	74.7
	0	0	121.0	187.0	231.0			
Karan 265 × UP 2121	0	9.2	9.9	10.0	13.6	134	3.0	62.0
	0	115.5	181.5	231.0	253.0			
Karan 265 × PBW 34	0	0	2.7	4.4	5.2	93.	3.2	55.7
	0	0	99.0	126.5	214.5			

1970, Lange and Wojciechowska 1976, Jalani and Moss 1980, Singh and Khanna 1988) and barley × wheat (Fedak and Jui 1982, Sudha 1991).

Within the selfings, barley showed high seed set. Since wheat selfings were made at the end of the crossing programme when the temperature was getting high, a low seed set of wheat may be attributed to that. A good seed set was recorded in barley × wheat crosses (53.7–74.9 per cent) while it was poor in the reciprocal crosses (2–6.7 per cent). These results were also reported by Fedak (1980), Islam et al (1981) and Sudha (1991).

An increased seed set was observed after application of three hormones (GA_3, IAA and KIN) in all the crosses except Karan 4 × PBW 34 and Karan 265 × UP 2121 (Table 2). Kinetin seemed to be more effective as it increased seed set over control in eight out of the twelve crosses. This was followed by GA_3 (seven out of the twelve crosses) whereas IAA was the least effective (four out of the twelve crosses). IAA may not be useful in wheat-barley crosses as it increased seed set over control in only wheat × barley, ie, UP 2121 × Karan 265 where GA_3 gave a still higher seed set.

In wheat × barley crosses where seed set in the control is quite low as compared to the reciprocal cross, GA_3 increased seed set over the control in 3 out of 4 crosses whereas KIN increased it in only 1 out of 4 crosses.

Table 2. Effect of GA_3, IAA and KIN on seed set in selfing and in reciprocal wheat-barley crosses.

Cross	Seed set (%)			
	Cont.	GA_3	IAA	KIN
Self				
common wheat (UP 2121)	46.5	60.4	43.7	56.6
durum wheat (PBW 34)	38.3	44.8	26.2	40.6
barley (Karan-4)	83.9	77.2	90.7	91.0
barley (Karan-265)	63.6	94.0	80.9	85.7
Wheat × barley				
UP 2121 × Karan 4	6.7	4.4	6.6	2.8
UP 2121 × Karan 265	2.0	8.7	7.3	2.0
PBW 34 × Karan 4	4.0	6.2	3.1	5.8
PBW 34 × Karan 265	4.0	13.3	6.2	3.3
Barley × wheat				
Karan 4 × UP 2121	55.5	70.4	27.5	65.0
Karan 4 × PBW 34	74.7	44.6	62.9	81.0
Karan 265 × UP 2121	62.0	44.4	32.9	58.3
Karan 265 × PBW 34	53.7	48.4	48.8	58.0

In barley × wheat crosses enough seeds were obtained in the control so the utilization of hormones may not be so important as in the reciprocal cross. In this cross KIN increased seed set over control in 3 out of 4 crosses as compared to 1 out of 4 with GA_3. It is suggested that spray of GA_3 would be more useful while making wheat × barley crosses whereas KIN may be effective in the reciprocal crosses to get more seed. Kaltsikes and Gustafson (1986) reported that dousing the floret after pollination with an aqueous solution of 50 ppm GA_3 every day for 4 days helps increase seed set in triticale.

In the present study, it seems that pollen tube length is more related to per cent seed set than the other parameters studied.

Embryo rescue technique was applied by using Murashige and Skoog's (1962) medium and hybrid plants were obtained, since the seeds have no endosperms and are filled with liquids. The hybrid 'seeds' cannot germinate to produce the F_1 plants, hence the use of embryo rescue technique would be useful for transferring desirable characters from barley to wheat. Further investigations would be necessary to increase the possibility for obtaining the hybrid plants by this technique.

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Catalogue of gene symbols for wheat: 1992 supplement

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During the next year a new edition of the Catalogue will be produced. Wheat scientists are invited to propose revision of any section of the Catalogue, and to offer suggestions or corrections, that will result in a more accurate document.

Additions to Symbols List.

Acl	Acyl carrier protein
Bdv	Reaction to barley yellow dwarf virus
Embp	b-ZIP class DNA binding protein
Cxp	Carboxypeptidase
Fed	Ferrodoxin
Glb3	(1-3)-b-glucanase (EC3.2.1.39)
	(*Glb33* and *Glb35* encode isozymes III and IV, respectively.)
Lec	Wheat germ agglutinin, lectin
Ltn	Leaf tip necrosis
or	Osmoregulation
Rbpa	Rubisco binding protein, a subunit
Sbp	Sedoheptulose-1,7-bisphosphatase
Tlp	Thiolprotease
Xcnl	DNA markers of unknown function: Cornell University, Ithaca, New York, USA
Xglk	DNA markers of unknown function: Genetic Laboratory, Kyoto, Japan

Anthocyanin Pigmentation

Purple grain/pericarp

.........complementry genes (....1321). For review see 1332.

Blue Aleurone

For review see 1332.

Crossibility With Rye and *Hordeum* spp.

For list of wheat/rye crossibilities see ....., 1330.

DNA Markers

Place the following sentence at the beginning of the DNA Markers section:

"Other chromosomes bearing markers detected with the same probe are indicated in parentheses after the probe designation."

Substitute each of the following for the corresponding previous entry:

Group 1L

XAdh-1A,B,D [936].	[*Adh-A,B,D2* (936), *Xadh3'* (1133)].	p3NTR (936).	

Group 1

XksuD16-1D (1133).		pTtksuD16.	(*Ae. squarrosa* 5D).

Group 2S

Xpsr108-2A,B,D (937,1150).		PSR108.	(7A,B,D).
Xpsr109-2A,B,D (937,1150).		PSR109.	(5A,B,D).
XRbcs-2A,B,D (976,956).	[*rbcs-2A,B,D* (956)].	pW9 (979), pTS512 (957).	
Xpsr130-2A,B,D (937,1150).		PSR130.	
Xpsr131-2A,B,D (937,1150).		PSR131.	

Delete the *Xpsr122* current entry.

Group 2L

Xpsr112-2A,B,D (937,1150).		PSR112.	
Xpsr102-2A,B,D (937,1150).		PSR102.	

Group 2

XksuD18-2D(1) [1133].	[*XksuD18(A)-2D* (1133)].	pTtksuD18.	(*Ae. squarrosa* 4D).
XksuD18-2D(2) [1133].	[*XksuD18(B)-2D* (1133)].	pTtksuD18.	
XksuF19-2D (1133).		pTtksuF19.	(*Ae. squarrosa* 6D).

Group 3

XksuD7-3D (1133).		pTtksuD7.	(*Ae. squarrosa* 7D).

Delete all previous listings for *XksuF43* in Groups 4 and 5 and substitute the following:

Group 4

XksuF43-4D(1) [1133].	[*XksuF43(A)-4D* (1133)].	pTtksuF43.	(5D, *Ae. squarrosa* 6D).
XksuF43-4D(2) [1133].	[*XksuF43(B)-4D* (1133)].	pTtksuF43.	(5D).

Group 5

XksuF43-5D(1) [1133].	[*XksuF43(A)-5D* (1133)].	pTtksuF43.	(4D, *Ae. squarrosa* 6D).
XksuF43-5D(2) [1133].	[*XksuF43(B)-5D* (1133)].	pTtksuF43.	(4D).

Group 6S

XksuG44-6D (1133).		pTtksuG44.	(*Ae. squarrosa* 5D).

Group 6

XksuF24-6D (1133).		pTtksuF24.	(7D).
XksuM9S-6D (1133).		pTtksuM9S.	(*Ae. squarrosa* 5D).

Group 7S

Xpsr108-7A,B,D (1150).		PSR108.	(2A,B,D).
Xpsr150-7A,B,D (1150).		PSR150.	(2A,B,D,5A,B,D).

Delete *XSs2* entry.

Group 7L

Xpsr56-7A,B,D (933,919,949).	[*Xpsr117*(933,919)].	PSR56.	(3A,B,D).

Group 7

XksuF2-7D(1), (2), (4), (5) (1133).	[*XksuF2(A), (B), (D), (E)-7D* (1133)].	pTtksuF2.	(*Ae. squarrosa* 2D).
XksuF2-7D(3) (1133).	[*XksuF2(C)-7D* (1133)].	pTtksuF2.	
XksuF24-7D(3) (1133).		pTtksuF24.	(6D).

