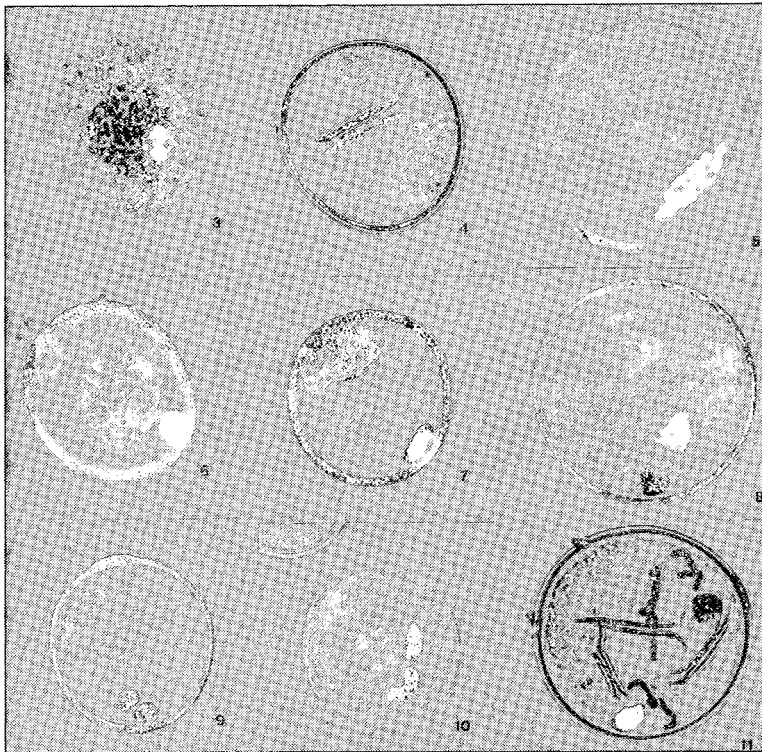


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Contents

	Page
I. Research Notes:	
Use of <i>Ae. spelthoides</i> and nulli-5B, Tetra-5D "Chinese Spring" for inducing homoeologous recombinations in a wheat- <i>Aegilops</i> addition line F. DOSBA	1
Chromosome pairing and chiasma formation in hybrids (ABRR) derived from 6x Triticale × 2x rye crosses P.K. GUPTA, I.C. TYAGI & J.R. BAHL	4
Differential suppression of homoeologous pairing in two recombinants of <i>Triticum persicum</i> × <i>T. dicoccoides</i> B. APOLINARSKA & A.J. ŁUKASZEWSKI	7
Meiotic associations in a <i>Triticum turgidum</i> L. var. <i>durum</i> Desf. em. Bowden × <i>Agropyron distichum</i> (Thunb.) Beauv. hybrid R. de V. PIENAAR	10
A fertile amphiploid from the cross <i>Triticum aestivum</i> L. em Thell. <i>Agropyron distichum</i> × (Thunb.) Beauv. R. de V. PIENAAR	13
Some cytological aspects of diploid wheat anther culture . . . B.H. TAN & G.M. HALLORAN	15
Analysis of wheat mutants for straw and leaf characteristics A.S. LARIK, H.M. HAFIZ & M.B. KUMBHAR	19
Study of allied species of <i>Triticum</i> against Indian cultures of leaf rust races L.B. GOEL & R.N. SAWHNEY	24
Performance of certain mutants of common wheat for yield and nutritional quality under salinity D. KUMAR, R.P.S. CHAUHAN & R.V. SINGH	26
Agronomic performance of randomly derived alloplasmic wheats . . K.D. KOFOID & S.S. MAAN	29
II. Gene Symbols:	
Catalogue of gene symbols for wheat, 1980 supplement R.A. McINTOSH	33
III. Editorial Remarks:	
Announcement for future issues	35
Membership fee	35
Acknowledgement	35
Coordinating committee	Cover iii
Explanation of the figure on the cover	Cover iii



I. Research Notes

**Use of *Ae. speltoides* and nulli 5B tetra 5D "Chinese Spring"
for inducing homoeologous recombinations
in a wheat-*Aegilops* addition line**

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Since KIMBER (1974) described a range of variation in *Ae. speltoides* and divided it into low, intermediate, high and super high pairing groups, it appears very important to select high or super high pairing *Aegilops* for inducing homoeologous recombinations. Thus, if the absence of recombination allows the obtention and the study of addition lines, such as wheat-*Aegilops ventricosa* lines (DOSBA *et al.*, 1978), the induction of homoeologous recombination is necessary to transfer the alien genetic information into wheat. The study reported in this paper was designed to evaluate the pairing group of different accessions of *Ae. speltoides* and to compare the efficiency of *Ae. speltoides* or "Chinese Spring" nulli 5B tetra 5D in inducing homoeologous recombinations into a wheat *Aegilops* addition line.

Four accessions of *Ae. speltoides* (included *Ae. speltoides* n°25 supplied by Dr G. KIMBER and considered as super high pairing) were crossed with *T. aestivum* cv Moisson. In these hybrids, the mean meiotic pairing reveals significant differences between *Aegilops speltoides* n° 25 and the three others (Table 1 and 2). Particularly, the univalent mean, is lower in the hybrids with *Ae. speltoides* n° 25 than with the other ones; and it appears that the decrease in univalent number is compensated by the formation of multivalents.

So, in the purpose of inducing homoeologous recombinations between the M^v chromosome of the addition line wheat *Ae. ventricosa* n° 255 and the wheat chromosomes, we tried to cross this line with *Ae. speltoides* n° 5 and n° 25, or with "Chinese Spring" nulli 5B tetra 5D. Concerning *Ae. speltoides*, only the crosses with *Ae. speltoides* n° 5 succeeded. The

1) With the technical assistance of Anne-Marie TANGUY.

Table 1. Meiotic pairing of F₁ hybrids between the french cultivar "Moisson" and different accessions of *Aegilops speltoides*

Name	nb. of plants	nb. of cells	2n	I	II	III	IV	other multivalents	nb. of chiasmata/cell	nb. of chiasmata/chromosome
Moisson × <i>Ae. speltoides</i> n°5	1	50	27	(1) 5.54 (2) 0-13	6.16 2-10	1.56 0-5	0.82 0-3	0.22 0-1	14.90	0.55
Moisson × <i>Ae. speltoides</i> n°17	1	50	28	6.50 2-12	7.08 1-13	0.90 0-3	1.08 0-3	0.06 0-1	15.50	0.55
Moisson × <i>Ae. speltoides</i> n°24	1	50	28	5.62 1-10	5.68 2-10	1.88 0-4	1.04 0-3	0.22 0-1	15.66	0.56
Moisson × <i>Ae. speltoides</i> n°5	3	123	28	5.58 0-12	6.55 1-13	1.58 0-5	0.90 0-4	0.18 0-2	16.36	0.58
Moisson × <i>Ae. speltoides</i> n°25	1	100	28	2.71 0-9	6.77 2-11	1.03 0-4	1.64 0-4	0.38 0-2	18.96	0.70

(1) mean (2) range

Table 2. Variance analysis of number of univalents (1), bivalents (2); and multivalents (3) per cell in four different crosses *T. aestivum* cv. Moisson × *Ae. speltoides* - (According to KRAMER, 1956).

Source	Df	Mean square	F calculated	F P<0.05	F P<0.01
1 between crosses error	3	229.79	44.62	S	S
	329	5.15			
2 between crosses error	3	18.95	3.85	S	NS
	329	4.92			
3 between crosses error	3	24.52	13.62	S	S
	329	1.80			

F (P<0.05)=2.64 S: Significant
F (P<0.01)=3.85 NS: Not Significant

analysis of the F₁'s meiotic pairing shows more associations than expected (19''+1''' +2') for the crosses 255 × nulli 5B tetra 5D and less for the cross 255 × *Ae. speltoides* n° 5 (Table 3). In the first case, the numerous multivalents observed are probably due to the presence of two reciprocal translocations (5B-7B, 1B-6B) which differentiate "Chinese Spring" from the recipient parent of the addition line, the french variety "Moisson" (BOURGEOIS *et al.*, 1978). One trivalent may be originated from trisomy 5D, the other from 7B/5B-5B/7B-7B and one quadrivalent from 1B-1B/6B-6B-6B/1B. However, it should be noticed 14.65% of cells do not present any univalent. So recombinations could occur between the added chromosome and those of wheat. Meiotic behaviour of the F₁ hybrid 255 × *Ae. speltoides* n° 5 compared to "Moisson" × *Ae. speltoides* n° 5 one's shows a decrease in the number of chiasmata per cell. The lack of pairing may be due to the fact that the accession n°5 was not fixed for inducing homeologous pairing.

Table 3. Meiotic pairing of hybrids between the wheat *Aegilops* addition line n° 255 and *Ae. speltoides* n° 5 or "Chinese Spring" nulli 5B-tetra 5D.

Name	nb. of plants	nb. of cells	2n	% of cells without univalent	I	II	III	IV	other multi-valents	nb. of chiasmata/cell	nb. of chiasmata/chrom
C.S. nulli 5B tetra 5D	1	90	42	—	(1)0.54 (2)0-3	19.19 15-21	0.24 0-1	0.59 0-1		37.46	0.89
line 255	2	100	44	74.00	0.61 0-4	21.68 20-22	0.01 0-1			40.28	0.92
F ₁ 255 × C.S. nulli 5B tetra 5D	9	226	43	14.65	1.84 0-8	15.55 10-20	1.95 0-5	1.02 0-4	0.03 0-1	35.70	0.83
"Moisson" × C.S.	11	367	42	69.70	0.60 0-7	13.01 13-21	0.17 0-3	1.14 0-3	0.05 0-1	38.22	0.91
255 × <i>Ae.</i> <i>speltoides</i> n°5	3	210	29	0	16.42 8-25	4.82 1-9	0.73 0-3	0.17 0-1	0.02 0-1	7.53	0.26
F ₂ 255 × C.S. nulli 5B tetra 5D	3	160	42	65.00	0.47 0-2	19.72 16-21	0.46 0-3	0.17 0-1		38.94	0.93
	6	261	43	49.81	0.83 0-5	13.57 15-21	0.80 0-3	0.64 0-2	0.01 0-1	38.91	0.90
	2	75	44	46.67	1.09 0-5	20.44 18-21	0.53 0-2	0.11 0-1		38.27	0.87

(1) mean (2) range

The progeny of these hybrids died before maturity except for the self-pollinated generation issued from 255 × "Chinese Spring" nulli 5B tetra 5D.

