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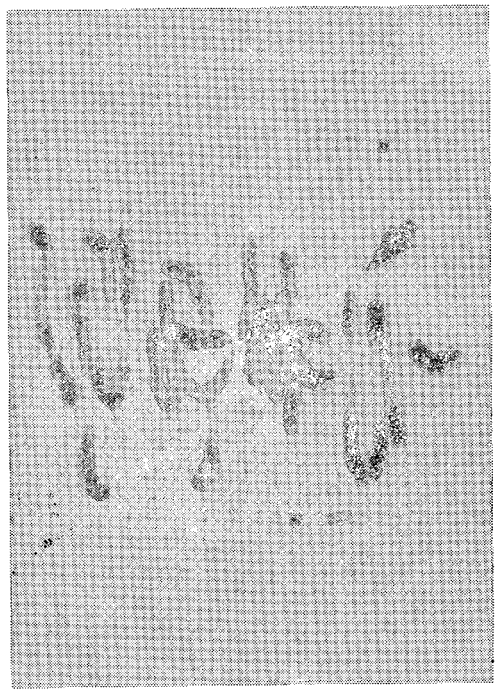

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CONTENTS

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I. Research Notes

A liguleless mutation radioinduced in *Triticum durum* Desf.

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Mutagenic treatments of dry seeds of *Triticum durum* cv. Capeiti and Ga B 125 (the latter being itself a radioinduced short straw mutant from the cultivar Garigliano) were made in 1967 in our Laboratory. Mutagens and doses applied are detailed in Table 1.

Table 1.

Varieties	Ga B 125	Capeiti
	Treatments	
Fast neutrons	700 reps	700 reps
〃 〃	550 〃	550 〃
Thermal neutrons	11.0×10^{12}/cm²/sec	11.91×10^{12}/cm²/sec
〃 〃	13.0×10^{12}/cm²/sec	13.52×10^{13}/cm²/sec
EMS	—	2%
〃	—	3%

Treated M_1 seeds were space planted and the main spike of each M_1 plant was bagged in order to prevent open pollination. M_2 generation was grown as M_1 spike progeny in spaced conditions.

Both Capeiti and Ga B 125 treated materials segregated in M_2 generation a mutation ("liguleless") for which "auricolae" are completely absent and "ligula" is strongly reduced. The leaf habit is consequently affected, being more erect not only in respect to mother variety but also to all other *durum* types. Studies in cereal crops have shown the higher efficiency in light utilization of erect leaves in respect to horizontal ones (Monsi and Saeki 1953, Saeki 1960). The positive correlation between erect leaves and a higher

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crop yield has also been proven in barley and wheat (TANNER *et al.* 1966) as well as in other cereals. The agronomic behaviour of the species is therefore presumably affected by the liguleless mutation.

In Capeiti, 2193 M_2 progenies were screened, out of which only one, from the treatment with fast neutrons at the dose of 700 reps, segregated the mutation. Segregation ratios in M_2 and M_3 and chi square of fitness under the hypothesis of monogenic inheritance and full dominance are given in Table 2:

Table 2.

Generation	Normal to liguleless segregation		Chi square	P
	observed	expected		
M_2	30 : 4	25.50 : 8.50	3.18	$0.10>P>0.05$
M_3	434 : 135	426.75 : 142.25	0.49	$0.50>P>0.25$

A slight deficit of liguleless individuals occurs in M_2 generation, presumably due to the chimeric structure of M_1 spike. As for other characters which can be of agronomic importance, a comparison is set in Table 3 between mother variety and mutant, grown in the same field environment. It is still to be ascertained whether the shorter culm and lower kernel weight exhibited by the mutant are due to side effects of the liguleless factor or to other modifications of the genetic background.

In Ca B 125, 1471 M_1 spike progenies were analyzed, and three of them were found to segregate liguleless plants. For each of them, Table 4 gives data about segregation ratios in M_2 and M_3 generations, under the hypothesis of monogenic inheritance and

Table 3.

Character	Liguleless mutant	Capeiti
Heading time*	8.56	8.44
(day of May)	0.27	0.22
No. of culms	2.63	2.82
	0.18	0.21
Culm length (cm.)	75.81	88.71
	1.41	1.40
No. of fertile spikelets	17.44	17.94
	0.53	0.45
Spikelet fertility	2.83	2.51
	0.15	0.07
1000 kernels weight (gr.)	36.13	49.07
	0.87	1.86

* For each character, values of the second row are standard errors.

Table 4.

M_2 progeny and mutagenic treatment	M_2 normal to liguleless		χ^2	P	M_3 normal to liguleless		χ^2	P
	observed segregat.	expected segregat.			observed segregat.	expected segregat.		
G1374 (Nf 700 r.)	13 : 2	11.25 : 3.75	1.09	$0.75>P>0.50$	160 : 38	148.5 : 49.5	3.56	$0.10>P>0.05$
G1008 (Nf 550 r.)	6 : 12	13.5 : 4.5	16.67	$P<0.01$	164 : 97	195.7 : 65.3	20.60	$P<0.01$
G624 (Nth 11.91×10^{12})	6 : 3	6.75 : 2.25	0.33	$0.75>P>0.50$	42 : 12	40.5 : 13.5	0.22	$0.75>P>0.50$

Table 5.

Character	Lines			
	G1374	G1008	G 624	Ga B 125
Heading time* (day of may)	10.70	10.25	8.94	10.70
	0.41	0.32	0.26	0.31
No. of culms	2.73	3.50	2.32	3.25
	0.30	0.32	0.22	0.27
Culm length (cm.)	82.67	84.67	73.58	89.20
	1.08	1.27	1.70	0.51
No. of fertile spikelets	16.73	17.22	17.32	17.90
	0.45	0.34	0.34	0.30
Spikelet fertility	2.10	2.36	2.46	2.26
	0.08	0.06	0.09	0.07
1000 kernels weight (gr.)	56.74	53.24	37.91	59.61
	1.42	1.52	1.51	1.07

* For each character, values of the second row are standard errors.

full dominance. Departures from expected ratios seem to occur in M_2 and M_3 segregations observed in G 1008 M_2 progeny. Data concerning other characters are given in Table 5 for each mutant progeny obtained from Ga B 125.

Mutant lines coming from both Capeiti and Ga B 125 are now being crossed each other with the purpose of checking whether the mutation has the same genetic basis. Transfer of the mutation itself to other genotypes for breeding purposes, as well as the agronomic evaluation of mutant lines, is also underway.

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Determination of the chromosome and its arm carrying the Ne_1-locus of *Triticum aestivum* L., Chinese Spring and the Ne_1-expressivity

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Summary

The Ne_1^w-locus of Chinese Spring was located on chromosome $5B^L$. It was found that the expressivity of three Ne_1^w-alleles of Chinese Spring is similar to one Ne_1^m-allele.

Introduction

The complementary genes Ne_1 and Ne_2 cause hybrid necrosis. The degree of necrosis depends on the nature and the dosage of the *Ne*-alleles and on the environment (HERMSEN 1962, 1963b). Three alleles of Ne_1 (Ne_1^w, Ne_1^m and Ne_1^s) and five alleles of Ne_2 (Ne_2^w, Ne_2^{mw}, Ne_2^m, Ne_2^{ms} and Ne_2^s) have been distinguished (HERMSEN 1963b).

Wheat varieties can be classified according to their *Ne*-genotype. Up to now about 597 Ne_1-, 654 Ne_2- and 1262 non-carriers have been identified (ZEVEN 1971).

The Ne_1^m-locus of Prelude is on 5B and the Ne_2^s-locus of Kharkov on 2B (TSUNEWAKI 1960). It is interesting to note that both loci are on chromosomes of the B genome.

Chinese Spring carries an extremely weak Ne_1-allele (HERMSEN 1964a). By using di-iso-$5B^L$ and di-telo-$5B^L$ of Chinese Spring it is possible to determine if chromosome 5B or rather its long arm also carries the Ne_1^w-allele.

Materials and method

Chinese Spring, and its di-iso-$5B^L$ and di-telo-$5B^L$ created by Dr. E. R. SEARS, Columbia, U.S.A., were received from Dr. R. RILEY, Cambridge, U.K.

These three lines and the F_1 (di-iso-$5B^L$ × di-telo-$5B^L$) were crossed with Touzelle á gros grains ($ne_1ne_1Ne_2^sNe_2^s$), and the number of green and necrotic plants counted in the F_1's and F_2's.

Results

Chinese Spring × Touzelle:

F_1 ($Ne_1^wne_1Ne_2^sne_2$) remains green, while only the F_2 plants with $Ne_1^wNe_1^wNe_2^sNe_2^s$ are necrotic. Plants which the have genotypes $Ne_1^wNe_1^wNe_2^sne_2$, $Ne_1^wne_1Ne_2^sNe_2^s$ and $Ne_1^wne_1Ne_2^sne_2$ do not show necrosis symptoms.

Chinese Spring di-iso-5B^L × Touzelle:

The F_1 plants remained green. In one F_2 24 green and 5 necrotic plants and in a second F_2 27 green and 6 necrotic plants were counted. This is in total 51 green : 11 necrotic plants.

Chinese Spring (di-iso-5B^L × di-telo-5B^L) F_1 × Touzelle:

Only two F_1's were grown. One consisted of 6 green and one necrotic plants and the other of 6 green plants only, which makes a total of 12 green : 1 necrotic plants.

Discussion

Localisation: If a chromosome other than 5B carries the Ne_1^w-locus of Chinese Spring the F_2 would have segregated into 15 green : 1 necrotic. In the F_2 (Chinese Spring di-iso-5B^L × Touzelle) our results deviate significantly from a 15 : 1 ratio ($\chi^2=13.80$, $P<0.0001$) so Ne_1^w-locus is not a chromosome other than 5B.

As necrosis was observed, the Ne_1^w-locus was present and hence must be on 5B. This is interesting because Ne_1^m of Prelude also is on 5B (see above). Furthermore as in the crosses only the long arm of 5B is involved the Ne_1^w-locus of Chinese Spring must be on this arm.

Dosage effect:

The expected *Ne*-genotypes and their necrotic experssion in the F_2 (Chinese Spring di-iso-5B^L × Touzelle) are shown in Table 1. The frequencies of these genotypes are not given because they are hard to predict.

Table 1. Expected *Ne*-genotypes, their expression for necrotic or green plants in an F_2 of Chinese Spring di-iso × Touzelle á gros grains

Expected *Ne*-genotype	Expression
$Ne_1^wNe_1^wNe_1^wNe_1^wNe_2^sNe_2^s$	necrotic
$Ne_1^wNe_1^wne_1Ne_2^sNe_2^s$	〃
$ne_1ne_1Ne_2^sNe_2^s$	green
$Ne_1^wNe_1^wNe_1^wNe_1^wNe_2^sne_2$	necrotic
$Ne_1^wNe_1^wne_1Ne^sne_2$	green
$ne_1ne_1Ne_2^sne_2$	〃
$Ne_1^wNe_1^wNe_1^wNe_1^wne_2ne_2$	〃
$Ne_1^wNe_1^wne_1ne_2ne_2$	〃
$ne_1ne_1ne_2ne_2$	〃

The genotypes $Ne_1^wNe_1^wNe_1^wNe_1^wNe_2^sne_2$ is also given as necrotic, because of the observation of one necrotic plant in the F_1 (di-iso-5B^L × di-telo-5B^L) × Touzelle. This necrotic plant must have had the genotype $Ne_1^wNe_1^wNe_1^wNe_2^sne_2$ as plants with $Ne_1^wNe_1^wNe_2^sne_2$ are green. In crosses of varieties with stronger Ne_1-alleles (Ne_1^w of some Italian varieties, Ne_1^m and Ne_1^s) with Ne_2^s-carrying varieties the F_1's ($Ne_1ne_1Ne_2^sne_2$) are necrotic. The degree

of necrosis observed in the necrotic plants of the F_2 (Chinese Spring di-iso-5B^L × Touzelle) (genotype $Ne_1^wNe_1^wNe_1^wNe_1^wNe_2^sne_2$) is similar to that of an $Ne_1^mne_1Ne_2^sne_2$-necrotic plants. This would suggest that the expressivity of four Ne_1^w-alleles of Chinese Spring is about equal to that of one Ne_1^m-allele, while the expressivity of two Chinese Spring-alleles is less than one of an Ne_1^w-allele of an Italian variety.

Acknowledgements

I am indebted to Dr. R. RILEY for providing me with seeds of Chinese Spring and its di-iso-5B^L and di-telo-5B^L and to Dr. J. G. Th. HERMSEN for advice.

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Path coefficient analysis of grain yield in wheat (*T. aestivum* L.)

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Introduction

In quantitative inheritance, a character is often influenced by variations in other traits. The covariation between traits as measured by the correlation coefficients have been studied by various workers viz., GANDHI *et al.* (1964), JAIN *et al.* (1969), VIRK and ANAND (1970). Such correlations, however, do not provide a clear picture of the relative contributions of direct and indirect influences of the component characters towards a complex character like yield. WRIGHT (1921) developed a technique to partition the correlation coefficients into direct and indirect effects on the basis of standardised partial regression analysis—path coefficient analysis.

Material and methods

The material consisted of eleven widely divergent wheat strains viz., NP825 and NP847 from Delhi, C306, C303 and C273 from Punjab, and S227, S210, S354, S355, S-409 and Mayo-64 from Mexico. These populations were grown in a randomised block design with six replications, consisting of paired 3.5 meter long rows in each replication. The plant to plant and row to row spacings were 15 cm and 22.5 cm respectively. The data were collected on 10 randomly selected plants from the paired plots in each replication. For the present analysis the overall means were used for the simple correlation coefficients. The path coefficient analysis was done according to DEWERY and LU (1959).

Results and discussion

The simple correlation coefficients and path coefficients of the components of yield have been set out in Tables 1 and 2 respectively.