New Entries

Group 1S

XGli-A,B,D1-1 (1144,1145).	pTag 1436 (1147).	
XIca1-1A,B,D (1145).	pcI-1-4 (1146).	
Xpsr168-1A,B,D (1144, 1145).	PSR168.	
Xpsr381-1A,B,D (1145).	PSR381.	
Xpsr393-1A,B,D (1144, 1145).	PSR393.	
Xpsr596-1A,B,D (1145).	PSR596.	
Xpsr688-1A,B,D (1145).	PSR688.	
Xpsr908-1B (1150).	PSR908.	(2A,D,6B).

Group 1L

XcnlCDO1312-1B [1163].		CDO1312.	(4B,D,5A).
XLec-1A,B,D (1144,1145).		PNVR1 (1149).	
Xpsr121-A,B,D (1161).		PSR121.	(7A,B,D).
Xpsr158-1A,B,D (1144,1145).		PSR158.	
Xpsr159-1A,B,D (1144,1145).		PSR159.	
Xpsr325-1A,B,D (1144).		PSR325.	
Xpsr330-1A,B,D (1144,1145).		PSR330.	
Xpsr343-1A,B,D (1145).		PSR343.	
Xpsr361-1A,B,D (1145).		PSR361.	
Xpsr385-1A,B,D (1145).		PSR385.	
Xpsr391-1A,B,D (1144,1145).		PSR391.	
Xpsr549-1A (949,1150).		PSR549.	(2B,3A).
Xpsr586-1A,B,D (1145).		PSR586.	
Xpsr626-1A,B,D (1145).		PSR626.	
Xpsr653-1A,B,D (1145).		PSR653.	

Group 1

Xglk90-1B (963).		pTag90.	
Xglk94-1D (963).	[*Xglk94d* (963)].	pTag94.	(2,3D,6A).
Xglk136-1B (963).		pTag136.	
Xglk163-1B (963).		pTag63.	
Xglk427-1B (963).		pTag427.	
Xglk483-1B (963).		pTag483.	
Xglk520-1B (963).	[*Xglk520a* (963)].	pTag520.	(2,5A,3,6B).
Xglk549-1B (963).	[*Xglk549b* (963)].	pTag549.	(7B).
Xglk558-1D (963).		pTag558.	
Xglk595-1B (963).	[*Xglk595b* (963)].	pTag595.	(3A).
Xglk652-1D (963).	[*Xglk652a* (963)].	pTag652.	(3B).
Xglk710-1A (963).		pTag710.	
Xglk732-1A (963).		pTag732.	
Xglk764-1B (963).		pTag764.	

Group 2S

XPer-2A,B,D (1150).		POX375 (1152).	
Xpsr100-2A,B,D (1150).		PSR100.	(5A,B,D).
Xpsr107-2A,B,D (1150).		PSR107.	
Xpsr135-2A,B,D (1150).		PSR135.	
Xpsr137-2A,B,D (1150).		PSR137.	
Xpsr143-2A (1150).		PSR143.	
Xpsr146-2A,B,D (1150).		PSR146.	
Xpsr150-2A,B,D (1150).		PSR150.	(5A,B,D,7A,B,D).
Xpsr379-2A,B,D (1150).		PSR379.	
Xpsr549-2B (1150).		PSR549.	(1A,3A).
Xpsr566-2A,D (1150).		PSR566.	
Xpsr593-2B (1150).		PSR593.	(4B,7B).
Xpsr649-2A,D (1150).		PSR649.	
Xpsr666-2A,B,D (1150).		PSR666.	
Xpsr899-2B (1150).		ABA7 (1153).	(6A,D).
Xpsr900-2A,B,D (1150).		PSR900.	

Xpsr903-2D (949,1150).		PSR903.	(3A,B,D,5D).
Xpsr908-2A,D (1150).		PSR908.	(1B,6B).
Xpsr912-2A,B,D (1150).		PSR912.	(5A,5D).
Xpsr928-2A,D (1150).		PSR928.	
Xpsr933-2A,D (1150).		PSR933.	
Xpsr946-2D (1150).		PSR946.	(7A,DL,DS).
XRbpa-2A,B,D (956).		pSV10 (956).	
XSbp-2B(1) (1162,949).		S9.2 (951).	(2BL,3A,B,D,7B).
XSs2-2A,B,D (1150,1151).		pST3 (914).	

Group 2L

Xpsr102-2A,B,D (1150).		PSR102.	
Xpsr151-2A,B,D (1150).		PSR151.	
Xpsr304-2A,B,D (1150).		PSR304.	
Xpsr331-2A,B,D (1150).		PSR331.	
Xpsr380-2A,B,D (1150).		PSR380.	
Xpsr388-2A,B,D (1150).		PSR388.	
Xpsr390-2A,B,D (1150).		PSR390.	
Xpsr540-2A,B,D (1150).		PSR540.	(7B).
Xpsr571-2A,B,D (1150).		PSR571.	
Xpsr609-2A,B,D (1150).		PSR609.	
Xpsr630-2A,B,D (1150).		PSR630.	
Xpsr641-2A,B,D (1150).		PSR641.	
Xpsr681-2A,B,D (1150).		PSR681.	(6D,7B).
Xpsr687-2A,B,D (1150).		PSR687.	(7A,B,D).
Xpsr692-2A,B,D (1150).		PSR692.	
Xpsr901-2A,B,D (1150).		PSR901.	
Xpsr919-2A,B,D (1150).		PSR919.	
Xpsr932-2A,B,D (1150).		PSR932.	
Xpsr934-2A,B,D (1150).		PSR934.	
XSbp-2B(2) (1162,1150).		S9.2 (951).	(2BS,3A,B,D,7B).

Group 2

Xglk76-2A,B (963).	[*Xglk76a,b* (963)].	pTag76.	
Xglk94-2D (963).	[*Xglk94c* (963)].	pTag94.	(6A,1,3D).
Xglk175-2D (963).		pTag175.	
Xglk222-2D (963).		pTag222.	
Xglk293-2D (963).		pTag293.	
Xglk302-2B (963).	[*Xglk302b* (963)].	pTag302.	(4A).
Xglk331-2B (963).		pTag331.	
Xglk370-2B (963).		pTag370.	
Xglk398-2B(1),(2) (963).	[*Xglk398a,b* (963)].	pTag398.	
Xglk400-2B (963).		pTag400.	
Xglk407-2B (963).		pTag407.	
Xglk431-2D (963).	[*Xglk431a* (963)].	pTag431.	(4B).
Xglk452-2A (963).	[*Xglk452b* (963)].	pTag452.	(4A).
Xglk460-2A (963).		pTag460.	
Xglk471-2B (963).	[*Xglk471b* (963)].	pTag471.	
Xglk520-2A (963).	[*Xglk520c* (963)].	pTag520.	(5A,1,3,6B).
Xglk529-2B,D (963).	[*Xglk529a,b* (963)].	pTag529.	
Xglk539-2B (963).		pTag539.	

Xglk546-2B(1),(2) (963).	[*Xglk546e,f* (963)].	pTag546.	(5,7A,3,6B).
Xglk554-2A,B (963).	[*Xglk554a,c* (963)].	pTag554.	(5B).
Xglk578-2B (963).	[*Xglk578b* (963)].	pTag578.	(4A,B).
Xglk592-2B (963).		pTag592.	
Xglk594-2B (963).		pTag594.	
Xglk600-2A,B (963).	[*Xglk600a,b* (963)].	pTag600.	
Xglk605-2B (963).		pTag605.	
Xglk609-2B,D (963).	[*Xglk609b,a* (963)].	pTag609.	
Xglk610-2A (963).	[*Xglk610a* (963)].	pTag610.	
Xglk613-2D (963).		pTag613.	
Xglk618-2B (963).		pTag618.	
Xglk632-2A,B (963).	[*Xglk632a,b* (963)].	pTag632.	
Xglk653-2A,B (963).	[*Xglk653a,b* (963)].	pTag653.	
Xglk661-2B (963).	[*Xglk661c* (963)].	pTag661.	(4A,B,D).
Xglk664-2A,B (963).	[*Xglk664a,b* (963)].	pTag664.	
Xglk684-2A (963).		pTag684.	
Xglk687-2B (963).		pTag687.	
Xglk699-2B (963).		pTag699.	
Xglk703-2B (963).		pTag703.	
Xglk734-2D (963).		pTag734.	
Xglk738-2A (963).		pTag738.	
Xglk740-2A,B (963).	[*Xglk740b,a* (963)].	pTag740.	