The analysis of some plants at the F₂ generation reveals an heterogeneity in the meiotic behaviour as well for univalents as for multivalents.

The line v 255 possesses no specific marker on its added chromosome. So it is difficult to assess the level of recombination between this chromosome and the wheat chromosomes. But occurrence of recombination can be assumed from the F₁ analysis.

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**Chromosome pairing and chiasma formation in hybrids (ABRR)
derived from 6x Triticale × 2x rye crosses**

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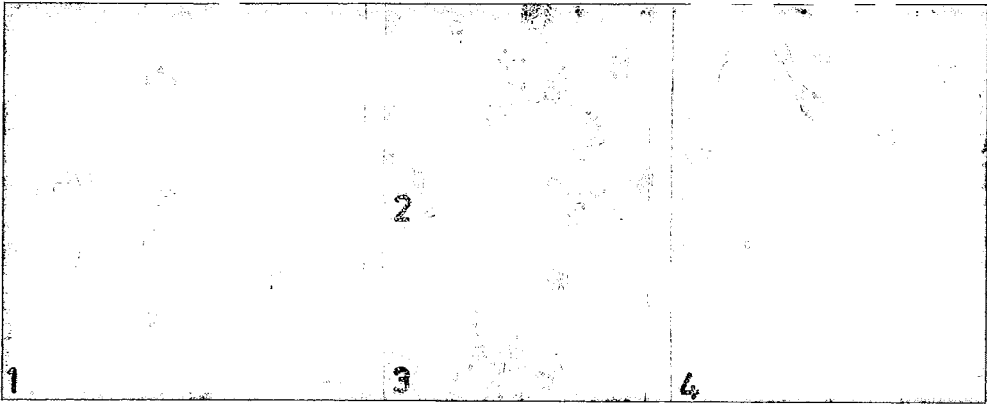
As a part of a research programme "*Cytogenetic Studies in Triticales*" sanctioned to us by Indian Council of Agricultural Research, we are planning to synthesize some tetraploid triticales. For this purpose, as earlier done by KROLOW (1973), we made crosses between 6x Triticale and 2x rye. The cross was easily successful and more than 500 seeds could be obtained by using 6x Triticale as the female parent. Seven different Triticale strains (DTS 30, DTS 205, ST 69-1, 6TA701, TL63A, JNK 6T192, JNK 6T214) and a single rye strain (persian rye) were used in the crosses.

Meiosis was studied in plants representing hybrids (ABRR) obtained from all the seven Triticale parents and the results are presented in Table 1. In the hybrids ABRR, one would generally expect the presence of 7''+14', the bivalents being contributed by rye chromosomes only. Since rye commonly shows seven ring bivalents (LAMM, 1936/37 and REES, 1955) one would also expect that in ABRR hybrids, the seven bivalents should be largely ring bivalents. The observed results deviated from this expectation and showed some agreement with earlier results of MILLER and RILEY (1972) and LELLEY (1975). It can be seen from Table 1 that although the average frequency of univalents in different hybrid lines ranged from 13.60-15.36 per p.m.c., in individual p.m.c. the number of univalents could be as low as five and as high as 22, the remaining chromosomes being associated as

Table 1. Chromosome associations and chiasmata frequencies in different F₁ hybrids (ABRR)

Triticale strain involved in F ₁ hybrid		Univalents	Bivalents			Trivalents	Quadrivalents	Chiasmata frequency/cell
			Ring	Rod	Total			
<i>DTS 30</i>	mean	14.65	0.55	5.52	6.07	0.06	0.26	7.52
	range	9-20	0-2	2-8	4-8	0-1	0-1	4-11
<i>DTS 205</i>	mean	15.32	1.14	4.94	6.08	0.08	0.06	7.62
	range	10-22	0-3	0-8	3-9	0-1	0-1	4-11
<i>ST 69-1</i>	mean	15.35	1.06	4.92	5.98	0.18	0.10	7.61
	range	9-20	0-3	1-8	3-8	0-1	0-1	5-12
<i>6TA701</i>	mean	14.00	1.92	4.92	6.84	0.04	0.06	9.02
	range	5-18	0-3	2-9	5-10	0-1	0-1	5-14
<i>TL63A</i>	mean	15.36	0.91	5.00	5.91	0.14	0.07	7.34
	range	12-22	0-3	2-7	3-8	0-1	0-1	5-11
<i>JNK 6T192</i>	mean	13.60	0.60	6.08	6.68	0.14	0.12	7.98
	range	4-20	0-3	4-9	4-12	0-1	0-1	5-14
<i>JNK 6T214</i>	mean	13.83	1.29	5.71	7.00	0.04	0.02	8.40
	range	8-18	0-3	3-8	5-10	0-1	0-1	6-14

bivalents and multivalents. (Figs. 1-4). It was also conspicuous that most of the bivalents were mainly rod bivalents as against the expectation of the formation of ring bivalents by the rye chromosomes. It is thus obvious that while increased chromosome pairing involving as many as 23 chromosomes was possible due to promotion of homoeologous chromosome pairing, there was also simultaneous reduction in the chiasmata formation in



Figures 1-4. Metaphase I chromosome associations in hybrids ABRR derived by crossing 6x triticale (AABBRR) and 2x rye (RR).

Fig. 1. 5'' (2 rods+3 rings)+18'; Fig. 2. 8'' (all rods)+12';

Fig. 3. Only 8' (remaining chromosomes associated as bivalents or multivalents); Fig. 4. A part of a cell showing a distinct chain quadrivalent.

individual chromosome association as revealed by the preponderance of rod bivalents and chain quadrivalents. Such increase in homoeologous chromosome pairing in hybrids was also inferred by RILEY and MILLER (1972) and LELLEY (1975) who attributed it to an increase in rye genome (relative to wheat). LELLEY (1975) also noticed a reduction in chiasma formation in 6x Triticale \times 2x rye hybrids and found that this reduction was observed even between homologous rye chromosomes, which is in agreement with our results. It is thus obvious that there are independent control systems for chromosome pairing and chiasmata formation. However, the frequency of multivalents and the total number of chromosomes involved in pairing during the present study was much higher than that observed by LELLEY (1975). Whether or not some of these quadrivalents are due to translocation differences can not be ascertained, but these multivalents were more frequent in some hybrids than others (Table 1). It can also be seen that chromosome pairing conspicuously differed in the different hybrid lines which as earlier explained by Rees and THOMPSON (1956) and LELLEY (1978), can be attributed to a polygenic control of chiasma formation.

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Differential suppression of homoeologous pairing in two recombinants
of *Triticum persicum* × *T. dicoccoides*

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The discovery of the genetic system controlling diploid-like pairing of chromosomes in wheat (OKAMOTO 1957, RILEY and CHAPMAN, 1958) opened new areas to wheat cytogenetics. However, due to lack of allelic variation, some aspects of this system were difficult or even impossible to study. To induce the variation some authors have undertaken mutation studies which resulted either in deletion in chromosome 5B (SEARS 1975) or in a weaker form of homoeologous pairing suppressor (mutant 10/13, RILEY 1973). In this paper we present results indicating that natural variation in the system controlling chromosome pairing may exist in tetraploid wheats.

Materials and Methods

Two recombinants of tetraploid wheats, Xu and Do, selected for good crossability with rye from *Triticum persicum* var. *rubiginosum* × *T. dicoccoides* var. *spontaneonigrum* hybrid by ŁAPINSKI (ŁAPINSKI, ŁUKASZEWSKI, SODKIEWICZ, APOLINARSKA 1979) were crossed to diploid winter rye *Secale cereale* commercial variety Dańkowskie Żłote. The resulting wheat-rye F₁ hybrids were backcrossed to the paternal rye. Out of the BC₁ generation 28 chromosome plants, believed to be of ABRR constitution, were selected and their meiotic behaviour was analysed along with ABR F₁ clones.

All spikes were fixed in absolute ethanol: glacial acetic acid (3:1) and refrigerated. For routine analysis anthers were squashed in 2% acetoorceine, while for chromosomes banding anthers showing desired stage of development were hydrolysed in 0.2N HCl for 45 min. at room temperature and squashed in a drop of 45% acetic acid on gelatine-coated slides. The procedure employed thereafter was essentially the same as used in the University of Manitoba, Canada, and described by BENNETT, GUSTAFSON and SMITH (1977).

Results and Discussion

The results obtained for routine and Giemsa banding analysis of chromosome pairing in MI of meiosis are given in Tables 1 and 2, respectively. Regardless of the variation between years, both in F₁ and in BC₁ the Xu wheat line derived hybrids showed significantly more chromosomes paired per PMC than the Do derived hybrids. The Giemsa banding allowed the authors to study the frequencies of wheat-wheat, rye-rye and wheat-rye associations in meiosis. In BC₁ it was found that not all rye chromosomes formed bivalents, 5II and 6II being the most frequent configurations, 33,3% and 25,5% for Xu hybrids and 29,6

Table 1. Chromosome pairing in MI of PMCs in ABR and ABRR hybrids from crosses/
Triticum persicum × *T. dicoccoides*/lines Xu and Do × *Secale cereale*.
Mean values, range given in brackets.

