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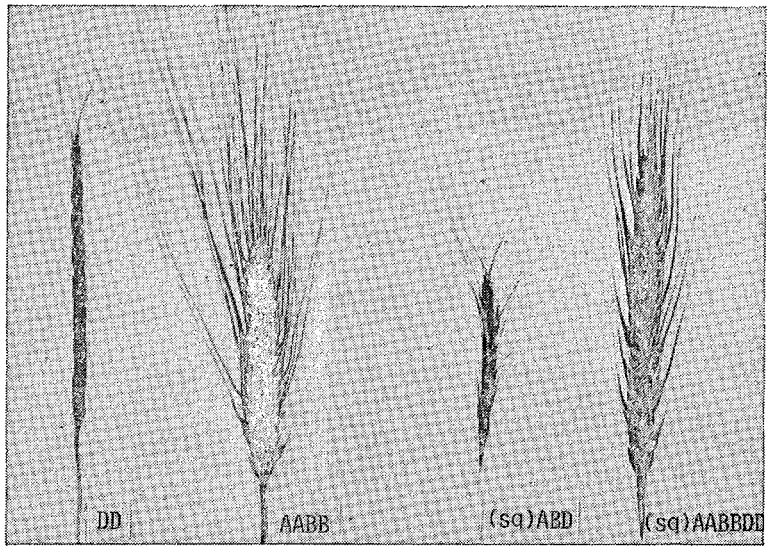

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I. Research Notes

Studies on multilines in Wheat (*Triticum aestivum L.*). 10. Genetic analysis of inter-genotypic interactions amongst components of Kalyansona multilines for agronomic characters

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In the breeding programme for the development of the component lines for multilines a breeder could follow one of the two approaches. First, a strict backcrossing may be adopted. In this procedure the final lines may recover the genotype of the recurrent parent most faithfully and these may not even be tested for the yield etc. The only difference which would occur among these isolines would arise from the genes conditioning the resistance to disease(s) the breeder is working for. In the second procedure (BORLAUG 1958) a limited back-crossing or even multiple crossing may be followed. The main idea behind this is that transgressive segregation may occur upon which selection may operate. Unlike the back-crossing, the multiple-crossing scheme may leave enough residual variability in addition to the one ascribable to re-genes, which may be having important bearing on the behaviour of the component lines. When grown in a mixture, the performance may vary depending upon the nicking ability of the component lines.

There have been some studies earlier (HARPER 1964; JENSEN & FEDERER 1965; JAIN & MOSHA 1974 etc.) where efforts have been made to find-out the performance of lines grown in a mixture. But in these studies the lines were morphologically different and at the time of recording of the observation the components could be separated. However, in multilines the concern is more as to how the mixture as such behaves rather than what happens to each component as has been the case with the earlier studies. The present study was, therefore, planned to investigate the behaviour of some of the component lines of Kalyansona multilines when grown in a mixture. The result are presented in the present paper.

Materials and Methods

Ten lines were selected for establishing a mechanically mixture diallel from among a larger number of component lines developed for multilines in Kalyansona cultivar. The 45 mixtures (1:1 ratio on grain weight basis) together with ten parental lines were grown in a randomised block design with three replications at the Punjab Agricultural University, Ludhiana. The plot size of each entry was 0.72 m×2.5 m. The row to row distance was 23 cm. The seed rate was used as recommended for commercial plantings. All the cultural practices as recommended for Kalyansona in this area were adopted.

The data were recorded for days to 50 per cent flowering, plant height (cm), ear length (cm), number of tillers per meter row length, number of spikelets per spike, seed size (g) and grain yield (g) per plot. The statistical analysis was conducted as suggested by GRIFFING (1956) model 1, method 2.

Results and Discussion

Progeny means and analysis of variance

There were highly significant differences among progenies for days to 50 per cent flowering (Table 1). All the three components of this variation viz: pure cultures, mixtures and pure cultures vs mixture showed highly significant variation. The range of variability among pure cultivars was from 107 to 122 days whereas the mixture showed a range from 108 to 120 days. This indicated that the variation in mixtures as a group was less as compared to that in case of pure cultivars which is apparent from the proportion of mean squares also. The variation in flowering period is useful in the sense that multilines with varying maturity period could be developed to fit in various crop sequences. In the multiline breeding programme being pursued at the Punjab Agricultural University an effort has been made to develop multilines with different flowering period.

As in case of flowering period, for plant height also there were significant differences among pure cultures as well as among mixtures. The contrast between the two groups was also highly significant. The range of variability for pure cultures was from 90.1 cm

Table 1. Analysis of variance for different characters

Source	D.F.	Days to 50% flowering	Plant height	Ear length	No. of tillers per mtr	Seed size	Grain yield
Replications	2	2.65	1.15	5.31	839.75	5.00	1615900
Progenies	54	15.35	24.16**	0.70	502.55**	32.43**	106176.25
Parents	9	31.30**	40.57**	0.46	1010.70**	53.37**	212425.55*
Mixtures	44	12.12**	21.16**	0.71	410.03**	28.73**	85991.84
P vs M	1	13.69**	8.78**	2.34	0.02	6.70**	38047.00*
Error	108	4.08	8.93	0.39	3.08	1.52	133951.68
General combining	9	195.42**	26.15**	0.75**	489.23**	2.78**	174476.12**
Specific combining ability	45	2.04*	4.38	0.14	103.18**	1.56**	22803.74**
Gca/Sca	-	96.01	5.47	5.47	4.74	1.46	7.65

Table 2. Progeny means for different characters

Sr. No.	Pedigree	Days to 50% flowering	Plant height	Ear length	No. of tillers	Seed size	Grain yield
1	ML 246 P_1	112	97.1	9.9	97.3	29.1	526.7
2	ML 267 P_2	114	100.7	9.9	92.3	28.8	853.3
3	ML 270 P_3	111	100.3	10.9	113.3	35.5	1216.7
4	ML 293 P_4	115	101.5	10.5	113.7	27.1	920.0
5	ML 319 P_5	114	103.3	10.1	113.3	28.8	980.0
6	ML 323 P_6	122	95.9	10.3	85.7	31.3	973.3
7	ML 326 P_7	109	97.8	10.1	106.7	28.9	776.7
8	ML 328 P_8	117	90.1	10.3	147.0	24.8	500.0
9	ML 412 P_9	107	98.3	11.1	99.3	34.1	1206.7
10	ML 419 P_{10}	112	97.1	10.1	84.3	32.3	1243.3
11	P_1+P_2	113	100.6	10.7	97.0	28.9	810.0
12	P_1+P_3	111	97.8	9.9	106.0	33.5	863.3
13	P_1+P_4	113	100.3	11.2	96.0	25.8	623.3
14	P_1+P_5	112	101.7	10.6	125.0	29.3	770.0
15	P_1+P_6	118	95.2	10.5	97.3	30.2	936.7
16	P_1+P_7	110	101.3	10.1	122.6	30.6	736.7
17	P_1+P_8	114	97.7	10.0	95.6	28.9	720.0
18	P_1+P_9	109	97.3	11.1	87.3	31.7	1056.7
19	P_1+P_{10}	112	93.5	10.3	81.7	32.1	1083.3
20	P_2+P_3	112	102.4	10.5	95.0	34.2	943.3
21	P_2+P_4	113	101.5	10.9	101.7	26.7	863.4
22	P_2+P_5	114	98.4	9.9	109.0	29.6	833.3
23	P_2+P_6	119	97.5	10.6	114.3	30.8	1123.3
24	P_2+P_7	110	98.0	10.5	114.3	28.4	756.7
25	P_2+P_8	115	103.7	10.5	120.0	30.1	916.7
26	P_2+P_9	116	96.4	11.1	99.0	32.4	1110.0
27	P_2+P_{10}	112	98.2	10.1	94.0	31.3	1103.3
28	P_3+P_4	113	103.3	11.0	137.3	32.3	1003.3
29	P_3+P_5	114	99.3	10.3	107.3	34.0	1063.3
30	P_3+P_6	118	99.5	10.9	103.0	32.3	1250.0
31	P_3+P_7	108	98.2	10.1	105.7	30.7	886.7
32	P_3+P_8	115	93.8	10.1	105.7	32.6	806.7
33	P_3+P_9	109	96.1	11.6	88.0	33.4	1130.1
34	P_3+P_{10}	111	97.5	10.8	95.0	32.9	1070.0
35	P_4+P_5	114	103.1	10.4	102.0	29.2	1006.7
36	P_4+P_6	120	97.6	10.5	103.3	32.1	876.7
37	P_4+P_7	113	101.1	10.5	95.7	30.2	740.0
38	P_4+P_8	116	101.4	11.5	109.7	24.9	770.0
39	P_4+P_9	113	97.5	10.5	102.3	29.3	980.0
40	P_4+P_{10}	114	102.8	11.0	110.3	31.1	1080.0
41	P_5+P_6	120	99.3	10.0	100.0	30.9	990.0
42	P_5+P_7	112	101.7	10.3	122.7	30.3	920.0
43	P_5+P_8	115	102.8	10.3	118.3	29.3	840.0
44	P_5+P_9	112	99.9	11.5	109.0	31.2	1180.0
45	P_5+P_{10}	113	99.6	9.8	106.0	32.1	1076.7
46	P_6+P_7	119	99.7	10.6	101.0	29.9	990.0
47	P_6+P_8	120	95.1	10.9	112.7	30.3	810.0
48	P_6+P_9	116	96.1	11.7	106.0	32.6	1383.3
49	P_6+P_{10}	118	95.8	10.5	84.3	31.4	1140.0
50	P_7+P_8	115	95.9	10.3	123.3	29.5	730.0
51	P_7+P_9	114	98.3	11.2	105.0	30.5	1190.0
52	P_7+P_{10}	112	100.3	10.3	95.3	32.5	970.0
53	P_8+P_9	113	95.1	11.5	105.7	36.7	876.7
54	P_8+P_{10}	111	95.8	10.9	109.7	31.4	1086.7
55	P_9+P_{10}	110	97.2	11.2	94.0	33.5	1310.0

(for ML–328) to 103.3 cm (for ML–319). The corresponding range for mixture was from 93.5 cm (ML–246+ML–419) to 103.7 cm (ML–267+ML–378). It may be observed that the variability in mixture is less than that in pure standards. It may be noted that in a mixture whenever a late flowering parent (ML–323 or ML–328) was used it resulted in delay in flowering. As far maturity period, efforts at this Uhiversity have been made to develop multilines in Kalyansona cultivar with varying height also so that multilines of different height could be released for different fertility levels. The indicated height differences in pure-cultures are being exploited in this direction.

It would be worthwhile to make two types of comparisons. First what is the performance of the mixture when two phenotypically divergent genotypes are mixed. The second would be the comparison of the performance of the mixture when the two phenotypically similar (almost same height) parents are grown in a mixture. In the present case if the mixture of ML–328 (the most dwarf parents) with other parents is observed it would be clear that the mixture is invariably the intermediate. Its mean value may be closer to the taller or dwarfer parent depending upon the plants sampled for recording the observation in mixture or it may be the result of the true intergenotype interaction. These two situations may be separated out in case the mixture has the phenotypically similar lines mixed. In the present study an interesting situation has been revealed. ML–246, ML–326 and ML–419 have almost same height (97.1, 97.3 and 97.1 cm respectively). The F_1s (ML–246+ML–326 and ML–246+ML–419) attained a height of 101.3 and 100.3 cm indicating that inter-genotypic competition has provided a stimulus to the growth. On the contrary the F_1 (ML–246+ML–419) had an average plant height of 93.5 cm only thus indicating that a retardation has occured. It may be noted that ML-246 has figured out in both the types of inter-action thus bringing out clearly that the interaction is highly specific. While mixing the components in a multiline, it may not be enough that the height of each of the components is taken into consideration. It should in fact be super-imposed with the performance. Only those lines should be mixed in the final make-up which have same height in a mixture as well.

There were no variation among pure cultures as well as in mixtures for ear length. This character was, therefore, not taken up for further analysis. For number of tillers per meter row length there were highly significant differences for pure cultures as well as for the mixtures. The range for parents was from 85.7 (ML–323) to 147.0 (ML–378) whereas for mixture it ranged from 81.7 (ML–246+ML–419) to 137.3 (ML–270+ML–293). Although the magnitude of mean squares due to pure cultures is much larger than that due to mixture the variation in the latter appeared to be larger. In the pure culture group one of the lines viz. ML–328 had exceptionally high tiller number and may have contributed to the variation. Otherwise the variation in mixture as a group seems to be more. This is encouraging because tiller number is one of the primary components of yield and if positively interacting genotypes could be spotted out these would result in increase in grain yield.

There were significant differences among progenies for seed size. The differences

due to pure cultures, mixtures and the contrast between the two groups were also highly significant. For pure cultures the seed size varied from 24.8 g for ML–328 g to 35.5 g for ML–270. The corresponding range in case of mixtures was from 25.0 g (ML–293+ML–328) to 34.2 g (ML–267+ML–270). The general trend appears that when two parents with almost similar seed size are mixed together the mixture also has the seed size in the same range. For instance ML–246, ML–267, ML–319 and ML–326 have a seed size of 29.1, 28.8 and 28.9 respectively. The mixtures ML–246+ML–267, ML–246+ML–319, ML–246+ML–326, ML–267+ML–319, ML–267+ML–326 and ML–319 +ML–326 had a seed size of 28,9, 29.3, 30.6, 29.6, 28.4 and 30.3 g respectively. Similarly, when two lines (ML–270 and ML–412) with bold seeds are grown in a mixture it results into bolder seeds. It is encouraging to note that the seed size is not reduced at least, even if only one of the parents is bold seeded in the mixture.

For grain yield the differences were highly significant for pure culture and the comparison pure culture vs mixtures. The range for pure cultures for grain yield from 500.0 (ML–328) to 1243.3 (ML–410). The corresponding range for the mixture was from 623.3 (ML–246+ML–293) to 1383.3 (ML–323+ML–412). Both the lower and the upper yield levels are higher in case of mixtures as compared with the pure cultures. It is, however, not possible to establish to definite trend between the pure cultures and mixtures. Although ML–323+ML–412 and ML–412+ML–419 two top yielding mixtures included one of the highest yielding pure cultures (ML–412) it did not maintain the high performance in all cases. On the contrary, however, wherever one of the two poorest yielding lines (ML–246 and ML–328) were present the mixture resulted into relatively lower yield level. It is thus clear that for obtaining good yield in a multiline the 'nicking ability' even of the high-yielding components must be high. The usefulness of the studies like the present one for plant height and seed size has already been brought out by JAIN & MOSHA (1974).

Combining ability analysis

The analysis of variance (Table 1) indicated that the variance due to *gca* was highly significant for all the characters studied. However, *sca* variance was important in case of days to 50 per cent heading, tiller number, seed size and grain yield. The ratio between the two variances ranged from 1.46 for seed size to 96.01 for days to 50 per cent heading. This indicated that the additive effects were much more important in the material and it may be possible to select for better general combining ability in case of all the characters studied.

The estimates of general combining ability effects for different characters in respect of the parents are given in Table 3.

The best general combining for days to earing was ML–412 followed by ML–326. ML–323 was the significantly poor general combiner for this character. For plant height the best general combining ability was exhibited by ML–328. This along with ML–323 and ML–412 were significantly better combiners. On the other hand ML–329 was

Table 3. Estimates of general and specific combining ability effects for different characters.

S. No.	Pedigree	Days to 50% flowering	Plant height	Ear length	No. of tiller P. Mtr.	Seed size	Grain yield
1	ML 246	−1.23	−0.50	−0.1783	−4.53	−0.68	−155.61
2	ML 267	0.10	1.02	−0.1450	−0.71	−0.62	− 29.52
3	ML 270	−1.48	0.32	0.0413	1.01	2.46	77.50
4	ML 293	0.68	2.17	0.1633	4.02	−1.80	− 61.45
5	ML 319	0.26	2.23	−0.2533	5.73	−0.33	9.94
6	ML 323	5.10	−1.52	0.0383	−0.32	0.47	77.16
7	ML 326	−1.65	0.37	−0.1867	3.46	−0.58	− 87.27
8	ML 328	1.43	−1.92	0.0050	11.44	−1.61	−163.66
9	ML 412	−2.07	−1.27	0.6050	−5.21	1.41	175.79
10	ML 419	−1.15	−0.89	−0.1033	−9.88	1.29	157.16
	S.E.	1.55	0.45	0.0880	0.28	0.18	52.27

the poorest combiner. For tiller number the differences were highly marked. ML–328 and ML–419 represented the best and the poorest combiners with other being intermediate. As for tiller number, the differences for seed size were also pronounced. ML–270 and ML–412 were better whereas ML–328 was the poorest combiner. For grain yield ML–412 and ML–419 were the significantly better combiners whereas ML–246 and ML–267 were the significantly poor combiners. Other parents were intermediate. Parent-wise it may be concluded that ML–412 is a better general combiner especially for heading date, plant height, ear length, seed size and grain yield. So this parent may be used in multilines more frequently. The only negative point in respect of this parent is the *gca* estimate for tiller number. ML–328 has shown a behaviour exactly opposite to that of ML–412. This is the poorest combiner for all the characters except for tiller number.