Group 3S

Xpsr305-3A,B,D (949).		PSR305.	
Xpsr383-3A,B,D (949).		PSR383.	
Xpsr598-3A,B,D (949).		PSR598.	
Xpsr689-3A,B,D (1150).		PSR698.	
Xpsr902-3A,B,D (949).		PSR902.	
Xpsr903-3A,B,D (949,1150).		PSR903.	(2D,5D).
Xpsr907-3B (949).		PSR907.	
Xpsr909-3A,B,D (1150).		PSR909.	
Xpsr910-3A,B,D (1150).		PSR910.	
Xpsr930-3A,B (1150).		PSR930.	
Xpsr1196-3A,B,D (1154,1150).		PSR1196.	

Group 3L

XCxp1-3A,B,D (949).		pkc.3 (948).	
XEmbp-3B (947).		pGC19 (950).	(5A,B,D,6A,B,7D).
XGlb33-3A,B,D (1150).		p7E (1156).	
XGlb35-3B,D (1150).		G5 (1156).	
XSbp-3A,B,D (1162,949).		S9.2 (951).	(2BS,BL,7B).
Xpsr56-3A,B,D (949,1150).		PSR56.	(7A,B,D).
Xpsr74-3A,B,D (949).		PSR74.	
Xpsr78-3A,B,D (949).		PSR78.	
Xpsr116-3A,B,D (949).		PSR116.	
Xpsr125-3A,B,D (949).		PSR125.	
Xpsr156-3A,B,D (949).		PSR156.	
Xpsr170-3A,B,D, (949).		PSR170.	(5A,B).
Xpsr347-3A,B,D (949).		PSR347.	
Xpsr354-3A,B,D (949).		PSR354.	

Xpsr394-3A,B,D (949).		PSR394.	
Xpsr454-3B (949).		PSR454.	
Xpsr543-3A,B,D (949).		PSR543.	
Xpsr570-3A,B,D (949).		PSR570.	
Xpsr578-3A,B,D (949).		PSR578.	
Xpsr549-3A (949,1150).		PSR549.	(1A,2B).
Xpsr754-3A,B,D (1150).		PSR754.	
Xpsr904-3A,D (949).		PSR904.	(6A).
Xpsr916-3A,B,D (1150).		PSR916.	
Xpsr923-3A,B,D (1150).		PSR923.	
Xpsr931-3A,B,D (1150).		PSR931.	
Xpsr1060-3A,B,D (1150,1154).		PSR1060.	
Xpsr1067-3D (1150,1154).		PSR1067.	
Xpsr1077-3A,B,D (1150,1154).		PSR1077.	
Xpsr1149-3A,B,D (1150,1154).		PSR1149.	
Xpsr1203-3A (1150).		PSR1203.	
Xpsr1205-3A,B,D (1150).		PSR1205.	
XTlp-3A,B,D (1150).		pHv14 (1155).	

Group 3

Xglk80-3B (963).		pTag80.	
Xglk94-3D (963).	[*Xglk94a* (963)].	pTag94.	(6A,1,2D).
Xglk118-3A (963).		pTag118.	
Xglk221-3A (963).		pTag221.	
Xglk223-3B (963).		pTag223.	
Xglk485-3A (963).		pTag485.	
Xglk520-3B (963).	[*Xglk520b* (963)].	pTag520.	(2,5A,1,6B).
Xglk538-3B,D (963).	[*Xglk538a,b* (963)].	pTag538.	
Xglk546-3B (963).	[*Xglk546c* (963)].	pTag546.	(5,7A,2,6B).
Xglk577-3A (963).		pTag577.	
Xglk595-3A (963).	[*Xglk595a* (963)].	pTag595.	(1B).
Xglk637-3B (963).		pTag637.	
Xglk645-3A (963).		pTag645.	
Xglk652-3B (963).	[*Xglk652b* (963)].	pTag652.	(1D).
Xglk683-3B (963).		pTag683.	
Xglk718-3A,B (963).	[*Xglk718a,b* (963)].	pTag718.	
Xglk724-3B (963).	[*Xglk724d* (963)].	pTag724.	(5A,6A,B,D).
Xglk747-3A (963).		pTag747.	
Xglk756-3B (963).	[*Xglk756a* (963)].	pTag756.	(5,6A).

Group 4S

XcnlBCD93-4A [1163].		BCD93.	(7A,D).
XcnlCDO484-4A [1163].		CDO484.	(5B,D).
XcnlCDO780-4A [1163].		CDO780.	(7A,D).
Xpsr115-4A (944).		PSR115.	(5B,D).
Xpsr139-4A,B,D (944).		PSR139.	
Xpsr147-4A,B,D (944).		PSR147.	(5A,B,D).
Xpsr153-4A,B,D (944).		PSR153.	
Xpsr166-4A,B,D (944).		PSR166.	
Xpsr580-4A (944).		PSR580.	(5B,D).
Xpsr593-4B (1150).		PSR593.	(2B,7B).

Group 4L

XcnlBCD1302-4B,D [1163].		BCD1302.	(5A).
XcnlCDO1312-4B,D [1163].		CDO1312.	(1B,5A).
XcnlWG114-4B,D [1163].		WG114.	(5A).
Xpsr164-4B,D (944).		PSR164.	(5A).

Group 4

Xglk128-4A (963).		pTag128.	
Xglk167-4A (963).		pTag167.	
Xglk210-4A (963).		pTag210.	
Xglk300-4B (963).		pTag300.	
Xglk302-4A (963).	[*Xglk302a* (963)].	pTag302.	(2B).
Xglk315-4A (963).		pTag315.	
Xglk335-4B (963).		pTag335.	
Xglk348-4D (963).	[*Xglk348a* (963)].	pTag348.	
Xglk354-4A (963).	[*Xglk354a* (963)].	pTag354.	(5B).
Xglk431-4B (963).	[*Xglk431b* (963)].	pTag431.	(2D).
Xglk450-4A (963).		pTag450.	
Xglk452-4A (963).	[*Xglk452a* (963)].	pTag452.	(2A).
Xglk512-4A (963).		pTag512.	(6A).
Xglk556-4B (963).		pTag556.	
Xglk578-4A,B (963).	[*Xglk578a,c* (963)].	pTag578.	(2B).
Xglk619-4A (963).		pTag619.	
Xglk650-4A (963).		pTag650.	
Xglk661-4A(1),(2),4B,D (963).	[*Xglk661a,e,d,b* (963)].	pTag661.	(2B).
Xglk694-4A,B (963).	[*Xglk694b,a* (963)].	pTag694.	
Xglk708-4A (963).		pTag708.	
Xglk752-4A (963).	[*Xglk752a* (963)].	pTag752.	(6B).

Group 5S

XAcl1-5A,B,D (961).		pACP11.	
Xpsr170-5A,B (949).		PSR170.	(3A,B,D).
Xpsr903-5D (949,1150).		PSR903.	(2D,3A,B,D).

Group 5L

XAcl3-5B (961).		pACP1.	(7A,B,D)
XcnlBCD87-5B,D [1163].		BCD87.	(7B).
XcnlBCD1302-5A [1163].		BCD1302.	(4B,D).
XcnlCDO484-5B,D [1163].		CDO484.	(4A).
XcnlCDO1312-5A [1163].		CDO1312.	(1B,4B,D).
XcnlWG114-5A [1163].		WG114.	(4B,D).
XEmbp-5A,B,D (947).		pGC19 (950).	(3B,6A,B,7D).
Xpsr79-5A,B,D [944].	[*Xpsr81* (944)].	PSR79.	
Xpsr100-5A,B,D (1150).		PSR100.	(2A,B,D).
Xpsr109-5A,B,D (1150).		PSR109.	(2A,B,D).
Xpsr115-5B,D (944).		PSR115.	(4A).
Xpsr120-5A,B,D(1),(2),(3) (944).		PSR120.	
Xpsr145-5A,B,D (944).		PSR145.	

Xpsr147-5A,B,D (1161).		PSR147.	(4A,B,D).
Xpsr150-5A,B,D (944).		PSR150.	(2A,B,D,7A,B,D).
Xpsr164-5A (944).		PSR164.	(4A,B).
Xpsr360-5A,B,D (944).		PSR360.	
Xpsr426-5A,B,D (944).		PSR426.	
Xpsr580-5B,D (944).		PSR580.	(4A).
Xpsr912-5A,D (1150).		PSR912.	(2A,B,D).
XRbcs-5A,B,D [956].	[*rbcs-5A,B,D* (956)].	pTS512 (957).	

