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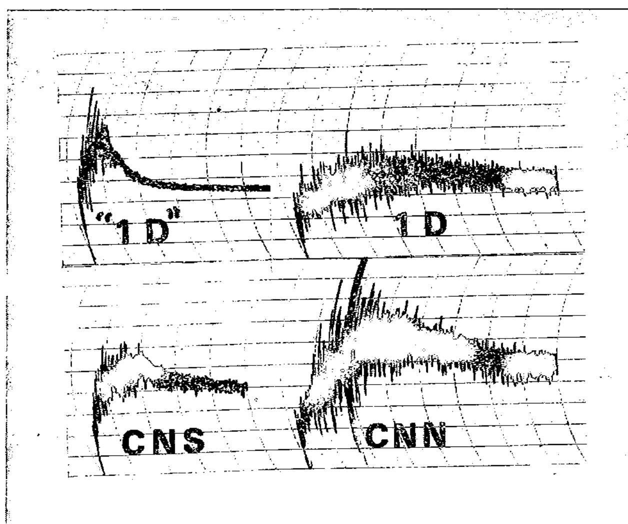

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CONTENTS

I. Research Notes: Page

Two new awn promoter genes in bread wheat..........J.W. GOUD and A.R. SADANANDA 1

Soft and hard grain mutants induced in common wheat variety K68 ....D. KUMAR 5

Chromosomal location of gene(s) for striata mutant in wheat .... M.P. JHA and K.M.P. SINGH 8

Quality tests of 'Cheyenne' wheat chromosome 1D substitution in 'Chinese Spring' .... R. MORRIS, P.J. MATTERN, J.W. SCHMIDT and V.A. JOHNSON 12

Mapping of the s and Ch 2 genes on chromosome 3D of common wheat .... T. KOBA and K. TSUNEWAKI 18

Variation and geographical distribution of esterase zymograms in *Aegilops squarrosa* .... Y. NAKAI 21

Preliminary report on shoot redifferentiation from wheat callus .... H. OGURA and T. SHIMADA 26

Identification of reciprocal translocation chromosome types in the emmer wheats I. *Triticum dicoccoides* KOERN. ....T. KAWAHARA and M. TANAKA 29

Formation of anaphase bridges with or without fragments in rye (*Secale cereale* L.) .... J.A. SÁIZ de OMEÑACA 32

Segregation in an F_2 population of *Aegilops longissima* × *Ae. bicornis* ....G. WAINES 36

Accessions collected by BMUK identified as *Aegilops searsii* FELDMAN & KISLEV .... G. WAINES 38

Aegilops searsii, a new species from Israel and Jordan ......M. FELDMAN and M. KISLEV 39

II. Genetic Stocks:

Mutants of *Triticum monococcum* ....M. SARVELLA and C.F. KONZAK 41

III. Gene Symbols:

Catalogue of gene symbols for wheat, 1977 supplement .................R.A. MCINTOSH 54

IV. Miscellaneus:

Recommendations of the Workshop on Rice Genetic Conservation, December 12–15, 1977, IRRI, Los Baños, Philippines 56

V. Editorial Remarks:

Announcement for future issues 61

Membership Fee 61

Acknowledgement 61

Coordinating Committee ....Cover iii

Explanation of the Figure on the Cover ....Cover iii

Nos. 45, 46 March, 1978

I. Research Notes

Two new awn promoter genes in bread wheat

J.V. GOUD and A.R. SADANANDA

Department of Agricultural Botany, College of Agriculture,
Dharwar, Karnataka, India

The most extensive genetic studies on inheritance of awning have been reported by WATKINS and ELLORTON (1940). They have shown that five major genes, viz., B_1 b_2^a, B_2, A, Hd determine awn development. The B genes act as awn inhibitors, A acts as awn promotors, b_1^a leads to half awned condition and Hd gives hooded condition. Different methods of aneuploid analysis generally have not only substantiated the above mentioned series, but have shown that additional chromosomes are also associated with some form of awn expression. WENZEL (1971) through monsomic analysis of cultivars Kurrachu and Norin-9 using Heines Koga-II monosomics, reported the presence of genes for awnedness on eight chromosomes of which 1B, 5D and 7A were reported for the first time, to carry genes responsible for this character. In the present communication presence of two new awn promotor genes has been indicated.

The material for the present investigation constituted the F_2 populations derived from crossing Red Bobs (Awnless), a Canadian cultivar and its monosomic lines for chromosomes 1A, 1B, 1D, 2D, 3D, 4A, 4D, 5A, 6A, 6D and 7B with Indian variety Sharbati Sonora (awned). The eleven monosomic F_2 populations were obtained by selfing the respective monosomic plants, selected after confirming the monosomic condition. The F_2 plants were classified into three categories based on awn characters, viz., i) awned – all spikelets having long awns, ii) hooded – only top spikelets having long awns and iii) awnless.

Awning in bread wheat is controlled by a series of awn promotor genes and three major epistatic genes Hd, B_1 and B_2. If any two or all the three of the genes were in homozygous condition, the plant would be awnless. If homozygous for only one dominant pair, it would be tipped or hooded and if all the three were in homozygous recessive state, it would give awned expression (WATKINS and ELLORTON 1940). Based on this hypothesis, the genotype of Red Bobs, an awnless variety was assumed to be AA Hd Hd b_1b_1 B_2B_2,

Table 1. Frequency of phenotypic segregation of different awn characters in monosomic and disomic F_2 populations

Population	Awnless	Hooded	Fully awned	Total	X^2 45:12:7
Mono 1A	94	35	28	157	10.33**
〃 1B	46	19	13	78	5.37
〃 1D	81	23	14	118	0.16
〃 2D	71	37	18	126	11.34**
〃 3D	131	49	27	207	4.98
〃 4A	85	38	18	141	7.52*
〃 4D	119	46	32	197	10.04**
〃 5A	75	28	10	113	3.88
〃 6A	123	24	23	170	3.09
〃 6D	87	14	18	119	5.13
〃 7B	121	41	25	187	2.85
Disomic	213	70	44	327	4.37

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

while that of awned variety, Sharbati Sonora as aahdhd $b_1b_1b_2b_2$ where 'a' is a multiple allelic series of awn promotors.

On these assumptions, the goodness of fit of frequencies of three phenotypic classes was tested against 45 awnless: 12 hooded: 7 awned ratio. The results obtained are presented in Table 1. A glance of the table would indicate significant deviations in the segregating pattern in monosomic populations for chromosomes 1A, 2D, 4D and 1% level and 4A as critical chromosome at 5% level.

Red Bobs, the monosomic parent, is an awnless variety, whereas the male parent Sharbati Sonora is a fully awned variety. The F_2 progenies of the eleven monosomic crosses and a disomic population segregated not only to the parental types but also to an array of intermediates. This segregation pattern showed a good fit for 45 awnless: 12 hooded: 7 awned ratio. This ratio was obtained after assuming the genotypes of Red Bobs, to be homozygous recessive to any of the two inhibitory genes i.e., either AA, HdHd, B_1B_1, b_2b_2 or AAHdHd b_1b_1. B_2B_2, whereas aahdhd $b_1b_1b_2b_2$ was assigned to Sharbait Sonora. The results indicated that the chromosomes, 1D, 2D, 4A and 4D as the critical chromosomes.

In bread wheat awning is controlled by a set of promotor genes and three major epistatic genes viz., Hd, B_1 and B_2. B_1 and B_2 act as awn inhibitors, while Hd confers hoodedness. If any two or three of them are present in homozygous condition, then the plant will be awnless. If the plant is homozygous for only one dominant pair, it will be tip awned or hooded and if all the three are homozygous recessives, the plants will be fully awned (WATKINS and ELLORTON 1940). The fully awned condition is due to the recessive allele 'a' which expresses only when it is inhibited by the partially epistatic Hd, B_1 or B_2 genes (HEYNE and LIVERS 1953). The awn promotor genes 'aa' have a multiple allelic series of 13 alleles from a_1 to a_{13}, reported to be situated on different chromosomes in different varieties (AUSEMUS *et al.*, 1968, BOZZINI and GIORGI 1971, BAIER *et al.*, 1974). The three major epiststic genes Hd, B_1 and B_2 have been assigned, beyond doubt to chromosomes 4B, 5A

and 6B respectively (SEARS 1953, SIKKA *et al.*, 1965, 1959 and AUSEMUS *et al.*, 1968).

Since the results of the present study do not show chromosome 5A as a critical line, it can be concluded that Red Bobs is homozygous recessive at B_1 locus i.e., b_1b_1. However, it is awneless, because of the presence of the other two genes 'Hd' and B_2 in dominant homozygous condition. The location of Hd and B_1 could not be confirmed because these two critical lines in 4B and 6B were not available for the present study. However, one thing is certain that there should be at least two major genes for awnless condition. Since the chromosome 5A in Red Bobs does not seem to possess B_1, the genotype of Red Bobs could be $AAHdHdb_1b_1B_2B_2$.

The critical chromosomes in the present study, viz., 1A, 2D, 4A and 4D do not possess any of the major genes but still they influence the character. Hence it is assumed that these critical chromosomes carry awn promotors. According to KUSPIRA and UNRAU (1957), either hd or b_2 or both together are epistatic to promotor genes and that Hd or B_2 or both together are non-epistatic or partially epistatic to these promoters. This is how the promotor genes influence awn condition.

There are reports that chromosomes 1A and 4A carry promotor genes designated as a_{12} and a_7 respectively (BAIER *et al.*, 1974). There are no reports of the presence of any promotor genes on chromosome 2D and 4D. However, in the present study, they are found to carry awn promotors on them. So the promotor genes present on chromosomes 2D and 4D are designated as a_{14} and a_{15} respectively.

In brief, based on the results of the present study for awn characters, the genotype of Red Bobs with respect to awnedness has been proposed as $AAHdHdb_1b_1B_2B_2$, whereas that of Sharbati Sonora as $aahdhdb_1b_1b_2b_2$. The 'a' gene of Sharbati Sonora has at least four multiple alleles a_7, a_{12}, a_{14} and a_{15} located on chromosomes 4A, 1A, 2D and 4D respectively.

Acknowledgement

The authors gratefully acknowledge the supply of complete set of monosomic lines of Red Bobs by Dr. Ruby I. LARSON of Department of Agriculture, Research Station, Lethbridge, Alberta, Canada.

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Soft and hard grain mutants induced in common wheat variety K68

Devender KUMAR

Department of Agricultural Chemistry, R.B.S. College,
Bichpuri, Agra 283105, U.P. India

Introduction

Concept of grain quality in wheat depends on the intended use and the consumers' preference. Hard wheats with strong gluten (AUSTIN and RAM 1971), a good balance of dough properties (SWANSON and JOHNSON 1943 and ABROL *et al.* 1972) and generally rich in protein are chiefly consumed for bread-making purposes. Soft wheats, on the other hand, with weak gluten and low in protein are consumed for biscuit and cake preparations. Thus, in view to meet the specific demands, it is imperative to develop soft and hard grain wheat varieties.

Protein content and the gluten strength are the chief components of baking quality. Besides, the attributes, viz., dough mixing, dough stability, mixing time etc. are also to be considered for this purpose. National-Swanson-Working-Dough-Mixer has widely been used to measure these properties (MEHDI *et al.* 1971 and ABROL *et al.* 1972). The present study was, therefore, initiated to classify thirteen homozygous mutants in soft and hard groups on the basis of their mixogram properties, total protein and gluten strength.

Material and Methods

Thirteen homozygous mutants were obstained from ^{60}Co gamma-ray treated seeds of common wheat variety K68. These mutants along with control were assessed for total protein and pelshenke value (gluten strength) in usual manner in M_4 generation. Mixogram characteristics were recorded from mixographs drawn by National-Swanson-Dough-Mixer in Cumming's Laboratory, IARI, New Delhi. Thirty gm of fine flour was used. Twenty one ml of water was added into mixing bowl and spring tension was set at 10. Measurements were recorded from the graphs according by SWANSON and JOHNSON (1943) and JOHNSON *et al.* (1943) as follow:

(1) Mixing time for dough development to maximum consistency (min).
(2) Height of the curve (cm)
(3) Rate of dough development (degrees)
(4) Rate of dough weakening (degrees)
(5) Dough development area (cm^2).

Results and Discussion

Data on mixogram characteristics total protein and pelshenke value of mutants

Table 1. Mixogram characteristics, total protein and pelshenke value of mutants and control in M_4 generation

Mutants and control	Mixing time for dough development (min)	Curve height (cm)	Angle of dough development	Angle of wea-kening	Dough development area (cm^2)	Total protein (%)	Pelshenke value (gluten strength) (min)
HUW-SDf1	1.6	4.4	45	85	9.0	14.1	62.5
〃 -SDf2	2.9	3.0	20	0	12.8	12.5	210.0
〃 -SDf9	1.4	3.6	30	10	7.5	12.0	50.5
〃 -SDf11	2.9	4.6	18	3	20.0	12.1	231.5
〃 -SDf16	2.0	4.7	33	2	12.8	13.2	232.0
〃 -SDf17	0.5	5.7	52	12	5.8	10.9	53.0
〃 -Df9	3.2	4.8	25	0	16.0	14.8	209.5
〃 -DfHp1	3.3	5.0	13	5	20.0	16.1	112.5
〃 -DfHp2	4.0	7.6	33	5	19.6	16.7	118.0
〃 -SStdHp1	5.0	6.2	15	4	24.5	17.1	266.0
〃 -SStd4	1.8	4.4	20	0	16.2	12.2	190.5
〃 -SStd8	0.5	5.4	40	10	7.4	11.0	37.5
〃 -SStd-Anl_1	1.8	3.9	23	3	13.7	11.9	220.5
Control	3.6	4.5	40	2	12.6	12.9	198.0

and control are presented in Table 1. The mutants HUW–SDf9, SDf17 and SStd8 were characterized as soft wheats. Which is evident from low pelshenke value (60 min), low mixing time (1.5 min), low dough development area and quite high angle of weakening (8°). WELSH and NORMAN (1972) have also reported that soft wheats possessed weak gluten and short mixing time. Such flour gives poor dough which tends to run out when fermentation proceeds and consequently may produce heavy loaves of unsatisfactory texture. Flour of these mutants is thus principally suited to biscuit and cake preparations.

High level of total protein (Ca 16%) of the mutants HUW-DfHp1 and 2 has probably led to increase in curve height and the mixing time; and thereby dough development was larger than the control (hard wheat). However, owing to medium pelshenke values (L 120 min) and the medium angle of weakening (5°), these mutants and HUW–SDf1 are characterized as medium hard or all purpose wheats. Flour of these mutants is basically suited to bread-mixing and secondary purposes, as well. VARUGHESE and SWAMINATHAN (1966) have also reported semi-hard mutants from soft wheat variety Larma Rojo.

The mutants HUW-SDf2, SDf4, SfD11, SDf16, Df9 and SStd-Anl_1 owing to strong gluten (120–160 min), high dough development area and quite low angle of weakening (3°) were considered as hard wheats. Flour of such mutants gives the dough of desirable elasticity and resistence, so that it produces when baked fine upstanding loaves of satisfactory volume and texture. Flour of these mutants is, therefore, best suited to bread-making purposes. KHROSTOVA (1969) also isolated some hard grain mutants after analysing 622 samples for pelshenke values. The mutant HUW-SStd-Hpl possessed considerably high protein (17%), and pelshenke value (266 min), Which contributed to highest dough development area (17.1^2 cm) probably through curve height and the angle of weakening. ABROL *et al.* (1972) have also noted that the varieties having high dough

development area showed high protein and pelshenke values. This mutant is thus regarded very hard and flour is suited to mix with the flour of soft wheats for blending purposes.

Gamm-ray treatment has thus proved much potent in inducing a wide range of variability for different dough properties, total protein and pelshenke values. Further, certain soft and hard grade mutants were induced from a hard wheat variety K68.

Summary

Thirteen ^{60}Co gamma-ray induced mutants in common wheat (*T. aestivum*) variety K68 were subjected to assessment for mixogram characteristics, total protein and pelshenke value in view to categorise them into soft and hard groups. Mutants reflected soft, medium hard, hard and very hard nature of grain flour as against hard nature of control K68.

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Chromosomal location of gene(s) for striata mutant in wheat

M.P. JHA and K.M.P. SINGH

Indian Agricultural Research Institute,
Regional Station, Pusa, Bihar, India

A classical example of spontaneous chlorophyll mutant is Neatby's virescent gene named after its discoverer (1933). Another natural viable mutant was isolated and described by HERMSEN (1966). SEARS (1957) located Neatby's virescent gene on chromosome 3B of wheat variety Chinese Spring and its near duplicate alleles on 3A and 3D. Interestingly the two recessive genes for Hermsen's virescence were also located on chromosomes 3A and 3B (SEARS and SEARS 1968). However, with the use of chemical mutagens all sorts of chlorophyll mutations are obtained which helped in further understanding of genetics of chlorophyll production. A hemizygous ineffective recessive gene for chlorina - 1 mutant isolated by Shama RAO and SEARS (1964) was located on chromosome 7A of Chinese Spring (SEARS and SEARS 1968). Another chlorina mutant, chlorina 448 was located on chromosome 7B by WASHINGTON (1969). JHA and SINGH (1977) located a dominant gene for another chlorina mutant isolated from the variety Sonora 64 in EMS treatment by VARUGHESE and SWAMINATHAN (1968) on chromosome 7D. The present study was undertaken to locate the chromosomes carrying the genes for yet another type of chlorophyll mutant designated as striata commonly observed after EMS treatment. The mutant used in this study was isolated from the variety Sonora 64 by VARUGHESE and SWAMINATHAN (1968) and is characterised by the longitudinal white (albino) stripe alternating with green area in the leaf right from the seedling stage. The white stripes are relatively more pronounced along the veins. This mutation affects the vigour of the plant although viable seeds are produced.

Materials and Methods

The materials comprised the striata mutant, the 21 monosomics of the wheat variety Pb C 591, their F_1, F_2 and F_3 progenies, the F_1's of striata × chlorina mutants (isolated from the same variety). The striata mutant used as male parent was crossed with cytologically identified monosomic plants of 21 monosomics and disomic Pb C 591. In addition, reciprocal crosses of striata with parent variety Sonora 64 and chlorina mutant were made. The F_1's were grown in 1970–71 at Indian Agricultural Research Institute, New Delhi in pots. Monosomic plants were identified cytologically in each of the 21 monosomic crosses for growing the F_2 generation. The F_2 populations from the monosomic as well as disomic crosses were grown at Regional Station, Pusa, Bihar in 1971–72. The F_3 progenies from randomely selected normal as well as striata plants in F_2 were grown in 1972–73. Segregation for striata types was recorded in the seedling stage before the plants were 45 days old.