Wheat genotype	Number of plants analysed	Number of PMCs analysed	Chromosome configurations			
			Univalents	Bivalents	Trivalents	Quadrivalents
F ₁ Xu/1977	3	200	17.91/12-21/	1.35/0- 4/	0.11/0-2/	0.015/0-1/***
Do/1977	4	200	19.10/15-21/***	0.85/0- 4/*	0.03/0-1/	
BC ₁ Xu/1977	2	100	9.39/ 2-14/	8.32/2-11/	0.41/0-2/	0.18/0-2/
Do/1977	2	100	10.92/ 4-16/***	7.88/4-11/***	0.40/0-2/	0.04/0-1/
Xu/1978	5	250	7.59/ 1-12/	8.22/3-13/	1.07/0-3/	0.16/0-2/
Do/1978	5	250	10.24/ 4-16/***	7.22/2-12/***	0.85/0-4/	0.16/0-2/

* significant difference, $p < 0.05$

*** interlocked bivalents

** significant difference, $p < 0.01$

B. Apolinarska, A.J. Łukaszewski, "Differential suppression of homoeologous pairing..."

Table 2. Configurations of wheat and rye chromosomes in MI of PMCs in ABR and ABRR hybrids from crosses/*Triticum persicum* × *T. dicoccoides*/lines Xu and Do × *Secale cereale*

	Line Do	Line Xu
F ₁ /ABR/:		
Number of PMCs analysed:	150	200
Configurations of wheat chromosomes:	12.27 _I +0.75 _{II} +0.03 _{III}	11.26 _I +1.11 _{II} +0.08 _{III}
Configurations of rye chromosomes:	6.85 _I +0.007 _{II}	6.65 _I +0.05 _{II}
Wheat-rye associations:	0.14 _{II}	0.19 _{II} +0.04 _{III}
Total F ₁ :	19.12 _I +0.90 _{II} +0.03 _{III}	17.91 _I +1.35 _{II} +0.12 _{III}
BC ₁ /ABRR/:		
Number of PMCs analysed:	54	51
Configurations of wheat chromosomes:	10.53 _I +1.24 _{II} +0.08 _{III}	8.29 _I +2.12 _{II} +0.27 _{III}
Configurations of rye chromosomes:	1.47 _I +5.65 _{II} +0.13 _{III}	1.98 _I +5.35 _{II} +0.12 _{III}
Wheat-rye associations:	0.06 _{II} +0.37 _{III} +0.09 _{IV}	0.22 _{II} +0.39 _{III} +0.01 _{IV}
Total BC ₁ :	12.00 _I +6.95 _{II} +0.58 _{III} +0.09 _{IV}	10.27 _I +7.69 _{II} +0.78 _{III} +0.01 _{IV}

B. Apolinarska, A.J. Łukaszewski, "Differential suppression of homoeologous pairing..."

% and 38,9% for Do, respectively. The remaining rye chromosomes were present either as univalents or they were involved in wheat-rye associations in which the presence of true chiasmata could not always be precisely determined. The evident secondary associations were not included into the data presented in Table 2. Stronger suppression of homoeologous pairing in Do resulted in more regular pairing of rye chromosomes in BC₁ and in reduction of wheat-rye associations, both in F₁ and BC₁. This indicates that pairing of rye chromosomes was affected by the system of pairing control of wheat, at least to certain extent.

Unfortunately, in this experiment it was impossible to determine whether the Do wheat line suppression of homoeologous pairing is equivalent to that in other wheats. In

general, ours involved hybrids show more chromosomes paired per PMC than those described in the literature. This may be due either to the difference in pairing control system or to the difference in external factors. Temperature is known to affect homoeologous pairing (KATO and YAMAGATA 1979). The between-year variation in pairing in BC₁ may reflect the influence of environmental factors. Moreover, the formation of trivalents (mostly wheat-wheat-rye type in this F₁) was rarely reported in ABR F₁.

The F₁ (*T. persicum* × *T. dicoccoides*) × *S. cereale* F₁ hybrid showed high pairing level (17,28_I+1,66_{II}+0,13_{III}+0,003_{IV}, ŁUKASZEWSKI, 1975). From indirect evidence based on the range of variation of the chromosome number in functional female gametes of F₁ it may be expected that all other lines selected by Łapiński (ŁAPINSKI *et al.* 1979) from this cross show pairing level simillair to Xu, the Do line being exceptional among all the selected progeny (ŁUKASZEWSKI, APOLINARSKA, ŁAPINSKI, SODKIEWICZ 1979).

NAKAJIMA (1956) found *T. persicum* to form more bivalents in F₁ hybrids with *S. cereale* than any other tetraploid wheat he studied. The described character of weaker suppression of homoeologous pairing might have been inherited from this species. DALAL and SADANAGA (1965) have shown *T. persicum* to carry reciprocal translocation involving chromosomes 2B and 3A. According to DRISCOLL (1972), 3A chromosome of Chinese Spring carries homoeologous pairing suppressor. However, presented results do not allow for any statement on mechanisms involved and this problem needs further studies.

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**Melotic associations in a *Triticum turgidum* L. var. *durum* Desf.
em. Bowden × *Agropyron distichum* (Thunb.) Beauv. hybrid**

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The successful crosses of the two hexaploid bread wheat cultivars Chinese Spring and Inia 66 with *Agropyron distichum* (PIENAAR *et al.*, 1977; PIENAAR, 1979), tempted us to produce a *T. turgidum* var. *durum* × *A. distichum* hybrid. The latter two species are both tetraploid with $2n=28$, and their amphiploid should therefore be octoploid with $2n=56$. Since the optimal chromosome number of many of the polyploid *Triticinae* is $2n=42$, it was thought that the *T. durum* × *A. distichum* octoploid would probably be more vigorous than the decaploid amphiploid obtained from the *T. aestivum* var. *aestivum* × *A. distichum* hybrid (PIENAAR, 1980).

During the early summer of 1977 and 1978 some 3744 *durum*-wheat florets were emasculated and pollinated with *A. distichum* (Table 1). None of these crosses yielded any filled kernels, but 23 shrivelled and 9 small kernels with undeveloped endo-sperm were obtained. The 9 embryos from the latter kernels were excised 18 days after pollination and cultured on sterile Orchid Agar in McCarthney bottles. Seven of these embryos developed into plantlets on the medium and were transplanted into pots at the three leaf stage. Five of these grew into vigorous F_1 hybrids with $2n=28$ chromosomes.

Table 1. Results of crossing *T. turgidum* var. *durum* with *A. distichum*.

<i>T. durum</i> cultivar, line, as ♀-parent	No. of florets pollinated	No. of kernels set			Kernel set (% polli- nated florets)	Kernels with embryo	Successful embryo cultures	Mature plants obtained
		filled	partly filled	shrivelled				
Calvin (D7047)	660	0	3	13	2.42	3	3	3
Cando	770	0	2	0	0.25	2	0	0
Gediz	124	0	0	0	0	0	0	0
Nordum (D6647)	740	0	4	1	0.67	4	4	2
Parana 66/270	32	0	0	0	0	0	0	0
Quilafen	94	0	0	0	0	0	0	0
Ward	106	0	0	0	0	0	0	0
A1345	174	0	0	0	0	0	0	0
D6962	500	0	0	7	1.4	0	0	0
7th IDSN 244	192	0	0	0	0	0	0	0
7th IDSN 245	40	0	0	0	0	0	0	0
6416-1-2-M	148	0	0	0	0	0	0	0
7214-1-1-1-M	118	0	0	2	1.69	0	0	0
7263-1-2-M	46	0	0	0	0	0	0	0
Total	3744	0	9	23	0.85	7	7	5

Both the Calvin and Nordum F_1 hybrids with *A. distichum* are much more vigorous than the F_1 hybrid of Inia 66 \times *A. distichum* and like the latter, tend to be perennial. They produce numerous tillers with large erect leaves. The height of the Calvin hybrid is 97 cm, that of the Nordum hybrid 122 cm, compared to the 97 cm of the Inia 66 hybrid. Although Calvin, Nordum and Inia 66 are awned cultivars, their hybrids with *A. distichum* differ in the expression of the awned character; the spikes of the Calvin and Nordum hybrids have short awns, whereas the Inia 66 hybrid has tip awns only. However, the latter hybrid resembles its Inia 66 parent in having a non-brittle spike with a strong rachis, whereas the durum-hybrids have brittle spikes like *A. distichum*.

The spikes of the Calvin and Nordum F_1 hybrids have 21 and 18 spikelets respectively, and the respective spikelets possess 8 and 6-7 florets. The spikes of the Calvin hybrid tend to be branched; the lower spikelets being replaced by branches with up to 7 spikelets. Both F_1 hybrids are completely selfsterile like the Inia 66 hybrid.

Young spikes of the F_1 hybrids were fixed in Carnoy's 6:3:1 fixative for 24 hours, stored in 70 per cent alcohol in a refrigerator for 48 hours, then placed in 45 per cent acetic acid overnight, rinsed in water and hydrolysed in N HCl at 60°C for 8 minutes. After staining the pollen mother cells according to the Feulgen procedures they were squashed in 1% Rosner aceto-carmine. The chromosome associations at the first meiotic metaphase were studied in 200 pollen mother cells (PMC's) in the Nordum \times *A. distichum* hybrid. The results given in Table 2 show that a mean of 13.88 chromosomes per PMC associate in bivalents and multivalents by means of 9.17 chiasmata of which 9.08 are terminalised. As many as 55.5 per cent of the PMC's have 14 or more chromosomes associated in bivalents and multivalents. This higher level of chromosome association than that reported for the Inia 66 \times *A. distichum* hybrid by PIENAAR (1979), is mainly due to the higher frequency of multivalents in the Nordum \times *A. distichum* hybrid.

The question which of the genomes of durum-wheat and *A. distichum* are sufficiently homologous to undergo synapsis and chiasma-formation in order to produce the large number of bivalents and multivalents, remains unsolved. Is it due to autosyndetic pairing between the two *A. distichum* genomes or due to allosyndetic pairing of one of the *Agropyron* genomes with either the A or B genome of the durum-wheat? The fact that 16 or more chromosomes are associated in bivalents and multivalents at first meiotic metaphase in 31.5 per cent PMC's indicates that at least some *A. distichum* chromosomes synapse with

Table 2. Mean chromosome associations at first meiotic metaphase in the PMC's of the F_1 hybrid *T. turgidum* var. *durum* cv. Nordum \times *A. distichum* (ranges in parentheses).

No. of PMC's examined	Metaphase I chromosome associations								Chiasmata per PMC	
	Univalents	Bivalents			Multivalents				Total	Terminal
		Rod	Ring	Total	III $\frac{1}{2}$	IV	V	VI		
200	14.12 (6-26)	3.55 (0-7)	1.26 (0-4)	4.81 (1-9)	0.375 (0-2)	0.75 (0-2)	0.01 (0-1)	0.01 (0-1)	9.17 (1-14)	9.08 (1-14)

wheat chromosomes and cross-over to produce chiasmata. It may then be possible to transfer useful genes from *A. distichum* to their wheat homoeologues by natural recombination.

An analysis of 30 PMC's at first meiotic anaphase showed a mean distribution of 8.03 and 7.63 chromosomes to the two poles with 12.33 univalents congregating on the equator of the spindle. The univalents divide during late anaphase I and many of the daughter chromosomes fail to reach the poles in time, and produce micronuclei. The daughter chromosomes that do reach the poles, fail to undergo division during the second meiotic division, and lag on the spindle. Many micronuclei were observed in the microspore tetrads. These meiotic abnormalities are responsible for the sterility of the hybrid.