It has been noted from the *sca* effects that there are no mixtures where all the characters are exhibited in the most desirable proportions. The estimation of specific combining ability effect may be more useful when F_1 is a normal cross between the two parents and the breeder is interested in the succeeding generations obtained through selfing or intermating. In case of studies like the present one the *per se* performance of the mixtures may be more meaningful rather than the specific combining ability effects.

There have been no studies already reported in literature on the lines of the present one. It has, therefore, not been possible to compare the present one with the previous one(s).

References

Borlaug, N.E. (1959). Proc. First Int. Wheat Genet. Symp. Winnipeg, pp. 12–26.
Griffing, B. (1956). Austr. J. Biol. Sci. **9**: 463–493.
Harper, J.L. (1964). Proc. XI Int. Genet. Cong, pp. 465–481.
Jain, K.B.L. and Mosha, A.S. (1974). Indian J. Genet. **34**: 1168–1181.
Jensen, N.F. and Federer, W.T. (1965). Wheat. Crop Sci. **5**: 449–452.

(Editorial Remarks: The present paper by K.S. Gill, G.S. Nanda & G. Singh was supposed to reach to the editorial office of WIS in January, 1979, but by unknown reason, the manuscript was lost during mailing. The editor asked the authors to resend it, and it is printed in WIS No. 52. The Editor)

Monosomic analysis of yield and yield components in wheat cultivars

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Through substitution lines, the genes responsible for quantitative characters have been located in specific chromosomes (KUSPIRA & UNRAU 1957; HERMSEN 1963; LAW 1967). Though the monosomic analysis is not very precise, but the results obtained were similar to the substitution lines (PETROVIC 1979).

To ascertain the contribution of individual chromosome in the expression of yield and yield components, two varieties having diverse dwarfing source were selected. Through 'F_2' monosomic analysis, the chromosome location of genes associated with yield trait were established. The data thus obtained is presented here and the results are discussed in the light of earlier observations.

Materials and Methods

The triple dwarf wheat genotypes (*Triticum aestivum*), Mex. C.B. 116 (Pedigree-Nai 60 × TT-Son. 64 × (LR×Son. 64) and Hira (Pedigree–E5477×Son. 64) were crossed as a donor parents with all 21 identified monosomic lines of Chinese Spring and also with the normal disomic. The F_1 plants were grown in the field and the monosomics were confirmed at meiotic metaphase. The identified monosomic F_1's were selfed. The progenies from selfed monosomic F_1 plants, and F_1 plants from normal cross were subsequently sown in a randomised block design with three replications. The material was sown in two seperate sets, one comprised of 22 F_2 populations derived from the crosses of Mex. C.B. 116 with 21 monosomic and one disomic Chinese Spring, and the other consisted of 22 F_2 progenies of crosses with variety Hira.

The observations were recorded on an individual plant basis and for that 40 plants were randomly selected from each plot. The means of different characters were determined per plot and the usual "F" test was applied to ascertain the differences between populations. The mean of parents were not included in statistical analysis.

The F_2 population derived from the crosses involving identified monosomic lines have been referred as 'F_2' monosomic population.

Results and Discussion

The data pertaining to "F_2" monosomic populations derived from crosses involving Mex. C.B. 116 and Hira for mean grain yield per plant and other yield components have been summarised in Table 1 and Table 2 respectively.

The results have indicated that absence of a single chromosome does not significantly alter grain yield in both the varieties, Mex. C.B. 116 and Hira. These observations have a supporting evidence from the earlier report of JOSHI & SINGH (1968). However, their studies were limited to eight monosomic lines where they recorded no difference in grain yield between monosomic and disomic populations. Furthermore, yield is a complex character and is considered the ultimate product of the action and interaction among a number of quantitative characters, which are known to be controlled by different sets of polygenes. Therefore, some workers have even doubted the individuality of this character and have raised a point, whether there are any genes governing the yield *per se* (GRAFIUS 1959; KOHLI 1973).

The results indicated that eleven chromosomes namely 1B, 2A, 2B, 2D, 3B, 3D, 4A, 4B, 6A, 6B and 7A in Mex. C.B. 116 and five chromosomes 1B, 2B, 2D, 3A and 3B in variety Hira increased the average number of ears per plant. It was interesting to notice that none of the F_2 monosomic population showed any significant reduction in the ear number per plant. SEARS (1954) observed that chromosomes 1B, 1D, 2A, 2B, 2D, 3B, 4B, 5D and 6A influenced this character, but their expression was variable. TSUNEWAKI & HEYNE (1959) reported all members of homoeologous group 4 and LAW (1966) associated

Table 1. Mean of grain yield and its components (Chinese Spring monosomics × C.B. 116-F_2)

Lines	Grain yield per plant (gm)	Ears per plant (Nos)	Spikelets per ear (Nos)	Grains per ear (Nos)	100-grains weight (gm)
Chinese Spring	14.81	21.26	25.20	66.80	2.26
Mex. C.B. 116	14.80	11.60	22.00	62.73	3.40
F_2 Normal	16.64	14.79	25.63	64.61	2.68
F_2 monosomics					
1A	15.72	15.04	23.73**	52.61**	3.09**
1B	15.39	18.78**	24.31**	51.46**	2.41
1D	18.99	15.61	24.08**	52.40**	3.17**
2A	19.46	16.95**	22.65**	54.53**	2.99*
2B	16.92	17.46**	24.02**	54.87**	2.90
2D	18.13	17.34*	24.74	54.59**	2.81
3A	16.39	14.83	23.73**	49.92**	2.93
3B	18.75	17.41**	24.63*	53.90**	2.92
3D	19.24	16.76*	24.59*	60.22	2.90
4A	15.86	17.97**	23.79**	50.42**	2.82
4B	20.31	20.01**	22.80**	51.53**	3.18**
4D	16.38	13.94	24.48*	56.16*	2.91
5A	16.31	16.64	24.54*	57.19	2.95
5B	17.43	15.30	23.71**	55.75*	2.77
5D	17.73	15.44	24.91	55.06*	3.26**
6A	19.05	17.36*	24.13**	61.89	2.92
6B	17.89	16.76*	25.10	58.24	2.72
6D	19.35	13.91	25.03	58.25	3.31**
7A	19.38	17.18*	24.29**	60.19	2.91
7B	18.21	16.30	24.16**	59.98	2.71
7D	19.22	16.44	24.38*	57.14	3.11**

* Significant at 5% level ** Significant at 1% level

Table 2. Mean of grain yield and its components
(Chinese Spring monosomics × Hira–F_2)

Lines	Grain yield per plant (gm)	Ears per plant (Nos)	Spikelets per ear (Nos)	Grains per ear (Nos)	100-grains weight (gm)
Chinese Spring	9.76	18.46	23.93	77.33	2.20
Hira	14.92	14.86	19.73	54.53	3.18
F_2 Normal	15.59	14.04	23.60	63.86	3.13
F_2 Monosomics					
1A	16.55	14.73	24.77**	67.56	3.18
1B	16.48	18.18**	23.15	48.13**	3.06
1D	15.09	14.64	24.38*	59.22	3.28
2A	15.35	13.44	23.02	55.24**	3.18
2B	15.58	17.18**	22.60**	49.98**	3.01
2D	16.30	17.50**	24.27	58.08*	3.06
3A	13.42	16.00*	23.19	51.18**	2.91
3B	14.31	15.92*	24.28	52.63**	3.00
3D	13.37	14.88	23.12	54.10**	3.13
4A	11.56	15.33	23.08	47.19**	3.54*
4B	12.68	15.63	21.98**	49.20**	3.14
4D	13.80	14.63	23.67	58.92	2.76*
5A	15.46	14.99	23.23	61.05	3.08
5B	14.21	14.59	22.40**	57.65*	3.30
5D	14.23	14.75	23.18	58.80	3.36
6A	16.08	15.68	23.24	60.55	2.97
6B	14.35	14.63	24.71**	58.43	2.97
6D	15.06	14.66	23.65	58.43	3.63*
7A	14.33	14.28	21.73**	57.38*	3.14
7B	14.75	14.88	23.03	59.83	3.18
7D	14.08	14.69	24.45*	59.44	3.10

* Significant at 5% level ** Significant at 1% level

chromosomes 1B, 3A, and 3D which distinctly influenced ears number per plant. SHARMA and BHOWAL (1973) attributed the increase in spike number per plant to the absence of chromosomes 4A, 4B and 7A, where as they found decrease was due to the absence of 2B and 4D chromosomes. BHAT & GOUD (1979) reported that monosomic population 3D and 4D had genes for low tiller number per plant, while 2B, 6D and 7B had genes with opposite effects.

The comparative observations have indicated that chromosomes namely, all members of 1, 3, 4 and 7 homoeologous and 2A, 2B, 5A, 5B and 6A showed variable range of reduction in the mean number of spikelets in variety Mex. C.B. 116. In variety Hira, eight F_2 monosomic lines (1A, 1D, 2B, 4B, 5B, 6B, 7A and 7D) had less number of spikelets. This finding is in agreement with previous reports on this trait (SASAKI *et al.* 1968; SHARMA & BHOWAL 1973). In addition, six chromosomes, 2A, 3A, 4A, 5A and 5B are reported for their effects on number of spikelets.

Joint consideration of the characters, spikelets per ear and grains per ear, revealed that most of the chromosomes like 1A, 1B, 1D, 2A, 2B, 3A, 3B, 4A, 4B, 4D and 5B in variety Mex. C.B. 116 and chromosomes like 2B, 4B, 5B and 7A in variety Hira are responsible for reducing the spikelets per ears as well as grains per ear. But the genes

located on the other chromosomes are not similar for the visual expression of both the characters. Among these chromosomes, some are responsible for spikelets per ear, while other's effect is confined to the grains per ear. On the basis of these observations, it can be suggested that there is some independence between these two characters, and different genotypes appear to have different chromosomes involved.

The present study, on 100-grain weight clearly indicated that seven monosomic, i.e. 1A, 1D, 2A, 4B, 5D, 6D and 7D increased the grain weight in variety Mex. C.B. 116. In other variety Hira, two chromosomes 4A and 6D increased the grain weight, whereas 4D chromosomes reduced the grain weight. All members of homoeologous group 1, 3, 6 and 7 and chromosomes 4A, 5A and 5B have been reported to effect the expression of grain weight by different workers, (KUSPIRA & UNRAU 1957; LAW 1966, 1967; SASAKI *et al.* 1968).

Taking into consideration the present observations and earlier reports on aneuploid analysis of yield and yield components, it would be evident that many chromosomes are involved and as such it may not be feasible to alter yield potentials of some selected wheat varieties by one or two chromosomes substitutions.

Literature Cited

BHAT, S.R. and J.V. GOUD 1979. WIS No. **50**: 14–17.

GRAFIUS, J.F. 1959. Agron J. **51**: 551–54.

HERMSEN, J.G. Th. 1963. Euphytica **12**: 126–129.

JOSHI, B.C. and D. SINGH 1968. Indian J. Genet. **28** (1): 66–67.

KOHLI, S.P. 1973. Proc. 4th Inter. Wheat Genet. Cymp. Columbia, Missouri, U.S.A. pp. 35–39.

KUSPIRA, J. and J. UNRAU 1957. Can. J. Plant. Sci. **37**: 300–306.

LAW, C.N. 1966. Genetics **53**: 487–498.

LAW, C.N. 1967. Genetics **58**: 445–461.

PETROVIC, S. 1979. WIS No. **49**: 19–23.

SASAKI, M.; M. MORIYASU; R. MORRIS and J.W. SCHIMIDT 1968. Proc. 3rd Inter. Wheat Genet. Symp. (Canberra) pp. 343–349.

SEARS, E.R. (1954). Missouri Agril. Exptl. Stn. Res. Bull. 572.

SHARMA, D.C. and J.G. BHOWAL 1973. Z. Pflanzenzuchtg **70**: 157–165.

TSUNEWAKI, K. and E.G. HEYNE 1959. Genetics **44**: 947–954.

Competitive abilities of the resynthesized hexaploid wheats

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The competitive ability of certain genotypes will play an important and direct role in the process of differentiation or adaptation to some environments. Under the natural selection, each of AABB genome and DD genome differentiated since the establishment of common wheats.

Tetra Canthatch was reconstituted by KERBER (1964) from Canthatch, a cultivar of common wheat after seven backcrosses to Canthatch of Canthatch-Stewart durum wheat hybrid. Five strains of the resynthesized hexaploid wheat used here were raise by KERBER from the cross between Tetra Canthatcth and each of five strains of *Aegilops squarrosa* (Table 1).

Table 1. Materials used in this study.

Code				
	Resynthesized hexaploid wheat			
ABD 5003	Tetra Canthatch	×	*Aegilops squarrosa*	RL 5003 ssp. *eu-squarrosa* Eig var. *typica* L.
ABD 5261	〃	×	〃	RL 5261 〃
ABD 5271	〃	×	〃	RL 5271 ssp. *strangulata* Eig var. *strangulata*
ABD 5288	〃	×	〃	RL 5288 〃
ABD 5289	〃	×	〃	RL 5289 ssp. *eu-squarrosa* Eig var. *meyeri* GRISEB
	Cultivated hexaploid wheat			
Canthatch	*Triticum aestivum* (L.) THELL. ssp. *vulgare* (VILL.) MAC KEY cv. Canthatch			
Chinese Spring	〃 cv. Chinese Spring			

Considerations of difference of competitive ability between Canthatch and each resynthesized hexaploid wheat make possible to analize the relative contribution among DD genomes in the hexaploidy level.

The competitive ability of each resynthesized hexaploid wheat strain and cultivar Canthatch was tested by comparing the relative response of strains to competitive conditions with a tester variety, cultivar Chinese Spring. Under the competitive conditions, plants of tested strains and those of tester variety were spaced in the row alternatively, that is;

Pure stand	Mixed stand with Chinese Spring	
x x x x x x x x x x	c c c c c c c c c c	(Chinese Spring)
x x x x x x x x x x	x x x x x x x x x x	(tested strain)
x x x x x x x x x x	c c c c c c c c c c	(Chinese Spring)

The plants of resynthesized strains were planted on Nov. 15th in 1979 in pure stands and in mixed stands, 10 cm apart in rows spaced 40 cm apart in a split plot arrangement

with three replications. Records were taken on ten plants from pure stand and from mixed stands for four vegetative and reproductive characters.

The average values of four characters taken as indications of competitive ability were compared on the basis of three replications in pure stands and as many from mxied stands. As shown in Table 2, almost all of the values of five resynthesized wheat strains in pure stands are high comparing to those in mixed stands. Therefore, it is clear that the competitive abilities of five resynthesized strains tested are generally lower than that of Chinese Spring. Results of analyses of variance of the above mentioned data are presented in Table 3. Competitive effects were observed in three characters, i.e. weight of whole plant (including root weight), weight of ears, number of ears in comparison with those of pure stand. The differences in decrements between the strains were not so striking, but it will be found commonly as a general tendency that competitive ability of Canthatch is greater than resynthesized hexaploid wheats. Among the resynthesized hexaploid wheats, the lowest competitive ability was observed in ABD 5003.

Table 2. Comparison of pure and mixed stand per individual basis.

Strain		Characters			
		Weight of whole plant (g)	Weight of ears (g)	Number of ears	Total grain yield (g)
Canthatch	P	67.7	17.9	20.5	7.80
	M	64.5	18.0	22.9	9.07
	M-P	−3.2 ns	−1.1 ns	2.4 ns	1.27 ns
ABD 5003	P	58.8	15.6	15.5	4.80
	M	32.5	8.0	11.1	1.91
	M-P	−26.3**	−7.6**	−4.4*	−2.89**
ABD 5261	P	52.6	17.1	13.9	6.08
	M	32.8	10.3	10.1	4.07
	M-P	−19.8**	−6.2**	−3.8*	−2.01 ns
ABD 5271	P	58.2	13.7	13.7	3.60
	M	36.9	8.1	10.0	2.65
	M-P	−21.3**	−5.6**	−3.7 ns	−0.95 ns
ABD 5288	P	59.3	14.7	15.3	3.12
	M	47.0	12.0	13.5	3.66
	M-P	−12.3*	−2.7 ns	−1.8 ns	0.54 ns
ABD 5289	P	52.3	13.1	16.6	3.53
	M	33.5	8.7	12.8	2.67
	M-P	−18.8**	−4.4*	−3.8*	−0.86 ns
Difference					
L.s.d. (0.05)		10.83	3.99	3.44	1.85
df=22 (0.01)		14.72	5.42	4.68	2.52

Abbreviations: P; Pure stand. M; Mixed stand with Chinese Spring.
*, **; significant at the 5 and 1% levels, respectively.
ns; non-significant.

Table 3. Analyses of variance on the competitive effects in four characters.

Source of variation	d.f.	Weight of whole plant	Weight of ears	Number of ears	Total grain yield
		Mean square			
Between blocks	2	58.05	12.26	3.78	2.038
(S) Between strains	5	475.99**	47.87**	79.10**	26.620**
Error (a)	10	58.85	4.37	5.83	0.775
(C) Competition	1	2582.84**	170.04**	56.75**	6.011
C×S	5	97.87**	15.26	9.74**	1.474
Error (b)	12	25.93	6.53	2.72	1.552

**; significant at the 1% level.

These results indicated that DD genome of Canthatch contributed to the adaptability of its strain more than DD genome of *Aegilops squarrosa*.