Results

F_1 results: The F_1's of disomic Pb C 591 looked normal in leaf colouration in the seedling stage. There was no difference between the monosomic and disomic plants in F_1 in any of the monosomic lines. The reciprocal cross of striata mutant with the parent variety Sonora 64 and disomic Pb C 591 did not show any maternal effects. The striata mutant behaved like a recessive character to normal leaf in both the crosses. The F_1 of chlorina × striata mutants (from the same variety) were also normal in the seedling stage; the colour, however, changing to chlorina type when the seedlings were 45 days old and subsequently to golden yellow by the flowering time. No reciprocal difference was observed in this cross whether chlorina was used as male or female parent.

Table 1: Segregation in F_2 generation of Pb C 591×striata cross.

Material	Number of plants					
	Normal		Striata		Total	Chi-square (15:1)
	Observed	Expected	Observed	Expected		
Disomic cross	286	282.180	15	18.812	301	1.312
Mono 1A	295	286.875	11	10.125	306	3.681
1B	315	311.25	17	20.75	332	0.721
1D	594	598.125	48	39.875	638	0.454
2A	339	342.180	26	22.812	365	0.472
2B	168	169.680	13	11.312	181	0.265
2D	273	268.125	13	17.875	286	1.417
3A	309	383.430	100	25.562	409	231.168*
3B	325	321.555	18	21.437	343	0.587
3D	287	276.555	8	18.437	295	6.300
4A	325	326.250	23	21.750	348	0.075
4B	385	389.005	30	25.937	415	0.675
4D	195	191.250	9	12.750	204	1.107
5A	296	302.805	27	20.187	323	2.445
5B	336	334.680	21	22.312	357	0.117
5D	351	352.500	15	23.500	376	0.105
6A	329	330.000	23	25.000	352	0.048
6B	176	180.930	17	12.062	193	2.148
6D	188	189.375	14	12.625	202	0.158
7A	407	394.680	14	26.312	421	6.145
7B	331	335.625	27	22.375	358	1.018
7D	300	336.555	59	22.437	359	63.525*

F_2 results: In F_2 generation segregation in a ratio of 15 normal: 1 striata was observed in the disomic cross of Pb C 591 × striata (Table 1). The same pattern of segregation was observed in the F_2 of all the monosomic crosses except in mono 3A, 7A, 3D and 7D where significant deviations from disomic were noted. In mono 3A approximately 24% of the plants were striata. In mono 7D the striata plants comprised about 18% of the population. In mono 7A and 3D the deviations from the expected ratio of 15 normal: 1 striata were due to significantly reduced proportions of striata plants in the F_2 in

Table 2 Segregation in F_3 progenies of normal F_2 in Pb C 591×striata

	True Breeding normal	Seg. in 15n: 1s	Seg. in 3n: 1s	Total
Obs.	12	9	9	30
Exp.	14	8	8	30

Chi-square (7:4:4) for 2 df.=0.580

comparison to disomic cross whereas in mono 3A and 7D the deviation was due to higher proportion of striata plants.

F_3 results: The single F_3 progenies of striata plants selected in F_2 did not show any segregation. All the 5 progenies bred true. Single plant progenies of normal F_2 plants showed three types of behaviour, certain families were true breeding, while others showed segregation. In segregating families, two types of segregation were noted; those segregating in a ratio of 15 normal: 1 striata and those segregating in the ratio of 3 normal: 1 striata. This gave a good fit to expected ratio of 7 true breeding: 4 segregating in a ratio of 3 normal: 1 striata: 4 segregating in ratio of 15 normal: 1 striata as expected (Table 2).

Discussion

Lack of maternal effect in reciprocal crosses of striata mutant with the parent variety Sonora 64, disomic Pb C 591 and chlorina mutant indicates that striata is a true gene mutation. The results from different crosses further indicate that the character is recessive. The F_2 segregation in a ratio of 15 normal: 1 striata in the disomic as well as monosomic crosses shows that the character is conditioned by two pairs of recessive genes. On the basis of deviations from the expected ratio of 15 normal: 1 striata due to higher proportions of striata plants in the F_2 of 3A, one of the two complementary genes are located on chromosome 3A where the percentage of striata types was 24%, almost approaching the expected proportion. Among the remaining three monosomics showing deviation from the disomic cross, the increase in the proportion of striata types was observed in 7D although the frequency of striata types was less than expected. In the remaining two monosomics, 7A and 3D, the deviation from disomic cross was due to reduction in the proportion of striata which is not expected if one of the complementary gene is assumed to be carried by them. In case of critical monosomic line approximately 96% of the plants will have one of the two complementary genes either in one or two doses. Thus the expected segregation will be in the ratio of 3:1 due to segregation for another gene only in 96% of the population. Thus the other recessive complementary gene is located on chromosome 7D. Limited data of F_3 generation confirm the assumption of two recessive genes controlling this character.

Summary

Identification of chromosomes carrying genes for striata mutant in wheat was under-,

taken through conventional monosomic method using Pb C 591 as female parent. The mutant was found to be controlled by two pairs of recessive complementary genes which were located on chromosomes 3A and 7D.

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Quality tests of 'Cheyenne' wheat chromosome 1D substitution in 'Chinese Spring'[1)]

R. Morris, P.J. Mattern, J.W. Schmidt and V.A. Johnson

North Central Region, U.S. Department of Agriculture,
Lincoln, Nebraska, U.S.A.

The dough-mixing and baking characteristics of individual 'Cheyenne' chromosome substitutions in 'Chinese Spring' background were reproted by Morris *et al.* (1966, 1968). The performance of the so-called "1D" substitution line was inferior to that of the low-quality parent, Chinese Spring. However, identity tests indicated that the Cheyenne chromosome substituted in this line was not 1D, so a new line was developed. We now report the milling and dough-mixing performance of the new 1D line.

Materials and Methods

The strong-gluten Cheyenne cultivar (C.I. 8885) was available in the wheat breeding program at the Nebraska Agricultural Experiment Station. The Chinese Spring aneuploid stocks were obtained from E.R. Sears, ARS, USDA, Columbia, Missouri.

After the initial cross between Chinese Spring 1D monosomics and Cheyenne, six backcrosses were made to Chinese Spring monotelosomic stocks. An identity test was made at the time of the sixth backcross using a Chinese Spring 1D ditelosomic stock. Five disomic sublines of the 1D substitution were developed. All were closely related because they were derived from the same series of crosses. Sublines 77 through 80 came from one disomic plant recovered after the sixth backcross and subline 76 came from a sister disomic plant.

The five 1D sublines were grown in a greenhouse soil bed in 1972 together with the parental cultivars, Cheyenne and Chinese Spring. Each subline or cultivar consisted of two rows, 20 plants per row, with 6,5 cm (2,5 in) between plants and 23 cm (9 in) between rows. Plants of Cheyenne, which had been vernalized in the field through the winter, were transplanted to the greenhouse on March 21, 1972. One row (20 plants) of the original line developed for 1D (in this paper referred to as "1D" because of uncertainty regarding the identity of the substituted chromosome) was included to compare its performance with that of the new line. The original line had four backcrosses to Chinese Spring.

Seeds harvested from the greenhouse planting were used for milling and dough-mixing tests. Seed samples were tempered to 12.5% moisture content and milled on the C.W.

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Brabender Quadrumat "Jr." Experimental Mill[2] with the sieve removed. The milled stock was separated on an auxiliary sieve shaker with 40, 60, and 100 mesh sieves.

AACC Method 50–10 (1962) was used to determine particle size distribution of the 100 mesh flour. Mass median particle diameters (MMD) were calculated. The MMD is the point at which 50% of the flour by weight is finer and 50% coarser.

One-gram samples were analyzed for nitrogen by AACC method 46–12 (1962) and protein percentages were calculated from percent N×5.73.

Flour from the 60 and 100 mesh sieves was composited for mixogram tests. Dough-mixing curves were recorded at 25°C with the Swanson-Working Mixograph[2] using 30g of flour, with absorptions adjusted to optimum for bread dough.

Results and Discussion

The identity test with the Cinese Spring 1D ditelosomic stock indicated that the Cheyenne chromosome substituted in the new line was 1D.

Data for kernel and flour characteristics of the new Cheyenne 1D substitution in Chinese Spring, the parental cultivars, and the "1D" substitution line appear in Table 1, and mixing curves in Figure 1.

Kernel length and weight were somewhat greater for Cheyenne than for Chinese Spring, but kernel width was similar in the two cultivars. The kernel weights and lengths of the 1D sublines were more like Chinese Spring than Cheyenne. The "1D" line matured about 1 month later than the other materials, and its kernel weight and width were reduced

Table 1. Kernel and flour characteristics of Cheyenne 1D substitution line in Chinese Spring back ground compared with the parental cultivars and a "1D" line of doubtful substitution

Line	Total yield† (g)	1000-kernel weight (g)	25-kernel size		Flour yield (%)	MMD (μ)	% Protein‡		Dough mixing (mixograph)	
			Av. length (mm)	Av. width (mm)			Kernel	Flour	Time (min)	Tolerance
Cheyenne	156	38.90	169	76	67.4	59.5	16.22	15.20	3	4−
Chinese Spring	254	35.68	151	78	60.7	43.0	16.10	14.15	1 1/2	1
1D(CS⁷×Cnn)§										
Subline 76	200	32.62	148	78	62.9	50.0	13.55	12.45	2 2/3	3+
〃 77	215	32.94	149	79	63.0	46.0	14.15	12.70	3 2/3	3+
〃 78	200	33.94	149	78	61.7	36.5	14.40	12.60	3 2/3	3
〃 79	216	34.24	148	80	61.4	23.0	13.50	11.80	4	3+
〃 80	297	35.75	151	82	61.8	51.5	13.95	12.05	3 2/3	3+
"1D"(CS⁵×Cnn)	35	24.17	149	69	56.9	44.5	19.65	-	2/3	0

† Based on 40 plants except for the "1D" line which had 20 plants.
‡ N×5.73; data based on 14% moisture.
§ 6 backcrosses after the initial cross to Chinese Spring.

2) Mention of trade products does not imply that they are endorsed or recommended by the U.S. Department of Agriculture over other products not mentioned.

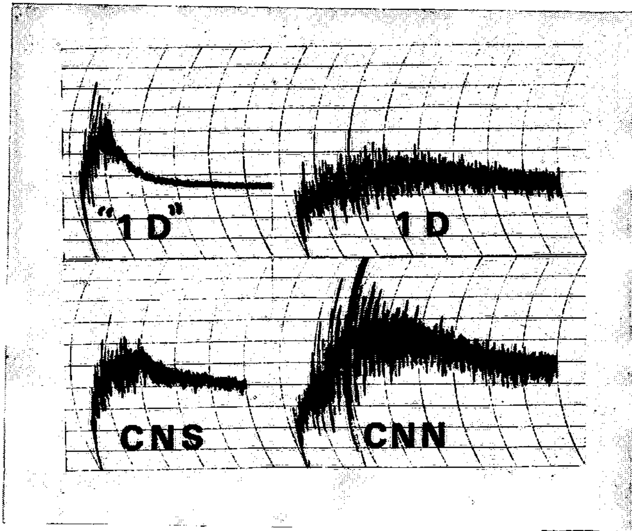

Figure 1. Mixing curves of the original "1D" chromosome substitution line with 4 backcrosses to Chinese Spring (top left), the new 1D line with 6 backcrosses (top right), Chinese Spring (CNS, lower left), and Cheyenne (CNN, lower right).

because of high temperatures in the greenhouse during early summer. The 1D sublines tended to be closer to Chinese Spring than to Cheyenne in flour yield and MMD values, and lower than either parent in percent protein. However, they resembled Cheyenne in having the desirable properties of increased mixing time and tolerance. The "1D" line, on the other hand, was inferior to Chinese Spring in mixing time and tolerance, as it had been in previous tests (Morris *et al.* 1966).

The effects of wheat chromosome 1D on kernel protein and various flour characters have been investigated in several studies. The monosomic state of 1D gave higher kernel protein values than the disomic state in 'Kharkof MC22' (Welsh and Watson 1965) and in Chinese Spring (Jha *et al.* 1971). Jha *et al.* also found that, in crosses between Chinese Spring 1D monosomics and 'Sonora-64' or 'Lerma Rojo', the F_1 monosomics and their F_2 and F_3 progenies all gave higher protein values than disomic counterparts. Yields and kernel weights were not reported in either of those studies, so it is not known whether increased protein values were associated with reduced yields or with lighter seeds. Joppa *et al.* (1975) added a pair of Chinese Spring 1D chromosomes to the tetraploid durum cultivar 'Langdon'. The semolina protein content was 2 to 3% higher in the 1D disomic addition line than in durum cultivars, including Langdon, but the grain yield was lower. The authors thought that the increased protein content might be associated with decreased yield.

Each of the Cheyenne 1D substitution sublines in the present study had lower kernel and flour-protein values than either parent. Yields of the sublines, except for Subline 80, were between those of the parental cultivars, and 1000-kernel weights were equal to or lower

than that of Chinese Spring, which had lighter kernels than Cheyenne. The "1D" line had a higher protein value than either parent, but its yield and kernel weight were markedly reduced by high temperatures.

Several studies have been made to determine the effect of chromosome 1D from different sources on flour characters. WELSH and HEHN (1964) considered 1D to be "extremely important in the determination of bread flour characteristics". They found that the monosomic state of 1D resulted in a deterioration of mixing quality and gas-retention capacity both in the weak-quality parent, Kharkof MC22, and in F_2 progenies of F_1 monosomic plants with 1D derived from the strong-quality parent,' 'Itana'. They concluded that genes carried by 1D could not function effectively in 3n–2 endosperm, which would occur in about 75% of the seeds produced by monosomic plants.

WELSH *et al.* (1968) tested 'Hope' 1D and 'Timstein' 1D substitutions in Chinese Spring for five flour quality characters. None of the characters in the Hope 1D line were significantly different from those in Chinese Spring. The Timstein 1D line had significant negative deviations for loaf volume and valorimeter (a measure of dough strength). On the other hand, our tests of the Cheyenne 1D substitution in Chinese Spring indicated a positive effect of 1D on dough characters. Thus, different sources of 1D can give a range of effects in the genetic bakcground of Chinese Spring.

The addition of two doses of chromosome 1D to durum wheat produced dough with strong mixing properties which were lacking in a sister line without 1D and in the durum cultivars (JOPPA *et al.* 1975).

KALTSIKES *et al.* (1968) identified a segment of the long arm of 'Prelude' 1D which conditioned the good bread-making quality of this cultivar. However, MAYSTRENKO *et al.* (1973a) concluded that, in Chinese Spring, genes enhancing flour quality were present on the short arm of 1D because its absence gave very poor physical properties of the dough.

In view of the important role of chromosome 1D in determining the flour characteristics of hexaploid wheats, it is not surprising that this chromosome has considerable genetic control over the aspects of protein composition that influence bread quality, namely, gluten and its principal components, gliadin and glutenin. 1D contributes genes for gluten quality (MAYSTRENKO *et al.* 1973b, SASAKI *et al.* 1973) and for components of glutenin (JOPPA *et al.* 1975) and gliadin (SOLARI and FAVRET 1970, KONAREV *et al.* 1972, WRIGLEY and SHEPHERD 1973, KASARDA *et al.* 1974). The short arm influences gluten composition (BOYD and LEE 1967, KHRABROVA *et al.* 1973) and gliadin components (SHEPHERD 1968). The long arm controls certain glutenin subunits (ORTH and BUSHUK 1974, BIETZ *et al.* 1975). Most of the studies on protein composition have tested chromosome 1D of Chinese Spring, which has poor dough-handling and baking properties. Chromosome 1D from some of the best bread cultivars should be tested in similar studies.

Identity tests of the "1D' line in the monosomic state indicated that 1A instead of 1D was the substituted chromosome. However, the disomic state of this line had much poorer mixing and loaf characteristics than the substitution line developed for 1A. Probably

a univalent shift occurred from 1D to 1A during the development of the "1D" line. In that case, both 1A in monosomic state and 1D in disomic state could have a mixture of genes from Cheyenne and Chinese Spring. The inferior performance of the line could be due to interactions of genes from the two parental cultivars or to unfavorable cytogenetic conditions of 1A or 1D. One exmaple of the latter might be a deficiency for a segment of 1D that contains essential genes for flour quality.

Summary

The 1D chromosome pair from the strong-gluten wheat cultivar Cheyenne was substituted for the homologous chromosome pair in the weak-gluten cultivar Chinese Spring by a series of six backcrosses after the initial cross. Dough-mixing tests demonstrated that the increased mixing time and tolerance of Cheyenne, in contrast to Chinese Spring, were controlled at least partially by a major gene(s) on chromosome 1D of Cheyenne. Another substitution line, which might involve the substitution of segments of Cheyenne chromosomes 1A and 1D (the so-called "1D" line), was inferior to Chinese Spring in mixing time and tolerance.

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Mapping of the s and Ch 2 genes on chromosome 3D of common wheat[1]

T. KOBA and K. TSUNEWAKI

Laboratory of Genetics, Faculty of Agriculture
Kyoto University, Kyoto, Japan

SEARS (1947) reported that the *sphaerococcum* gene, *s*, is located on chromosome 3D, and is ineffective in hemizygous state. One of the two complementary genes, *Ch2*, for hybrid chlorosis is known to locate on the same chromosome, 3D (TSUNEWAKI and KIHARA 1961). We investigated the genetic distance between the centromere of this chromosome and two genes, *s* and *Ch2*, using the ditelo-3DL of Chinese Spring wheat. The results are reported in this paper.