Table 1. Simple correlation coefficients among various quantitative characters

Trait	Plant height	Grains/ear	100-grain weight (gm)	Ears/plant
Grain yield (gm)	0.858*	−0.406	0.847*	0.672*
Plant height (cm)		−0.465	0.846*	0.593
Grains/ear			−0.793*	−0.848*
100-grain weight (gm)				0.829*

* Significant at 1% level.

Table 2. Path coefficients of the components of yield

Character	Plant height	Grains/ear	100-grain weight	Ears/plant	Correlation with grain yield
Plant height	−0.0273	−0.4579	1.0501	0.2931	r=0.858
Grains/ear	0.0127	0.9848	−0.9843	−0.4191	r=−0.406
100-grain weight	−0.0231	−0.7809	1.2413	0.4097	r=0.847
Ears/plant	−0.0162	−0.8351	1.0291	0.4942	r=0.672

Residual effect=0.2800 ; The underlined figures denote the direct effects.

The grain yield had strong positive correlations with plant height, 100-grain weight and ears per plant. The observed correlations between the characters associated with grain yield were also positively high except plant height×eras per plant. These correlations were similar to VIRK and ANAND (1970). Plant yield have also been found to have close association with plant height, ears per plant and 100-grain weight by SIKKA and JAIN (1958), NANDPURI (1959), and GANDHI *et al.* (1964).

Grain yield being a complex character is influenced by many factors. Selection based on simple correlations without determing the interactions between the ancilliary

traits can be misleading. It is amply revealed from the Table 2 where plant height showed negligible direct effect (−0.0273) though it had a high positive correlation with yield which was mainly through 100-grain weight and to some extent through ears per plant. The grains per ear had high direct effect (0.9848) on the yield, though it had negative and non-significant correlation with grain yield. Its associations with 100-grain weight and ears per plant were highly negative which was confirmed by the path coefficient analysis. The ears per plant also had good direct effect but the indirect effect through 100-grain weight was considerably high (1.0291). The direct contribution of 100-grain weight and its indirect importance from plant height and ears per plant very clearly emphasised the value of this character in practical selection procedures. However, due weight age should also be given to ears per plant whereas practically no significance should be attached to grains per ear and plant height. VIRK and ANAND (1970) also observed similar weightage for these traits.

Summary

Simple correlations and path coefficients were worked out in a collection of eleven wheat varieties. The study of path coefficients revealing the direct and indirect effects showed that 100-grain weight was the most important character influencing yield followed by the ears per plant. This analysis also very clearly showed that only the simple correlations were not sufficient to formulate appropriate selection procedures.

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Orientation of homoeologous chromosomes in the somatic cells of wheat

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FELDMAN *et al.*, (1966) have shown that with the normal two doses of chromosome 5B of *Triticum aestivum*, homologous telocentric chromosomes are located near each other in root tip cells oftner than was at all likely on the basis of chance alone. FELDMAN (1968) has indicated that there is some evidence that in the somatic cells of *T. aestivum* the homoeologous chromosomes are also associated but lie much less close than homologous chromosomes. We have obtained evidence to support this contention.

Ditelo $7B^L$ of Chinese Spring was crossed with Ditelo $7D^S$ and the F_1 seeds were germinated and root tip squashes prepared by the Feulgen technique. Distances between the mid points of the two homoeologous telocentrics $7B^L$ and $7D^S$ and between two satellited homologous chromosomes were measured with an ocular micrometer. To minimise differences due to degree of squashing of cells, each distance between the telocentrics and the homologous chromosomes was divided by the distance between the two chromosomes farthest apart in the cell concerned (FELDMAN *et al.* 1966). This corrected distance was taken as the distance between the two homoeologous telocentrics and the two satellited homologous chromosomes. Forty-three flat circular cells were used for measurement.

It was observed that the distance between the homologous chromosomes was 0.186 ± 0.017 and between the homoeologous telocentrics was 0.321 ± 0.020. These distances were significantly different from each other and also from the distance of 0.452, the theoretical distance between two chromosomes randomly oriented in a cell. This observation has thus indicated that, 1) in the presence of two doses of chromosome 5B the homoeologous telocentrics are not randomly distributed in the somatic cells of *T. aestivum*, 2) they are placed near each other in the somatic cells but significantly less than the homologous chromosomes.

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On the use of the 5B genetic system in wheat breeding: The allosyndetic pairing in nulli-5B amphidiploids

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It is known that chromosome 5B of common wheat, *Triticum aestivum* L, carries a genetic system which inhibits or suppresses homoeologous pairing. Meiotic pairing between wheat chromosomes and those of related species (and its consequent interspecific gene recombination) is possible in appropriate hybrids lacking chromosome 5B (RILEY, CHAPMAN and KIMBER 1959).

In order to break down the barrier of sterility of hybrids RILEY and CHAPMAN (1963) pointed out the possibility of using nulli-5B amphidiploids in the breeding programs in which is aimed to introduce into common wheat the alien genetic variation.

Allosyndetic pairing (and its consequent interspecific gene recombination) in interspecific hybrids is cytologically proved by the occurrence of quadrivalents or higher meiotic associations, while heptavalents or higher associations are the cytological proof in their corresponding amphidiploids. Since homoeologous pairing competes with the pairing between homologous chromosomes in nulli-5B amphidiploids, a reduction in the amount of the interspecific gene recombination can take place and, consequently, in the main aim of the breeding program; i.e. the introduction into wheat of the alien genetic variation.

So, for the same combination *T. aestivum-Aegilops longissima*, RILEY and CHAPMAN (1963) found that the mean values of quadrivalent and heptavalent meiotic associations per pollen mother cell in, respectively, hybrids and amphidiploids were 1.04 and 0.10 in the most favourable case; that is to say, ten-fold higher in mono-5B hybrids than in their corresponding nulli-5B amphidiploids.

In the hybrids *T. aestivum-Secale cereale* and *T. aestivum-Aegilops columnaris* deficient for chromosome 5B, LACADENA (1967) found quadrivalent and/or higher meiotic associations at first metaphase with a frequency of 0.04 and 0.56, respectively, per pollen mother cell. Nevertheless, on analyzing cytologically at the present time their corresponding nulli-5B amphidiploids we have not found any heptavalent or higher associations among, respectively, 518 and 500 pollen mother cells observed at first metaphase; i.e., it has not been found (but not excluding its possibility) the cytological proof of allosyndetic pairing and subsequent interspecific gene recombination.

This is the reason why we consider interesting to emphasize that previously stated elsewhere on the use of the 5B genetic system in order to gain the most profit in wheat

breeding. The two following alternatives were proposed: i) to make successive backcrosses of the 5B-deficient hybrids to wheat as the male recurrent parent (RILEY and KIMBER 1966), or ii) to restore the lost fertility of hybrids by duplicating the chromosomes of the offspring obtained from the first backcross and then to backcross successively to wheat as the male recurrent parent (LACADENA 1967). In any of both alternatives hexaploid forms can be obtained in which wild genes have been introduced into the wheat genome as a consequence of the interspecific gene recombination which took place at the meiosis of the original hybrid deficient for chromosome 5B.

Although the two proposed methods seem to assure the highest level of interpsecific gene recombination, the use of nulli-5B amphidiploids may also be of interest as reported by RILEY, KIMBER and LAW (1967); they were able to transfer the resistance to *Puccinia recondita* from *Aegilops umbellulata* to wheat by backcrossing the nulli-5B amphidiploid *T. aestivum-Ae. umbellulata* to wheat as recurrent parent.

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Identification of univalents in synthesized wheat, ABD-12

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For the purpose of identifying the univalents found in synthesized wheat ABD-12, an amphiploid of *T. dicoccoides spontaneo-nigrum* × *Ae. squarrosa strangulata* by TANAKA (1961), chromosome pairing of F_1 hybrids between ditelosomes of Chinese Spring wheat and ABD-12 was investigated. Identification of univalents was deduced from the percentage of cells with heteromorphic bivalent. As shown in Table 1, out of 19 combinations, a combination ditelo 3B long × ABD-12 revealed only 3.1% of cells with heteromorphic bivalent. In short it seems to indicate that a univalent of ABD-12 is 3B. In other 2 combinations, ditelo 4Aα × ABD-12 and ditelo 2B long × ABD-12, the frequencies were 42.1% and 33.4% respectively. These facts seem also to show that two univalents are 4A and 2B.

Table 1. Frequency of cells with heteromorphic bivalent in F_1 hybrids between ditelosomes of Chinese Spring wheat and ABD-12

Combination	No. of cells observed	No. of cells with heteromorphic bivalent	% of cells with heteromorphic bivalent
ditelo 1A long × ABD-12	53	51	96.2
〃 3A 〃 × 〃	166	154	92.8
〃 4A α × 〃	513	216	42.1
〃 5A long × 〃	154	153	99.4
〃 6A short × 〃	34	28	82.4
〃 7A long × 〃	248	240	96.8
〃 1B 〃 × 〃	376	341	90.7
〃 2B 〃 × 〃	42	14	33.4
〃 3B 〃 × 〃	453	14	3.1
〃 4B 〃 × 〃	468	463	98.9
〃 5B 〃 × 〃	422	374	88.6
〃 6B 〃 × 〃	70	43	61.4
〃 1D 〃 × 〃	179	175	97.8
〃 2D α × 〃	126	118	93.7
〃 3D 〃 × 〃	213	157	73.7
〃 4D 〃 × 〃	104	85	81.7
〃 5D long × 〃	110	104	94.5
〃 6D α × 〃	67	65	97.0
〃 7D short × 〃	152	151	99.3

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Induced mutations for amber grain color in two varieties of wheat

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Hexaploid wheat varieties HP (M) 549 and HP (M) 574, which were introduced to India as S549–1–1 and S574–1–2 respectively, from Mexico, possess potential for very high yields as observed in the yield trials conducted in the North-Eastern Plain zone of India. However, these varieties were not accepted for commercial cultivation because of red grain color. With a view to rectify this defect, mutations for amber grain color were induced.

Seeds of both the varieties were treated with gamma rays (30 kR), N-nitrosomethyl urea (0.01%) and Ethyl methanesulphonate (0.5%). Seeds from selfed M_1 spikes were collected separately. The frequency of mutants with amber grains isolated in M_1 generation is presented in Table 1. The M_1 spikes were either completely mutated or were

Table 1. Frequency of amber grain mutants in M_1 genertaion

Treatment	Var. HP(M)549				Var. HP(M)574			
	M_1 plants studied	M_1 spikes studied	Mutation frequency		M_1 plants studied	M_1 spikes studied	Mutation frequency	
			% seg. plants	% seg. spikes			% seg. plants	% seg. spikes
Control	95	429	0	0	52	200	0	0
Gamma-rays (30 kR)	133	337	0	0	113	433	0	0
NMU (0.01%)	141	566	0	0	203	622	2.46	1.12
EMS (0.5%)	150	583	0.66	0.55	125	458	3.20	1.52

chimeral for amber and red grains. Morphologically the amber grain mutants resembled the parent varieties. The mutants bred true in the M_2 generation. Induction of amber grained mutations did not affect the yielding potential. Nature of the induced mutations is being investigated.

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Genetic cooperation in early growth characteristics of red and amber grained strains of variety Pb C591

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It was shown that the roots of red grained varieties of wheat grow faster and are longer than the amber grained strain of the same variety and the gene producing red colored grain in hexaploid wheat (*Triticum aestivum*) is associated with faster root growth (JOSHI *et al.* 1970). Experiments were conducted with a view to finding out, (i) if this differential growth in red and amber grained strains of the variety is restricted to roots or is expressed in coleoptile and (ii) if the factor (s) responsible for faster growth in red strain would also accelerate the growth of amber strain when the two are grown in mixture. The results are presented in this communication.

The two strains of Pb C591 having red and amber grains with the same genetic background except for the gene governing red color were used in these studies. The red grained euploid strain was developed from Mono-5A of Pb C591 which had gotton the red grain gene from Chinese Spring (JOSHI *et al.* 1970).

Replicated sets of 40 seeds of each of the strains were sown in petridishes when sown separately, but when the two strains were sown mixed then 20 seeds of each were put in the same petridish, a red seed alternating with amber one. Identical conditions of temperature (20°±1°C) and watering in an incubator were provided to all the germinating seeds. Measurements of the main root and coleoptile were taken after 36 and 60 hours of sowing, of the amber and red grains separately when either grown individually or mixed.

The mean lengths of main root and coleoptile of these strains are given in Table 1. Statistical analysis of the data were made to test the significance of the differences of means.

Table 1. Mean length (±SE) of main root and coleoptile of red and amber strains of Pb C591 after 36 and 60 hrs. of germination

	Material	Growth period (hrs.)	Length of main root (cm)	Length of coleoptile (cm)
Separately grown	Red	36	1.005±0.219	0.465±0.081
		60	1.995±0.458	0.655±0.179
	Amber	36	0.850±0.331	0.340±0.153
		60	1.505±0.341	0.520±0.115
Grown mixed	Red	36	0.810±0.144	0.325±0.063
		60	2.280±0.423	0.790±0.172
	Amber	36	0.665±0.225	0.278±0.111
		60	1.780±0.537	0.640±0.189

The results show that when grown separately, the root and coleoptile of red strain were significantly longer than amber strain upto 60 hrs. of growth. These results further confirm the results of JOSHI *et al.* (1970), indicating the association of the red gene not only with the faster root growth rate but also that of the coleoptile. However, when both the strains were grown in mixture, there was a depression in the growth of root and coleoptile in both the strains at 36 hrs. of germination. But after 60 hrs. of germination the growth of root and coleoptile showed acceleration in both the strains, resulting in longer root and coleoptile as compared to when grown separately. The red strain had longer root and coleoptile length than amber strain. The accelerated growth in mixture after 60 hrs. in comparison to when grown separately indicates a genetic cooperation between the two strains which are genetically identical except for the gene for the red grain color. This phenomenon of genetic cooperation between two strains to mutually accelerate growth demonstrable in petridishes, opens a practicable and easy approach to determine genetic cooperation between isogenic lines, differing only in one character like disease resistance, in the production of successful multiline varieties. Field trials conducted this year have shown a positive increase in yield of mixtures of two strains over their pure stands, confirming the genetic cooperation tests made in petridish (UPADHYA and BANSAL, in preparation).

