Langley

MAIZE GENETICS COOPERATION

NEWS LETTER

31

March 15, 1957

Department of Botany
University of Illinois
Urbana, Illinois

CONTENTS

******

I. GENETIC NOMENCLATURE IN MAIZE

The International Committee on Genetic Nomenclature will submit its recommendations on nomenclature and symbolization to the forthcoming International Congress at Montreal. So far the Committee has not agreed upon its recommendations and some feel that no attempt should be made at this time to establish a rigid system. In order to aid the International Committee I have been asked to obtain the views of maize geneticists with respect to certain suggestions. Given below is a summary of the nomenclatorial system now used by maize geneticists.

1. The linkage groups and chromosomes are designated by Arabic numerals. Linkage group 1 includes those genes which lie in the longest chromosome, etc. The longest chromosome of the monoploid set of 10 is called chromosome 1 and the shortest chromosome 10.

2. Whenever biliteral symbols are used the second letter shall not be dropped as a subscript. Italicize gene symbols.

3. Literal or numeral superscripts shall be used to represent different members of an allelic series, e.g. R^r, R^g, r^r, r^g. Superscripts in italics.

4. Numeral subscripts shall be used to represent different (polymeric) genes which give phenotypically similar effects, e.g. v_1, v_2, v_3, etc. The subscripts are also italicized.

5. The normal allele of a recessive mutant gene shall be designated as has been customary in the past, i.e. either by a + sign or by a capital letter; e.g. the normal allele of su can be either Su or +, depending upon which is the most convenient to use. The normal allele of what are commonly considered dominant genes can be designated, as in the past, by either a + sign or by small letters, i.e. the normal allele of Tu can be either + or tu.

6. The letter T shall denote translocations. T 1-2a would represent the first case of reciprocal translocation between chromosomes 1 and 2, T 1-2b the second, etc. A reciprocal translocation involving one of the normal A set of chromosomes and a B chromosome shall be designated TB. TB-9a would represent the first case of a reciprocal translocation between chromosome 9 and a B chromosome. All symbols are in italics and on the same line -- i.e. no subscripts are used.

7. The symbol Df shall be used for deficiency. The first deficiency involving chromosome 10 will be represented as Df 10a; the second as Df 10b, etc. All parts are italicized and are on the same line. In practice this has not been followed since some maize workers use numerals to designate different deficiencies. Agreement is needed here.

8. The symbol In shall stand for inversion. An inversion involving chromosome 4 will be represented as In 4a, the second case as In 4b, etc. All parts are italicized and are on the same line.

9. The symbol K shall be used to designate chromosome knobs. A knob on chromosome 9, for example, would be K9, one of chromosome 10 would be K10. When more than one knob is found on a specific chromosome arm the proximal one would be designated by the letter p, the more distal one by the letter d, and a terminal knob by the letter t. If it is necessary to denote the arm of the chromosome this can be done by using the letter S for the short arm and the letter L for the long arm. On this scheme the terminal knob on the short arm of chromosome 9 would be designated K9St. All parts are italicized.

10. X-ray induced mutants are indicated by the letter x. For example, the recessive mutations at the A_1 locus found by Stadler and Roman are represented by the symbols $a\text{-}x_1$, $a\text{-}x_2$, $a\text{-}x_3$. All parts are italicized.

An unresolved problem confronting maize workers is the symbolization of the different sources of male sterile cytoplasm and of fertility restoring genes. At recent Southern and North Central Corn Conferences approval was given to the following recommendations:

Different sources of male sterile cytoplasm be designated as cms_1, cms_2, etc. The symbol Rf be used for fertility restoring genes (Rf_1, Rf_2, etc.).

However, the Committee on Nomenclature at the Northeastern Corn Conference had the following recommendations:

(1) Capital letters be used to designate the source of sterile cytoplasm--e.g. the letter T for the Mexican June source from Texas, the letter S for the U.S.D.A. source, etc.

(2) Preference was indicated for the use of R or F for fertility restoring loci but they are willing to accept Rf if this meets with general approval.

(3) When an inbred such as C103 has been converted to type in a sterile cytoplasm it could be represented as C103T if the Texas source was used, etc. If such a sterile inbred as C103T is restored to fertility it is written C103TF (if F represents fertility restoration).

It has been the common practice in genetic literature to designate cytoplasmic differences or factors by Greek letters. This appears singularly inappropriate for maize where it is conceivable that numbers of different cytoplasms will exceed the number of letters in the Greek alphabet.

Although no consensus has yet been reached by the corn breeders it is to be hoped that some definite system can be agreed upon which can be transmitted to the International Committee. I do not believe an attempt will be made to insist on adherence to a rigid nomenclatorial system but maize workers may be called upon to examine their system in the hope that it may be brought into closer agreement with that used for other plants and animals.

I believe that the maize nomenclatorial system agrees on the whole with that used by most other investigators but there is a difference on several points. For example, there is considerable sentiment for the use of Roman rather than Arabic numberals to designate linkage groups and chromosomes. Personally I feel this is undesirable. The designation T7-8a is unquestionably to be preferred to TVII-VIIIa. A second point of difference is the designation of the normal allele of a mutant locus. The suggestion has been made to represent the normal allele by the mutant symbol with the + sign as a superscript (i.e., the Wx allele would be wx^{+}).

I would appreciate any comments or criticims which you may care to send me and I will attempt to fairly present your views to the International Committee.

M. M. Rhoades

II. REPORTS FROM COOPERATORS

ALABAMA POLYTECHNIC INSTITUTE
Auburn, Alabama
Department of Botany and Plant Pathology

1. A study of reciprocal crossover differences in the presence of heterozygous translocations involving the short arm of chromosome 9.

In 1950 Burnham reported in the Corn News Letter that when $\frac{C + + T\ 5\text{-}9a}{c\ sh\ wx\ +}$ was used as the female there was 6.6% recombination between sh and wx, whereas when it was used as the male there was 12.5% recombination. To study this phenomenon further the following translocations were selected:

Table 1.

Group*	Identification in this study	Translocation with Longley's 1950 Ident. No.	Break-Points		Source	
A	2	23-19	9S .51	5S .28	Anderson	6057-1
	3	37-32	9S .46	5L .67	"	4871-3
	4	37-84	9S .36	5L .28	"	4997-6
	5	30-96	9S .15	5S .25	"	5614-8
	6	31-4	9S .08	5L .07	"	4817-7
	7	5-9a	9S .40	5L .85	Burnham 11910-5 X 11911-6	
B	8	38-48	9S .32	2L .36	Anderson	6656-1
	9	27-1	9S .27	8L .06	"	5391-3
	10	3-9c	9S .20	3S .15	Burnham 11885-2 X 11886-6	
C	14	X7-39	5L .68	9L .44	Anderson	X7-39
	15	24-17	5L .86	9L .76	"	6200-1
	16	39-81	5L .51	9L .63	"	4352-7
	1	X14-111	5L .46	9L .74	"	1330
D	12	26-50	5L .81	10S .38	"	5290-4
	13	30-89	5L .82	2L .74	"	5602-2

* Group A includes translocations with breaks at different points in the short arm of 9, and the chromosome 5 break in the long arm at different points when possible. Group B includes translocations with breaks near .30 in the short arm of 9 and involving a chromosome other than 5. Group C includes translocations with breaks in the long arm of 5 near .80 and in the long arm of 9. Group D includes translocations with breaks near .80 in the long arm of 5 and involving some chromosome other than 9.

These translocations were first crossed to the recessive stock c sh wx gl_{15} and then exact reciprocal backcrosses were made to study recombination in the sh wx and wx gl_{15} regions.

Table 2 is a summary of recombination tests in the sh wx region for all heterozygous translocations involving chromosome 9. The translocations are listed in order of the position of the break-point in the short arm of 9. Included in the table are the ranges and average recombination values in the male and female, the average of the differences ($\bar{d}$), and their significance as measured by "Student's" paired comparison test. Note that when the break in 9S is near the centromere there is little difference between the male and the female in recombination between sh and wx. As the distance from the centromere increases, the difference becomes increasingly great but at 9S .51 there is again little difference.

In this study these observations were made:

1. Recombination in the male was always higher than in the female.
2. The magnitude of the difference between male and female had no relationship to the chromosome which was translocated with 9, or to the position of the break in that chromosome.
3. The magnitude of the difference had no relationship to the length of the interstitial segments.
4. The magnitude of the difference had no relationship to the formation of chromatids of unequal length as the result of crossing over in the interstitial segment.
5. The magnitude of the difference had no relationship to the amount of general reduction from the normal of 21% recombination between sh and wx.

The simultaneous study of recombination in the wx gl_{15} region showed some reduction from normal for most of the translocations but no pattern of differences between reciprocal crosses such as was observed in the sh wx region. Recombination between pr and v2 on chromosome 5 was studied for the translocations involving 5L. Here also recombination was reduced in most cases and usually the difference between reciprocal crosses was not significant.

This work was done at the University of Minnesota under Dr. C. R. Burnham.

E. M. Clark

Table 2. Summary of recombination tests in the sh wx region.

Translocation	Break-points	Exact reciprocals	Total seeds classified		Range in recombination values		Average Recombination		$\bar{d}$	p
			Male	Female	Male	Female	Male	Female		
#		#			%	%	%	%		
2	9S .51 5S .28	5	1717	1686	0.3-6.1	1.8-7.1	3.2	4.1	1.22	.2-.3
3	9S .46 5L .67	6	2341	1918	10.8-26.8	1.7-9.2	18.4	6.0	12.21	.001-.01**
7	9S .40 5L .84	8+1 Θ	3722	1774	10.0-15.0	0.0-3.8	14.0	1.8	11.37	<.001**
4	9S .36 5L .28	6	2063	1486	12.0-30.2	6.8-15.7	21.2	11.7	8.82	.001-.01**
8	9S .32 2L .36	6	2234	1165	12.3-20.7	3.6-19.4	17.7	8.5	8.97	.001-.01**
9	9S .27 8L .06	7	2118	1409	13.9-21.2	8.3-18.3	16.2	11.2	4.19	.02-.03*
10	9S .20 3S .15	6	2339	2203	17.4-27.0	14.2-22.3	22.1	16.7	5.27	.04-.05*
5	9S .15 5S .25	6	1897	1349	15.6-23.6	13.0-19.1	18.5	15.0	3.58	.08-.1
6	9S .08 5L .07	6	2099	1271	13.7-26.9	13.4-20.9	20.5	17.9	2.40	.2-.3
14	9L .44 5L .68	6	2137	1691	21.7-30.2	20.5-28.1	26.4	24.8	1.78	.1-.2
15	9L .76 5L .86	4+1 Θ	1735	1062	18.2-29.6	17.9-24.9	25.5	21.4	4.84	.05-.1
16	9L .63 5L .51	4	1144	1217	20.9-29.2	23.9-25.2	24.5	24.7	0.03	>.9
1	9L .74 5L .46	4	1218	1170	16.3-22.1	17.5-26.4	21.8	21.6	1.57	.6-.7

* Significant at 5% level.
** Highly significant.
Θ Same heterozygote used as male and female but with different recessive parents.

BEAR HYBRID CORN COMPANY, INC.
Decatur, Illinois

1. Radiation as a breeding tool.

The primary aim of this project was to investigate radiation as a practical method of inducing endosperm and plant mutations in agronomically desirable corn inbred lines.

During the summer of 1954, Dr. W. Ralph Singleton, then associated with the Brookhaven National Laboratory, was kind enough to assume responsibility of the irradiation and pollination of three inbred lines, B14, Hy_2, and 07. Seeds from these irradiated plants were grown and selfed in our nursery in 1955.

Additional lines, M14 and C103, as well as B14 were sent to Brookhaven for irradiation in 1955. Also in 1955, we grew inbred lines M14, B14, and C103 in buckets and through the courtesy of St. Marys Hospital in Decatur and Dr. Glenn E. Ross, radiologist, tassels of these plants were exposed to 600r and 700r from a General Electric deep therapy x-ray machine seven days prior to pollen shed. Seeds from all of these irradiated plants were grown and selfed in 1956.

Listed are observations made on the 1955 and 1956 plantings:

1955 Data	B14	Hy	07	
Total Plants Observed	522	239	124	
Plant Aberrations	103	49	24	19.9%
Total Selfed, Ears Screened	143	115	42	
Ears with Endosperm Segregations	3	4	1	2.7%

1956 Data

Plant Aberrations - Seed from Irradiated Generation

Inbred Line	M14	B14	C103	07	% Aberrations by Method
Thermal Neutrons (BNL)					
Normal Plants	75	103	28		
Aberrant Plants	29	29	81		27.7%
1300r ♂ and ♀ (BNL)					
Normal Plants	57				
Aberrant Plants	6				9.5%

Plant aberrations - Seed from Irradiated Generation (Cont'd)

Inbred Line	M14	B14	C103	07	% Aberrations by Method
1300r ♂ (BNL)					
Normal Plants	62		35	101	
Aberrant Plants	22		11	8	17.2%
600r X-ray					
Normal Plants	63	121			
Aberrant Plants	12	17			13.6%
700r X-ray					
Normal Plants	56		87		
Aberrant Plants	0		12		7.7%
% Aberrations by Line	18.0%	17.0%	22.7%	7.3%	

Endosperm Segregations - Selfed Ears from Irradiated Generation

Inbred Line	M14	B14	C103	07	% Segregations by Method
Thermal Neutrons (BNL)					
Normal Plants	71	89	17		
Endosperm Segregates	2	2	1		2.8%
1300r ♂ and ♀ (BNL)					
Normal Plants	55				
Endosperm Segregates	2				3.6%
1300r ♂ (BNL)					
Normal Plants	56		26	40	
Endosperm Segregates	2		2	0	3.3%
600r X-ray					
Normal Plants	66	111			
Endosperm Segregates	1	1			1.1%
700r X-ray					
Normal Plants	51		78		
Endosperm Segregates	1		2		2.3%
% Segregations by Line	2.7%	1.5%	4.1%	0%	

Aberrant plant types include several different categories. For example, M14 plants irradiated by thermal neutrons in 1955 and grown in 1956 had 29 aberrant plants in a total population of 104. In classification, some plants were listed under two categories.

Plants shorter than normal	7	Completely sterile tassels	10
Very narrow leaves	1	Kernels formed in tassel	1
Extremely late	7	Shoot with no silks	1
Semi-sterile tassels	10		

Endosperm segregations observed in all lines included wx, su_1, y, and various defective types. Differences in aberration rates were noted according to inbred, type of irradiation, and amount of irradiation.

Difficulty was encountered in obtaining good seed sets by selfing even when the pollen appeared normal and abundant. The low number of ears classified for endosperm segregations in relation to the plant characters classified both in 1955 and 1956 bears this out.

The S_2 generation from plants irradiated in 1954 were grown in 1956 to observe possible desirable recessive plant characteristics. In this material we noticed several ear-rows which were segregating for various plant characteristics. We did not keep detailed data on obvious deleterious segregations -- our main screening was to detect obvious improvements of undesirable line characteristics. We found none.

As we see it, the chief objection to using radiation as a breeding tool is the same as is encountered with many other breeding techniques, namely, the testing of a large progeny to identify desirable agronomic characteristics.

Marvin L. Vineyard
Robert P. Bear

BLANDY EXPERIMENTAL FARM
University of Virginia
Charlottesville, Virginia

1. The Blandy Experimental Farm.

The Blandy Experimental Farm has joined the ranks of research institutions working on corn. Although it has been in operation for some 30 years comparatively little corn has been grown. Research at the Farm has consisted mainly in genetics, cytogenetics, and cytotaxonomy. Men who have taken their degrees at the Blandy Experimental Farm are now holding positions of responsibility in all sections of the country, particularly in the South.

The Blandy Experimental Farm is located in the Shenandoah Valley of Virginia. It consists of slightly more than 700 acres, 100 acres of which is the Orland E. White Arboretum named after the first director of the Blandy Experimental Farm. This arboretum consists of more than

5,000 species of plants. The farm was willed to the University by the late Graham F. Blandy. It was put into operation as a biological laboratory in 1927 when Dr. O. E. White became the first director. There are working and living facilities for a number of graduate students, also two furnished apartments for guests and investigators. The staff, students and guests take their meals in a common dining room provided by the Farm. There are available a number of fellowships paying $1200 a year for the graduate students. Since the students spend at least half of the year at the Blandy Farm where the cost of living is merely the cost of food, or about $30 a month, the stipends of $1200 a year are adequate for living throughout the year. Fees and tuition are taken care of by the University for students on fellowships. At least two or three of these Fellowships will be open in the fall of 1957 and we would be pleased to have applications from anyone interested in doing genetic research, particularly with corn.

2. Blandy Radiation Field.

Beginning in the summer of 1957 there will be a Cobalt-60 radiation machine installed in a small circular field which is completely shielded by concrete wall and earth embankments. The radiation field is in some ways similar to the first radiation field established at the Brookhaven Laboratory with the difference mentioned that we are using concrete and soil for shielding instead of distance as is done at the Brookhaven Laboratory. Also this source will be considerably smaller, between 100 and 200 curies instead of the 1800 curie source in use at Brookhaven. It is not planned to grow plants for their entire life in the field at the Blandy Farm but rather grow them in pots or pails and move them in for a short radiation of fairly high intensity at different periods in the life of the plant. With a 200 curie source it would be possible to get around 3,000 r per day at a distance of 1 1/2 meters from the source. At 3 meters from the source the radiation will be 720 r per day which is sufficient for inducing changes in the growing corn plant. There are great differences in the sensitivity as the corn goes through the meiotic cycle. The short note to follow by Alan Caspar will give a few of the details of the difference observed. We will be happy to have investigators spend some time at the Blandy Farm and make use of the radiation facilities there. In future years it may be possible to make service irradiation for investigators, although for the present year we are not prepared to do this.

3. Plastic Tags for Labelling Hand Pollinated Ears of Corn.

In the 1955 edition of the Maize Genetics Cooperation News Letter we had a short item entitled "Hurricane Proof Tags." Our primary object in using the plastic tag there was so that the hurricanes could not obliterate the records on our hand pollinated ears. However, since that time we have found these tags most useful even when we do not have

hurricanes. They are especially useful in making mass pollinations where we have been testing mutation rates induced in radiated developing pollen. The tags are all stamped prior to pollination with the data which we wish on the tag. Stamping is done by a "Crown" stamping machine which has 12 bands each containing a complete alphabet and numbers so that any combination can be stamped onto the tag. The tags are 3 1/2 inches by 5/8 inch, large enough for at least 12 letters or figures. The ink used is waterproof since these tags must stay out in the weather. Tags have been exposed continuously to the weather since last summer and the ink has not faded at all. Where a number of pollinations are to be made from the pollen of a single plant the tags can be stamped and hung on the plant desired and they serve as a reminder of how many pollinations are to be made. When the tags are used up the pollinations are complete. They come in five different colors, red, yellow, blue, green and white. Different experiments can be labelled automatically with a different color which makes sorting of the ears at harvest time an easy chore. The plastic tags are wired onto the plant with copper wire. At harvest time a quick jerk cuts through the plastic tag leaving the tag free without the wire. These are then strapped onto the ears with a rubber band. We have been using rubber bands for fastening labels onto hand pollinated ears for about 20 years and they give good results and hardly ever is a band broken. One precaution in using bands on the plastic tags is not to wrap the rubber band too tightly as it might be cut by the plastic tag. The advantage of rubber bands in fastening the tags to the ear is that as the ear shrinks the band also shrinks and remains tight to the ear.

One of the biggest advantages of using prelabelled tags for hand pollinated ears is that it is not necessary to transfer any data from the tag used in the hand pollination which cuts down materially on the errors in labelling the hand pollinated ears. The plastic tags can be obtained from the National Band and Tag Company, Newport, Kentucky.

W. Ralph Singleton

4. Radiation Induced Pre-meiotic Mutation.

A series of experiments was started in 1953 and 1955 to determine the relative sensitivity of the various stages of maize microsporogenesis to gamma radiation. The results reported here are from the 1955 experiment in which plants homozygous dominant for the endosperm characters Su, Y, Sh, and Wx were placed in the Brookhaven gamma field for two day periods where they were radiated for 20 hours each day. The first group of plants was placed in the field 36 days before the pollen was shed. The first group was removed after 40 hours of gamma radiation given at the rate of 50 r per hour, and another group placed in the field. This was continued until the last group to go in the radiation field was shedding pollen when removed from the field. Pollen was collected from all the plants in the experiment on this day and placed on silks of a

multiple recessive tester stock. Ears were harvested and scored for su, y, sh, and wx endosperms.

Nine recessive endosperms were recovered from a population of 18,000 seeds produced from pollen which had been radiated for a two day period between 36 and 14 days before pollen shedding. 7,100 seeds were produced from plants which had received their radiation during the last twelve days of microsporogenesis, and there were 262 mutant endosperms recovered from these seeds.

F_1's were grown from seeds with mutant endosperms. It was found that of the nine recessive endosperms from the early radiated group five showed the mutant phenotype on the F_1 ears. All these ears were normal with full seed sets. Two of the remaining four seeds did not produce F_1 seedlings, one was lost in the seedling stage to cutworms, and the last produced a normal non-mutant ear. Three of the mutations were from Sh to sh, on chromosome 9, one was from Wx to wx, also on 9, and the last one was from Su to su on chromosome 4. Pollen was not examined from these mutants but transmission of the mutant through the megaspore was apparently normal.

F_1 plants were grown from 130 seeds of the 262 mutant endosperms produced from the pollen radiated during the last 12 days of microsporogenesis. 27 or 20% of the F_1's showed the same recessive endosperm as the seed which was planted. However, all of these ears were semi-sterile, which would indicate that all of the mutant endosperms produced by radiation of pollen late in the microsporogenesis were the result of chromosomal aberrations.

3.7% of the endosperms scored for the four recessive endosperm characters showed the mutant phenotype in the F_0 when the pollen was radiated during the last 12 days of microsporogenesis. When the mutant types were planted 60% of the resulting F_1's were semi-sterile while the non-mutant seeds from the same radiation period produced F_1's of which 30% were semi-sterile.

Since we are more interested in the possibilities of using radiation to produce gene mutations we are more concerned with the five F_1's showing the mutant phenotype that were produced from pollen radiated early in microsporogenesis. These have not yet been examined cytologically and it is not known whether these are "gene mutations" or simply small deletions. There is ample evidence in the literature that maize chromosomes can carry deletions which are inherited as simple recessive genes.

At this point I should like to do some speculating as to the stages of microsporogenesis during which the five mutants without megaspore sterility could have been produced. Sparrow (Annals of the New York Academy of Science 51: 1508-1540, 1951) showed that the interphase of Trillium is the least sensitive to radiation damage as measured by breakage and states that the effects recovered in the F_1 would be

greatest from stages least sensitive to radiation breakage as damage produced from sensitive stages would be least likely to produce viable F_1's.

We have some fragmentary data on stage sensitivity in our material as measured by F_o seed sets. If this is correlated with maize microspore development as described by Kiesselbach (Univ. of Nebraska Agr. Exp. Sta. Res. Bul. 161: 1-96, 1949), it would appear that the three may have been produced during one of the interphases preceding pollen mother cell formation, and the other two may have come from the interphase between meiosis II and the first microspore mitosis.