The reproductive abilities of the strain such as grain yields must affect the survival rate, even though total grain yields produced by certain tested strains was not modified significantly according to their competitive abilities, but in ABD 5003. Competitive effects would rather be observed in vegetative characters such as weight of whole plant. Because competitive effects in total grain yield in four resynthesized hexaploid wheat strains were not observed, but in vegetative character (weight of whole plant), more allocation of photosynthate into reproductive character will represent in resynthesized wheat than in common wheat in competitive condition.

Literature Cited

KERBER, E.R. 1964. Wheat: reconstitution of the tetraploid component (AABB) of hexaploids. Science **143**: 253–255.

A synthesized common wheat obtained from a triploid hybrid, *Aegilops squarrosa* var. *strangulata*(♀) × *Triticum durum*(♂)[1)]

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It is known that about 70% of plant species are polyploidy, and many are allopolyploidy. Allopolyploid species might have evolved through following three processes; (i) compatible crossing between two species, (ii) chromosome doubling in the F_1 hybrid, and (iii) producing fertile gametes accompanied with stable chromosome pairing among progenies.

In *Triticinae*, fertile F_1 hybrids and natural amphiploidization have been reported in the crosses of *Secale* × *Triticum* (ROBBELIN & SMUTKUPT 1968), *T. dicoccoides* × *Aegilops ovata* (KIHARA 1931), *T. dicoccoides* × *Ae. squarrosa* (KIHARA & LILIENFELD 1949), *Ae. speltoides* × *Ae. umbellulata* (MITSUOKA 1953), *T. persicum* × *Ae. squarrosa* (TABUSHI 1956), *T. boeoticum* × *Ae. squarrosa* (SEARS 1941), *Ae. heldreichii* × *T. durum* (MAAN & SASAKUMA 1977), and *T. aestivum* × *Agropyron disticum* (PIENAAR 1980). These data indicated that the three processes above mentioned were independent events each other and was subjected to genic control as well as environmental one. Most of these amphiploids were obtained only in uni-directional crosses except one involving *Ae. heldreichii* × *T. durum*, mainly because of cross-incompatibility in the reciprocal crosses including zygotic lethality.

On the other hand, many lines of synthesized 6x wheat with the genome constitution of AABBDD have been produced through spontaneous or colchicin-induced amphiploidizations, and they have been utilized for evolutional and genetical analyses, as well as for breeding programs (KIHARA 1944; MCFADDEN & SEARS 1946; TABUSHI 1956; KERBER & DYCK 1978; MAAN & SASAKUMA 1978). All these synthesized wheats were produced from the crosses of various Emmer wheats (AABB) as female parents with the pollen of *Ae. squarrosa* (DD), and the reciprocal cross (*squarrosa* × Emmer) was reported to be of zygotic lethal. A review on cross-compatibility among *Triticum* and *Aegilops* indicates that it is controlled by ploidy balance, genic compatibility, or nucleus-cytoplasm interaction between parental species (KIHARA 1937; SEARS 1941; NISHIYAMA 1979; MAAN 1977). Cross-incompatibility might be overcome with polyploidization of female parent, chromosomal manipulation, or embryo-culturing.

We have obtained lines of synthetic 6x wheat from the crosses involving *Ae. squarrosa* as female parents, of which breeding processes are described in the present paper.

1) The present study was conducted as a part of the Cooperative Project on NC-Heterosis Breeding directed by H. Kihara, and financially supported in part by the Grant-in-Aid No. 1445 (1980) of Ministry of Agr. Forest. and Fish. of Japan.

Materials and Methods

Ae. squarrosa var. *strangulata* (2n=14;DD) was used as female parent in the crosses with *T. boeoticum* (2n=14; AA), *T. monococcum* (2n=14; AA), *Ae. speltoides* (2n=14; SS), *T. timopheevi* (2n=28; AAGG), or Emmer (2n=28; AABB) and Dinkel (2n=42; AABBDD) wheats. Their crossed seed-set, seed plumpness, and germination ability of produced seeds were examined. From the seeds obtained from *Ae. squarrosa* (♂) × *T. durum* Selection 56–1(♀), young embryos were aseptically removed at 14 days after pollination, and placed on the agar media in test tubes each containing 10 ml of RM–64 medium (LINSMAIER & SKOOG 1965) supplemented with 10 mg/l of GA_3 and 0.1 mg/l of kinetin. Young embryos were cultured under continuous illumination at 20°C until seedlings with roots grew up. The F_1 hybrids obtained were grown in pots with soil, and their PMC's and microspores were sampled to provide for cytological observations of microspore development of the interspecific F_1 hybrids. Also, chromosome pairing at MI and fertility of their progenies from selfing and crossing were examined.

In order to obtain the auto-tetraploid lines, seedlings of 10 accession lines of *Ae. squarrosa* at tillering stage were treated with 0.2% colchicine in 2% dimethyl sulfoxide (DMSO) solution for 5 hr after leaves and roots of seedlings were cut back to about 5 cm. The treated seedlings were re-potted after washing in running water and grown with sufficient moisture in greenhouse. Their chromosome constitutions were cytologically examined with renewed roots and PMC's. The efficiency of colchicine treatments for obtaining auto-tetraploids were described in the report by SASAKUMA & KIHARA (1981). The autotetraploid lines were crossed with *T. durum* Sel. 56–1 or *T. aestivum* cv. Chinese Spring and the chromosome pairing and fertility of F_1 hybrids were examined.

Results and Discussion

No plump seed was obtained from the crosses of *Ae. squarrosa* as female parents with any species of *Aegilops* and *Triticum* used (Table 1). More than 50% of the crossed florets in these crosses produced the residues of undeveloped seeds, which were categorized as shrivelled seed in this paper. In fact, fertilization and early embryogenesis were recognized by observing disected young seeds at 10–14 days after pollination. These young seeds were filled with fluid, and lost the moisture along the plants matured, resulting in dry residues of about 0.1–0.2 cm in size. On the other hand, plump seeds were obtained from the crosses of the colchicine-treated *Ae. squarrosa* as female parents with Emmer or Dinkel wheats although they produced shrivelled seeds in certain proportion (Table 1). The reciprocal crosses (Emmer or Dinkel × *Ae. squarrosa*) set plump seeds. These facts suggest that the compatible balances of D genome dosage between embryo and endosperm may determine the seed plumpness with some other modifying factor(s). It was reported that the crosses of *Ae. squarrosa* (♀) × Emmer wheat (♂) resulted in zygotic lethality, and that an induced autotetraploid line of *Ae. squarrosa* set seeds in the cross with Emmer wheats, of which progenies were utilized for breeding alloplasmic wheat lines

Table 1. Crossability of *Ae. squarrosa* var *strangulata* with *Triticum* and *Aegilops* species.

Female parent	Male parent	Genome constitution		No. florets crossed	No. seeds obtained	
		Embryo	Endosperm		Plump	Shrivelled[4]
squarrosa (2x)	*boeoticum*	AD	ADD	38	0	19
〃	*monococcum*	AD	ADD	22	0	8
〃	*speltoides*	DS	DDS	24	0	12
〃	Emmer[1]	ABD	ABDD	186	0	117
〃	*timopheevi*	AGD	AGDD	24	0	12
〃	*aestivum*	ABDD	ABDDD	118	0	98
squarrosa (4x)	Emmer[1]	ABDD	ABDDDD	42	18	17
〃	*aestivum*[2]	ABDDD	ABDDDDD	22	8	3
durum	*squarrosa* (2x)	ABD	AABBD	44	12	1
aestivum	〃	ABDD	AABBDDD	36	18[3]	0

1) Involving *T. durum, turgidum, polonicum, dicoccoides* and *dicoccum.*
2) Involving *T. aestivum* cv Chinese Spring, Selkirk and *T. macha.*
3) Seeds were plump but did not germinated.
4) All shrivelled seeds were residues of undeveloped seeds and did not germinate.

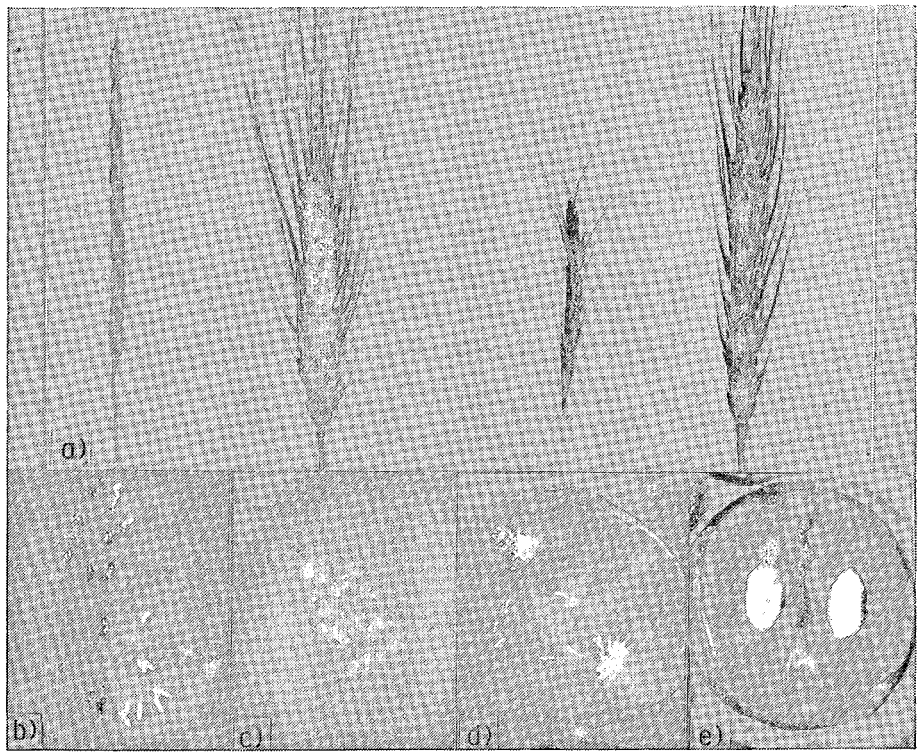

Fig. 1. Spike morphology and microsporogenesis in natural amphiplodization from the cross of *Ae. squarrosa* var. *strangulata* (♀) × *T. durum* Sel. 56–1 (♂).
a) From left to right, *Ae. squarrosa, T. durum*, F_1 and F_2 plants, respectively. b)-e) Microsporogenesis in the F_1 hybrid; complete asynapsis at MI(b), restitution nucleus(c), equational division(d), and synmetrical dyad formation(e).

having cytoplasm of *Ae. squarrosa* (KIHARA 1973, 1979).

Seven seedlings were obtained from germinating embryos in the test tubes out of 62 embryos cultured, and five were grown till mature plants. All five plants had 21 chromosomes in somatic tissues, and their morphological appearrances were of wheat type with long awns, although they were weak in vigor in comparison with the parental *T. durum* Sel. 56–1 (Fig. 1-a). All five F_1 hybrids produced fertile pollen grains and set F_2 seeds on bagged spikes. The F_2 progenies had 42 chromosomes of 2.58I+19.70II+0.02III on average in PMC (Table 2). These facts indicated that the natural amphiploidization had occured in the F_1 hybrids of *Ae. squarrosa* (♀) × *T. durum* (♂). In general, natural amphiploids might originate by the spontaneous doubling of chromosomes in somati ctissues of interspecific hybrids, producing fertile sectors, or by the production of the unreduced functional gametes and self-fertilization. In *Triticinae*, the latter event has been experimentally observed (KIHARA 1949). MAAN *et al.* (1980) suggested a pairing suppression system of homoeologous chromosomes involved in the induction of the unreduced gamete formation. Cytological observations on PMC's of the F_1 hybrids in the present experiment indicate the following meiotic process and microsporogenesis; (i) complete asynapsis at MI without any chromosome pairing (Fig. 1-b), (ii) univalent chromosomes showing x-shape, gathered in the center of the cells (Fig. 1-c), (iii) equational division of univalent chromosomes at the first division of PMC's (Fig. 1-d), (iv) synmetrical dyad formation as product of 'meiosis', which is characterized to have large obscure nuclei (Fig. 1-e), and (v) production of fertile pollen grains with three nuclei filled with starch granules. This meiotic process is characteristic for the meiotic non-reduction and the unreduced gamete formation in interspecific hybrids, resulting in amphiploid production observed by KIHARA (1949), MAAN *et al.* (1980) and others.

Out of 46 plants obtained from the fertile F_1's, one plant had 41 chromosomes and the others had 42 with relatively stable chromosome pairing (Table 2). The plants obtained from the crosses of the F_1's with *T. aestivum* cv Chinese Spring and *T. durum* Sel. 56–1 showed pairing conformations of 3.80I+19.10II, and 7.82I+13.59II, respectively, which indicated that there was no significant reduction of pairing stability in these hybrids. Many lines of synthetic hexaploid wheat (AABBDD) have been obtained by KIHARA and his co-

Table 2. Chromosome pairing and fertilities of hybrids involving 2x and 4x *Ae. squarrosa*.

Female parent	Male parent	Genome const.	Chromosome pairing at MI			Pollen fert.	Selfed seed-set	Crossed seed-set[1]
			I	II	III			
2x	*durum*	ABD[2]	20.80	0.10	0.00	58.2%	16.6%	25.3%
Selfed	F_2[3]	AABBDD	2.58	19.70	0.02	98.7	97.5	95.8
4x	*durum*	ABDD	16.26	5.87	0.00	0.0	0.0	3.6
4x	*aestivum*	ABDDD	20.75	6.56	0.38	0.0	0.0	2.8

1) Seed-set (%) in the crosses with pollen of *T. durum* Sel. 56–1.
2) Obtained through embryo culture.
3) F_2 plants having 42 chromosome obtained from selfing the fertile ABD.

workers (KIHARA *et al.* 1957; TABUSHI 1957; TANAKA 1961) and KERBER & DYCK (1978). All of them were from the crosses between Emmer wheats as female and *Ae. squarrosa* as male parents. Some of them were natural and others are colchicine-induced. The newly induced AABBDD amphiploid in this experiment is unique because this synthesized common wheat have *squarrosa* cytoplasm.

In the present experiment, auto-tetraploid lines of *Ae. squarrosa* including four subspecies (*typica, strangulata, meyeri,* and *anathera*) were induced. They showed partially reduced fertility probably because of multivalent formations and irregular segregations of the duplicated chromosomes. Various F_1 hybrids were obtained from the crosses of these auto-tetraploids with *T. durum* Sel. 56–1 and *T. aestivum* cv Chinese Spring. Their paring conformations on over-all average were 16.26I+5.87II in ABDD and 20.75I+6.56II+0.35III in ABDDD, respectively. They were highly sterile but a few seeds were obtained from the crosses of each F_1 line with *T. durum*.

The lines obtained in the present experiments will be used as the maternal plants for introducing cytoplasmic variability in NC-heterosis breeding program.

Literature Cited

KERBER, E.R. & P.L. DYCK 1978. Proc. 4th Int. Wheat Genet. Symp. (New Delhi): 358–364.
KIHARA, H. 1931. Cytologia **26**: 301–324.
———— 1944. Agr. & Hort. **19**: 13–14.
———— 1973. Seiken Ziho **24**: 5–9.
———— 1979. Seiken Ziho **27/28**: 1–3.
———— & F. LILIENFELD 1936. Jap. J. Genet. **12**: 236–256.
———— & ———— 1949. Proc. 8th Inter. Congr. Genet. Hereditas Suppl. vol.: 307–319.
————, K. YAMASHITA, M. TANAKA & J. TABUSHI 1957. Wheat Inf. Serv. **6**: 14–15.
LINSMAIER, E.M. & F. SKOOG 1965. Physiol. Plant **18**: 100–127.
MAAN, S.S. 1977. Proc. 8th Congr. EUCARPIA (Madrid): 201–214.
———— & T. SASAKUMA 1977. J. Hered. **68**: 87–94.
———— & ———— 1978. Proc. 4th Int. Wheat Genet. Symp.: 322–331.
MCFADDEN, E.S. & E.R. SEARS 1946. J. Hered. **37**: 26–32.
MITSUOKA, S. 1953. Seiken Ziho **8**: 91–96.
NISHIYAMA, I. 1979. Wheat Inf. Serv. **49**: 32–34.
PIENAAR, R.V. 1980. Wheat Inf. Serv. **51**: 13–14.
ROBBELEN, G. & S. SMUTKUPT 1968. Wheat Inf. Serv. **27**: 10–13.
SASAKUMA, T. & H. KIHARA 1981. Jap. J. Breed. **31**, Suppl. vol.
SEARS, E.R. 1941. Mo. Agr. Exp. St. Res. Bull. **337**: 1–20.
TABUSHI, J. 1956. Wheat. Inf. Serv. **4**: 11–12.
TANAKA, M. 1961. Wheat Inf. Serv. **12**: 11.