Group 5

Xglk83-5B (963).		pTag83.	
Xglk157-5D (963).		pTag157.	
Xglk165-5B (963).		pTag165.	
Xglk251-5D (963).		pTag251.	
Xglk278-5A,B (963).	[*Xglk278a,b* (963)].	pTag278.	(6B).
Xglk317-5A(1),(2)(963).	[*Xglk317a,b* (963)].	pTag317.	(6A).
Xglk319-5B (963).		pTag319.	
Xglk354-5B (963).	[*Xglk354b* (963)].	pTag354.	(4A).
Xglk424-5A (963).		pTag424.	
Xglk505-5A (963).		pTag505.	
Xglk510-5A,B (963).	[*Xglk510a,b* (963)].	pTag520.	
Xglk520-5A (963).	[*Xglk520e* (963)].	pTag520.	(2A,1,3,6B).
Xglk546-5A(1),(2)(963).	[*Xglk546a,g* (963)].	pTag546.	(7A,2,3,6B).
Xglk554-5B (963).	[*Xglk554b* (963)].	pTag554.	(2A,B).
Xglk587-5A,D (963).	[*Xglk587a,b* (963)].	pTag587.	
Xglk612-5A (963).		pTag612.	
Xglk614-5A (963).		pTag614.	
Xglk621-5D (963).		pTag621.	
Xglk629-5B (963).		pTag629.	
Xglk644-5A (963).		pTag644.	
Xglk695-5D (963).		pTag695.	
Xglk701-5A (963).		pTag701.	
Xglk724-5A (963).	[*Xglk724a* (963)].	pTag724.	(6A,B,D,3B).
Xglk756-5A (963).	[*Xglk756c* (963)].	pTag756.	(6A,3B).
Xpsr170-5B (949).		PSR170.	(5AS,3A,B).

Group 6S

XEmbp-6B (947).		pGC19 (950).	(6AL,3B,5A,B,D,7D).
Xpsr681-6D (1150).		PSR681.	(2A,B,D,7B).
Xpsr899-6A,D (1150).		ABA7 (1153).	(2B).
Xpsr904-6A (949).		PSR904.	(3A,D).

Group 6L

XEmbp-6A (947).		pGC19 (950).	(6BS,3B,5A,B,D,7D).
Xpsr908-6B (1150).		PSR908.	(1B,2A,D).

Group 6

Xglk94-6A (963).	[*Xglk94b* (963)].	pTag94.	(1,2,3D).
Xglk172-6A (963).	[*Xglk172a* (963)].	pTag172.	(7A,B).

Xglk229-6B (963).		pTag229.	
Xglk259-6A (963).		pTag259.	
Xglk299-6A,D (963).	[*Xglk299a,b* (963)].	pTag299.	
Xglk317-6A (963).	[*Xglk317c* (963)].	pTag317.	(5A).
Xglk334-6A (963).		pTag334.	
Xglk479-6A (963).		pTag479.	
Xglk495-6D (963).		pTag495.	
Xglk512-6A (963).	[*Xglk512a* (963)].	pTag512.	(4A).
Xglk520-6B (963).	[*Xglk520d* (963)].	pTag520.	(2,5A,1,3B).
Xglk537-6A (963).		pTag537.	
Xglk546-6B (963).	[*Xglk546b* (963)].	pTag546.	(5,7A,2,3B).
Xglk547-6A(1),(2),(3),6B (963).	[*Xglk547a,b,d,c*(963)].	pTag547.	
Xglk562-6A (963).		pTag562.	
Xglk582-6B (963).		pTag582.	
Xglk680-6B (963).		pTag680.	
Xglk705-6B (963).		pTag705.	
Xglk724-6A,B,D (963).	[*Xglk724e,c,b* (963)].	pTag724.	(5A,3B).
Xglk736-6B (963).		pTag736.	
Xglk744-6B (963).		pTag744.	
Xglk752-6B (963).	[*Xglk752b* (963)].	pTag572.	(4A).
Xglk756-6A (963).	[*Xglk756b* (963)].	pTag756.	(5A,3B).
Xglk762-6A (963).		pTag762.	

Group 7S

XAcl3-7A,B,D (961).	pACP1 (1160).	(5B).
XcnlBCD87-7B [1163].	BCD87.	(5B,D).
XcnlBCD93-7A,D [1163].	BCD93.	(4A).
XcnlCDO780-7A,D [1163].	CDO780.	(4A).
Xpsr540-7B (1150).	PSR540.	(2A,B,D).
Xpsr946-7D(1) (1150).	PSR946.	(2D,7AL,7DL).

Group 7L

XEmbp-7D (947).	pGC19 (950).	(3B,5A,B,D,6A,B).
XFed-7A,B,D (960).	1.3 Kb *Hind*III fragment of a wheat gene.	
Xpsr121-7A,B,D (933,919).	PSR121.	(1A,B,D).
Xpsr593-7B (1150).	PSR593.	(2B,4B).
Xpsr681-7B (1150).	PSR681.	(2A,B,D,6D).
Xpsr687-7A,B,D (1150).	PSR687.	(2A,B,D).
Xpsr946-7A,7D(2) (1150).	PSR946.	(2A,7DS).
XSbp-7B (1162,949).	S9.2 (951).	(2B,3A,B,D).

Group 7

Xglk35-7A,B (963).	[*Xglk35b,a* (963)].	pTag572.	
Xglk61-7B (963).		pTag61.	
Xglk172-7A,B (963).	[*Xglk172b,c* (963)].	pTag172.	(6A).
Xglk184-7D(1),(2) (963).	[*Xglk184a,b* (963)].	pTag184.	
Xglk197-7B (963).		pTag197.	
Xglk301-7A (963).		pTag301.	
Xglk341-7A,D (963).	[*Xglk341b,a* (963)].	pTag341.	

Xglk349-7B (963).		pTag349.	
Xglk356-7B (963).		pTag356.	
Xglk439-7B (963).		pTag439.	
Xglk478-7B (963).		pTag478.	
Xglk536-7B (963).		pTag536.	
Xglk546-7A (963).	[*Xglk546d* (963)].	pTag546.	(5A,2,3,6B).
Xglk549-7B (963).	[*Xglk549a* (963)].	pTag549.	(1B).
Xglk576-7A (963).		pTag576.	
Xglk598-7B (963).		pTag598.	
Xglk642-7A (963).		pTag642.	
Xglk651-7A (963).		pTag651.	
Xglk658-7A (963).	[*Xglk658a* (963)].	pTag658.	
Xglk686-7A (963).		pTag686.	
Xglk702-7D (963).		pTag702.	
Xglk750-7B (963).		pTag750.	

Leaf Tip Necrosis

Ltn (1324). 7D. v: Wheats with *Lr34/Yr18* (1317, 1324).

Male Sterility

ms3. v: KS87UP9 (1333).

Nucleolus organizer regions

In the sentence which ends, ". . . . restriction endonuclease-treated DNA on Southern blots . . . .", delete "7" and "19" as references and substitute "719."

Osmoregulation

Osmoregulation is a specific form of solute accumulation regulating turgor pressure and hydration during periods of stress with positive effects on growth. Wheat lines selected for higher osmoregulation in the greenhouse have greater growth and seed yields under water limited conditions in the field.

High osmoregulation
or (1312). 7A(1312). v: Chinese Spring, Songlen, Condor, Takari (1312).

Low osmoregulation
Or (1312). s: CS(Red Egyptian 7A).
v: Red Egyptian, Capelle Desprez, Condor*4/3Ag#14(1312).

Proteins

2. Enzymes

IV. *a*-Amylase

After *a-Amy-R*^{m}*1*, insert

"It has been estimated (945) that there are two *a-Amy-1* genes in 6A and five or six in both 6B and

6D and three or four *a-Amy-2* genes at each of the 7A, 7B, and 7D loci."

Add the following sentences to the last paragraph in the *a*-Amylase section:

"Only one gene copy appears to be present at each locus. In rye, evidence has been obtained for three *a-Amy-1* genes, two or three *a-Amy-2* genes and three *a-Amy-3* genes (946)."

VI. Endopeptidase

Change the *Ep-A1a* entry to the following:

Ep-A1a (245,359). v: CS.