This is not the first case of radiation induction of pre-meiotic mutation in maize. Dollinger (Maize Genetics Cooperation News Letter 28: 11-12, 1954) reported finding two pre-meiotic mutations. One of these was a mutable involving the $\underline{A}_1$ and $\underline{Sh}_2$ loci, the other was $\underline{Bt}_2$ to $\underline{bt}_2$. Cytological examination of his material revealed no pollen sterility or detectable chromosomal alteration.

Based on these results, it would seem that if one were interested in producing chromosomal aberrations one should radiate mature pollen or the interphase between the first and second microspore division. If one is interested in events inherited as "gene mutations" one should try and hit one of the interphases preceding the pollen mother cell formation in order to use the later division of microsporogenesis to screen out the larger types of chromosomal aberrations.

The control population of 6000 seeds grown for this experiment gave no recessive endosperms and a semi-sterile rate of 2.6% in the F_1. However, it may be of interest to consider the results of some experiments we did to determine the spontaneous mutation rate in pollen homozygous for Su, Pr, Y, Sh, and Wx. In 1953 an experiment was conducted in which 83,000 seeds were examined. There were 46 recessive endosperms and when these were planted six or 19% showed the recessive character in the F_1. Of these only one, a Pr to pr, showed full normal seed set, the other 5 were semi-sterile. A control population of 25,000 seeds grown in 1955 gave 35 mutant endosperms in the F_o and when these were planted five or 16% showed the same phenotype in the F_1. In this case all of the F_1's were semi-sterile. It would appear that mutant phenotypes found when dominant pollen is placed on recessive ears results from spontaneous chromosomal aberrations probably produced in the same stages of microsporogenesis which are most sensitive to the production of aberrations from radiation.

Alan Caspar

5. Chimera in maize.

A corn plant, 6-601-7, was accidentally found in the corn field of the Blandy Experimental Farm, University of Virginia, in the summer of 1956 which possessed chimerical branches on its tassel. The normal diploid branches had the 2n number 20, while the chimerical branches were tetraploid, having 40 chromosomes in their pollen mother cells.

A detailed meiotic study was made on the tetraploid branches. Tetravalents in the form of rings, chains, or figures-of-8 were frequently found in diakinesis and first metaphase of the pollen mother cells. There was only one case out of 50 cells observed which had no tetravalent. One hexavalent, two octavalents, and two crosses-of-4 were found, which indicates that a reciprocal translocation is involved.

A morphological comparison between 6-601-7 and its sister plants was made. No gross morphological differences were found, but the spikelets and the florets of the tetraploid branches were slightly larger than those of the diploid branches.

15 seedlings, siblings of plant 6-601-7, were examined cytologically; all had somatic numbers of 20. The ear resulting from selfing of plant 6-601-7 had a full set of kernels. The progeny will be tested in 1957.

Te Hsiu Ma

UNIVERSITY OF CALIFORNIA CITRUS EXPERIMENT STATION
Riverside, California

1. Effects of the genes du and su_2 in sweet corn at eating stages.

These two genes have been introduced, separately, into several inbreds including P39A; P51B; Iowa 45, 2000, and 3001; Conn. 22 and 68; Maine 23 and 41; and into the varieties Hayes White and Luther Hill. Most of the lines have been carried through 4 backcrosses and 3 or 4 selfing generations. Studies of carbohydrate balance at eating stages in several of these inbreds indicate that the gene effects vary with the background. Table 1 shows the sucrose, water-soluble polysaccharide, and starch levels found at 5 sampling dates. On P39A background, sucrose was higher at each date when du or su_2 was homozygous than when they were absent; on the Connecticut 68 background these genes made little consistent difference in sucrose levels.

Table 1. (Data given in mg. per whole kernel.)

Genotype	Purdue 39A background, Days after pollination 16	19	22	25	28	Connecticut 68 background, Days after pollination 16	19	22	25	28
Sucrose										
su_1	2.5	6.8	9.3	7.8	5.5	5.3	5.4	7.5	9.1	6.9
su_1 du	4.1	8.6	10.7	13.5	9.0	7.2	6.8	7.2	7.2	7.7
su_1 su_2	6.6	9.7	14.1	13.1	10.7	7.0	5.7	8.5	9.4	7.2
Water-soluble Polysaccharides										
su_1	9.6	17.6	24.5	31.8	36.9	7.5	15.6	21.4	29.7	36.3
su_1 du	9.5	21.6	22.9	34.2	38.1	8.3	16.8	24.2	30.7	39.1
su_1 su_2	10.5	21.6	26.7	35.3	41.6	7.9	17.2	23.0	31.1	35.5
Starch										
su_1	8.9	13.1	17.3	21.6	26.4	5.7	8.5	16.2	20.5	27.8
su_1 du	2.6	4.7	6.1	9.6	13.2	2.8	4.9	8.3	12.4	16.5
su_1 su_2	3.5	5.0	5.8	10.1	14.0	2.7	4.1	6.7	11.5	9.8

There was little difference in content of water-soluble polysaccharides in either inbred, due to the addition of du or su_2, although the trend was to slightly higher quantities in P39A. There was a marked effect, however, on starch accumulation in both inbreds, with both the du and su_2 lines showing much lower starch content at every sampling date. This is in line with earlier assays of mature seed of various backgrounds, by Dunn et al., and by Cameron, which showed that final starch content was lower when du or su_2 was homozygous. Present assays of these genotypes on backgrounds of P51B, Maine 41, and Hayes White show the same trend toward lower starch at eating stages, expecially in P51B.

Samples on the Hayes White background at 19 days after pollination were tested after immediate preservation at picking, and after preservation following 30 hours storage at room temperature. Table 2 shows the behavior of the carbohydrates.

The su_1 su_2 combination was the most effective in slowing the loss of total sugars, and likewise in slowing the accumulation of starch. Both du and su_2, in combination with su_1, appeared to condition greater increases of water-soluble polysaccharides during storage than did su_1 alone.

Table 2. (Hayes White background. Data given in mg. per whole kernel.)

Genotype	Immediate preservation	Stored 30 hours at room temp.	% loss or gain
	Total Sugars		
su_1	14.3	6.8	-52.4
su_1 du	14.6	8.0	-45.2
su_1 su_2	22.4	19.1	-14.7
	Water-Soluble Polysaccharides		
su_1	14.4	17.2	+19.4
su_1 du	17.8	22.9	+28.7
su_1 su_2	11.8	17.0	+44.1
	Starch		
su_1	5.7	6.6	+15.8
su_1 du	6.0	6.4	+ 6.7
su_1 su_2	4.5	4.7	+ 4.4

Hybrids among several of these converted lines have been grown and evaluated for eating quality. Taste tests were arranged by presenting each taster with a sibbed ear from each of the following four F_1 plant types: su_1su_1 dudu Su_2Su_2; su_1su_1 DuDu su_2su_2; su_1su_1 Dudu Su_2su_2; su_1su_1 DuDu Su_2Su_2. The four members of each such F_1 hybrid background and all ears were the same age from pollination. Of a total of 42 such taste trials on cooked corn, involving 8 F_1 hybrid sets and about 14 tasters, hybrids homozygous for su_1 su_2 were rated better than su_1 in 40 trials, and were rated best of the four types in 20 trials. Genotype su_1 du was rated better than su_1 in 28 trials, and best of all in 5 trials. The rating was based on a combination of sweetness and/or tenderness.

Tenderness tests on raw corn with a Chatillon tenderness gauge did not indicate a consistent effect of du or su_2 on pericarp tenderness.

Ear mold on field-matured seed ears of su_1 du and su_1 su_2 was not significantly worse than on su_1 ears in 1956, except where earworm was present. In areas of higher humidity and frequent summer rains the mold problem might be different, however.

James W. Cameron
Donald Cole

UNIVERSITY OF CALIFORNIA AT LOS ANGELES
Los Angeles 24, California

1. Growth response of dwarf mutants of maize to the gibberellins produced by the fungus Fusarium moniliforme (Gibberella fujikuroi).

The dwarf mutants, anther-ear-1, dwarf-(5232), dwarf-1, dwarf-2, and dwarf-(8201) responded by normal growth to microgram amounts of gibberellic acid (gibberellin A_3), $C_{19}H_{22}O_6$; gibberellin A_1, $C_{19}H_{24}O_6$; and gibberellin A_2, $C_{19}H_{26}O_6$. Mutants treated with a total of 200 micrograms gibberellic acid per plant reached a tassel height approaching that of normals. Leaf color, size and form of leaf and stem were comparable to those of normals from the same culture. Tassels and ears of treated dwarfs varied considerably. Some remained similar to those of non-treated dwarfs, others were intermediate between those of non-treated dwarfs and normals, and a few approached the size and form of normals.

The dwarf mutants, dwarf-(4963), dwarf-(8043), nana-1, nana-2, midget, and dominant-dwarf showed no response or only a slight response to the three known gibberellins. Dwarf-(4963) and nana-1 mutants showed a slight response in the early seedling stage and no response or inhibition in later stages of growth. Mature plants of the mutant, dwarf-(4963) were smaller than non-treated dwarfs, having leaves that were twisted and pale-green in color. Treated nana-1 mutants reached a height at maturity no greater than the height of non-treated mutants. Dominant-dwarf mutants gave no growth response at any stage of development. Dwarf-(8043), nana-2, and midget mutants have been tested only in the seedling stage. They show no response or only a slight response to the gibberellins.

Bernard O. Phinney

2. Growth response of dwarf mutants of maize to "gibberellin-like" substances from flowering plants.

"Gibberellin-like" substances obtained from the seed or fruit of species representing seven different families of flowering plants have been found to give a response with the dwarf mutants indistinguishable from the gibberellin response. These substances are active for the five mutants that respond to gibberellins and inactive or slightly active for the five mutants that do not respond or respond only slightly to gibberellins. Paper partition chromatography suggests that: (1) A family of "gibberellin-like" substances may exist in higher plants, (2) None of these substances are identical to the three known gibberellins. The active substances do not give an indole test, nor a leucoanthocyanin test. They do not fluoresce in concentrated sulfuric acid as does gibberellic acid.

Charles A. West
Bernard O. Phinney
Mary Ritzel

3. Movement of gibberellins in maize tissue.

Gibberellic acid applied to the distal portion of a leaf blade will cause elongation of the sheath of that leaf and also of succeeding leaves at later stages of development. This response would suggest that gibberellic acid must enter the leaf and move from the site of application to the site of action. To test whether gibberellic acid itself is moving, and to obtain data on the rate of movement, the following experiments have been carried out.

(1) An agar strip containing 15 micrograms of gibberellic acid was applied to the distal portion of the first leaf blade of a dwarf-1 seedling. After two hours the leaf blade was removed by a transverse cut 1 cm. proximal to the agar block. Four days later a detectable growth response was evident in the leaf sheath. From experiments of this kind, it would appear that gibberellic acid was moving at a minimal rate of 5 mm. per hour.

(2) To test for the actual movement of gibberellic acid, blocks of internode tissue, 2 1/2 mm. thick and 3 mm. square, were prepared and placed between two agar blocks, the upper block containing 5 micrograms gibberellic acid. Presence of gibberellic acid in the lower block was observed using the fluorescence test for gibberellic acid. Under these conditions, the maximum rate of movement was about 1 mm. per hour. The amount detected in the lower block varied with the age of the tissue, the older the tissue the greater the amount of detectable gibberellic acid. No polarity of transport has yet been demonstrated. The rate of movement is greater in the direction of the vascular bundles than at right angles to the bundles.

Peter M. Neely

4. The anatomical basis for the gibberellin response in the first leaf sheath of dwarf-1 mutants.

Under the conditions of the experiments reported here, the average final length of the first leaf sheath of dwarf-1 seedlings was found to be about one-third that of normals. Treatment of dwarf-1 seedlings with gibberellins resulted in elongation of the first leaf sheath to a length equal to that of non-treated normals.

To investigate the anatomical basis for this response, counts of parenchyma cells were made along the entire length of the first leaf sheath of treated dwarf-1, non-treated dwarf-1, and non-treated normal seedlings. Records of cell number were taken by counting number of cells per unit distance from the ligule to the base of the leaf sheath. Average cell lengths at different positions along the sheath were obtained by dividing the cell number in a unit distance by the unit distance. From preliminary observations the following statements can be made:

(1) Cells of non-treated dwarf-1 leaf sheaths were fewer in number and smaller than those of normals.

(2) Dwarf-1 seedlings treated with gibberellins had a cell number and cell length that approached the cell number and cell length of non-treated normals. In the region of the ligule, cell lengths of treated dwarfs were characteristically shorter than those of the normals. In the median portion of the sheath, cell lengths of treated dwarfs were found to be the same or greater than cell lengths of non-treated normals.

Table 1. Length of first leaf sheath, total cell number and maximum cell length within this leaf sheath for dwarf-1 and normal seedlings.*

	non-treated dwarf-1	treated dwarf-1	non-treated normal
Length of sheath	18 mm.	55 mm.	50 mm.
Total number of parenchyma cells along a linear file from the ligule to the base of the leaf sheath	248	405	437
Maximum cell length in the parenchyma of the leaf sheath	95 microns	205 microns	165 microns

* values are averages from 4 leaf sheaths.

Kenneth R. Skjegstad

CALIFORNIA INSTITUTE OF TECHNOLOGY
AND UNITED STATES DEPARTMENT OF AGRICULTURE
Pasadena 4, California

1. The gametophyte factor of chromosome 5.

The translocation #5L.09-9L.06 brought into one linkage group the characters shrunken, waxy, gametophyte, brittle, necrotic and red aleurone. The necrotic character is a seedling abnormality recently observed by Dr. Anderson, that causes parts of the young leaf tissue to become watery and die, and it produces zebra-like stripes of lighter green tissue in the leaves of mature plants. The gametophyte character is detected only when pollen carrying this character falls on pistils that possess an inhibitor, preventing it from effecting fertilization. This inhibitor factor seems to be dominant and at present has not been

tied to any linkage group. Since it seems to eliminate all pollen carrying the ga factor it eliminates all other genes on the same chromosome.

Since egg transmission is normal for semisterile plants carrying the inhibitor or the ga factor or both, selfed plants heterozygous for ga, a second linked character and the inhibitor show directly 1/2 the recombination between them by the departure of the second character in seed or progeny classes from 50%, if the second character is not on the ga bearing chromosome, or by the departure from 0% if the second character is on the ga chromosome. When the recombination value is too low to show in some small samples these were not included in determining the value and consequently the determinations in this group given below are slightly too high. Back cross seeds or progenies, obtained when pollen from semisterile plants was used on testers carrying the inhibitor, gave a direct measure of the recombination value between ga and a second linked character by the departure of the second character from 100% or 0%.

Character	Recombination value	
	Back Cross %	Self %
sh - ga	---	27.1
wx - ga	7.6	9.0
♀ - ga	---	3.0
ga - bt	---	4.3
ga - nc	---	7.2

A. E. Longley

2. List of translocation stocks.

List of translocation stocks obtained from the "Crossroads" material (Bikini able bomb and x-ray controls). The cytological positions given are the average measurements of camera lucida drawings of three or more pachytene figures.

Symbol	Chromosomes	Chromosomal Designation	
4301- 39	3-8	3L.92	8L.82
4301-111	2-3	2 near cent.	3 near cent.
4302- 31	1-7	1S.16	7L.08
4302-116	5-8	5L.06	8S.11
4303- 9	9-10	9L.26	10S.44

Symbol	Chromosomes	Chromosomal Designation	
4303- 12	3-8	3 near cent.	8 near cent.
4303- 74	2-3	2L.73	3L.68
4304- 82	4-9	4S.22	9L.37
4305- 8	4-5	4S.27	5L.28
4306- 4	5-7	5S.32	7L.35
4307- 4	1-7	1S.42	8L.66
4307- 12	4-9	4S.48	9L.55
4308	1-4	1S.65	4L.58
4314	1-3	1L.81	3L.89
4331	1-5	1L.03	5S.02
4337	6-7	6L.37	7L.13
4340	3-8	3L.88	8L.72
4341	4-6	4S.37	6S.81
4347	6-10	6L.65	10S.81
4349	3-6	3S.58	6L.70
4352	5-9	5L.48	9L.61
4356	7-10	7L.70	10 near cent.
4363	7-9	7 near cent.	9 near cent.
4369	2-3	2S.19	3S.26
4372	2-6	2S.37	6S.81
4373	4-9	4L.29	9L.39
4374	2-4	2L.15	4L.23
4382	3-10	3S.38	10L.29
4383	3-10	3S.18	10L.84
4384	5-10	5L.13	10L.79
4394	2-6	2S.91	6L.12
4398	1-9	1L.51	9S.19
4400	2-7	2L.24	7L.32
4405	1-7	1S.43	7S.46
4413	2-4	2S.84	4S.32
4414	2-8	2L.12	8L.14
4420	1-7	1L.47	7L.90
4422	7-10	7L.79 (also 7L 10L)	10S.43
4444	1-7	1S.65	7S.50
4447	4-6	4S.28	6L.14
4453	8-9	8L.86	9S.68
4456	1-6	1L.71	6L.30,
4461	4-6	4S.86	6L.17
4464	1-2	1S.53	2L.98
4472	4-5	4S.25	5S.19
4483	4-7	4L.34	7L.57
4484	2-10	2S.09	10L.14
4505	6-9	6L.13	9 near cent.

Symbol	Chromosomes	Chromosomal Designation	
4519	2-7	2L.65	7L.66
4536	7-8	7L.38	8L.47
4545	6-7	6L.25	7S.73
4573	6-7	6L.22	7L.27
4578	2-5	2L.92	5S.71
4593	8-9	8L.69	9L.65
4594	6-7	6L.52	7S.67
4597	1-5	1L.52	5S.43
4613	1-5	1S.78	5L.22
4626	3-8	3S.30	8L.31
4635	3-5	3S.44	5S.48
4636	5-8	5L.23	8L.79
4643	8-9	8S.37	9L.11
4662	3-4	3S.24	4S.16 .67
4666	5-6	5L.35	6L.86
4669	5-6	5L.13	6L.40
4670	3-7	3S.20	7L.76
4676	1-8	1L.04	8S.06
4685	1-8	1S.20	8L.21
4692	1-4	1L.46	4L.15
4698	4-7	4L.08	7L.74
4711	2-8	2S.86	8L.64 67
4713	3-4	3L.21	4S.59
4717 5-9	2-6	2L.77 .70	6L.27
4726	3-4	3S.16	4L.15
4727	3-9	3L.54	9L.42
4741	2-5	2S.47	5L.47
4742	1-7	1S.95	7L.03
4748	1-8	1L.12	8L.15
4759	1-3	1L.37 .39	3L.20
4773	3-7	3S.11 .12	7L.08 .07
4775	8-9	8L.42	9L.68
4778	6-9	6S.80 .78	9L.30
4790	5-9	5L.34	9L.45
4801	5-10	5L.91	10L.23
4817	5-9	5 near cent.	9 near cent.
4824	7-8	7L.83	8L.25
4832	1-5	1S.20	5L.12
4833	6-10	6L.83	10S.78
4837	1-7	1S.73	7L.55
4871	5-9	5L.71	9S.38
4872	3-8	3L.18	8L.15
		3S.22	8S.37
4873	3-5	3S.24	5S.16
4874	3-8	3L.28	8L.32
4880	3-5	3S.25 .27	5S.12 .05
	3-5	3L.18	5L.18

Symbol	Chromosomes	Chromosomal Designation	
4885	1-10	1 near cent.	10 near cent.
4891	1-7	1L.12	7L.69
4898	3-5	3 near cent.	5 near cent.
4933	5-6	5S.23	6L.89
4934	5-6	5L.34	6L.89
4937	1-2	1L.10	2S.15
4963	3-9	3L.76	9L.55
4964	6-7	6S.76	7L.72
4986	1-6	1S.21	6S.78
4995	1-9	1L.19	9S.20
4997	1-9	1L.37	9S.28
5013	5-8	5S.67	8L.59
5028	6-8	6L.21	8L.31
5045	1-5	1S.94	5L.50
5072	1-6	1S.17	6L.45
5074	7-9	7S.48	9L.53
5074	3-4	3 near cent.	4 near cent.
5077	1-6	1S.20	6L.60
5098	2-5	2L.13	5S.20
5143	5-7	5S.51	7L.10
5144	2-7	2S.35	7L.08
5156	3-4	3S.47	4L.08
5157	2-4	2S.86	4L.06
5179	5-7	5L.58	7L.75
5181	6-7	6S.79	7L.86
5188	5-10	5L.37	10S.65
5201	3-6	3S.37	6S.82
5208	2-9	2L.76	9L.68
5225	1-6	1L.61	6L.72
5227	4-6	4S.46	6S.84
5242	1-3	1L.90	3L.65
5253	6-10	6S.80	10L.41
5255	1-2	1S.25	2S.31
5257	2-9	2L.28	9L.20
5267	1-3	1L.72	3L.73
5273	1-10	1L.17	10L.69
5279	2-7	2S.93	7L.25
5285	3-9	3L.51	9L.49
5287	8-10	8L.17	10S.33
5290	5-10	5L.78	10S.49
5300	8-9	8L.85	9S.43
5304	2-3	2S.68	3L.29
5339	1-7	1L.24	7L.14
5339	4-8	4S.22	8L.71
5355	5-10	5S.77	10L.45

Symbol	Chromosomes	Chromosomal Designation	
5358	5-10	5L.10	10L.76
5368	5-9	5L.87	9L.95
5368	3-6	3L.22	6L.20
5373	1-4	1L.17	4S.29
5376	1-2	1L.77	2L.08
5378	3-7	3L.13	7L.73
5381	7-9	7L.85	9L.78
5384	1-8	1L.10	8L.59
5386	6-8	6S.78	8S.83
5391	8-9	8L.07	9S.33
5412	4-8	4L.59	8L.95
5413	7-8	7L.09	8L.77
5419	2-6	2L.82	6S.79
5438	1-4	1L.93	4L.81
5453	1-2	1L.11	2S.58
5454	6-9	6 near cent.	9S.75
5454	2-8	2L.21	8S.39
5471	3-7	3L.64 2S.25	7L.58 6L.15
5472	2-6	~~2L.27~~	~~6L.28~~
5476	1-3	1L.66	3L.87
5479	7-8	7L.70	8S.21
5484	2-8	2L.24	8S.58
5488	9-10	9L.57	10L.89
5495	1-6	1S.25	6S.80
5499	7-8	7L.05	8L.08
5512	1-5	1S.08	5L.70
5519	6-10	6S.75	10L.17
5521	3-5	3L.17	5L.48
5523	1-2	1L.27	2S.62
5525	1-5	1S.75	5L.53
5529	4-5	4S.37	5L.46
5537	1-5 1-6	1S.11 1S.31	5S.15 6L.22
5539	1-2	1L.21	2L.61
5557	5-10	5L.92	10S.39
5558	3-8	3S.26	8S.74
5561	2-10	2L.35	10S.16
5566	1-4	1S.21	4L.26
5570	5-8	5S.47	8L.35
5574	4-9	4L.80	9L.87
5575	5-8	5S.21	8S.22
5585	8-10	8 near cent.	10 near cent.
5588	1-8	1S.10	8S.32
5597	1-3	1S.77	3L.48
5602	2-5	2L.73	5L.77