New hybrids between *Agropyron* and wheat. I. *A. ciliare*×wheat and *A. smithii*×wheat[1]

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Four *Agropyron* species, *A. distichum* (Thumb.) Beauv. (2n=4x=28), *A. elongatum* (Host) Beauv. (2n=2x=14 and 2n=10x=70), *A. intermedium* (Host) Beauv. (2n=6x=42, syn. *A. trichophorum*, *A. glaucum*, *A. amurense*) and *A. junceum* (L.) Beauv. (2n=2x=14 and 2n=4x=28) have been successfully crossed with wheat (PIENAAR *et al.*, 1977; CAUDERON, 1979; ALONSO and KIMBER, 1980). All seven wheat – *A. elongatum* (2n=14) disomic addition lines and six wheat – *A. intermedium* disomic addition lines have been produced (CAUDERON *et al.*, 1973; DVOŘÁK, 1980). Several of these lines are resistant to leaf rust, stem rust and wheat-streak mosaic virus (WSMV). Disease resistant *Agropyron* genes have been transferred into wheat by induced homoeologous pairing and by X-ray irradiation (SEARS, 1977; KNOTT *et al.*, 1977). One notable example is the Lr24 gene derived from *A. elongatum* (SMITH *et al.*, 1968) present in several commercial winter wheat cultivars (BROWDER, 1980).

It is obvious that *Agropyron* is a useful source of alien genetic variation in wheat. Several attempts to cross some other *Agropyron* species with wheat have failed, primarily because of early seed abortion. We successfully hybridized two additional species – *A. smithii* Rydb. (2n=4x=28) and *A. ciliare* Trin. (Fanch) (2n=4x=28) with wheat.

Triticum aestivum L. cv. 'Chinese Spring' and winter cvs. 'Newton', 'TAM 105', 'Turkey' and 'Vona' were crossed in reciprocal combinations with *A. smithii* (TA2052) and *A. ciliare* (TA2006). In the cross *T. aestivum* (♀) × *A. smithii* (♂), 615 florets were pollinated and 5 seeds began to develop but aborted early. In the reciprocal combination, *A. smithii* × *T. aestivum* 268 florets were pollinated and 18 seeds began to develop. The embryos were cultured at day 12 on MURASHIGE and SKOOG (1962) medium supplemented with 0.4 mg/l thiamine-HCl, 10 mg/l each L-arginine HCl, glycine and L-tyrosine and containing 0.8% Bacto agar, and 2 hybrid plants *A. smithii* × 'Chinese Spring' and *A. smithii* × 'TAM 105' grew to maturity. The cross *T. aestivum* (♀) × *A. ciliare* (♂) was unsuccessful, but in the reciprocal combination one hybrid plant *A. ciliare* × 'Chinese Spring' was obtained by embryo culture from pollination of 350 florets. All three *Agropyron* – wheat hybrids were cytologically analyzed.

The three hybrids were vigorous and tillered profusely. The spike and spikelet morphology was intermediate. *A. smithii* is rhizomatous and *A. smithii* × wheat hybrids developed some rhizomes. The white scales on the stem in 'TAM 105' and in *A. ciliare*

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were also in the *A. smithii* × 'TAM 105' hybrid and in the *A. ciliare* × 'Chinese Spring' hybrid. The hybrids were totally sterile.

Chromosome numbers in the *A. smithii* × *T. aestivum* 'Chinese Spring' hybrid varied from 29 to 42 in root tip cells (Fig. 1a) and from 26 to 36 in pollen mother cells (PMC's). The *A. smithii* × 'TAM 105' hybrid also showed range in chromosome variation, 34 to 36 in root tips and 30 to 38 in PMC's. In both these hybrids, of the 33 PMC's scored, 22 had fewer than 35 chromosomes (Table 1). It seems likely that *A. smithii* chromosomes are

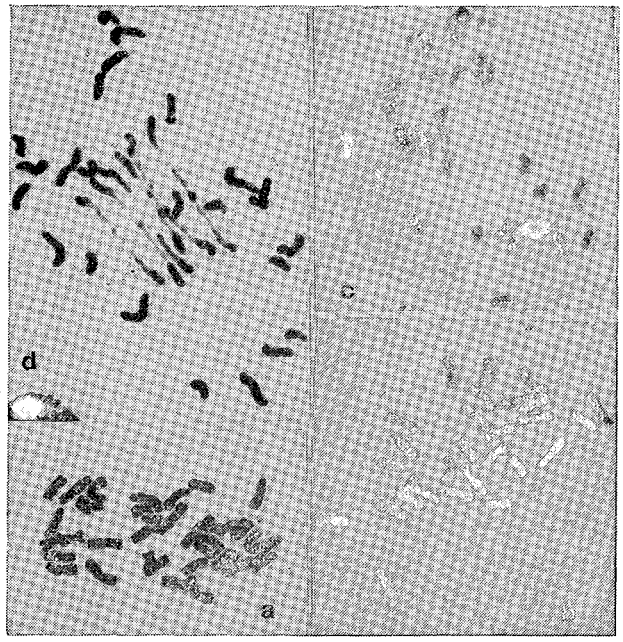

Fig. 1 a) Somatic cell of *A. smithii* × *T. aestivum* cv. 'Chinese Spring', 2n=35
b) Somatic cell of *A. smithii*, 2n=28
c) Pollen mother cell of *A. smithii* × *T. aestivum* cv. 'Chinese Spring', 1 rod II+28 I
d) Pollen mother cell of *A. ciliare* × *T. aestivum* cv. 'Chinese Spring', 6 rod II+23 I

Table 1. Chromosome pairing in *A. smithii* × *T. aestivum* 'Chinese Spring' and 'TAM 105' hybrids (Range values given in brackets).

Chromosome number	Number of cells	Univalents	Bivalents			Chiasma frequency
			Rod	Ring	Total	
26	1	26	0	0	0	0
30	11	27.33[24-30]	0.82[0-2]	0.18[0-2]	1.00[0-2]	1.2[0-4]
31	3	27.67[25-31]	1.67[0-3]	0	1.67[0-3]	1.7[0-3]
32	3	29.30[28-30]	1.00[0-2]	0.33[0-1]	1.33[0-2]	1.7[1-2]
34	4	32.00[30-34]	1.00[0-2]	0	1.00[0-2]	1.7[0-2]
35	9	33.11[24-35]	0.44[0-2]	0.11[0-1]	0.56[0-2]	0.7[0-2]
36	1	32	1	1	2	3
38	1	34	2	0	2	2

preferentially eliminated in these hybrids. Chromosomal instability was also present in the *A. smithii* parent used to produce these hybrids. *A. smithii* showed 2n=28 (Fig. 1b) with a range of 2n=24 to 38. There was very little pairing between *A. smithii* and wheat chromosomes in *A. smithii* × wheat hybrids (Table 1, Fig. 1c). Meiotic abnormalities, like anaphase bridges (in 12 of 30 cells), laggards (in 17 of 19 cells) and quartets with micronuclei (in 33 of 44 cells), were abundant.

A. ciliare × *T. aestivum* 'Chinese Spring' hybrid had the expected chromosome number of 35. The chromosome pairing was 4.25 II and 0.11 III per cell and an average chiasma frequency of 4.9 (Table 2, Fig. 1d). Meiotic abnormalities, such as laggards (in 12 of 15 cells) and quartets with micronuclei (in 15 of 33 cells), were frequent.

Table 2. Chromosome pairing in F_1 hybrid *A. ciliare* × *T. aestivum* 'Chinese Spring'.

	Univalents	Bivalents			Trivalents	Chiasma frequency	Number of cells
		Rod	Ring	Total			
Mean	26.18	3.84	0.41	4.25	0.11	4.9	130
Range	14-35	0-9	0-3	0-9	0-1	0-11	

Attempts to obtain amphiploids by colchicine treatment (0.05% for 6 hrs) so far have been unsuccessful. However, backcross-1 seedlings from both *A. smithii* × wheat and *A. ciliare* × wheat hybrids with wheat have been obtained. Eventually, we hope to obtain whent-*Agropyron* addition lines involving different *A. smithii* and *A. ciliare* chromosomes. Preliminary results indicate that *A. ciliare* is resistant to barley yellow dwarf virus (BYDV) and WSMV. Apart from cytogenetic analysis of *Agropyron* species genomes, obtaining BYDV and WSMV resistant germplasm is another major objective.

Literature Cited

ALONSO, L.C. and G. KIMBER 1980. A hybrid between diploid *Agropyron junceum* and *Triticum aestivum*. Cereal Res. Commun. **8**: 355–358.

BROWDER, L.E. 1980. A compendium of information about named genes for low reaction to *Puccinia recondita*. Crop Sci. **20**: 775–779.

CAUDERON, Y. 1979. Use of *Agropyron* species for wheat improvement. Proc. Conf. Broadening Genet. Base Crops, Wageningen, 1978. Pudoc, Wageningen 1979. pp. 175–186.

CAUDERON, Y., B. SAIGNE and M. DAUGE 1973. The resistance to wheat rusts of *Agropyron intermedium* and its use in wheat improvement. Proc. 4th Int. Wheat Genet. Symp., Univ. Missouri, Columbia. pp. 401–407.

DVOŘÁK, J. 1980. Homoeology between *Agropyron elongatum* chromosomes and *Triticum aestivum* chromosomes. Can. J. Genet. Cytol. **22**: 237–259.

KNOTT, D.R., J. DVOŘÁK and J.S. NANDA 1977. The transfer to wheat and homoeology of an *Agropyron elongatum* chromosome carrying resistance to stem rust. Can. J. Genet. Cytol. **19**: 75–79.

MURASHIGE, T. and F. SKOOG 1962. A revised medium for rapid growth and bioassay with tobacco tissue culture. Physiol. Plant. **15**: 473–497.

PIENAAR, R. de V., H.S. ROUX, E.C. VERMEULEN and M.G. LOMBARD 1977. An intergeneric hybrid

from the cross bread wheat (*Triticum aestivum* L. em. Thell. v. *aestivum* cv. Chinese Spring) × Coastal wheat grass (*Agropyron distichum* (Thumb.) Beauv.). Proc. 6th Congr. S. Agr. Genet. Soc. p. 76.

SEARS, E.R. 1977. Analysis of wheat – *Agropyron* recombinant chromosomes. Proc. 8th Eucarpia Congr., Madrid, Spain. pp. 63–72.

SMITH, E.L., A.M. SCHLEHUBER, H.C. YONG and L.H. EDWARDS 1968. Registration of Agent wheat. Crop Sci. **8**: 511–512.

Classification of tetraploid wheats based on differential response of their genomes to *Aegilops squarrosa* cytoplasm[1)]

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In 1934, LILIENFELD and KIHARA divided the tetraploid wheats into two groups based on genome analysis; Emmer group with the AABB genome constitution and Timopheevi group having the AAGG genome constitution. Since then, many workers have been discussing on the relationship between these two groups (KOSTOFF 1936; WAGENNAAR 1961, 1966; FELDMAN 1966), because of their genetical similarity and continuous variation. The continuous variations of the cytological and morphological characters between Emmer and Timopheevi groups are more remarkable in their wild species than in their cultivars (TANAKA & KAWAHARA 1976; TANAKA *et al.* 1978, 1979; TANAKA & SAKAMOTO 1979).

Recently, MAAN (1975) and KIHARA & OHTSUKA (1975) reported that the successive back-crossed lines of Emmer wheats to an induced autotetraploid *Aegilops squarrosa* had 29 chromosomes even after back-crossing more than ten times, and that many abortive seeds were produced in the back-crossed spikes as the result of lethality of zygotes which did not receive an extra chromosome from female gametes. This extra chromosome was indispensable for the compatible relation between the AB genome of Emmer wheats and the cytoplasm of *Ae. squarrosa* in zygote and in male gamete (OHTSUKA & KIHARA 1976; OHTSUKA 1980). This chromosome was identified to be homologous to *1D* chromosome of Dinkel wheat (OHTSUKA & KIHARA 1976; TSUJI & MURATA 1976; OHTSUKA 1980). On the other hand, two alloplasmic lines of Timopheevi wheats (*Triticum timopheevi* and *T. araraticum*) with the cytoplasm of *Ae. squarrosa* showed the chromosome configuration of 14_{II} in their PMC's and did not produce the abortive seeds in back-crosses (OHTSUKA 1980). OHTSUKA (1980) suggested that the AG genome of Timopheevi wheats had factor(s) which controlled the compatible relation between wheat genomes and the cytoplasm of *Ae. squarrosa*.

Present experiments attempt to use the differential response of AB and AG genomes to *Ae. squarrosa* cytoplasm for classifing the tetraploid wheats.

Materials and Methods

Thirty-nine strains of tetraploid wheat including cultivars and wild species were used as male parent in the crosses. Twenty-seven strains of the wild tetraploid wheat used were collected from northern highlands of Mesopotamia by Dr. TANAKA *et al.* in the

1) The present study was conducted as a part of the Cooperative Project on NC-Heterosis Breeding directed by Dr. H. Kihara, and financially supported in part by the Grant-in-Aid No. 1445 (1980) of Ministry of Agri. Forest. and Fish. of Japan

Botanical Expedition of Kyoto University to the Northern Highlands of Mesopotamia (BEM) in 1970. The other strains have been maintained in Kihara Institute for Biological Research. They were shown in the column of male parent of Table 1 and 2.

Three species of Emmer wheat (2n=28; AABB), *T. turgidum*, *T. durum*, and *T. dicoccoides* were successively back-crossed to the colchicine-induced autotetraploid line of *Ae. squarrosa* (2n=28; DDDD). During the back-crosses, Emmer wheat lines of *1D* monosomic-addition or 1D(1A) monosomic-substitution having *Ae. squarrosa* cytoplasm were obtained (OHTSUKA 1980). These lines were designated as (*squarrosa*) *T. turgidum* +*1D*, (*squarrosa*)*T. durum*+*1D*, and (*squarrosa*) *T. dicoccoides*+*1D*–*1A*, respectively, and used as female parents in the present experiment.

The crosses were conducted in 20 to 50 florets/spike, on two or more spikes/individual, with two or more individuals for each combination, in the field at Yokohama. The percentage of abortive seeds in seed-set was scored in the crosses. The tetraploid wheats used as pollen parents were classified as AB type in the response to the cytoplasm of *Ae. squarrosa* when many abortive seeds were produced in the crosses, and as AG type when the abortive seeds were not produced with some exceptional cases having 2–3% abortive seed production.

Table 1. Frequency of abortive seeds produced in the crosses between the alloplasmic Emmer wheat having *Ae. squarrosa* cytoplasm and various tetraploid wheat species

Male parent	Female parent		Type of response to *squarrosa* cytoplasm
	(*squarrosa*)-AABB+*1D*	(*squarrosa*)-AABB+*1D*−*1A*	
Cultivated Emmer wheat			
T. dicoccum var. *liguliforme*	61.7%	44.7%	AB
T. durum var. *reichenbachii*	85.2	38.1	AB
T. turgidum var. *nigro-barbatum*	75.2	—	AB
T. polonicum var. *vestitum*	62.2	54.5	AB
T. isphahanicum	78.6	61.9	AB
Wild emmer wheat (Palestine)			
T. dicoccoides var. *Aronshoni*	68.8	40.6	AB
T. dicoccoides var. *spontaneo-nigrum*	86.0	49.7	AB
Timopheevi wheat (Transcaucasia)			
T. timopheevi var. *typicum* (KU–107–1)*	0.0	0.0	AG
T. araraticum var. *thumaniani* (KU–196–2)*	0.8	0.0	AG
T. araraticum var. *thumaniani* (KU–1908A)*	0.0	—	AG
Transcaucasian endemic species			
T. palaeocolchicum var. *schwamilicum*	0.0	0.0	AG
T. persicum var. *stramineum*	—	0.0	AG

* Genetic stock number in Plant Germ-plasm Institute, Faculty of Agr., Kyoto Univ.

Table 2. Frequency of abortive seeds produced in the crosses between the alloplasmic Emmer wheat having *Ae. squarrosa* cytoplasm and wild tetraploid wheats collected from the northern highlands of Mesopotamia

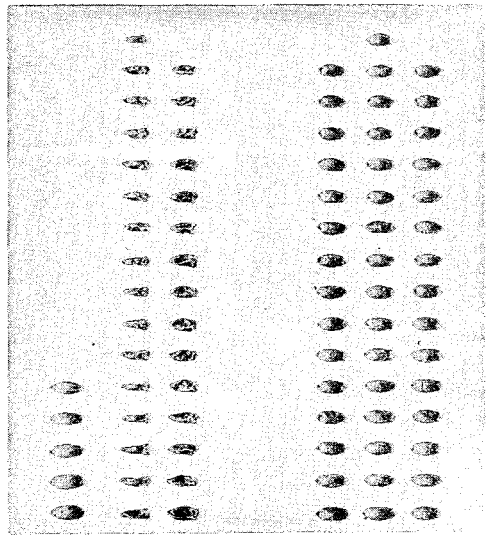
Male parent		Female parent		Type of response to *squarrosa* cytoplasm
stock No.* (KU)	genome**	(*squarrosa*)-AABB+*1D*	(*squarrosa*)-AABB+*1D*−*1A*	
8478	AAGG	0.0%	0.0%	AG
8539	AABB	71.4	35.8	AB
8544	AAGG	0.0	0.0	AG
8601	AAGG	0.0	0.0	AG
8685	AAGG	0.0	0.0	AG
8700	AAGG	0.0	0.0	AG
8719	AAGG	0.0	0.0	AG
8732	AAGG	0.0	0.0	AG
8736A	AABB	—	49.1	AB
8770	AAGG	0.0	2.6	AG
8784	AAGG	0.0	0.0	AG
8808	AABB	—	0.0	AG
8821A	AABB	—	0.0	AG
8821B	AAGG	0.0	0.0	AG
8821C	AABB	—	0.0	AG
8822	AAGG	0.0	0.0	AG
8866	AAGG	0.0	0.0	AG
8884	AAGG	—	0.0	AG
8912	AAGG	0.0	0.0	AG
8915A	AABB	—	31.5	AB
8919	AAGG	0.0	0.0	AG
8933	AAGG	0.0	0.0	AG
8937B	AABB	83.3	39.3	AB
8940	AAGG	0.0	0.0	AG
8942	AABB	89.7	33.3	AB
8944	AAGG	0.0	0.0	AG
8947	AAGG	0.0	0.0	AG

* Genetic stock number in Plant Germ-plasm Institute, Faculty of Agr., Kyoto Univ.
** After Dr. M. Tanaka and coworkers (1973, 1976, 1978, 1979, and personal communication)

Results and Discussion

The differential response between *T. turgidum* (AABB) and *T. timopheevi* (AAGG) was shown by the proportion of abortive seed production in the crosses to (*squarrosa*)AABB+*1D* lines as seen in Fig. 1. Fig. 1-a shows the crossed seeds obtained from one spike of (*squarrosa*) *T. turgidum*+*1D* line fertilized by the pollen of *T. turgidum*, in which five normal seeds (in left) had the genetic constitution of (*squarrosa*)AABB+*1D*, and were capable to germinate. The other thirty-one abortive seeds (in right) were zygotic lethal, and were presumed to have the genetic constitution of (*squarrosa*)AABB. In these abortive seeds, the seed coat that originated from tissue of female parent developed, while the embryo and the endosperm did not differenciate.