For the mapping of the *s* gene on chromosome 3D, two strains of common wheat were used; those are a ditelocentric line of the long arm of chromosome 3D of a cultivar Chinese Spring (abbreviated to CS ditelo-3DL), supplied by Dr. E.R. SEARS, and an isogenic marker line of a cultivar S615 with the *s* gene (abbreviated to *s*–S615) that was introduced from *T. sphaerococcum* PERC. through ten backcrosses. The breeding procedure taken for mapping this gene is illustrated in Fig. 1. The genotype of the F_1 hybrids of the cross, CS ditelo-3DL (*SS* or - -) × *s*–S615 (*ss*), was assumed to be either *Ss* or *s*-. All three F_1 plants produced did not show the *sphaerococcum* character, for its recessiveness in the former case and/or its ineffectivceness in the latter case. Therefore, it could not be determined in the F_1 generation

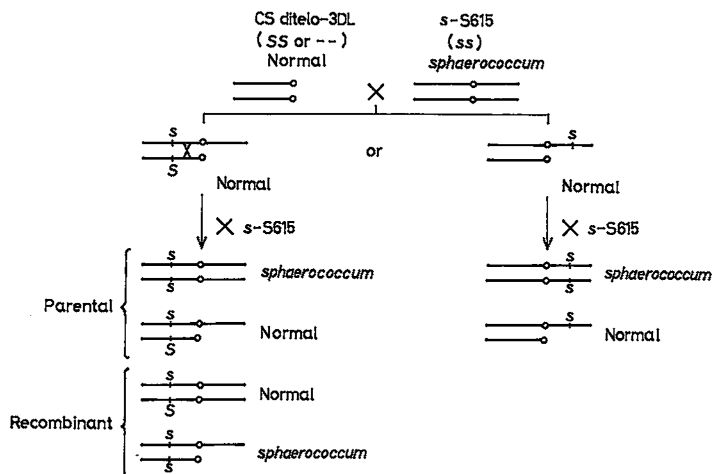

Fig. 1. Procedure used for locating the *s* gene on chromosome 3D.

1) The work was supported in part by a Grant-in-Aid (No. 048310) from the Ministry of Education.

Table 1. Number of plants having different chromosome constitutions and *sphaerococcum* phenotypes

Chromosome constitution	Phenotype	
	Normal	*sphaerococcum*
Normal	1	57
Monotelodisomic	49	5

whether the *s* gene locates on the long arm or short arm of the chromosome 3D. The F_1 plants were, then, pollinated by *s*–S615 (*ss*). In the offspring of this cross, chromosome constitutions and phenotypes (normal vs. *sphaerococcum*) were investigated with individual plants, the results being summarized in Table 1. If the *s* locus is on the short arm, it is expected that all individuals which have 42 normal chromosomes should have *sphaerococcum* character, while all those which have 41 normal plus one telocentric chromosome should exhibit normal phenotype due to the ineffectiveness of the *s* gene in hemizygous state. In this experiment, however, six recombinants were produced, i.e., five individuals having 41 normal plus one telocentric chromosome and *sphaerococcum* character, and one having 42 normal chromosomes and normal character. It is, therefore, concluded that the *s* locus is on the long arm of chromosome 3D, the genetic distance between the locus and the centromere being estimated to be 6/122 or 5.0±2.0%.

For the mapping of the *Ch*2 gene, three strains of common wheat, NIG 1, NIG 7, and CS ditelo-3DL, were used. Their genotypes for hybrid chlorosis are shown as follows:

CS ditelo-3DL *ch*1*ch*1*Ch*2*Ch*2 or *ch*1*ch*1 - -
NIG 1 *ch*1*ch*1*ch*2*ch*2
NIG 7 *Ch*1*Ch*1*ch*2*ch*2.

The breeding procedure taken for mapping the *Ch*2 gene is illustrated in Fig. 2. The

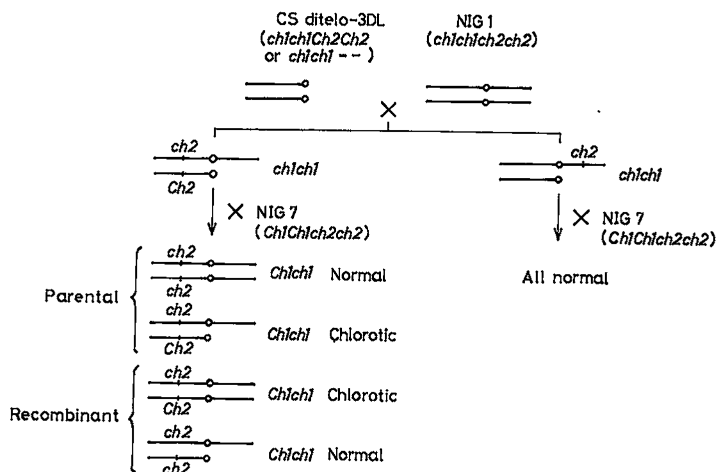

Fig. 2 Procedure used for locating the *Ch*2 gene on chromosome 3D.

Table 2. Number of plants having different chromosome constitutions and chlorosis phenotypes

Chromosome constitution	Phenotype	
	Normal	Chlorotic
Normal	48	16
Monotelodisomic	37	46

eight F_1 plants from the cross, CS ditelo-3DL×NIG 1, were pollinated by NIG 7. Because the offspring of this cross segregated two phenotypes, chlorotic and normal, it can be concluded that the *Ch2* locus locates on the long arm of chromosome 3D (Fig. 2). All of the plants in this segregating generation were divided into four classes according to their chromosome constitutions and their chlorosis phenotypes (Table 2). In total, 53 recombinants were obtained among 147 plants tested. Thus, the crossing over value between the *Ch2* locus and the centromere is estimated to be 53/147 or 36.1±4.0%. However, the frequency of the non-chlorotic monotelodisomics (one of the recombinant classes) was in great excess, and that of the chlorotic disomics was in shortage, comparing to their expected frequencies. Reasons for this discrepancy must be elucidated in further works.

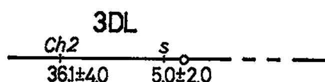

Fig. 3 Locations of the *s* and *Ch2* genes on the long arm of chromosome 3D (Numerals indicate map units in centimorgans).

From the results described above, the first linkage map to chromosome 3D was constructed as shown in Fig. 3. It appears that the *Ch2* gene locates on the distal part, while the *s* gene locates on the very proximal region of the long arm of chromosome 3D. To confirm this map, distance between the *s* and *Ch2* genes must be measured, that is now under investigation.

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Variation and geographical distribution of esterase zymograms in *Aegilops squarrosa*[1)]

Yasuo NAKAI

Laboratory of Genetics, Faculty of Agriculture,
Kyoto University, Kyoto, 606.

Introduction

The hypothesis that *Ae. squarrosa* is the D genome donor to common wheat has been widely accepted. However, many differences in morphorogical and physiological characteristics are found in *Ae. squarrosa* (KIHARA and TANAKA 1958). Johnson (1972) showed that albumin bands of the common wheat have homology with those of *Ae. squarrosa*. As to the esterase isozymes, three types of the zymogram were found in *Ae. squarrosa*. Among those, only one type has the homologous bands with that of present-day common wheat, the two rest types having non-homologous bands.

In the present paper, the variation of esterase isozymes was investigated, and its genetic basis was also analyzed.

Materials and Methods

In total 136 strains of *Ae. squarrosa* were used in this investigation. The large number of strains were collected by the Kyoto University Scientific Expedition to the Karakoram and Hindukush (abrebiated as KUSE) in 1955, the Botanical Expedition to Caucasus (BEC) in 1966 and the Botanical Expedition to the Northern Highlands of Mesopotamia (BEM) in 1970.

Electrophoresis of esterase isozymes was performed using the ordinary gel isoelectric-focusing method (NAKAI 1973). About 40 mg of soaked seeds of each strain were homogenized in 0.5 ml of potassium phosphate buffer (0.05 M, pH 7.0), and the homogenate was centrifuged at 20,000 $\times$g for 15 min. The supernatant was placed on polyacrylamide gel containing a carrier ampholite with a pH range of 6.0 to 8.0. The electrophoresis was carried out at 200 volts and was run for 3 hours. After electrophoresis, gels were stained with 0.1% Fast Blue RR Salt and 0.01% α-naphtyl acetate (w/v) in the phosphate buffer (0.07M, pH 7.0) for 10–20 minutes.

Results and Discussion

1) Variation on the esterase zymogram

In *Ae. squarrosa*, three zymograms were found which were designated as type 1, type 2 and type 3, respectively (Fig. 1). Type 1 had three major bands, 3E, 5E and 6E (Fig.

1) The work was supported in part by a Grant-in-Aid (No. 134050) from the Ministry of Education.

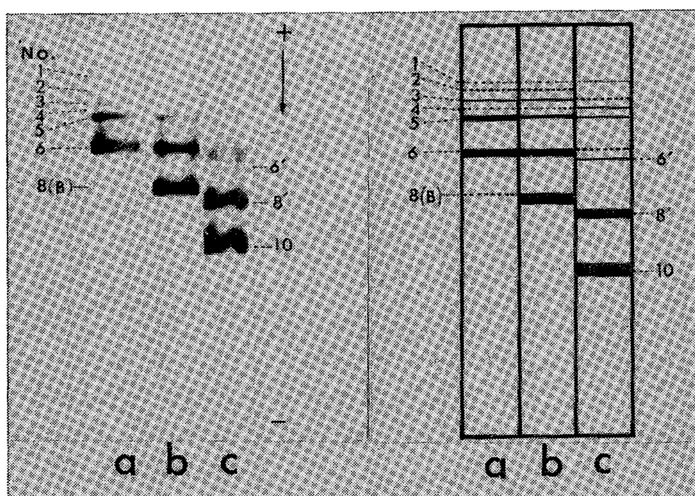

Fig. 1. Three types of esterase zymograms found in *Ae. squarrosa* strains.
a: Type 1 zymogram of *Ae. squarrosa* var. *strangulata* KUSE 2135, b: Type 2 zymogram of *Ae. squarrosa* var. *meyeri* KUSE 2144, c: Type 3 zymogram of *Ae. squarrosa* var. *typica* No. 2.

Table 1. Number of *Aegilops squarrosa* strains having different types of esterase zymogram

Strain or variety	No. of strains tested	Zymogram		
		type 1	type 2	type 3
typica	107	0	19	88
intermediate	6	0	0	6
anathera	8	0	0	8
meyeri	7	0	2	5
strangulata	8	1	4	3
Total (%)	136 (100)	1 (0.7)	25 (18.4)	110 (80.9)

1–a). Type 2 had one extra major band, 8E-B (Fig. 1-b). Type 3 differed greatly from types 1 and 2, by having two major bands, 8'E and 10E, and six minor bands, 1E, 3E, 4E, 5E, 6E and 6'E (Fig. 1-c). Type 1 was found only a single strain of var. *strangulata*, and type 2 in var, *typica*, var. *meyeri* and var. *strangulata*. All varieties of *Ae. squarrosa* contained the type 3 zymogram (Table 1).

2) Factorial basis of the three zymograms

The type 1 lacked major band 8E-B as compared to the type 2 zymogram. While the type 3 had extra bands 8'E and 10E. To clarify the factorial basis of 8E-B band, F_1 and F_2 generations of the cross, *Ae. squarrosa* var. *strangulata* KUSE 2118 (type 2)×*Ae. squarrosa* var. *strangulata* KUSE 2135 (type 1), were studied, In the F_1, type 2 zymogram was observed. In the F_2, type 1 and type 2, segregated in a 1:3 ratios as shown in Table 2, indicating that the production of 8E-B bands is controlled by a single dominant gene.

Table 2. F_2 ratios for esterase bands, 8E, 8'E and 10E of *Aegilops squarrosa*

Cross	F_1 genotype	No. plants	F_2 zymogram			X^2 value
(type 1) × (type 2)			(tpye 1):		(type 2)	(1:3)
KUSE 2135 × KUSE 2118	Est^1/Est^2	61	15		46	0.006
〃 × 〃 2144		65	19		46	0.625
Total		126	34		92	0.264
(type 2) × (type 3)			(type 2):	F_1:	(type 3)	(1:2:1)
KUSE 2118 × *typica* No. 2	Est^2/Est^3	55	13	26	16	0.065

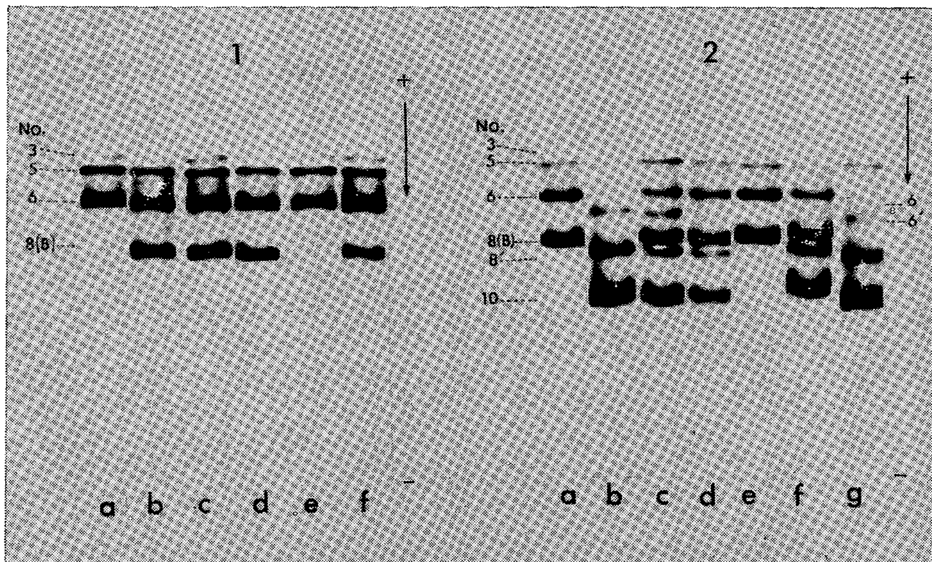

Fig. 2. Segregation of the carrier and non-carrier of the 8E-B, 8'E and 10E bands in the F_1 generation of various crosses of *Ae. squarrosa*.
1: KUSE 2135 (type 1) × KUSE 2118 (type 2).
a: KUSE 2135, b: KUSE 2118, c: mixture of seed extracts of KUSE 2135 and KUSE 2118, d: F_1, e & f: F_2.
2: KUSE 2118 (type 2) × *typica* No. 2 (type 3).
a: KUSE 2118, b: *typica* No. 2, c: 1:1 mxiture of seed extracts of KUSE 2118 and *typica* No. 2, d: F_1, e & f: F_2.

The F_1's between KUSE 2118 (type 2) and *Ae. squarrosa* var. *typica* No. 2 (type 3) showed an intermediate zymogram (Fig. 2–2). In the F_2 generation, type 2, the intermediate, and type 3 segregated to a 1:2:1, ratio as shown in Table 2. Therefore it is concluded that a pair of allelic genes is responsible for the difference between type 2 and type 3 zymograms.

3) Geographical distribution of the three zymograms

The geographical distribution of the three esterase zymograms of *Ae. squarrosa* along

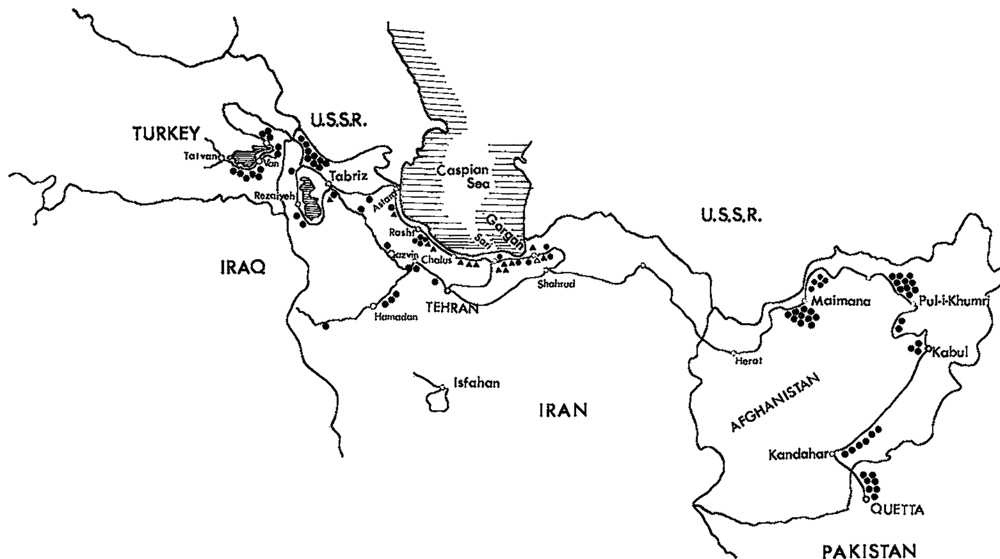

Fig. 3. Geographical distribution of *Aegilops squarrosa* strains having different esterase zymograms in Turkey, Iran, Afghanistan and Pakistan.
Explanation of symbols: △: type 1, ▲: type 2, ●: type 3.

the expedition route is shown in Figs. 3 and 4. It is well known that *Ae. squarrosa* distributes from the Caucasus to Iran, Afghanistan, Pakistan and Uzbek S.S.R., and ussally occurs in wheat fields or along field borders. Var. *typica* has the largest distribution among all varieties, and var. *meyeri* and var. *strangulata* distribute within small area along the Caspian Sea coast.

The strain having type 1 zymogram was found in Behshar, Iran. This strain belong to var. *strangulata*. Strains having type 2 zymogram were found in Elburz mountains along the coast of the Caspian Sea. Strains having type 3 zymogram had the widest distribution, though the strains from Pakistan and Afghanistan were all of this type. All strains from eastern Turkey were, also, of this type (Fig. 3).

As to the distribution in Caucasus, samples from seven different areas were investigated (Fig. 4), all of which belonged to var. *typica*. Though the samples from Baku, Azerbaijan were type 3, those of Shemakha (110 km west of Baku) were all type 2. Materials from Yerevan, Armenian S.S.R., exhibited type 3. A mixed population of type 2 and 3 was found in Tbilisi, Georgian S.S.R. A sample from Derbent collected by Dr. Vavilov was type 3. Type 1 was not found in Caucasus.