Symbol	Chromosomes	Chromosomal Designation	
5605	6-8	6L.36	8L.22
5614	5-9	5L.09	9L.06
5619	1-8	1L.07	8L.16
5622	1-9	1L.10	9L.12
5622	5-6	5S.94	6L.42
5629	1-4	1L.10	4L.10
5634	1-8	1L.08	8S.28
5643	3-9	3S.55	9L.64
5645	2-5	2L.60	5S.85
5648	2-6	2L.25	6L.19
5651	2-10	2S.71	10L.62
5653	5-10	5S.76	10L.71
5657	4-9	4L.33	9S.25
5679	5-10	5S.16	10L.15
5680	1-4	1S.87	4L.45
5685	5-6	5L.27	6L.20
5688	5-10	5L.78	10L.53
5693	1-7	1L.92	7L.18
5711	2-9	2S.24	9L.23
5724	3-7	3 near cent.	7 near cent.
5752	1-8	1L.36	8L.24
5756	1-4	1L.89	4L.81
5765	5-6	5S.19	6L.32
5775	3-9	3L.09	9S.24
5777	5-8	5 near cent.	8 near cent.
5780	6-10	6L.93	10L.13
5783	2-7	2L.66	7L.10
5788	4-9	4L.72	9L.82
5800	2-3	2S.73	3S.81
5821	1-8	1L.65	8L.31
5828	7-8	7S.31	8L.10
5831	2-10	2 near cent.	10 near cent.
5866	5-8	5L.32	8L.77
5871	3-7	3S.29	7L.13
5874	3-5	3L.16	5L.21
5876	2-5	2L.47	5L.46
5883	1-3	1S.88	3S.60
5884	4-9	4L.40	9L.49
5891	3-4	3 near cent.	4 near cent.
5892	3-10	3S.17	10L.25
5896	1-2	1S.22	2S.30
5906	5-6	5S.15	6L.13
5910	1-8	1L.93	8L.67
5918	4-9	4S.24	9L.18

Symbol	Chromosomes	Chromosomal Designation	
5920	3-4	3S. 28	4L. 73
5944	8-10	8L. 75	10L. 40
5946	1-2	1 near cent.	2 near cent.
5951	2-4	2L. 18	4S. 26
5955	3-7	3L. 10	7L. 59
5964	6-9	6L. 47	9L. 83
5982	1-3	1S. 77	3L. 66
6019	6-9	6L. 27	9L. 26
6057	5-9	5S. 15	9S. 52
6061	5-10	5S. 60	10L. 57
6062	5-6	5L. 20	6L. 78
6063	4-8	4S. 02	8L. 05
6128	8-10	8L. 43	10S. 47
6178	1-5	1L. 04	5L. 05
6187	6-8	6L. 19	8L. 51
6189	1-6	1S. 23	6L. 17
6197	1-5	1S. 02	5L. 02
6200	5-9	5L. 81	9L. 71
6222	4-9	4L. 03	9S. 68
6225	7-9	7 near cent.	9 near cent.
6261	3-8	3L. 49	8L. 40
6266	2-4	2L. 40	4L. 27
6270	2-3	2S. 46	3L. 60
6270	6-9	6L. 19	9L. 28
6284	2-3	2L. 81	3L. 96
6289	5-8	5L. 06	8L. 54
6293	5-7	5L. 26	7L. 63
6328	1-9	1L. 79	9L. 40
6346	3-5	3L. 94	5L. 83
6349	3-6	3L. 10	6L. 15
6363	4-8	4L. 76	8L. 30
6372	2-7	2S. 21	7L. 11
6373	3-8	3S. 53	8L. 68
6401	1-5	1L. 14	5S. 20
6402	5-8	5S. 07	8L. 07
6406	5-8	5 near cent.	8 near cent.
6422	1-4	1L. 16	4S. 11
6427	7-8	7L. 96	8L. 28
6439	3-8	3S. 30	8L. 15
6462	3-5	3S. 31	5L. 47
6466	3-7	3L. 36	7L. 14
6473	3-5	3S. 32	5L. 26
6482	5-6	5S. 22	6S. 77
6482	7-9	7L. 01	9S. 97
6488	8-10	8L. 14	10S. 34

Symbol	Chromosomes	Chromosomal Designation	
6498	6-7	6L.16	7S.48
6504	4-9	4L.09	9S.83
6522	5-6	5S.87	6L.87
6531	7-8	7 near cent.	8 near cent.
6534	3-4	3L.48	4L.89
6557	3-7	3 near cent.	7S.59
6559	5-6	5S.72	6L.09
6560	4-5	4S.32	5S.21
6566	3-6	3L.41	6L.35
6575	4-7	4S.38	7S.32
6580	2-5	2L.09	5S.09
6587	4-10	4L.55	10L.53
6591	1-8	1S.18	8S.43
6598	6-7	6L.43	7L.61
6612	5-8	5S.59	8L.66
6623	4-6	4L.18	6L.31
6653	8-10	8L.04	10L.06
6656	2-9	2L.32	9S.31
6662	4-10	4L.04	10L.03
6671	2-6	2S.23	6L.22
6673	8-9	8L.32	9S.33
6691	3-10	3L.30	10L.87
6695	3-5	3 near cent.	5 near cent.
6697	1-8	1L.89	8L.52
6722	3-9	3S.66	9S.66
6743	4-5	4L.56	5S.59
6750	2-3	2L.76	3S.53
6760	5-10	5S.78	10S.40
6762	1-9	1S.16	9L.53
6766	1-8	1L.54	8L.77
6796	1-7	1S.40	7S.39
6830	5-10	5 near cent.	10 near cent.
6831	4-5	4S.32	5S.59
6853	2-10	2L.79	10L.86
6861	1-3	1L.04	3L.65
6862	2-3	2S.39	3L.20
6873	6-8	6L.21	8L.29
6883	1-2	1L.63	2L.52
6884	1-3	1L.17	3L.19
6885	6-7	6L.33	7S.58
6885	2-5	2L.63	5S.79
6891	1-2	1S.14	2S.83
6892	1-2	1L.30	2L.35
6899	1-5	1S.32	5S.20

Symbol	Chromosomes	Chromosomal Designation	
6921	8-9	8L.85	9L.15
6926	4-8	4L.60 .61	8L.~~71~~ .80
6931	2-6	2L.24	6L.23
6978	7-9	7L.62	9S.83
		7L.15 .14	8S.49
6981	7-8	7S.45 .46	8L.09
6994	2-4	2S.61 .59	4L.95
7036	6-7	6S.90 .89	7L.~~70~~ .63
7037	4-6	4L.61	6S.77
7041	3-9	3S.59	9L.70
7043	3-5	3L.63	5L.61
7067	4-7	4L.14 .17	7S.60
7067	3-6	3L.07	6L.75
7068	5-8	5S.18	8L.18
7069	2-8	2L.13 .14	8L.~~14~~ .15
7074	7-9	7L.03 .08	9S.~~80~~ .85
7078	4-5	4L.05	5L.~~10~~ .08
7096	2-9	2S.57	9L.66
7097	1-6	1S.46	6L.62
7102	5-8	5L.48	8S.10
7103	9-10	9L.73	10L.88
7108	4-7	4S.17	7S.45 .48
7136	4-5	4L.45	5L.33
7142	5-10	5L.73	10L.17
7149	7-8	7L.~~56~~ .53	8L.65
7162	3-6	3L.~~52~~ .53	6L.~~53~~ .55
7205	5-9	5L.21	9L.90
7211	1-2	1L.57	2L.79
7212	1-5	1L.~~44~~	5S.~~28~~
7267	1-5	1L.92	5L.82
7285	2-3	2L.26	3L.39
7309	1-2	1S.90	2S.89
7328	4-6	4S.53	6S.89
7362	3-8	3L.07	8L.69

E. G. Anderson
Albert E. Longley

CALIFORNIA INSTITUTE OF TECHNOLOGY
Pasadena 4, California

1. Dwarfs.

(a) The following four mutant dwarfs in chromosome 9 were found to be allelic to each other and to $\underline{d}_3$ - $\underline{d}_{5588}$, $\underline{d}_{8004}$, $\underline{d}_{8054}$, $\underline{d}_{8201}$.

(b) Anther-ear$_2$ ($\underline{an}_2$) is an allele of $\underline{d}_1$.

(c) Five anther-ears ($\underline{an}_{7281}$, $\underline{an}_{7752}$, $\underline{an}_{8083}$, $\underline{an}_{8379}$, $\underline{an}_{8704}$) from different sources all proved allelic to $\underline{an}_1$.

2. Frazzled (fz).

A recessive character which results in a splitting of the leaves along the veins. Plants are so distorted that many do not appear above soil surface. Plants have been kept alive three months at which time they are approximately one inch tall. In selfings of heterozygous fz 501 normal seedlings to 165 fz seedlings resulted. fz has shown close linkage with translocations 1 - 9c and 1 - 9a, but is not obviously linked with 1 - 4a. This would indicate fz to be in the short arm of chromosome 1.

	n	fz	n	fz
wx T 1 - 9c	79	33	50	0
wx T 1 - 9a	41	25	21	0
su T 1 - 4a	168	41	36	8

Fred D. Pettem

3. The green mosaic allele of viviparous-2.

The green mosaic allele of vp-2 was found by Dr. Anderson in a stock derived from seed exposed to the Bikini atom bomb. Like vp-2 this mutant has a pale yellow endosperm and albino seedlings. But unlike vp-2, it shows back mutations to normal in both the endosperm and seedling, resulting in a pale yellow endosperm with patches of yellow and in white seedlings with a mosaic of green tissue. This allele has been difficult to study since it has the tendency to produce small viviparous seeds such as are typical of vp-2. However, it has been possible to get stocks that give a fair proportion of mosaic seedlings by selecting lines that are not strongly viviparous. Using such stocks, we have learned something about the inheritance of the green mosaic character.

4. Allele tests with vp-2.

The early allelic tests with vp-2 established that the mosaic condition was dominant. However, nothing more was learned about the relationship of vp-2 and green mosaic because of the vivipary and small seed size which was very prevalent in these crosses. These tests will be repeated with our improved stocks.

5. Levels of mutability.

Not all stocks of the mutant show the same level of mutability. Five different classes have been designated: 1) Very strong, many flecks and streaks of green; 2) Strong, liberal number of flecks and streaks; 3) Light, few scattered back mutations to normal; 4) Light-minus, very few small flecks of green; and 5) Weak, with only one to several small green spots. These classes have been selected for convenience of classification and do not necessarily indicate any basic genetic differences. They might be a reflection of the variability in our stocks. To reduce such variability to a minimum, plans are being made to convert these mosaic stocks to a more uniform background. Pure breeding strong and weak mosaic lines which consistently give uniform seedlings have been isolated. The relationship of the other three classes to these is not certain.

6. Intercrosses between mosaic classes.

Crosses between several of the classes of mosaic seedlings have been made this past year with the following results:

Very strong mosaic X White Very strong mosaic X Weak mosaic Strong mosaic X White	all gave light mosaic seedlings
Weak mosaic X White	gave weak mosaic seedlings.

7. White green mosaic lines.

Two true breeding white lines have been selected from mosaic stocks. The first was obtained from the progeny of an ear that was segregating mosaic and white seedlings. The record on the original ear was made before the various classes of mosaic seedlings were recognized. However, the second white line had its origin in a progeny that was segregating strong and weak mosaics. This year seven apparently new true breeding lines were isolated. One was from a line segregating strong and weak mosaic. The others were from lines segregating strong mosaic, weak mosaic, and white seedlings.

8. Modifying factor.

The segregation of white and mosaic seedlings on the same ear indicate that the mutable condition is controlled by a modifying factor that can be separated from the vp-2 locus. This modifier must be closely linked to the vp-2 locus or widely spread in our stocks since most outcrosses of mosaic to standard lines give only mosaic seedlings.

Donald S. Robertson

CARNEGIE INSTITUTION OF WASHINGTON
Department of Genetics
Cold Spring Harbor, Long Island, N. Y.

1. Continued study of stability of location of Spm.

The mode of operation of the a_1^{m-1} - Spm system was outlined in the last two issues of this News Letter and evidence was presented indicating that the Spm element undergoes frequent changes in location. To obtain further evidence of the degree of stability of location of Spm, two additional tests were conducted this past summer. Each involved determination of Spm constitution and linkage relations in the progeny of a plant having one Spm whose location was known. In both cases, the location of Spm in the chromosome complement differed from that of other determined locations of it. In one parent plant, Spm was linked with Wx in chromosome 9. In the other parent plant, it was located close to Y in chromosome 6. The history of the first mentioned parent plant is referable to a culture grown in the summer of 1954. The plants in this culture were Wx/wx and either a_1^{m-1}/a_1^{m-1} or a_1^{m-1}/a_1 in constitution. In one plant of this culture, two independently located Spm elements were present, one of which was linked with wx. When pollen of a plant homozygous for a_1^{m-1} and wx and having no Spm (standard Spm tester stock) was used on the silks of an ear of this plant, there appeared 130 pale colored kernels (no Spm) and 335 kernels that had A_1 spots in a colorless background (Spm present), indicating the presence in this plant of two independently located Spm elements. From the ratio of Wx to wx in each class (100 Wx : 30 wx in the no Spm class and 123 Wx : 212 wx in the Spm class) it was evident that one of the two Spm elements was located in the wx carrying chromosome of this plant. In order to obtain plants with a single Spm element located in a chromosome 9 carrying Wx, and to test for its stability in this location, 29 plants derived from the variegated, Wx class of kernels on the above described ear were again tested by crossing them with plants that were homozygous for a_1^{m-1} and wx but in which no Spm was present. The first ear on the main stalk was always used for this test and when possible, other ears of the plant were so used. Among these 29 plants, 1 had no Spm; 20 plants had one Spm but it was not linked with Wx; 4 plants had two Spm elements

that were not linked to each other but in 3 of these plants, one of the two Spm elements was linked with Wx. One plant had three independently located Spm elements. In the remaining 3 plants, a single Spm element was present and it was linked with Wx. Among the 1918 kernels appearing on five ears obtained from these three plants, the following types appeared: 1 A_1 wx, 1006 uniformly pale colored (no Spm) of which 222 were Wx and 784 were wx, and 911 in which spots of A_1 appeared in a colorless background (Spm present) of which 747 were Wx and 164 were wx. Linkage of Spm with Wx is obvious and the value of the "recombinant" classes is 20.1%.

Thirteen plants derived from the Spm Wx class of kernels on one of the five above mentioned ears were grown this past summer under culture number 7285. Each was used as a female parent in crosses with plants homozygous for a_1^{m-1} and wx and carrying no Spm, and all fertile ears produced by each plant were so used. One of the 13 plants had no Spm but in the remaining 12 plants, one or two Spm elements were present. The number of ears obtained from each plant, the Spm constitution in the cells that produced each ear, and the linkage relations of Spm and Wx, are indicated in table 1. The tiller ear produced by one plant had no Spm but in the remaining 25 ears obtained from these twelve plants, one or two Spm elements were present. In 16 ears, one Spm element, linked with Wx, was present. In 5 ears, two Spm elements were present, one of which was linked with Wx. In 4 ears, one Spm was present but it was not linked with Wx. The ratio of kernel types appearing on these ears is given in table 2 for each of these three categories of Spm constitution and location. From table 1, it may be seen that correspondence in Spm constitution and location is shown in the cells that produced the 1st and 2nd ears on the main stalk. Differences with respect to this were expressed only in tillers. This suggests that the mechanism responsible for change in number and location of Spm elements was operating relatively early in development of these plants.

The second test of stability of location of Spm was conducted with the progeny of a plant having a single Spm element located close to Y in chromosome 6. The parent plant was one of 5 in a culture and it was the only plant in this culture that showed close linkage of Spm with Y. This plant was homozygous for a_1^{m-1} and heterozygous for Y, Pr, and Wx. It was used as a female parent in a cross with a plant that was homozygous for a_1^{m-1}, y, pr, and wx, and had no Spm. The ear this cross produced had a small, well defined sector in which Spm was absent. All the kernels within this sector were uniformly pale colored (no Spm); 21 were Y and 26 were y. Among the other 329 kernels on this ear, 167 were uniformly pale colored (no Spm) and 162 showed A_1 spots on a colorless background (Spm present). In the pale colored class, 10 were Y and 157 were y. In the variegated class, 153 were Y and 9 were y. It could be concluded, therefore, that a single Spm element was present in the part of the plant that produced most of this ear and that this element was closely linked with Y (5.6% "recombinants"). No linkage with Pr or with Wx was expressed. This past summer, 17 plants derived

Table 1.

Plant Number in culture 7285	Number of ears tested per plant	Position of ear on plant	Spm constitution and linkage with Wx
A-6, B-1, and B-6	1	1st ear, main stalk.	1 Spm; linked with Wx (each ear)
B-4	1	"	2 Spm; one linked with Wx
A-5	2	1st and 2nd ear, main stalk.	2 Spm; one linked with Wx (both ears)
B-2 and B-5	2	1st ear, main stalk; tiller ear.	1 Spm; linked with Wx (all four ears)
A-1	3	1st and 2nd ear, main stalk; tiller ear.	1 Spm; linked with Wx (1st and second ear, main stalk) 1 Spm; not linked with Wx (tiller ear)
A-3	3	"	2 Spm; one linked with Wx (1st and 2nd ear, main stalk) 1 Spm; linked with Wx (tiller ear)
A-4	3	"	1 Spm; not linked with Wx (all three ears)
A-2	3	1st ear, main stalk; ear on each of 2 tillers.	1 Spm; linked with Wx (1st ear, main stalk; 1 tiller ear) No Spm (1 tiller ear)
A-7	4	1st and 2nd ear, main stalk; ear on each of 2 tillers.	1 Spm; linked with Wx (all four ears)

Table 2.

Spm constitution of tested plants (Culture 7285)	A_1	Phenotype of kernel: Pale color (No Spm)		Colorless with spots of A_1 (Spm present)		
		Wx	wx	Wx	wx	Total
1 Spm; linked with Wx	1	418	1539	1512	356	3826*
2 Spm; one linked with Wx	0	79	267	594	323	1263
1 Spm; not linked with Wx	0	190	168	140	174	672

* 20.2% are "recombinants".

from the variegated, Y, Pr, Wx class of kernels on this ear were tested for Spm constitution and location. The silks of all fertile ears produced by each plant received pollen from plants that were homozygous for a_1^{m-1}, y, pr, and wx and had no Spm. One ear was obtained from 3 plants, two ears were obtained from 4 plants, three ears were obtained from 7 plants, and four ears were obtained from 3 plants. That a single Spm element was present in all tested parts of each plant was indicated by the approximate 1 : 1 ratio of presence and absence of Spm among the kernels on each of the 44 ears. And, in 43 of these 44 ears, linkage of Spm with Y was expressed. Only on the ear produced by a tiller of one plant was evidence of this linkage absent. The proportion of kernel types with respect to presence and absence of Spm and to Y and y among the kernels appearing on the ears of 15 of the 17 plants is given in A of table 3. One plant, number 17, was small and defective in appearance. The ear it produced was partially sterile and from the ratio of kernel types on this ear, it was evident that the Y chromosome carrying Spm was not being transmitted normally. Nevertheless, close linkage of Spm with Y is indicated (B, table 3). The types of kernels appearing on each of two ears produced by plant number 2 is shown in C of table 3. On the 1st ear of the main stalk, linkage of Spm with Y was clearly expressed. However, the ratio of kernel types that appeared on the ear produced by a tiller of this plant gives no evidence of such linkage. Also, there was no evidence of linkage of Spm with either Wx or Pr.

Table 3.

A. Plant number in culture 7260	Phenotype of Kernel: A_1	Pale color (No Spm) Y	Pale color (No Spm) y	Colorless with spots of A_1 (Spm present) Y	Colorless with spots of A_1 (Spm present) y	Total
1	0	25	345	360	18	748
3	0	16	308	272	9	605
4	0	14	389	387	9	799
5	0	2	55	48	2	107
6	1 Y	17	367	364	13	762
7	0	17	252	257	18	544
8	1 y	16	530	520	38	1105
10	0	19	318	295	11	643
11	1 y	20	468	436	13	938
12	0	28	548	540	12	1128
14	0	24	271	251	12	558
15	0	19	302	305	17	643
16	0	5	75	81	5	166
18	0	7	122	125	2	256
19	1 Y	18	358	310	13	700
Totals	4	247	4708	4551	192	9702*
B. Plant No. 17	0	1	91	20	1	113
C. Plant No. 2 main ear	0	25	203	171	11	410
tiller ear	0	65	47	48	59	219

* 4.5% are "recombinants"

With regard to stability of location of Spm, the results obtained from the two experiments, outlined above, differ markedly. The first gave evidence of relatively frequent changes in location of Spm. This is in contrast to the experiment just described where an unusual degree of stability of location of Spm was made evident. Nothing is yet known about genetic or other factors that may be responsible for controlling the time during development of a tissue when change in location of Spm will occur, or the frequency of this.

2. Continued study of a structurally modified chromosome 9.

In last year's News Letter, a description was given of a modification affecting the organization of chromosome 9. Two chromosomes instead of one carry the substance of this chromosome. One of these is composed of the distal third of the short arm and it was referred to as the fragment chromosome. The centromere is situated at the proximal end of this component of chromosome 9. The longer segment is composed of the proximal two-thirds of the short arm of chromosome 9 and all of its long arm, and it was referred to as the deficient chromosome. Interest in this case was centered on the aberrant behavior of the fragment chromosome in somatic cells, and this was outlined briefly last year. Further examination of this case required more exact knowledge of the composition of the two components of this structural modification. Therefore, an extensive series of tests of this were continued during the past year. The fragment was known to carry the locus of C and preliminary evidence presented in the News Letter last year, suggested that it also carried the loci of sh and bz. Since the deficient chromosome was known to have the loci of Sh and Bz, with Sh situated very close to the end of its short arm, the genetic composition of the structurally modified chromosome 9 would then include a duplication of a segment composed of the region from the locus of sh to one that is proximal to bz. Recent tests have confirmed the presence of sh and bz in the original fragment chromosome and they also have revealed the relative length of the segment that extends from bz to the centromere of the fragment. It is equivalent to a segment in the normal chromosome 9 that is 5 crossover units proximal to Bz.

Genetic study of the constitution of the fragment and the deficient chromosome makes it clear that a segment in the fragment,--from the locus of sh to the centromere--, duplicates a segment in the deficient chromosome that is located at the very end of its short arm. Examination of the chromosomes at the pachytene stage in structural heterozygotes did not reveal the physical length of the duplicated segment with the desired degree of certainty. It can not include more than 1 or 2 small chromomeres, if matching chromomeres in synapsed regions may be used as a reliable criterion of homology.