Fig. 1-b shows the crossed seeds which were obtained from one spike of the same plants as Fig. 1-a fertilized with pollen of *T. timopheevi*. Majority of female gamete of this (*squarrosa*) AABB+*1D* plant must not have *1D* chromosome, because the transmission rate



(a) (b)

Fig. 1. Differential responses of AB and AG genome to *Ae. squarrosa* cytoplasm
(a): Normal and abortive seeds production from the cross of (*squarrosa*)*T. turgidum*+*1D* × *T. turgidum* var. *nigro-barbatum*.
(b): Normal seed production from the cross of (*squaarrosa*)*T. turgidum*+*1D* × *T. timopheevi* var. *typicum*

of the additional *1D* chromosome through female gamete was 24.8% on average. In spite of this low transmission rate of *1D* chromosome through female gametes, all zygotes developed to normal seeds, and were able to germinate. This result and the observation of OHTSUKA (1980) suggest that genetic factor(s) of G genome for the genome compatibility with the cytoplasm of *Ae. squarrosa* is equivalent to that of *1D* chromosome.

The differential response of AB and AG genomes to *Ae. squarrosa* cytoplasm was also observed when (*squarrosa*)*T. dicoccoides*+*1D–1A* and (*squarrosa*)*T. durum*+*1D* were used as female parents in the crosses. The ratio of normal to abortive seeds on female plants of (*squarrosa*) *T. durum*+*1D* was similar to that on (*squarrosa*) *T. turgdium*+*1D*. However, this ratio on (*squarrosa*) *T. dicoccoides*+*1D–1A* line was different from that on either of *1D* monosomic-addition lines as shown in Table 1. This might be due to the difference in their transmission rates of *1D* chromosome through female gametes.

The results from the crosses of eleven species or strains of tetraploid wheat as pollen parents to the monosomic-addition lines and the monosomic-substitution line having *Ae. squarrosa* cytoplasm were showed in Table 1. Five species of Emmer wheat and two varieties of Palaestaine-*T. dicoccoides* were classified as AB type, because many abortive seeds were produced. Percentage of abortive seeds in the crossed seeds were 61.7%–86.0% and 38.1 %–61.9% when (*squarrosa*)AABB+*1D* and (*squarrosa*)AABB+*1D–1A* line were used as female parent, respectively. These figures reflected the frequency of the female gametes without *1D* chromosome.

Three strains of Trans·Caucasian-Timopheevi wheat, and two species of Trans·Caucasian-endemic species, *T. palaeocolchicum* MEN. (=*T. georgicum* DEK.) and *T. persicum* VAV. (=*T. carthlicum* NEVSKI) showed the AG type response, because abortive seeds were not or almost not produced in the crosses. However, *T. palaeoclchicum* and *T. persicum* have been classified as Emmer group with AABB genome.

The distribution of *T. palaeocolchicum* is restricted in West-Georgia of Trans·Caucasia and overlapped with that of *T. timopheevi*. Morphologically, *T. palaeocolchicum* is difficult to be distinguished from *T. macha* which is the Trans·Caucasian-endemic Dinkel wheat (JAKUBZINER 1958). *T. palaeocolchicum* appears as a bridging type between *T. timopheevi* and *T. dicoccum* (MAC KEY 1963). Therefore, even after the genome of this species was designated as AABB by MATSUMURA (1958), MAC KEY (1963) discussed the phylogenic relationship among *T. palaeocolchicum*, *T. macha* and *T. timopheevi*. The present results indicates the presence of the genetic factor(s) for genome compatibility to the cytoplasm of *Ae. squarrosa* in *T. palaeocolchicum*, and suggests that *T. palaeocolchicum* might receive the genetic factor(s) from *T. timopheevi* through the introgressive hybridization.

Another Trans·Caucasian-endemic species of *T. persicum* was also classified as AG type in the present experiment. The status of this species in wheat phylogeny has been discussed frequently after it was discovered. LILIENFELD & KIHARA (1934) included this species in Emmer group. VAVILOV (1926) suggested that *T. persicum* had originated from a pentaploid hybrid between Emmer and Dinkel wheats. MAC KEY (1963) and KUCKCUK (1979), in studies of the *Q* factor and resistance to mildew and rust respectively, supported the hypothesis of VAVILOV (1926). Taking together the previous works, there is a possibility that *T. persicum* obtained the genetic factor(s) for the genome compatibility to the cytoplasm of *Ae. squarrosa* through the translocation between *1D* chromosome and a chromosome of AB genome in the evolution of *T. persicum* (AABB) from pentaploid hybrid (AABBD).

TANAKA and co-workers collected many strains of wild tetraploid wheats in 'Botanical Expedition of Kyoto University to the Northern Highlands of Mesopotamia' (BEM) in 1970. These strains were classified as *T. dicoccoides* (AABB) and *T. araraticum* (AAGG) by the morphological and cytological studies (TANAKA & ISHII 1973; TANAKA & KAWAHARA 1976; TANAKA *et al.* 1978, 1979; TANAKA & SAKAMOTO 1979). Twenty-seven lines of these wild tetraploid wheats collected by BEM were used in the present experiment. These lines were classified as AB type or AG type depending on the differential response to the cytoplasm of *Ae. squarrosa*. The results were shown in Table 2 together with the classification of TANAKA and co-workers (1973, 1976, 1978, 1979, and personal communication).

The present classification of AB or AG types agrees with TANAKA's classification of AB or AG genomes in twenty-four strains. However, three strains of KU–8808,–8821 A, and –8821 C which were classified as AABB genome species by TANAKA and co-workers (1976, 1978, 1979) showed AG type response to the cytoplasm of *Ae. squarrosa*. TANAKA & KAWAHARA (1976), and TANAKA *et al.* (1978, 1979) classified KU–8821 A and –8821 C as *T. dicoccoides* (AABB) because these two lines showed morphological similarities and cytological

affinities with Palestaine-*T. dicoccoides*. However, they also observed high chromosome pairing in PMC's of F_1 hybrids between these two strains and Trans·Caucasian-*T. araraticum* (AAGG), although the F_1 hybrids were completely sterile. The present result also indicates that KU–8821 A and –8821 C are not typical AABB genome species. Since these two strains were collected from the northern highlands of Mesopotamia where *T. araratcium* distributed dominantly, TANAKA and co-workers (1978, 1979) suggested that *T. dicoccoides* and *T. araraticum* were differentiated from a common tetraploid ancestor in that region. The present results of KU–8821 A and –8821 C support the hypothesis of TANAKA and co-workers (1978, 1979).

The present classification of the tetraploid wheats by the response to *Ae. squarrosa* cytoplasm coincides with the classification of Emmer and Timopheevi groups in most strains. MAAN (1975) and TSUNEWAKI *et al.* (1976) indicated that the genetic differentiations of the cytoplasms among wheats and its relatives are corresponding to their genomic differentiations. The genetic factor(s) for the compatible relation between the genomes and cytoplasms may reflect the differentiation of the species, and the system used in the present experiments may be useful for the classification among related species of *Triticinae*.

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Literature Cited

FELDMAN, M. 1966. Can. J. Genet. Cytol. **8**: 144–151.
JAKUBZINER, M. M. 1958. Proc. 1st Int. Wheat Genet. Symp.: 207–220.
KIHARA, H. & I. OHTSUKA 1975. Japan. J. Genet. **50**: 470.
KOSTOFF, D. 1936. Z. Ind. Abst. Vererb. **72**: 115–118.
KUCKUCK, H. 1979. Wheat Inform. Serv. **50**: 1–5.
LILIENFELD, F. and H. KIHARA 1934. Cytologia **6**: 87–122.
MAAN, S.S. 1975. Prairie. Univ. North Dakota Press: 255–281.
MAC KEY, J. 1963. Proc. II Wheat Genet. Symp.: 237–276.
MATSUMURA, S., M. Nezu & Y. Koshiba 1958. Wheat Inform. Serv. **7**: 7–8.
OHTSUKA, I. 1980. Seiken Zihô No. 29: 18–39.
——— & H. KIHARA 1976. Japan. J. Genet. **51**: 433–434.
TANAKA, M. & H. ISHII 1973. Proc. 4th. Int. Wheat Genet. Symp.: 115–121.
——— & T. KAWAHARA 1976. Wheat Inform. Serv. **43**: 3–4.
———, T. KAWAHARA & J. SANO 1978. Proc. 5th Int. Wheat Genet. Symp. Vol. **1**: 73–80.
——— & S. SAKAMOTO 1979. Rep. Plant Germ-plasm Inst. Kyoto Univ. No. **4**: 12–17.
———, T. KAWAHARA & J. SANO 1979. Rep. Plant Germ-plasm Inst. Kyoto Univ. No. **4**: 1–11.
TSUJI, S. & M. MURATA 1976. Japan. J. Genet. **51**: 327–336.
TSUNEWAKI, K., Y. MUKAI, T.R. ENDO, S. Tsuji & M. Murata 1976. Japan. J. Genet. **51**: 175–191.
VAVILOV, N.I. 1926. – Inst. Bot. Appl. Amél. Pl., Leningrad, 248pp.
WAGENAAR, E.B. 1961. Can. J. Genet. Cytol. **3**: 47–60.
——— 1966. Evolution **20**: 150–164.

C-banding technique for wheat chromosomes

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C-banding techniques applicable to plant chromosomes have been reported in several crops; wheat (GILL & KIMBER 1974a), maize (HADLACZKY & KALMAN 1975), rye (SARMA & NATARAJAN 1973, DARVEY & GUSTAFSON 1975), barley (LINDE-LAURSEN 1975) and rice (KURATA & OMURA 1978). These techniques are mainly based on the Sumner's BSG (Barium/Saline/Giemsa) method (SUMNER 1972). However, the BSG technique has the technical difficulties in making well-separated chromosome preparations. GILL & KIMBER (1974a) added a emzyme maceration step to BSG method. NODA & KASHA (1978), using barley chromosomes, applied hot HCl treatment, which was the maceration step of the Feulgen stain procedure, and 0.07 N NaOH instead of $Ba(OH)_2$ solution. The present experiment was attempted to examine if the method of NODA & KASHA (1978) is applicable to wheat chromosomes.

Materials and Methods

Seeds of *Triticum monococcum* var. *vulgare* and *Aegilops speltoides* var. *typica* (KU-2), which were kindly provided by Dr. M. Tanaka, Plant Germ Plasm Institute, Kyoto University, were germinated and about 2 cm long root-tips were placed in ice-cold water for 20 hr to accumulate cells at metaphase stage. They were fixed in freshly prepared acetic-alcohol (1:3) and stored in a refrigerator until used.

Maceration: The root-tips were placed in 1N HCl at 60°C for 10 min. This step was important to differentiate C-bands. The root-tips were treated with 100x diluted pectinase solution (Pectinase Solution, 10000 units/104 ml, Sigma Co.) at 35°C for 15 min when further maceration was required.

Slide preparation: The meristematic part of root-tips was removed by a razor blade and placed on a clean slide in a drop of 45% acetic acid. The root-tip was squashed under a cover slip with no adhesive applied to slide or cover slip. The slides were examined under a phase contrast microscope to determine if cells with well-separated chromosomes were present. Cover slips were removed by dry ice method. The slides were dried at room temperature overnight.

C-banding: The slides were placed in 1N HCl solution at 60°C. The treatment time of hot 1N HCl was different depending on species used. It was five minutes for *T. monococcum* chromosomes and nine minutes for *Ae. speltoides* chromosomes. After the hot HCl treatment, the slides were rinsed in tap water and placed in 0.07N NaOH solution for 35 seconds. Chromosomes were stained in 60x diluted Giemsa solution (BDH Giemsa Staining Solution) or 5x diluted Leishman solution (BDH Leishman Staining Solution) in 1/15 M phosphate

buffer (pH 6.8). The slides were rinsed in tap water, air-dried and mounted in Canada balsam.

Results and Discussion

In the present experiment, ten minutes treatment of the first hot·HCl was required for chromosomes of *T. monococcum* and *Ae. speltodies* to differentiate C-bands. NODA and KASHA (1978), using barley chromosomes, reported that seven minutes of treatment of hot HCl in the maceration step was appropriate to produce C-bands. Also there is a difference in the time of the second hot HCl treatment between *T. monococcum* and *Ae. speltoides* chromosomes. It was five minutes for *T. monococcum* chromosomes and nine minutes for *Ae. speltoides* chromosomes. These differencies in the treatment time of hot HCl among different species may reflect chemical and/or structural variation in the constitutive heterochromatin.

In the present experiment, stain ability of Giemsa stain solution was compared with that of Leishman stain solution. Leishman solution gave better differential staining of heterochromatin and euchromatin than Giemsa solution as DARVEY and GUSTAFSON (1975) reported.

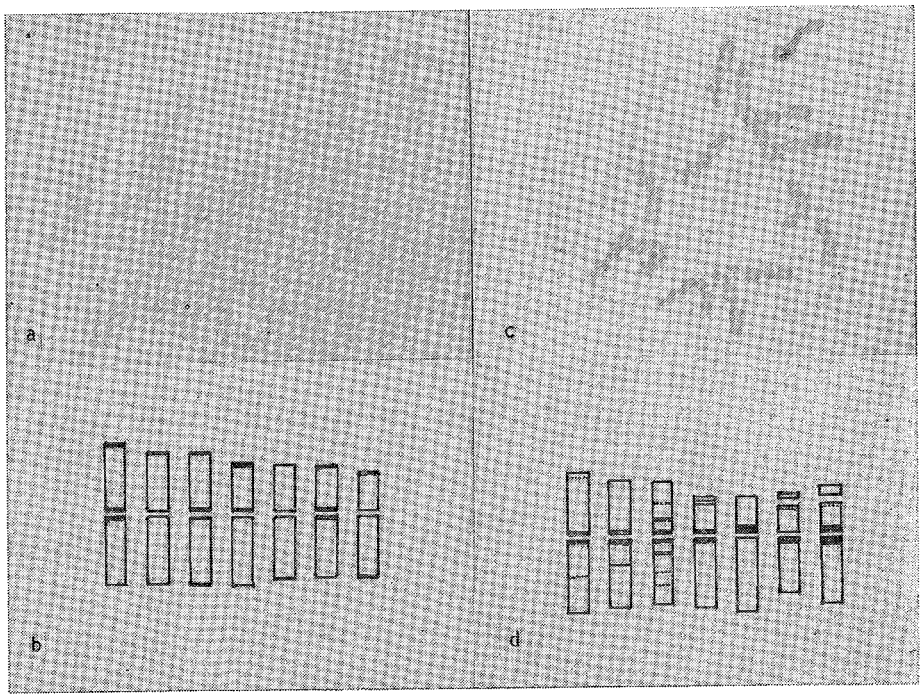

Fig. 1. (a) C-banded chromosomes of *T. monococcum* var. *vulgare*
(b) Idiogarm of *T. monococcum* var. *vulgare* chromosomes
(c) C-banded chromosomes of *Ae. speltoides* var. *typica*
(d) Idiogram of *Ae. speltoides* var. *typica* chromosomes

T. monococcum chromosomes showed a few C-bands (Fig. 1a & b). These C-bands located mainly in centromere and telomere regions of the chromosomes, and were allocated tentatively to each chromosomes. Characteristics of C-banding patterns of *T. monococcum* chromosomes was telomere bands in comparison with those of *Ae. speltoides* chromosomes (Fig. 1c & d). KOSTOFF (1938) stained *T. monococcom* chromosomes by gentian violet, and reported that *T. monococcum* chromosomes had heterochromatic segments at the distal ends. The present results agree with his observation although he did not detected centromere heterochromatin.