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Isozymes of Ae. triuncialis and its parental species

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A large interspecific variation was found in two genera, *Aegilops* and *Triticum* (NAKAI and TSUNEWAKI 1971).

Aegilops triuncialis has the genome formula, CCC^uC^u and is assumed to have originated from the hybrid between *Ae. caudata*(CC) and *Ae. umbellulata* (C^uC^u) (SEARS 1939, KONDO and KIHARA 1943). In one of the many recent studies on the relationships between phosphatase isozymes and phylogeny, BREWER (1969) indicated that in bread wheat part of the alkaline phosphatase activity is controlled by genes on chromosomes 4B and

4D. In our previous work (NAKAI *et al.* 1969), esterase zymograms of *Ae. triuncialis*, obtained with pH 3–10 carrier ampholite, showed a good correspondence to those of *Ae. caudata* and *Ae. umbellulata*. WAINES and JOHNSON (1971) also found that the electrophoretic pattern of seed protein in an amphidiploid between *Ae. caudata* and *Ae. umbellulata* is very similar to that of *Ae. triuncialis*.

I. Esterase isozymes

The materials used were about 100 mg of germinating seeds soaked in petri-dishes for 24 hours in a growth chamber (23°C). Electrophoresis and esterase analysis were performed with the polyacrylamide disc isoelectrofocusing technique used by NAKAI & TSUNEWAKI in 1971. Two kinds of ampholite with differing pH ranges were used. The results were somewhat different, and are described separately.

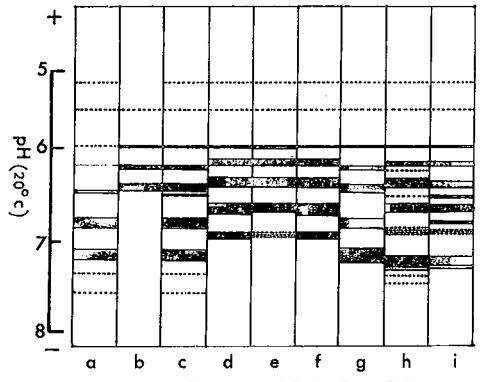

Fig. 1. Esterase zymograms of an amphiploid and its parental species obtained with a pH 5–8 carrier ampholite.
a. *Ae. caudata* var. *polyathera*, b. *Ae. umbellulata*, c. mixture, d. amphiploid (KONDO's CCC^uC^u), e. amphiploid (Sears' CCC^uC^u), f. *Ae. triuncialis* ssp. *eu-triuncialis* (Rumanian strain), g. *Ae. triuncialis* ssp. *eu-triuncialis* var. *typica*, h. *Ae. triuncialis* ssp. *orientalis* var. *persica*, i. an exceptional spectrum of Kondo's amphiploid.

Results with pH **5–8** *carrier ampholite*: Zymograms of *Ae. caudata* (2n=14) and *Ae. umbellulata* (2n=14) differed. Almost all strains of *Ae. caudata* (10 strains in total) showed the same esterase zymogram (Fig. 1a). Highly active bands were found at pI 6.7, 6.9 and 7.2, and bands of low activity at pI 5.3, 5.7, 6.0, 6.3, 7.4 and 7.6. Whereas, *Ae. umbellulata* showed three highly active bands at pI 6.0, 6.2 and 6.5, and a band at pI 5.7 with low activity (Fig. 1b). The esterase pattern of a 1:1 mixture by weight of these two species was compared to esterase patterns of two artificialy synthesized CCC^uC^u strains (KONDO's and SEARS' strains), and natural *Ae. triuncialis* (Fig. c-i). The mixture showed a zymogram equal to the sum of both parents, *Ae. caudata*, *Ae. umbellulata* (Fig. 1c) zymo-

grams. The two synthesized CCC^{u}C^{u} strains resembled each other, though the pI 6.95 band of SEARS' strain was much weaker than that of KONDO's. Natural strains of *Ae. triuncialis* are classified in two subspecies based on their morphological characters; ssp. *eu-triuncialis* (var. *typica*) and ssp. *orientalis* (var. *persica* and *assiriaca*). Esterase patterns (Fig. 1f-h) can be classified into three types. Type 1 (two strains from Rumania) showed five bands at pI 6.0, 6.2, 6.4, 6.6 and 6.65 (Fig. 1f). These strains belong to ssp. *eu-triuncialis* var. *typica*, and their zymogram is the same as that of the synthesized strains. Type 2 (also, ssp. *eu-triuncialis* var. *typica*) showed five bands at pI 6.0, 6.3, 6.6, 6.9 and 7.2 (Fig. 1g). The characteristic of band at pI 6.0 separated two bands by condition. This zymogram is similar to that of the 1 : 1 mixture of the two parental species. While, ssp. *orientalis* var. *persica* showed five active bands at pI 6.0, 6.2, 6.5, 6.75 and 7.3, weak bands at pI 5.8, 6.4, 6.8, 7.5 and 7.6 (Fig. 1h), only once in the trial did KONDO's CCC^{u}-C^{u} strain show a similar pattern (Fig. 1i). Two bands at pI 6.4 and 6.8 were never found in either *Ae. triuncialis* ssp. *orientalis* or the 1 : 1 mixture.

Result with pH **6–8** *carrier ampholite:* A photograph of zymograms obtained with this ampholite is shown in Fig. 2. The 1 : 1 mixture, KONDO's CCC^{u}C^{u} and *Ae. triuncialis*

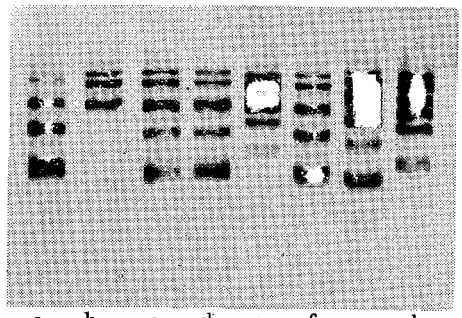

Fig. 2. Comparison of esterase patterns of the amphiploid and its parental species using pH 6–8 carrier ampholite.
a. *Ae. caudata* var. *polyathera*, b. *Ae. umbellulata*, c. mixture, d. amphiploid (KONDO's strain), e. amphiploid (Sears' strain), f. *Ae. triuncialis* var. *typica*, g. *Ae. triuncialis* var. *persica*, h. *Ae. triuncialis* (Rumanian strain).

var. *typica* all showed the same zymograms, identical to the sum of the zymograms of both parental species. Rumanian strains and the var. *persica* of *Ae. triuncialis* showed different zymograms. SEARS' CCC^{u}C^{u} had a somewhat similar zymogram to that of the Rumanian strains of *Ae. triuncialis*. The difference found in zymograms of two strains of CCC^{u}C^{u} may be due to a difference in the parental materials used for their synthesis. Parental strains (both for *Ae. caudata* and *Ae. umbellulata*) of SEARS' CCC^{u}C^{u} were not available in this experiment. *Ae. caudata* populations, particularly, may be due to interspecific variations by outcrossing many times in the field, therefor, the genetic background is

heterogenous. But, in this experiment, many strains of *Ae. caudata* were not used. Results indicated that ssp. *eu-triuncialis* and ssp. *orientalis* of *Ae. triuncialis* differed in their esterase zymograms. SENJANINOVA-KORZAGINA (1932) treated ssp. *orientalis* var. *persica* as an independent species, *Ae. persica*, based on her Karyo-morphological study. ZOHARY and FELDMAN (1962) concluded that the ear type of var. *persica* is due to an introgression of genes from *Ae. crassa*. KIHARA *et al.* (1965), on the other hand, suggested that ssp. *orientalis* derived from ssp. *eu-triuncialis*. The present results favor KIHARA's hypothesis that ssp. *eu-triuncialis* is a progenitor type in *Ae. triuncialis*.

II. Acid phosphatase isozymes

About 100 mg of seeds of each strain were soaked in petri-dishes for 24 hours in a growth chamber (23°C). Polyacrylamide gel electrofocusing of seed extracts was carried out using a minor modification of DAVIS' (1962) method of disc electrophoresis. This method was described in detail in a previous publication (NAKAI and TSUNEWAKI 1971). The procedure for staining acid phosphatase isozymes was the same as that described by ALLEN *et al.* (1963).

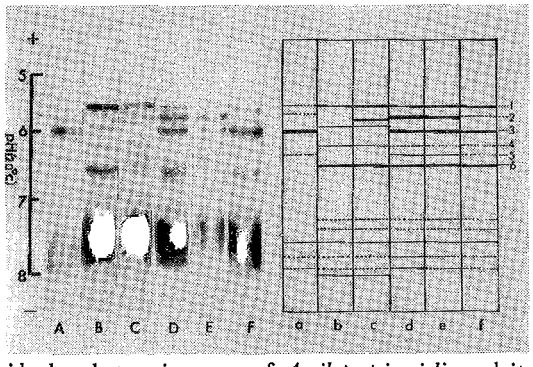

Fig. 3. Acid phosphatase isozymes of *Aegilops triuncialis* and its parental species.
A & a. *Ae. umbellulata*, B & b. *Ae. caudata* var. *polyathera*, C & c. *Ae. caudata* var. *typica*, E & e. amphidiploid (KONDO's strain) F & f. 1 : 1 mixture of seed extracts of *Ae. caudata* and *Ae. umbellulata*.

The acid phosphatase of *Ae. umbellulata* showed a simple zymogram (Fig. 3a); the pI 6.0 band showed high activity, while three bands of pI 5.7, 5.8 and 6.4 had low activities. Separation of bands at pI 7.4–7.7 was very poor. In general, both varieties of *Ae. caudata* (var. *typica* and var. *polyathera*) showed similar zymograms with two highly active bands at pI 5.7 and 6.5, and three other bands at pI 6.0, 6.3 and 7.1 (Fig. 3b). However, a single strain of var. *typica* differed from the other strains of *Ae. caudata* in that the pI 5.85 band showed high activity (Fig. 3c). Zymograms of both natural and arti-

ficially synthesized strains were similar, i.e., they had bands at pI 5.7, 5.8, 6.0, 6.3, 6.4, 6.5, 6.85 and 7.5–7.7 in common (Fig. 3d, e). However, the activities of two bands at pI 6.4 and 6.5 were low in the synthesized strains as compared to those of the natural strain. The zymogram of *Ae. triuncialis* involved all the bands of *Ae. caudata* (pI 5.7, 6.3 and 6.5) and *Ae. umbellulata* (pI 6.0, 6.4). The pI 5.8 band (No. 2 band) of natural and synthesized *Ae. triuncialis* was not found in either of the parental species. Furthermore, this band did not appear in a 1 : 1 mixture by weight of the extracts of *Ae. caudata* and *Ae. umbellulata* (Fig. 3f). These results suggest that the pI 5.8 band in *Ae. triuncialis* is a hybrid enzyme.

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Natural hybridization of male sterile lines of common wheat *Ae. cylindrica* × Host

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Natural hybrids of soft wheat × *Aegilops*, as Vavillov states (1966), were observed over hundred years ago. This warranted some scientists to suggest and, thereafter, experimentally prove that some species of this genera had taken part in the origination of wheat.

We have been facing, in our expansive scale research work at the Wheat and Sunflower Institute, with natural hybrids of wheat × *Aegilops cylindrica*, quite a bit recently. This *Aegilops* has, to our conditions, a wide spread, particularly in the field margins and roads where no cultivation is carried out. It goes into a nearly simultaneous blossoming with wheat and favourably pollinates male sterile lines with cytoplasm of *T. timopheevi*. Natural hybrids of common wheat × *Aegilops* have not been evident in this country so far, but male sterile plants have a continuous blossoming with widely open flowers, thus enabling the pollination of other plant species and obtaining of intergeneric hybrids with a pretty good density at that. An example of this is the 1971 counting of plants from a relatively small plot, where of the 13,100 available plants of the male sterile line of Bezostaya 1, 65 proved hybrids, which represents a 0.5 per cent value. These hybrid plants differ greatly to those of wheat and *Aegilops*. They manifest a far big hybrid vigour, the plants being up to 1.10 or 1.20 m. in height; see Fig. 1.

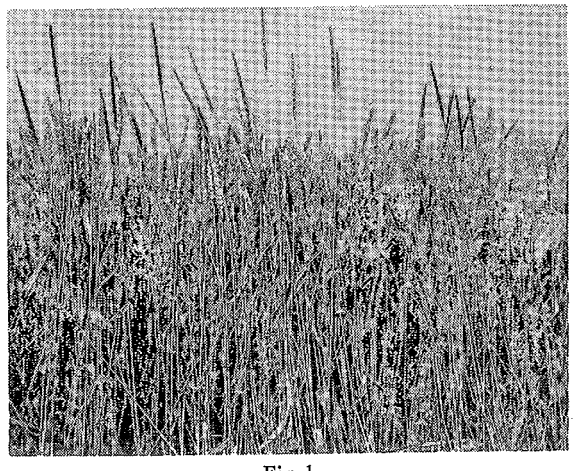

Fig. 1

The number of the tillers per plant goes as far as 20 or 30, or even more; the plants are completely sterile, with a pollen fertility of 2.4 per cent.

Additional investigations were carried out in 1971 for a fuller elucidation of the problem of common wheat × *Aegilops cylindrica* hybridization as well as of the nature of the hybrids obtained.