In structural heterozygotes whose chromosome 9 components are appropriately marked for crossover studies (an example: normal chromosome 9 with I Sh Bz wx/ deficient chromosome 9 with Sh Bz Wx/ fragment

with C sh bz) an exchange occurring in the region between sh and bz of the fragment (region 1) or between bz and the centromere of the fragment (region 2) would give rise to a structurally normal chromosome 9 carrying sh and Bz or one carrying sh and bz. The presence of such a normal chromosome 9 was confirmed in 48 plants that were derived from kernels exhibiting a phenotype expected from a crossover in one or the other of these regions. In 9 of these 48 plants, an unmodified fragment chromosome carrying sh and bz was also present. (The fragment could not carry the reciprocal product of the crossover. If it had, the kernel would not have exhibited the crossover phenotype.) A normal chromosome 9 would be obtained from a crossover in region 1 or 2 either between the fragment and the normal chromosome or between the fragment and the deficient chromosome. Evidence obtained from the test crosses did not allow definite conclusions to be drawn regarding the relative frequency of the exchanges that occur in these regions between the fragment and the normal and deficient chromosomes. It did suggest, however, that most of the crossing over may take place between the fragment and the normal chromosome and that a crossover in either region 1 or 2 does not interfere with another occurring between the normal and the deficient chromosome. Evidence for the latter statement is conflicting, however, and some of the difficulties encountered in these analyses may derive from differences in behavior of the fragment among the tested plants, as illustrated below.

Four plants having two deficient chromosomes 9, each carrying Sh, Bz, and Wx, and a single fragment chromosome carrying C, sh, and bz, were used as pollen parents in crosses to plants that were homozygous either for C, sh, bz, and wx, or c, sh, bz, and wx, or for c, sh, Bz, and wx. The only functional pollen grains produced by such plants are those having either a deficient chromosome and the fragment, a deficient chromosome and the fragment that has become attached to the end of another chromosome (which sometimes occurs), or a structurally normal chromosome 9 produced by a crossover, however it may be initiated, between the homologous segments of the fragment and the deficient chromosome. Crossovers of this latter type would give rise to structurally normal chromosomes having either C sh Bz Wx or C sh bz Wx. The number of kernels having such phenotypes that appeared on the ears produced by test crosses with these four plants is given in A of table 4. In the cross entered in B of this table, only the sh kernels could be recorded for all of them received Bz from the female parent. Pollen used in the test crosses was collected from each plant over many days, and from tillers as well as from the main stalk. Regardless of the date or the part of the plant from which the pollen was collected, the frequency of appearance of the sh class of kernels on the test cross ears was the same for an individual plant. However, as table 4 shows, wide differences in this respect are exhibited among these plants. Such differences would not be anticipated unless it was known or suspected that some genetic system was controlling the type of behavior of the fragment chromosome. There is some evidence to suggest that this system may be related to the one that controls the behavior of the

fragment in somatic cells. In somatic cells, the fragment may undergo types of events that effect its non-disjunction or its removal during a mitotic cycle from one or both sister cells. Differences in type of genetic control exist and these may be recognized readily, for they give rise to different patterns of variegation in plant and endosperm cells when proper genetic markers are present to allow detection of those events that affect fragment distributions. The behavior of the fragment in the two plants in table 4 that produced the lowest percent of sh kernels, i.e., plants 6971A and 7174A-2, was similar in endosperm development. The pattern of variegation each produced indicated a low rate of loss of the fragment and these losses occurred late in endosperm development. On the other hand, the behavior of the fragment in plants 7169-10 and 7176B-3 resulted in a pattern of variegation in the endosperm that indicated frequent loss of the fragment and often this occurred early in development.

Table 4.

	A				B		
	♀ C sh bz wx or c sh bz wx x ♂ Fragment: C sh bz; Deficient: Sh Bz Wx Deficient: Sh Bz Wx				♀ c sh Bz wx x ♂ Fragment: C sh bz; Deficient: Sh Bz Wx Deficient: Sh Bz Wx		
Plant No.	Total No. kernels	Phenotype of sh kernels C sh Bz Wx	Phenotype of sh kernels C sh bz Wx	% sh	Total No. kernels	C sh Bz Wx	% sh
6971A	371	1	2	0.8	742	4	0.5
7167-10	3294	9	44	1.6	1589	23	1.4
7174A-2	3750	5	14	0.5	1361	5	0.3
7176B-3	1638	7	51	3.5	1763	63	3.5
	Totals	22	111				

That the kernels showing the crossover phenotypes received a structurally and functionally normal chromosome 9 from the male parent was demonstrated by cytological and genetical studies conducted with 2 plants derived from the C sh Bz Wx class of kernels and with 8 plants

derived from those in the C sh bz Wx class. Among the latter, two plants had received an unmodified fragment chromosome in addition to the structurally normal chromosome 9. It is of interest to note that the ratio of Bz to bz among the sh class of kernels in A of table 4 (22 : 111) is much the same as the ratio of these two phenotypes among the sh class that was obtained from heterozygotes (normal chromosome 9 with I Sh Bz wx/ deficient chromosome 9 with Sh Bz Wx/ fragment with C sh bz) when these were used as pollen parents in crosses to plants that were homozygous either for C, sh, bz, and wx, or for c, sh, bz, and wx. This ratio was 57 C sh Bz (6 Wx : 51 wx) to 206 C sh bz (27 Wx : 179 wx).

Barbara McClintock

CENTRO DI GENETICA DEL C. N. R.
Pavia, Italy
and
INSTITUTO DI GENETICA VEGETALE DELLA FACOLTA' DI AGRARIA
Piacenza, Italy

1. Defective endosperm factors from maize-teosinte derivatives.

Evidence is being accumulated that most of the defective endosperm factors from maize-teosinte derivatives are highly unstable. In several cases all sizes of kernels can be obtained from selfed de^t/de^t plant. In a few other types of de^t factors three distinct "states" seem easily distinguishable; besides the normal, a weak and an extreme defective class appear on the defective-segregating ear. At least a few de^t factors, when placed in a genetic background other than A158, seem to "recover." Apparently some genotypes "restore" de^t factors to De^t. Several de^t factors, which arose in different derivatives, turned out to be allelic, which, together with the instability, seems to support the hypothesis that the cause of such de^t factors could be of extragenic nature (in McClintock's sense). The factors de^{t4}, de^{t5}, de^{t10}, de^{t11}, de^{t17}, de^{t18}, de^{t19}, de^{t23}, de^{t24} are probably identical or allelic; the same is possibly true for the series de^{t13}, de^{t22}, de^{t26}, de^{t27}, de^{t29}; and is well established for the series de^{t14} and de^{t20} (on chromosome 4).

2. Endosperm chimeras on ears segregating de^t factors.

Endosperm chimeras have been observed in derivatives of crosses to testers of the stocks showing the de^t factors. Their rate of appearance, when no teosinte segments are present, is unknown. The chimeras can be observed for characters whose genetic factors are carried by any chromosome, including the de^t carrier. Out of 17 chimeric kernels (12 Su-su, 3 De^t-de^t, 1 Pr-pr, 1 Wx-wx) 8 were found in ears segregating genetic

marker and *de*^{t} factor on the same chromosome, while the linkage relationships for the others were not evident. Out of 112 ears segregating *de*^{t} factors linked to *su*, 9 showed *Su-su* chimeras. In 37 ears segregating *de*^{t} not linked to *su* the *Su-su* chimeras were 3.

3. *Ga factors in maize-teosinte derivatives.*

The maize kernel, and especially its highly evolved endosperm, is a structure where mutant factors are susceptible to prompt detection. But when appropriate genetic tests are performed the maize gametophyte turns out to be, as expected, the first place in which mutant factors may show, in some way, their presence. The majority of the many mutants which have been detected in maize-teosinte derivatives (Mangelsdorf 1955, Maize News Letter 29:23) were recognized as defective endosperm factors. However, such derivatives crossed to multiple testers showed that several *Ga* factors should be postulated to account for aberrant segregation data. A male gametophyte factor has been found on the short arm of chromosome 9, strongly linked to *Wx*. Self-pollination of plants whose genotype is probably *Ga Wx/ ga wx* yielded the following segregations:

Plant No.	*Wx*	*wx*	%*wx*
55-356-5	273	2	.73
-10	356	5	1.38
-1	155	2	1.27
-13	225	3	1.31
Total and average	1009	12	1.17

5 sib ears segregated *wx* with percentages ranging from 21.4 to 24.9.

55 selfed plants from *Wx* kernels of low *wx* ears, in 1956 yielded:

2 ears segregating waxy close to 25%,
18 ears segregating low waxy (80 *wx* out of a total of 4269 kernels),
35 ears non-segregating.

As the last two classes are expected to be almost equally represented (exactly 27:26; Emerson, Genetics 19: 149) it is quite possible that in the non-segregating class some ears occurred whose constitution actually was *Ga Wx/ ga wx*; the chance for the *ga wx* gametes to fertilize was probably so low that no *wx wx* recombinations occurred in some ears.

Twelve low waxy ears were studied, classifying separately the kernels on the upper, middle and lower part of the cob. The three ratios are not very different: 2.43-1.25 and 1.93 respectively (chi square 3.75; P = .15). A slight negative correlation however exists between

the total number of the kernels on the ears and the ratio of wx. That, together with the appearance of the two regular wx ears in a population of 55 ears, seems compatible with an hypothesis that some ga pollen grains are functioning and that some crossing-over occurs between wx and ga. In backcrosses of heterozygous Ga Wx/ga wx as the male on homozygous waxy plants 32 wx kernels were obtained out of 672 (4.76%). All the reported data indicate that the Ga factor detected in the maize-teosinte derivative is identical or allelic to Gag, described by Schwartz (Maize News Letter 25:30).

Another aberrant ratio perhaps caused by a ga factor on chromosome 9 has been found which, however, gives minor deviations of the wx classes. The family in which it was detected showed 21% wx; its progeny gave 3 Wx Wx ears, 3 low wx ears (20.2%), 2 normal wx ears (24.7%) and 1 high wx (30.8%). These data suggest that, if actually a ga factor is involved, it should be a very weak allele of gag or, as seems more likely, a ga factor loosely linked to wx.

A ga factor should be postulated in the family 56-488, too, where the su class ranges from 28.5 to 35.1% and in the family 56-392 in which the su percent is 21.3 (17.5 to 24.3). In both these cases progeny tests are not yet available.

A ga factor that has been lost may have been present on chromosome 7 in a cross in which the percentage of gl_1 was as low as 7.2% instead of the expected 25%.

4. Incomplete synapsis in a multiple tester.

Incomplete synapsis has been found in the multiple tester stock bred by Dr. P. C. Mangelsdorf. In almost every pollen mother cell one or more of the pachytene chromosomes show usually one or two non-paired regions. These asynaptic segments cover one fourth to one half of the arm length. The centromere region is almost always regularly paired. The stock is wholly fertile. Specific linkage data are not yet available, but indirect evidence suggests that possibly the irregularity does not effect appreciably the crossing-over.

5. Mitotic disjunction and non-disjunction in the case of interchanges involving the B-type chromosomes.

One of the two gametes of the mature pollen grain unites with the polar nuclei in the embryo sac to form the triploid endosperm; the other fertilizes the egg. The two gametes of a single pollen grain are usually identical, with the exception of plants carrying B-chromosomes or interchanges between a B-type chromosome and a member of the A complement. The B-type centromere with the translocated A-segment undergoes non-disjunction in the second microspore mitosis. Thus one

of the gametes has two of these chromosomes; its partner none. If fertilization were at random one would expect the hyperploid and the deficient gametes to fertilize the egg with equal frequency. Actually the egg receives the hyperploid gamete more frequently than the deficient one, and a low rate of regular disjunction occurs in the second microspore division. As a consequence, three types of kernels are expected: (1) normal chromosome complement both in embryo and in endosperm because of normal disjunction, (2) hypoploid endosperm with hyperploid embryo or, (3) vice versa, hyperploid endosperm with hypoploid embryo because of non-disjunction. The relative frequency of the three kernel types can easily be determined by crossing TB-A translocation stocks on testers possessing two recessive markers in the segment homologous to the translocated A-segment. One marker should affect an endosperm character; the second one a seedling trait.

The multiple tester for the short arm of chromosome 9 yg C sh_1 bz wx has been pollinated by a TB-9b stock. Because the break in chromosome 9 occurs somewhere between bz and wx loci, the resulting endosperms should be classified according to their phenotypes in the classes sh_1 bz and Sh_1 Bz. The figures found were 237 and 231 respectively. As expected, the first class turned out to be all regularly green, Yg with ten exceptions due possibly to hetero-fertilization or to some other unusual event. The second class gave 116 yg and 100 Yg. The high proportion of the Yg seedlings in the Sh Bz class may be accounted for by regular disjunction of the B9 chromosome in the division of the generative nucleus. These results, as compared with those reported by Roman (Proc. Nat. Acad. Sci. 34. 2: 36-42) who, using C-c segregation, found very low B9 regular disjunction, indicate that disjunction occurred in an appreciable rate and suggest that the residual inheritance may affect the behavior of the chromosomes at the second division of the microspore. A fairly high disjunction has to be postulated, too, in later results by Roman and Ullstrup (Agron. Jour. 43: 450-454) in the case of TB-1a, and may be inferred in Randolph's findings (Genetics 26: 608: 631).

6. Balanced lethals for determining linkages.

The methods of locating inherited factors on the chromosomes in maize are based (1) on multiple testers with at least a marker for each of the 10 chromosome pairs, (2) on the use of a series of reciprocal translocations, (3) on the exploitation of the characteristics of A-B chromosome translocation stocks used as pollinator.

An additional method may rely on a series of balanced lethal systems, one for each chromosome pair. The defective endosperm factors may be useful for this purpose. Such balanced lethal stocks can be crossed with the unplaced mutants. In the non-lethal class of the following selfed progenies an excess of the mutants is expected, as

compared with the usual 25%, when they are in repulsion with respect to the lethals. Further tests are, of course, needed to verify the linkage which is indicated by an excess of mutants.

Angelo Bianchi

THE CONNECTICUT AGRICULTURAL EXPERIMENT STATION
New Haven 4, Connecticut

1. Estimating pollen restoration.

In the process of converting inbreds to the cytoplasmic pollen sterile condition and the conversion of these sterile inbreds to restorers it is necessary to have some reliable measure of normal pollen production. The examination of anthers from small pieces of tassel under a low power microscope gives a fairly accurate measure of the amount and degree of pollen abortion. The staminate flowers are collected shortly before the time of normal dehiscence and usually preserved in acetic-alcohol until they can be examined. The proportion of normal, well filled pollen grains can be determined approximately but this method is slow and tedious. It also gives no information about dehiscence and ability of the pollen to function.

Pollen examinations over a period of years indicated that there was a close correlation between the amount of normal pollen produced and the time and pattern of pollen shedding. Tassels with anthers well filled with normal pollen grains begin shedding at the time of first silk emergence or before. Anthers that had any unusual amount of partially filled or completely aborted pollen were usually delayed in appearance until after the first silks appeared, and the anthers did not follow the usual pattern of emergence. The normal pattern of pollen shedding is for the anthers to be extruded first below the tip of the central spike. Extrusion then extends evenly to the tip and the base of the central spike, followed or accompanied by the appearance of anthers on the lateral branches near the tips of the upper branches extending evenly to the tips and the bases of all the branches. Any delay in the appearance of anthers beyond the appearance of the first silk on any part of the tassel, or the first appearance of anthers on the lateral branches or at the tip or base of the main spike, or gaps without anthers is usually an indication of some degree of pollen abortion. In some partially or completely sterile plants the anthers may be well filled with normal appearing pollen grains but these anthers are not extruded, or if extruded the pollen may not be released.

By using these manifestations plants can be easily and quickly classified in the field at the time of silking. We usually put the plants in a segregating population in four arbitrary categories:

(1) normally fertile, (2) partially fertile with about 50 percent or more of normally released pollen, (3) partially fertile with about 50 percent or less of normally released pollen, (4) completely sterile. In the first category the normal functioning of the pollen has been checked many times by self and cross pollinations made by hand. The last category shows no anthers as long as the silks are receptive, and the anthers are devoid of any normally appearing pollen grains.

For convenience in classification the first three categories are lumped together to compare the effectiveness of this method of testing segregation. In 1956 six progenies were grown in replicated plantings, about 100 plants in each replication. Five of the lots were F_2 selfed progenies of crosses of S and T sterile inbreds by the pollen restoring inbreds NC77, Tx127 and Ky21. One lot was the F_1 cross of a T sterile inbred by the single cross (Ky21 x Tx127). The differences in the percent of plants with or without anthers appearing ranged from 0 to 12 percent. None of these differences is significant.

2. Seasonal differences in pollen restoration.

Using this method of field examination and the same arbitrary classification of plants with and without anthers the differences shown by the same F_2 segregating progenies were determined for the two growing seasons of 1955 and 1956. The same lots of seed were planted each year and the results averaged for the three pollen restoring inbreds given above. In 1955 the growing season up to the time of flowering was unusually dry and above normal in temperature. The leaves were wilted and rolled on many days. The 1956 season was quite adequate in moisture before flowering and temperatures were normal. The results combined from the three inbreds used as pollinators in 18 different selfed F_2 progenies are as follows:

	Number of Plants		Percent	
	With Anthers	Without Anthers	With Anthers	Without Anthers
1955 Observed	480	356	57	43
Calculated 9:7	470	366	56	44
1956 Observed	1014	331	75	25
Calculated 3:1	1009	336	75	25

The agreement in 1955 with a 9:7 calculated ratio and in 1956 with a 3:1 calculated ratio is remarkably close. This indicates that in the relatively unfavorable season of 1955 two restoring genes were needed for the plants to show any anthers. In the more favorable season of 1956 only one restoring gene was necessary.

3. Segregation of pollen restoring genes in inbreds used as pollen parents and seed parents.

When the inbreds NC77, Tx127 and Ky21 used as restorers on T cytoplasm are studied separately it is found that they segregate differently in F_2 selfed progenies. All of these inbreds used alone or in single cross combinations produced all normally fertile plants in the F_1 generation grown in 1954, 1955 and 1956 in combination with WF9T, 38-11T, C106T, KysT, K4T, CI7T; not all combinations were grown in each of the three years. These F_1 fertile plants were selfed and the F_2 segregating progenies were grown in 1955 and 1956 and the results combined.

Of the three restoring inbreds used as pollen parents Tx127 segregated in a 9:7 ratio, Ky21 and NC77 segregated in 3:1 ratios. The differences between observed and calculated are not significant. Of the inbreds used as seed parents with these pollinators WF9T and 38-11T segregated in a 9:7 ratio, while C106T, KysT and K4T segregated 3:1. Again the differences between observed and calculated are not significant. However, in view of the wide differences in the two different years and in different progenies the results are only indicative of differences in the number of restoring genes involved in the crosses of the different inbreds used.

4. Segregation of fertile and sterile plants in backcrossed progenies of different inbreds.

That different numbers of genes are involved in the restoration of different sterile inbreds is also borne out by the behavior of backcrossed lines in the process of conversion to complete restoration. Many of the standard corn belt inbreds widely used in the northeastern and northcentral corn growing regions are in process of conversion by taking the S or T cytoplasmic sterile versions of these inbreds, crossing them as females by several different restoring inbreds followed by backcrossing the restored fertile plants repeatedly on the sterile inbreds. These inbreds have been backcrossed from two to six generations and then self pollinated for one or two additional generations. The segregation of fertile and sterile plants is quite different in many inbreds. A few illustrations are given here.

A158 is completely sterile in both S and T types of cytoplasm and in five additional sources. No anthers shedding pollen appeared on any plants in 10 backcrossed generations in the S cytoplasm and 5 generations in the T cytoplasm. Both the S and T steriles are completely restored by Ky21. Anthers appear and pollen is shed in normal amount about 5 days before the first silks appear in the original, fertile inbred, and this same pattern is shown by the restored fertiles. The backcrossed S steriles in 5 generations of backcrossing and 1 generation selfed usually produced no sterile plants. Small progenies of 15 to 20 plants were grown each generation but several progenies were grown each year.

The fact that few sterile plants appeared indicates that there are a large number of genes any one of which alone can restore pollen production to the S type of sterile cytoplasm.

The backcrosses on the T type of sterile cytoplasm have segregated approximately 1:1 sterile and fertile in each backcrossed generation, and 3:1 in each selfed generation although the total numbers are small.

The inbreds C103 and Kr (187-2) also give clear cut segregation, 1:1 in backcrossed, and 3:1 in selfed progenies having T sterile cytoplasm. They have not been tested with the S type. A fairly large number of progenies have been grown. The Kr inbred has been selfed twice after backcrossing 4 and 5 generations, and a number of progenies in F_3 give all fertile plants as expected.

The behavior of WF9 and Hy inbreds is quite different. WF9 is completely sterilized by both S and T cytoplasms, also by four other sources. Five additional sources have given a few partially fertile plants in the first or second generations of backcrossing.

WF9T and S sterile plants are completely restored by Tx127, Ky21, and WF9T by I153 and many other lines. These restored T steriles have been backcrossed on WF9T sterile for 1 to 3 generations and have all segregated into fully fertile or completely sterile plants. In 22 progenies grown in 1956 there are 382 fertile and 933 sterile plants. This is a significant departure from a 1:1 ratio being a 1:2.4 ratio. This indicates that WF9T sterile requires more than one restorer gene to produce pollen and these genes must all be present to be effective.

One selfed progeny of (WF9T x Ky21) grown in 1955 gave 58 fertile and 36 sterile plants which is fairly close to a 9:7 ratio, and two back-crossed progenies gave 39 fertile and 120 sterile plants, a very close 1:3 gametic ratio, again indicating two dominant complementary genes for fertility. The F_2 generation of crosses with Tx127 and Oh41 gave fewer fertile plants, indicating more than two genes involved or less potency in the dry year of 1955.

In contrast to the results with WF9 is the behavior of Hy. Five slightly different lines have been sterilized by T cytoplasm and restored to full fertility. Hy has been a difficult line to sterilize and to restore. After 5 generations of backcrossing both S and T sterile lines produce some partially fertile plants. When restored by Ky21 and C236 (an inbred out of the same Chester Leaming variety from which Hy was derived) the backcrossed lines give 108 fertile to 39 sterile plants, which is close to a 3:1 gametic ratio. These same backcrossed lines self-fertilized give 109 fertile and 7 sterile plants, which is remarkably close to a 15:1 F_2 ratio. Both results indicate two genes of which either one alone or both together can restore fertility. WF9 therefore seems to be recessive for at least two complementary genes and Hy recessive for at least two duplicate genes for pollen restoration, and the dominant alleles of all these genes are present in the restorers used.

5. The use of restoring inbreds in commercial double crosses.

One question needs answering as soon as possible. How much pollen restoration is necessary or desirable in the production of hybrid seed corn? In the last News Letter it was stated that WF9T restored by I153 and related lines and used as a pollinator on standard sterile seed parents restored at least 50 percent of the plants to full fertility. Several of these combinations were grown again in 1956 in Connecticut and throughout the corn belt and again produced about 50 percent of the normal amount of pollen. Since they were grown in trial plantings no reliable test of their pollen production was possible, but in time and amount of pollen shedding they were considered to have sufficient pollen for normal grain production. Other hybrids restored by various combinations of Oh29, Oh41, and M14 were also grown in many locations and produced 50 percent or more of the normal amount of pollen. Many of these restored steriles were outstanding in yield of grain and stalk quality.