Ae. speltoides chromosomes had more C-bands in comparison with *T. monococcum* chromosomes, especially in intercalary regions of the chromosomes (Fig. 1c & d). GILL and KIMBER (1974B), and GUSTAFSON and KROLOW (1978) reported that C-band patterns of *T. aestivum* cv. Chinese Spring and *T. turgidum* cv. '20' chromosomes, respectively. GUSTAFSON and KROLOW (1978) indicated that C-banding patterns of A- and B- genomes chromosomes of *T. turgidum* cv. '20' were similar to those of *T. aestivum* cv. Chinese Spring. When the present results of C-banding patterns of *T. monococcum* and *Ae. speltoides* chromosomes are compared with the results of GILL and KIMBER (1974) and GUSTAFSON and KROLOW (1978), it appears that the banding patterns of several chromosomes of *T. monococcum* and *Ae. speltoides* are corresponding with those of A- and B- genomes chromosomes of *T. aestivum* cv. Chinese Spring and *T. turgidum* cv. '20'. Further studies of C-banding patterns of other *Aegilops* species chromosomes will provide informations on the evolution of wheat and origin of B genome.

Literature Cited

DARVEY, N.L., & J.P. GUSTAFSON 1975. Identification of rye chromosomes in wheat-rye addition lines and triticale by heterochromtin bands. Crop Sci. **15**: 239–243.

GILL, B.S. & G. KIMBER 1974a. Giemsa C-banding technique for cereal chromosomes. Cereal Res. Comm. **2**: 87–94.

GILL, B.S. and G. KIMBER 1974b. Giemsa C-banding and the evolution of wheat. Proc. Nat. Acad. Sci. **71**: 4086–4090.

GUSTAFSON, J.P. & K.D. KROLOW 1978. A tentative identification of chromosomes present in tetraploid triticale based on heterochromatic banding patterns. Can J. Genet. Cytol. **20**: 199–204.

HADLACZKY, Gy & L. KALMAN 1975. Descrimination of homologous chromosomes of maize with Giemsa staining. Heredity **35**: 371–374.

KOSTOFF, D. 1938. Heterochromatin, somatic "crossing over" and the interchange hypothesis between non-homologous chromosomes. Proc. Indian Acad. Sci. **8**: 11–44.

KURATA, N. & T. OMURA 1978. Karyotype analysis in rice. I. A new method for identifying all chromosomes pairs. Jap. J. Genet. **53**: 251–255.

LINDE-LAURSEN, I. 1975. Giemsa C-banding of chromosomes of "Emir" barley. Hereditas **81**: 285–289.

NODA, K. & K.J. KASHA 1978. A modified Giemsa C-banding technique for *Hordeum* species. Stain Tech. **53**: 155–162.

SARMA, N.P. and AT. NATARAJAN 1973. Identification of heterochromatic regions in the chromosomes of rye. Hereditas **73**: 233–238.

SUMNER, A.T. 1972. A simple technique for demonstrating centromeric heterochromatin. Exptl. Cell Res. **75**: 304–306.

II. Records

ABSTRACTS OF THE 16th WHEAT GENETICS SYMPOSIUM OF JAPAN

Kihara Institute for Biological Research
Oct. 26, 1980

Wheat Genetics Symposium of Japan has been held every two years to exchange ideas in the field of wheat genetics. In the 16th Symposium, Drs H. Kihara and S. Sakamoto were invited as guest speakers. Dr. Kihara spoke about "Nucleus-Cytoplasm Heterosis in Wheat". Dr. Sakamoto participated in "the survey of emmer wheat in Spain" supported by FAO in 1980. He talked about "Collection of Spelta Wheats in Spain".

Followings are the abstracts of papers presented in the general session of the 16th Wheat Genetics Symposium.

A strain of tetraploid wheat with homoeologous chromosome pairing derived from the *Aegilops speltoides-Triticum boeoticum* amphiploid

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In order to understand the relationship between the gene *Ph* (suppressor of homoeologous chromosome pairing) on chromosome 5B of polyploid wheats and the promoter(s) of homoeologous chromosome pairing present in *Aegilops speltoides*, transfer of the promoter(s) into tetraploid wheat was attempted as the first step.

For this purpose an F_2 plant with somatic chromosome number 2n=30 derived from the cross *Ae. speltoides-Triticum boeoticum* amphiploid × *T. dicoccum* (TANAKA *et al.* 1979, Rep. Pl. Germ-plasm Inst., Kyoto Univ. 4: 1–11) was backcrossed to *T. dicoccum*. Among the resulting B_1F_2, three plants, designated A, B and C, had 2n=27, 28 and 29, respectively. These plants were crossed by *Ae. sharonensis* (2n=14) whose genome is not homologous to those of the tetraploid wheat, and triploid hybrids were obtained. The occurrence of the homoeologous pairing in these hybrids was tested by examining the amount of chromosome pairing at MI of PMC's.

Homoeologous chromosome pairing was observed in all cross combinations between A, B, or C and *Ae. sharonensis*. Sixteen hybrid plants of B × *Ae. sharonensis* were classified into four pairing-level groups in terms of the mean number of chiasmata per cell, *i.e.* five plants in Level I (2.4–3.8 per cell), seven in Level II (4.7–6.4), three in Level III (7.5–8.4) and one in Level IV (11.1). These results suggest that the plants in Level I have the gene *Ph* but do not have the promoter, those in Level IV have the promoter but do not have *Ph*, and those in the Levels II or III have both or neither. From the frequency distribution of individuals in the four pairing-levels, it seems probable that the gene *Ph* and the promoter segregate independently. In contrast with this, out of 16 hybrid plants of C × *Ae. sharonensis*, 13 fell into Level III, which suggests that the plant C had a pair of homologous chromosomes causing homoeologous pairing. Then these chromosomes will show regular meiotic pairing and one of them may be transmitted to almost all the hybrid plants, causing homoeologous pairing. They may explain the hypertetraploid chromosome number (2n=29) of plant C.

The plants A, B, and C had one to two multivalents and several univalents per cell on the average. The multivalent formation is probably due to homoeologous pairing. The mean chiasma frequency per cell in plant C was higher than both A and B.

Intraspecific differentiations in chromosome structures of the wild tetraploid wheats

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Intraspecific differentiations in chromosome structures of the two wild tetraploid wheats, *Triticum dicoccoides* Körn. and *T. araraticum* Jakubz. were analyzed through hybridization experiments. In *T. dicoccoides*, three chromosome types differing with reciprocal translocations were reported by KAWAHARA and TANAKA (1978). While, seven chromosome types (A-G type) were found in *T. araraticum* (TANAKA *et al.* 1979). In the present study, a total of 190 strains, 40 *dicoccodies* strains and 150 *araraticum* strains, collected from the whole range of their distribution area were analyzed using strains belonging to those chromosome types as tester strains.

Two new chromosome types were recognized in *T. dicoccoides* in addition to the three reported earlier. Those five types were designated from the E1 to the E5 type, respectively. The E1 type was the most common and 80 per cent of the *dicoccoides* strains observed were of this type. Five strains belonged to the other four types. Three strains from Southern Turkey had chromosome structures other than E1, but their chromosome type remained unidentified. Types other than E1 were restricted to a single locality in Turkey or Palestine, respectively. The number of translocations between the E1 and the other four types was lower than that found among the types other than E1. Based on those observations, the E1 type was considered to have the original chromosome structures. The other four types seem to be differentiated from this original type by one reciprocal translocation.

Of the 150 *araraticum* strains observed, 90 belonged to the B type and seven strains were of the other six types. The remaining 53 strains had chromosome structures other than B, but their chromosome type did not be identified yet. The number of interchanges between the B and the other six types was lower than that found among the types other than B. The B type was found in all the regions where samples were collected. Those observations lead to the conclusions that the B type is the original chromosome structure of *T. araraticum* and that the other six types were derived from B type by one or two reciprocal translocations. Strains of the derived types were found in the whole distribution area. In Southeastern Turkey and northern tip of Iraq, most strains were of the original type. While, a population in Southern Turkey was marked by its very low proportion of the original type.

The present study revealed the wide geographical distribution of the original chromosome types and the sporadic occurence of the derived types in both *T. dicoccoides* and *T. araraticum*. This would indicate that the intraspecific differentiation in chromosome structures of the two wild tetraploid wheats occured after the extension of their distribution area from their birthplace, the eastern part of the Fertile Crescent, to the present regions showing disjunct patterns of distribution.

Reconsideration of the genome of *Aegilops mutica* Boiss. based on the chromosome pairing in interspecific and intergeneric hybrids

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The purpose of the present work is to estimate chromosome homology between the genome of *Ae. mutica* and those of other diploid *Aegilops* species and a diploid *Triticum* species. Eight diploid species, *Ae. longissima* (S^1S^1), *Ae. bicornis* (S^bS^b), *Ae. speltoides* (SS), *Ae. comosa* (MM), *Ae. uniaristata* (M^uM^u), *Ae. caudata* (CC), *Ae. umbellulata* (C^uC^u) and *T. boeoticum* (AA) were crossed by *Ae.*

mutica (MtMt) with or without B-chromosomes, and the pairing of A-chromosomes at MI of PMCs in these F_1 hybrids was observed.

A very high chromosome pairing with a quadrivalent or a trivalent, many bivalents and a few univalents was observed in hybrids without B-chromosomes (OB hybrids) of *Ae. longissima* × *Ae. mutica* and *Ae. comosa* × *Ae. mutica*. On the contrary, in almost all cells of hybrids with two B-chromosomes (2B hybrids) of these two cross combinations, only 14 univalents were characteristically observed. And the amount of chromosome pairing in hybrids with one B-chromosomes (1B hybrids) was intermediate between those of OB and 2B hybrids mentioned above. In *Ae. bicornis* × *Ae. mutica*, only OB hybrids were obtained. These hybrids formed almost 7 bivalents. Only OB hybrids were obtained from *T. boeoticum* × *Ae. mutica*. They showed a very high chromosome pairing and the formation of a ring-shaped quadrivalent was observed only in this cross combination. Hybrids without B-chromosomes of *Ae. uniaristata* × *Ae. mutica*, *Ae. caudata* × *Ae. mutica* and *Ae. umbellulata* × *Ae. mutica* formed much more univalents than OB hybrids of other cross combinations. Moreover, many multivalents were observed in the latter two combinations. And 2B hybrids of *Ae. caudata* × *Ae. mutica* formed 14 univalents in most of cells observed.

In contrast with the above-mentioned hybrid combinations, a very high chromosome pairing with 10.91 chiasmata per cell was observed in the 1B hybrid of *Ae. speltoides* × *Ae. mutica*. This mean chiasma frequency was the highest among all the 1B hybrids obtained in the present work. Moreover, the 2B hybrid of this cross combination showed an evidently high chromosome pairing with 5.14 chiasmata per cell, though some reduction of chromosome pairing compared with the 1B hybrid was observed. Not a few ring-shaped bivalents were observed but no PMCs with 14 univalents were found in this 2B hybrid.

It is well-known that the B-chromosomes of *Ae. mutica* suppress homoeologous chromosome pairing but not homologous one. Considering this fact and the present data, it is clear that the genome Mt is very closely related to S. Mt is also closely related to S^1, S^b, M and A, but not so closely related to M^u, C and C^u. At present, no data are available with the 2B hybrids in *Ae. bicornis* × *Ae. mutica* and *T. boeoticum* × *Ae. mutica*.

Transmission of D genome chromosome in alloplasmic pentaploid wheat

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In order to determine the cytoplasmic control of *Aegilops squarrosa* (2n=14; DD) on chromosome pairing, fertility and chromosome transmission, the AABBD pentaploid lines having *squarrosa* cytoplasm were produced from the crosses of alloplasmic Dinkel having *squarrosa* cytoplasm × Emmer, and alloplasmic Emmer × Dinkel. As the parental lines, *Triticum spelta* var. *duhamelianum* (6*x*), *T. vulgare* var. *erythrospermum* (6*x*), *T. polonicum* var. *vestitum* (4*x*), *T. durum* var. *reichenbachii* (4*x*) and their alloplasmic lines having *squarrosa* cytoplasm were used. Germination ability, chromosome configuration in PMC's, pollen fertility and selfed seed-set of the (*squarrosa*)-5*x* lines were compared with the respective control 5*x* lines having Dinkel or Emmer cytoplasm.

There was a significant reduction of germination rate of 5*x* hybrid seed in 4*x* (♀)×6*x* (♂) in comparison with that of 6*x* (♀)×4*x*(♂), but no difference was detected between 5*x* lines having *squarrosa* cytoplasm and those having Dinkel or Emmer cytoplasm. On the other hand, significant differences were observed in pollen fertility between (*squarrosa*)-5*x* and (wheat)–5*x*, 35.4% and 82.5% on average, respectively. Also, significant increase of trivalent formation in PMC's at MI was observed in three (*squarrosa*)–5*x* lines in comparison with respective controls.

Equation and certation crosses were conducted by crossing (*squarrosa*)-5*x* lines with *T. durum* or T.v.e. reciprocally. A part of data were shown in Table 1 and Fig. 1. The data on chromosome transmission indicate that no 14-chromosome gamete was transmited through male in (*squarrosa*)-5*x*, and significant reduction was observed in transmission rates of 14- and 15-chromosome gametes through female in equational crosses involving (*squarrosa*)-5*x* in comparison with those of the

Table 1. Observed frequencies in female gametes* of pentaploids with normal and *squarrosa* cytoplasms

Chromosome No. of female gamete	5*x*–3**	(*squarrosa*) 5*x*–3
14	11 (11.0%)	2 (3.3%)
15	18 (18.0)	3 (4.9)
16	16 (16.0)	12 (19.7)
17	22 (22.0)	17 (27.9)
18	15 (15.0)	13 (21.3)
19	14 (14.0)	8 (13.1)
20	3 (3.0)	4 (6.6)
21	1 (1.0)	2 (3.3)
Total	100 (100.0)	61 (100.0)

* Frequencies of female gametes were estimated from the chromosome numbers of B_1 plants in the equational type of crossings; 5*x*–3 × Tve and (*squarrosa*) 5*x*–3 × Tve

** 5*x*–3 indicates the pentaploid hybrid between Tve × *T. durum*

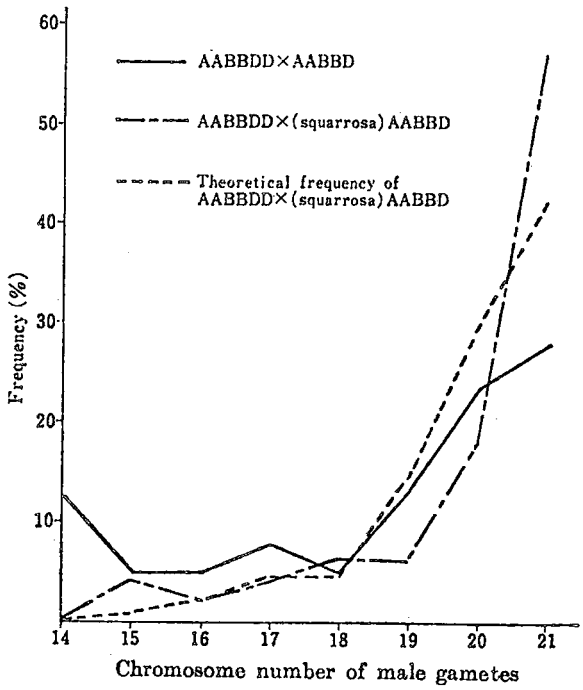

Fig. 1. Theoretical and observed frequency of male gametes with different chromosome number fertilized in certation crossing using Tve as female

control 5*x*. In certation crosses involving (*squarrosa*)-5*x*, the following formulas were introduced for calculating the chromosome transmission rates on the assumption that 1*D* chromosome is essential to avoid incompatibility between the nuclear genome and *squarrosa* cytoplasm (OHTSUKA 1980);

$$f_p = \frac{b}{\sum_{p=14}^{21} b} \times 100 \qquad b = \frac{{}_2C_{p-15}}{{}_7C_{p-13}} \times a_n$$

$(f_{14} = 0)$

p: Chromosome number of male gametes ranging 15–21

a_n: Observed number of male gametes in pentaploid hybrids with normal cytoplasm

The observed data fit well the theoretical ones as seen in Fig. 1.

Conclusionaly, the experiment showed that male gametic sterility and zygotic lethality were detected in the interaction between *squarrosa* cytoplasm and AB genome, and that the *squarrosa* cytoplasm affect the chromosome paring, fertility, and chromosome transmission to the progenies in $5x$ hybrid of wheat.