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**A fertile amphiploid from the cross *Triticum aestivum* L. em
Thell. × *Agropyron distichum* (Thunb.) Beauv.**

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By using the embryo culture technique, F₁ hybrids were obtained from the crosses of the two hexaploid bread wheat (*Triticum aestivum* var. *aestivum*) cultivars, Chinese Spring and Inia 66, with the single indigenous tetraploid and perennial *Agropyron* species, *A. distichum* (PIENAAR *et al.* 1977; PIENAAR, 1979).

The self-sterile F₁ hybrids on open-pollination with bread wheat set a few kernels which produced plants with chromosome numbers ranging from 43 to 68 (Table 1).

Table 1. Results of open-pollinating the F₁ hybrids of (a) Chinese Spring × *A. distichum*, and (b) Inia 66 × *A. distichum* with bread wheat.

No. of (spikes) and spikelets openpollinated	No. of kernels set	No. of kernels germinated	Number of progeny with chromosome number of:							
			43	45	54	55	56	59	62	68
a: (14) 308	10	8	1	1	1	2	1	1	1	0
b: (82) 1432	2	2	0	0	0	0	1	0	0	1

Colchicine treatment of the Chinese Spring × *A. distichum* F₁ hybrids yielded no fertile amphiploid spikes. The single Inia 66 × *A. distichum* F₁ hybrid plant was cloned to produce 13 plants, 10 of which were treated with 0.1% colchicine in 2% DMSO for 24 hours. Nine of the 10 plants had no fertile sectors, but one plant produced a spike with a few dehiscent anthers. It was decided to back cross the spike to Inia 66, and 40 kernels were obtained which produced plants with chromosome numbers ranging from 52 to 69 (Table 2).

Table 2. The frequency distribution of chromosome numbers in the BC₁ progeny of
(C₁: Inia 66 × *A. distichum*) × Inia 66

No. of C ₁ (spikes) and spikelets pollinated	No. of kernels set	No. of kernels germinated	Number of progeny with chromosome number of:							
			51	52	53	54	55	56	57	69
(1) 17	40	38	0	3	5	10	13	6	0	1*

*C₂ monosomic decaploid amphiploid resulting from self-pollination.

Only 6 of the 38 backcross progeny had the expected chromosome number of 2n=56; one plant resulted from selfpollination and was a monosomic decaploid with 2n=69, the

others had chromosome numbers ranging from 52 to 55. It was evident from these results that the meiosis in the fertile sector of the C_1 plant must be slightly irregular. This was borne out by a meiotic study of a few PMC's – see below.

The tiller which produced the fertile spike was cut back after the spike was harvested, and repotted. It sprouted again and produced six partly fertile spikes, one of which was sacrificed for meiotic investigations. The other five spikes produced 25 kernels in 87 spikelets after self-pollination. These C_2 kernels will most likely produce a new fertile decaploid *Agroticum* species which will be of use in wheat breeding programmes. It will resemble the semi-fertile C_1 plant which developed from the repotted fertile tiller reported above. This plant is approximately 1 meter tall and produces spikes which are 15 cm long and contain up to 20 spikelets. Each spikelet is composed of 5 to 6 florets. The spikes have a strong rachis and except for a very short tip awn, are awnless—the awned spikes of Inia 66 is therefore recessive to the awnless spikes of *A. distichum*. The plant has a strong perennial tendency and can be readily maintained by cloning. It has no vernalization requirement and is insensitive to daylength, coming into flower any time of the year, unlike *A. distichum* which flowers only during the latter part of November and early December.

The meiotic investigation of the semi-fertile spike revealed that it was mixoploid – partly pentaploid and partly decaploid. Meiotic prophase in the decaploid pollen mother cells (PMC's) appears to be quite normal because the 7 PMC's observed at diakinesis had a mean bivalent frequency of 33.86 (range 33–35). Some bivalents, however, must disjoin before metaphase I, since the mean univalent frequency per PMC at metaphase I as deduced from the 20 scored cells at this stage, is 6.1 (range 2–10). In spite of this the anaphase I distribution appears to be fairly regular – the mean distribution in 20 scored PMC's is 34, 1–1–34, 9.

In order to produce a fully fertile amphiploid, selection for meiotic stability will have to be practiced in the C_2 and subsequent generations.

This investigation was financed from funds obtained from the Department of Agricultural Technical Services and the University of Stellenbosch. The technical assistance of Mr. H.S. ROUX and Mrs. M.H. LAMBRECHTS is gratefully acknowledged.

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Some cytological aspects of diploid wheat anther culture

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Previous attempts (FUJII 1970, HESZKY and MESCH 1976) at inducing callus in anthers of diploid wheat (*Triticum monococcum* L., $2n=14$) were unsuccessful.

Recently we studied the responses of eight *T. monococcum* lines collected by one of us (G.M.H.) in Asia Minor. Callus induction was feasible only in three of these lines.

In that preliminary study we noted the occurrence of pollen dimorphism (Fig. 14), which was manifest in the late uninucleate and later stages of pollen development. The phenomenon has also been reported in certain cultivar(s) of hexaploid wheat, barley, oats, tobacco and *Paeonia* (SUNDERLAND 1978). The cytoplasm of the larger and predominant delete form is rich in starch granules and stains readily with acetocarmine, both characteristics of which are absent in the smaller form. According to DALE (1975) only the latter type is potentially morphogenic in barley.

The developmental sequences from meiosis to the tetrad *in vivo* (Figs. 1-2), and from early-uninucleate to the mature trinucleate pollen (Figs. 3-10) both *in vivo* and *in vitro* are similar to those already described for other cereal species.

During anther culture a variable proportion of pollens at the mid- or late-uninucleate stage is capable of unrestrained mitotic division to form multi-cellular pollens (m.c.p.'s) within the anther sac — which in essence is the cytological basis toward callus formation *in situ*. The so-called 'A-Pathway' (SUNDERLAND and DUNWELL 1974), whereby the vegetative nucleus divides repeatedly in contrast to the quiescence of the generative nucleus(i), appeared to be the more common pathway in pro-callus morphogenesis (Figs. 16-19). Although the 'B-Pathway' was also represented it is insignificant in *T. monococcum*. The latter mode of morphogenesis is often arrested at the bicellular stage. Non-haploid nuclei are common in such pollens (Fig. 15), probably as a result of endo-mitosis or endo-replication. Free nucleus(i) are sometimes observed following the first mitotic division (Fig. 11); SUNDERLAND (1978) suggested that the parallel orientation of the spindles, in relation to the intine, could be responsible for the absence of cell wall formation.

Of considerable interest was the observation that an inoculated anther was either *inductive*, in which case about 5-40% of (uninucleate) pollens developed into m.c.p.'s and pro-calli after about three weeks, or that it was otherwise non-supportive of morphogenesis (Fig. 12-13): m.c.p. induction is thus *sine qua non*.

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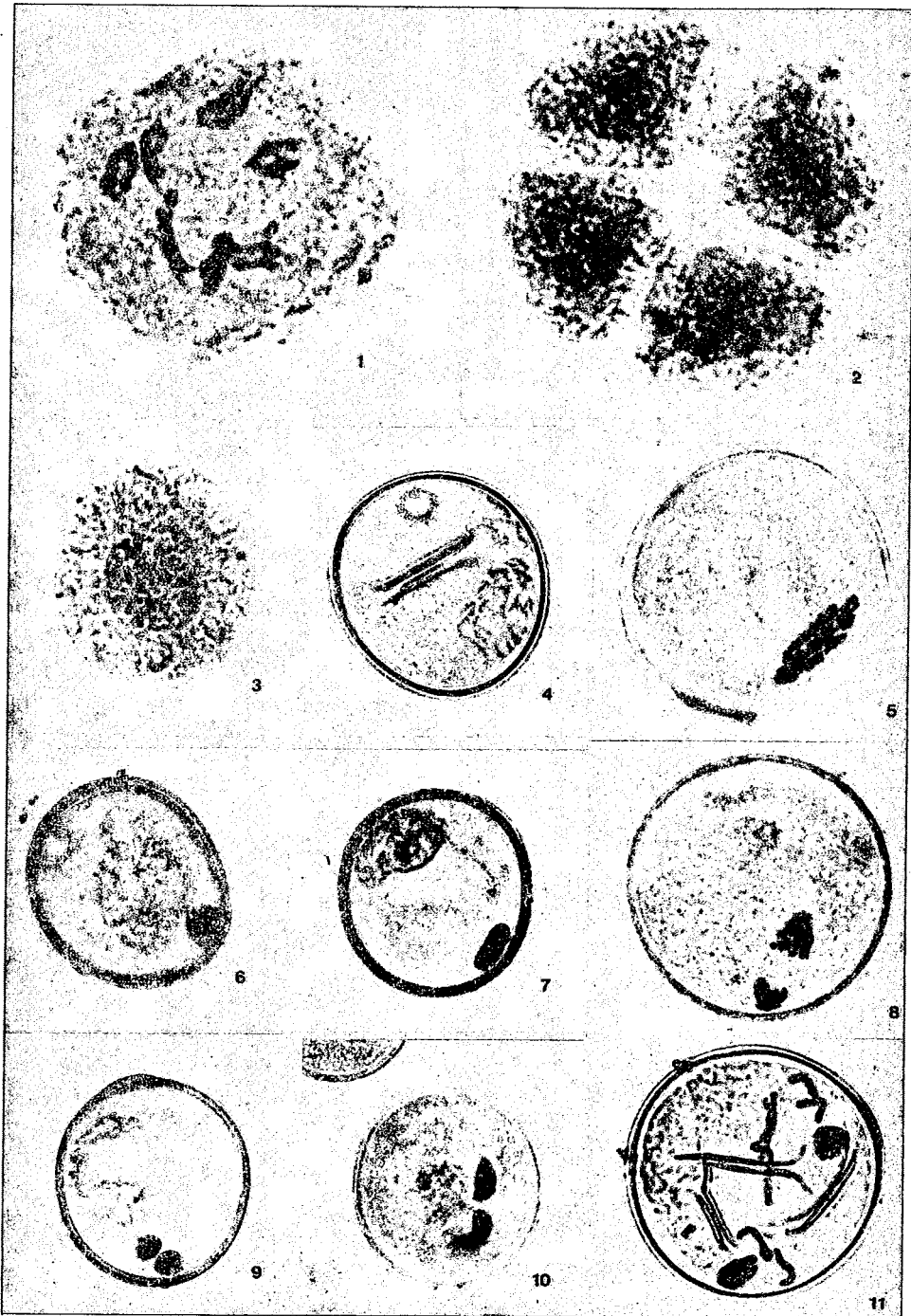


Plate I (Figs. 1-11)

Rarely was more than one sister anther from the same floret found to be inductive, which suggests that the inductive stimulus is not ubiquitous. It is sheer speculation to suggest what the inductive stimulus (i) or substance (s) might be, but it probably holds the key to putting anther culture on a more predictable basis. It could be hormonal, or, it could involve the removal of an inhibitory substance (s) present in excess or only in some but not all the anthers. The presence of activated charcoal in the culture medium should be beneficial in the latter situation, but comparative studies examining the value of adsorbents are not always conclusive.