Table 1. Seed set at natural and manual pollination of common wheat × *Aegilops cylindrica* HOST

Cross	Pollination	No. of pollinated florets	No. of seed set	Seed set per cent
Male Sterile Bez. 1 × *Aegilops cylindrica*	natural	—	—	0.50
〃 × 〃	manual	570	4	0.70
Ae. cyl. indica × normal Bezostaya 1	〃	125	15	12.0
(Male Sterile Bez. 1 × *Ae. cylindrica*) × Bez. 1	natural	6670	50	0.75
(〃 × 〃) × *Ae. cylindrica*	manual	366	4	1.09

The results on Table 1 present the seed set, through manual pollination of the male sterile line of Bezostaya 1 variety be almost equal (0.70 per cent) to that of the natural pollination.

A comparatively bigger amount of seed set may be obtained by a reciprocal combination when *Aegilops cylindrica* was used as a mother plant; the seed set then amounts up to 12 per cent. Very few seeds were obtained when a backcross was made by using wheat (RB_1) or *Aegilops* (SB_1).

The frequent cases of natural hybridization of sterile common wheat × *Aegilops* is not, of course, an obstacle for our program of producing hybrid wheat, but very probably will influence on the homogeneity and uniformity of the hybrids and should be taken into consideration for our future investigations.

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Variation of chromosome numbers in different seed size classes of hexaploid triticale[1)2)]

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In order to study the frequency of euploids in the different seed size classes, the chromosome number of bulk populations of nine hexaploid strains of triticale were studied. The materials used in this study are shown in Table 1.

Table 1. Experimental materials

Group	Strain U.M. No.	Cross combinations
A	6211, 6211-2	6A189 (*T. durum* var. "Ghiza" × *S. cereale*) × 6A20 (*T. durum* var. "Carlton" × *S. cereale*)
B	6242, 6408	6A20 × 6A66 (*T. dicoccoides* × *S. cereale*)
C	6250, 6250-2	6A69 (*T. persicum* × *S. cereale*) × 6A67 (*T. persicum* × *S. cereale*)
D	6432-3	Group A × Group C
E	6606	6A250 (*T. persicum* × *S. cereale*) × (6A67 × 6A69) F_8
F	6608	6A250 × 6A190 (*T. durum* var. "Stewart" × *S. cereale* var. "Prolific")

The groups A, B and C have been used in the previous experiments (TSUCHIYA 1968a, b; 1969a, b). The euploid frequency of these six strains was 85 to 90% in the bulk populations (TSUCHIYA 1968a). The other three strains showed an extremely high frequency of aneuploids. The average frequencies of euploids and aneuploids for these three strains were 61 and 39% (TSUCHIYA and LARTER 1971). The bulk seeds were sieved through round-holed sieves, 9/64, 10/64 and 11/64 inches in diameter. The seeds were thus separated into three size classes: large, medium and small. Chromosome numbers were counted by acetocarmine squash technique and/or the Feulgen method for root tip mitosis.

Since the details of this experiment will be published elsewhere, only the results of chromosome counts are given in Tables 2 and 3.

Table 2 shows the variation of chromosome numbers in the low aneuploid materials (groups A, B and C). The results showed that the average frequency of euploids was similar to the previous one (TSUCHIYA 1968a).

Table 3 shows the variation of chromosome numbers in the high aneuploid materials (groups D, E and F). The average frequencies of euploids and aneuploids were also very similar to the previous results (TSUCHIYA and LARTER 1971).

The fact that a greater variation in chromosome numbers was found in the low aneu-

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2) This work was supported by the Research Grant from the Rockefeller Foundation and the National Research Council of Canada during the period of 1964~1968.

Table 2. Chromosome numbers in the low aneuploid groups

Chromosome number	A				B				C				Total			
	L	M	S	Total	L	M	S	Total	L	M	S	Total	L	M	S	Total
34+1 telo											1	1			1	1
38							1	1							1	1
39		1		1										1		1
40	1	3	2	6		1	6	7	1		3	4	2	4	11	17
40+1 telo			1	1	1	1	1	3					1	1	2	4
40+2 telo											1	1			1	1
41	10	6	11	27	3	5	15	23	9	19	13	41	22	30	39	91
41+1 telo						2	3	5			1	1		2	4	6
41+2 telo										1	1	2		1	1	2
42	86	64	75	225	96	68	57	221	101	70	66	237	283	202	198	683
42+1 telo	2			2			2	2	2	4		6	4	4	2	10
42+2 telo		1		1										1		1
43	2	6	3	11	3	3		6	5	3	2	10	10	12	5	27
43+1 telo							1	1	1			1	1		1	2
44										1	1	2		1	1	2
60		1		1										1		1
Total	101	82	92	275	103	80	86	269	119	98	89	306	323	260	267	850
Euploid (%)	85.1	78.1	81.5	81.8	93.2	85.0	66.3	82.1	84.9	71.4	74.1	77.8	87.6	77.7	74.2	80.4

Table 3. Chromosome numbers in the high aneuploid groups

Chromosome number	UM6432-3(D)				UM6606 (E)				UM6608 (F)				Total			
	L	M	S	Total	L	M	S	Total	L	M	S	Total	L	M	S	Total
39		1		1										1		1
40	1		2	3						2	4	6	1	2	6	9
41	3	7	4	14	4	7	8	19	16	16	10	42	23	30	22	75
41+1 telo		1	1	2	1	2		3	1			1	2	3	1	6
42	19	17	16	52	22	17	19	58	15	17	19	51	56	51	54	161
42+1 telo	1		1	2			2	2		2		2	1	2	3	6
43	2	2	2	6	1	1	1	3	2		1	3	5	3	4	12
Total	26	28	26	80	28	27	30	85	34	37	34	105	88	92	90	270
Euploid (%)	73.0	60.7	61.5	65.0	78.5	63.0	63.3	68.2	44.1	46.0	56.0	48.5	63.6	55.4	60.0	

ploid groups (Table 2) than in the high aneuploid groups could be ascribed to some extent to the fact that a larger number of plants was studied in the former (850) compared to the latter (270).

From the results shown in Tables 2 and 3, it may be concluded that the euploid frequency is higher in the large seed class than in the medium and small seed classes with an exception of UM6608 (group F) in which the euploid frequency was highest in the small seed class.

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Chromosome associations and seed fertility in five strains of hexaploid triticale[1)2)]

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Chromosome associations and fertility were studied in five advanced strains of hexaploid triticale. The materials used in the experiment are shown in Table 1.

1) Contribution No. 272 of the Department of Plant Science, the University of Manitoba, Winnipeg, Canada.

2) This work was supported by Research Grants from the Rockefeller Foundation (RF65019) and National Research Council of Canada.

Table 1. Five advanced strains used and their parentage of hexaploid triticale

U. of M. Strain	Parentage
6316	6A189 (*T. durum* var. "Ghiza" × *S. cereale*) × 6A20 (*T. durum* var. "Carlton" × *S. cereale*)
6242, 6408	6A20 × 6A66 (*T. dicoccoides* × *S. cereale*)
6250, 6250.2	6A69 (*T. persicum* × *S. cereale*) × 6A67 (*T. persicum* × *S. cereale*)

Chromosome associations were analyzed at metaphase I of meiosis in the materials grown in the experimental field of the University of Manitoba, Winnipeg, Canada, in the summer of 1966. The materials were fixed with 1:3 acetic alcohol solution and

Table 2. Chromosome associations at metaphase I of meiosis and seed fertility in five strains of hexaploid triticale

Material*	Number of bivalents per PMC			No. univalents/ PMC	No. of PMC	Seed fertility (%)**
	Closed	Open	Total			
6316- 1	17.25	3.19	20.44	1.12	100	—
〃 - 4	16.54	3.71	20.25	1.50	100	79.1
〃 - 9	13.62	5.46	19.08	3.84	100	41.2
〃 -13	16.59	3.73	20.32	1.36	100	—
〃 -14	18.09	2.35	20.44	1.12	100	—
〃 -15	15.99	4.19	20.18	1.64	100	—
〃 -20	15.83	4.30	20.13	1.74	100	—
Average (Total)	16.27	3.85	20.12	1.76	700	(65.7)
6408- 1	15.35	4.57	19.92	2.16	100	57.3
〃 - 2	16.61	3.57	20.18	1.64	100	66.6
〃 - 3	16.27	3.95	20.22	1.56	100	—
〃 - 4	17.11	3.23	20.34	1.32	100	62.0
〃 - 7	16.31	4.07	20.38	1.24	100	63.0
Average (Total)	16.33	3.88	20.21	1.58	500	(66.5)
6242-12	14.79	5.26	20.05	1.90	100	(62.7)
6250- 2	14.82	5.06	19.88	2.24	100	87.5
〃 - 5	14.26	5.63	19.89	2.22	100	87.2
〃 - 7	14.57	5.15	19.72	2.56	100	68.4
〃 -14	14.04	5.89	19.93	2.14	100	—
Average (Total)	14.42	5.43	19.86	2.29	400	(75.5)
6250.2- 2	16.12	4.38	20.50	1.00	100	83.6
〃 - 5	15.63	4.40	20.03	1.94	100	71.0
〃 - 7	15.53	4.80	20.33	1.34	100	81.7
Average (Total)	15.76	4.53	20.29	1.42	300	(81.1)
Average (Grand Total)	15.77	4.35	20.12	1.78	2000	—

* Somatic chromosome number of all plants was 2n=42.
** Seed fertility shown in parentheses is the average of 5 to 11 euploid plants (2n=42) in each strain.

preparations were made by acetocarmine squash technique. Fertility was shown by the percentage of seed set in the primary florets (the first and second florets of a spikelet) of two to three spikes collected from each plant.

The number of closed and open bivalents and the number of univalents per sporocyte are shown in Table 2 with seed fertility in some plants.

These results indicated that meiotic association of chromosomes are almost normal with high average number of bivalents (20.1) per sporocyte in combination with low number of univalents (1.78 per sporocyte) on an average. The variation of the number of bivalents and univalents per sporocyte was not great in different plants within a variety with a few exception (6316–9, 6408–1). The chromosomal associations in 6250 were slightly lower than the other four strains. The average seed fertility was, however, even higher in 6250 than the other strains studied as partly shown in Table 2.

These results shown in this brief note suggest that the chromosome association may not be the only factor affecting the seed fertility expressed by the seed set percentage in the primary florets. However, as shown in 6316–9, the abnormal meiotic behaviour may be directly reflected to the lower seed fertility when the abnormality is beyond some points, though more data should be obtained to give definite conclusion about the relationship between meiotic abnormalities and the seed set reduction.

At any rate, the results obtained suggest that the selection should be made in triticale breeding towards at least two directions: Selection of the plants or strains with high fertility and selection of materials with regular meiotic behaviour of chromosomes.

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Recombination between the chromosomes of wheat and rye— A possibility

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In an attempt to transfer desirable characters from *Secale cereale* ($2n=14$) to *Triticum aestivum* ($2n=42$), F_1 hybrids were produced between them. We have isolated presumably a spontaneous mutation at the 5B locus of *T. aestivum*, in one of the 28 chromosome F_1 hybrids leading to pairing of the presumably homoeologous chromosomes of wheat and rye, with the result that several bivalents, trivalents and occasional quadrivalent were formed (as given in Table 1). The normal control cross showed very little pairing among its 28 chromosomes.

Table 1. The chromosome configuration at metaphase I in the F_1 hybrid of *T. aestivum* and *S. cereale*, 5B mutant and the control

Material	2*n*	I	II	III	IV	X ta
aestivum × *cereale* (5B mutant)	28	13.0±0.2	6.2±0.1	0.6 ±0.05	0.1±0.02	9.3±0.2
aestivum × *cereale* (control)	28	25.1±0.2	1.4±0.1	0.03±0.01	Nil	1.5±0.1

In the 5B mutated hybrid there were several cells in which there were 11 bivalents, out of which many were close-ring type with distinct interstitial chiasmata and several cells showed quadrivalents. Since BIELIG and DRISCOLL (1970) have provided evidence that in the absence of long arm of chromosome 5B the wheat and a rye telocentric chromosomes pair, we postulate that in the F_1 hybrid reported here there is pairing between wheat and rye chromosomes.

NAKAJIMA (1952) also reported the cytological analysis of an F_1 hybrid between wheat and rye which was also a mutation at a locus suppressing pairing of homoeologous chromosomes in which as many as from 5 to 11 bivalents and trivalents and quadrivalents per cell were formed. Since at the time the 5B system was not discovered and there was no evidence to suggest that the wheat and rye chromosomes can pair, it was postulated by NAKAJIMA that there would not be any syndesis between the genomes of wheat and rye.

The extremely low frequency (3.5 percent) of pairing between wheat and rye chromosomes, in the absence of $5B^L$ of *T. aestivum*, as reported by BIELIG and DRISCOLL (1970), is probably due largely to asynchronous replication of the chromosomes of wheat and rye. SINGH, JOSHI and SHARMA (unpublished) have observed in a cross of wheat and rye that not only there is asynchronous replication of their chromosome complements, in the presence of one dose of chromosome 5B, but the whole genomes of wheat and rye were distinctly separate within the same pollen mother cell. However, in the F_1 hybrid between *T. aestivum* and *S. cereale*, where apparently the 5B gene has mutated, the genomes of wheat and rye are not separate within a pollen mother cell at the early stages of meiosis. This observation also suggests that there is pairing between wheat and rye chromosomes and would rather imply that the mutated 5B gene is responsible for the pairing of the homoeologous chromosomes of wheat and rye as well as synchronising the replication of their chromosomes.

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Effect of B chromosomes on chiasma frequency of A chromosomes in rye

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It has been reported that the variation in chiasma frequency of A chromosomes among PMC's increases with the increase of B chromosome frequency in rye (JONES and REES 1969). In this connection two different inbred rye lines with B chromosomes from the same origin were cytologically studied.

The plants examined in this report were F_2 progenies of the B_4F_1 with 2 B chromosomes for inbred rye line 10 (IR 10) and of the B_3F_1 with 2 B chromosomes for inbred rye line 14 (IR 14). Using IR 10 and IR 14 from MÜNTZING, and the B chromosome of standard type from KISHIKAWA (1965), as the original materials, these two lines were developed following the procedures below.