D. F. Jones
H. T. Stinson, Jr.

6. Free amino acid differences between cytoplasmic sterile and normal fertile anthers.

The free amino acid content of cytoplasmic sterile and fertile anthers was investigated in the hybrids C106T8 x A158, C106 x A158, and C106TF5(Ky21) x A158 by the application of paper chromatographic techniques. The C106 parent used in the last mentioned hybrid was derived from a C106 T sterile line which was restored to normal fertility by crossing with Ky21. Restored fertile plants were backcrossed to a C106T line, which had been converted to C106 type, for five generations.

Chromatograms of anthers in stages beyond meiosis showed distinct differences between sterile and fertile anthers. The first difference seen was in the alanine content, this amino acid being accumulated precociously in sterile anthers. A detailed and quantitative study of the pattern of alanine accumulation in the development of anthers revealed little or no differences in the amount of the substance between sterile and fertile anthers in the premeiotic or meiotic stages of development. Occasionally, diads from sterile plants had noticeably larger quantities of alanine, but in all cases, quartets from sterile plants had considerably more alanine (at least a two-fold increase). This disparity became still more pronounced as the age of the anther advanced, although at maturity, sterile anthers had somewhat less alanine than fertile anthers per anther. However, if the alanine content of anthers was compared on an equivalent dry weight basis, it was found that sterile anthers continued to have a large excess of the substance over the fertile counterpart throughout development. This precocious accumulation of alanine in the spore quartets of sterile anthers is of particular interest in

view of the fact that it precedes any detectable morphological differences. Young microspores from sterile and fertile anthers also are indistinguishable, but soon after, it is possible to tell them apart. Fertile microspores increase rapidly in size, develop heavy walls and a definite pore whereas sterile microspores do not enlarge greatly and wall thickening and pore-development are limited.

At later stages of anther development, further differences became apparent. Chromatograms of sterile anthers with old microspores had two other ninhydrin-positive spots absent or less intense in chromatograms of normal anthers. One spot, designated as Y, was distal to alanine and has not been identified, while the other was asparagine. In mature anthers (4-5 days prior to anthesis in the normal plant and later), large quantities of proline are characteristic of normal anthers but not present in sterile ones. This accumulation of asparagine in the mature sterile anther, together with the lack of proline, has been reported by Fukasawa (1954).

Since the restored C106 parent used in the hybrid (C106TF5(Ky21) x A158 was heterozygous for the restorer gene(s), segregation for fertile and sterile plants occurred in the F_1 hybrid families. Anthers from sterile plants followed the chromatographic pattern of the sterile C106T8 x A158. Anthers from restored fertile plants were chromatographically identical in appearance to the normal C106 x A158. Thus, the deviation from the normal free amino acid content associated with T cytoplasm does not take place when the T cytoplasm is combined with restorer genes of Ky21.

These chromatographic investigations were extended to several other lines of corn which had been sterilized by male sterile cytoplasm from different sources, namely, the A, B, and S steriles. It was found that in all lines tested (C106, A158, WF9, WF9-4, W22) T cytoplasmic sterile anthers invariably developed alanine precociously, and always before morphological differences became apparent. A, B, and S types of sterility did not, at all stages of development, affect the ninhydrin-positive patterns of the anthers.

Uheng Khoo
Harry T. Stinson, Jr.

CORNELL UNIVERSITY
Department of Plant Breeding
Ithaca, New York

1. Studies on the longevity of corn pollen.

This program was initiated as a portion of a study of the male gametophyte. Experiments were conducted in 1955 and 1956 to ascertain the effect of the environment upon the viability of the pollen grain, and, in addition, to determine the optimal conditions under which to store the pollen. The criterion of viability used was the ability to set seed.

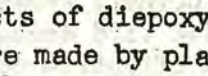
Five ranges (15% - 60%) of relative humidity at each of 5 temperatures (-79°C to+16°C) represent the bulk of our treatments. A preliminary interpretation of data indicates that we were able to obtain seed from pollen approximately 150 hours old, at temperatures from -10°C to +5°C, with a reduction in the percentage of viability, however. Pollen that was 95-100% fertile at collection time showed a decrease in viability to approximately 15% after 150 hours. As mentioned, the test criterion was the ability to set seed.

If pollen could be stored for a week or longer and retain a small percentage of viability, it is probable that this would be advantageous to the corn breeder and geneticist, especially in the early stages of a program when the number of seed is not too important. It might also prove to be a profitable method by which to exchange pollen with cooperators separated by relatively great distances.

We plan to increase the precision of our experiment in 1957 and test some of these additional hypotheses.

D. B. Walden
R. E. Anderson
H. L. Everett

2. Mutagenic effect of diepoxybutane.

Experiments have been conducted for several seasons to determine the possible mutagenic effects of diepoxybutane,  , on Zea mays. Treatments were made by placing the cut ends of newly shedding tassels taken from homozygous multiple dominant stocks in 0.2 per cent solutions of the chemical for 18 hours. Pollinations were made immediately and after a 24 hour period on homozygous multiple recessive stocks. Losses of dominant marker genes in the endosperm of the resulting kernels were used to evaluate the mutagenicity of the diepoxybutane.

Most of the experiments utilized a multiple recessive stock having the chromosome 9 markers c sh wx, all of which affect the endosperm. These linked genes were used to determine whether the appearance of the recessive characters involved chromosomal deficiency, gene mutation, or genic instability. The number of kernels showing single or multiple gene losses ranged from 8 to 12 per cent over a three year period. This compares with a control rate of less than 1 per cent. The extent of loss varied from a tiny spot to the entire kernel being affected, with all intermediate types occurring. Mosaic types also occurred in which there was an all over web-like appearance of the loss. Since the order of these loci with reference to the centromere is Wx, Sh, and C, coincident losses of all three loci or of Sh and C indicate chromosomal loss while a loss of Wx alone indicates a small intercalary deletion or mutation. Thus far the greatest percentage of observed deficiencies involved (1) all three loci, (2) Sh - C, or (3) C alone and can easily be explained as losses of terminal segments of chromosome 9. However, losses of Wx without losses of C and Sh did occur and must be explained in some other way. Mosaic patterns may be the result of either breakage - fusion - bridge cycles or genic instability induced by the chemical. No instance of the mosaic type of pattern was found in the controls.

Jean D. Kreizinger

3. Bird Repellants.

Results of a study on the sense of taste in birds by the New York State College of Veterinary Medicine prompted an investigation of the bird repelling properties on ripening corn of the most promising of the compounds. A single spray application on a small isolated block of inbred material gave complete control; the untreated half of the field showed only light damage, however. One application of spray to small areas in a large field of commercial corn reduced subsequent bird damage to approximately one-fourth of that in check areas. The compound used was easily handled, reasonable in price, and slightly objectionable in odor. Since it is primarily used as a food additive, it is presumably non-toxic.

Further investigations indicate that other more potent materials are available for tests of repellant effect during the coming season. Since many of the areas where Cornell grows breeding and testing material of corn are subject to extensive bird damage, we are hopeful that further investigations will produce an effective control.

R. E. Anderson

CROW'S HYBRID CORN COMPANY
Milford, Illinois

1. Mutations affecting carotenoid synthesis.

Seeds of the M14 mutant and of the Ohio 7 mutant described last year were sent to California for comparison with other known types. No report has been received as to whether these are identical with other mutations of a similar type that have already been described.

2. Semi-dwarf.

The F_2 generation of crosses between our lines and semi-dwarf strains from Guatemala segregated for semi-dwarf this past year, and the dwarf plants were selfed. Crosses will be made in 1957. One of the problems with dwarf hybrids will be weed control in the seedling stage. Chemical weed killers may help solve the problem.

3. Twin shoots.

We had one line of twin-shoot material that was homozygous for the character this year. We made reciprocal crosses between single twin shoot plants and single plants of a normal single-eared line to make a more careful study of the mode of inheritance.

4. Siberian corn.

We obtained some seed of a very early strain of Siberian corn from Herbert Plambeck, Des Moines, Iowa who made a trip with American farmers to Russia. We selfed a number of the plants and divided the pollen to make crosses on our early inbreds. The crosses all set seed but the selfs did not. The only seed we got was from a sib-pollinated ear. I made the pollinations myself and have no explanation for the results. We will repeat the work this year to see whether there is some incompatability that prevents seed setting when the plants are selfed.

5. Pollen restorers.

We have a large number of lines that have been recovered from crosses with Guatemalan, Puerto Rican and Cuban varieties. These were all crossed on our male-sterile lines in 1955. In 1956, we found that 14 of these lines were good restorers of pollen. Further tests will be made to see whether these are all carrying the same gene for restorer.

W. J. Mumm

DE KALB AGRICULTURAL ASSOC., INC.
De Kalb, Illinois

1. Cytoplasmic influence on internode length in maize.

I. The stunting effect of cytoplasm on plant height has been reported in Epilobium by Michaelis (Advances in Genetics, vol. 6. 1954. pp. 287-401) and also in Zea mays by Briggle (Agronomy Journal, vol. 48. 1956. pp. 569-573) and others.

In 1955 and 1956 an attempt was made to determine whether this stunting phenomenon in maize took place in the tassel internode only or if it was a general effect involving all internodes. Preliminary observations also seemed to suggest the possibility that one or more nodes was actually missing in the cytosterile strain.

Fertile and sterile counterparts of both S and T type inbred lines and single crosses were grown in alternating rows. In all comparisons listed in the tables below plants from sterile rows were compared with plants in fertile rows adjacent to them. After the plants had obtained their maximum growth and were still green, they were cut between the lowest visible node and the surface of the ground. These plants were then stripped of their leaves. Internode No. 1 is the distance in inches between the lowest tassel branch and the uppermost leaf node. Internode No. 2 is the length between the uppermost leaf node and the next leaf node below and so on down the stalk. All internode lengths were measured but only the upper three including the tassel internode are listed on the accompanying tables.

All lengths and node numbers in the following data are average lengths in inches of ten plants with the exception of table A where Wf-9 F internode lengths are the average of 20 plants compared with 29 plants in Wf-9 S. Also, 12 plants of Wf-9 F are compared with 14 plants of Wf-9 T. In the single crosses, table B, the average internode lengths of 21 plants of (Wf-9 x 38-11)F were compared with 19 plants of Wf-9 x 38-11)S.

II. The following tables show the comparison between fertile and sterile counterparts of inbred and single crosses. Average internode length of 10 or more plants (see last paragraph in section I) is given in inches. "S" and "T" refer to the cytosterile source.

1955 Data

Table A.

	Internode No. 1		Internode No. 2		Internode No. 3	
	Fertile	Sterile	Fertile	Sterile	Fertile	Sterile
Wf-9 S	7.07	6.17	3.75	3.70	4.29	4.15
Wf-9 T	6.74	5.71	4.15	3.80	4.77	4.52
Sum	13.81	11.88	7.90	7.50	9.06	8.67
F	11.75*		0.88		0.44	

Table B.

Wf-9 x M14)S	8.90	6.92	5.67	4.54	5.25	5.02
Wf-9 x 38-11)S	8.40	6.92	5.17	5.06	5.06	5.24
Sum	17.30	13.84	10.84	9.60	10.31	10.26
F	50.00*		2.92		1.00	

1956 Data

Table C.

Wf-9 T	9.00	6.67	4.85	3.99	4.64	4.41
M14 T	8.26	7.57	5.45	4.64	4.89	4.58
W22 T	7.89	7.47	4.66	4.45	4.50	4.45
Sum	25.15	21.71	14.96	13.08	14.03	13.44
F	65.66**		4.21		2.00	

Table D.

Wf-9 S	8.16	7.20	4.35	3.82	4.25	4.07
M14 S	8.31	7.14	5.34	4.17	5.15	4.21
W22 S	7.69	7.79	5.03	4.92	4.90	4.90
Sum	24.16	22.13	14.72	12.91	14.30	13.18
F	5.81		1.88		1.02	

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

	Internode No. 1		Internode No. 2		Internode No. 3	
	Fertile	Sterile	Fertile	Sterile	Fertile	Sterile
Table E.						
Wf-9 x Oh43)T	11.34	9.37	7.20	5.97	6.66	6.30
Wf-9 x Pal.8)T	12.32	9.20	6.80	5.97	6.52	6.16
Wf-9 x 38-11)T	10.63	7.62	6.42	5.68	6.44	5.98
Wf-9 x Hy)T	12.27	9.83	7.60	6.69	7.28	6.93
Sum	45.56	36.02	28.02	24.31	26.90	25.37
F	17.58**		7.71*		1.83	
Table F.						
Wf-9 x M14 S	11.11	8.19	6.92	5.69	6.91	5.85
Wf-9 x W22 S	11.10	9.71	7.08	6.55	7.07	6.96
Wf-9 x Pal.8 S	11.82	9.57	6.48	6.10	6.25	6.46
Wf-9 x 38-11 S	10.97	8.44	6.36	5.75	6.24	6.01
Wf-9 x Hy S	12.15	11.21	7.17	7.39	7.15	7.67
Sum	57.15	47.12	34.01	31.48	33.62	32.95
F	11.69**		1.89		.106	

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

III. When the "F test" is applied significant differences exist in the internode length of single crosses and inbred lines between fertile and sterile counterparts of both cytoplasms with the exception of the inbreds in table D. In table E a significant difference at the 5% level was found in the second internode of four single crosses involving the T cytoplasm. No significant differences exist in internode lengths below the 3rd internode down to the internode above ground. Whether or not stunting takes place in the internodes of the root system below ground or in the floral parts other than glumes, anthers, and pollen is not known.

IV. Slight differences in the actual number of nodes was also observed between inbred lines and single crosses involving the S and T cytoplasm. However, when the "F test" is applied these differences are not significant at either the 1% or 5% level. The results from 1956 data are summarized in the following tables where each number represents the average number of nodes in 10 plants.

Table G.

	S - Type		T - Type	
	Fertile	Sterile	Fertile	Sterile
Wf-9	14.9	14.6	13.1	12.7
M14	12.0	12.1	11.6	11.8
W22	12.8	12.0	12.6	12.3
Sum	39.7	38.7	37.3	36.8
F	.072		.127	

Table H.

	Fertile	Sterile		Fertile	Sterile
Wf-9 x M14)S	13.6	13.8	Wf-9 x Oh43)T	13.2	13.5
Wf-9 x W22)S	14.7	14.1	Wf-9 x Pal.8)T	14.8	14.3
Wf-9 x Pal.8)S	15.4	15.0	Wf-9 x 38-11)T	15.0	14.6
Wf-9 x 38-11)S	15.4	14.7	Wf-9 x Hy)T	14.4	14.2
Wf-9 x Hy)S	15.3	14.4			
Sum	74.4	72.0	Sum	57.4	56.6
F	1.38			.184	

Loring M. Jones

EAST AFRICAN AGRICULTURE AND FORESTRY RESEARCH ORGANIZATION
Kenya Colony, East Africa

1. Breeding maize for resistance to Puccinia polysora Underw.

Puccinia polysora was first recorded in East Africa in 1952. Genetic studies, by seedling tests in glasshouses and breeding from plants selected in these tests, were undertaken at Muguga, Kenya; and field breeding by collaborators on three stations in Kenya, Uganda and Tanganyika.

Only one physiologic race, termed "EA.1", has yet been detected in the field. A second race, "EA.2", appeared in the glasshouses in 1955.

No resistance to either race was found in any African maize. Through the generosity of correspondents, a collection of over 200 maizes from Central America and the Caribbean area was assembled. In 45 of

these, plants showing the hypersensitive type of resistance were detected. True immunity was not found.

Two genes conferring the hypersensitive reaction have been recognized. Rppl, from the variety "Colombia 2" (AFRO.29), confers reaction "01" (chlorotic - necrotic lesions, probably close to the "0;" of the Stakman system) to EA.1, but full susceptibility to EA.2. Rpp2, from a Mexican line (AFRO.24), and also probably from several other sources including certain plants of "Colombia 2", confers reactions "01" to "1" (necrotic lesions with small sori) or sometimes "X" (mixed) against both races of P. polysora. Rpp2 is incompletely dominant; Rppl apparently fully dominant.

These two genes have been transferred by the plant breeders to a number of East African maizes; and in 1957 bulks of several pure resistant stocks will be available for issue to cultivators.

H. H. Storey
Audrie K. Ryland

ESCUELA NACIONAL DE AGRICULTURA
Lima, Peru

1. Geographic distribution of pericarp and cob color gene frequencies of Peruvian Highland corn.

A survey of pericarp and cob color gene frequencies was started in 1955, and is being continued at the present time on all collections made in Peru.

Five ears selected at random from each collection are scored according to a conventional classification (Emerson, Beadle and Fraser's) for pericarp and cob color alleles. While the survey is being made for the initial purpose of studying geographical variation in gene frequencies, the distribution of the different corn races is disregarded and counts are made on all collections from a given Department, considering for the time being only areas above 1800 meters above sea level. Later, the same data will be rearranged to provide information on gene frequencies within races, and in interaction with geographical areas.

Table No. 1 shows zygotic frequencies for some of the Sierra (Highland) Departments of Peru, without discriminating for altitude and races. Evidence appears there that Ancash is a center for a^{pl} (reddish-brown pericarp), while Ancash, Apurímac, Ayacucho, and Huancavelica have a very high frequency of a^{pl} (brown pericarp). We may also point out the high frequencies of P^{wr} in Cuzco and Cajamarca (notice also high frequencies of A in these two Departments), which

indicated an entirely different pattern of selection (against pericarp color) in those regions.

Table 1. Zygotic frequencies of pericarp and cob color alleles.

	Ancash	Apurimac	Ayacucho	Cajamarca	Cuzco	Huancavel	Junin	Puno
A	0.465	0.552	0.300	0.700	0.800	0.566	0.639	0.806
$a^{p'}$	0.114	0.013	0.025	---	0.021	0.037	0.033	---
$a^{b'}$	0.421	0.434	0.675	0.300	0.177	0.397	0.328	0.193
P^{rr}	0.577	0.486	0.725	0.325	0.237	0.452	0.409	0.207
P^{rw}	0.044	0.105	0.050	0.150	0.029	0.105	0.098	---
P^{wr}	0.052	0.092	0.100	0.400	0.410	0.288	0.229	0.483
P^{cr}	0.179	0.144	0.025	---	0.187	0.037	0.098	0.010
P^{cw}	0.075	0.052	0.050	---	0.028	0.009	0.033	0.034
P^{vv}	0.031	0.092	---	0.125	0.072	0.082	0.131	0.172
P^{mo}	0.019	0.026	---	---	0.014	0.023	---	---
P?*	0.021	---	0.050	---	0.022	0.005	---	---

* New P allele, undescribed yet.

2. Association between imbrication and pericarp color in Peruvian Highland corn.

A study of association between imbrication and pericarp color disclosed that within collections originating in nine Sierra Departments there was a positive and highly significant association between those two characters, in the sense that ears with high score for kernel imbrication were more likely to be colored in the pericarp.

Table 2. Association between imbrications and pericarp color.

Score for Imbrication	Observed Pericarp Color Yes	No	Expected Yes	Increase of Observed Yes over Expected
0	630	767	698.5	- 9.8 %
-1	102	53	77.5	31.6 %
1	147	75	111.0	32.4 %
2	66	33	49.5	33.3 %
3	8	1	4.5	77.7 %

$\chi^2 = 34.35^{**}$ d.f. = 5

Discriminating between three pericarp colors: brown, red, and reddish-brown (Table 3) there was evidence in favor of a positive association of red pericarp and high score for imbrication. Studies within each Department for the same associations have been carried on, and will be published elsewhere. These data might serve to support the hypothesis that primitive corn in the highlands of Peru, which was highly imbricated, had a pigmented pericarp, probably red. This is also supported by findings of ears of corn in pre-Inca graves along the Peruvian coast, where red pericarp and high imbrication were dominant associations.

Table 3. Association between specific pericarp colors and imbrication.

Pericarp Color		Imbrication				
		0	-1	1	2	3
Red	Obs.	95	10	26	15	1
	Exp.	98.47	11.99	23.97	11.51	0.94
	Dev.	-3.47	-1.99	2.03	3.49	0.06
Brown	Obs.	283	27	57	27	3
	Exp.	266.07	32.39	64.77	31.11	2.54
	Dev.	16.93	-5.39	-7.77	-4.11	0.46
Reddish-brown	Obs.	41	14	19	7	0
	Exp.	54.47	6.63	13.26	6.37	0.52
	Dev.	-13.47	7.37	5.74	0.63	-0.52

$\chi^2 = 19.808^{**}$ d.f. = 8

3. Association between cob color and endosperm color and texture.

A high association between red cob color and yellow endosperm exists both for floury and flint highland Peruvian corn, the same being true for white cob and white endosperm. As for reddish brown and brown cob colors, they are well below expected zygotic frequencies when flint endosperm is present, but, on the other hand, their zygotic frequencies in association with floury endosperm are very high, regardless of endosperm color.

The significant deviation from randomness in the association of these characters might lead us to confirm the hypothesis that there is a high positive selection pressure (presumably human) in favor of some phenotypic associations.

Table 4. Association between cob color and endosperm color and texture. Percent increase over expected zygotic frequencies.

Cob Color	Endosperm			
	Flint		Floury	
	Yellow	White	Yellow	White
Red	50.0	-40.7	29.4	-22.0
White	-13.7	54.4	-32.1	1.6
Brown	-20.4	-32.7	15.3	13.5
Reddish-Brown	-59.8	-91.9	42.9	42.5

4. Studies on corn from archaelogical findings.

A survey and study of archaelogical corn material stored in public and private museums, as well as that from new digging, has been continued. It can be stated that, before the Spaniards arrived in Peru, the natives had at least the following recognized races under cultivation in the Coast: (a) Mochero, (b) Pagaladroga, (c) Confite Puneño, (d) Alazán. Alazán appeared in a later period, as did also an 8-rowed corn, either as a derivative of Pagaladroga or as an introduction from the highlands, via Tiahuanacoid influence, in pottery of whose period in the Coast, it has been found as mouldings.

Piricinco (Cutler's Coroico) a present-day jungle corn was found moulded in three pottery vases of the Muchik culture of the northern coast, indicating that this race was in existence at that time (before 800 A.D.) and was known, at least incidentally, to coastal people.

From their seeming resemblance to modern races, ancient coastal corn plants should have been rather short (around 1.50 meters), with one to two ears well covered with smooth soft husks, early (four months to maturity), and highly drought resistant.

All ear shape and size variants of coastal archaelogical corn have been found in self pollinations made on the variety "Blanco Local de Lambayeque", a representative of the race Mochero.