Our current investigations, focusing on the influence of medium and effect of spike pre-treatment on the frequencies of anther induction and subsequent callus formation, will be reported at a later date.

Acknowledgements

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Stages of pollen development in *T. monococcum*.

- Fig. 1: ($\times 3950$) Pollen mother cell at Metaphase I of meiosis with 7 bivalents;
Fig. 2: ($\times 3950$) Tetrad;
Fig. 3: ($\times 3630$) Early-uninucleate stage, non-vacuolated, nucleus occupying central position;
Fig. 4: ($\times 2200$) Mid-uninucleate stage;
Fig. 5: ($\times 2750$) Late-uninucleate stage;
Fig. 6: ($\times 2420$) After the first mitotic (unequal) division — a large vegetative and a small generative (*g*) nucleus;
Fig. 7: ($\times 2420$) Vegetative nucleus migrates towards germ-pore;
Figs. 8-9: ($\times 2750$, $\times 2420$) Second mitotic (equal) division — 2 *g*'s formed;
Fig. 10: ($\times 2420$) Generative nuclei differentiate into sperm nuclei (crescent-shaped);
Fig. 11: ($\times 2750$) Free vegetative nucleus at metaphase ($n=7$).

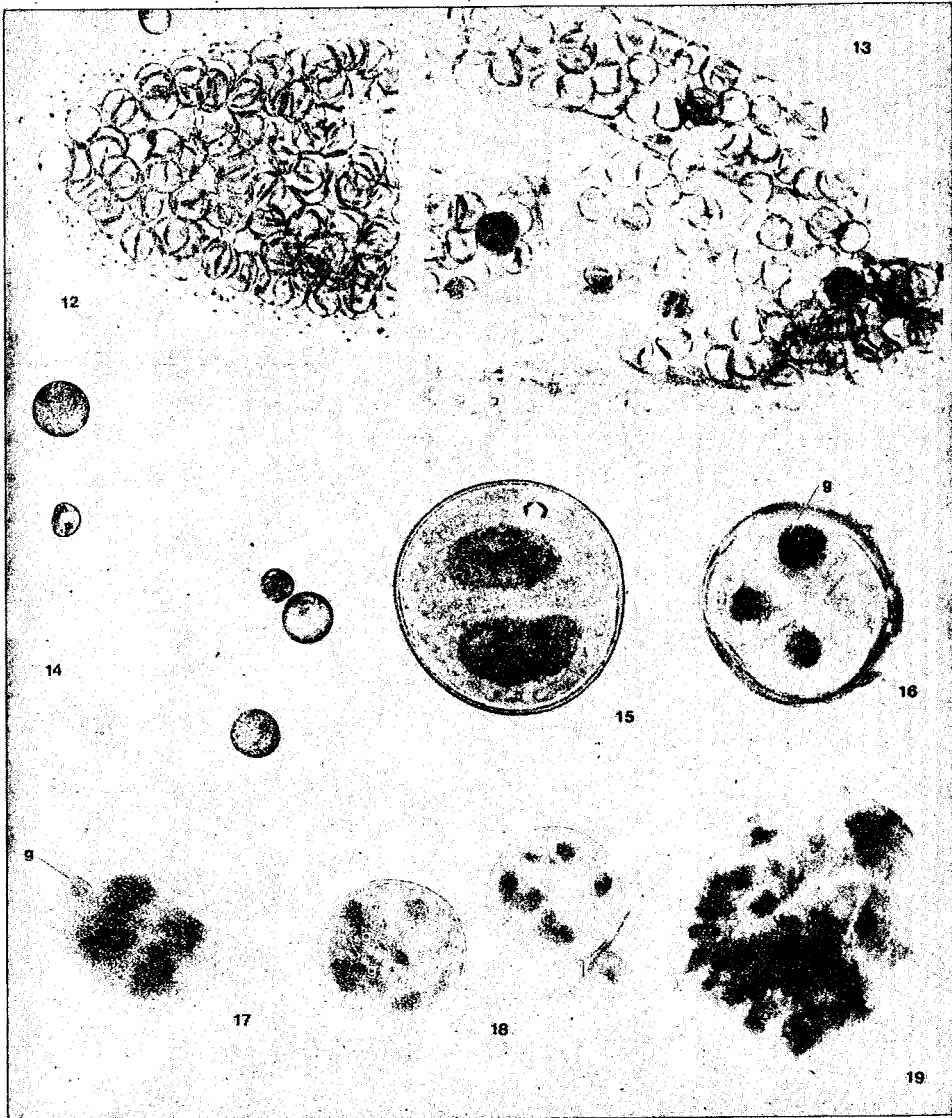


Plate II (Figs 13-19)

- Fig. 12: ($\times 440$) Non-inductive anther after three weeks' culture on Nitsch & Nitsch's medium supplemented with 1.0 mg l^{-1} 2,4-D and 0.3 mg l^{-1} kinetin;
- Fig. 13: ($\times 440$) Inductive anther containing m.c.p.'s after four weeks' culture on same medium;
- Fig. 14: ($\times 440$) Pollen dimorphism at pollen shed;
- Fig. 15: ($\times 2260$) Bicellular pollen, nuclei non-haploid;
- Fig. 16: ($\times 2260$) Five-celled pollen comprising 3 haploid (1 with *g*), 1 diploid, and 1 anucleate cell;
- Fig. 17-18: ($\times 1650$) M.c.p.'s with one or more *g*'s;
- Fig. 19: ($\times 2200$) Pro-callus unit, *g* not conspicuous.

Analysis of wheat mutants for straw and leaf characteristics

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In recent years very useful models of production processes have been developed by DEWITT (1965) and DUNCAN *et al* (1967), using straw and leaf characteristics as architectural elements influencing grain yield. The recognition of genetic variation in any character which is involved in the synthesis of yield leads to the possibility of crop improvement and in this context all stages of plant growth and development are of importance (BELL and KIRBY, 1966). Enhanced characters may be transferred from the donor parent to a gene pool from which improved genotypes may be developed. This assembling of attributes into a genotype follows the concept of ideotypes (DONALD, 1968), although the success of such improvement programme depends on the expression of the enhanced characters in the new genetic background and against the interaction of environmental factors.

In present studies data on straw and leaf characteristics of wheat mutants were analysed and correlated with grain yield. While operating a breeding methodology, it seems obvious that selection is likely to change two or more characters simultaneously and a plant breeder must therefore exert different magnitude of pressures on various attributes.

Material and Methods

Four high yielding mutants (No's 27, 31, 35 and 44) derived from Nayab (Mexican origin) were investigated along with control during Rabi 1978-79. Morphological traits of agronomic significance were studied with reference to straw architecture and leaf characteristics that contributes toward yield. The first three spikes (ontogenetically) of each M_6 mutants were used to raise M_{10} generation. Sowing of homogeneous seeds of mutants and cultivar was done by dibbling single seed per hole at 30.5 cm intervals in single row each 3.1 m long with 30.5 cm interrow distance with path ways 1.0 m wide between blocks of a plot in randomized block design with four replications accomodating 31 plants in each replication on fertile soil type at the Botanical Garden, Sind Agricultural University, Tando Jam, Pakistan.

Data on 10 randomly selected M_{10} plants in each replication were recorded for ten metrical traits Viz., plant height, first internode length, second internode length, third internode length, harvest index, first flag leaf length, first flag leaf width, second flag leaf length, second flag leaf width and first flag leaf L/B ratio. Thus 40 plants were studied from each mutant genotype. The data was analysed statistically and the mean values were

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Table 1. Analysis of variance for straw and leaf characteristics of

Source of variation	D. D.F.	Plant height		First internode length		Second internode length	
		M.S.	F-value	M.S.	F-value	M.S.	F-value
Replications	3	40.85		2.89		3.14	
Genotypes	4	108.34	9.52**	78.32	24.32**	19.26	9.16**
Error	12	11.37		3.22		2.10	
Total	19						
S.E for genotype mean		1.871		.915		4.212	
C.V. %		2.13		3.10		4.21	

** Denote significant at

used to calculate coefficient of correlation. Harvest index was calculated after DONALD (1962). HI expressed in percentage, gives the ratio of the economic yield (grain yield) and the biological yield (total dry matter) as follows:

$$\text{Harvest Index (HI)} = \frac{\text{Economic Yield}}{\text{Biological Yield}} \times 100$$

Results and Discussion

Among the plant characters associated with lodging and nitrogen responsiveness, plant height is predominant factor affecting lodging resistance (SCARASCIA-MUGNOZZA, 1970) and characters such as straw architecture exert an influence on polygenic traits like grain yield and protein quality (LARIK, 1978; SIDDIQUI & DOLL, 1972, 1979). It is therefore necessary to take into consideration all the related plant attributes in any meaningful genetic evaluation of wheat mutants. Studies are therefore conducted of the straw architecture and leaf characteristics. Analysis of variance for straw characters indicate that mutant genotypes differed significantly ($P \geq 0.01$) from common parental variety Nayab. Mean values of the characters associated with straw architecture are given in Table 2. Mutants 27 and 44 displayed reduction in plant height at 1% level of significance. The first internode of mutants 27, 31 and 35 reduced significantly ($p \geq 0.01$) whereas, second and third internode length of all mutant strains increased significantly ($p \geq 0.01$) as a consequence of gamma irradiation.

Semi-dwarf mutant genotypes has spectacularly increased the yielding ability of wheat due to increased resistance to lodging. In relation to photosynthesis - respiration balance, shorter culms may minimize respiration loss by the culm, thereby improving net grains. All the mutants produced highest yield (economic as well as biological yield) and high harvest index in comparison to the mother variety. This appears to be an additive effect of positive genes which has increased the grain yield in all the mutant genotypes. This also confirms the significant role of gamma radiation in improving grain yield of mutants.