(1) Cross a certain inbred rye line, say A line, with a rye line having B chromosomes.

(2) Backcross A line repeatedly to the hybrids to get B_1F_1, B_2F_1 and so on after selecting the plant, as a female parent, which is being apparently like the A line and checking for B chromosomes at each generation.

In Table 1 are presented the chiasma frequencies converted to the frequencies of failures in chiasma formation of A chromosomes per cell at metaphase I of meiosis of PMC's in those IR 10 and IR 14 lines with various number of B chromosomes. In taking the data on the chiasma frequency a rod bivalent was treated as having 1 chiasma and a ring bivalent 2 and ca. 50 cells per plant were checked with some exceptions. As for the IR 10 series the modes of chiasma frequency of A chromosomes per cell in IR 10, recurrent parent, and B_4F_1 plants with 0 B, 2 B, 3 B, and 4 B chromosomes, were 13, 13, 11, 12, and 11, respectively. As for the IR 14 series, on the other hand, those in IR 14, recurrent parent, and B_3F_2 plants with 0 B, 1 B, 2 B, and 4 B chromosomes were 13, 13, 13, 14 and 14, respectively. Thus it is apparently clear that the more the number of B chromosomes, the less the number of chiasmata of A chromosomes per cell in the genetic background of IR 10, while the more the former the more the latter in the genetic background of IR 14. This tendency is also clearly seen on the mean chiasma frequency per cell. In addition the variance of the chiasma frequency calculated here as the variance of the number of failures in chiasma formation, providing these data follow the Poisson distribution, increased with increasing B chromosome numbers in the IR 10 series, whereas it decreased in the IR 14 series.

From the above mentioned results it is quite apparent in rye that the influence of B chromosomes on the mean and the variance of the chiasma frequency of A chromosomes is dependent on what kinds of inbred lines are used as a genetic background where B chro-

Table 1. Distribution, mean and variance of the number[1] of failures in chiasma formation (chiasmata) of A chromosomes at metaphase I of two different inbred rye lines with 0~4 B chromosomes

Line	No. B chromosomes	No. cells (plants) observed	No. failures in X-ma formation per cell (No. X-mata per cell)												Mean	Variance[2]	Mean X-ma freq.	No. Univalents per cell
			0 (14)	1 (13)	2 (12)	3 (11)	4 (10)	5 (9)	6 (8)	7 (7)	8 (6)	9 (5)	11 (4)	12 (3)				
IR 10	0	40 (1)	30.0[3]	50.0	10.0	10.0									1.0	1.0	13.0	0.00
B_4F_2	0	248 (7)	16.9	32.3	30.6	15.7	3.6	0.4	0.4						1.6	1.6	12.4	0.24
〃	2	199 (4)	7.5	19.6	15.6	23.1	16.1	8.5	4.5	4.0	1.0				2.4	2.4	11.6	0.60
〃	3	86 (2)	14.0	26.7	30.2	15.1	8.1	4.7		1.2					2.0	2.0	12.0	0.40
〃	4	346 (8)	2.6	13.9	19.7	22.3	11.0	11.3	11.0	4.6	2.3	0.9		0.6	3.5	3.5	10.5	1.06
IR 14	0	50 (1)	18.0	54.0	12.0	12.0	2.0		2.0						1.3	1.3	12.7	0.20
B_3F_2	0	296 (6)	32.1	40.2	15.9	9.1	2.7								1.1	1.1	12.9	0.12
〃	1	200 (4)	38.0	42.0	16.5	2.5	1.0								0.9	0.9	13.1	0.03
〃	2	319 (8)	48.3	37.6	11.0	2.8	0.3								0.7	0.7	13.3	0.01
〃	4	100 (2)	74.0	18.0	7.0	1.0									0.3	0.3	13.7	0.00

Rod and ring bivalents were scored as having 1 and 2 chiasmata and ca. 50 cells per plant were checked with some exceptions.
___shows the mode of the frequency.

1) Cells with 14 and 3 chiasmata were treated as cells with 0 and 11 failures in X-ma formation, respectively.

2) Provided the Poisson distribution.

3) Numerals are shown in percentage.

mosomes are introduced. And it seems to suggest that the genetic effect of B chromosomes is not only additive.

Heading date did not differ much among the plants with various numbers of B chromosomes. However, the pollen and seed fertilities decreased proportionally with the increase of B chromosomes.

The meiotic behavior of B chromosomes was as regular as it was in the report by KISHIKAWA (1965).

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Induction of chlorophyll deficient mutations in *Secale cereale*

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Seeds of self fertile diploid *Secale cereale* ($2n=14$) were treated with the mutagens gamma rays, nitrosomethyl urea (NMU) and ethyl methanesulphonate (EMS). Gamma rays were delivered from Cobalt^{60} in the Gamma Cell 200 of Atomic Energy of Canada, Ltd., at a dose rate of 5.1 kR/minute. For EMS and NMU treatments seeds were soaked in aqueous solutions of the mutagens for 20 hours. Irradiated or chemically treated seeds were immediately sown in the field to give M_1 generation. In each treatment 300

Table 1. Dose rate, sample size and frequencies of chlorophyll mutations induced by gamma rays, EMS and NMU in *Secale cereale*

Mutagen	Dose kR or %	Number of M_1 spikes tested	Number of segregating M_1 spike progenies	M_1 spike progenies segregating (%)
Gamma rays	7.5	131	11	8.4
	10.0	70	9	12.8
	12.0	42	6	14.2
	15.0	11	2	18.1
EMS	0.1	191	18	9.4
	0.2	200	27	13.5
NMU	10^{-3}	196	29	14.8
	2×10^{-3}	149	16	10.7
	5×10^{-3}	181	28	15.5
	10^{-2}	82	17	20.7
Control	—	103	0	0

seeds were sown. Three spikes per M_1 plant were used to raise M_2 generation and score chlorophyll deficient mutations.

In Table 1 are given the sample sizes and chlorophyll mutation frequencies for different doses of gamma rays, EMS and NMU. The response to gamma rays in the range of doses from 7.5 kR to 15 kR is linear. With NMU (10^{-2} to 10^{-3}) and EMS (0.1 and 0.2 percent) generally more mutations are induced as the dose increases but the relationship is complex.

Ninety-two percent of the chlorophyll mutations were of three types: albina, striata and tigrina. Out of these, on an avarage, about 79 percent were striata, 15 percent albina and 6 percent tigrina. The frequencies of chlorophyll mutations induced by gamma rays, EMS and NMU among these three classes of mutants obtained, by pooling the data for all the concentrations of each of the chemical, are given in Table 2. It is seen that with

Table 2. Relative frequencies of induced albina, striata and tigrinamutations in *Secale cereale*

Mutagen	Albina	Striata	Tigrina
Gamma rays	37.8	56.8	5.4
NMU	11.5	80.2	8.3
EMS	8.9	89.3	1.8

both EMS and NMU the frequencies of albina (8.9, 11.5 percent) and striata (89.3, 80.2 percent) are comparable. However, frequency of tigrina is higher with NMU (8.3 percent) than with EMS (1.8 percent). The frequencies of the three kinds of mutations with gamma rays are markedly different from that obtained with EMS and NMU, the frequency of albina being higher (37.8 percent) and that of striata being lower (56.8 percent).

The spectrum of induced chlorophyll mutations in rye differs significantly from that observed in diploid barley (*Hordeum vulgare*, $2n=14$). In barley, albina, tigrina and striata mutations account for an average of only about 56 percent of the total chlorophyll mutations. In this 56 percent portion of the mutant population the three types of mutations induced by gamma rays, EMS and NMU occur with frequencies given in Table 3. As seen from the Table, in barley, with all the three agents the albina mutation is predominant (53 to 69 percent) and the frequencies of striata (3 to 17 percent) and tigrina (27 to 34 percent) are very low.

Table 3. Relative frequencies of induced albina, striata and tigrina mutations in barley (*Hordeum vulgare*)

Mutagen	Albina	Striata	Tigrina
Gamma rays	69.0	3.5	27.5
NMU	52.8	16.6	30.6
EMS	57.9	7.9	34.2

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Failure of cytokinesis in *Secale cereale*

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This communication reports the observed failure of cytokinesis in control population of *Secale cereale* (2n=14). While studying meiosis in cut spikes of *Secale cereale*, maintained in Hoagland solution for 8 hours at 25°C, it was observed that in some of the spikes meiosis proceeded normally up to first metaphase by forming seven bivalents, followed by proper disjunction of homologous chromosomes. However, in other anthers, analysed at first anaphase, the 14 chromosomes were found scattered in the cytoplasm, indicating the failure of cell wall formation between the products of first meiotic division. At the second metaphase the chromosomes had an 'X' shaped morphology. At second anaphase two types of cells were observed, 1) which had 28 chromatids distributed randomly in the cytoplasm and 2) cells in which there were two groups of 14 chromatids each at the two poles.

Since diploid rye has $2n=14$ chromosomes, the normal execution of different steps of meiosis is expected to give rise to gametes with seven chromosomes each. Realization of microsporocytes with 28 and 14 chromosomes at second anaphase in the present study suggests the failure of cytokinesis at either first or second or both the anaphases of meiotic division.

The failure of cytokinesis reported in the present study was observed in spikes from 6 plants out of 10 picked at random from the field and therefore, it is unlikely that mutants for abnormal cytokinesis have been picked up. The failure of cytokinesis therefore, is to be attributed to disturbed metabolic processes incident on excision of the spikes from the plants and subsequent culture conditions to which it had been exposed. The process of meiosis is a very delicately balanced one and a large number of seemingly trivial conditions can upset it. Our observations, therefore, stress the need for a study of adequate controls in experiments done with excised spikes.

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The homoeologous group 4 in the Triticinae

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In the recent months, important work in wheat has been done using the techniques of molecular biology. The compensating nullisomic-tetrasomic lines were used by SHEPHERD (1968), BREWER *et al.* (1969) and HART (1970) in order to find out the variability in proteins or enzyme products of the genes located on the homoeologous chromosomes. While definite differences were recorded in the seed proteins (SHEPHERD 1968), remarkable homogeneity was observed in the isozymes tested (BREWER *et al.* 1969). Out of the 12 isozyme systems, for which the tests were conducted, variability was observed only in case of alkaline phosphatase. The genes for this enzyme could thus be located on the wheat chromosomes 4B and 4D. In another recent report (HART 1970), 40 strains of wheat, including 38 of the 42 possible combinations of compensating nullisomic-tetrasomic lines, were tested for alcohol dehydrogenase. It was concluded that the genes for alcohol dehydrogenase should be located on the chromosomes of the homoeologous group 4. It can perhaps be inferred, therefore, that the chromosomes of the homoeologous group 4 have differentiated to a greater degree than those of other groups. However, BELFIELD and RILEY (1969) concluded on the basis of meiotic pairing, that there was no evidence of any appreciable difference in the closeness of the chromosomes in the different homoeologous groups. SEARS (1966) on the basis of phenotypes, did find such differences and in his study, homoeologous group 4 was one such group where differences were rather prominent.

With this information available about wheat chromosomes, we can perhaps have a look on the chromosomes of the alien species from the sub-tribe Triticinae. Relationships of some of the chromosomes from three of the four alien genera in the Triticinae, have been established with wheat chromosomes. One chromosome from *Aegilops comosa*, was found to belong to homoeologous group 2 and was consequently designated as 2M (RILEY *et al.* 1966). Recently another chromosome from *Aegilops umbellulata* was shown to belong to homoeologous group 5 and was designated as $5C^u$ (CHAPMAN and RILEY 1970). Three chromosomes from *Agropyron elongatum* were shown to belong to homoeologous groups 3, 6 and 7 (BAKSHI and SCHLEHUBER 1959, JOHNSON 1966, QUINN and DRISCOLL 1967). Similarly chromosomes from *Secale cereale* could be shown to belong to homoeologous groups 1, 2 ,3, 5 and 6 (See GUPTA 1971). Out of these alien chromosomes, whose homoeologous relationships are known, only one (3R, BARBER 1969) was studied using biochemical techniques and it was shown that the biochemical techniques were useful in establishing homoeologous relationships. It should be noted that among the

chromosomes from the alien species, whose homoeologous relationships are known, none has so far been assigned to the homoeologous group 4. If this observation is considered in the light of the variability for alkaline phosphatase and alcohol dehydrogenase in the wheat chromosomes of the homoelogous group 4, we may expect that the chromosomes from homoelogous group 4 in the Triticinae have perhaps differentiated to a higher degree than the chromosomes of other homoeologous groups. It is also possible, therefore, that no disomic alien substitution may be obtained for any of the wheat chromosomes belonging to this group, because the differentiation of high degree would not allow compensation possible. However, JENKINS (1966) reported the substitutions of rye chromosome V for 4B and 4D, although the correctness of wheat chromosomes was not checked. GUPTA (1971) pointed out that rye chromosome V (designated after JENKINS 1966) did not show any compensation for any chromosome of the D genome in the pollen. He also indicated that this rye chromosome may be 4R, which lost much of its homoeology. However, using amphiploids, alien addition lines and the six nullisomic-tetrasomic lines belonging to the group 4, it should be possible to find out which chromosome in an alien species is having genes for alkaline phosphatase and alcohol dehydrogenase. In the absence of sustitution lines this technique may give valuable information regarding the relationship of a chromosome, which has lost most of its similarity due to differentiation. Alien chromosomes belonging to homoeologous group 4 can thus be identified. Rye chromosome V referred above may be particularly tested for the presence of the genes for alkaline phosphatase and alchool dehydrogenase. This would confirm whether this chromosome is really 4R. We would have liked to undertake such a project ourselves, but for the lack of facilities in this laboratory. It is hoped, therefore, that such a project will be undertaken elsewhere.