Alexander Grobman
Wilfredo Salhuana
P. C. Mangelsdorf

HARVARD UNIVERSITY
Cambridge, Massachusetts

1. The blotching system involving the c locus.

Three of the four genes involved in the blotching system which causes color to develop in the aleurone in the presence of recessive c have now been located on the chromosomes through backcross linkage tests. The data follow:

Row	Genes	Number of Individuals					Recombinations	
		XY	Xy	xY	xy	Total	No.	Percent
184	Bh Su	169	148	130	198	645	278	43.1
186	Bh Y	378	168	158	304	1008	326	32.3
181	Bh Wx	248	306	300	245	1099	493	44.8

The Bh gene on chromosome 4 shows very weak linkage with De^{t-1}. Since this locus appears to be on the short arm of chromosome 4 (Bianchi) it is probable that Bh is on the long arm. Rhoades (MNL, 1948) has already shown that the Bh on chromosome 6 is closely linked to Pl and, therefore, is on the long arm of that chromosome. Since the Bh locus on chromosome 9 shows 44.9 per cent of crossing over with Wx, it could be on either arm and, if on the short arm, is probably near Yg. If this is true, then the experiment reported by Rhoades (MNL, 1945), in which he found less blotching in the aleurone of kernels carrying a chromosome 9 deficient for the c locus than in kernels with normal chromosomes, may involve the loss of the Bh factor on chromosome 9 and thus represents a case of dosage differences with respect to Bh factors rather than an indication that c is mutating to C.

2. The blotching system affecting the r locus.

Three of the five or more loci involved in the system in which blotches of color appear in the aleurone in the presence of recessive r have been located through backcross linkage tests. Two of the genes are linked with Su. Earlier data had indicated that two of the genes in this system were linked with each other. This occurred in modifications of 9:7 ratios as follows:

Ear	Total	No. Bh	Percent Bh
241A-1	582	401	68.9
2	513	317	61.8
3	546	366	67.0
4	372	249	66.9
243-3	409	267	65.3
4	425	258	60.7
5	340	226	66.5
Totals	3187	2084	65.4

This deviation from the 56.75 percent of Bh seeds expected in a normal 9:7 ratio can be explained in terms of linkage between two Bh factors on the same chromosome with crossing over of the order of 25 percent.

There is no doubt that one of these Bh loci is on chromosome 4, as the following data from backcross linkage tests show:

		Number of Individuals					Recombinations	
Row	Genes	XY	Xy	xY	xy	Total	No.	Percent
188	Bh Su	262	205	204	261	932	409	43.9
189	Bh Su	325	211	156	322	1014	367	36.2
	Totals	587	416	360	583	1946	776	39.9

Since the two Bh loci are linked, and one is definitely on chromosome 4, the other must also be on chromosome 4 and may show strong linkage or weak linkage with Su depending on the sequence of the genes. The data from two ears in which Bh-bh segregated in a 1:1 ratio, and Su-su, in a 3:1 ratio, follow:

Ear	Su Bh	Su bh	su Bh	su bh	Totals
178-1	95	116	35	54	300
1-2	153	157	45	53	408
Totals	248	273	80	107	708

The deviation from independent inheritance is not significant, although there is in both ears a higher percentage of Su seeds in the Bh class than in the bh class.

The data so far available indicate that the sequence is Bh, Bh, Su, and that it involves a total map distance of the order of 80 units. This suggests that both Bh genes occur in the long arm of chromosome 4.

The third Bh gene in this system appears to be linked with Fl. Following are the data from three backcross ears:

	Number of Individuals					Recombinations	
Row	Bh Fl	Bh fl	bh Fl	bh fl	Total	No.	Percent
190	241	295	275	261	1072	502	46.8

If the Fl gene is the one on chromosome 2, then Bh is almost certainly on the short arm of this chromosome, near the lg locus. Crosses have been made to test this possibility.

3. Bh genes in common in the two blotching systems.

Since the two blotching systems involving the c and r genes are similar in their manifestations, and since both involve a locus on chromosome 4 with 40-45 percent crossing over between Bh and Su, the question arises whether the two systems have loci in common. In preliminary tests in 1955, stocks lacking one Bh gene in the c system were crossed with stocks lacking one Bh in the r system. The F_1 seeds were, of course, completely colored because of the complementary action of C and R. Blotched seeds appeared in the F_2 in about one half of the progenies. This indicated that stocks from one system were carrying Bh genes of the other, but did not prove that the Bh genes themselves were identical since many stocks which have no blotching do carry one or more Bh genes.

A more critical test was made in 1956. Fifteen different stocks of the composition cc rr but carrying all four of the Bh genes of the c system, were pollinated by two stocks of the r system, each lacking one Bh gene. It was assumed that if only part of the fifteen stocks carrying the four Bh genes of the c system were capable of producing blotches in crosses with stocks lacking one Bh gene in the r system, then it could not be concluded that the two systems had genes in common. But if all of the stocks carrying the four Bh genes of the c system were capable of completing the r system, then there would be at least a strong indication, if not final proof, that one of the four genes in the c system is identical with one of the five or more in the r system.

All fifteen of the crosses with row 162 showed blotching. All fifteen of the crosses with row 163 lacked blotching. Other tests showed that row 162 involves the same Bh gene as rows 188 and 189 above, in which linkage of Bh with Su is shown.

Our conclusion from the data now available is that the two systems have a Bh gene on chromosome 4 in common. Further tests could show, however, that there are two distinct Bh genes on this chromosome - one involved in the c system, one involved in the r system - and that these two genes are so closely linked that crossing over between them is rare.

4. The blotching inhibitor appears to affect both systems.

In last year's News Letter it was reported that the inbred Conn. P39 carries an inhibitor of blotching in the r system which is closely linked or allelic to one of the Bh genes. The question is whether this gene also inhibits blotching in the c system. To determine this a stock carrying all four of the Bh genes in the c system was crossed with Conn. P39. The F_1 seeds were Cc Rr and completely colored. The F_2 seeds segregated in a 9:7 ratio for self-colored and colorless or blotched. If the F_1 was heterozygous for all four Bh factors, then 31.6 percent (81:175 ratio) of all cc RR/Rr seeds should be blotched (31.6% x 75% x 25% = 5.925%). If the inhibitor from Conn. P39 suppressed blotching in the c system, then only one fourth of this percentage (1.48 percent) blotched seeds should occur. The data from six ears follow:

Number of Kernels				Percent Blotched
Total	Colored	Blotched	Colorless	
2219	1221	49	949	2.2

The percentage of blotched seeds, 2.2 percent, is nearer the percentage expected, 1.48 percent, from the action of an inhibitor than the 5.9 percent expected if the inhibitor does not act on this system.

The inhibitor of blotching has no discernible effect upon the development of self-color, but the chromosome 9 inhibitor of aleurone color, the I gene, completely inhibits blotching.

5. The possible utilization of Bh genes in the classification of maize.

The four Bh genes in the c system and the five or more Bh genes in the r system may prove to be quite useful in the classification of races, varieties and inbred strains of maize. If the maize in question is

recessive for both c and r, it is very easy to determine its genotype with respect to the Bh genes by simply crossing with a series of stocks, each one of which lacks one of the Bh genes. If the stock being tested is not recessive, then an F_1 plant to furnish the F_2 endosperm generation would have to be grown. In either case, the tests for blotching will also tell the genotype of the stock with respect to c and r so that the genotype for ten different loci can be determined from nine different pollinations. This assumes that the two systems have only one Bh gene in common.

Stocks which prove to be identical or nearly so in these ten loci are very likely to be closely related.

6. Half-tunicate from Peru, Ecuador and Paraguay.

The half-tunicate character, which originally occurred as a mutation in one of our tunicate stocks, has been picked up in collections from Peru, Ecuador and Paraguay. When repeatedly backcrossed to the inbred A158, the half-tunicate from these exotic races is indistinguishable from the mutant half-tunicate. Half-tunicate is especially common in the Peruvian coastal race, Perla. Mr. Alexander Grobman of the National School of Agriculture near Lima tells me that 1-2 percent of the inbred strains isolated from this race are segregating for this character.

Half-tunicate should not be confused with papyrescent, another character involving prominent glumes described in this Letter, which also occurs in South American maize.

7. An inhibitor of half-tunicate.

We have for some years past assumed that pcd corn, if it is the ancestral type, is not inherently monstrous and that its frequent monstrousness can be explained in terms of a relict "wild" gene superimposed upon the genetic background of modern, highly domesticated maize. On this assumption, we have selected for modifier complexes which would reduce the expression of the tunicate character, and we have found such complexes to be especially common in the pop corns. This in itself is significant since the pop corns as a class are the most primitive types of maize extant.

We have now found that, in addition to the complex of minus modifiers for tunicate which many pop corn varieties carry, there are in some varieties of pop corn a gene which strongly inhibits the expression of half-tunicate. This gene, which in preliminary tests appears to be linked with Y on chromosome 6, has so far been studied only in half-tunicate stocks; it is recessive and acts only in the homozygous condition. It causes $tu^h tu^h$ to act like $tu^h tu$ and it renders $tu^h tu$ almost indistinguishable from tu tu.

We have crossed the inhibitor with Tu stocks. If it has a similar effect upon these, as it almost certainly will, then the genotype Tu Tu should become more or less similar to $tu^h tu^h$ in ordinary stocks and should not be monstrous.

That a major inhibitor of the expression of genes at the Tu locus, as well as minus modifying complexes, should be found in pop corn varieties, which are primitive in other respects, is highly significant and is probably more than mere coincidence.

Paul C. Mangelsdorf

8. Genotypes involving the Tu-tu locus compared in isogenic stocks.

In an earlier News Letter (1953) we compared a number of genotypes involving the Tu-tu locus in characters of the ears and tassels. However, the stocks then available were not completely isogenic and not all genotypes were included. We now have data involving a comparison of six genotypes in isogenic stocks resulting from repeated backcrossing to the inbred A158. These are shown in the table on the following page.

A study of the data show that four profound changes of obvious evolutionary significance are involved in the transition through the genotypes from Tu Tu to tu tu.

A. The terminal inflorescences, the tassels, decline and the lateral inflorescences, the ears, gain in prominence. The fact that the gain in weight of the ears (line 11) greatly exceeds the loss of weight of the tassels (line 1) suggests that the shortened lateral branch is more efficient in laying down dry matter than the terminal inflorescence. Indeed, it may be this fact which renders maize more productive, on the average, than any other cereal.

B. The ratio of pistillate and staminate spikelets in the tassel is drastically changed (line 10).

C. The central spike of the tassel becomes relatively more prominent at the expense of the branches (line 4). Since the ears are the counterpart of the central spike, this change accounts for the fact, previously noted in other studies, that branched ears are more common among tunicate stocks than among non-tunicate.

D. The rachises of both inflorescences become more prominent at the expense of the glumes (lines 6, 8 and 15-16). This is especially significant in the ear, since a large rachis offers a greater grain-bearing surface and at the same time is capable of containing a larger system of supply. These facts are reflected in the increased number and weight of the kernels and the higher shelling percentage (lines 17-19).

A comparison of six genotypes involving the Tu-tu locus in isogenic stocks.

Characters	Genotypes					
	Tu Tu	Tu tu^h	Tu tu	$tu^h tu^h$	tu^htu	tu tu
1. Weight tassels, gms	28.9	18.3	12.7	9.2	6.7	4.9
2. Weight peduncles, cgms	264	220	130	111	109	106
3. Weight central spikes, gms	6.6	4.8	3.5	2.9	2.1	1.5
4. Percent: central spikes/ tassel weight	22.8	26.2	27.6	31.5	31.3	30.6
5. Weight rachises, gms	4.6	2.9	2.1	1.4	1.3	1.1
6. Percent: rachis weight/ total weight	15.9	15.8	16.5	15.2	19.4	22.5
7. Weight spikelets, gms	24.3	15.4	10.6	7.8	5.4	3.8
8. Percent: spikelets/ total weight	84.1	84.2	83.5	84.8	80.6	77.5
9. Average length glumes, cms	2.7	1.9	1.7	1.4	1.2	1.0
10. Percent pistillate spikelets	79.9	0.9	0.0	0.0	0.0	0.0
11. Weight ears, gms		21.6*	59.5	89.7	126.6	125.2
12. Weight cobs, gms		6.4*	20.6	24.5	24.0	22.7
13. Weight glumes		5.3*	16.5	17.7	14.2*	8.7*
14. Weight rachises gms		1.1*	4.1	6.8	10.5*	10.9*
15. Percent: glumes/cob		82.8*	80.1	72.2	57.5*	44.4*
16. Percent: rachis/cob		17.2*	19.9	27.8	42.5*	55.6*
17. Weight kernels, gms		15.2*	39.0	65.2	102.6	102.5
18. Percent: kernels/ear		70.3*	65.6	72.7	81.0	81.8
19. Number of kernels		76 *	282	371	532	477
20. Average weight of kernels, gms		20 *	13	17	19	21

* Data based on a single ear.

There is little doubt that changes of the four types described above have occurred in the maize plant during its evolution under domestication. It cannot yet be proved that such changes were wrought by genetic changes at the Tu-tu locus, but it would be strange indeed if this were not the case. At least no other locus has yet been discovered in maize which is capable of so drastically changing the maize plant in the direction of greater usefulness to man.

Paul C. Mangelsdorf
Helen P. Mangelsdorf

9. Mutation rates in teosinte derivatives.

In previous News Letters we have recorded the occurrence of a wide variety of mutations in modified strains of the inbred A158 in which one or more teosinte chromosomes have been substituted for maize chromosomes. No mutation was ever observed in the original inbred A158.

During the past year we have conducted a controlled experiment in which the mutation rates for seed and seedling characters of the teosinte-modified strains were compared directly to the original strain. In 100 ears of A158 there was one mutation to defective seeds. In 435 ears of teosinte derivatives there were 32 mutations involving 12 defective seeds, one brittle endosperm and 19 seedling defects of various types.

The mutations which have now occurred in the teosinte derivatives include most of the categories of inherited defects found in open-pollinated maize: gametophyte factors, defective seeds, chlorophyll deficiencies (albinos, virescents, stripes), brittle and sugary endosperm and dwarfs.

Paul C. Mangelsdorf
Walton C. Galinat

10. Papyrescent maize.

The dominant gene which produces this glume character has been designated previously as "pseudopod" (Pp) (Galinat and Mangelsdorf, MNL, 1955) but it now seems more appropriate to use the name "papyrescent" and the symbol Pn in order to call attention to its papery character and its similarity to the "papyrescens" character of Sorghum (Rangaswami) as well as to avoid confusion with the symbols for heterozygous pericarp color (Pp).

When we first obtained the Pn character from a Peruvian variety, it was closely linked to another mutant form resembling branched silkless (bd) reported as near the long arm of chromosome 7. The associated

mutant in our stock has now been definitely located on chromosome 7 by use of E. G. Anderson's a-b translocation tester for that chromosome. Although we have grown families from about 30 Pn ears, we have only obtained one cross-over between Pn and bd.

The Pn mutant is characterized by prominent but defective glumes which consist largely of undifferentiated parenchyma cells. When the Pn glumes dry down during final maturation of the ear, they shrink to a thin, almost transparent, layer with the vascular bundles becoming prominent ridges. The glumes do not contract much in length and continue to partially cover the grains. At maturity they are papery and brittle, and are distinctly different from the glumes of tunicate maize or the normal glumes which serve to protect the caryopses of other grasses.

Walton C. Galinat
Paul C. Mangelsdorf

11. Half-tunicate teosinte, a possible "synthetic" prototype of maize and Tripsacum.

The structure of half-tunicate teosinte fits the theoretical requirements for a common ancestor of maize and Tripsacum. Also the general structure of this synthetic derivative approximates a typical condition for the Andropogoneae. The resemblance is closest to Elyonurus tripsacoides. The slender rachis segments of half-tunicate teosinte differ from those of Elyonurus by the presence of a shallow cupule in the former and its absence in the latter. This cupule (or adnate-prophyll part of a cupule) is a definitive character separating the Andropogoneae from the American Maydeae.

If maize and Tripsacum had such a common ancestor, then evolution toward these species could have followed certain general tendencies which are prevalent in the grasses. The evolution toward primitive maize from our synthetic common ancestor would have involved longitudinal compaction and reduction to unisexual flowers. The factors for a polystichous thickened and continuous rachis in modern maize appear to represent acquisitions made chiefly during domestication as is suggested by recent studies on primitive archaeological maize. In the evolution of Tripsacum, reduction would have proceeded toward solitary instead of paired spikelets in the pistillate region. Also there would have been specialization of the cupule and outer pistillate glume as integral parts of a new protective device, the cupulate fruit case.

12. The effect of weak tunicate alleles on the expression of the Vg gene.

A collection of weak alleles at the tunicate locus has been assembled in isogenic stocks (Mangelsdorf, MNL, 1953) and these are now

being combined with the vestigial glume (Vg) gene for comparative studies. One of these from Mangelsdorf's collection came from Chapalote maize and it modifies the expression of the Vg gene in a manner identical to that of the Chapalote factor which was isolated independently (Galinat, MNL, 1955) and is presumed to be the same gene. Weak tunicate alleles derived from other races (Wilburs Flint, Guatemala 197, and Mexico 1740) tend to have a similar, although less pronounced, effect in restoring tassel glumes to Vg plants bearing glumeless ears.

13. A minus-modifier for the Vg gene from Nobogame teosinte.

During the course of incorporating the Vg gene into Nobogame teosinte, a minus-modifier which restores tassel glumes to Vg plants was encountered in heterozygous condition in the recurrent parent. This modifying factor, which appeared in 50 percent of the Vg plants in the BX-3 generation, could only have come from teosinte because any accidental outcrossing to maize would have been readily apparent. Previous crosses to teosinte involving the F_1 and first two backcrosses yielded essentially glumeless tassels, indicating that not all plants of Nobogame teosinte carry the modifier. When the Vg teosinte plants with long tassel glumes were outcrossed to normal (non-tunicate) maize, normal tassel glume development reappeared in 50 percent of the Vg progeny. Thus this modifying factor is dominant. Its effect on the expression of the Vg gene is quite similar to that of the tunicate factor from Chapalote.

14. Occurrence of bifurcated midrib in the first leaf above the coleoptile.

Bifurcation of the midrib to the first leaf above the coleoptile was observed in 18 out of 22 related families of 30 seedlings each. It occurred at various frequencies ranging from 3 to 63 percent. The average frequency was 18 percent.

If such bifurcation is inherited, the penetrance of the genes is not complete or uniform. Perhaps the double midrib in this leaf results from an intergrading influence between that which normally results in the development of two main ribs in the coleoptile and the single midrib of most other leaves. Sometimes this bifurcation will extend to several leaves or, more rarely, the shoot itself becomes involved.

15. Leaf bloom in the corn grass and teopod mutants.

A waxy bloom occurs on the upper side of the leaf blades in these narrow-leafed mutants as it does in certain other grasses (sorghum) as well as on the narrow leaves (the lowermost or seedling leaves) of normal maize. Pubescence replaces the bloom on the broad, more distal

leaves in normal maize. When corn-grass leaves are somewhat broader than those of the original grass-like extreme, as may result from minus modification, then the upper leaves have streaks of bloom interspersed with pubescent areas.

Another peculiarity of the original grass-like type of corn grass plant, which has not been recorded previously, is a convex rolling of the leaves. The direction of this roll is opposite to that which occurs in normal leaves which have been subjected to drought.

Walton C. Galinat

16. Further cytological studies of maize-teosinte derivatives.

Materials and techniques used and some of the results of the cytological studies of maize-teosinte derivatives were reported in last year's News Letter. The following is a brief account of additional studies.

A. Asynapsis: Asynaptic configurations varying in size, shape, location, and the chromosomes involved were observed at pachytene. Involved in this type of irregularity were chromosomes 1 and 4 of Florida teosinte, and chromosomes 8 and 10 of Durango teosinte.

B. Non-homologous association: In the derivatives of Durango teosinte foldback types of non-homologous association involving chromosomes 2, 4, 5 and 8 were observed, while in Florida-teosinte derivatives non-homologous association between two different pairs involving chromosomes 7 and 8 were found. The length of the chromosome segments within various non-homologous associations varied in different collections.

C. Chromosome knobs: In Durango-teosinte derivatives additional knobs were recorded on chromosomes 2, 5 and probably 8. In Nobogame-teosinte derivatives an additional knob was present on chromosome 4.

D. Inversions: Since the last report a terminal inversion on the short arm of chromosomes 8 was found in three more progenies of Durango-teosinte. At diakinesis the chromosomes, heterozygous for this inversion, usually did not pair normally. Among 151 cells studied in the progeny No. 5913, 29 had the two chromosomes completely dissociated and acting as univalents. In the remaining 122 cells some of the chromosome 8 bivalents were associated only at one end. Bridges and fragments at anaphase I or early telophase were found. However, frequencies of the appearance of bridges and fragments were very low (see table). Furthermore, no bridges were recorded at anaphase II among 1090 cells studied.

It was also observed that at anaphase I the heterozygous chromosomes 8 frequently underwent precocious division. These early-divided chromosomes were always found persistent in the center of the cells, while the other diads had approached the poles.

Number of bridges and fragments found at anaphase I in the progenies of maize-Durango teosinte derivatives which are heterozygous for In8.

Progeny	no bridge no fragment	1 bridge no fragment	1 bridge 1 attached fragment	1 bridge 1 free fragment	2 bridges no fragment
5911	638	5	1	5	0
5913	353	4	6	8	0
5915	567	34	1	11	0
5919	400	4	0	2	1
Total	1958	47	8	26	1
Percent of total	96	2.3	0.3	1.3	0.004

E. Binucleated sporocyte: In the progeny No. 5915 of a Durango-teosinte derivative several sporocytes were found to have two nuclei at mid-prophase of meiosis. The two nuclei were different in the stage of division in all of the cases. These two nuclei were undergoing prophase division within a common cell wall but were not within a common nuclear membrane. Perhaps caryokinesis accompanied by a failure of cytokinesis, just before the sporocyte division, may result in this kind of irregularity.

F. Heterochromatic fragments: Several heterochromatic fragments, smaller than regular B-chromosomes, were observed in two progenies of Florida-teosinte derivatives and one progeny of a Nobogame-teosinte derivative. At pachytene these heterochromatic fragments had an average length of less than 20 μ, and they varied in configurations, although most of them appeared to fold back upon themselves. All of them occupied a relatively peripheral region of the cells. Meanwhile, the other chromosomes of the cells in which these fragments were found, appeared normal; no translocation, deficiency or any other chromosome alterations could be identified.

All of the chromosome irregularities such as asynapses, non-homologous associations, binucleated sporocytes and heterochromatic fragments described above were not found in the checks. It appears certain that these irregularities were induced by hybridization between maize and teosintes. The additional knobs present in both Durango- and Nobogame-teosinte derivatives were undoubtedly inherited from teosinte.

17. Cytological observations of the F_1 hybrids between maize and Nobogame teosinte.

Cytological study was made on the F_1 plants of reciprocal crosses of maize (Wilburs Flint) and Nobogame teosinte. It was consistently found that, at pachytene, all of the chromosomes from Nobogame teosinte are equal in length to the chromosomes from maize, despite the fact that in the parental Nobogame teosinte, chromosome 6 was found shorter than the average chromosome 6 from maize.

At pachytene, when any two homologues are heterozygous for either a terminal or an internal knob, the knob-bearing chromosome always appeared longer, at least for a knob length, than its partner. Such was the case for both chromosomes 7 and 9 in the present study.

A terminal inversion on the short arm of chromosome 9 was observed. The length of the inverted segment is approximately one-third of the length of that arm. In addition to a less frequently found ring-shaped configuration, the arms heterozygous for this inverted segment, often formed a V-shaped figure.