Using straw as architectural element, the plant height and other related characters of

different mutants of hexaploid wheat in M_{10} generation (1978-79)

Third internode length		First Flag leaf length		First Flag leaf width		Second Flag leaf length		Second Flag leaf width	
M.S.	F-value	M.S.	F-value	M.S.	F-value	M.S.	F-value	M.S.	F-value
3.94	13.74**	2.35	25.71**	.073	5.27**	10.03	11.53**	.012	4.46**
25.18		80.93		.099		40.24		.025	
1.83		3.12		.018		3.48		.005	
.891		.732		.066		.958		.045	
4.95		4.52		5.75		3.96		3.50	

1% level of probability.

Table 2. Estimates of mean values for straw and leaf characteristics of different mutants of hexaploid wheat in M_{10} generation (1978-79)

Genotypes	Plant height (cm)	First internode length (cm)	Second internode length (cm)	Third internode length (cm)	Harvest index (Kg/plot)	First flag leaf length (cm)	First flag leaf width (cm)	Second flag leaf length (cm)	Second flag leaf width (cm)	First flag leaf L/B ratio
Nayab (Control)	85.24	42.18	17.10	8.30	28.67	23.95	1.42	31.70	1.25	16.86
Mutant-27	76.12	37.10	20.78	13.50	31.58	24.50	1.38	31.78	1.29	17.75
Mutant-31	83.00	39.00	20.50	13.00	29.89	26.10	1.30	31.82	1.26	20.07
Mutant-35	84.00	38.80	21.35	13.18	32.85	23.45	1.33	30.00	1.31	17.63
Mutant-44	80.11	40.10	19.20	11.00	33.00	24.00	1.40	32.00	1.27	17.14
Significance										
LSD (.05) = 3.21		2.40	2.24	1.75	—	3.13	0.23	3.43	0.23	—
(.01) = 5.10		3.25	2.95	2.37	—	3.23	0.29	4.61	0.35	—

mutants were correlated with grain yield. Results in Table 3 reveal that in all mutants plant height expressed strong positive correlation ($p \geq 0.01$) with grain yield and other straw characters. First and second internode displayed significant negative association with grain yield whereas, third internode showed weaker association ($p \geq 0.05$) with grain yield. Similar conclusions were drawn earlier by LARIK (1978, 1979) in wheat and reported the selection and improvement of high yielding wheat mutants on the basis of straw characters.

Leaf Characters.

The present investigation was confined to the morphological study of leaf characters of the mutants derived from Nayab cultivar. The results of analysis of variance (Table 1), showed highly significant ($p \geq 0.01$) differences amongst various genotypes which suggest that genotypes varied significantly for leaf characters. Mean values of the leaf characters are presented in Table 2. Data reveal that in all the mutants leaf characters did show slight

improvement in the leaf length and breadth but not to the level of significance. Leaf length/breadth ratio, which affect Carbon-Nitrogen ratio and ultimately the productivity in present studies also displayed some improvement in the mutant strains. These results are in good agreement with the results obtained by LARIK (1977) in mutants of wheat.

Table 3. Phenotypic correlation coefficients among all possible combinations of the five different traits

Characters correlated	Plant height (1)	First internode length (2)	Second internode length (3)	Third internode length (4)	Grain yield (5)
Plant height	1.000	.6810**	.8320**	.8132**	.7981**
First internode length		1.000	.2987*	.1652	-.0238
Second internode length			1.000	.9038**	-.5201**
Third internode length				1.000	.2996*
Grain Yield					1.000

*,** Denote significant at $P \geq .05$ and $P \geq .01$ respectively.

Leaf characters of the mutants were correlated with grain yield. Results in Table 4 reveal that first flag leaf length displayed significant negative correlation (-.2913) with grain yield whereas it showed strong positive association ($P \geq 0.01$) with next flag leaf length and weaker association with next flag leaf width. First flag leaf width also revealed highly significant ($P \geq 0.01$) association with next flag leaf length and next flag leaf width. SIDDIQUI (1978) and TANNER *et al.* (1966) also obtained similar results. They reported the selection of high yielding mutants on the basis of leaf characters.

Leaf characters are important parameters in determining dry matter production of a plant community and affect biochemical activities such as nitrate assimilation and synthesis of nucleic acid and protein (LOOMIS and WILLIAM, 1972). Leaf area was found to be the trait that could account for higher yielding ability of mutant strains. By developing a larger leaf blade area and delaying senescence, the cultivar had the potential to produce more photosynthate than control. Leaf blade area before anthesis could affect grain yield indirectly (THORNE, 1966) through influences the number and potential size of the sites (seeds) at which the photosynthate could accumulate. Leaf blade area of mutant strains in present

Table 4. Phenotypic correlation coefficients among all possible combinations of the five different traits

Characters correlated	First flag leaf length (1)	First flag leaf width (2)	Next flag leaf length (3)	Next flag leaf width (4)	Grain yield (5)
First flag leaf length	1.000	.3014*	.5809**	.0811	-.2913*
First flag leaf width		1.000	.5312**	.7934**	.1105
Next flag leaf length			1.000	.3716*	.1209
Next flag leaf width				1.000	.1931
Grain Yield					1.000

*,** Denote significant at $P \geq .05$ and $P \geq .01$ respectively.

study was reasonably larger than those of the control before anthesis to have given the mutant strains an advantage in the size of spike (No. of spikelets/spike) and ultimately contributed towards higher harvest index.

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Study of allied species of *Triticum* against Indian cultures of leaf rust races.

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Variability in genes for resistance is essential for the success of breeding resistant cultivars. The variation and parallel evolution in the wheat rust pathogen, in particular, demand continued effort in search of new resistances and in this direction study of allied species for their effectiveness against the local virulences in the country offer rich dividends. The use of rust resistance from allied species of *Triticum* goes back to 1930, when McFadden developed Hope and H44 from the cross Yaroslov Emmer (*T. turgidum dicoccum* group) × Marquis. These varieties were responsible for the largest rust free situation (1938-49) in the United States. SHANDS (1941) could transfer successfully the stem rust, leaf rust and powdery mildew and other disease resistant properties of *T. timopheevi* to common wheat. A number of *T. timopheevi* lines and a few *T. aestivum* lines having derived their resistance from *T. timopheevi* were studied for their resistance to Indian cultures of stem rust races (SAWHNEY and GOEL, 1980). In this communication, we report the resistance of a number of *Triticum* species of tetraploid group against Indian cultures of leaf rust (*Puccinia recondita* f. sp. *tritici*) races.

Seven species of *Triticum* viz., *T. compactum* var. *fitosodi*, *T. dicoccum* var. *rufum*, *T. carthlicum* var. *faligirresum*, *T. polonicum* var. *gorskyis*, *T. turgidum* var. *lusitanicum*, *T. timopheevi* var. *typicum* and *T. timopheevi* var. *viticulosum*, maintained at the Indian Agricultural Research Institute, were tested against the Indian cultures of leaf rust races viz., 10, 11, 12, 17, 20, 63, 77, 77A, 104, 107, 108, 162 and 162A at the seedling stage in the green house at a temperature ranging 8°C-22°C. The results are presented in Table 1. The important conclusions drawn were:

(1) *T. timopheevi* var. *typicum* and *T. timopheevi* var. *viticulosum* were found resistant to all the cultures of Indian leaf rust races used. Complete effectiveness of both the varieties of *T. timopheevi* against all the races, however, provides no information on the relationship of resistance in the two lines.

(2) Variation for resistance in the three species, *T. compactum* var. *fitosodi*, *T. dicoccum* var. *rufum* and *T. carthlicum* var. *faligirresum* to different race or group of races suggests that the leaf rust resistance in these three sources is different.

(3) *T. polonicum* var. *gorskyis* and *T. turgidum* var. *lusitanicum* were observed completely ineffective against the races tested and thus have no value for breeding resistance to leaf rust.

Table 1. Seedling tests of allied species of *Triticum* against Indian cultures of leaf rust (*P. recondita*) races.

Species	Races												
	10	11	12	17	20	63	77	77A	104	107	108	162	162A
<i>Triticum compactum</i> var. <i>fitosodi</i>	+	+	+	+	-	+	+	+	+	+	+	+	+
<i>Triticum dicoccum</i> var. <i>vifum</i>	+	-	+	+	+	-	+	+	+	+	+	+	+
<i>Triticum carthlicum</i> var. <i>faligerresum</i>	+	+	+	+	-	-	+	+	+	+	+	-	-
<i>Triticum polonicum</i> var. <i>gorskyis</i>	+	+	+	+	+	+	+	+	+	+	+	+	+
<i>Triticum turgidum</i> var. <i>lusitanicum</i>	+	+	+	+	+	+	+	+	+	+	+	+	+
<i>Triticum timopheevi</i> var. <i>typicum</i>	-	-	-	-	-	-	-	-	-	-	-	-	-
<i>Triticum timopheevi</i> var. <i>viticulosum</i>	-	-	-	-	-	-	-	-	-	-	-	-	-

+ = Compatible (susceptible) - = Incompatible (resistance)

High degree of resistance in *T. timopheevi* lines to stem rust (SAWNEY and GOEL, 1980) and to leaf rust reported in the present study suggests that *T. timopheevi* lines could be an excellent source for imparting high degree of resistance against Indian races of stem and leaf rust pathogen. Resistance from other allied species at (2) above could be useful as diverse source of resistance against the race or group of races to which these were found effective.

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Performance of certain mutants of common wheat for yield and nutritional quality under salinity

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The magnitude of the severity of salinity problems and the consequent losses to the field crops in the areas where the use of underground saline water for irrigation is a common practice has long been established (BERNSTEIN and HAYWARD, 1958; JADAV *et al.* 1976; GIRIRAJ *et al.* 1977; KUMAR 1978). The use of salt tolerant genotypes in such condition is known to show edge over other procedures management practices, reclamation of soils etc. This implies the immediate need for the salt tolerance evaluation of agronomically superior genotypes. Present study is aimed to supplement the informations regarding the performance of certain improved mutants (from common wheat varieties HD 1553 and HD 2009) at the application of synthetic saline waters for irrigation.