After the *Ep-A1c* entry, add the following:

"An EP isozyme encoded by *Ep-A1a* of CS is visible on zymograms following starch gel electrophoresis (245). The product of this allele is not observable, however, on zymograms following isoelectric focusing (359)."

Ep-D1b. v: H-93-70 (1335); 5L 219 (1335).

Ep-R1 (955). 6RL (955). ad: CS/Imperial.

VII. Esterase

Est-B5: Substitute (7) for (293) as reference for 3BL location.

Add immediately after *Est-D5* entries:

"Encoding of the endosperm esterases of hexaploid wheat by 12-15 genes in five compound loci located in 3AL, 3BL, 3DL, 3AS and 3DS has been postulated (952)."

Add:

Est-H1 (1140). 3H (1140). ad: CS/Betzes.

XII. Malate dehydrogenase

add

Mdh-R4 (1141). 1RL (1141). v: various crosses.

XVII. Superoxide dismutase
add

Sod-H1 (1140). 2H (1140). ad: CS/Betzes.
Sod-E1 (1140). VI (1140). ad: CS/*Ag. elongatum*.

XXII. NADH dehydrogenase

Modify,

Ndh-R1 (1125).	4RS (1125),	ad:	CS/Imperial, King II (1125, 1142).
	4R (1142).		CS/Dakold (1142).

Add

Ndh-E1 (1142).	4E (1142).	ad:	CS/*Ag. elongatum*.
Ndh-U1 (1142).	A (1142).	ad:	CS/*Ae. umbellulata*.

3. Endosperm Storage Proteins

II. Gliadins

Add:

Gli-S^{l}1 (943).	$1S^{l}$ (943).	ad:	CS/Ae. longissima
Gli-S^{l}2 (943).	$6S^{1}$ (943).	ad,su:	CS/Ae.longissma
Gli-V1 (953).	1V (953).	ad:	Creso-*D. villosum*.
Gli-V2 (953).	6VS (953).	ad:	Creso-*D. villosum*.
Gli-V3 (953).	4VL (953).	ad:	Creso-*D. villosum*.
Glu-V1 (953).	1V (953).	ad:	Creso-*D. villosum*.

4. Protease inhibitors

at end of section add:

'Three subunits of the wheat tetrameric inhibitor of insect *a*-amylase, CM1, CM3 and CM16, with homology to the dimeric and monomeric *a*-amylase inhibitors and the trypsin inhibitors, were located by Southern analysis of cDNAs pCT1, pCT2, and pCT3 to 4A, 4B, 4D; 7A, 7B, 7D; and 4A, 4B, 4D, respectively (1143).'

Restorers for Cytoplasmic Male Sterility

T.timopheevi cytoplasm

Rf1.	v:	R113 *Rf4* (1318).
Rf4.	v:	R113 *Rf1* (1318).

Ribosomal RNA

Substitute the following for the earlier listing:

5S rRNA genes

Within the Triticeae there are basically two 5S rRNA loci. One locus identified by repetitive units 320-468 bp in length is located on group 1 chromosomes. The other locus identifed by repetitive units 469-500 bp in length is on group 5 chromosomes. Within species the repetitive units at a locus are extremely uniform in size and sequence. They remain stable in foreign genetic backgrounds.

5S-Rrna-A1.	[*5SDna-A1* (1076)].	1AS (1076).	dv:	*T. monococcum*
5S-Rrna-B1.	[*5SDna-B1* (1076)].	1BS (29, 1076).	v:	CS.
5S-Rrna-D1.	[*5SDna-D1* (1076)].	1D (1076,1077).	v:	CS (1076, 1077).

		1DS (1076).	dv:	*T. tauschii* (1077).
5S-Rrna-E1.	[*5SDna-E1* (962)].	1E (1097).	dv:	*L. elongatum*.
5S-Rrna-R1.	[*5SDna-R1* (1078)].	1RS (29, 1078).	al:	*S. cereale*.
5S-Rrna-S^{c}*1*.	[*5SDna-*S^{c}*1* (962)].	1S^{c} (1097).	al:	*Elymus ciliaris*.
5S-Rrna-S^{t}*1*.	[*5SDna-*S^{t}*1* (962)].	1S^{t} (1097).	al:	*E. trachycaulus*.
5S-Rrna-Y1.	[*5SDna-Y1* (962)].	1Y (1097).	al:	*E. ciliaris*.
5S-Rrna-A2.	[*5SDna-A2* (1076)].	5AS (1076).	v:	CS.
			al:	*T. monococcum*.
5S-Rrna-B2.	[*5SDna-B2* (1076)].	5BS (1076).	v:	CS.
5S-Rrna-D2.	[*5SDna-D2* (1076)].	5D (1076,1077).	v:	CS (1076, 1077).
		5DS (1077).	dv:	*T. tauschii* (1077).
5S-Rrna-R2.	[*5SDna-R2* (1078)].	5RS (1078).	al:	*S. cereale*.
5S-Rrna-H^{t}*2*.	[*5SDna-*H^{t}*2* (962)].	5H^{t}(1097).	al:	*E. trachycaulus*.
5S-Rrna-U2.	[*5SDna-U2* (1076)].	5U (1076).	al:	*T. umbellulatum*.
5S-Rrna-V2.	[*5SDna-V2* (962)].	5V (1097).	al:	*D. villosa*.

A single 5S rRNA hybridization site was observed in barley. The chromosome involved was not one of those identified by the presence of secondary constrictions (29), but Kolchinsky *et al.* (1084) located a predominant short repetitive sequence (320 bp) to 2H.

Pathogenic Disease/Pest Reaction

Reaction to Barley Yellow Dwarf Virus

Bdv1 (1325). v:

Reaction to *Diuraphis noxia*

Dn3 (recessive)(1311).	v:	*T. tauschii* SQ24/T. *turgidum* TD65(1311).
	tv:	*T. tauschii* SQ24 (1311).

Reaction to *Erysiphe graminis*

Pm1.	v:	Anfield *Pm9*, Pompe *Pm9*(1331), Ring *Pm9*.
Pm9.	v:	Anfield *Pm1* (1331), Pompe *Pm1* (1331), Ring *Pm1* (1331).

Complex genotypes: Drabent* *Pm2 Pm4b Pm9/Pm1 Pm2 Pm4b Pm9* (1331); Nemares *Pm1 Pm2 Pm4b Pm6 Pm9* (1331); Sappo *Pm1 Pm2 Pm4b Pm9* (1331).

Reaction to *Mayetiola destructor*

H7.	5D (1309).		
H21.	2B (1328) (2BS.2RL).	v:	Hamlet = KS89WGRC8 (1336); KSWR 69-2-4-3 (1328); KS85HF 011-5 (1328).
		ad:	KSWR 297-1-1-9 (1328).
		al:	Chaupon rye (1328).
H22.	1D (1329).	v:	KS86WGRC1 (1329).
H23.	6D (1334).	v:	KS89WGRC3 (1334).

H24. 3D (1334). v: KS89WGRC6 (1334).

H25. 6B (1337) (T 6BS.6BL-6RL). v: 88HF16 (1337).
4B (1337) (T 4BS.4BL-6RL). v: 88HF79, 88HF80, 88HF81, 88HF117 (1337).
4A (1337) (Ti 4AS.4AL-6RL-4AL). v: 89HF17, 89HF18, 89HF25, 88HF32, 88HF51, 88HF89 (1337).
6R (1337). al: Balbo rye (1337).

Reaction to *Pseudocercosporella herpotrichoides*

Pch. v: H-93-70 (1335); 5L 219 (1335).

Reaction to *Puccinia graminis*

Sr39 (1319). 2B (1071). v: RL5711 (1319, 1071). Amphiploid RL5347 (*Ae.speltoides / T.monococcum*) (1071).

Although *Sr39* produces similar responses to *Sr32*, also derived from *Aegilops speltoides*, recombination studies based on three crosses showed independent inheritance (1319). *Sr39* segregated independently of *Lr13* (1071).

Sr40 (1322). 2BS (1322). v: RL6087 = RL6071*7/PGR 6126;
RL6088 = RL6071*7/PGR 6195.
tv: *T. araraticum* PGR 6126; PGR 6195.

Reaction to *Puccinia recondita*

Lr12. v: Chinese Spring *Lr34* (1317); Sturdy *Lr13* (1317).

Lr34. v: Chinese Spring *Lr12* (1317), Sturdy *Lr12* (1317).