In common wheat, ten esterase zymgorams were found, and chromosomal localization of genes responsbile for the individual isozyme band was previously reported (Nakai 1973). Among the three zymograms found in *Ae. squarrosa*, type 2 best fits to that of the D genome donor to common wheat. This hypothesis was derived from the results of an investigation with synthesized hexaploid wheats (Nakai unpublished). Many strains of

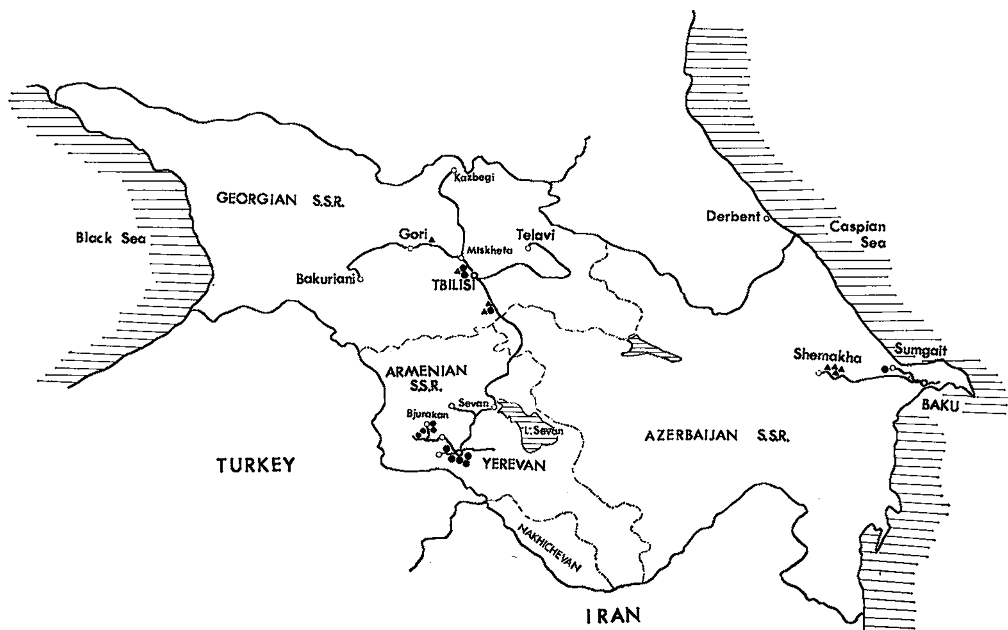

Fig. 4. Distribution of *Aegilops squarrosa* strains having different esterase zymograms in Caucasus. Explanation of symbols: ▲: type 2, ●: type 3.

Ae. squarrosa having type 2 zymgoram were found to distribute in Behshar to Pahlavi of Iran.

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Preliminary report on shoot redifferentiation from wheat callus

H. OGURA* and T. Shimada

Laboratory of Genetics, Faculty of Agriculture,
Kyoto University, Kyoto 606, Japan

It seems to be of valuable importance in basic studies on breeding and genetics of wheat plant to establish the conditions for shoot redifferentiation from wheat callus. However, only a few investigators have reproted occasional shoot redifferentiation from wheat callus of somatic tissue origin, by decreasing auxin level (SHIMADA *et al.* 1969) or application of zeatin (DUDITS *et al.* 1975) in the medium.

In attempts to improve the conditions for shoot redifferentiation, preliminary data are here presented on the relationship between "callus age" and shoot regeneration, and kinetin-IAA (indole-3-acetic acid) interaction. Presoaked and sterilized seeds of *Triticum aestivum* cv. Chinese Spring were placed aseptically on an RM–1964 agar slant medium (LINSMAIER and SKOOG 1965) containing 3.0 mg/l of 2,4-dichlorophenoxyacetic acid (2,4-D) and cultured *in vitro* under continuous fluorescent illumination of about 1,200 luxes and the constant temperature of 25±1°C. The pH of the medium was adjusted to 5.8±0.1 before autoclaving.

Callus formation from germinated seedling roots was observed about 25 days after inoculating the seeds. Primary callus cultures were obtained by transferring these induced callus masses into new fresh RM–1964 medium in test tubes (18×180 mm), each containing 10 ml of the same medium as used for callus induction. These calluses were

Table 1. Responses of different aged calluses on shoot and green spot formation in *Triticum aestivum* cv. Chinese Spring. RM–1964 basal medium supplemented with 2.0 mg/l of kinetin and 0.2 mg/l of IAA was used under continuous fluorescent illumination of about 1,200 luxes. Data were taken after 50 days of culture

Callus* age	No. calluses inoculated	Number of calluses manifesting	
		shoot redif.	green spot form.
14	6	3	6
19	9	1	3
26	16	1	2
less than 26 days	31	5	11
ca. 180	40	0	0

* Number of days maintained as callus cultures after inoculation in the primary subculture medium.

* Present address: Laboratory of Crops and Plant Breeding, Ishikawa Pref. College of Agr., Nonoichi, Ishikawa-gun, Ishikawa Pref. 921, Japan.

Table 2. Organ redifferentiation and green spot formation from two week-aged wheat callus. Data were taken about two months after inoculation in the medium

Growth regulator (mg/1)		Number of test tubes			
kinetin	IAA	total	shoot redif.	root redif.	green spot
0	0	10	1	4	3
0	0.2	10	1	4	3
0	2.0	10	2	4	2
0.02	0	10	1	6	3
0.02	0.2	10	1	4	0
0.02	2.0	10	1	6	2
0.2	0	10	1	6	3
0.2	0.2	10	1	4	2
0.2	2.0	10	1	4	3
2.0	0	10	0	4	3
2.0	0.2	10	2	4	3
2.0	2.0	10	2	5	2

subcultured every *ca.* two months in the same RM–1964 medium supplemented with 3.0 mg/1, of 2,4-D. and maintained in our Laboratory. Differing callus cultures of other higher plants, the wheat callus cultured in the conditions is especially characterized that roots or root-like tissues were frequently accompanied. When 2,4-D concentration was higher than 5.0 mg/1, comparatively uniform callus with no roots was obtained, but the growth was highly inhibited. In case of shoot redifferentiation experiment, root or root-like tissue was aseptically removed from the callus by a scalpel prior to inoculation.

Effect of callus age, *i.e.*, time length as a callus state before placing onto the shoot redifferentiation medium (RM–1964+2.0 mg/1 kinetin+0.2 mg/1 IAA), on shoot regenerative ability and green spot formation is presented in Table 1. The data suggest that shoot regenerative ability decreased in proportion to callus age. Calluses cultured for about six months gave rise no shoot. Also, light condition seems to be necessary, because, in the dark, even young-age callus (less than 30 days of culture in the primary subculture medium) significantly decreased shoot formation, and no green spots were formed. Table 2 shows influence of the combination of kinetin and IAA on organ formation from two week-aged callus. It seems there are no significant differences in shoot and root as well as green spot formation due to combinations or concentrations of growth regulators. Almost all calluses with green spots did not redifferentiate shoots. Several combinations of a morphactin, chlorflurenol-methyl-ester (CFM) and kinetin were tested on shoot organogenesis from wheat callus, however, no shoot morphognesis was observed. Several combinations of these substances have been successful for 100% of shoot redifferentiation in tobacco callus (Ogura 1975).

So far as the wheat callus of seedling root origin is concerned, the results may be interpreted that shoot regeneration depends on (1) callus age, (2) light condition and (3) medium composition and/or growth regulators.

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Identification of reciprocal translocation chromosome types in the emmer wheats, I. *Triticum dicoccoides* KOERN.

Taihachi KAWAHARA and Masatake TANAKA

Plant Germ-plasm Institute, Faculty of Agriculture,
Kyoto University, Kyoto, Japan

The presence of reciprocal translocation in polyploid wheats offers us valuable clues in pursuing the evolution of wheat. RILEY *et al.* (1967) were the first to use informations on chromosomal interchanges in discussing the phylogeny of hexaploid wheat. However, most studies have not been conducted on a large enough scale to identify the "wild" chromosome type neither of each polyploid level nor of each species. This series of study is planned to clarify the "wild" chromosome structure with regard to reciprocal translocations in the Emmer group of tetraploid wheats. This paper deals with wild Emmer, *T. dicoccoides*.

Materials used were 22 strains of *T. dicoccoides* from Palestine, Southeastern Turkey, Northern Iraq and Western Iran (Table 1). A Palestinian strain, 108–3, was arbitrarily chosen as a tester strain and later another strain, 108–5, was also used as a male parent. For cytological observations, young anthers were fixed in Farmer's solution and the aceto-carmine squash method was used. The average seed fertility was calculated from seed setting on three bagged spikes from a single plant.

Chromosome parings and seed fertilities of F_1 hybrids between various *dicoccoides* strains and strain 108–3 and/or 108–5 are shown in Table 2. So far as major reciprocal translocations are concerned, 108–5 shows similar cytogenetical behavior to 108–3 when

Table 1. *T. dicoccoides* used in the present study

Strain No. (KU-)*	Collection site	Source
108-1	unknown	unknown
108-2	20 km NW of Sueida (Cheikh Meskine–Sueida), Syria	BMUK (1959)**
108-3	〃 〃	〃
108-5	unknown	Collection of Mac Key
109	Palestine	Vavilov (1930)
110	Suburbs of Tiberias, Palestine	〃
195	Palestine	Collection of All Union Institute of Plant Industry, Leningrad, U.S.S.R. No. 20403 (1964)
198	Mt. Canaan, Palestine	Aaronsohn (1906)
8536	20.3 km S from Sulaymaniyah to Qara Dagh, NE slope of Shakh i Baranan, Iraq	BEM (1970)***
8539	〃 〃	〃
8541	〃 〃	〃
8736A	SSW of Rowanduz, Iraq (alt. 850 m)	〃
8736B	〃 〃	〃
8737	〃 〃	〃

Table 1. *T. dicoccoides* used in the present study(continued)

Strain No. (KU-)*	Collection Site	Source
8804	North Slope of Jabal Sinjar, South of Kursi, Iraq	BEM (1970)***
8816B	〃 〃	〃
8817	〃 〃	〃
8821A	15.3 km ENE from Dohuk to Amadiyah, Iraq (alt. 780 m)	〃
8935	9.3 km SE from Ergani to Diyarbakir, Turkey (alt. 780 m)	〃
8937B	〃 〃	〃
8941	58.8 km N from Kermanshah to Ravansar, Iran (alt. 1610 m)	〃
8943	〃 〃	〃

* Stock No. of the Plant Germ-plasm Institute, Faculty of Agriculture, Kyoto University

** the Botanical Mission of the University of Kyoto, 1959.

*** the Botanical Expedition of Kyoto University to the Northern Highlands of Mesopotamia, 1970.

crossed to other strains. Table 2 shows that of 22 strains examined, 20 belong to the same reciprocal translocation chromosome type as 108–3, but that the remaining two strains, 109 and 195, have different chromosome structures from 108–3. Hybrids 109× 108–3 and 195×108–3 formed a tetravalent at meiosis. In the former combination, 65 per cent of the cells were $1_{IV}+12_{II}$. In hybrid 109×195, $2_{IV}+10_{II}$ were observed in 57 per cent of the PMCs. Based on the present data, chromosome type of 108–3 was designated as the EA type and those of 109 and 195 were named the EB and the EC type, respectively. The formation of a tetravalent indicating a major reciprocal translocation is expected in

Table 2. Chromosome pairings and seed fertilities of F_1 hybrids of strains of *T. dicoccoides*

Cross combination	No. of PMCs observed	Chromosome pairings					Seed fertility (%)
		I	II	III	IV	VI	
108-1 ×108-3	50	0.24	13.80	-	0.04	-	69.1
108-2 ×108-3	50	0.16	13.92	-	-	-	83.3
108-5 ×108-3	63	-	13.97	-	0.015	-	48.2
109 ×108-3	83	0.08	12.28	0.08	0.65	0.08	63.0
〃 ×195	44	0.18	10.66	0.14	1.52	-	-
110 ×108-3	83	0.14	13.88	-	0.02	-	88.2
195 ×108-3	25	-	12.00	-	1.00	-	3.2
198 ×108-3	50	0.42	13.72	0.02	0.02	-	75.0
8536 ×108-5	50	-	13.96	-	0.02	-	-
8539 ×108-3	50	0.32	13.80	-	0.02	-	-
8541 ×108-5	50	0.04	13.98	-	-	-	50.5
8736A ×108-5	50	-	13.96	-	0.02	-	39.4
8736B ×108-3	50	0.90	13.46	0.06	-	-	76.0
〃 ×108-5	50	-	14.00	-	-	-	47.7

Table 2. Chromosome pairings and seed fertilities of F_1 hybrids of strains of *T. dicoccoides* (continued)

Cross combination	No. of PMCs observed	Chromosome pairings					Seed fertility (%)
		I	II	III	IV	VI	
8737 ×108-5	100	0. 04	13. 98	–	–	–	12. 7
8804 ×108-3	50	0. 20	13. 90	–	–	–	74. 0
8816B ×108-3	50	0. 12	13. 86	–	0. 04	–	77. 5
8817 ×108-5	50	–	14. 00	–	–	–	–
8821A ×108-3	50	0. 04	13. 86	–	0. 06	–	72. 0
8935 ×108-5	50	–	14. 00	–	–	–	74. 4
8937B ×108-3	50	0. 12	13. 94	–	–	–	31. 2
〃 ×108-5	50	0. 12	13. 94	–	–	–	72. 4
8941 ×108-5	50	0. 08	13. 88	–	0. 04	–	40. 3
8943 ×108-5	50	0. 08	13. 96	–	–	–	54. 8

the PMCs of hybrids between the EA and EB types and between the EA and EC types. Two reciprocal translcoations are expected between the EB and EC types. The present data indicate that the EA is the "wild" chromosome type of *T. dicoccoides*.

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Formation of anaphase bridges with or without fragments, in rye (*Secale cereale* L.)

J.A. Sáiz de Omeñaca

E.T.S.I. Agrónomos, Universidad de Córdoba, Spain

Dicentric bridges at meiosis have been found in inbred plant material. Several causes have been mentioned as the origin of anaphase bridges. Anaphase bridges originated by crossing-over in inversion heterozygotes and not accompanied by fragments were explained in several ways, such as difficult observation by the presence of numerous univalents (Koller 1938) and small size (Blanco 1948). Anaphase bridges have been found in rye populations in many instances. Inbreeding in rye increases the frequency of bridges with or without fragments; Rees and Thompson (1955) found asymmetrical bivalents and interpreted them as acentric fragments originated by chromosome breakage and retained by chiasmata. Later there would be a U-type sister union between chromatids and the bridges can be formed at the first or the second anaphase division. In 1966, Lewis and John proposed that U-type changes could result from erroneous crossing-over. Jones (1967, 1968 and 1969) and Jones and Brumpton (1971) obtained results which reinforce the hypothesis of both types being due to breakages and U-type reunions resulting from alterations in the normal crossing-over process. Lewis and John (1966) and Stutz (1976) explained the bridge formation as the result of genetically controlled chromatid and subchromatid breakage.

Eight inbred lines of rye and their F_1 hybrids were studied. Table 1 gives in columns 2nd to 4th respectively: the frequency of abnormal cells, the frequency of cells with one bridge and one fragment, and the frequency of cells with one bridge and no detectable fragment. These bridges, showing no knobs, were formed between sister chromosomes of a bivalent or between the sister chromatids of an univalent undergoing equational division. Even in this last case fragments can occasionally being present. The fragments are usually rather small, punctiform and variable in size even between PMC from the same anther. Fragments unaccompanied by bridges were also observed and their frequencies are recorded in the 5th column.

The presence of bridges without fragments is constant in our material. The fragments can pass unnoticed on occasions, but not in the proportion necessary to support the assumption that all the bridges formed are accompanied by fragments. In our material the presence of bridges is surely not a consequence of inversion heterozygosis because of the material's inbreeding history. On the other hand, we observed spontaneous chromosome breakage in our material, a high frequency of bridges in lines and F_1s with relatively low chiasma frequencies, and a pointed discrepancy between the number of bridges and the number of fragments observed, apart from other irregularities such as interweaven bivalents.

Table 1. Percent of PMC at AI showing

Line or F_1	Abnormalities	1 birdge + 1 fragment	1 bridge, no fragment	fragments, no bridge
4	38.9	6.0	19.1	2.9
5	30.0	2.1	12.0	1.6
5a	23.6	2.4	11.1	0.6
6	25.7	1.0	10.6	1.1
6a	31.9	5.5	13.9	1.2
9	31.9	2.6	12.9	0.7
9a	63.6	7.7	23.8	3.4
14	30.9	4.3	11.2	3.3
4 × 5	30.9	4.4	11.9	2.6
4 × 5a	41.3	2.9	18.9	0.9
4 × 6	73.6	13.9	21.6	12.3
4 × 6a	45.7	4.5	18.7	2.1
4 × 9	39.9	5.1	16.1	0.6
4 × 9a	27.2	4.1	9.7	0.3
4 ×14	37.5	4.0	25.2	7.6
5 × 5a	37.8	4.7	12.8	5.2
5 × 6	36.1	1.9	24.9	0.3
5 × 6a	28.9	3.4	14.8	1.3
5 × 9	26.5	0.3	9.9	0.2
5 × 9a	16.4	0.3	9.6	0.2
5 ×14	50.2	7.9	14.1	5.3
5a × 6	24.9	1.5	6.2	3.8
5a × 6a	23.7	0.2	9.2	0.9
5a × 9	33.9	0.5	18.9	1.4
5a × 9a	22.9	1.1	9.5	0.2
5 ×14	3.7	0.0	2.2	0.0
6 × 6a	5.8	0.2	2.8	0.0
6 × 9	20.5	0.0	11.0	0.2
6 × 9a	10.7	2.5	6.9	0.5
6a ×14	8.4	0.1	6.6	0.1
6a × 9	26.5	0.6	6.8	0.9
6a × 9a	18.7	0.1	2.7	0.1
6a ×14	39.4	5.0	12.4	1.2
9 × 9a	17.5	7.1	24.4	4.4
9 ×14	10.1	0.0	3.6	0.4
9a ×14	24.5	0.3	12.7	0.0

All these abnormalities indicate (LEWIS and JOHN 1966) that bridges and fragments can be a result of chromosome breakage. The usually small size of the fragment is in harmony with the localization of chiasmata, which even in inbred rye is distal, with some exceptions. All this supports the assumption that the place in which the crossing-over occurs in the chromosome is the same in which the U-type changes giving rise to bridges accompanied fragments take also place. JOHN and LEWIS (1965) and LEWIS and JOHN (1966) proposed that breakage and reunion at half-chromatid level is a cause-mechanism of anaphase bridges. The change could take place between half chromatids of sister chromatids or between half chromatids of non-sister chromatids. If the union is U-type, dicentric bridges and acentric fragments would form, the latter retained in the middle part forming a knob, which does not coincide with what we observed in our material. Should a fragment break free, it would not be easy to distinguish the bridges originating at half-chromatid level of

the resulting U-type union between chromatids. A half-chromatid breakage followed by and X-type union could possibly cause the appearance of anaphase bridges without fragments, but with a knob in its middle. These bridges have not been observed in our material, with few exceptions, and can be due to other causes. STAR (1970), STUTZ (1976) and others also explained irregularities on the basis of subchromatid exchanges during synapsis. But there are still more reasons not to consider that anaphasic bridges are a result of changes at half-chromatid level; by instance, there have been considerable efforts to demonstrate the existence of the half-chromatid unit, but the proofs against its existence are strongly enough to think that each chromatid is formed by a single molecule of DNA.