Genetic diversity of the cytoplasm among *Triticum* and *Aegilops* species having S and M group genomes, revealed by the fertility spectrum

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Cytoplasms of diploid species having the genomes of group S or M, and those of polyploid species which were assumed by Tsunewaki *et al.* (1980) to have received the cytoplasm from the donor of an S or M (or related) genome were transferred by repeated backcrosses from their carriers to 12 common wheats, i.e., *T. aestivum* var. *erythrospermum* (abbrev. Tve), strain P168 (P168), cv. Chinese Spring (CS), cv. Norin 26 (N26), strain Salmon (Slm), cv. Jones Fife (JF), cv. Selkirk (Sk) and cv. S–615 (S615), *T. sphaerococcum* (Sphr), *T. compactum* (Cmp), *T. spelta* (Splt) and *T. macha* (Mch). The 21 cytoplasms used were first introduced into common wheat at Kyoto University, Japan, North Dakota State University, USA (Dr. S.S. Maan), and the Institute for Wheat and Sunflower, Bulgaria (Dr. I. Panayotov), indicated by K, M and P, respectively. The fertility spectrum of these cytoplasms was examined against the 12 tester wheats, and the following results were obtained:

The genetic diversity of the cytoplasm among diploid species having the S group genomes was great; the cytoplasms of *Ae. speltoides*-K, *Ae. bicornis*-M and *Ae. longissima*-P gave high fertility to all testers, while the cytoplasms of *A. speltoides*-M, *Ae. aucheri*-P and *Ae. sharonensis*-K caused complete or almost complete sterility in the testers at different combinations. The fertility spectrum of the first 3 species was essentially the same as that of Emmer (*T. dicoccoides* var. *spontaneonigrum*-K and *T. dicoccum*-K) and common wheats, which supports our previous proposal (Tsunewaki *et al.* 1980) that the cytoplasms of those polyploid wheats were derived from either *Ae. speltoides*, *Ae. bicornis* or *Ae. longissima*. The fertility spectra of the cytoplasms of Timopheevi wheats (*T. dicoccoides* var. *nudiglumis*-K, *T. araraticum*-M, *T. timopheevi*-K and *T. zhukovskyi*-M) closely resembled each other; the fertility spectrum of the *Ae. aucheri*-P cytoplasm was most similar to these spectra. These findings suggest that their cytoplasms originated from some form of diploid species having S genomes. The *Ae. speltoides*-M had an intermediate cytoplasm between the *Ae. speltoides*-K and *Ae. aucheri*-P cytoplasms, giving high fertility to 5 testers, Tve, P168, CS, Splt and Mch. Although no diploid species with the S group genomes had a cytoplasm identical to those of *Ae. kotschyi*-K and *Ae. variabilis*-K, the *Ae. speltoides*-K, *Ae. bicornis*-M and *Ae. longissima*-P cytoplasms were the same as those cytoplasms in their response to 9 of the 12 testers.

Cytopalsms of *Ae. comosa*-K, *Ae. heldreichii*-P, *Ae. uniaristata*-M, and *Ae. mutica*-M and -P, all having the M group genomes were distinctly different with each other, although the *Ae. heldreichii*-P

and *Ae. mutica*-P cytoplasms caused complete or almost complete sterility to all testers, and the *Ae. uniaristata*-M and *Ae. mutica*-M cytoplasms gave high fertility to 8 to 10 testers. None of them showed a fertility spectrum identical to that of the *Ae. ovata*-K cytoplasm. However, the *Ae. mutica*-P cytoplasm gave some fertility to P168, CS and Mch, all of which were fully fertile when the cytoplasm was introduced from *Ae. ovata*-K. Thus, the *Ae. ovata*-K cytoplasm seems to be somewhat related to the *Ae. mutica*-P cytoplasm.

The present results on the fertility spectrum clearly demonstrate that; 1) great genetic diversity of the cytoplasm exists among diploid species having both the S and M group genomes, and 2) genetically similar cytoplasms to those of all polyploid wheats, *Ae. kotschyi-Ae. variabilis* complex, and *Ae. ovata* exist among these diploid species.

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Chromosomal locations of genes controlling the seed fertility of Chinese Spring against to the alien cytoplasms

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Ditelocentric lines of Chinese Spring (CS) developed by Dr. E.R. SEARS are being introduced into certain cytoplasms of *Aegilops* and *Secale* (SASAKI *et al.* 1977, 1978).

Table 1. Chromosomal locations of genes controlling the seed fertility of Chinese Spring (CS) with four alien cytoplasms

Cytoplasm	1BS	1BL	1DL	2AL	2BS	3AL	3BS	4Aβ	4BS	4DS	5DS	6BL	7AS	7BS	7BL
Original			F[1]	m[2] 50*	m[3] 42**										
Ae. ovata	*Rfo*2[4] 10**	—[5]	—		m 34**	m 45*	m 21**	—		m 41*	*Rfo*1 0**			m 39*	—
Ae. speltoides		—	—	m 31**	m 38**			m 13**		m 12**		m 45**	m 54**		*Rfs*1 0**
Ae. squarrosa			(*Rfq*)[6]		—					—	—				
Ae. variabilis	m 11**	m 32**	—		m 36**				m 54*						

1) F indicates one of 8 major genes for the seed fertility of CS against to the original "normal" cytoplasm. Each of these 8 major genes (or gene blocks) was located on the 8 chromosome arms, 1DL, 2AS, 2BL, 4Aα, 4BL, 5AL, 5BL and 5DL, of which 7 arms are not shown in the Table, because ditelocentrics missing each of these arms was sterile according to SEARS and SEARS (1978).

2) m indicates a modifier gene(s).

3) Numerals in the Table are means of at least 2 experiments and shown as the relative fertility to that of CS with respective cytoplasm on the row.

4) Only monotelodisomic F_1 plants were observed.

5) — indicates the line missing the arm was not produced yet.

6) In this case the fertility of ditelocentrics 1DL, and the results by OTSUKA and KIHARA (1976) and TSUJI and MURATA (1976) were considered.

*, **: Significantly lower than that of CS with respective cytoplasm at the 5% and 1% levels, respectively.

From the results obtained on the pollen and selfed seed fertilities of ditelocentrics with each of the *Ae. ovata*, *Ae. speltoides*, *Ae. squarrosa* and *Ae. variabilis* cytoplasms, it is induced that some major and a number of modifier genes locating on certain chromosome arms are controlling the fertility of CS against these alien cytoplasms. Those are summarized in Table 1.

Each of the following chromosome arms carry a major gene(s) for the fertility of CS: Chromosome arms 5DS and 1BS against to the cytoplasm of *Ae. ovata*; 7BL to that of *Ae. speltoides*; 1DL to that of *Ae. squarrosa*. A number of modifier genes for the fertility were also located: Five on each of the chromosome arms, 2BS, 3AL, 3BS, 4DS and 7BS, to the cytoplasm of *Ae. ovata*; six (2AL, 2BS, 4Aβ, 4DS, 6BL, 7AS) to that of *Ae. speltoides*; four (1BS, 1BL, 2BS, 4BS) to that of *Ae. variabilis*.

As seen in Table, the *Rfo*1 gene located on chromosome arm 5DS was active to the *Ae. ovata* cytoplasm but ineffective to the original, *Ae. speltoides* and *Ae. variabilis* cytoplasms whereas the *Rfs*1 gene on 7BL acting to the *Ae. speltoides* cytoplasm was not effective to the original, *Ae. squarrosa* and *Ae. variabilis* cytoplasms. Such a nucleo-cytoplasmic interaction on the gene expression for the fertility could be used for hybrid wheat breeding systems by searching an appropriate alien cytoplasm where *ms* mutants found in the original cytoplasm would become fertile. All gene symbols used here are tentative.

Characterization of mitochondrial DNAs in two alloplasmic and a normal line of common wheat by four restriction enzymes

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It is well known that some genetic factors are located in cytoplasm and transmitted uniparentally in most plants, involving wheat. Various cytoplasms in two genera *Triticum* and *Aegilops* were introduced into common wheat by repeated back crosses, and were classified into twelve cytoplasm types depending upon the nucleus-cytoplasm interaction (TSUNEWAKI *et al.* 1980). It is also well established that an appreciable amount of DNA is contained in various cytoplasmic organelles, such as the chloroplast and mitochondrium. Unique behaviors of the twelve cytoplasms against the common wheat nucleus might be due to the presence of unique DNAs in their organelles.

Now, we started studies on the diversity of organella DNAs using their cleavage by several restriction endonucleases. I herewith report some differences between the cleavage patterns of mitochondrial DNAs isolated from two alloplasmic and a normal line of common wheat.

Mitochondrial DNAs were isolated from etiolated seedlings (5 days old) of a normal and two alloplasmic lines of a common wheat, Chinese Spring (abbrev. CS). The alloplasmic lines used were (*kotschyi*)- and (*timopheevi*)-CS. Plasma types of normal CS, (*kotschyi*)-CS and (*timopheevi*)-CS were S, G and S^{V}, respectively. The DNAs isolated were digested by four restriction endonucleases, Eco RI, Bam HI, Hind III and Bst EII. The digests were separated by 1% agarose slab gel electophoresis.

The mitochondrial DNA of the normal line was digested by all four enzymes to form about 50 separable bands, whose molecular weights varied from ca. 15×10^6 to 0.1×10^6 dalton. The number of DNA bands observed was similar to that previously reported in wheat (Vedel *et al.* 1978) and maize (Pring and Levings 1978).

The electrophoretic patterns of the mitochondrial DNAs isolated from three different cytoplasms showed detectable differences from each other at least in the digest of one restriction enzyme. This result suggests that mitochondrial genomes have been differentiated clearly among the three different cytoplasms.

References

PRING, D.R. and C.S. LEVINGS III. 1978. Heterogeneity of maize cytoplasmic genomes among male-sterile cytoplasms. Genetics **89**: 121–136.

TSUNEWAKI, K., Y. MUKAI and T. Ryu ENDO. 1980. Genetic diversity of the cytoplasm. In "Genetic diversity of the cytoplasm in *Triticium* and *Aegilops*." Ed. K. Tsunewaki. Japan Soc. Promotion of Science.

VEDEL, F., F. QUETIER, F. DOSBA and G. DOUSSINAULT. 1978. Study of wheat phylogeny by Eco RI analysis of chloroplastic and mitochondrial DNAs. Plant Sci. Letters **13**: 97–102.

DNA synthesis and cell division in alloplasmic lines of common wheat, *Triticum aestivum* cv. Chinese Spring

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As the one way to elucidate the nuclear genome functions, especially for chromosomal DNA replication, in alien cytoplasms, the duration of the mitotic cycle and its component periods were measured in root meristem cells of alloplasmic lines of a common wheat, *Triticum aestivum* cv. Chinese Spring (2n=42, AABBDD).

After the seeds were germinated in the dark at 25°C for 36 hrs on wet filter papers in petri dishes, 20-min pulse labelling with 1 μCi/ml of [^{3}H-met] thymidine (40 Ci/mM) were performed. Rinsed seeds were further germinated and their root tips were collected at intervals of 2 h up to 48 h after the end of the ^{3}H-thymidine labelling. Slides were prepared autoradigoraphy using Kodak NTB 2 emulsion and they were exposed in dark boxes for 3 weeks at 4°C. Labelled mitotic cells were counted and the per cent was plotted against time after ^{3}H-thymidine labelling. The duration of the mitotic cycle (CT), and its parts: the presynthetic (G_1), DNA synthetic (S), postsynthetic (G_2) and mitotic (M) periods were estimated from the curves of per cent of labelled mitotic cells vs. hrs after labelling.

Any allocytoplasm tested in this study, *Ae. squarrosa*, *Ae. comosa* or *Ae. speltoides*, did not preferentially affect a given mitotic stage or the duration of the mitotic cycle of the original nuclear donor, *T. aestivum* cv. Chinese Spring. Their G_1, S, G_2+M/2 and CT were 0.8, 10.0, 2.6 and 14.0 h, respectively.

This work was supported in part by grants from the Ministry of Education, Science and Culture of Japan. The author is grateful to Dr. K. Tsunewaki for generous provision of alloplasmic lines of Chinese Spring.

Aegilops-Triticum hybridization in view of PNA hypothesis

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18, Hazamacho, Shugakuin, Sakyoku, Kyoto

In recent papers published in WIS, Nos. 49 and 50 (NISHIYAMA 1979a, b) abortive interspecific crosses in *Aegilops*, and *Triticum* were almost successfully interpreted by means of polar-nuclei activation (PNA) hypothesis.

The hypothesis is now applied to intergeneric hybridizations between *Aegilops* and *Triticum* which were previously made by many workers (Tables 1, 2). Eleven *Aegilops* and eight *Triticum* species are used in the present work. And their activating values, AV, (or response values, RV,) which are the same as those adopted in the previous interspecific crosses, are listed in the following:

Aegilops	Genome	AV	*Triticum*	Genome	AV
Ae. squarrosa L.	D	0.6	*T. monococcum* L.	A	0.9
Ae. uniaristata Vis.	M^u	0.7	*T. boeoticum* Boiss,	A	1.0
Ae. umbellulata Zhuk.	C^u	0.9	*T. timopheevi*	AG	1.5

Aegilops	Genome	AV	*Triticum*	Genome	AV
Ae. comosa Sibth. et SM.	M	1.1	*T. dicoccoides* Kön.	AB	1.7
Ae. caudata L.	C	1.4–(1.7)	*T. dicoccum* Schrank.	AB	1.7
Ae. speltoides Tausch.	S	1.5	*T. durum* Desf.	AB	1.75
Ae. ventricosa Tausch.	D M^v	1.6	*T. spelta* L.	ABD	2.9
Ae. ovata L.	C^u M^c	1.65	*T. aestivum* L. (T. vulgare Host.)	ABD	3.0
Ae. triaristata Willd, 4x	C^u M^t	2.1			
Ae. cylindrica Host.	C D	2.2			
Ae. triuncialis L.	C^u C	2.2			

The activation index of polar nuclei by a male nucleus in double fertilization is calculated from the formula AV/2RV(%) in each cross (Tables 1, 2). The index is closely related with development of hybrid seeds (Fig. 1). That is, in a total of 69 reciprocal crosses, AI less than 10 or 20%, 20–80%, 80–110%, and 110–250% generally indicate weakly developed seeds (W-type), barely viable; nearly normal seeds (N-type), viable; intermediate (P_s-type) between N- and E-type, partially viable; and empty, shrivelled seeds (E-type), inviable, respectively. However the hypothesis is hardly applicable to a few cases. In most of them crossing data were insufficient. Therefore, it has need to check them in detail.

Table 1 Reciprocal crosses between *Aegilops* and *Triticum* species, I.

Triticum AV / *Aegilops* RV	*monococcum* 0.9			*boeoticum* 1.0			*timopheevi* 1.5			*dicoccoides* 1.7		
	AI[1]	Germ.[2]	Auth.[3]	AI	Germ.	Auth.	AI	Germ.	Auth.	AI	Germ.	Auth.
squarrosa				83.3	0	Ka'33				—	—	—
0.6				30.0	62	Ka'33[4]				17.6	+	T'59
uniaristata				—	—	—						
0.7				35.0	+	S'41						
umbellulata				—	—	—	—	—	—			
0.9				45.0	+	S'41	30.0	+	MT'56			
comosa	—	—	—	45.5	50	Ka'33	68.2	61	LK'34			
1.1	61.1	+	S '41	55.0	+	S'41						
caudata				35.7	+	K'37	36.8	18	LK'34			
1.4–(1.7)												
speltoides	30.0	+	KL '32				50.0	61	LK'34			
1.5			P '30									
ventricosa	28.1	+	B '30	31.3	+	KL'32	46.9	13	LK'34	53.1	+	P'30
1.6												
ovata	27.3	+		30.3	+	KL'32	45.5	83	Ka'33	51.5	71	Ka'33
1.65							55.0	53	Ka'33	48.5	+	K'29
triaristata				23.8	0	Ka'33	105.0	0	Ka'33			
2.1				105.0	0	Ka'33						
cylindrica				22.7	+	KL'32	34.1	78	LK'34	38.6	+	P'30
2.2							73.3	0	Ka,33			
triuncialis							34.1	+	K '29	38.6	+	K'29

1) Activation index (%), 2) Seed germination (+ or %), 3) Author and year reported, 4) Lower line indicates the reciprocal cross.

Abbreviation: A Aase, B Bleier, BK Bochev and Kostova, DC Dosba and Cauderon, K Kihara, Ka Katayama, Kg Kagawa, KL Kihara and Lilienfeld, KT Kihara and Tanaka, LK Lilienfeld and Kihara, MT Matsumoto and Tabushi, P Percival, S Sears, T Tanaka.

Table 2 Reciprocal crosses between *Aegilops* and *Triticum* species, II.

Triticum AV / *Aegilops* RV	*dicoccum* 1.7			*durum* 1.75			*spelta* 2.9			*aestivum* 3.0		
	AI	Germ.	Auth.	AI	Germ.	Auth.	AI	Germ.	Auth.	AI	Germ.	Auth.
squarrosa 0.6	—	—	—	145.8	0	Ka'33				250.0	0	Ka'33
	17.6	+	T'59	17.1	23	Ka'33				10.0	0	Ka'33
comosa 1.1				79.5	45	Ka'33				136.3	0	Ka'33
caudata 1.4–(1.7)				62.5	23	Ka'33				107.1	22	Ka'33
speltoides 1.5										100.0	0	Ka'33
ventricosa 1.6				54.7	23	Ka'33				93.8	0	Ka'33
				45.7	83	Ka'33				26.7	50	DC'72
ovata 1.65	51.5	50	BK'73	53.0	91	BK'73	87.9	+	P'30	90.9	56	BK'73
				47.1	+	K'29				27.5	+	P'30
triaristata 2.1				41.7	75	Ka'33				71.4	40	Ka'33
				60.0	0	Ka'33				35.0	0	Ka'33
cylindrica 2.2	38.6	+	Kg'29	39.8	+	B'30	65.9	+	B'30	68.2	+	Kg'28
							37.9	+	A'30	36.7	+	Kg'28
triuncialis 2.2	38.8	+	K'29	39.8	77	BK'73	65.9	+	K'29	68.2	82	BK'73
							37.9	+	K'29	36.7	+	K'29

Explanation of the abbreviation and symbol is shown in Table 1.