Lr38 (1313). 2A. v: W49.
(2AS.2AL-7Ai#2)su: W44 (7Ai #2 [7D]); W52 (7Ai #2 [7A]).
ad: T2.
Lr38 is derived from *Agr. intermedium.*

Lr39 (1320). Proposal still under discussion.

Lr40 (1320). Proposal still under discussion.

Lr41 (1326). 1D (1326). v: KS90WGRC10 = TAM107*3/*T. tauschii* TA 2460 (1327).
dv: TA 2460 (1327).

Reaction to *P. striiformis*

Yr2. v: HD2329 (1314); Kalyansona (1314); PBW54 (1314); PBW120 (1314); WG377 (1314); WH147 (1314); WL711 (1314); WL1562 (1314). Sonalika *YrA* (1314).

Yr7. v: PBW12 (1314); WL2265 (1314).

Yr18 (1323). 7D (1323). v: Jupateco 73R, Wheats with *Lr34* (See *Lr34*).

Lr34/Yr18 is also closely associated with *Ltn*, a gene for leaf tip necrosis (1324).

Reaction to *Shizaphis graminum*

Gb5. 7S (1315). s: CI17882, CI17884, CI17885 (798).
In all these wheats chromosome 7S substitutes for 7A (1315).

Genetic Linkages

Chromosome 1DS

Gli-D1	-	*Rg2*	1.4 +/- 1.4 cM	(1316).
	-	*Lr21*	5.6 +/- 2.7 cM	(1316).
	-	*Glu-D1*	I	(1316).
Rg2	-	*Lr21*	4.2 +/- 2.4 cM	(1316).
	-	*Glu-D1*	I	(1316).
Lr21	-	*Glu-D1*	I	(1316).

Gene order *Gli-D1* - *Rg2* - *Lr21* (1316).

Chromosome 2B

Sr39	-	*Lr35*	3.0 +/- 1.1%	(1071).

Chromosome 4B

Adh-B1	-	centromere	20.0 +/- 3.5%	(1310).

Chromosome 6BS

telomere	-	*Lr36*	<9.9%	(1072).
centromere	-	*Lr36*	46.3 +/- 4.0 cM	(1072).
			26.0 +/- 7.9 cM	(1072).

Lr36 is distal to *Gli-B2* (1072).

Chromosome 6D

H13	-	*H23*	25 cM	(1329).

Chromosome 7AL

Pm1	-	*Pm9*	8.5 cM	

Chromosome 7D

Ltn	-	*Lr34/Yr18*	<0.013	(1324).

Chromosome 6D

H13	-	*H23*	25 cM	(1329).

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Number 74: 54 – 60 (1992)

Information

1. Symposium/Workshop

The 8th International Wheat Genetics Symposium

(July 20–25, 1993 in Beijing, China)

In this symposium scientific program will place emphasis of the most recent and exciting developments in wheat genetics. Following topics are suggested for the program: Evolutionary and genome relationship, Cytogenetics/Transfer of alien genetic material/Genetic resources, Molecular genetics/Biotechnology, General genetic analysis/Gene mapping and marker systems, Genetics of resistance to pathogens and pests, Genetical approaches to breeding.

The first announcement is now available from secretary-general of this symposium. More detailed information will appear in the next issue of Wheat Information Service (No. 75).

Prof. Chen Shouyi
Secretary-General of 8th IWGS
Institute of Genetics, Chinese Academy of Sciences
Beijing, 100101, CHINA
FAX: 86–1–4914896, Tel: 86–1–4914896, Telex: 222337ICCST CN

Evaluation and Utilization of Biodiversity in Wild Relatives and Primitive Forms for Wheat Improvement: An International Workshop

(12–15 October 1992 in Aleppo, Syria)

Worldwide concern has been expressed that agricultural production needs to be increased using ecologically responsible farming systems with long-term sustainablility. This requires plant breeding and agronomic solutions to crop improvement. Several wheat cultivars have been developed with specific nutritional qualities that allow production on soil where yield is limited by salinity and poor nutrient availability. Future progress, therefore, will depend on identifying agronomically important genes and understanding their physiological, biochemical, and genetic behavior when transferred to cultivated species.

Wheat is one of the earliest crops to be brought under cultivation through domestication, and has now acquired a wide range of distribution throughout the world. To realize further advance in its breeding and address new demands for improved yields with tolerance to stresses, it has become increasingly urgent to broaden its genetic base with the introduction of genes from other sources, such as wild relatives and previously cultivated species.

Present-day crop plants were domesticated from wild progenitors and selected from a primitive genepool. The former's usefulness in modern plant breeding depends on their cytogenetic affinity and barriers to hybridization, the amount of available germplasm for

evaluation, and the presence of desirable traits, and also on whether repeated backcrossing is needed to eliminate undersirable characteristics introduced from the wild or primitive parent.

This workshop over a period of four days will review progress toward evaluation and utilization of wild relatives of wheat and its primitive forms, identify areas of research where emphasis needs to be placed, and indicate possible imbalances between theoretical and taxonomic studies and experimental verification.

The program: The Workshop will bring together scientists from diverse disciplines, such as germplasm collectors, genebank personnel, cytogneticists, biochemists, stress physiologists, pathologists, etc. to exchange ideas and information about the status of wild relatives and primitive forms and their usefulness in wheat improvement. Emphasis will be on methods of evaluating genetic variability and recognizing desirable genes, studies in crossability of wild germplasm with cultivated wheat, as well as biotechnological advances in overcoming barriers to crossing and difficulties in chromosome pairing. It will feature invited and contributed papers in all areas of research and particularly in: Taxonomy, Germplasm evaluation, Disease resistance, Tolerance to salinity, Grain quality of primitive forms, Utilization of germplasm, Constraints to use of wild relatives, Use of biotechnology, Development of networks.

Invited papers will be sought from scientists who have achieved international recognition for their work in areas of interest to the Workshop.

A program of activities for persons accompanying Workshop delegates will be prepared if there is sufficient interest. A tour of the ancient and historic city of Aleppo will be arranged.

Proceedings: Proceedings of the Workshop will be published in English.

Location: The Workshop will be held at Tel Hadya, ICARDA's principal research station, located 37km south of Aleppo.

Accommodation: Rooms at specially discounted rates will be available at a Hotel (4-star). Average temperature during October is 22–25C. Light rain is possible for a short period.

For further information and registration (no fee), please contact:

Dr. A. B. Damania
Genetic Resources Unit,
ICARDA, P. O. Box 5466,
Aleppo, Sylia
Telex: 331206, 331208, 331263 ICARDA SY. Fax: (963–21) 225105 or 213490

Mendel Forum

(July 20–22, 1992 in Brno, Czechoslovakia)

This Forum will be held in honor of the 170th anniversary of birth of Gregor Johann Mendel (1822–1884).

Mendelianum Musei Moraviae, Gregor Mendel Genetical Society of the Czechoslovak Biological Association, Czechoslovak Socity of Medical Genetics of the Medical Association of J. E. Purkyne, and Czechoslovak Committee for the History of Science and Technology invite you to participate in the Mendel Forum to be held directly in the place where Mendel lived and worked, and to discuss the latest achievements in the following thematic groups: Concept of Gene, Interrelations between Molecular and Organismal Genetics, Acceptance of Mendel's theory in different countries, and Ethical problems in Genetics. English is working language. Contact the head of Mendelianum Musei Moraviae for detailed information:

Dr. Anna Matalova
Head, Mendelianum Musei Moraviae
Mendelovo namesti
603 00 Bruno
Czechoslovakia

Forth International Workshop on Seeds. Basic and Applied Aspects of Seed Biology
(20–24 July, 1992 in Angers, France)
Place of the Meeting: Centre de Congres, 33 boulevard Carnot, 49100 Angers, France.
Travel to Angers: It is easy to get to Angers. By train, from Paris (gare Montparnasse); 11 trains per day. Journey time: 90 minutes. By road: 300 km from Paris.
Official Language: French and English. Simultaneous translation will be provided in all sessions.
Registration Final Date: 15 April, 1992 (increased charge after this date).
Date of final manuscript of oral communication and poster papers: 1, July, 1992.
For detailed information contact:

Professeur D. Come,
Universite Pierre et Marie Curie
-Physiologie Vegetable Appliquee, Tour 53, 1er etage
4, place Jussieu – 75252 Paris Cedex 05 – France
Tel: (33–1) 44.27.59.26, Fax: (33–1) 44.27.59.27, Telex: 200 145 UPMC SIX F

Sixth International Symposium on Pre-Harvest Sprouting in Cereals
(July 25–29, 1992 in Coeur d'Alene, Idaho USA)
This interdisciplinary symposium is designed to facilitate communication among those who are actively interested in and working on problems related to pre-harvest sprouting in cereals. Topics include mechanisms of dormancy, influence of environmental and agronomic factors, molecular regulation of seed development and germination, genetics and plant breeding, effects of sprouting damage on cereal end products, and sprouting damage assay methods.
Final Call of Papers: Research reports and critical reviews on all aspects of preharvest

sprouting in cereals are invited. Participants wishing to present an oral paper or poster should complete the Abstract from of the Second Circular. The completed form and one copy should be sent by air mail to M. K. Walker-Simmons, and received before May 15, 1992.
Proceedings: The proceedings will be published by the American Association of Cereal Chemists (AACC) in a volume entitled *Pre-Harvest sprouting in Cereals 1992.*
For detailed information contact:

Dr. M. K. Walker-Simmons
Symposium Director
USDA-ARS, Pulluman, WA, U.S.A.