Centromeres of all the chromosomes in the hybrids were not so easily identified as they were in the parental species, suggesting that hybridization may perhaps have some effect on the centromere organization.

18. Internal knobs on the chromosomes of two tropical forms of Tripsacum.

Inflorescences of the two tropical forms of Tripsacum were collected by Dr. William Hathaway in Colombia in the summer of 1956. Taxonomically one form probably belongs to Tripsacum laxum Nash, the other, probably to T. australe Cutler and Anderson.

Cytological investigation of the forms showed that, in addition to terminal knobs, internal knobs are also present at pachytene. In the clones of T. laxum there are three chromosomes, probably 3, 5 and 8, having internal knobs on the long arm. Only chromosome 8 has an internal knob on the long arm in the smears of T. australe.

Pachytene chromosomes in Tripsacum laxum were very sticky and difficult to identify. Chromosome behavior was extremely irregular at both anaphase I and anaphase II. Mitotic chromosomes in the tapetal cells of the anthers proved superior to pachytene chromosomes for chromosome count in this species. It was found that there are 54 chromosomes in such cells. This particular clone of T. laxum is therefore triploid. Meiosis in the clones of T. australe is regular. The number of pairs of chromosomes was counted to be of 18 at both pachytene and diakinesis stages. Therefore, the clone of this species is diploid.

Y. C. Ting

UNIVERSITY OF ILLINOIS
Urbana, Illinois
Department of Agronomy

1. Linkage of the S factor of the "Kys" type of male sterility.

The S factor of the "Kys" type of male sterility (Schwartz 1951, Bauman 1956) has been tested against a number of genetic testers to determine its linkage relationship. The crosses made were as follows:

Msms ss AA (male sterile) x MsMs SS aa (tester)

F_1 Ms-- Ss Aa (partial pollen plant)

The F_1 with partial pollen was used in reciprocal backcrosses to the tester. Depending on the direction of the cross, the following genotypes may be expected in the B.C. progeny:

F_1 used as male	F_1 used as female
Ms-- SS Aa	Ms-- SS Aa
Ms-- SS aa	Ms-- SS aa
	Ms-- Ss Aa (partial pollen)
	Ms-- Ss aa (" ")

When the F_1 is used as the male parent, the gametes with s are non-functional; in the case of linkage of gene A with s, the transmission of A will be reduced, the reduction depending on the proximity of A to s. In the reciprocal cross the linkage of s and A may be ascertained by the non-random distribution of plants with partial and normal pollen in the Aa and aa progeny classes.

The tests with all but chromosome 2 linkage groups were negative. In the case of lg_1 and gl_2 (chromosome 2) the following phenotypes were obtained when the F_1 was used as the male parent: Lg_1: 133, lg_1: 205; Gl_2: 113, gl_2: 225. All plants tested had normal pollen. Using the F_1 as the female parent, 1 : 1 ratios of Lg_1:lg_1, Gl_2:gl_2, and Fl_1:fl_1 were obtained. On the basis of 893 plants from two crosses involving lg_1 and gl_2, and 289 plants from a cross involving lg_1, gl_2 and fl_1, the following map distances were calculated: lg_1-gl_2: 13.84, lg_1-fl_1: 50.87, lg_1-s: 61.25, gl_2-fl_1: 37.02, gl_2-s: 47.40, and fl_1-s: 10.38.

The map values for lg_1, gl_2, and fl_1 have been established at 11, 30, and 68 respectively (Rhoades 1950). The position of s may therefore be mapped in the vicinity of 78 on chromosome 2.

Wolf Prensky

UNIVERSITY OF ILLINOIS
Urbana, Illinois
Department of Botany

1. Crossover data for chromosome 3.

Three point backcross data were obtained from plants homozygous for In 3a. Since Rg is not included in the inverted segment the linear order in the inverted chromosome should be Rg A Lg instead of the usual Rg Lg A order.

In 3a Rg A Lg / In 3a rg a lg X rg lg a pollen

(0) Rg A Lg	(0) rg a lg	(1) Rg a lg	(1) rg A Lg	(2) Rg A lg	(2) rg a Lg	(1-2) Rg a Lg	(1-2) rg A lg	Total
317	279	123	126	191	195	52	52	1335

Recombination: Rg-A = 26.4%
A-Lg = 36.7%

Sibling plants of the above tested individuals were heterozygous for the Gl_6 locus rather than Rg. Using these plants as pollen parents the following backcross data were obtained:

gl lg a X In 3a gl A Lg / In 3a Gl a lg

(0) gl A Lg	(0) Gl a lg	(1) gl a lg	(1) Gl A Lg	(2) gl A lg	(2) Gl a Lg	(1-2) gl a Lg	(1-2) Gl A lg	Total
275	254	71	64	174	158	27	40	1063

Recombination: Gl-A = 19.0%
A-Lg = 37.5%

Since the Rg-A recombination percentage was 26.4 and that for Gl-A was only 19 percent, the linear order in a structurally normal chromosome, starting from the centromere, appears to be Rg-Gl-Lg-A.

The probable correctness of this order is suggested by the following backcross data from structurally normal chromosomes 3:

Rg gl lg a / rg Gl Lg A X rg gl lg a

(0)	(0)	(1)	(1)	(2)	(2)	(3)	(3)	(1-3)	(1-3)	(2-3)	(2-3)
Rg	rg	Rg	rg	Rg	rg	Rg	rg	Rg	rg	Rg	rg
gl	Gl	Gl	gl	gl	Gl	gl	Gl	Gl	gl	gl	Gl
lg	Lg	Lg	lg	Lg	lg	lg	Lg	Lg	lg	Lg	lg
a	A	A	a	A	a	A	a	a	A	a	A
87	97	1	3	19	34	45	38	0	1	6	10

Total = 341
Recombination: Rg-gl = 1.5%
gl-lg = 20.2%
lg-a = 29.3%

Backcross data from structurally normal chromosomes 3 came from the following cross:

Gl Lg A Et / gl lg a et X gl lg a et *

(0)	(0)	(1)	(1)	(2)	(2)	(1-2)	(1-2)	Total
Gl	gl	Gl	gl	Gl	gl	Gl	gl	
Lg	lg	lg	Lg	Lg	lg	lg	Lg	
A	a	a	A	a	A	A	a	
329	215	86	122	108	209	40	12	1121

Recombination: Gl-Lg = 23.2%
Lg-A = 33.0%

* No classification was made for et since it was not well expressed. The marked deficiency of the a class is due to the semi-lethal effect of the et allele.

2. Preferential pairing in structurally heterozygous triploids.

A triploid plant found in the progeny of the cross of In 3b X In 3a came from a diploid egg with two In 3b chromosomes. One In 3a chromosome was contributed by the pollen parent. (For information about the extent of these inversions see the 1956 News Letter). Both In 3b chromosomes carried the A_1 allele and the recessive a_1 allele was in the In 3a chromosome. Although a large progeny from triploid plants is rather difficult to obtain, reciprocal crosses were made with a_1 testers and the ensuing kernels classified for the A and a phenotypes. Using the triploid as the female parent there was a ratio of 225 colored:43 colorless kernels (83.9% A) in the backcross. The reciprocal crosses gave 405 colored: 75 colorless kernels (84.4% A). Control data were available from backcrosses of triploids with three structurally normal chromosomes 3, two with the A allele and one with the a allele. When these structurally homozygous triploids were used as the female parent in backcrosses there was a ratio of 874 colored:276 colorless kernels (76.0% A). The

reciprocal mating gave 225 colored:80 colorless (73.8% A). These data, limited though they are, suggest that pairing was not at random in the structurally heterozygous triploid but tended to occur preferentially between the two In 3b chromosomes. If these two chromosomes always formed a bivalent and disjoined normally, only colored kernels would be found in backcrosses. If pairing between the three chromosomes were at random, then the ratio of colored: colorless kernels should be that found in the control matings with structurally identical chromosomes. The observed data fall between these two extremes and are indicative of some degree of preferential pairing. These data are of interest in connection with the problem of pairing in allopolyploids with partially homologous chromosomes.

M. M. Rhoades

3. Further studies on the Li pericentric inversion in chromosome 9.

Li reported (M. N. L. 1950) that the break points in In 9a were at 0.7 in 9S and 0.9 in 9L. The sh locus was distal to the break point in 9S while wx was included in the inverted segment. Crossovers within the inversion loop give rise to two kinds of deficient-duplicate chromosomes. One is a Dp 9S Df 9L chromatid which has in duplicate the distal .3 of 9S and is deficient for the terminal .1 of 9L. The complementary duplicate-deficient strand is Df 9S Dp 9L. This chromatid is deficient for the distal .3 of 9S and has the distal .1 of 9L in duplicate. Li found that 2.4 percent of the functioning megaspores had the Df 9S Dp 9L chromosome. No statement was made about the functioning of the Dp 9S Df 9L megaspores. The following data afford additional information on the cytogenetics of this inversion:

$$\frac{\text{Sh Bz In Wx}}{\text{sh bz N wx}} \times \text{sh bz wx pollen}$$

Sh Bz Wx	sh bz wx	Sh bz Wx	sh Bz wx	Sh bz wx	sh Bz Wx	sh bz Wx	Sh Bz wx	Total
1104	1099	0	2	10	11	142	720	3088

1834 Sh:1254 sh 1837 Bz:1251 bz 1257 Wx:1831 wx

The greater number of Sh and Bz kernels compared to those homozygous for the sh and bz alleles is due to the large Sh Bz wx class which comes in large part from Dp 9S Df 9L gametes produced by crossing over within the inversion. It is evident that the Bz locus is distal to the break point in 9S. However the Sh Bz wx can also come from single exchanges between bz and the In and from 2- and 2-strand doubles within the inversion where one exchange is between wx and the break point in 9L. These should be relatively infrequent. The complementary class,

sh bz Wx, occurred much less frequently (142 vs 720) than the Sh Bz wx class. This is indicative that the Df 9S Dp 9L megaspores do not function as frequently as do the Dp 9S Df 9L spores.

Data from the reciprocal cross are as follows:

Sh Bz Wx	sh bz wx	Sh bz Wx	sh Bz wx	Sh bz wx	sh Bz Wx	sh bz Wx	Sh Bz wx	Total
754	540	0	0	13	9	31	40	1387

Here the Sh Bz wx and sh bz Wx classes are approximately equal in size since neither type of duplicate-deficient microspore develops into functioning pollen and both classes stem from singles between bz and the In or 2- and 3-strand doubles within the In where one exchange is between wx and the break point in 9L. In the female backcross the Sh Bz wx class constituted 23.3 percent of the progeny but only 2.9 percent in the male backcross. The difference may be ascribed to functioning Dp 9S Df 9L megaspores. Likewise in the female backcross the sh bz Wx class was 4.6 percent of the total while in the male backcross the percentage was 2.2. Here also the difference is due to functioning Df 9S Dp 9L megaspores which according to Li's data amount to 2.4% of the functioning ovules.

When plants heterozygous for this inversion were pollinated by bm$_4$ pollen, some of the F_1 plants were phenotypically bm. These arose from functioning Dp 9S Df 9L megaspores which are deficient for the tip of 9L. The F_1 bm plants are hemizygous for the bm locus and show the bm phenotype. The bm locus can be placed in the distal end of 9L.

M. M. Rhoades
E. B. Patterson

4. Further studies on preferential segregation.

Plants of abnormal 10/normal 10 and K 3L/k 3L constitution were used as the female parent in crosses with a gl$_6$-lg$_2$-a$_1$ tester which had knobless chromosomes 3. (The symbol K 3L represents a chromosome 3 possessing the knob at position 0.6 in the long arm while k 3L denotes a knobless chromosome 3.) Both the K 3L and k 3L chromosomes of the female parent were carrying the Gl, Lg and A alleles. The A locus is distal to the knob while Gl is proximal. The location of Lg with respect to the knob is uncertain as yet. Four types of F_1 plants are expected although not with equal frequencies inasmuch as both the abnormal 10 and K 3L chromosomes undergo preferential segregation. In a total of 50 F_1 plants which were studied cytologically for the presence or absence of the abnormal 10 and K 3L chromosomes, and from which backcross progenies were obtained, there were 25 plants

heterozygous for abnormal 10 and K 3L, 10 heterozygous for abnormal 10 but homozygous for k 3L, 11 homozygous for normal 10 but heterozygous K 3L, and 4 which were homozygous normal 10 and knobless 3. The following backcross data were obtained using the F_1 plants as the egg parent:

	(0) Gl Lg A	(0) gl lg a	(1) Gl lg a	(1) gl Lg A	(2) Gl Lg a	(2) gl lg A	(1-2) Gl lg A	(1-2) gl Lg a	Total
abn 10/N 10; K 3L/k 3L	2529	871	663	2060	859	474	309	662	8427
abn 10/N 10; k 3L/k 3L	730	656	425	465	471	493	210	178	3628
N 10/N 10; K 3L/k 3L	954	870	514	525	274	326	121	143	3727
N 10/N 10; k 3L/k 3L	286	259	122	118	174	159	67	38	1223

Analysis of these data gave the results shown below:

	% Gl	% Lg	% A	Recombination Gl-Lg	Lg-A	Total
abn 10/N 10; K 3L/k 3L	51.7	72.5	63.6	43.9	27.3	71.2
abn 10/N 10; k 3L/k 3L	50.6	50.8	52.3	35.2	37.3	72.5
N 10/N 10; K 3L/k 3L	50.0	50.9	51.7	35.0	23.2	58.2
N 10/N 10; k 3L/k 3L	53.1	50.4	51.5	28.2	35.8	64.0

One of the unusual features of these data is the increase in crossing over found in plants heterozygous for abnormal 10. The average total recombination for the Gl-Lg-A regions in the two classes carrying abnormal 10 is 72 percent while it is 61 percent in the two classes homozygous for normal 10. Another point of interest is the reduction in crossing over in the Lg-A region when the knob is heterozygous. The average value for this region in the two classes homozygous for knobless chromosomes 3 is 36.5 percent and only 25.2 percent in the two classes heterozygous for the knob. It is obviously desirable to ascertain the location of the Lg_2 locus with respect to the knob; no accurate placement is possible at this time but the Lg locus most likely lies proximal to the knob. Another matter of some importance is that the decrease in recombination in the Lg-A region found in plants heterozygous for the knob is accompanied by an increase in the Gl-Lg region. Comparing first the two classes each heterozygous for abnormal 10 but differing in that one is heterozygous for K 3L while the other is homozygous for k 3L, we find a decrease in the Lg-A region and an increase in the Gl-Lg region in K 3L/k 3L plants as compared to k 3L/k 3L. The total amount of recombination is essentially equal. A comparison of the data from N 10/N 10 K 3L/k 3L and N 10/N 10 k 3L/k 3L plants also indicates a decrease in the Lg-A region in K 3L heterozygotes as compared to homozygous k 3L plants and an increased amount of recombination in the Gl-Lg

region in the K 3L heterozygotes. It should be stressed that these crossover data come from sibling plants.

Studies are underway to see if the increase in crossing over in the long arm of 3 found in abnormal 10 heterozygotes will also occur in other chromosomes and to determine what the frequency of crossing over will be in homozygous abnormal 10 plants.

Preferential segregation for the chromosome 3 markers occurred in only one of the four F_1 classes--namely the class heterozygous for both abnormal 10 and K 3L. Plants heterozygous for abnormal 10 and homozygous k 3L exhibited random segregation for genes in 3L as did plants in the two classes homozygous for normal 10. Before discussing the varying extent of preferential segregation for the Gl, Lg and A loci, it is necessary to consider what is known of the cytological locations of these loci. Studies with In 3a show that Gl_6 is proximal to position 0.4 and Dempsey (1955 News Letter) has shown that it is distal to point 0.1. There are approximately 20 crossover units between Gl_6 and the centromere. The Lg_2 locus cannot be accurately assigned at this time. It is known to be distal to point 0.4 and probably lies proximal to the knob (0.6) but this conclusion is not soundly based. The distal-most locus A is situated in the segment delimited by positions 0.8 and 0.9; it lies therefore beyond the knob.

The low degree of preferential segregation for the Gl allele is understandable on the hypothesis that preferential segregation takes place only when crossing over occurs resulting in anaphase I dyads having one knobbed chromatid with the Gl allele and one knobless chromatid with the gl allele. Heterozygous dyads of this type arise from tetrads with single exchanges between the centromere and gl and from all kinds of double exchanges where one exchange is in the centromere-gl region and the second exchange is between the knob and A. All other double exchanges with one crossover to the left of gl give random segregation for the gl locus.

The high degree of preferential segregation for the Lg allele is expected since there is more opportunity for the appropriate crossovers which lead to heteromorphic dyads and hence to preferential segregation. If the order is centromere (1) Gl (2) Lg (3) K (4) A, singles in regions 1 and 2, 3-strand doubles in 1-2, and all doubles in 1-4 and in 2-4 lead to preferential segregation for Lg. Preferential segregation for the A allele comes from singles in 1, 2, and 3, from 3-strand doubles in 1-2, from 3-strand doubles in 1-3 and from 3-strand doubles in 2-3. The higher degree of preferential segregation for the Lg allele as compared to the A allele is due to the frequent occurrence of double exchanges in regions 2 and 4 which lead to preferential segregation for Lg but not for A.

In the 1955 News Letter we presented data showing preferential segregation for the knobbed chromosome 9 in heteromorphic bivalents

in plants both homozygous and heterozygous for abnormal 10. Additional data have since been obtained which are in agreement with this conclusion. It now appears, however, that preferential segregation for the knobbed 9 is higher in plants homozygous for abnormal 10 than in heterozygous plants. The following data have been obtained using the wd character which is always associated with a knobless 9 since it is due to a deficiency for the tip of 9S.

N 10/N 10; K Wd/k wd	1629 Wd : 1618 wd (control data)			
	Wd Wx	wd Wx	Wd wx	wd wx
abn 10/N 10; K Wd Wx/k wd wx	3676	1504	2198	2546
	(59.2% Wd and 52.2% Wx)			
abn 10/abn 10; K Wd Wx/k wd wx	967	225	591	430
	(69.8% Wd and 53.9% Wx)			

An unusual situation was encountered when plants of abnormal 10/normal 10; K 8L j/k 8L J constitution were used as the egg parent in backcrosses. Since the knobbed chromosome 8 carried the j allele it was anticipated that preferential segregation would occur for the j allele which is situated in the distal portion of 8L not too far removed from the knob. The data are listed below:

G J	g j	g J	G j	
1936	518	682	138	= 3274
59.1%	15.8%	20.8%	4.2%	
(63.3% G and 79.9% J)				

The high percentage of functioning megaspores apparently carrying the J allele was wholly unexpected and disturbing since the J allele was carried by the knobless chromosome 8. Indeed, the frequency of the j class should have been much higher than that of the J class. This finding, which was contrary to the data obtained with other heteromorphic chromosome pairs, could be explained if the abnormal 10 chromosome carried a dominant suppressor of j. Stocks carrying abnormal 10 are known in which the j phenotype is suppressed. Thus many plants of the J phenotype actually were homozygous for the j allele whose action was inhibited by a dominant suppressor of j in the distal portion of the long arm of abnormal 10. Approximately 70 percent of the functioning megaspores had abnormal 10 with the suppressor. Therefore 70 percent of the backcross progeny would be phenotypically J even if all chromosomes 8 in the basal megaspores possessed the j allele.

M. M. Rhoades
Ellen Dempsey

5. "Kys" male sterility.

In the 1956 News Letter a case of male sterility was reported in which the male sterile plants first occurred in a backcross of as/ Kys egg parents to Kys. On further analysis it appears that this occurrence of male sterility is simply another instance of the so-called "Kys" male sterility, which appears in the second cross to Kys (with Kys as pollen parent) of any strain of Ms __ S __ constitution. The data presented below are consistent with a two factor system in which Ms __ s s types are male sterile and Kys is homozygous for both recessives. Moreover, plants of Ms ms S s genotype produce 50% partially filled pollen as was observed by Bauman in his study of the Kys male sterility. The only discrepancy to date between my results and those reported by others working with Kys male sterility is the progeny of a single selfed plant which segregated male steriles. None of the genotypic combinations of the Ms and S factors would be expected to give male sterile plants in the F_2 because the s allele is not transmitted through the pollen by Ms ms S s plants. The F_2 populations examined in the field in 1956 did not segregate male sterility, but none were duplicates of the aberrant population mentioned above.

An adequate test of a cytoplasmic effect has not yet been completed in the present case. Leng and Bauman (1955) and Ogle (1956 News Letter) have shown that no cytoplasmic sterility is involved in the Kys male sterility. This is undoubtedly true in the present case also, especially since plants with "partial" pollen occur in the progeny of Kys X Ms ms S s as well as in the progeny of Ms ms S s X Kys where the Ms ms S s egg parent was derived from as/Kys X Kys. In the former cross the cytoplasm was from normal Kys and in the latter it came from the asynaptic stock.

Results of crosses of Ms ms S s and Ms ms s s egg parents by ms ms s s (Kys) pollen.

	Normal	Male sterile
Ms ms S s		
	79	25
	8	5
	21	12
	23	6
	18	10
	24	10
	19	12
	6	3
	75	16
	59	32
	58	21
	390	172
Expect (3:1)	421.5	140.5

	Normal	Male sterile
Ms ms s s		
	46	27
	33	34
	19	21
	31	24
	129	106
Expect (1:1)	117.5	117.5

Simultaneous tests in which male sterile plants were classified:

		♀ B.C.	♂ B.C.	as ♂ X MS sib	⊗
Ms ms S s	19147 (2)	75 N: 16 MS	all N	all N	-----
	19147 (12)	59 : 32	all N	all N	-----
	19147 (47)*	---------	all N	all N	all N
	19147 (54)*	---------	all N	all N	all N
		χ = 134 48			
		Expect (3:1) 136.5: 45.5			
ms ms S s	19147 (13)	---------	all N	65 N: 26 MS	all N
	19147 (34)	all N	all N	63 : 12	-----
				χ = 128 38	
				Expect (3:1) 124.5: 41.5	
ms ms s s	19147 (5)	---------	-----	29 : 54	all N
	19147 (30)	---------	all N	45 : 47	all N
				χ = 74 :101	
				Expect (1:1) 87.5: 87.5	

* Genotypes of these plants were determined after examination for "partial" pollen.

Classification for "partial" pollen:

		♀ B.C.	♂ B.C.	as ♂ X MS sib	♀
Ms ms S s	19147 (47)	------	35 N: 56	19 N: 68 : 0 MS	54 N: 34
	19147 (54)	------	37 56	9 13 1	47 20
	17150	------	------	9 27	------
	17150	------	------	16 28	------
	19151 (3)	------	------	----------	27 11
	17150 (94)	------	------	----------	36 23
			χ = 72 :112		
		Expect (1:1)	-- 92 : 92	χ= 53 :136 : 1*	χ=164 : 88
				Exp.	
			Expect (1:3)	--47.3:141.7 (5:3)	-157.5: 94.5
ms ms S s	19151 (1)	------	------	----------	33 : 0
	19151 (2)	------	------	----------	40 0
	19147 (34)	all N	all N	41 : 22 :12	------
			Expect (2:1:1)	--37.5: 18.7:18.7	

* Probably due to contamination.