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Homoeologous pairing of specific *Agropyron elongatum* (2n=70) chromosome with wheat chromosomes

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The gene pool present in taxons closely related to the genus *Triticum* represents a valuable source of genetic variability for wheat breeding. The transfer of genes for disease resistance from related genomes and their fixation in the wheat genome is an important task in wheat genetics. The method of translocating alien chromosome segment into the wheat genome by irradiation was pioneered by Sears (1956) and Knott (1961). However, it appears that the appropriate manipulation of the diploidizing genetic mechanism found in wheat (Sears and Okamoto 1958, Riley 1958) might provide a more efficient method for gene transfer. The pairing between homoeologous chromosomes is prevented in wheat by the activity of a gene located on the longer arm of chromosome 5B. The removal of the pair of 5B chromosomes or the addition of the *Aegilops speltoides* or *Ae. mutica* genomes suppresses the activity of the wheat diploidizing mechanism (Riley 1960) and results in pairing between homoeologous chromosomes. A method based on this principle has been successfully applied to transfer a gene for resistance to yellow rust from *Ae. comosa* to common wheat (Riley *et al.* 1968). Success with this procedure is, however, limited by the degree of pairing between alien chromosomes and wheat chromosomes.

The species of the section *Elytrigia* of the *Agropyron* genus have proved to be a valuable source of genes for resistance to various diseases of wheat. The successful transfer of genes from *Agropyron* to wheat by homoeologous recombination depends on pairing between *Agropyron* and wheat chromosomes. An *Agropyron* chromosome homoeologous with the 6th wheat group was found to pair with wheat chromosomes with an average frequency of 4.8% when homoeologous pairing was restored by adding the *Ae. speltoides* genome (Johnson and Kimber 1967). Homoeologous pairing between the chromosomes of *Ae. squarrosa*, the donor of the wheat D genome, and the chromosomes of diploid *Ag. elongatum* (2n=14) also suggests fair pairing affinity (Dvořák 1971a).

A chromosome pair of *Ag. elongatum* (2n=70) carrying a gene for leaf rust resistance was substituted into the genome of common wheat by Caldwell *et al.* (1956). This wheat derivative was released under the name Agrus. Knott produced disomic, monotelocentric and ditelocentric additions of the alien chromosome by backcrossing Agrus to the common wheat cultivar Thatcher. This *Agropyron* chromosome has been shown to be homoeologous with the 7th homoeologous group of wheat (Nanda 1968, Quinn and Driscoll 1967, Knott 1968).

The monotelocentric addition line was crossed with *Ae. speltoides*. Hybrid seedlings were obtained by means of embryo culture and plants having 28+I chromosomes were selected. The plants were transferred into a growth chamber prior to meiosis and were grown under the following conditions: 10 hours of full light at 26°C and 39% relative humidity (RH), 4 hours at 22°C and 50% RH, 6 hours of darkness at 13°C and 85% RH and 4 hours again at 22°C and 50% RH. Thus the plants received 16 hours of light and 8 hours of darkness each day. Spikes for cytological analysis were collected between 2 and 3 hours after the start of full light. The affinity of the *Agropyron* telocentric for either wheat or *Ae. speltoides* chromosomes was estimated by scoring the frequency of PMC's in which the telocentric was found to be paired. Chiasma frequency was scored as a measure of the uniformity of conditions.

Chinese Spring ditelo 7A was crossed with *Ae. speltoides* and pairing of the telocentric 7A with its homoeologues was scored in the same way.

Results

The 29-chromosome plants from the cross with *Ae. speltoides* were of two types (Table 1). In two plants PMC's showed about 15 chiasmata per cell and the *Agropyron* telocentric was paired in 12.9% of the cells. Surprisingly, one plant had only 6.7 chiasmata per cell and the *Agropyron* telocentric was not paired in any of 200 cells. Since the wheat parent had been backcrossed 7 times to Thatcher and should have been essentially homozygous, it appears that the variability must have come from *Ae. speltoides*. Presumably the *Ae. speltoides* parent was segregating for at least two genotypes having different effects in suppressing the 5B diploidizing system in wheat. Further data on the suppression of the diploidizing system in wheat by the activity of *Ae. speltoides* suppressor genes will be published later.

By comparison, in 28-chromosome plants from the cross, Chinese Spring ditelo 7A × *Ae. speltoides*, the telocentric paired in 77% of the PMC's (Table 1). In similar crosses JOHNSON and KIMBER (1967) found 56.0 and 59.0% pairing for telocentrics 7B and 7D, respectively.

Table 1. Pairing affinity of an *Ag. elongatum* telocentric and wheat telocentric 7A with the chromosomes of wheat and *Ae. speltoides*

Cross	Number of cells	% of PMC's with a heteromorphic association	Chiasma frequency per cell
Agrus Tc^r × *Ae. speltoides*	114	12.3	14.96±0.21
〃 × 〃	103	13.5	14.98±0.18
〃 × 〃	200	0.0	6.70±0.17
Chinese Spring ditelo 7A × *Ae. speltoides*	100	77.0	15.76±0.10

Present data indicate that the Agrus chromosome arm carrying the gene for leaf rust resistance shows sufficient pairing with wheat chromosomes that the gene can be transferred by means of homoeologous recombination.

Pairing affinity with wheat chromosomes has been estimated also for three different telocentrics of diploid *Ag. elongatum* chromosomes (Dvořak 1971b). These telocentrics were also found to pair with their wheat homoeologues. The chromosome homoeology between *Agropyron* and wheat genomes appears to be generally high enough to make gene transfer by means of homoeologous recombination practical.

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Inheritance of field reaction to wheat rusts

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I. Stripe rust

Inheritance of mature plant reaction to stripe rust of wheat was studied in six crosses making a dial between the four vulgare wheat cultivars Tosson, (Hindi 62×Hindi 722), Kenya Farmer and F.K.N. These studies were carried out in season 1967~68 on F_1, F_2 populations and backcrosses where the epiphytotic of the natural infection during this season was severe.

According to mature plant reaction to stripe rust, the cultivars were classified in these classes—.;

Resistant	:	F.K.N.
Moderately resistant	:	Kenya Farmer
Susceptible	:	Tosson and (Hindi 62×Hindi 722)

Crosses studied were grouped in four groups:

(1) Moderately resistant×susceptible crosses:

This group was represented by two crosses, including Kenya Farmer as a moderately resistant parent crossed with each of the two susceptible cultivars Tosson and (H. 62×H. 722). F_1 of each cross was nearly as susceptible as the susceptible parents, showing nearly complete dominance of susceptibility to stripe rust. From these results, it could be suggested the presence of two duplicate genes (Ys_1 and Ys_2) for susceptibility carried by the susceptible cultivars Tosson and (H. 62×H. 722) respectively, while their recessive alleles (ys_1 and ys_2 were carried by the moderately resistant Keyna Farmer cultivar.

(2) Resistant×susceptible crosses:

This group was represented by two crosses including FKN as a resistant parent crossed with the susceptible cultivars Tosson and (H. 62×H. 722). The F_1 plants showed resistance to stripe rust (type 1), indicating incomplete dominance of resistance. Data indicated that resistance to stripe rust was due to the presence of three pairs of gene difference between the parents, and suggesting that the resistant parent carried one dominant gene for resistance. The resistant cultivar FKN might carry the dominant gene (Yr) for resistance, while for the two susceptible cultivars Tosson and (H. 62×H. 722), it was suggested previously that they carried the two dominant duplicate genes for susceptibility (Ys_1 and Ys_2) respectively. Gene (Yr) for resistance was epistatic to genes Ys_1 and Ys_2 for susceptibility.

(3) Resistant × moderately resistant crosses:

This group was represented by the cross FKN × Kenya Farmer. All F_1 plants showed resistance to stripe rust (Type 0) as in FKN parent, indicating complete dominance of resistance. Results indicated the presence of one pair of genes controlling resistance to stripe rust. The cultivar FKN was suggested to carry the dominant gene (*Yr*) for resistance, while the moderately resistant cultivar Kenya Farmer carried the recessive allele (*yr*).

(4) Susceptible × susceptible crosses:

One cross between the two susceptible parents Tosson and (H. 62 × H. 722), represented this group. The F_1 plants, F_2 population and progenies of backcrosses were all susceptible as the parents. It was previously suggested that the two duplicate genes for susceptibility (Ys_1 and Ys_2) respectively are found in the two parents. This conclusion agreed also with the results obtained in this group of crosses.

To explain the previous results, obtained from the F_1, F_2 and backcrosses of these four groups of crosses on a factorial basis, the following genes were suggested:

Yr	:	a gene for resistance to stripe rust, epistatic over genes Ys_1 and Ys_2.
Ys_1, Ys_2	:	two duplicate genes for susceptibility epistatic over gene *yr*.
yr	:	recessive allele for moderate resistance.
ys_1, ys_2	:	two recessive alleles for moderate resistance.

According to these assumptions the genetic constitutions of the parents would be:

Resistant	:	FKN *YrYr* ys_1 ys_1 ys_2 ys_2
Moderately resistant	:	Kenya Farmer *yryr* ys_1 ys_1 ys_2 ys_2
Susceptible	:	Tosson and (H. 62 × H. 722) *yryr* ys_1 ys_1 ys_2 ys_2

II. Leaf rust

Inheritance of mature plant reaction to leaf rust of wheat was studied in six crosses constituting a complete dial between the three susceptible vulgare wheat cultivars; Tosson, (H. 62 × H. 722) and Kenya Farmer, and the resistant cultivar FKN (Fn-K58-N11-50–18. These studies included F_1, F_2, backcrosses and F_3 families, which were tested during the two successive seasons 1967~68 and 1968~69. Parents were included in the two seasons under natural leaf rust epiphytotic, which was fortunately severe during both seasons, and susceptible plants were severely infected.

Crosses studied were grouped into two groups:

(1) Resistant × susceptible crosses:

This group was represented by three crosses including the cultivar FKN as a resistant parent crossed with each of the three susceptible cultivars Tosson, (H. 62 × H. 722) and

Kenya Farmer. All F_1 plants in the three crosses were completely resistant as in the resistant parent FKN, indicating complete dominance of resistance to leaf rust. Results showed that leaf rust resistance was simply inherited in these crosses. The resistant cultivar FKN might possess one dominant gene for leaf rust resistance designated as (*Lr*), while the susceptible cultivars Tosson, (H. 62×H. 722) and Kenya Farmer carried the recessive allele (*lr*) for leaf rust susceptibility.

II. Susceptible×susceptible crosses:

This group was represented by three crosses; Tosson×(H. 62×H. 722), Tosson×Kenya Farmer and (H. 62×H. 722)×Kenya Farmer. The F_1 plants were as susceptible as the parents. Results showed clearly that all these susceptible parents possessed the same genetic constitution or similar genes for susceptibility. Nevertheless, it was previously proposed the presence of the recessive allele (*lr*) for leaf rust susceptibility, which also confirmed the present finding in this group of crosses.

From these results, it could be suggested that the genetic constitution of the parental cultivars would be:-

Resistant: FKN *LrLr*

Susceptible: Tosson, (H. 62×H. 722) and Kenya Farmer *lrlr*

III. Stem rust

Inheritance of mature plant reaction to stem rust of wheat was studied in six crosses forming a complete dial between the four common wheat cultivars; Tosson, (Hindi 62×Hindi 722), Kenya Farmer and FKN (Fn-K58-N 11–50–18). The parents, F_1, F_2 populations and backcrosses were grown in season 1967~68 while parents, F_1 and F_3 families were grown innseason 1968~69. Artificial epidemics were created, including the prevalent stem rust races, during the two successive seasons and caused severe infections to the susceptible plants.

According to mature plant reactions to stem rust, the cultivars were classified into three classes:-

Resistant	: FKN
Moderately resistant	: Kenya Farmer
Susceptible	: Tosson and (H. 62×H. 722)

Crosses studied were grouped into four groups:

(1) Moderately resistant×Susceptible group, represented by the two crosses; Kenya Farmer crossed with each of the susceptible cultivars Tosson and (H. 62×H. 722). F_1 plants showed susceptibility to stem rust as in the susceptible parent indicating complete dominance of susceptibility. Data in F_2 and F_3 indicated the presence of two pairs of gene difference between parents. It could be assumed that each of the susceptible cultivars Tosson and (H. 62×H. 722) carried the dominant gene (*S*) for stem rust suscep-

tibility while the moderately resistant cultivar Kenya Farmer might carry the dominant gene (R_1) for moderate resistance. The gene (S) for susceptibility was epistatic over the gene (R_1) for moderate resistance.

(2) Resistant × susceptible group, represented by two crosses, FKN crossed with each of the two cultivars Tosson and (H. 62 × H. 722). The F_1 plants in these two crosses were as resistant as the resistant parent, showing complete dominance of resistance to stem rust. Results from F_2 and F_3 showed that the resistant cultivar FKN might carry a dominant gene (R) for resistance, while its allele (r) would be present in the susceptible cultivars, Tosson and (H. 62 × H. 722). However, it was previously detected that the dominant gene for susceptibility (S) in the two susceptible cultivars was epistatic over (R_1) in the cultivar Kenya Farmer. However, gene (S) appeared from the results, to be hypostatic to the gene (R) carried by FKN.

(3) Resistant × moderately resistant crosses; represented by the cross FKN × Kenya Farmer. The F_1 plants were as resistant as the resistant parent FKN, indicating complete dominance of resistance to stem rust. Results in F_2 and F_3 indicated the presence of two pairs of genes, including gene (R_1) for moderate resistance in Kenya Farmer and gene (R) for resistance in FKN, as was previously assumed. Their recessive alleles (r and r_1) gave susceptible plants.

(4) Susceptible × susceptible group, represented by the cross Tosson × (H. 62 × H. 722). All F_1, F_2 populations, F_3 families and backcrosses plants were as susceptible as both parents. These results showed clearly that the two susceptible parents possessed the same genetic constitution or possessed similar genes for susceptibility, which was previously suggested to be gene (S).