Material and Methods

A field study on seven stable mutants (M_4) alongwith parental wheat varieties was carried out in micro-plots (2.50×1.00 m) at this college experimental sites during 1977-78. A split-plot design with three repeats was used. Salinity levels (control; 6, 12×16 mmhos/cm) were assigned to main plots, whereas the genotypes to 2.50 m long rows of each main plot. Twenty plants at a distance of 5 cm apart were maintained in each row. Saline waters were synthesized keeping in view the cations (Na:Mg:Ca) and anions (Cl:SO₄:HCO₃) in ratio 60:25:15; 2:1:1, respectively. Data were recorded for grain yield/plant. Analysis of grains for protein, P, K, Ca, Mg and Na was done following the usual laboratory procedures.

Results and Discussion

The saline water of 6 mmhos/cm onwards gave significant adverse effects of salinity on grain yield; and a reduction by 32.89% was noticed at the abrupt salinity (16 mmhos/cm) over control (Table 1). Earlier reports (TORES and BINGHAM 1973; JADAV *et al.* 1976; KUMAR 1978) also indicate detrimental effects of salinity on grain yield of wheat. Osmotic inhibition of water uptake and the greater influx of salts into the plants are known to show such adverse effects. Mean values on mineral nutrients showed varied impacts of salinity. For instance, protein and Na contents increased, whereas that of P, K and Ca contents decreased with the salinity. No definite response was, however, noticed for Mg. Results reported by UPRETY (1970) on protein; NOURI *et al.* (1970) and SINGH *et al.* (1974) on K; and MEHROTRA and DAS (1973) on Ca are similar to our results. Suppression effects of Na

on absorption has been reported responsible for decreased contents of K and Ca by these workers.

None of the mutants induced from HD 1553 yielded significantly higher to it (Table 2). Grain yield, however ranged from 5.72 gm (Bhp 11) to 8.07 gm (Bhp 29) as against 6.80 gm for the control. The mutant Bhp 29 though yielded higher to control and was equally

Table 1. Effect of different levels of water salinity on grain yield and mineral nutrients.

Salinity (mmhos/cm)	Grain yield/plant (gm)	Total protein (%)	P (%)	K (%)	Ca (%)	Mg (%)	Na (%)
2.1 (control)	8.39	9.59	0.30	0.19	0.18	0.13	0.01
6	8.02	9.78	0.28	0.19	0.16	0.12	0.01
12	6.56	10.64	0.27	0.11	0.13	0.13	0.02
16	5.63	12.03	0.26	0.10	0.12	0.13	0.02
C.D. (5%)	0.73	—	—	—	—	—	—

Table 2. Effects of saline irrigation waters on grain yield

Genotypes	Mean yield across salinity levels	Per cent decreased over control salinity	Per cent reduction at 16 mmhos/cm over control salinity	Regression of yield on salinity
HD 1553 (cont.)	6.87	8.40	34.00	$y = -0.187x + 8.287$
Bhp 11	5.72	25.71	61.03	$y = -0.356x + 8.931$
Bhp 12	6.20	13.88	27.77	$y = -0.121x + 7.291$
Bhp 14	5.85	18.75	37.50	$y = -0.291x + 6.693$
Bhp 29	8.07	12.28	34.78	$y = -0.218x + 10.036$
HD 2009 (cont.)	7.62	8.74	20.95	$y = -0.142x + 8.901$
Bhp 18	9.11*	22.45	40.42	$y = -0.351x + 12.267$
Bhp 19	6.42	8.00	25.00	$y = -0.134x + 7.629$
Bhp 22	9.03	14.81	20.00	$y = -0.271x + 11.474$
C.D. 5%	1.60	—	—	—

good to it in respect to yield reduction at abrupt salinity over control. It however showed higher yield reduction to control salinity and the magnitude of regression slope was also higher to HD 1553, hence the mutant can't be regarded salt tolerant. On the contrary, the mutant Bhp 12 with rather poor yield return exhibited lower yield reduction at the abrupt salinity and the regression slope was also of lower magnitude, hence this mutant could be regarded better tolerant to HD 1553. Reports of SAINI *et al.* (1975) and GILL and DATT (1976) are similar that salt tolerant genotypes show low degree of regression slope for grain yield/germination of seeds and salinity. The mutant Bhp 18 (from HD 2009) yielded significantly higher to control, was not considered salt tolerant owing to higher yield breakdown at abrupt salinity and regression slope also indicated higher rate of yield decline. The mutant Byp 19 on the other hand, with lower degree of regression slope was considered better salt tolerant to HD 2009.

The mutants also exhibited varied and wide impacts of saline water on mineral

Table 3. Effect of saline irrigation waters on grain mineral nutrients

Genotype	Total protein (%)	P (%)	K (%)	Ca (%)	Mg (%)	Na (%)
HD 1553 (control)	9.27	0.25	0.13	0.18	0.12	0.01
Bhp 11	11.55	0.30	0.15	0.16	0.13	0.02
Bhp 12	10.40	0.29	0.15	0.15	0.14	0.02
Bhp 14	11.38	0.33	0.16	0.14	0.20	0.02
Bhp 29	10.87	0.31	0.22	0.15	0.19	0.02
HD 2009 (control)	9.99	0.27	0.14	0.16	0.16	0.01
Bhp 18	10.21	0.25	0.16	0.15	0.11	0.02
Bhp 19	10.41	0.25	0.17	0.12	0.14	0.01
Bhp 22	10.55	0.30	0.19	0.20	0.12	0.02

contents of grains (Table 3). It is worth mentioning that all the mutants showed higher protein content to respective control varieties. However, Na content was comparatively less affected. Interestingly, the salt tolerant mutant Bhp 12 was improved to HD 1553 in mineral contents i.e. protein, P, K and Ca. It was however, inferior in Mg content. In contrast, other salt tolerant mutant Bhp 19 was improved to HD 2009 with regard to protein and K contents only. The salt tolerance nature of these two mutants seems to be different. For instance, Bhp 12 looks to be Na-tolerant as it showed higher Na content. On the other hand, mutant Bhp 19 may be considered Na excluder as it showed lower Na content.

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Agronomic performance of randomly derived alloplasmic wheats¹

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Utilizing alien cytoplasm has been suggested as a method to increase the genetic variability of wheat (*Triticum aestivum* L.) (1, 2). However, little work has been done to determine if lines can be extracted from segregating populations in an alien cytoplasm which equal or exceed the performance of lines extracted from segregating populations in normal wheat cytoplasm. BUSCH and MAAN (2) reported that some of the progeny of alloplasmic 'Chris' in *Aegilops squarrosa* L. cytoplasm exceeded the yield of euplasmic Chris, while none of the progeny of alloplasmic Chris in *Ae. cylindrica* Host., *Ae. ventricosa* Tausch, or *Ae. juvenalis* (Thell) Eig cytoplasm equalled the check. Their study was with nonsegregating genotypes and the expression of heterosis of segregating nuclear genes was not evaluated. The objectives of this study were to compare the agronomic performance of randomly derived lines from crosses involving euplasmic and alloplasmic parents and to determine if superior individuals could be obtained in an alien cytoplasm.

Materials and Methods

Two hard red spring wheat cultivars, 'Chris' and 'Selkirk', were used as male recurrent parents to substitute their nuclear genomes into the cytoplasm of *Ae. squarrosa* and *Ae. bicornis* (Forsk.) Jaub. & Spach. The alloplasmic lines thus produced were reciprocally crossed to Chris and Selkirk. The F₁ was selfed and 20 F₂ plants were randomly selected from each set of crosses. In addition, 20 plants were randomly selected from each of the euplasmic and alloplasmic parents. Each individual progeny was advanced as a bulk to the F₃. The pedigree, cytoplasm source, and number of F₂-derived F₃ lines from each parent and cross are given in Table 1. The lines were tested in an incomplete block arrangement of a randomized complete block design with two replications at Fargo, ND in 1979. Each incomplete block consisted of all lines from any individual family. Each line was evaluated in two 2.4 m rows with 0.3 m between the rows. The traits measured on each line were: days to head, days from planting until 50% of the spikes had emerged from the flag leaf sheath; plant height, height from the ground to the tip of the spike in cm; grain yield, weight of the grain harvested from each plot converted to kg/ha; and test weight, weight of a given volume of grain expressed as kg/hl.

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Table 1. Pedigree, cytoplasm source, and number of randomly derived F₃ progeny from each family grown at Fargo, ND, in 1979.

Family no.	Pedigree	Cytoplasm source†	No. of F ₃ lines tested
1	Chris (euplasmic control)	aes	19
2	<i>Ae. bicornis</i> /8* Chris	bic	18
3	<i>Ae. squarrosa</i> /4* Chris	squ	20
4	Chris// <i>Ae. bicornis</i> /8* Chris	aes	20
5	Chris// <i>Ae. squarrosa</i> /4* Chris	aes	19
6	Selkirk (euplasmic control)	aes	19
7	<i>Ae. bicornis</i> /8* Selkirk	bic	19
8	<i>Ae. squarrosa</i> /12* Selkirk	squ	20
9	Selkirk// <i>Ae. bicornis</i> /8* Selkirk	aes	19
10	Selkirk// <i>Ae. squarrosa</i> /12* Selkirk	aes	20
11	Chris/Selkirk (euplasmic control)	aes	20
12	Chris// <i>Ae. bicornis</i> /8* Selkirk	aes	20
13	Chris// <i>Ae. squarrosa</i> /12* Selkirk	aes	20
14	<i>Ae. bicornis</i> /8* Chris//Selkirk	bic	18
15	<i>Ae. squarrosa</i> /4* Chris//Selkirk	squ	20
16	Selkirk/Chris (euplasmic control)	aes	20
17	Selkirk// <i>Ae. bicornis</i> /8* Chris	aes	20
18	Selkirk// <i>Ae. squarrosa</i> /4* Chris	aes	20
19	<i>Ae. bicornis</i> /8* Selkirk//Chris	bic	12
20	<i>Ae. squarrosa</i> /12* Selkirk//Chris	squ	20

† aes=*T. aestivum*, bic=*Ae. bicornis*, and squ=*Ae. squarrosa*.