The appearance of bridges with fragments, of lone fragments, or even bridges with knob can be explained by means of the processes outlined previously, but not the appearance

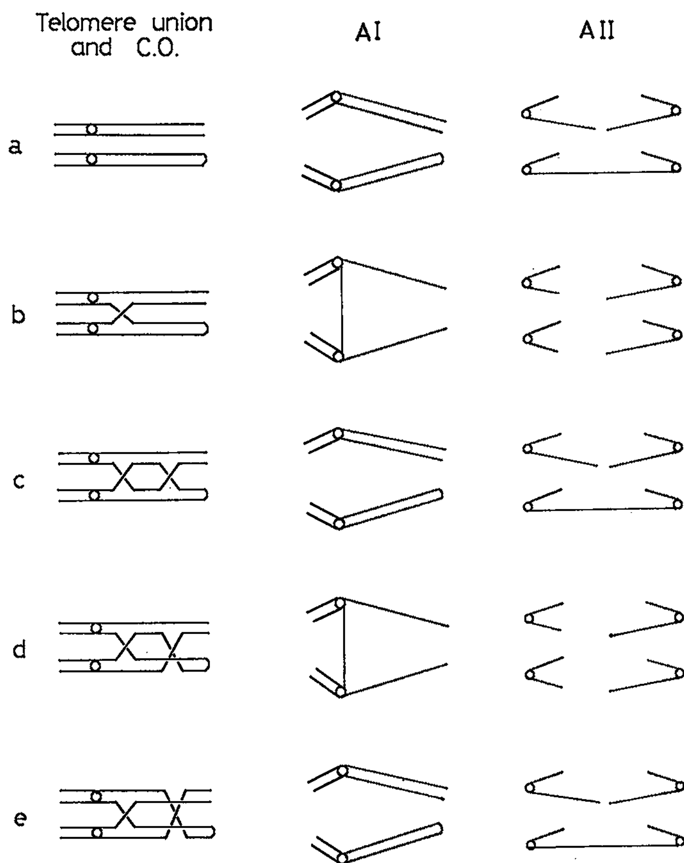

Fig. 1. The sister telomeric union at pachitene, and its consequences in first and second meiotic anaphase configurations in accordance with crossing-over combinations. a) no C.O.; b) single C.O.; c) double C.O., reciprocal chiasmata; d) double C.O., diagonal chiasmata; e) double C.O., complementary chiasmata.

of anaphase bridges without knobs unaccompanied by fragments, keeping in mind the frequency of such bridges in our material. During the meiotic prophase a telomeric union should occur between chromatids in a certain percentage of chromosome pairs. The different possibilities are shown in Fig. 1 as well as its consequences during the first and second anaphase, in accordance with the cross-over combinations.

The frequency of bridges without fragments is much lower during the second division in our material. Likewise, we only observed 21 bridges with fragments among 6623 PMC at AII. JONES and BRUMPTON (1971) came to the conclusion that even keeping in mind the conversion due to crossing-over, estimated according to the frequencies of chiasmata in MI, in 94% of the cases the U-type changes occur between non-sister chromatids, as in the X-type changes, which also implicate generally the non-fraternal chromatids. As can be seen in the corresponding figures, this is valid if it is assumed that the U-type changes are a result of an erroneous crossing-over, because this would correspond in reality to less number of "conversions" being due to crossing-over, the number of correct crossing-overs being smaller. But it is also logical that bridges appear in the first anaphase due to sister telomeric union, since a crossing-over is necessary for them in the affected chromosome arm, and we have seen that this situation is the most common one at diakinesis. The double fraternal union originates a double bridge or linked bivalents in AI, or bridges in AII, but this happens in very few cases. Acentric fragments without bridges is an infrequent succes and can be a result of stretchness and breakage.

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Segregation in an F_2 population of *Aegilops longissima* $\times$ *Ae. bicornis*

Giles WAINES

Department of Plant Sciences, University of California,
Riverside, CA 92521, U.S.A.

A possible origin for *Aegilops sharonensis* EIG as a segregant from a hybrid between *Ae. longissima* SCHWEINF. & MUSCH. and *Ae. bicornis* (FORSK.) JAUB. & SP. was put forward by WAINES and JOHNSON (1972), based on the ethanol-extracted, seed-protein electrophoretic patterns of *sharonensis*, which are intermediate to those of *longissima* and *bicornis*. This note reports preliminary results to resynthesize *sharonensis* from such a parentage.

Since 1972 the cross *Ae. longissima*$\times$*Ae. bicornis* has been made many times using several different genotypes of each species. The F_1 hybrids grow vigorously and cytogenetic analyses of pollen-mother cells show 5 closed bivalents and a chain quadrivalent, which confirms previous reports (KIMBER 1961), of a translocation difference between the two species. KIMBER (1961) recorded that his F_1 hybrid was more or less self-sterile. I was surprised to find, however, that under greenhouse conditions at Riverside, F_1 hybrids are very fertile and appear to produce as many seeds as parental plants. The F_1 hybrids of *longissima/sharonensis* and *sharonensis/bicornis* are known to produce fertile seed (ROY 1959, TANAKA 1955).

If *longissima* is used as the female parent, and *bicornis* as the male parent, true hybrids can be easily identified. *Ae. longissima* has spikes that remain intact, or break at one weak point approximately 5 spikelets up from the spike base, whereas *bicornis* has spikes in which the top part of the spike breaks up into individual spikelets. The F_1 hybrids all disarticulate similarly to *bicornis*. Moreover, the hybrid-spike morphology is intermediate between that of *longissima* and *bicornis* for lateral awns.

Over 1,000 F_2 seeds of *longissima* G1306, collected 25 km south of Beersheba, Israel, and *bicornis* G1299, collected 2 km north of Gvulot, Israel, were sown in the field at Riverside in early February, 1977 along with plots of the parental lines. A considerable number of plants were killed by barley-yellow-dwarf virus, but a sufficient number flowered to collect data. Pollen viability in the F_2 population ranged from 0%–90%, whereas in *bicornis* viability averaged 60% and in *longissima* 80%. If we assume that viabilities greater than 60% indicate the translocation present in homozygous forms, and viabilities below 50% represent plants with the translocation in heterozygous form, then of the 82 plants tested, the 42 homozygous: 40 heterozygous represents a reasonable fit to the expected 1:1 ratio.

Of 293 plants scored for disarticulating or intact rachis, 223 plants disarticulated and

70 plant remained intact, or had spikes that broke only at one point. These values approach a 3:1 ratio and are consistent with the interpretation that intact rachis is controlled by a single recessive gene. If we consider the range of types for spike disarticulation listed for *longissima* by EIG (1929), the control of intact rachis in *longissima* may be more complicated.

Spikes of some of the segregants from the F_2 population approached the morphology of *sharonensis* spikes, and F_3 seed of these plants will be grown in 1978. These results are consistent with the interpretation that *Ae. sharonensis* may have originated as a hybrid segregant.

I hope that taxonomists will not use these results to merge *Ae. longissima* into *Ae. bicornis*, as they ealier used chromosome pairing and fertility studies to merge *sharonensis* into *longissima*. All these three species have different morphologies and different ecological requirements (ANKORI and ZOHARY 1962).

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Accessions collected by BMUK identified as *Aegilops searsii* FELDMAN & KISLEV

Giles WAINES

Department of Plant Sciences, University of California,
Riverside, CA 92521, U.S.A

Recently Dr. M. FELDMAN has collected material of a new diploid species of *Aegilops* in Israel which has been called *Ae. searsii* (FELDMAN and KISLEV 1977). It has been known for some time that a new variety of *Aegilops longissima* SCHWEINF. & MUSCH. was collected by BMUK in Jordan (YAMASHITA and TANAKA 1967). These two new taxa appear to be one and the same. The ethanol-extracted, seed-protein electrophoretic patterns of 5 accessions made by BMUK are different from those of *Ae. longissima* and will be described elsewhere. In particular, all have a band faster than any so far found among *Aegilops* species. There are also other protein band differences. The BMUK accessions are Nos. 5751, 5755, 5756, 5758, 5760, and there may be others. Collection data for these accessions are listed by YAMASHITA and TANAKA (1967).

Literature Cited

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(Received Aug. 2, 1977)

Aegilops searsii[1], a new species from Israel and Jordan[2]

Moshe FELDMAN[3] and Mordechai KISLEV

Plant Genetics, Weizmann Institute of Science, Rehovot and
Department of Life Sciences, Bar-Ilan University,
Ramat-Gan, Israel

A new species of *Aegilops* named *Ae. searsii* FELDMAN et. KISLEV, from Judean Mountains and Samaria in Israel and Gilead, Ammon and Moav in Jordan, was recently described. The formal publication of this species as *Ae. searsii* and as *Triticum searsii* is at present in press (FELDMAN and KISLEV, in press). It belongs to section *Sitopsis* ZHUK. (*Platystachys* EIG). *Ae. searsii* is most closely related to *Ae. longissima* SCHWEINF. et MUSCH. Both have a 1-rowed ear which generally disarticulates only very close to its base, and its awns are restricted to the uppermost spikelet. Other common features such as very few fertile florets per spikelet and 2-toothed apex of glume of the lateral spikelets, characterized subsection *Emarginata* EIG, to which they belong together with *Ae. sharonensis* EIG and *Ae. bicornis* (FORSK.) JAUB. et SP.

Ae. searsii differs from its related species by various principal characters such as the proportionate length of glume and lemma and adaptation to a certain type of soil. A peculair character of *Ae. searsii* is the single, terminal, arched or diagonally oriented awn of the dispersal unit, and the ±free kernel.

Cytogenetic studies show that the F_1 hybrid between *Ae. searsii* and *Ae. longissima* exhibits meiotic irregularities and is highly sterile (FELDMAN *et al.*, submitted).

Ae. searsii, like all other members of section *Sitopsis*, is a diploid with $2n=14$. All the chromosomes are large, with median or submedian centromeres. Like all other species of this section, *Ae. searsii* contains two pairs of satellited chromosomes. However, while the related species of subsection *Emarinata* contains one pair of large and one pair of small satellites, the karyotype of *Ae. searsii* is characterized by one chromosome pair with large satellites and one pair with median-sized satellites. The karyotype of *Ae. searsii* differs from those of other *Emarginata* species also by the arm ratio of several chromosomes.

Ae. searsii, which is endemic to the hills of both sides of the Jordan, has an unusual habitat as compared to that of other members of subsection *Emarginata*. While the other species grow on light and sandy soils in relatively dry climate, the habitat of *Ae. searsii* has typically terra rossa soil and sub-Mediterranean climate.

Section *Sitopsis* contains the *Aegilops* species which are morphologically most similar to wild and cultivated wheats (ZHUKOVSKY 1928, EIG 1929). Species of both subsections were

1) Named in honor of E.R. Sears from the University of Missouri, U.S.A.

2) Supported in part by a grant from the Stiftung Volkswagenwerk, Az. 112073.

3) The Marshall and Edith Korshak Professor of Plant Cytogenetics.

regarded as the putative donors of genome B of polyploid wheats, e.g., *Ae. speltodies* by SARKAR and STEBBINS (1956) and Riley *et al.* (1958), and *Ae. bicornis* by SEARS (1956). However, of all the *Sitopsis* species, *Ae. searsii* is the only one which is distributed sympatrically and forms mixed populations with the wild tetraploid wheat, *Triticum dicoccodies* KOERN, in Israel and Jordan. In southern Syria material described as *Ae. longissima* but may well be *Ae. searsii*, is distributed together with *T. dicoccodies.* This ecogeographical resemblance as well as several morphological and karyotypical similarities suggest that *Ae. searsii* (and/or *Ae. longissima*) is the likliest donor of genome B of polyploid wheats.

Seeds of *Ae. searsii* can be obtained from the authors.

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———, I. STRAUSS and A. VARDI Chromosome pairing and fertility of F_1 hybrids between *Aegilops searsii* and *Ae. longissima.* (submitted to the Can. J. Genet. Cytol.).

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II. Genetic Stocks

Mutants of *Triticum monococcum*

Patricia SARVELLA† and C.F. KONZAK

Cell Culture and Nitrogen Fixation Laboratory, Agricultural Research Service,
United States Department of Agriculture, Beltsville, Maryland 20705,
and Department of Agronomy and Soils, Washington State
University, Pullman, Washington 99163, U.S.A.

Mutagens have been used to obtain genetic variants in wheat (KONZAK 1973). In the present study eleven lines from mutagen-treated *Triticum monococcum* L. which had different heights but all shorter than normal were selected. Normal *T. monococcum* was described by PERCIVAL, 1921; BOWDEN, 1959, and Box and GUEST, 1968.

Plants were grown in the field at Pullman. Washington in 1973. Eleven lines were selected on the basis of plant height and harvested. These eleven lines were numbered 2, 3, 4, 6, 10, 11, 17, 20, 25, 26, and 29. Line 14 is representative of normal *T. monococcum*. Mature plants and seeds were shipped to Beltsville, Maryland. They were grown in the winter greenhouse in 1974. Photographs were made of the whole plant at maturity; flower at anthesis; mature spikelet; mature grain; glumes, palea, lemma, and remaining florets; and the mature spike.

Whole plant at maturity. There was considerable difference in plant height. Four of

Table 1 Height of *Triticum monococcum* mutants grown in the field at Pullman, Washington, 1973 and in the greenhouse at Beltsville, Md., 1974.

Line	CI #	Ht. (cm) Pullman	Ht. (cm) Beltsville
2	17652	64	104
3	17653	88	127
4	17654	74	79
6	17655	81	131
10	17656	78	99
11	17657	53	88
17	17658	68	112
20	17659	74	84
25	17660	81	99
26	17661	48	72
29	17662	74	112
14	—	99	

† It is regretable to note here that our beloved Dr. Patricia Sarvella passed away last year (K. Yamashita, the Managing Editor)

the selected lines at Pullman were classed as short, four intermediate, and three tall (Table 1, Plates 1–11A). Two of the four short lines remained short at Beltsville; however, two were classed as intermediate. Two of the four intermediates at Pullman were again classed as intermediate and two as short. Of the three tall lines, two were tall and one intermediate at Beltsville. Lines 17 and 26 tillered profusely while lines 3, 10, 25, and 29 had fewer tillers. Line 3 had a chlorina coloration. Lines 10, 11, 17, 20, 25, 26, and 29 had later maturities at Washington.

Flowers at anthesis (Plates 1-11B). Four lines have shortened filaments. Stigmas in these lines appeared normal.

Spike (Plates 1-11F) Three lines (4, 10, and 11) had shorter awns and four lines (4, 20, and 25) shorter spikes. Line 25 also had nodding heads. Spikes in line 29 shattered easily.

Spikelets, glumes, lemmas, and paleas. (Plates 1–11, C and E). Glumes were generally shorter than the lemmas. Lines 2, 10, and 29 have broader glumes. Beaks on the glumes were more prominent in line 25. Some of the lemmas contained grain (3, 4, 17, 20, 25, 26, 29). The paleas of lines 4, and 20 were shorter than the lemmas and were shorter than the paleas of the other lines.

Grain (Plates 1-11, D). The grains in the various lines appeared to have the same length. Four lines (3, 6, 20, 26) had narrow grain.

Conclusion. Thus, the eleven different lines varied not only in plant height but also in several other morphological characters.

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(Received Nov. 30. 1977)

Explanatian of Plates

Plates 1–11. *Triticum monococcum* mutant lines.

A-Whole plant at maturity 0.13 X; B-Flower at anthesis 4.1 X; C-Mature spikelet 1.9 X; D-Mature grain front, side, and back 3.4 X; E- Glumes, palea, lemma, remaining florets, R. to L. 1.9 X; F- Mature spike 0.9X.

Pl. 1-Line 2; Pl. 2-Line 3; Pl. 3-Line 4; Pl. 4-Line 6; Pl. 5-Line 10; Pl. 6-Line 11; Pl. 7-Line 17; Pl. 8-Line 20; Pl. 9-Line 25; Pl. 10-Line 26; Pl. 11-Line 29.

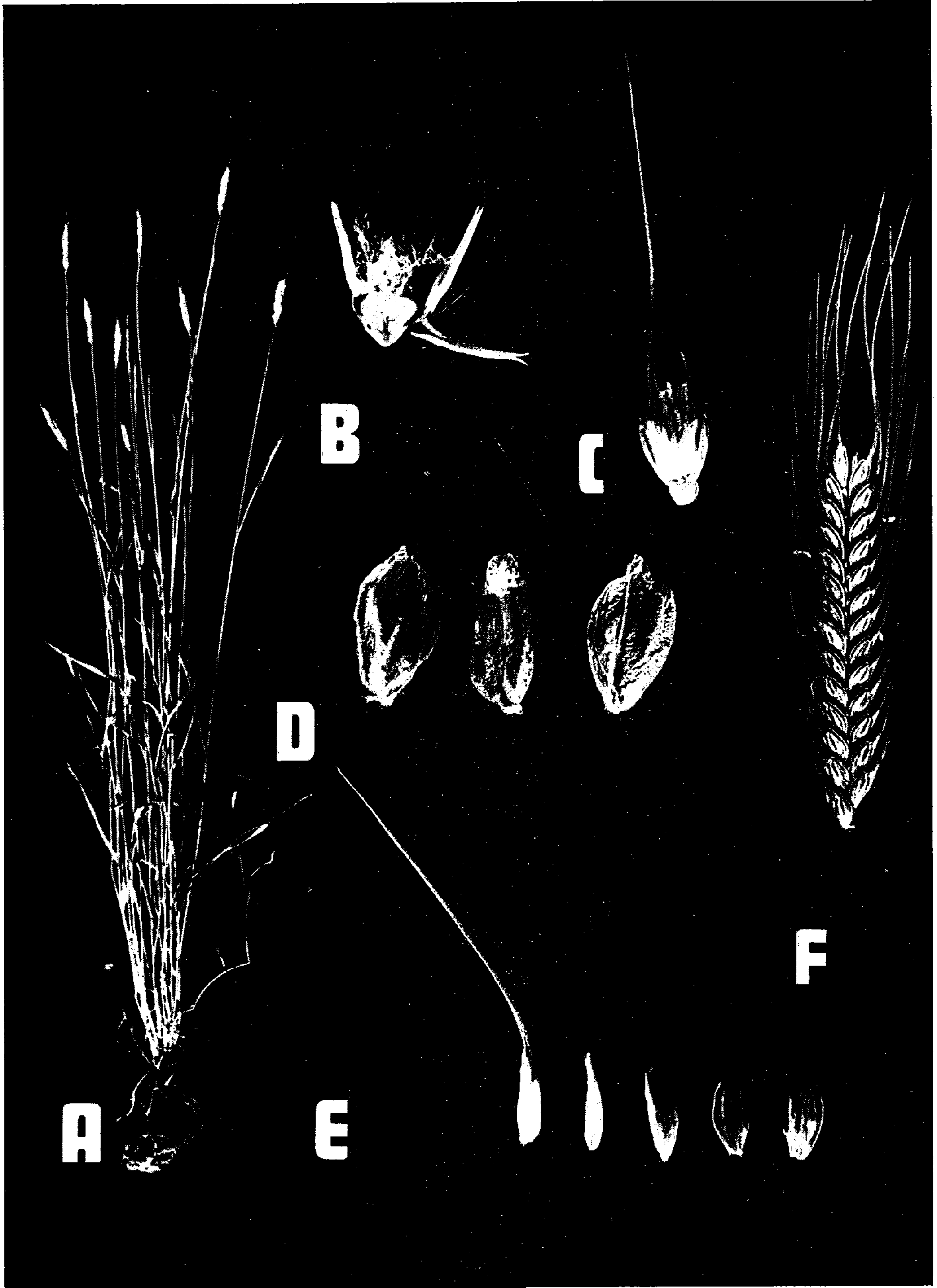

Plate 1.