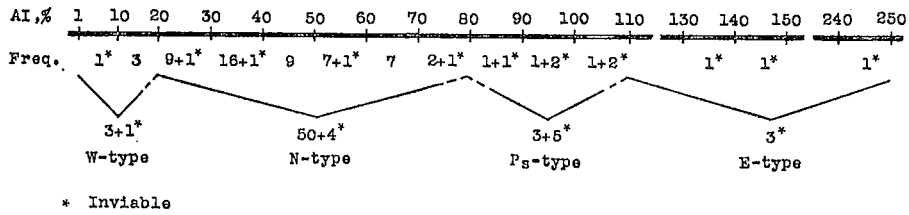

Fig. 1. *Aegilops-Triticum* cross-incompatibility system, especially indicating a relationship between the activation index series and development of hybrid seeds in 69 reciprocal crosses.

The efficient means of the nurse-seedling and planting

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The manual works in cultivation of crops and plants are troublesome and laborous. Recently, the mechanizations in agriculture have been carried out, but the agricultural machines are high prices and need expensive fuels, furthermore it is not effective but for large scale farming.

Any agricultural works are under various influences by the environments, stand and season, hour, weather, and can not be continuous in a stand. So the use of the agricultural machines is often uneconomical and brings so-called mechanization poverty to the farmer. The convenient

planting method by the use of strings or tapes was devised and the apparatuses for it were invented by the author.

It's principle for cultivation is as the followings. The several strings or tapes adhered the seeds or seedlings of plants with any adequate intervals on it can be easily streched out parallelly with any suitable spaces between the columns on the ground surface which have proper soil moisture and temperature. Then the seeds or seedlings shall soon strech out new roots into the soil and shall simultaneously sprout, stand up itself naturally. And it can grow vigorously in accordance with ecological and physiological theories for growth of plants body.

After development of the roots, the strong dural tapes can be taken away from the ground and plants, and it can be used again economically. This mean needs not heavy machine and is very convinient. There are able to mulch plastic films or straws between the parallel columns of the plants for preventing weeds and keeping soil moisture and ground temperature. So the agricultural products by this cultivation can be good yields by convenient practices economically. There are some secrets how the seeds or seedlings are adhered with adequate intervals on the strings or tapes conveniently and extended with adequate spaces on the ground surface.

It will be awarded by the training course for the memberships of "the Shokubyokai" (or "the Cultural Society") for the purpose of right progress of the proper practices in cultivation and agriculture.

The alien chromosome substitution line of *durum* wheat I. Substitution of the chromosome e_1 of *Agropyron elongatum* for the chromosome 1B of *Triticum durum* cv. Stewart

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Out of eighteen F_1 plants obtained from the cross between monosomic 1B of *Triticum durum* cv. Stewart and disomic addition of the chromosome e_1 of *Agropyron elongatum* (2n=14) to the *durum* wheat, 10 monosomic substitution e_1(1B) having 13''+2' at meiotic metaphase were selected. The alien monosomic substitution was indistinguishable from *durum* wheat in morphology, except for fertility. Seed-set in the monosomic substitution was approximately 0.57 per spilelet, whereas 1.1 in monosomic 1B and 2.4 in euploid *durum*.

Mochizuki (1962) reported that e_1 chromosome which was added to the chromosomes of *durum* wheat paired with wheat chromosomes in 2.62% of PMCs. In the present experiment, however, no pairing of the alien chromosome with any wheat chromosomes was found. Since it was ascertained that the substitution gametes, [(AB)–1B+e_1], more or less involved in fertilization for the production of F_1s from *durum* × monosomic substitution e_1(1B) and its reciprocal crosses, the plants having 28 chromosomes from self-pollinated monosomic substitution will be expected to include the disomic substitution e_1(1B), [(AABB)–1B1B+e_1e_1].

The number of root tip chromosomes and chromosome configurations at meiotic metaphase in 114 plants from self-pollinated monosomic substitution e_1(1B) were given in Table 1. In Table 1, 38 plants having 14'' at meiosis were similar in morphology, however, 8 of those expressed the different rate of fertility from the remaining 30 plants. Average seed-set in the formers was 0.47

Table 1. Somatic chromosome numbers and meiotic configuratios in 114 plants from self-pollinated monosomic substitution e_1(1B)

Somatic number Configuration	27 13''+1'	28 13''+2' 14''	29 14''+1'	30 15''
	18	39 38	19	0

per spikelet and 2.1 in the latters. This greater reduction of fertility suggest that alien chromosome substitution occurred in the former 8 plants. To verify the substitution occurred actually, each plant with 14" and low fertility was crossed with durum wheat. 58 F_1 plants from this cross had 13"+2' at meiosis without exception. This provided a evidence that a pair of *Agropyron* chromosomes indeed had replaced a pair of wheat chromosomes.

The alien chromosome substitution line of *durum* wheat II. Substitution of the chromsome e_7 of *Agropyron elongatum* for the chromosome 4A of *Triticum durum* cv. Stewart

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A monosomic substitution line of *Agropyron elongatum* chromosome e_7 designated by Mochizuki (1962) for the chromosome 4A of *Triticum durum* cv. Stewart was produced by crossing monosomic 4A of *durum* wheat [2n=27, (AABB)–4A] as a female with disomic addition line of e_7 chromosome [2n=30, (AABB)+e_7e_7] as a male. This monosomic substitution [2n=28, (AABB)–4A+e_7] is morphologically distinct different from normal *durum* wheat by observing number of tillers, thickness of culm and length of awn. There is, however, no significant difference in plant height between the substitution and the euploid *durum*. The plants of the monosomic substitution grew vigorously, but had reduced fertility. This is presumably due to the presence of two univalents at meiotic metaphase I (Table 1).

The transmission rate of chromosome e_7 through pollen grains was determined by crossing this monosomic substitution line as a male with *durum* wheat. From the number of the F_1 plants with 13"+2' at meiotic metaphase I, the male transmission rate of chromosome e_7 of *Agropyron* was 38.8%. Considering the facts that the competition takes place generally between the euploid and the substitution pollens in fertilization and that the nullisomic 4A pollens[(AB)–4A] do not participate in fertilization, this value implies that chromosome e_7 fairly well compensates for the lack of chromosome 4A.

The female transmission rate of the alien chromosome e_7 determined from the reciprocal cross was unexpected high as shown in Table 2.

The observed frequencies of 7 types of chromosome constitution derived from the selfed progeny of monosomic substitution e_7 (4A) were in agreement with the expected frequencies of those estimated from the data of male and female transmission rates of chromosome e_7.

Table 1. Morphological traits of normal Stewart *durum* and its monosomic substitution e_7 (4A)

	No. of tillers	Thickness of culm (mm)	Length of awn (mm)	Seeds/ spikelet	Plant height (cm)
normal *durum*	10.8	2.30	140	2.25	167.0
monosomic sub. e_7(4A)	15.2**	2.51**	124**	0.96**	174.4

** Significant at 1% level

Table 2. Female transmission rates of four types of gametes

Chromosome number	13	14		15
Chromosome constitution	[AB]–4A	[AB]	[AB]–4A+e_7	[AB]+e_7
Transmission rate	50.0%	10.7%	32.1%	7.1%

Among the plants having 27 chromosomes obtained from self-pollinated monosomic substitution e_7(4A), two types were recognizable from their awn length. One was almost the same as monosomic 4A and the other had shorter awn than that of monosomic 4A. The plants with short awn was mononullisomic e_7 (4A), [2n=27, (AABB)–4A4A+e_7]. In this case, single dose of chromosome e_7 of *Agropyron* sufficiently compensates for double doses of chromosome 4A.

According to cytological observation, the PMCs of monosomic substitution e_7(4A) had 2 univalents, but cells with 14'' were not observed at meiotic metaphase I. At diakinesis, however, majority of PMCs had 14'', suggesting homoeologous pairing between 4A and e_7. From the results, it seems that *Agropyron* chromosome e_7 is related to the homoeologous group 4, i.e., the e_7 chromosome might be considered as 4E.

Analysis of primary infection and host response of wheat to powdery mildew fungus

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The six-day old seedlings of 24 different strains of wheat and their hybrids were inoculated with the conidiospores of wheat powdery mildew fungus, *Erysiphe graminis* f. sp. *tritici*, race t_2. The number of germinated spores with the elongated secondary hypha (ESH) of more than 12.5 μ in length was counted with time until 32 hours after inoculation and expressed as ESH % (a ratio in percent of the spores with ESH to the spores with matured appressorium). Further examination of the fungus development and host response was made until 6 days after inoculation.

There observed four types of resistance in the host plants to fungal infection. The first was a type of strong protection to the invasion of the fungus into the host epidermal cell. The spores were able to germinate and form appressoria, but fail to form haustorial bodies. *Triticum dicoccoides* var. *spontaneonigrum* and a variety of *T. dicoccum* (No. 189) were recorded as this type. The second was a type exhibiting an abnormal development of haustorium. The spores were allowed to grow and form haustorial bodies, but their growth ceased and then the secondary hypha was not formed. *T. dicoccum* var. *atratum* (No. 122) was recorded as this type. The third was a type, in which the mycelial growth was inhibited within 2–3 days after inoculation. The spores having ESH were approximately 5%. *T. monococcum* var. *vulgare* and *T. paveocolchicum* var. *shwamilicum* were recorded as this type. The fourth was a type which formed a few pustules. The earlier process of infection looked like to that of the third type, however, some of the spores finally grew into maturation and a few pustules were visible at 6 days after inoculation. *T. aestivum* var. *pseudoingredieńs* was recorded as this type. The remaining 18 strains were fully susceptible, in which many pustules were observed on the leaves at 6 days after inoculation.

The genetical analysis on 21 F_2 hybrids and 6 F_2 populations suggested that two recessive genes were involved in the expression of the first type of resistance and a dominant gene in the second and third types of resistance, respectively.

III. Gene Symbols

Catalogue of gene symbols for wheat, 1981 supplement

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Reprints of the original Catalogue (1973) and some Annual Supplements are available. A consolidation of the first five Annual Supplements appeared in the Proceedings of the Fifth International Wheat Genetics Symposium, Volume 2, 1299–1309, but reprints are not yet available. Supplementary lists appear annually in Cereal Research Communications, Wheat Information Service and Annual Wheat Newsletter.

A completely revised Catalogue is to be prepared for the Sixth International Wheat Genetics Symposium in 1983. Revisions, additions, corrections and suggestions on the organisation and presentation of the Catalogue will be appreciated. Information for inclusion should be accompanied by appropriate references or by permission to cite.

Reduced Height

Rht7	(317AA)	v:	Bersee Mutant A (317AA); Bersee Mutant C (317AA).	2A(317AA)

Reaction to *Puccinia recondita*

Lr28				4BL(163)
Lr30	58	i:	Tc*6/Terenzio, R.L. 6065 (58).	4BL(58)
		v:	Terenzio (58).	
Lr13		v:	Timvera (163); Sabikei 12(163).	5BL(163)

Reaction to *Puccinia striiformis*

To conform with reference 153A the 1977 listings for *Yr9* and *Yr10* should be reversed, i.e. the gene in Aurora, Kavkaz, etc. should be designated *Yr9*, and that in Moro and P.I. 178383 should be *Yr10*.

Reaction to *Mayetiola destructor* (Say)

*H5**		v:	Abe (43A); Arthur 71 (43A).
		*H5	is temperature sensitive (266A).
H7 } *H8*	74A	Duplicate partially dominant factors	
		v:	Seneca (74A).

H9 (268A) v: Line 822–34(43A); 5A(43A) Elva C.I. 17714 *H10* (43A).

H10(196B) v: Line 812–24(43A); Line 817–2 5A(43A) (43A); Elva C.I. 17714 *H9* (43A).

H11 v: Line 916, a hexaploid derivative of P.I. 94587 with resistance to biotype D. Closely linked to *H5* (196B).

Genetic Linkages

4BL	*Lr30* – Centromere	2.9±1.3%	(58)
5A	*H3* – *H5*	15.5%	(268A)
	H9 – *H10*	36.0%	(43A)

References

43A. CARLSON, S.K., F.L. PATTERSON and R.L. GALLUN. 1981. Inheritance of resistance to hessian fly derived from *Triticum turgidum* L. Crop Sci. **18**, 1011–1014.

196B. PATTERSON, F.L. personal communication.

266A. SOSA, O. Jr. and J.E. FOSTER 1976. Temperature and the expression of resistance to the hessian fly. Environ. Entomol. **5**, 333–336.

268A. STEBBINS, N.B., F.L. PATTERSON and R.L. GALLUN 1980. Interrelationships among genetic factors in wheat for resistance to hessian fly. Crop Sci. (In press).

317AA. WORLAND, A.J., C.N. LAW and A. SHAKOOR 1980. The genetical analysis of an induced height mutant in wheat. Heredity **45**, 61–71.

IV. News

SIXTH INTERNATIONAL WHEAT GENETICS SYMPOSIUM

The International Organizing Committee

Dr. M.S. Swaminathan (Chairman), Dr. M. Feldman,
Dr. C.N. Law, Dr. S.S. Maan, Dr. R.A. McIntosh,
Dr. D. Mettin, Dr. G.T. Scarascia-Mugnozza and
Dr. M. Tanaka (Secretary)

The Organizing Committee of the Sixth International Wheat Genetics Symposium takes pleasure of inviting you to attend the Sixth International Wheat Genetics Symposium to be held in Kyoto, Japan, from November 28 to December 3, 1983.

The six-day Symposium will cover the following tentative topics:

1. Evolution and Speciation
2. Induced and Natural Variation
3. Alien Genetic Material
4. Genetic Analysis
5. Cytogenetics
6. Biochemical and Molecular Genetics
7. Ecological Genetics
8. Cytoplasmic Genetics
9. Quantitative Genetics
10. Tissue and Cell Culture
11. Breeding and Breeding Method
12. Disease and Pest Resistance
13. Wheat Quality
14. Triticale and Hybrid Wheat

There will be both invited papers and contributed papers. The poster demonstration may also be accepted.

Provisional Registration

Those who intend to participate in the Symposium are asked to return the Provisional Registration Form to the Local Coordinating Secretary of the Symposium not later than August 31, 1981.

Submitting this Provisional Registration Form does not imply any obligation, but ensures receiving the Second Circular which will contain detailed informations concerning registration procedures, submission of abstracts and full papers, hotel accommodation, ladies programmes, passports, visas, etc.

If any of your colleagues have not received this notice and will like to make a provisional registration, they may do so by writing directly to the Local Coordinating Secretary.

Expected Schedules before the Symposium

Sending of the First Circular	April, 1981
Closing date of the Provisional Registration	August 31, 1981
Sending of the Second Circular	August, 1982
Closing date of the registration (registration fee, proposal of contribution, abstract of paper, space of poster demonstration, hotel accommodation and ladies programmes)	December, 1982
Sending of the Third Circular	April, 1983
Closing date of manuscript for the proceedings	June, 1983

Weather and Dress

The weather in Kyoto during the period of the Symposium is cool and changeable, the temperature averaging 9°C (max. 14° – min. 4°C). Light winter dress is recommended.

Local Organizing Committee: M. Tanaka (Chairman), M. Muramatsu, K. Nishikawa, M. Okamoto, H. Ono, S. Sakamoto, M. Sasaki, H. Suemoto and K. Tsunewaki.

Please address all correspondence to:

Dr. S. Sakamoto
Local Coordinating Secretary
Sixth International Wheat Genetics Symposium
Plant Germ-plasm Institute
Faculty of Agriculture
Kyoto University
Mozume, Muko, Kyoto 617,
Japan

PROVISIONAL REGISTRATION FORM
SIXTH INTERNATIONAL WHEAT GENETICS SYMPOSIUM

1983

Kyoto, Japan

Please fill in this Form and return it not later than August 31, 1981.

Are you interested in attending the Symposium ?

Yes ☐ No ☐

Do you wish to contribute a paper ?

Yes ☐ No ☐

If so, to which session ?

Session no.

1st preference ☐

2nd preference ☐

3rd preference ☐

Do you wish to present a poster demonstration ?

Yes ☐ No ☐

Tentative title of your paper or poster demonstration:

_____

_____

Do you wish to purchase a copy of the Proceedings though not intending to attend the Symposium ?

Yes ☐ No ☐

(Please type or write in block letters.)

NAME: Mr.
Miss
Mrs. _____

(Family name) (First name) (Second name)

MAILING ADDRESS:

V. Editorial Remarks

Announcement for Future Issues

WIS No. 53 will be planned for publication in October, 1981. Manuscripts for this issue are most welcome and accepted any time, not later than September 30, 1981.

WIS is open to all contributions regarding methods, materials and stocks, ideas and research results related to genetics, breeding and cytology of *Triticum*, *Aegiolops*, *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 cm^2). Lists of stocks are exempted from this page limit. Authors receive 50 reprints of their contributions free of charge. Extra copies are printed by order at cost price. Communications regarding editorial matters should be addressed to:

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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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The Managing Editor

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