Plant Genome I

(November 9–11, 1992, at Town & Country Hotel, San Diego, CA, U.S.A.)
Sponsors: Agricultural Research Service, USDA/ARS; National Agricultural Library, USDA/NAL; John Innes Centre (U.K.); National Institute of Agrobiological Resources, NIAR (Japan).
Chairmen: S. Heller (USDA/ARS), J. Miksche (USDA/ARS), M. Gale (John Innes Center), K. Takayanagi (NIAR).
Scientific Program: Purpose, Management & Organization; Mapping Projects; Informatics; Beyond the Map.
Proposed Satellite Sessions: Forest Tree Genome Mapping; Map Generation & Analytical Mapping Software Workshop.
Organizer:

Scherago International, Inc.
11 Penn Plaza, Suite 1003, New York, NY 1001, U.S.A.
Tel: (212) 643–1750, Fax: (212) 643–1758

Genome Mapping of Wheat and Related Species

(Sept. 23–25, 1992, at CIMMYT Headquater, Mexico)
The third annual international workshop on genome mapping of wheat and related species is open to anyone interested in the use of molecular markers for genetics and breeding of cereal crops, which is sponsored by the International Triticeae Mapping Initiative (ITMI). The objectives of the workshop will be to provide up-to-date reports on progress in molecular genetic mapping, and to provide a setting for interaction between scientists and the cereal crop industry.

The workshop will include the invited presentations which will adress strategies and techniques of genetic and physical mapping, the use of genetic stocks in mapping, and the progress of mapping in wheat and related species. Oral or poster presentations on related topics are invited. No registration fee will be charged, but space is limited to apporoximately 60 participants, so advance registration is required. Registration deadline is 1 June,

1992, mailing to;

Dr. David Hoisington
CIMMYT
Lisboa 27
Apdo. Postal 6-641
06600 Mexico, DF MEXICO

or FAX to;

Ms. Susana Vefazquea 52-5-954-1069

ITMI bussiness office
Calvin O. Qualset, Director
US Genetic Resouces Conservation Program
Univ. of California, Davis, CA 95616 USA
Phone: (916) 757-8920, FAX: (916) 757-8755

2. Book

Proceedings of International Symposium: Wheat Breeding Prospect and Future Approaches

(400 pages with 86 scientific papers)

The present collection comes as a result of the efforts and work of scientists in the field of genetics and selection of wheat, who have participated in the International Symposium "Wheat Breeding — Prospects and Future Approaches" held on 4-8 June 1990 in the resort of Albena, Bulgaria. The aim of the Symposium was to gather in one place scientists in the fields of selection and biotechnologies, phytopathologists and other researchers, in order to exchange views regarding the future development and direction of wheat selection.

During the past 20 years, selection has demonstrated marked achievements, especially as concerns productivity. At the present time, however, new problems arise, mostly concerning the protection of the environment. This has meant the creation of new varieties, resistant to diseases, which do not require chemical treatment. The creations of varieties with minimal requirements regarding nitrates, especially nitrogen, the assimilation of hard to acquire phosphates, the processing of these elements and their storage in the grains, are of paramount importance. Draught-resistance is also of significant importance for obtaining stable crop yields. Resistance against other stress factors assumes primary importance for certain regions. Evidently selection aiming toward increase of productivity in linked above all to ecological flexibility and resistance to stress factors. Undoubtedly, a principal condition in wheat cultivation is that production should be cheaper and possess a much higher quality. All this predetermines the need for creation of diverse varieties of wheat from fodder-wheat of high agrotechnical quality to high grade flexible and economically effective varieties. This aim, coupled with the efforts of many scientists in the field of selection, agrochemists, physiologists and other specialists, will find their relization

in new varieties, suitable for cultivation in the year 2000. We hope that varieties of this kind will correspond to the greatest extent to the complex environmental condition of the future. The experience of numerous specialists, without a shadow of doubt will contribute towards the attainment of this goal, which was one of the foremost tasks of the Symposium. Prof. I. Panayotov, Ph. D. (from Preface of the proceedings)

To purchase or get detailed information, contact:

Prof. I. Panayotov
Institute for Wheat and Sunflower "Dobroudja"
Agricultural Academy of Bulgaria
near General Toshevo
Bulgaria

Nuclear and Organellar Genomes in Wheat Species: Proceedings of Dr. H. Kihara Memorial International Symposium on Cytoplasmic Engineering in Wheat

International symposium on Cytoplasmic Engineering in Wheat (ISCEW) was held at Hokkaido University, Sapporo Japan in July 4–6, 1991, in commemoration of Dr. Hitoshi Kihara (See WIS 73: 60–62). The symposium was organized to exchange information and ideas between molecular biology and classical genetics from basic evolutionary studies to applied breeding. Proceedings from the symposium have been just published from Kihara Memorial Foundation, entitling "Nuclear and Organellar Genomes in Wheat Species" (edited by T. Sasakuma, Kihara Institute for Biological Research)

The 310-page book contains 35 research articles, consisting of the five sections: 1) Histrical backgrounds of cytoplasmic genetics in wheat species, 2) Nuclear genomes, 3) Organellar genomes and genes, 4) Nucleus-cytoplasm interactions, and, 5) New approaches of wheat breeding. Four special lectures were also included, namely; 1) Progress of NC-heterosis studies in wheats by Dr. T. Kinoshita (Hokkaido University), 2) Histrical review of studies on cytoplasms in wheat and its relatives by Dr. K. Tsunewaki (Kyoto University), 3) mRNA editing and tRNA import in plant mitochondria by Dr. J. H. Weil (University of L. Pasteur), and 4) Nuclear and cytoplasmic control of anther culture in responses in wheat by C. F. Konzak (Washington State University).

Price of the book is 5000 yen (including mailing cost), and can be purchased by mail order to;

Kihara Memorial Foundation
Mutsukawa 3–122–20, Minami-ku,
Yokohama 232, Japan
Fax: 045–715–0022

3. Database

Wheat Database as Part of the U. S. Department of Agriculture's Plant Genome Initiative
The United States Department of Agriculture's Plant Genome Initiative Program includes support for the establishment of plant database at the National Agricultural Library in Washington, D. C. The database will be publically accessible via telephone and network connections, and will eventually be distributable on CD-ROM. The database is currently being prototyped using five plants as models in the design phase.
The five include three crops (maize, soybeans, and wheat) plus pine trees and the laboratory model plant *Arabidopsis*. Types of data in the databases include genetic maps, loci, probes, germplasm and connections among the different data types. Data for each of the five plants is being examined to determine what specific data needs may exist for different plants and the specific interested scientific plant communities. At a latter date the five individual databases will be merged into the master database at the National Agricultural Library along with all other plant data. It is planned to be settle on wheat prototype design by May, 1992, with a version of the database running for evaluation by September, 1992.

The wheat database prototype is being set up at the USDA's Western Regional Research Center, Albany, California, and is being coordinated by Dr. Olin D. Anderson. The database is being designed and implemented in association with the Computing Science Group at the Lowrence Berkeley Laboratory. In addition to the computer database, a repository for the storage and distribution of clones, probes, and libraries will be established, and some technical resources research carried out to contribute to genome mapping of Triticeae.