Results and Discussion

All of the traits studied in the parents were affected by the *Ae. bicornis* cytoplasm (Table 2). The *Ae. bicornis* cytoplasm caused a significant delay in days to head with a significant decrease in plant height, grain yield, and test weight in both alloplasmic Chris (family 1 vs family 2) and Selkirk (family 6 vs family 7). The only significant effect of the *Ae. squarrosa* cytoplasm was a decrease in test weight of alloplasmic Chris (family 1 vs family 3). When the alloplasmic lines were crossed as male to the euplasmic lines, the mean performance of the progeny indicated that the deleterious effects of the alien cytoplasm were not transmitted to the progeny (family 2 vs family 4, and family 7 vs family 9). Thus, the deleterious effects observed in the alloplasmic lines with the *Ae. bicornis* cytoplasm were caused by the *Ae. bicornis* cytoplasm. The yield level of the euplasmic lines derived from crosses of euplasmic controls by alloplasmic parents equalled the euplasmic controls, (families 4 and 5 vs 1, and families 9 and 10 vs 6) and in the case of crosses involving alloplasmic Chris, the derived euplasmic progeny exceeded the control, although not significantly.

The performance of randomly selected progeny from the segregating populations was similar to that of the parents (Table 3). The reciprocal control crosses, Chris/Selkirk and Selkirk/Chris, gave similar responses. The performance of progeny in the *Ae. bicornis* cytoplasm was significantly lower than the controls for plant height, grain yield, and test weight, (family 14 vs family 11, and family 19 vs family 16). The performance of progeny in the *Ae. squarrosa* cytoplasm was also lower for grain yield and test weight, but was higher

Table 2. Mean of traits studied in randomly derived progeny from euplasmic and alloplasmic parents grown at Fargo, ND, in 1979.

Family no.	Trait			
	Days to head	Plant height (cm)	Grain yield (kg/ha)	Test weight (kg/hl)
1	55.1	101.8	2180	72.2
2	56.7	91.8	1875	68.9
3	54.6	105.9	1935	69.1
4	55.0	106.1	2305	72.0
5	52.8	100.3	2200	70.6
6	56.6	98.3	2405	70.2
7	58.4	92.9	2020	68.3
8	57.4	101.4	2305	69.7
9	56.6	99.9	2200	69.7
10	56.6	100.5	2395	69.8
LSD 0.05	1.0	5.0	240	0.8

Table 3. Mean and range of traits studied in randomly F_2 -derived F_3 progeny from crosses of euplasmic and alloplasmic parents grown at Fargo, ND, in 1979.

Family No.	Trait							
	Days to head		Plant height (cm)		Grain yield (kg/ha)		Test weight (kg/hl)	
	\bar{X}	Range	\bar{X}	Range	\bar{X}	Range	\bar{X}	Range
11	55.6	50.0-62.0	99.7	90.0-107.5	2025	1610-2590	68.4	64.5-71.6
12	54.8	52.0-62.0	100.6	92.5-107.5	2005	1415-2435	69.7	64.5-73.5
13	56.1	50.0-61.5	99.1	94.0-106.0	2165	1475-2850	69.2	60.6-72.2
14	55.9	51.0-62.0	90.5	84.0-95.0	1780	1230-2255	66.8	60.3-71.6
15	58.5	54.0-61.5	103.2	94.5-114.0	1960	1520-2460	68.0	64.5-70.9
16	54.2	50.0-62.0	98.7	87.5-107.0	1995	1450-2420	69.1	62.6-72.2
17	55.0	50.0-59.5	100.0	86.5-110.5	1945	1490-2435	69.3	66.7-72.5
18	56.9	50.5-61.0	96.1	89.0-102.5	2050	1370-2610	69.6	65.5-71.6
19	56.5	49.5-62.0	88.7	78.5-101.5	1635	1220-2125	66.4	63.2-69.6
20	54.7	51.0-61.0	101.5	94.0-110.5	1875	1410-2350	68.2	65.5-72.5
LSD 0.05	1.0		5.0		240		0.8	

for plant height, although none of these differences were significant from the respective control progeny (family 15 vs family 11, and family 20 vs 16). The progeny of crosses involving euplasmic parents of one cultivar with alloplasmic parents in either *Ae. bicornis* or *Ae. squarrosa* cytoplasm of the other cultivar produced results similar to euplasmic parents formed by crossing euplasmic control with alloplasmic parents of the same cultivar. The male parent in *Ae. bicornis* cytoplasm, increased plant height and test weight beyond the respective control progeny with grain yield being equal, (family 12 vs family 11, and family 17 vs family 16). The male parent in *Ae. squarrosa* cytoplasm gave higher grain yield and test weight with shorter plants (family 13 vs family 11, and family 18 vs family 16).

The range in individual progeny performance was essentially the same among all crosses

for days to head and test weight. However, genes for plant height were cytoplasm sensitive. The *Ae. bicornis* cytoplasm gave the shortest individual line while the *Ae. squarrosa* cytoplasm gave the tallest individual line. The response of grain yield to the two alien cytoplasmic backgrounds was similar. The highest yielding individual line in each cytoplasm did not exceed the highest yielding individual line in the respective controls. However, the grain yield of progeny from crosses of euplasmic parents of one cultivar as female with alloplasmic parents of the other cultivar as male responded in a positive manner. In this type of cross, grain yield was enhanced over the reciprocal cross and, in fact, the highest yielding individual lines were in crosses in which the alloplasmic *Ae. squarrosa* line was used as the male. These individual lines showed 8 to 10% heterosis over the highest yielding individual in the respective control crosses. The alloplasmic parents may have differential transmission of male gametes with a more desirable genetic constitution when returned to the normal cytoplasm. This possibility is consistent with certain alloplasmic pentaploid wheat hybrids having a strong influence on the preferential transmission of male gametes with specific chromosomal constitution which was not observed in euplasmic control pentaploid wheat hybrids (3).

Conclusion

The relationship between the performance of alloplasmic lines and segregating populations having the same cytoplasm appears to be stable and predictive. The mean yield of alloplasmic lines in the *Ae. bicornis* cytoplasm was 86 and 84% of the euplasmic Chris and Selkirk controls, respectively. The mean yield of crossed progeny in the *Ae. bicornis* cytoplasm was 88 and 82% of the respective controls while the yield of the best individual line in the crossed progeny in *Ae. bicornis* cytoplasm was 87 and 88% of the best individual in the corresponding euplasmic control cross. Similar responses were noted with the *Ae. squarrosa* cytoplasm. Thus, knowing the performance of an alloplasmic line in comparison to the respective euplasmic control should give a reliable estimate of the performance of the alien cytoplasm in crosses. However, when the alloplasmic line is used as a male parent in crosses, performance of the progeny may be improved beyond the performance of the euplasmic control.

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II. Gene Symbols

Catalogue of gene symbols for wheat, 1980 supplement

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Reprints of the original Catalogue (1973) and some of the Annual Supplements are available. A consolidation of the first five Annual Supplements will appear in the Proceedings of the Fifth International Wheat Genetics Symposium Volume 2. Supplementary lists appear annually in Cereal Research Communications, Wheat Information Service and Wheat Newsletter.

Height

Reduced height

- rht4* v: Burt *ert937 rht6* (127AAA).
rht5 v: Marfed *ert1* (127AAA).
rht6 v: Brevor (99D), Burt (99D), Norin 10-Brevor 14 *Rht1 Rht2* (99D).

Proteins

8. Nitrate Reductase Activity

- Nra* (73G) v: UC44-111 (73G)
nra (73G) v: Anza. (73G)

Pathogenic Disease Reaction

Reaction to *Erysiphe graminis*

- Pm9* 66AA v: Normandie *Pm1 Pm2* (66AA) 7A (66AA)

Reaction to *Puccinia graminis*

- Sr33* *SrSQ* (111B) v: RL5405=Tetra Canthatch/ 1DL (111B)
Aegilops squarrosa,
R.L. 5288 (111B)
Sr34 163 v: Compair; CS2A/2M 4/2; 2D
CS2D/2M 3/8; CS2M(2A) -
alien substitution line.

Reaction to *Puccinia recondita*

<i>Lr22b</i>	58A	s: CS (Hope 3B); CS (Ciano 3B);	3B
<i>Lr27</i> (163)	<i>LrGi</i>	CS (Ciano 5B).	
		v: Gatcher; Timgalen <i>Lr3*</i> <i>Lr10</i> .	
		* heterogeneous.	
<i>Lr28</i>	163	s: CS2A/2M 4/2; CS2D/2M 3/8	4B
<i>Lr29</i>	163	s: CS7D/7Ag #11	7DS

Reaction to *Tilletia* spp.

<i>Bt9</i>	177A	Reference 177A replaces 175	
		P.I. 167822 (177A); P.I. 166910 (177A)	
		P.I. 166921 (177A).	

Reaction to *Mayetiola destructor*

<i>H7*</i>	74A	v: Seneca (74A)	
<i>H8*</i>	74A	v: Seneca (74A)	
		* duplicate partially dominant factors.	

Genetic Linkages

1DL	<i>Sr33</i> - centromere	Independent	111B
	<i>Sr33</i> - <i>Lr21</i>	21.4±2.7%	111B
	<i>Sr33</i> - <i>Rg2</i>	35.0±5.2%	111B
2Dα	<i>Lr22b</i> - <i>W2^I</i>	10.6±2.9%	58A
	<i>Lr22b</i> - <i>Tg</i>	11.6±3.1%	58A
	<i>Tg</i> - <i>W2^I</i>	21.9±4.2%	58A
7AL	<i>Pm1</i> - <i>Pm9</i>	Linked	66AA

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III. Editorial Remarks

Announcement for Future Issues

WIS No. 52 will be planned for publication in March, 1981. Manuscripts for this issue are most welcome and accepted any time, not later than February 28, 1981.

WIS is open to all contributions regarding methods, materials and stocks, ideas and research results related to genetics, breeding and cytology of *Triticum*, *Aegilops*, *Secale*, *Haynaldia* and related genera. Manuscripts should be typewritten (double-space) in English, and submitted with duplicates. One article should not exceed five printed pages, including one textfigure (smaller than 7×7 cm²). Lists of stocks are exempted from this page limit. Authors receive 50 reprints of their contributions free of charge. Extra copies are printed by order at cost price. Communications regarding editorial matters should be addressed to:

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Membership Fee

Yearly Membership Fee has been raised up to ¥2,000 for foreign as well as Japanese members from the fiscal year beginning April 1980. The money should be paid by the Foreign Postal Money Order, otherwise considerable loss is caused due to the bank charges. Back numbers are available.

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Explanation of the Figure on the Cover

Cf. text figure in page 16 of an article by TAN and HALLORAN

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