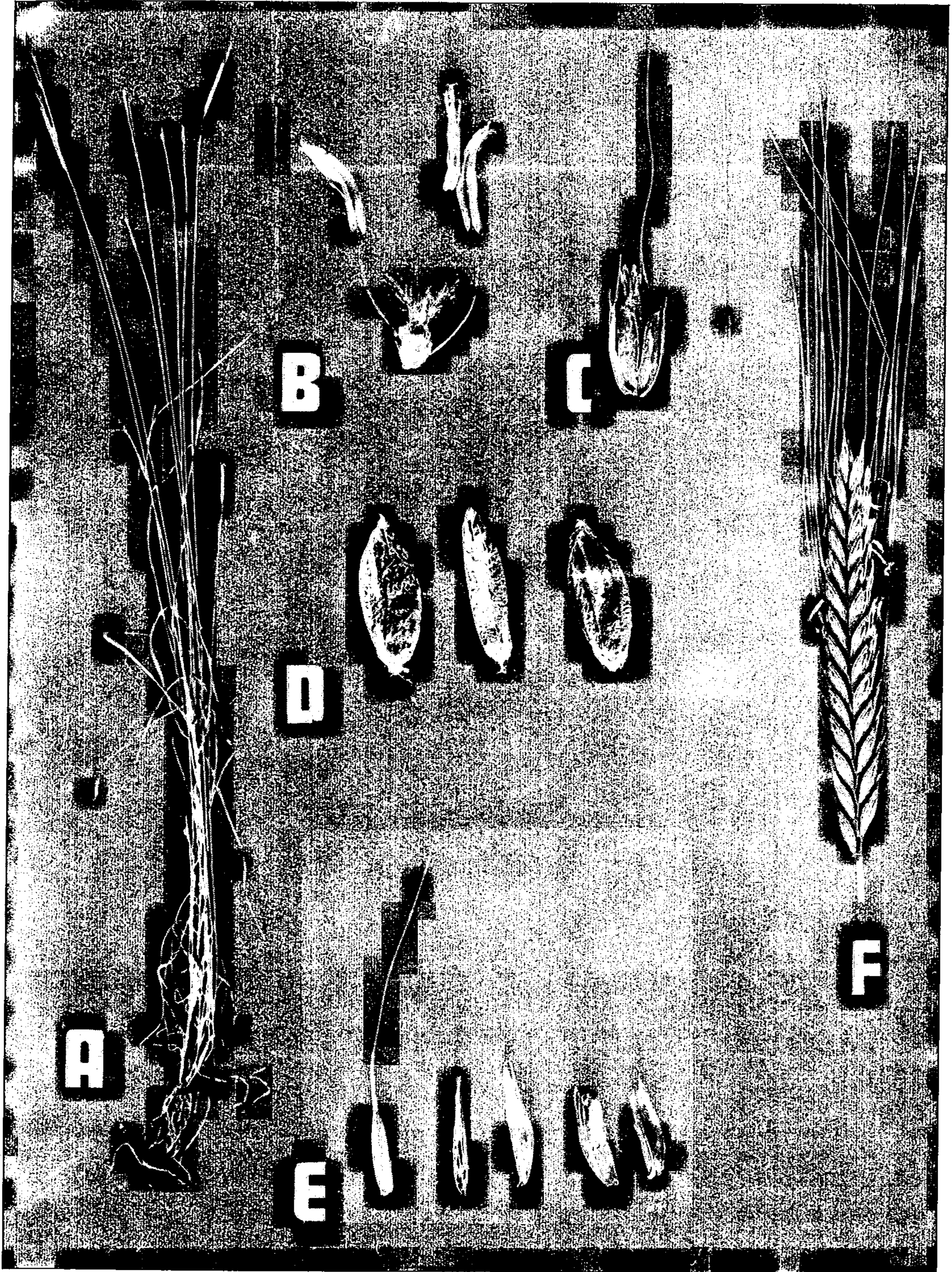

Plate 2.

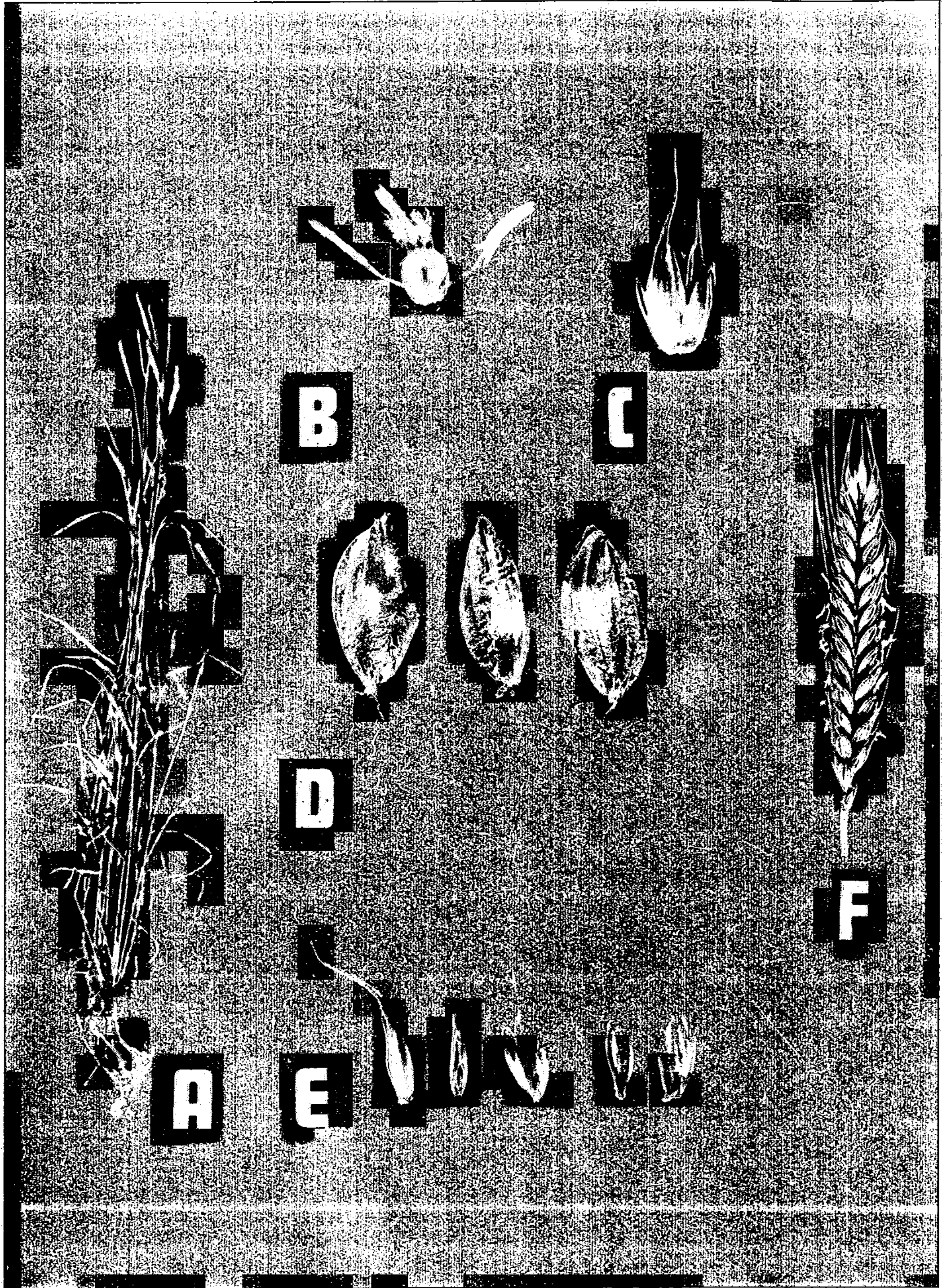

Plate 3.

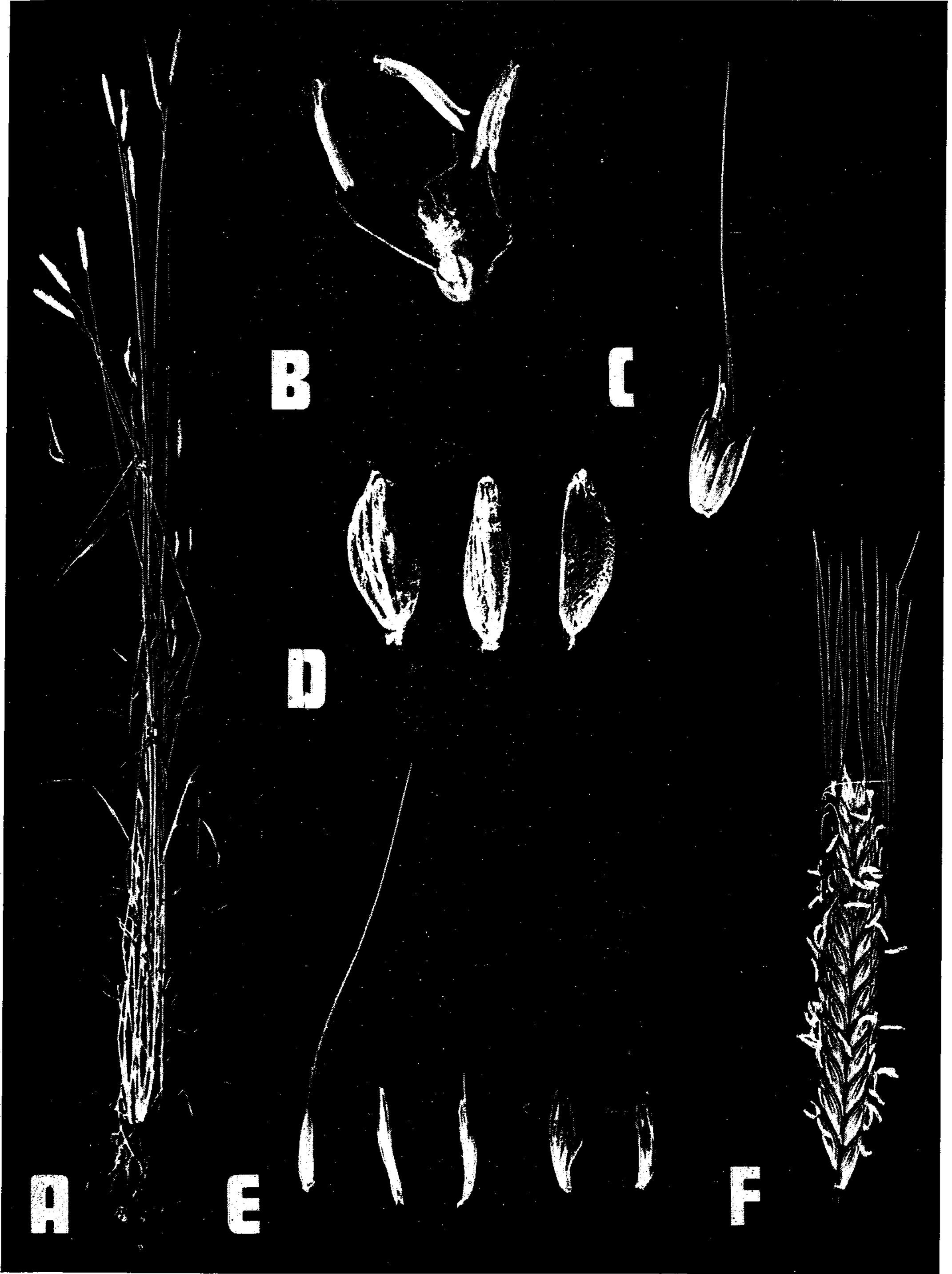

Plate 4.

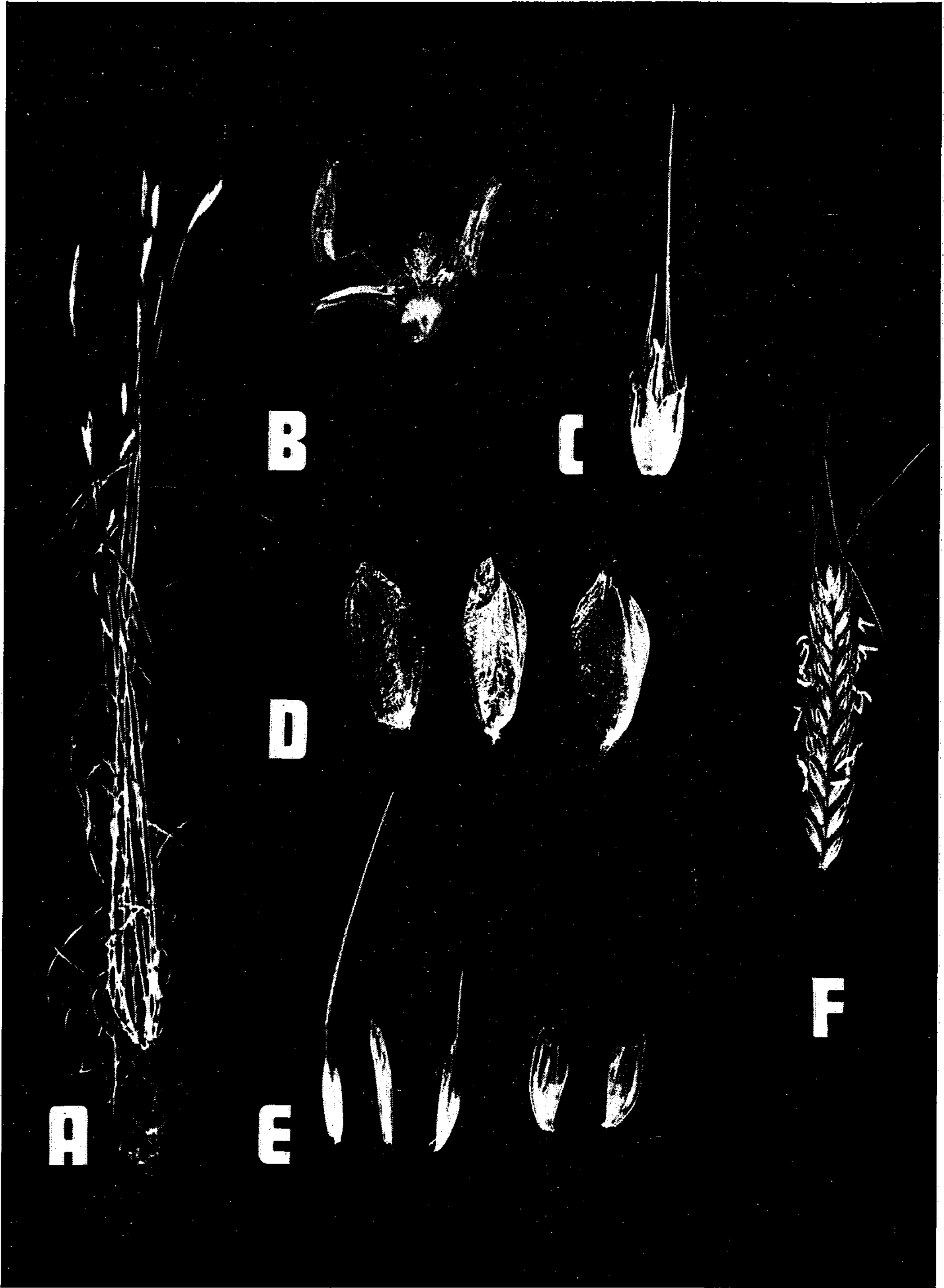

Plate 5.