For explaining the previous results obtained from the F_1, F_2, backcrosses and F_3 of these groups of crosses on a factorial basis the following genes were suggested:

R: dominant gene for resistance to stem rust, epistatic over gene (S) for susceptibility.

R_1: dominant gene for moderate resistance to stem rust.

S: dominant gene for susceptibility, epistatic over gene (R_1) for moderate resistance.

r, r_1, and S: recessive alleles giving susceptibility.

According to these assumptions the genetic constitutions of the parents would be:

Resistant: FKN RRr_1r_1ss

Moderately resistant: Kenya Farmer rrR_1R_1ss

Susceptible: Tosson and (H. 62 × H. 722) $rr\ r_1r_1\ SS$.

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RNA synthesizing activity of wheat chromatin from germinating embryos and aleurone layers

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It has been assumed that embryonic cells have many sistes of gene activation while differentiated cells have only limited sites. In this point of view it is interesting to compare the chromatin properties between wheat germinating embryos and aleurone cells. Aleurone cells have differentiated extremely and do not divide any more, but have considerably high activity of RNA synthesis. The present preliminary report deals with the RNA synthesizing activity of chromatin prepared from germinating embryos and aleurone layers by DNA-dependent RNA polymerase obtained from *Escherichia coli*.

Seeds of *Triticum aestivum* (Cultivar. Shirasagi) were germinated in dark at 25°C. After 40 h incubation, embryos and endosperm portions were separated each other.

Chromatin preparation followed essentially the method of SHIN and BONNER (1969). DNA was isolated according to MARMUR (1961) from 3-day-old seedlings. Template activity of chromatin or DNA to support RNA synthesis was assayed by the method of CHAMBERLIN and BERG (1962) with *Escherichia coli* RNA polymerase purified up to the step of fraction IV. The standard reaction mixture (0.25 ml) contained 10 μmoles of tris buffer, pH 7.9, 0.25 μmoles of $MnCl_2$, 1.0 μmole of $MgCl_2$, 100 μmoles each of CTP, GTP, and UTP, and 50 μmoles of ^{14}C-ATP (specific activity: 8 μCi/μM).

Table 1. Template activity of wheat chromatin isolated from germinating embryos and aleurone layers

Exp.	Template	Amount of DNA μg	^{14}C-AMP incorp. (mμmole)
1	Embryo chromatin	2.4	0.281
	Aleurone layer chromatin	2.4	0.133
2	DNA from seedlings	3.4	0.801
	Embryo chromatin	3.4	0.406
	Aleurone layer chromatin	3.4	0.232

Assay conditions described in text, incubating for 10 min at 37°C.
Each incubation was performed in triplicate.

It was found that the isolated chromatin of wheat germinating embryos and aleurone layers can prim RNA synthesis in the presence of exogenous RNA polymerase. As shown in Table 1, the abilities of embryo chromatin and aleurone layer chromatin to support RNA synthesis are different. The template activity of embryo chromatin is about a half of the activity of wheat seedling DNA, and further the activity of aleurone layer chromatin is about a half of that of embryo chromatin.

The results may suggest that more genes are available for transcription in embryo chromatin. However, endogenous RNA polymerase activity was very low in the chromatin prepared by the present method. Therefore, a comparison of real RNA synthesizing ability between the two chromatins has need of more precise investigation.

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II. Genetic Stock

Necrosis genes in Chinese and Indian common wheat

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Since 1965, we are investigating distribution of necrosis genes in various geographical populations of wheat. This time we completed analysis of about 200 common wheat cultivars (or strains) from China and about 60 cultivars from India. Chinese materials were obtained from the Central Agricultural Experiment Station, Konosu, Japan. Information about their origin was also supplied. Indian materials were provided by the Indian Agricultural Research Institute, New Delhi, India.

All those cultivars were crossed to three necrosis testers, Jones Fife (genotype ne_1-$Ne_2ch_1Ch_2$), Prelude ($Ne_1ne_2ch_1Ch_2$) and Macha ($Ne_1ne_2Ch_1ch_2$). F_1 hybrids obtained were grown in field, and occurrence of necrosis or chlorosis was observed. Based on this record, genotype for necrosis type 1 (caused by two complementary genes Ne_1 and Ne_2) and chlorosis type 1 (caused by Ch_1 and Ch_2) of the tested cultivars was determined.

At the same time, three other characters, i.e. growth habit, awnedness and glume hairiness were observed. Growth habit was tested in greenhouse conditioned at 18～20°C with 14～16 hr illumination. Depending upon their heading response, they were classified as spring (S), winter (W) and intermediate (I) types. For awnedness, all materials were classified to four types, fully awned (++), half awned (+), awnletted (±) and awnless (−). Glume hairiness was expressed by either+(hairy) or−(glabrous).

Results are summarized in the following table. Detailed treatment of the results with Chinese wheat was already published in Japan. J. Genet. 46: 103～107, 1971.

Cult. No.	Cultivar	Locality	Tester[1]			Genotype of tested strains	Growth habit[2]	Awnedness[3]	Glume hair[4]
			Jones Fife $ne_1Ne_2ch_1Ch_2$	Prelude $Ne_1ne_2ch_1Ch_2$	Macha $Ne_1ne_2Ch_1ch_2$				
Chinese	wheat								
3251		Manchuria	+	+	+	$ne_1ne_2ch_1ch_2$	S	±	−
3252	Chichihaerh	〃	+	+	+	$ne_1ne_2ch_1ch_2$	S	++	−
3253	Chuyehching	Middle China	n	+	c	$Ne_1ne_2ch_1Ch_2$	I	++	−
3254	Chenshantsaosheng	Shantung	n	+	?	$Ne_1ne_2ch_1$?	I	+	−
3255	Chingtaotsailai No. 1	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	−	−
3256	〃 No. 2	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	?	−	−
3257	Changchiakou 1	Changchiakou, Hopei	n	+	c	$Ne_1ne_2ch_1Ch_2$	S	++	−
3258	〃 2	〃	+	+	+	$ne_1ne_2ch_1ch_2$	W	−	−
3259	Changchun	Manchuria	+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3260	Changshan No. 1	Chingtao, Shantung	+	+	c	$ne_1ne_2ch_1Ch_2$	W	++	−
3261	〃 No. 2	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3262	〃 No. 3	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3263	〃 No. 4	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	W	±	−
3264	〃 No. 6	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	W	+	−
3265	〃 No, 7	〃	n	+	?	$Ne_1ne_2ch_1$?	W	−	−
3266	〃 No. 8	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	−
3267	Middle China No. 1	Middle China	+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3268	〃 No. 2	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3269	〃 No. 3	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3270	〃 No. 4	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3271	〃 No. 5	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	−	−
3272	〃 No. 6	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3274	Tatungkou	?	+	+	c	$ne_1ne_2ch_1Ch_2$	W	++	−
3275	Tatoukou	?	+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3276	Thungshanpo	Chingtao, Shantung	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	−
3277	Yunghsing	?	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	−
3278	〃	?	+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3279	Yingchou	?	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	−

(Continued)

3280	Iwei	Ichang, Hupei	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	−	−
3281	Wuhuatou	?	+	n	c	$ne_1Ne_2ch_1Ch_2$	S	?	−
3282	Yulinpo	?	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	−
3284	Yinchunhsi No. 21	Manchuria	+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3286	Pochiehliangmai	Chinan, Shantung	n	+	+	$Ne_1ne_2ch_1ch_2$	S	±	−
3287	Pokukuotzuwei	Chintao, Shantung	n	+	c	$Ne_1ne_2ch_1Ch_2$	S	?	−
3288	Potoupokai	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	+	−
3289	Potutouerhmeimai	〃	+	n	c	$ne_1Ne_2ch_1Ch_2$	W	−	−
3290	Yunerhpang	Manchuria	+	+	c	$ne_1ne_2ch_1Ch_2$	S	−	−
3291	Huamai	?	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	−
3292	〃	Manchuria	n	+	c	$Ne_1ne_2ch_1Ch_2$	S	++	−
3293	Pin	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3294	Penchang No. 4	Chingtao, Shantung	+	n	c	$ne_1Ne_2ch_1Ch_2$	W	++	−
3295	〃 No. 7	〃	+	n	+	$ne_1Ne_2ch_1ch_2$	W	±	−
3296	Pukou	Chiangsu	+	+	c	$ne_1ne_2ch_1Ch_2$	W	++	−
3297	Fangcheng	Manchuria	+	+	+	$ne_1ne_2ch_1ch_2$	I	++	−
3298	Fengtientsailaichung	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3299	Fengshanhsiao	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	W	+	−
3300	Putung	Chiansu	+	+	c	$ne_1ne_2ch_1Ch_2$	W	−	−
3301	Pingyüan 50	?	+	+	+	$ne_1ne_2ch_1ch_2$	W	±	−
3302	Piensui	?	+	+	c	$ne_1ne_2ch_1Ch_2$	W	?	−
3303	Weihsintsailai	?	n	+	c	$Ne_1ne_2ch_1Ch_2$	I	++	−
3304	Hsüchou	Hsuchou, Chiangsu	+	+	c	$ne_1ne_2ch_1Ch_2$	I	++	−
3305	〃 2	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	−
3306	Hsüchouhsiaomai	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	S	++	−
3307	Hsüchoupohsiaomai	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	S	++	−
3308	Chiehshouhsiaomai	Chiehshou	+	+	c	$ne_1ne_2ch_1Ch_2$	S	+	−
3310	Honantangyinpofu	Honan	+	+	?	$ne_1ne_2ch_1$?	W	++	−
3312	Helungching	Manchuria	+	+	c	$ne_1ne_2ch_1Ch_2$	I	±	−
3313	Chinmai	Chihfu, Shantung	+	+	c	$ne_1ne_2ch_1Ch_2$	I	−	−
3314	Hungmangcha	Chintao	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	−

(Continued)

3315	Hunghoshangtou	Peking, Hopei	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	−
3316	Hunghuamai	Chungking, Ssuchuan	n	+	c	$Ne_1ne_2ch_1Ch_2$	I	±	−
3317	Hunghuohsiaomai	Middle China	+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3318	Hungtungmen	Chingtao, Shantung	+	+	c	$ne_1ne_2ch_1Ch_2$	W	++	−
3320	Kochunhsi No. 787	Manchuria	+	+	c	$ne_1ne_2ch_1Ch_2$	W	+	−
3323	Huangpaochu	?	+	+	c	$ne_1ne_2ch_1Ch_2$	S	±	−
3324	Huanglungching	?	+	n	c	$ne_1Ne_2ch_1Ch_2$	S	++	−
3325	Huangliaomaitzu	?	n	+	c	$Ne_1ne_2ch_1Ch_2$	S	++	−
3326	Kaomipomai	?	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	−
3327	Kaoyu	?	+	+	?	$ne_1ne_2ch_1$?	W	+	−
3328	Hunchun	Manchuria	+	n	c	$ne_1Ne_2ch_1Ch_2$	W	++	−
3329	Kuangtou	〃	+	+	+	$ne_1ne_2ch_1ch_2$	S	±	−
3330	Hungchou	Hangchou, Chechiang	+	+	?	$ne_1ne_2ch_1$?	I	+	−
3331	Chingnung No. 1	Peking, Hopei	?	+	c	? $ne_2ch_1Ch_2$	W	++	−
3332	〃 No. 2	Chinan, Shantung	+	+	?	$ne_1ne_2ch_1$?	W	±	−
3333	Chiuchiang	Chiuchiang, Chianghsi	+	+	c	$ne_1ne_2ch_1Ch_2$	W	++	−
3334	Hungmacha	?	n	+	c	$Ne_1ne_2ch_1Ch_2$	S	±	−
3335	Minghsien No. 169	Shansi	n	+	?	$Ne_1ne_2ch_1$?	S	±	−
3336	〃 No. 204	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	W	++	−
3337	Menghsienhuamai	Menghsien	n	+	c	$Ne_1ne_2ch_1Ch_2$	S	+	−
3338	Wumangpomai	Chinan, Shantung	+	n	c	$ne_1Ne_2ch_1Ch_2$	S	−	−
3339	Wumanghungkai	Chingtao, Shantung	n	+	c	$Ne_1ne_2ch_1Ch_2$	I	++	−
3340	Wumanghungku	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	−	−
3341	Wumangtsungku	〃	+	+	?	$ne_1ne_2ch_1$?	W	++	−
3342	Mingkuang	Shanghai, Chiangsu	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	±	−
3343	Nanching	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	I	++	−
3344	Nanchingchihku	Chingtao, Shantung	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	−
3345	Nanchingtayühua	Nanking, Chiangsu	?	+	?	? ne_2ch_1 ?	W	++	−
3347	Peiching No. 1	Hopei	+	+	c	$ne_1ne_2ch_1Ch_2$	W	?	−
3348	〃 No. 2	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	−	−
3349	〃 No. 4	Chingtao, Shantung	+	+	c	$ne_1ne_2ch_1Ch_2$	S	−	−

(Continued)