It is the intent of the program to solicit as much international coordination and cooperation as possible to maximize both the amounts of useful information gathered, and the most useful presentation and accessibility possible for cereal researchers. Dr. Anderson is cooperating with the International Triticeae Mapping Initiative (ITMI) organization in the database design and information assembly. Although there is currently support for establishment of the wheat database, coodination and cooperation in data assembly will be critical to the project's success and maintenance of the database once established. Any individuals, departments, groups, etc., wishing more information on wheat database, and especially those able to contribute information and/or ability to participate in the data assembly and maintenance are urged to contact:

Dr. Olin Anderson
ARS, USDA, WRRC
800 Buchanan Street
Albany, CA, 94710
U. S. A.
Tel: 510-559-5773
FAX: 510-559-5777

White Board

1. Comment to Dr. Tsunewaki's proposal on symbol designations (ref. WIS 73: 59)

1. If we use the plasmon donor's genome symbol to start the genome symbol, such as BAD for *T. aestivum,* we can recognize that it has the B plasmon.
2. Need the footnotes for the "Code".
3. Genome for *Ae. juvenalis* should be DMU, not DMJ.

Received in March 3, 1992 from:

Dr. Richard Wang
USDA-Agricultural Research Service
Forage and Range Research Laboratory
Utah State University
Logan, UT 84322-6300
U.S.A.

2. Remarks on the comments of Dr. R. Wang regarding the plasmon and organellar genome designation

1. On the nuclear genome designation:

It is a good idea to consider the donor of cytoplasm in formulating the nuclear genome constitution of amphiploid species, because it is a general rule to indicate the female parent first followed by the male parent in showing a hybrid cross combination.

However, the presently used nuclear genome formulae recognize the priority for the genus specific (in the case of *Triticum* species) or the section-specific genome (in the case of *Aegilops* species), placing these genomes in the top of the genome formulae. Those are the A genome of the *Triticum* genomes, the C genome of Cylindropyrum, the C^u genome of Polyeides, and D genome of Vertebrata, the sections of *Aegilops.* I am in favor of retaining the present genome formulae because the species characteristics are mainly controlled by the nuclear genomes.

2. On the code number of the cytoplasm:

This is the accession number given to each cytoplasm. Nos. 1–20 are reserved for the cytoplasms of diploid species, nos. 21–50 for those of tetraploids, and no. 51 and above for those of hexaploids. The sources of the cytoplasms corresponding to the presently used code numbers are given in the following table;

Code number	Source (cytoplasm donor)		Remarks
	Taxon	Strain or cultivar	
01	*T. boeoticum* var. *aegilopoides*		
02	*Ae. caudata* var. *polyathera*		H. Kihara
03	*Ae. umbellulata*		M. Muramatsu
04	*Ae. squarrosa*	No. 2 (4x)	H. Kihara
05	*Ae. comosa*	No. 2	
06	*Ae. heldreichii*		I. Panayotov
07	*Ae. uniaristata*		S. S. Maan
08	*Ae. speltoides* var. *ligustica*	(SSAA of R. Riley)	
09	*Ae. speltoides* var. *aucheri*		I. Panayotov
10	*Ae. sharonensis*		S. Sakamoto
11*			I. Panayotov
12	*Ae. bicornis*		S. S. Maan
13	*Ae. mutica*	M	S. S. Maan
14	*Ae. mutica*	P	I. Panayotov
15	*Ae. speltoides* var. *ligustica*		S. S. Maan
16	*T. monococcum* var. *flavescens*		I. Panayotov
17	*Ae. speltoides* var. *aucheri*	KU2201B	
18	*Ae. searsii*	(S^sS^sAA of Feldman)	
19	*Ae. squarrosa* var. *anathera*	KU2009	T. Sasakuma
20	*Ae. longissima*	(S^lS^lAABB of H. Tsujimoto)	
21	*T. dicoccoides* var. *spontaneonigrum*		
22	*T. dicoccum*	cv. Vernal	
23	*T. araraticum*		
24	*T. araraticum*		S. S. Maan
25	*T. timopheevi*		J. W. Schmidt
26	*Ae. triuncialis*		
27	Synthetic *Ae. triuncialis*	(C^uC^uCC of N. Kondo)	
28	*Ae. cylindrica*		
29	*Ae. biuncialis*	No. 1	S. Sakamoto
30	*Ae. columnaris*	No. 2	S. Sakamoto
31	*Ae. ovata*		H. Fukasawa
32	*Ae. triaristata*	No. 7 (4x)	
33	*Ae. kotschyi*	No. 2	S. Sakamoto
34	*Ae. variabilis*	No. 1	S. Sakamoto
35	*Ae. crassa*	(4x)	S. S. Maan
36	*Ae. ventricosa*	No. 4	
37	*Ae. biuncialis* var. *macrochaeta*		I. Panayotov
38	*Ae. triuncialis*		I. Panayotov
39	*Ae. triuncialis*	BEC2926	
51	*T. zhukovskyi*		S. S. Maan
52	common wheat		
53	*Ae. juvenalis*		S. Sakamoto

54	*Ae. triaristata*	No. 1 (6x)	S. Sakamoto
55	*Ae. crassa*	No. 2 (6x)	S. Sakamoto
56	*Ae. vavilovii*		I. Ohtsuka
57	*Ae. triuncialis* var. *recta*		I. Panayotov
58	*T. aestivum* ssp. *tibetanum*		

Remarks: Names of the persons from whom an alloplasmic line of common wheat having the respective cytoplasm was received, that was used as the source of the cytoplasm in the production of our own alloplasmic lines. Non-remarked cytoplasms were introduced by K. Tsunewaki and his coworkers.

*: Originally tagged as an *Ae. longissima* cytoplasm that was later found to be the cytoplasm of common wheat by its mitochondrial DNA analysis.

Received in April 4, 1992 from:

Dr. K. Tsunewaki
Laboratory of Genetics
Kyoto University
Kyoto 606, Japan

Editorial Remarks

Since the reorganization of Wheat Information Service had been announced in 1991, valuable advice and information have been sent to the business office to improve the quality and reputation of WIS. Some of the advice are realized in the present issue, in which an invited review article appears by Dr. K. Nishikawa, a member of Advisory Board. WIS has decided to expand the pages for various information concerning wheat researches, and, also, incorporate the space called "White Board" for the purpose of comments, opinions etc. from readers.

The following table shows the recent statistics of WIS distibution covering 45 countries of the world. We should be proud of having this wide distribution of membership, from which we can expect further contributions to wheat researches. Newly organized members of International Advisory Board and Editorial Board are glad to have your contribution on research article, record or list of genetic stocks, as well as various information.

The next issue (No. 75) will be published in October 1992. Deadline for publication to the issue is September 15, 1992. Research articles accepted by the time, and information, genetic lists and records received by the time will appear in this issue. Facsimile is convenient for business correspondence (Country code of Japan 81, FAX No. 45-715-0022). Please notify us whether you want to be listed or withdrawn from the mailing list.

Distribution of Wheat Information Service (1992, 3, 30)

Country	Personal	Institution	Total	Country	Personal	Institution	Total
Argentina	7	1	8	Japan	89	25	114
Australia	8	14	22	Jordan	1	0	1
Austria	1	0	1	Kenya	0	1	1
Brazil	6	0	6	Mexico	8	2	10
Bulgaria	1	0	1	New Zealand	2	1	3
Canada	16	4	20	Pakistan	6	1	7
Chile	1	0	1	Philippine	3	1	4
China	3	0	3	Poland	5	1	6
CIS (USSR)	1	0	1	Portugal	2	0	2
Czechoslovakia	2	1	3	Rumania	2	0	2
Egypt	6	0	6	Saudi Arabia	2	0	2
Finland	1	0	1	South Africa	4	1	5
France	5	4	9	South Korea	1	0	1
Germany	10	5	15	Spain	4	0	4
Greece	2	0	2	Sweden	9	5	14
Holland	2	4	6	Swizerland	0	2	2
Hungary	3	0	3	Syria	2	0	2
India	28	4	32	Taiwan	1	1	2
Iran	1	0	1	Turkey	3	0	3
Iraq	4	1	5	UK	8	8	16
Ireland	1	0	1	USA	74	16	90
Israel	6	2	8	Yugoslavia	4	2	6
Italy	12	5	17				
Total			45 countries		357	112	469

International Advisory Board

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Explanation of the picture on the cover

Types of primary and tertiary monosomics concerning A and B chromosomes. (See the review of K. Nishikawa in this volume for the detail.)

WIS No. 74

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