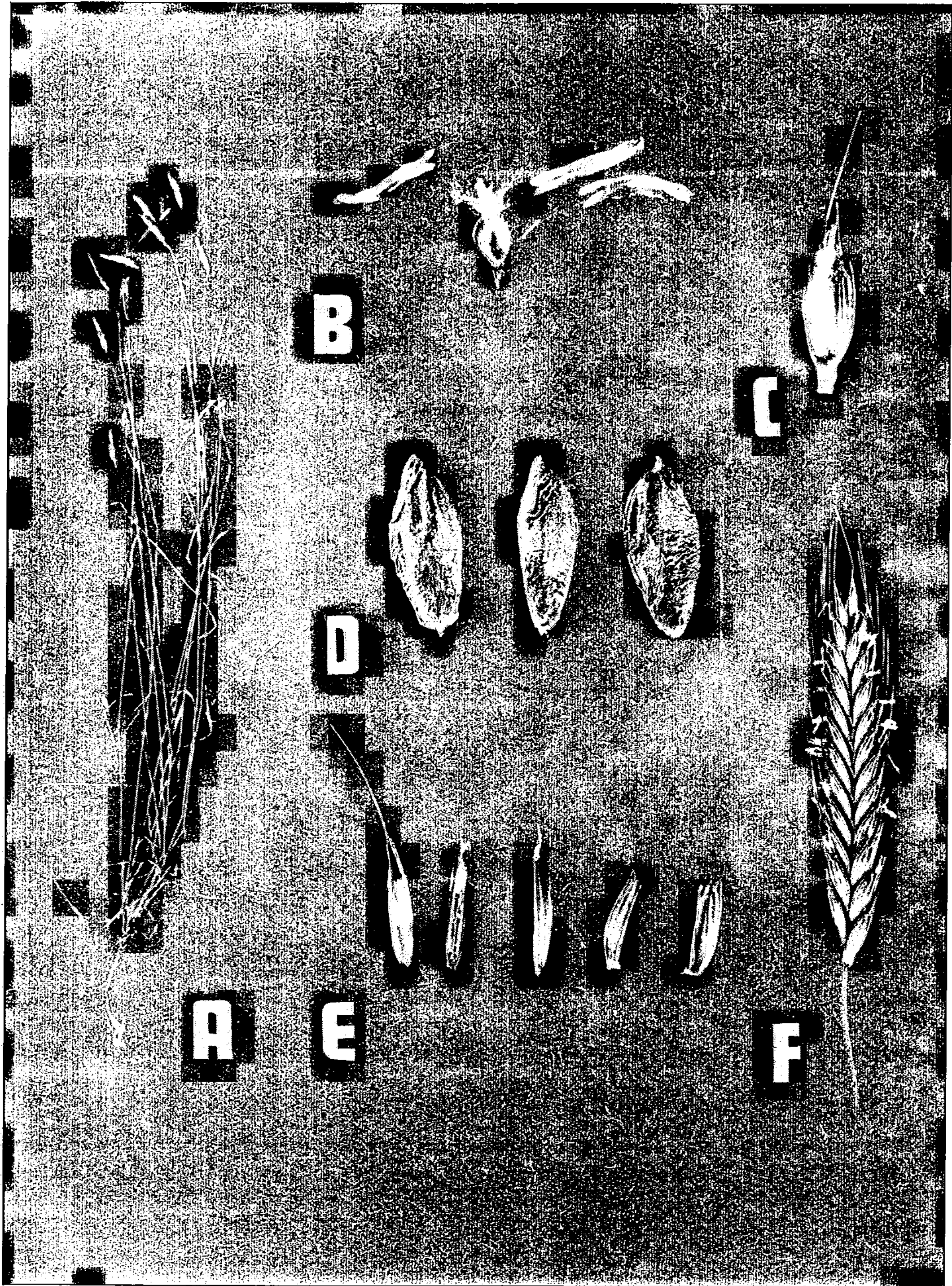

Plate 6.

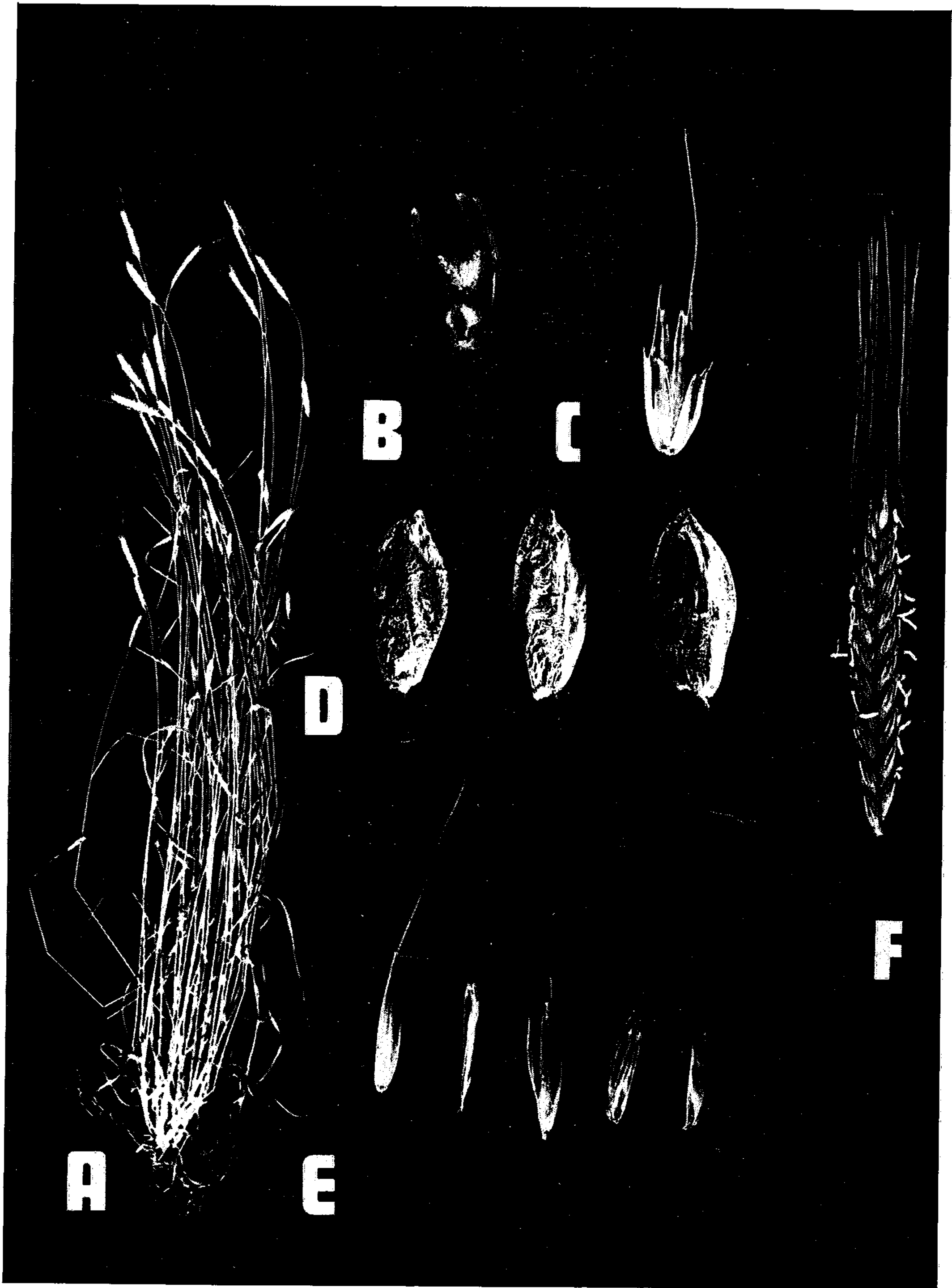

Plate 7.

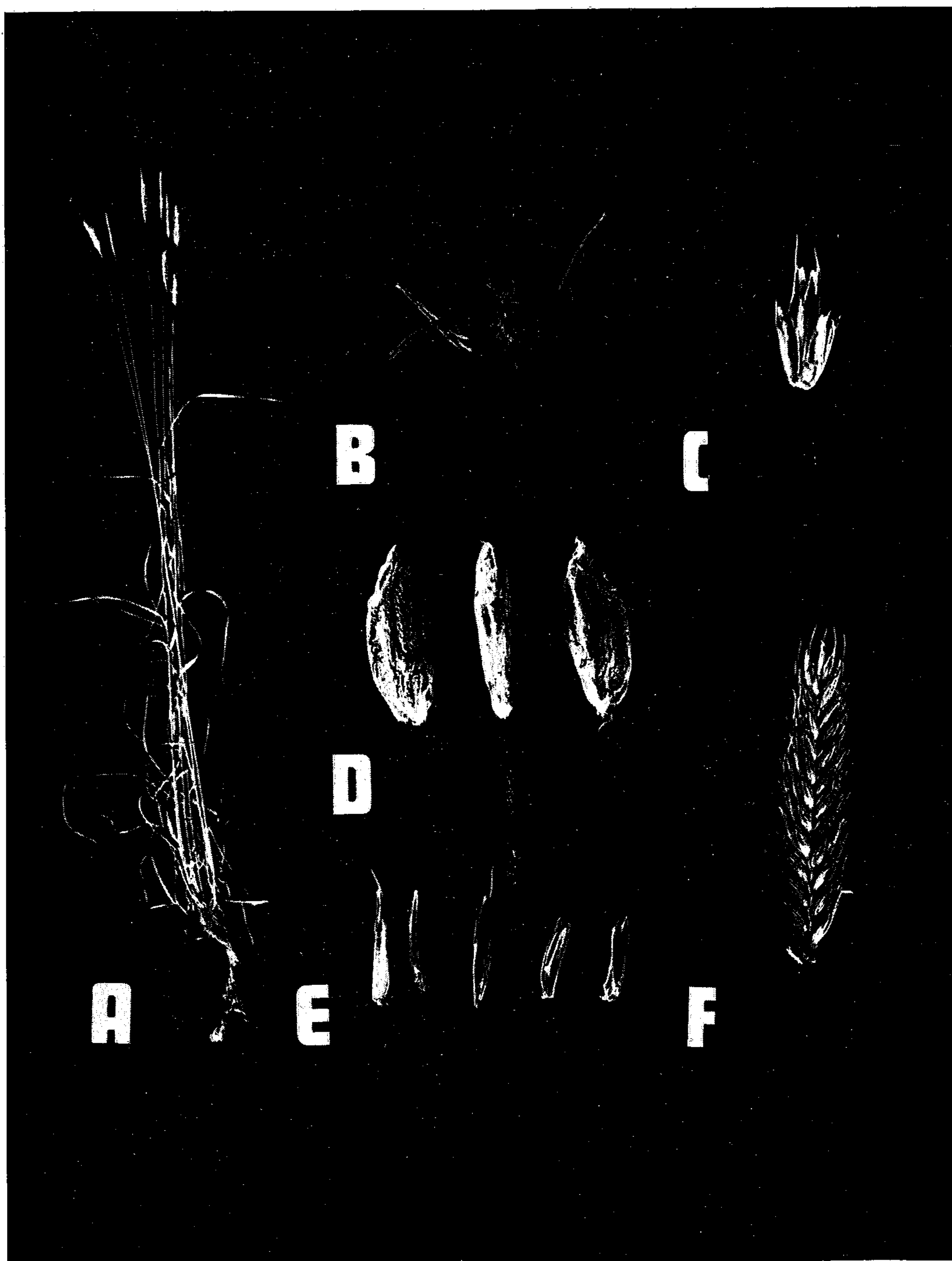

Plate 8.

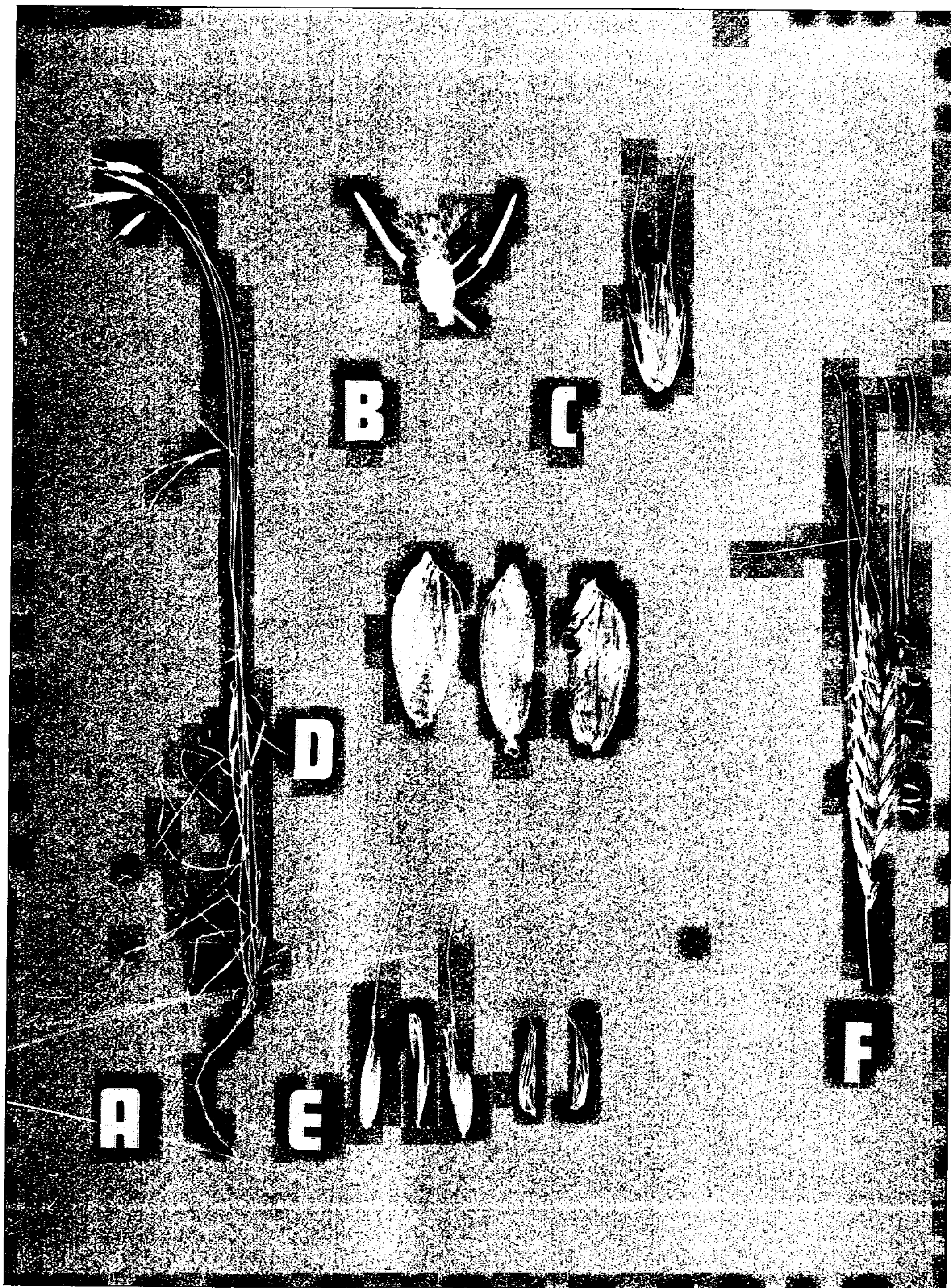

Plate 9.

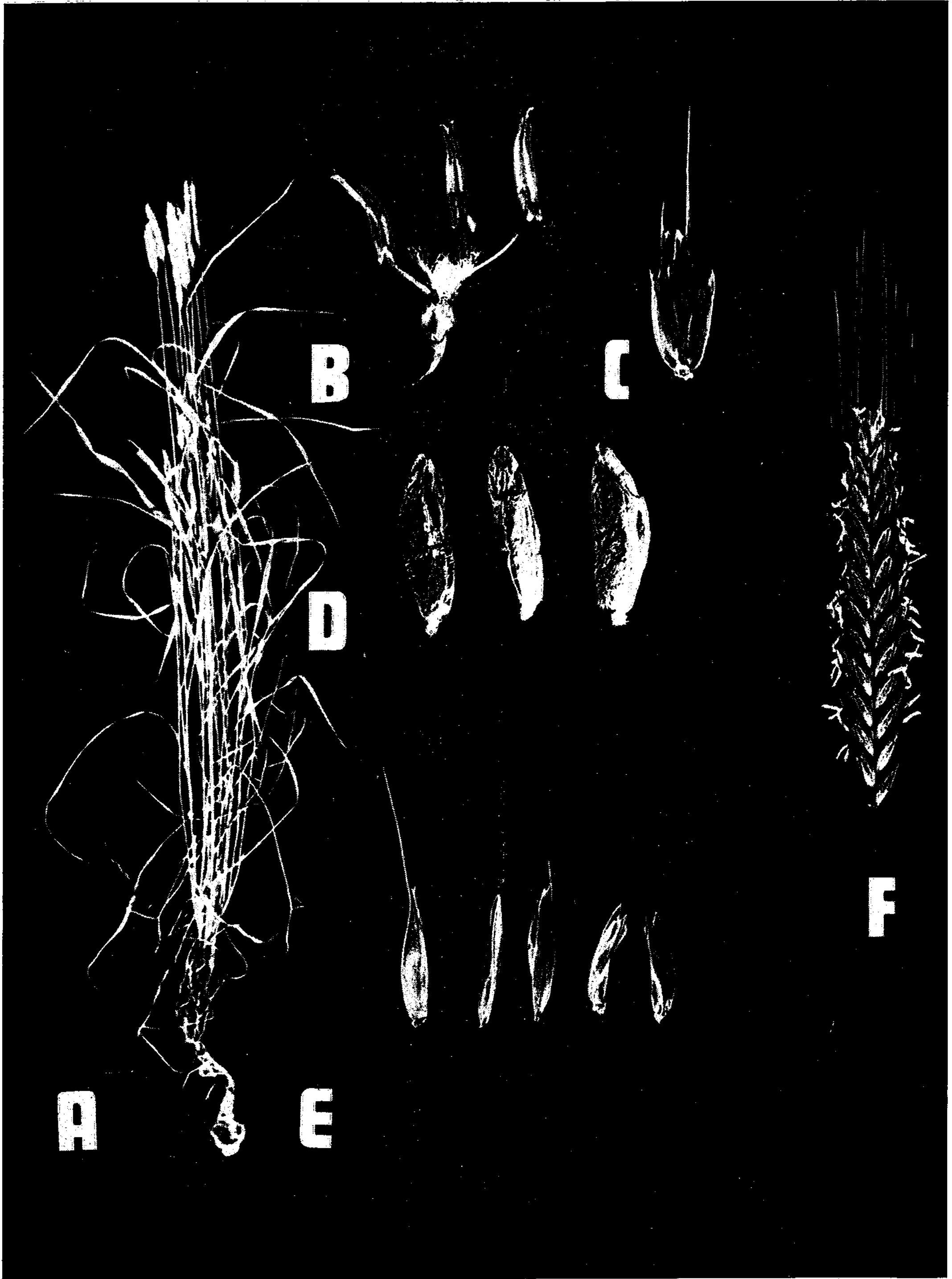

Plate 10.