3350	Peiching No. 5	Chingtao, Shantung	?	+	c	? $ne_2ch_1Ch_2$	S	—	—
3351	〃 No. 6	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	—
3352	Peichingpo	〃	?	+	c	? $ne_1ch_1Ch_2$	S	±	—
3353	Peichingyumang	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	W	++	—
3354	Peichinghsihsiaotsailaichung	Peking, Hopei	+	+	c	$ne_1ne_2ch_1Ch_2$	W	++	—
3355	〃 (chih)	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	—
3356	〃 (5)	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	I	++	—
3357	Lichengtaipo	Shantung	?	+	c	? $ne_2ch_1Ch_2$	W	++	—
3358	Lishantaipo	〃	+	n	?	$ne_1Ne_2ch_1$?	S	++	—
3359	Luho	?	?	+	?	? ne_2ch_1 ?	W	—	—
3360	Chinan No. 1	Shantung	n	+	?	$Ne_1ne_2ch_1$?	W	—	—
3361	〃 No. 2	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	—
3362	〃 No. 4	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	—
3363	〃 No. 5	〃	+	n	?	$ne_1Ne_2ch_1$?	W	++	—
3364	〃 No. 7	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	+	—
3365	〃 No. 9	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	I	++	—
3366	Chinantsailai No. 2	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	—
3367	Tsainingpo	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	—
3368	Tsainingpomai	〃	+	+	?	$ne_1ne_2Ch_1$?	W	++	—
3369	Chitouliangku	〃	+	?	c	ne_1 ? ch_1Ch_2	W	±	—
3370	Sanhsing	Manchuria	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	—
3372	Shihchiachuangwumang	Chichiahuang, Hopei	+	+	c	$ne_1ne_2ch_1Ch_2$	I	+	—
3373	〃 -hofuwumang	〃	?	+	?	? ne_2ch_1 ?	W	—	—
3374	Chüanchou	Chuanchou, Fuchien	n	+	?	$Ne_1ne_2ch_1$?	S	++	—
3375	Tangshan	Chingtao, Shantung	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	—
3376	Tangshantufeng	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	I	±	—
3377	Tangshanhsiaomai	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	—
3378	Tangshanpo	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	W	++	—
3379	Hsiaowangmai	Fushanhsien	+	n	c	$ne_1Ne_2ch_1Ch_2$	W	++	—
3380	Tzukan	Wuhu, Anwei	+	+	c	$ne_1ne_2ch_1Ch_2$	W	++	—
3381	Sangpao No. 291	?	?	?	c	? ? ch_1Ch_2	S	++	—

(Continued)

3382	Sangpao No. 328	?	+	+	c	$ne_1ne_2ch_1Ch_2$	W	++	−
3383	〃 No. 6	?	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	−
3384	Salachi 1	Manchuria	n	+	c	$Ne_1ne_2ch_1Ch_2$	S	++	−
3386	Hsipei 501	?	+	+	?	$ne_1ne_2ch_1$?	W	++	−
3387	Shihchiachuang 407	Chihchiachuang, Hopei	+	+	?	$ne_1ne_2ch_1$?	W	++	−
3388	Shihte 14	?	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	+	−
3389	Taian No. 2	Chingtao, Shantung	+	+	c	$ne_1ne_2ch_1Ch_2$	W	++	−
3390	Ihsienhuamai	?	+	+	c	$ne_1ne_2ch_1Ch_2$	W	++	−
3391	Tinghsien No. 72	Hopei	+	+	c	$ne_1ne_2ch_1Ch_2$	W	−	−
3392	Tingchoutsailai No. 1	?	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	±	−
3396	Chinshih	Changsha, Hunan	+	+	?	$ne_1ne_2ch_1$?	W	++	−
3397	Ailimai	?	?	+	?	? ne_2ch_1 ?	W	++	−
3398	Yumangpokai	?	+	+	c	$ne_1ne_2ch_1Ch_2$	W	++	−
3399	Yumanghsiaomai	Chinan, Shantung	?	+	?	? ne_2ch_1 ?	W	++	−
3404	Chungchu 68	?	+	+	c	$ne_1ne_2ch_1Ch_2$	W	±	−
3405	Yenta No. 1817	Hopei	?	+	?	? ne_2ch_1 ?	?	?	?
3406	〃 No. 1885	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	−
3420	Peiching No. 3	Peking, Hopei	+	+	c	$ne_1ne_2ch_1Ch_2$	I	±	−
3421	Peking No. 7	〃	+	n	c	$ne_1Ne_2ch_1Ch_2$	I	−	−
3422	〃 No. 8	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	I	±	−
3424	Liying No. 3	Chekiang	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	+	−
3425	Chinan No. 8	Shantung	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	−
3426	〃 No. 10	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	−	−
3427	Chita 195	Chinan, Shantung	+	+	c	$ne_1ne_2ch_1Ch_2$	W	++	−
3428	Taian No. 3	Chingtao, 〃	+	+	c	$ne_1ne_2ch_1Ch_2$	W	+	−
3429	Anta	Manchuria	+	n	c	$ne_1Ne_2ch_1Ch_2$	S	++	−
3430	Wuchin	Chingtao, Shantung	+	+	?	$ne_1ne_2ch_1$?	W	±	−
3431	Chingtaotsailaifenhsi	〃	+	+	?	$ne_1ne_2ch_1$?	W	−	−
3432	Chungta 2419	?	+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3433	Chungnung	Italy	?	+	?	? ne_2ch_1 ?	W	±	−
3434	Hahsi 122-4	Manchuria	n	+	c	$Ne_1ne_2ch_1Ch_2$	S	++	−

(Continued)

3435	Hahsi 126–1	Manchusia	+	+	?	$ne_1ne_2ch_1$?	S	±	+
3436	Pima No. 1	?	+	+	?	$ne_1ne_2ch_1$?	W	++	−
3437	〃 No. 4	?	+	+	?	$ne_1ne_2ch_1$?	W	++	−
3438	Peiyüan No. 3	?	?	+	c	? $ne_2ch_1Ch_2$	W	++	−
3439	Huang No. 16	Shanghai, Chiangsu	+	+	c	$ne_1ne_2ch_1Ch_2$	W	++	−
3440	Huanghai No. 26	〃	?	+	c	? $ne_2ch_1Ch_2$	W	±	−
3441	〃 No. 103	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	S	−	−
3442	Huangpi	Nanking, 〃	+	+	?	$ne_1ne_2ch_1$?	I	+	−
3443	Huanung No. 9	Kaifeng, Honan	n	+	?	$Ne_1ne_2ch_1$?	W	++	−
3444	Chingyang	?	+	+	?	$ne_1ne_2ch_1$?	W	+	−
3445	Kaifêng 124	Kaifeng, Honan	+	+	+	$ne_1ne_2ch_1ch_2$	W	+	−
3446	Chinta 2905	?	+	+	?	$ne_1ne_2ch_1$?	W	++	−
3447	〃 4197	?	?	+	c	? $ne_2ch_1Ch_2$	W	±	−
3448	Huapei 187	Huapei	?	+	c	? $ne_2ch_1Ch_2$	W	++	−
3449	〃 497	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	W	−	−
3450	〃 672	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	±	−
3451	M3	Manchuria	+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3452	M19	〃	n	+	c	$Ne_1ne_2ch_1Ch_2$	I	++	−
3453	M22	〃	?	+	c	? $ne_2ch_1Ch_2$	W	±	−
3454	M25	〃	+	+	?	$ne_1ne_2ch_1$?	S	±	−
3455	Manchou No. 3	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	S	±	−
3456	〃 No. 5	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	I	±	−
3457	Nungta 16	Peking, Hopei	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	±	−
3458	〃 36	〃	+	+	c	$ne_1ne_2ch_1Ch_2$	W	+	−
3459	〃 183	〃	?	+	?	? ne_2ch_1 ?	W	+	−
3460	Peiching No. 8	〃	+	+	?	$ne_1ne_2ch_1$?	W	+	−
3461	Liying	?	n	+	c	$Ne_1ne_2ch_1Ch_2$	I	++	−
3462	Chinan No. 3	Shantung	+	+	?	$ne_1ne_2ch_1$?	W	++	−
3463	〃 No. 6	〃	?	+	c	? $ne_2ch_1Ch_2$	W	++	−
3464	Hsiuchouhsiaomai	?	+	+	?	$ne_1ne_2ch_1$?	I	++	−
3465	Tsaoyangmai	America	?	+	c	? $ne_2ch_1Ch_2$	W	++	−

(Continued)

3466	Chienchiaomai	?	+	+	c	$ne_1ne_2ch_1Ch_2$	S	+	−
3467	Hsinung 6028	?	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	−
3468	Chientoupokai	?	n	?	c	$Ne_1ne_2ch_1Ch_2$	W	−	−
3469	Taian	Shantung	n	+	c	$Ne_1ne_2ch_1Ch_2$	W	++	−
3470	Tungnung 55-825	Huatung	+	+	c	$ne_1ne_2ch_1Ch_2$	I	++	−
3471	Hatiehhsi No. 11	Manchuria	+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3472	Yenchiao 35368	Peking, Hopei	n	+	c	$Ne_1ne_2ch_1Ch_2$	S	++	−
3473	Yüpimai	?	?	+	?	$?\,ne_2ch_1?$	S	±	−
Indian	wheat								
3501	NP 4		+	+	c	$ne_1ne_2ch_1Ch_2$	S	−	+
3503	〃 165		+	+	c	$ne_1ne_2ch_1Ch_2$	S	−	−
3505	〃 718		+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3506	〃 761		+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3507	〃 770		+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	+
3509	〃 798		+	+	c	$ne_1ne_2ch_1Ch_2$	S	±	−
3511	〃 824		+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	+
3512	〃 825		+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	+
3513	〃 830		?	+	c	$?\,ne_2ch_1Ch_2$	S	++	−
3514	〃 839		?	n	c	$ne_1Ne_2ch_1Ch_2$	S	++	+
3515	〃 852		?	+	c	$?\,ne_1ch_1Ch_2$	S	++	+
3516	〃 860		+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	+
3517	〃 862		?	+	c	$?\,ne_2ch_1Ch_2$	S	++	−
3518	〃 864		+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3519	〃 871		+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	−
3520	〃 872		+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	+
3521	〃 874		+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	+
3522	〃 876		n	+	?	$Ne_1ne_2ch_1?$	S	++	+
3523	〃 880		+	+	?	$ne_1ne_2ch_1?$	S	++	+
3524	〃 884		?	+	c	$?\,ne_2ch_1Ch_2$	S	++	−
3525	〃 887		+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	+
3526	HD-60-534		n	+	?	$Ne_1ne_2ch_1?$	S	++	+

(Continued)

3527	HD–60–563		+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	+
3528	HD–60–565		+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	+
3529	HD–60–566		n	+	c	*Ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	+
3530	HD–60–839		+	+	?	*ne*$_1$*ne*$_2$*ch*$_1$?	S	++	–
3531	HD–60–851		+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	–
3532	HD–60–854		?	+	c	? *ne*$_2$*ch*$_1$*Ch*$_2$	S	++	–
3533	HD–60–929		?	n	?	*ne*$_1$*Ne*$_2$*ch*$_1$?	S	++	–
3534	HD–60–1371		+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	–
3535	HD–63–1357		+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	+
3536	HD–63–1395		+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	–
3537	HD–64–1396		+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	+
3538	HD–64–1396A		n	+	c	*Ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	+
3539	HD–64–1408		+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	–
3540	HD–450–9–1		n	+	c	*Ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	+
3541	HW–45–239–19		+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	–
3547	Sorona 63	(Mexican origin)	+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	–
3548	〃 64	〃	+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	–
3549	Lema Nata	〃	+	n	c	*ne*$_1$*Ne*$_2$*ch*$_1$*Ch*$_2$	S	++	–
3877	India 3		n	+	c	*Ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	W	++	–
3878	〃 4		n	+	c	*Ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	–
3881	Pusa 6		+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	±	–
3883	NP 52		+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	–
3884	〃 54		+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	–
3885	〃 80–5		+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	–	–
3586	〃 90		+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	–	–
3587	〃 101		+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	–
3889	〃 112		+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	–	+
3890	〃 120		+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	–
3891	〃 123		+	+	?	*ne*$_1$*ne*$_2$*ch*$_1$?	S	++	–
3892	〃 124		+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	–
3893	〃 125		+	+	c	*ne*$_1$*ne*$_2$*ch*$_1$*Ch*$_2$	S	++	–

(Continued)

3894	NP 163–2		+	+	c	$ne_1ne_2ch_1Ch_2$	S	−	−
3896	〃 715		+	+	?	$ne_1ne_2ch_1$?	S	++	−
3897	〃 720		+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	+
3898	〃 721		+	+	c	$ne_1ne_2ch_1Ch_2$	S	++	+

1) n, c and + : necrotic, chlorotic and normal hybrid, respectively.
2) S, W and I : spring, winter and intermediate type, respectively.
3) ++, +, ± and − : fully awned, half awned, awnletted and awnless, respectively.
4) +and − : hairy and glabrous, respectively.

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III. News

INDIAN AGRICULTURAL RESEARCH INSTITUTE, NEW DELHI.

(Division of Genetics)

Indian Wheat Varieties as Sources of Fertility Restoration in Wheat

A research programme on the development of hybrid wheat has been in progress at the Indian Agricultural Research Institute for the past 5 years. In the course of this work, *T. timopheevi* cytoplasm was incorporated into Kalyansona, a dwarf (Norin) wheat variety developed from breeding material of Mexican origin. Five completely male sterile lines of Kalyansona were crossed as female parents with 29 of the more important Indian wheat varieties. The F_1 plants from the crosses involving the varieties NP 839, NP 883 and NP 880 were almost completely fertile. The fertility observed in the F_1 plants suggests that these three varieties carry genes for fertility restoration. A number of other Indian wheat varieties have also been identified, which partially restore fertility. Seeds of all these varieties would be made available on request. The request should be addressed to Dr. H.K. JAIN, Head, Division of Genetics, IARI, New Delhi-12, India.
(M. S. SWAMINATHAN)

IV. Editorial Remarks

Announcement for future issues

WIS No. 35 will be planned for publication in August 1972. Manuscripts for this issue are accepted any time, not later than July 15, 1972.

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

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The Managing Editor

Explanation of the Figure on the Cover

Fig. 1. Metaphase in PMC of a 29-chromosome plant of the cross, Agrus $Tc^{r} \times$ *Ae. spelteides*, showing $6_{I}+7_{II}+3_{III}$ (the *Agropyron* telocentric is in a heleromorphic bivalent). (cf. J. DVOŘÁK and D. R. KNOTT, pp. 35~37)