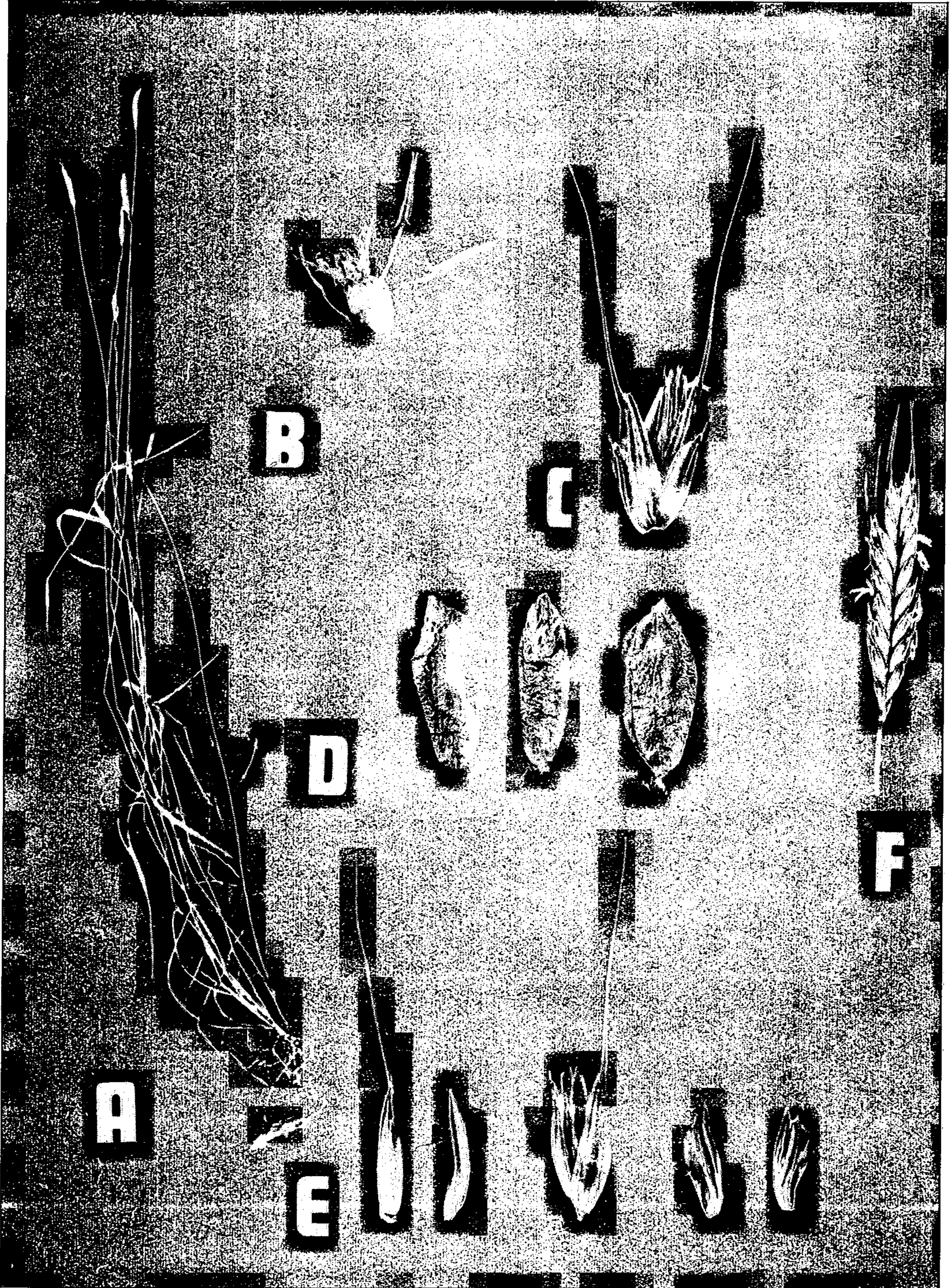

Plate 11.

III. Gene Symbols

Catalogue of gene symbols for wheat, 1977 supplement

R.A. McIntosh

Plant Bseeding Institute, University of Sydney,
N.S.W., Australia, 2006.

Reprints of the original Catalogue and the 1975 and 1976 Supplements are available. Three are no reprints of the 1974 Supplement. Supplementary Lists appear annually in Cereal Research Communications, Wheat Information Service and Wheat Newsletter.

Proteins

1. Alcohol dehydrogenase

Adh-R_1 (276A) Chinese Spring+Imperial Rye chromosome C 4R (276A)

3. **Glutamate oxaloacetate transaminase**

Gene	Ref.	Stock	Chromosome	Ref.
Got-A_1	(82B)	Chinese Spring	6A	(82B)
Got-B_1	(82B)	〃	6BS	(82B)
Got-D_1	(82B)	〃	6D	(82B)
Got-A_2	(82B)	〃	6A	(82B)
Got-B_2	(82B)	〃	6BL	(82B)
Got-D_2	(82B)	〃	6D	(82B)
Got-R_2	(276A)	Chinese Spring+6R	6R	(276A)
Got-A_3	(82B)	Chinese Spring	3A	(82B)
Got-B_3	(82B)	〃	3BL	(82B)
Got-D_3	(82B)	〃	3D	(82B)
Got-Ag_3	(82)C	Alien chromosome substitution line CS*3/TAP67 and certain 3D/3Ag translocation lines (82C)	3Ag	(82C)
Got-R_3		Chinese Spring+3R	3R	(276A)

Reduced Height

Rhtl	4A	(73E)

Response to Gibberellic Acid

Gail	4A	(73E)

Response to Vernalization

Vrnl	5AL	(136A)
Vrn3	5DL	(136A)

Reaction to *Puccinia graminis*

Sr9g (163) s: CS*7/Marquis 2B Sr_{16}; CS*4/Thatcher 2B Sr_{16}

v: Acme; Iumillo; Kubanaka;

Celebration Sr_{12} Sr_{16}: Lee Sr_{11} Sr_{16};

Hochzucht Sr_5 Sr_{12}; Thatcher Sr_5 Sr_{12} Sr_{16}.

Sr_{29} SrEC (169B) i: Prelude/8*Marquis/Etoile de Choisy (61A)(6D (61A)
v: Etiole de Choisy Sr_{23} (169B)

Sr_{30} (125A) SrW v: Festiguay (125A); Webster (125A) 5DL (125A)

Reaction to *Puccinia striiformis*

Yr_9 (153A) v: Moro (153A); P.I. 178383 1B (179)

Yr_{10} (153A) v: Aurora (319A); Kavkaz (319A); Irlando (319A); Neuzucht (319A) Saladan (174A); St 2153/63 (174A); Salzmunder Bartweizen (319A); Riebesel 47/51 (153A, 319A); Wentzel (319A); Weihenstephan 1007/53 (319A). 1B/1R or 1R(1B) (319A)

Genetic Linkages

Chromosome 3DL	*Got-D*$_3$	– centromere	Approx. 4.3% (82C)
Chromosome 4A	Gai_1	– Gai_3	No recombination (74E)
Chromosome 5AL	Vrn_1	– centromere	Independent (136A)
Chromosome 5DL	Vrn_3	– centromere	Independent (136A)
Chromosome 7AL	Sr_{22}	– *cn-A*$_1$	2% (278A)
	Sr_{22}	– Pm_1	41%(278A)

Literature Cited

61A DYCK, P.L., and E.R. KERBER. In preparation.

73E GALE, M.D., and G.A. MARSHALL. 1976. The chromosomal location of Gai_1 and Rht_1, genes for gibberellin insensitivity and semi-dwarfism, in a derivative of Norin 10 wheat. Heredity 37, 283–289.

82B HART, G.E. 1975. Glutamate oxaloacetate transaminase isozymes of *Triticum*: evidence for multiple systems of triplicate structural genes in hexaploid wheat. *In* Isozymes III. Developmental Biology. C. Marker (Edit.), Academic Press. New York 637–657.

82C HART, G.E., D.E. MCMILLAN and E.R. SEARS. 1976. Determination of the chromosomal location of a glutamate oxaloacetate transaminase structural gene using *Triticum-Agropyron* translocations.

125A KNOTT, D.R. and R.A. MCINTOSH In preparation.

136A LAW, C.N., A.J. WORLAND and B. GIORGI. 1975. The genetic control of ear-emergene time by chromosomes 5A and 5D of wheat. Heredity 36: 49–58.

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174A METTIN, D., W.D. BLUTHER and G. SCHLEGEL. 1973. Additional evidence on spontaneous 1B/1R wheat rye substitutions and translocations. Proc. 4th Int. Wheat Genetics Symp. Columbia Missouri 179–184.

276A TANG, K.S. and G.E. HART. 1975. Use of isozymes as chromosome markers in wheat-rye addition lines and in triticale. Genet. Res. Camb. **26**: 187–201.

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(Received Feb. 24, 1977)

IV. Miscellaneus

Recommendations of the Workshop on Rice Genetic Conservation[1]
December 12-15, 1977
IRRI, Los Baños, Philippines

Participants in the Workshop on Rice Genetic Conservation recognzied the extreme urgency of collecting, preserving, and evaluating all of the older, unimproved cultivars and wild relatives of *Oryza sativa* and *O. glaberrima* wherever they exist.

Recommendations of the participants follow.

I. General considerations related to field collection

a. All national and regional centers concerned with the genetic conservation of rice and IRRI should accelerate and intensify their collection rates in the next 5 years.

b. Definite guide lines are needed to determine which areas and countries should be assigned the highest priority for exploration and collection of traditional, unimproved varieties and wild relatives of both *O. sativa* and *O. glaberrima*. Criteria to be considered should include:

1. the rate at which improved cultivars are replacing local or traditional varieties;
2. the richness of genetic diversity and range of environments within the country or area;
3. the time and extent of past collection efforts.
4. the accessibility of potentially rich germ plasma areas to field collectors; and
5. the extent of local (in-country) support for collecting.

c. The priority for collection should be primitive cultivars, wild species of the A-genome (which can contribute to the breeding programs), improved local varieties, mutants (including structural chromosome variants), and wild species distantly related to the cultivated species.

d. The participants recognize the relative priorities of geographical areas for collection of rice cultivars and their closely related wild and weed taxa. The participants recommend that IBPGR, FAO and national governments consider these proposals in the respective regional symposia before initiating on field collection programs.

e. Not distracted by the size of existing collections, the participants recommend that all collaborating scientists continue to identify the gaps in world wide collections and communicate with respective regional and national programs to ensure that missing cultivars and wild taxa are collected.

f. The participants recommend that field workers collect enough seed of each sample

1) The Workshop was cosponsored by the International Board for Plant Genetic Resoruces (IBPGR) and the International Rice Research Institute (IRRI), and was attended by Dr. H. Kihara and Dr. K. Yamashita.

and send a portion directly to IRRI or a regional center that participates in the coordinated collection activities, or both. This will help ensure against loss of any accession.

g. Where possible, the germplasm collectors should be trained within the country. International institutes can provide suitable literature and training opportunities to ensure uniformity of criteria for collection, evaluation, and data collection.

II. Plan of action for collection

The action plan for the next 5 years developed by the participants is summarized below. For each country, the agency responsbile for coordination of collection activities is given in italic.

a: Africa:
1. All of Africa, particularly Gambia, Mali, Ghana, Benin, Togo, and Nigeria – IITA.
2. Tanzania and Zambia, and all French-speaking African countries, particularly Senegal, Mali, Upper Volta, Guinea, Guinea-Bissau, Niger, Cameroon, Chad, and Malagasy — IRAT and ORSTOM.
3. All West African countries, particularly Senegal, Gambia, Mali and Upper Volta — WARDA.

b. Southeast Asia:
1. Burma* — *ARI*, Central Farm, and Extension Service
2. Thailand* — Rice Division
3. Philippines* — *UPLB*, BPI, BAEx
4. Indonesia* — CRIA
5. Malaysia* — MARDI

c. South Asia:
1. Bangladesh* — *BRRI* and Department of Agriculture
2. India* — *NBPGR*, CRRI, ICAR-Complex, agricultural universities, and state departments of agriculture
3. Nepal* — *NRIP*, ICP
4. Pakistan* — *ARC*
5. Sri Lanka* — *CARI* (Sri Lanka-IRRI collaboration was agreed on early in 1977).

d. West Asia:
1. Iran* — *Rasht* and Amol Rice Research Stations
2. U.S.S.R. — *VIR*, AURRI

e. South America:
1. Brazil* — *EMBRAPA*, EMBRATER
2. Colombia, Equador, Guyana, Mexico, and Surinam — CIAT-IRRI.

f. Other countries – the participants request that IRRI contact officials in other countries

* Participation of IRRI staff members may be required in collection activities.

rich in germ plasm such as China, Vietnam, Cambodia, and Laos, whose scientists were not present at the Workshop, and invite them to participate in the collaborative collection scheme.

G. The participants urge all collaborating national governments to endorse and implement their portions of the proposed action programs as completely as possible before their irreplaceable germ plasm is lost.

H. Participants urge that IRRI coordinate and pool technical and finanical support for these collection activities where needed.

III. Collaborative plan to preserve and rejuvenate conserved rice seedstocks

The following comprehensive plan of action suggests a division of responsbilities among the participating countries and international institutes.

A. A complete set of conserved stocks (the base collection) should be preserved in long-term seed stroage at IRRI. National and international centers should provide to IRRI fresh and healthy seed of those stocks not already conserved there and of stocks that IRRI cannot effectively rejuvenate (see points C,D,E, and H).

B. IRRI should preserve, rejuvenate and distribute the indica and javanical cultivars and breeding lines of *O. sativa* and other *Oryza* species except for those from Africa.

C. Japan should preserve, rejuvenate, and distribute as many of the japonica varieties of East Asia as possible.

D. The United States should preserve, rejuvenate, and distribute varieties from the U.S., temperate South America, and the Mediterranean area; the U.S. also should continue to store duplicate samples of conserved IRRI stocks.

E. IITA should preserve, rejuvenate, and distribute cultivars of *O. glaberrima* and wild species of Africa. IRTA plans to collaborate with IITA on seed multiplciation. IRAT, ORSTOM, and WARDA plan to collaborate with IITA on medium-term storage.

F. The above centers should exchange and carefully compare accession lists to minimize the maintenance of obviously duplciate accessions within single collections and to ensure that no distinct accession or ecostrain is overlooked in the inventorial process.

G. Major germ plasm centers are urged to keep complete duplciate sets of accession records at separate locations to avoid loss through fire or other disasters. In the acquisition or exchange and use of accessions from major collections, original names and accession numbers should be included in the continuing records for cross reference purposes. Major germ plasm centers are encouraged to standardize record systems. Where such standardization is impractical, compatibility of separate systems should be assured.

H. Each national and regional center should preserve and rejuvenate its complete collection or at least a working collection, and assist the major germ plasm centers to increase and rejuvenate accessions that are porrly adapted to the growing conditions at the centers.

IV. Specific considerations related to management of genentic reosurces

A. National collections should continuously replace the missing accessions with stock from the base collection at IRRI and vice versa

B. Procedures and guidelines should be developed for collecting and cataloguing of minor variants such as ecostrains, induced mutants, and other genetic manipulations of varieties.

C. Participants recommend that germplasm conservationists at some locations try to "trap" genes from closely related wild species (for example, by growing domesticated and wild types in close proximity to take advantage of the natural crossing).

D. Countries that plan to initiate rice breeding programs may need a minimum working collection. The International Rice Observation Nursery of the International Rice Testing Program will provide widely divergent varieties and information to fulfill this need.

E. For the identification and avoidance of duplciates, observations on biochemical characters and root characters may be included in addition to the conventional agro-morphological characters currently taken on each accession.

F. Realizing that geographic environments differentially affect field performance and agronomic characters of varieties, stored data on such characters should include the date and location where such data were taken.

G. Participants urge countries that lack adequate facilities for medium-term seed storage to send duplciate samples of all accessions in their collections to IRRI for safe storage. National programs should give high priority to the establishment of facilities for medium-term storage.

H. Participants recognzie that variation may exist within a collected sample or population. In order to fully utilize such material, it is suggested that the original sample designation should retain as part of the continuing identification in any division of the sample according to type.

I. Apparent off-types within named varieties should be retained in the collections — not discarded — unless they are obviously mechanical mixtures. Otherwise they should be designated as subsamples of the original accessions. When seedstocks are rejuvenated, the same care should be taken to not rogue out variants in the original sample and thus lose potentially valuable genes forever.

J. Morphologic and other economic traits recorded in the data systems of the germ plasm centers should be expanded periodically to include data collected at other

locations. Also the inclusion of additional characteristics in the data system may be desirable.

K. The participants recommend further standardization of terminology used in collection, preservation, and utilization of germ plasm.

L. Recognizing the frequent changes in taxonomic nomenclature, the participants recommend that synonyms be identified in all rice collection catalogues.

M. The participants stressed the importance of having continuity in personnel experienced in germ plasm conservation and in accurate record keeping for the proper maintenance, evaluation, and utilization of rice germ plasm.

N. Participants recognize an urgent need to collect germfls plasm of wild and weed races of rice. To properly carry out such collection activities, specialized training conducted in the locality of the materials is highly desirable.

O. Participants expressed the desirability of adequate training of workers for field collection, maintenance, storage, and utilization of valuable germ plasm.

V. Future plans

A. Participants strongly recommend to IBPGR and collaborating national governments that another workshop similar to this one be organized and held within 3 to 4 years. IBPGR and collaborating international agricultural research institutes might sponsor such a workshop to assess progress and to develop continuing action plans for conservation for ice genetic resources.

B. An organizing committee should be set up in the immediate future to develop plans for a comprehensive Seed Science Workshop to be held within the next 2 years.

C. Definite plans should be made to request nations that have areas of rich diversity of wild types to preserve such areas as natural reserves. Living collections, particularly of wild species, should also be maintained at two or more locations.

V. Editorial Remarks

Announcement for future issues

WIS Nos. 47 & 48 will be planned for publication in December 1978 and March 1979. Manuscripts for these issues are accepted any time, not later than October 30, 1978 and Jan. 31, 1979.

WIS is open to all contributions regarding methods, materials and stocks, ideas and reserach results related to genetics and cytology of *Triticum*, *Aegiolops*, *Secale*, *Haynaldia* and related genera. Manuscripts should be typewriten in English, and submitted with duplicates. One article should not exceed five printed pages, including one textfigure (smaller than $7 \times 7\ cm^2$). 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:

Kosuke YAMASHITA
Wheat Information Service
Kihara Institute for Biological Research
3-122-2, Mutsugawa-cho, Minami-ku,
Yokohama 232, Japan

Membership Fee

Due to the economic situations, the yearly Membership Fee has been raised up to ¥ 1,000 for foreign as well as Japanese members from the fiscal year beginning April 1978. The money should be paid by the Foreign Postal Money Order, otherwise considerable loss is caused due to the bank charges. Back numbers are available.

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Explanation of the Figure on the Cover

Mixing curves of the original "1D" chromosome substitution line with 4 backcrosses to Chinese Spring (top left), the new 1D line with 6 backcrosses (top right), Chinese Spring (CNS, lower left), and Cheyenne (CNN, lower right). (Cf. Fig. 1, p. 14, present issue of WIS, R. MORRIS, P.J. MATTERN, J.W. SCHMIDT and V.A. JOHNSON)

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発行者　山　下　孝　介

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