In the above 2 tables, all columns labelled B.C. refer to backcrosses to Kys.

Pollen grains from Ms ms S s and Ms ms s s plants were stained with carmine and examined. In Ms ms S s samples, about half the grains are normal in appearance and half are smaller and partially filled with starch. The latter presumably are of Ms s and ms s constitution. Some of the small grains contained two sperm nuclei and a vegetative nucleus while others apparently had only one nucleus. In Ms ms s s samples, there is no normal pollen and none of the grains contains starch. Some of the cells have a single nucleus and others show signs of degenerate nuclear material. Both S and Ms may produce a transient conditioning of the cytoplasm of the microspores. Grains of identical genotypes (Ms s and ms s) are present in the two samples examined yet in the Ms ms S s sample the abortive grains are much more normal in appearance. This difference may be due to the action of the S factor. Moreover, the ms s genotype in itself cannot produce abortion in the microspore since normal Kys pollen is of this constitution. It would seem that the Ms factor also has a conditioning effect on the cytoplasm of the PMC prior to meiosis which determines whether a microspore of ms s constitution will be entirely normal or will abort.

Ellen Dempsey

6. Heterotic effects of a chromosomal segment.

Tests for heterotic genes in the long arm of chromosome 3 were continued in 1956. A homozygous inversion 3a strain carrying the recessive a_1 allele in the inverted segment was crossed to a number of inbred lines with the A_1 allele. F_1 plants, all heterozygous for the inversion and for A:a, were backcrossed by the recessive a_1 inversion stock. On the F_1 backcrossed ears there was a ratio of 1 colored: 1 colorless kernels. The colored kernels are heterozygous for the inversion and for A:a and the colorless kernels homozygous for the inversion and for a:a. The kernels of the 2 classes were planted in replicated plots. Data for grain yield, ear height, kernel weight, ear number, and maturity are given in the following tables:

	Ave. yield per rep. in lbs.				Ave. ear height per plant in cms.			
	No. reps.	Aa	aa	't' value	No. reps.	Aa	aa	't' value
R 4	12	3.89	3.58	6.20**	12	114	106	4.60**
R 2	12	3.37	3.36	0.17	12	129	124	6.28**
O 45	12	3.35	3.17	2.00	12	115	100	7.91**
O 41	12	3.49	3.24	4.17**	12	128	120	5.65**
M 14	12	3.57	3.48	1.50	12	108	103	6.42**
K 4	12	3.55	3.41	1.52	12	131	121	6.85**
I 205	12	3.05	3.11	0.90	12	108	109	0.51
C 103	12	3.38	3.29	1.32	12	122	116	3.67**
5120 B	12	3.79	3.58	2.14	12	125	114	7.46**
K 187-2	12	2.92	2.65	2.45*	12	113	93	10.41**
38-11	12	3.62	3.39	2.88**	12	128	120	5.37**
O 7	12	3.56	3.19	3.36**	12	113	98	12.16**
WF 9	12	3.36	3.41	1.40	12	107	105	2.44*
W 26	12	3.29	3.40	1.11	12	120	112	7.07**
R 59	12	4.05	3.92	1.55	12	125	114	10.37**

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

	Ave. weight of 1000 kernels in gms.				Ave. ear no. per rep.			
	No. reps.	Aa	aa	't' value	No. reps.	Aa	aa	't' value
R 4	6	187	166	2.94*	12	17.7	16.9	1.51
R 2	6	192	181	2.57*	12	14.2	14.8	2.23*
O 45	6	231	201	3.17*	12	13.1	13.2	0.27
O 41	6	199	173	3.93**	12	16.9	16.0	1.96
M 14	6	189	173	4.07**	12	15.8	16.7	1.99
K 4	6	178	159	2.28	12	18.5	18.2	0.48
I 205	6	197	184	1.86	12	12.6	13.0	2.19
C 103	6	221	205	2.48	12	13.5	13.2	0.72
5120 B	6	235	207	8.80**	12	15.5	14.3	2.17
K 187-2	6	202	177	4.41**	12	15.1	13.0	4.75**
38-11	6	218	188	6.06**	12	16.0	14.5	2.57*
O 7	6	214	205	1.59	12	18.0	14.5	6.44**
WF 9	6	223	186	12.41**	12	12.5	12.8	1.08
W 26	6	220	197	3.71**	12	13.5	14.8	2.79*
R 59	6	246	228	1.62	12	16.8	17.6	1.46

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

	Ave. days from planting to half silking			
	No. reps.	Aa	aa	't' value
R 4	12	69.2	69.7	2.08
R 2	12	68.8	69.1	1.73
O 45	12	66.3	65.2	3.67**
O 41	12	69.7	69.4	1.42
M 14	12	68.4	68.3	0.36
K 4	12	71.9	71.3	1.87
I 205	12	66.9	66.2	1.85
C 103	12	68.3	68.9	2.22*
5120 B	12	67.4	67.5	0.50
K 187-2	12	65.2	64.9	1.43
38-11	12	67.0	66.9	0.40
O 7	12	65.3	65.2	0.40
WF 9	12	62.9	64.1	6.32**
W 26	12	66.1	66.5	1.43
R 59	12	66.2	66.5	2.64*

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

The kernels from selfed ears of F_1 plants were planted at random in the field without classifying for aleurone color. The F_2 plants were detasseled and the intervening rows of an $\underline{a}_1$ tester used as pollen source. Plants having ears with only colored kernels are homozygous for the chromosome 3 segment from the inbred line, those with half colored and half colorless kernels are heterozygous for the inverted segment, and those with only colorless kernels are homozygous for the inversion. Data for grain yield, ear height, ear number, and maturity are presented below:

	Ave. yield per plant in gms.						't' value		
	No. plants	AA	No. plants	Aa	No. plants	aa	AA vs Aa	AA vs aa	Aa vs aa
R 4	36	72.9	86	96.2	34	101.8	3.58**	4.60**	1.54
R 2	70	99.2	120	116.0	52	108.5	2.42**	1.65	1.48
O 45	61	118.2	124	131.2	61	108.9	2.52**	1.52	4.82**
O 41	35	110.5	90	116.4	31	103.3	1.00	0.99	2.11*
M 14	67	106.8	124	125.8	53	113.7	4.23**	1.34	2.43**
I 205	42	94.7	64	104.2	39	107.3	1.44	1.59	0.42
C 103	27	99.1	82	122.9	32	103.7	3.08**	0.47	2.53**
5120 B	42	101.8	86	117.6	44	109.5	2.68**	0.99	1.28
K 187-2	47	116.0	119	113.7	59	103.5	0.38	2.06*	1.96
38-11	32	95.1	77	111.4	35	98.1	2.04*	0.36	1.76
O 7	44	119.0	71	133.6	33	113.1	1.98*	0.71	2.74**
WF 9	53	112.1	109	116.8	66	116.5	0.74	0.59	0.05
W 26	60	82.3	119	101.1	52	98.2	4.29**	3.15**	0.58
R 59	36	92.1	85	115.3	32	88.2	3.22**	0.52	3.74**

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

	Ave. ear height per plant in cms.						't' value		
	No. plants	AA	No. plants	Aa	No. plants	aa	AA vs Aa	AA vs aa	Aa vs aa
R 4	36	91	86	94	34	90	1.52	0.15	1.62
R 2	70	106	119	105	52	96	0.16	3.28**	4.16**
O 45	61	94	124	88	61	77	2.04*	5.78**	4.61**
O 41	35	100	90	110	31	100	2.66**	0.15	2.63**
M 14	67	70	124	76	53	73	2.95**	1.11	0.87
I 205	42	90	64	105	39	111	5.15**	6.38**	1.98
C 103	27	84	82	85	32	82	0.32	0.53	1.13
5120 B	42	106	86	111	44	105	1.68	0.57	2.31**
K 187-2	47	107	119	104	59	85	1.42	7.24**	7.36**
38-11	32	128	76	122	35	100	1.87	7.24**	6.31**
O 7	44	126	70	124	33	109	0.39	4.32**	4.37**
WF 9	53	101	109	102	66	96	0.25	1.30	2.15*
W 26	56	100	113	102	49	88	0.58	3.62**	5.37**
R 59	36	125	84	122	32	108	0.71	4.47**	4.98**

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

	Ave. ear number per plant						't' value		
	No. plants	AA	No. plants	Aa	No. plants	aa	AA vs Aa	AA vs aa	Aa vs aa
R 4	36	1.03	86	1.18	34	1.18	1.93	1.85	0
R 2	70	1.21	120	1.15	52	1.09	1.05	1.68	0.99
O 45	61	1.13	124	1.18	61	1.05	0.81	1.52	2.45**
O 41	35	1.20	90	1.31	31	1.13	1.22	0.74	1.96
M 14	67	1.03	124	1.14	53	1.13	2.33**	2.07*	0.17
I 205	42	1.02	64	1.08	39	1.18	1.30	2.48**	1.53
C 103	26	1.04	82	1.00	32	1.00	1.79	1.15	0
5120 B	42	1.12	86	1.14	44	1.23	0.31	1.33	1.31
K 187-2	47	1.36	119	1.36	59	1.07	0	3.99**	4.21**
38-11	32	1.00	77	1.16	35	1.00	2.47**	0	2.61**
O 7	44	1.17	71	1.25	33	1.00	0.92	2.24*	2.89**
WF 9	53	1.19	109	1.10	66	1.06	1.45	2.03*	0.65
W 26	60	1.07	119	1.19	52	1.15	2.16*	1.24	0.60
R 59	36	1.22	85	1.35	32	1.19	1.36	0.27	1.67

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

	Ave. days from planting to silking						't' value		
	No. plants	AA	No. plants	Aa	No. plants	aa	AA vs Aa	AA vs aa	Aa vs aa
R 4	36	65.1	85	64.9	31	64.6	0.54	1.28	0.54
R 2	67	63.7	111	62.4	49	63.2	3.52**	1.12	1.98*
O 45	56	63.4	113	61.3	54	61.4	5.38**	3.89**	0.10
O 41	31	65.5	81	65.6	28	64.8	0.32	1.68	2.61**
M 14	56	62.3	107	61.8	48	62.6	1.41	1.00	2.17*
I 205	42	62.1	60	62.8	36	63.0	1.33	1.89	0.68
C 103	27	65.2	78	65.0	29	65.5	0.37	0.47	0.95
5120 B	38	65.3	82	65.1	41	65.9	0.51	1.18	1.87
K 187-2	42	63.7	104	63.6	50	63.0	0.15	1.35	1.32
38-11	22	66.5	57	66.6	32	65.9	0.12	0.78	1.05
O 7	43	66.4	65	65.5	31	65.5	2.18*	1.63	0
WF 9	49	62.4	104	62.7	63	64.4	0.72	3.35**	3.41**
W 26	54	63.9	104	63.0	44	63.2	2.05*	1.26	0.50
R 59	26	72.6	60	70.2	24	70.9	4.06**	2.15*	1.08

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

After 3 successive years' tests it is concluded that certain inbred lines carry genes in the long arm of chromosome 3 which give a heterotic effect when tested against the same segment in the inversion strain. This heterotic effect is shown in both grain yield and ear height. The grain yield data obtained from 1954 to 1956 and the maturity data obtained in 1955 and 1956 are not consistent. This might be attributed to differences in the conditions of different growing seasons. As indicated in the tables of grain yield and ear number of both backcrossed and F_2 materials, the larger ear number is, in most cases, related to the greater yield in the heterozygous classes over the homozygous classes in those inbred lines which show significant differences. Data for ear height obtained in the last two years from backcrossed materials show highly significant differences between heterozygous and homozygous inversion classes, except in one inbred line, I 205, which showed a significant difference in 1955 but not in 1956. This is also true in the F_2 materials as shown in the table presented in this paper. The differences in kernel weight are highly significant in most inbred lines in both years. These differences are either due to the heterotic genes from the inbred lines or the 15.75% ovule abortion in the class heterozygous for inversion (3.31% in the class homozygous for inversion). From these experiments it is also concluded that the method of using paracentric inversions for testing genes affecting agronomic characters, such as yield and ear height, as suggested by Dobzhansky and Rhoades in 1938, is effective.

Chuan-Ying Chao

7. Unstable genes.

Five mutable alleles of pr have been found which are not Ac controlled. Each of these mutable genes was crossed to an Ac tester that was I Ds/I Ds in constitution. No evidence of Ac activity was obtained.

One other mutable gene which occurred at the R locus also failed to show any Ac activity when crossed to an Ac tester. This unstable gene effects both the aleurone and plant color components. Four different phenotypes were observed in the aleurone. The seeds that were fully colored and spotted-dilute gave rise to fully colored plants, but the seeds that were spotted produced variegated color in the tassels. The plant color from colorless seeds appeared somewhat diluted, but only four plants were observed from this class.

8. Pre-meiotic mutation at the R locus.

Several somatic sectors involving pre-meiotic mutations of R to r have occurred spontaneously in female gametes. The cultures in which the sectors originated were marked to the left and right of the R locus to determine whether crossing over was involved.

One relatively large sector including 24 colorless seeds was produced by the cross $g\ R^r\ K/G\ R^r\ k \times g\ r^g\ k/g\ r^g\ k$. Since the colorless seeds were found in positions clustered on the ear. the mutation must have occurred in a somatic cell. The table (p. 89) shows the positions of the mutants on the ear and also the g and knob-10 classification.

It will be noted that 15 of the 19 mutants analyzed are of $g\ r^r\ K$ type that could occur by mutation of the $g\ R^r\ K$ allele. If pre-meiotic mutation resulted in the production of $g\ r^r\ K/G\ R^r\ k$ cells, the two $G\ r^r\ K$ mutants (positions I-3 and A-4) could be ascribed to coincident crossing over between g and r at meiosis. This interpretation is plausible since 14% of the mutants analyzed should show crossing over in the g - r segment.

In addition to these 17 mutants with knob-10, two were found without the knob. They included one $g\ r^r\ k$ mutant (position C-20) and one $G\ r^r\ k$ mutant (position A-1). On the assumption that the original mutation occurred in the $g\ R^r\ K$ allele, the compound $g\ r^r\ K/G\ R^r\ k$ could yield a $g\ r^r\ k$ mutant by crossing over between r and K in the following meiosis. However, only 1% crossing over is known to occur between r and K. Another possible interpretation is that unequal crossing over occurred at meiosis independent of the sector. The other seed color mutant without the knob ($G\ r^r\ k$) could be attributed to a double crossover in the g-r segment and the r-K segment, assuming the somatic mutation involved the $g\ R^r\ K$ chromosome. Both of these considerations, however, require a high percentage of crossing over in a relatively short segment.

Ear Diagram of Sector

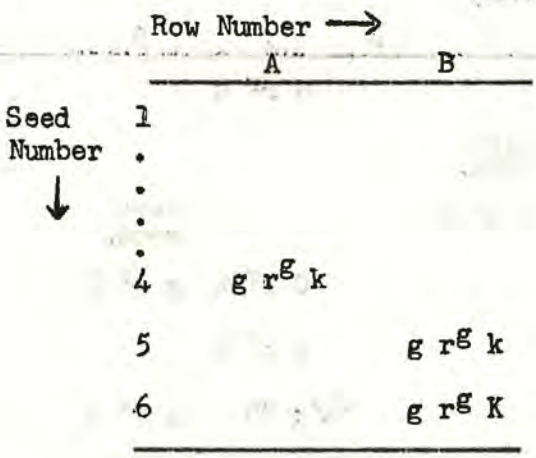
($g\ R^r\ K/G\ R^r\ k \times g\ r^g\ k/g\ r^g\ k$)

Seed Number ↓	Row Number → H	I	J	A	B	C . . . . . G
1				G r^r k		
2		zero germ.				
3	g r^r K	G r^r K			zero germ.	
4	g r^r K			G r^r K	g r^r K	
5				g r^r K		
6			[1]	g CD	g r^r K	
7			[1]	g CD	g r^r K	
8						
9					g r^r K	
10					g r^r K	g r^r K
11						
12						
13					g r^r K	
14						
15						
16					g r^r K	
17					g r^r K	g r^r K
18						g r^r K
19						[2] g CD
20					g r^r K	g r^r k

[1] Died before maturity. Both mutants were colored plant and golden.

[2] Sterile plant.

A second sector involving loss of aleurone color occurred in the compound g R^g co-7 k/G R^r K. In this case the sector included only three colorless seeds. The location of these mutants is given in the following diagram:



These results indicate that the pre-meiotic mutation involved the g R^g k allele since two of the three cases were g r^g k. If the pre-meiotic mutation produced g r^g k/G R^r K cells, the g r^g K mutant (position B-6) could be attributed to a coincident crossover between r and K. As mentioned previously, coincident crossovers are expected in only 1%.

In addition to these large sectors, three others were found which involved only two seeds. In the first case two adjacent mutants were identified in the compound g R^g co-6 k/G R^r K. The two mutants were of the g r^g k type which occurred by mutation of the R^g k parental allele.

A second case with two adjacent mutants was identified in the compound g R^g-14 K/G R^r k. Both mutants were of type G r^r K which could represent somatic mutation of the G R^r k allele with coincident crossing over between r and K. An alternative explanation is that both mutants represent independent events of unequal crossing over.

The third case with two adjacent mutants occurred in the compound g R^g co-8 k/g R^r K. One of the mutants was of type g r^g k and the other was g r^r k. Presumably these mutants represent meiotic events. The r^g k case could be attributed to mutation of the R^g k allele and the r^r k case to unequal crossing over.

M. H. Emmerling

UNIVERSITY OF ILLINOIS
Urbana, Illinois
Department of Horticulture

1. An apparent effect of manganese on rate of crossing over in maize.

Recent work by Demerec and Hanson on Escherichia coli, and Mazia's discovery of calcium - magnesium chromosome linkages in Arbacia, followed by Steffensen, Levine, and Eversoll and Tatum's work on Tradescantia, Drosophila and Chlamydomonas respectively, makes it seem reasonable that applications of the manganous ion would affect the rate of crossing over and/or rate of chromosome aberration in maize.

The results of a preliminary experiment seem striking enough to be worth reporting.

Two rates and 5 times of manganous ion application were employed as follows:

Treat No.	Rate and Nature of Application							
1.	.2 molar	$MnSO_4$	50	days	before	meiosis,	}	repeated each 5 days thereafter until meiosis.
2.	"	"	40	"	"	"		
3.	"	"	30	"	"	"		
4.	"	"	20	"	"	"		
5.	"	"	10	"	"	"		
6.	.02	"	50	"	"	"		
7.	"	"	40	"	"	"		
8.	"	"	30	"	"	"		
9.	"	"	20	"	"	"		
10.	"	"	10	"	"	"		

Treatments were made as foliar sprays. The upper surfaces of the leaves were thoroughly wetted at each treatment.

Rate of crossing over in treated plants was determined for 3 segments. In each case, plants heterozygous for marker loci were treated with manganous ion, and the proportion of crossover male gametes was determined by means of appropriate untreated female tester plants.

The three segments tested were as follows:

C $\overset{(1)}{\text{wx}}$ 0 (Chrom. 9) $\text{lgl}\overset{(2)}{\text{gl2}}\overset{(3)}{0}\text{v}_4$ (Chrom 2)

The results are given in the table on page 92.

Treat. No.	C - wx			$lg_1 - gl_2$			$gl_2 - v_4$			doubles in (2)-(3)		
	Size Prog.	% X-over	P	Size Prog.	% X-over	P	Size Prog.	X-over	P	Size Prog.	% double X-over	P
1.	131	45.0	.05*	20	40.0	.001**	20	40.0	.99	20	25.0	<.0005**
2.	391	36.1	.99	266	19.9	.01 **	192	33.0	.20	192	4.7	.80
3.	426	34.5	.40	87	13.8	.99	87	31.0	.20	87	4.6	.95
4.	273	38.8	.50	418	17.5	.05 *	141	39.7	.80	141	2.1	.20
5.	179	37.4	.90	465	18.9	.01 **	212	34.0	.20	212	4.7	.80
6.	381	34.4	.40	83	12.0	.60	83	34.9	.50	83	1.2	.20
7.	266	36.8	.99	315	17.5	.10	227	40.5	.60	227	2.2	.05 *
8.	251	35.9	.80	290	20.0	.005**	290	33.4	.10	290	3.8	.30
9.	155	29.7	.10	79	10.1	.40	79	41.8	.60	79	2.5	.30
10.	522	39.8	.20	--	--	--	--	--	--	--	--	--
Control	414	36.7	--	424	14.2	--	267	38.6	--	267	5.2	--

The effects of the manganous ion have been explained as a function of the ability of this ion to replace the calcium-magnesium ions of the divalent cation bonds, resulting in a net weakening of the chromosome structure.

The rates of crossing over in the C - wx and the lg_1 - gl_2 segments appeared to be correlated throughout the 9 comparable treatments. The coefficient of correlation test gave a highly significant r value of .9134, with a probability of $<.01$.**

It is apparent from the data that crossing over in the lg_1 - gl_2 segment was most noticeably affected, while only one treatment affected the C - wx segment, and no significant effects occurred in the gl_2 - v_4 segment. These results are precisely comparable to those of Eversoll and Tatum, who studied the effects of calcium and magnesium deficiency on crossing over in 3 segments in Chlamydomonas. (They reported a drastic effect for one segment, a slight effect for another, and no effect in a third segment.) It is an obvious conjecture that the effects of Mn^{++} may be modified by the proximity of the centromere and/or degree of chromaticity.

One aberrational progeny from treatment 2 was noted during the process of germinating seedlings for lg_1 - gl_2 - v_4 classification. All seedlings grown from one pollination were uniformly retarded and of uniformly spindly growth. Transmission of minus types in this progeny was drastically altered:

Size of Prog.	% transmission of lg_1	P	% transmission of gl_2	P	% transmission of v_4	P
39	28.2	.01**	7.7	<.0005**	3.04	<.0005**

More striking was the fact that minus types were recovered only in crossover strands.

Since most of the several possible explanations for this progeny involve pre-meiotic events, it would seem that a complete analysis of the effects of Mn should include a study of somatic aberrational tendencies. This estimation is strengthened by Steffensen's finding that a 12-fold increase in frequency of micronuclei present at prophase I occurred in Tradescantia plants grown in a Ca - Mg deficient nutrient solution. (These were clearly a result of pre-meiotic events.)

The most severe Mn treatments markedly retarded the growth of maize. Two plants of treatment one were "thrown" into a "rosette" type of growth for about two weeks. Normal symmetry was finally restored in spite of continued Mn treatments, and the plants matured in a normal, though diminutive, fashion.

If the rather frequent estimation is creditable that the rate of breeding progress in maize is limited by the rate at which genes may be "reshuffled," i.e., the rate of crossing over, it would seem worth while to further investigate the possibilities of utilizing agents affecting the cation linkages of the chromosomes in lifting this ceiling, if it exists.

The writer is indebted to Dr. E. B. Patterson and Dr. E. R. Leng for materials and guidance in this pilot experiment.

2. An effect of beta-hydroxyethylhydrazine on time of flowering in maize.

.075, .15, .3, and .6% concentrations of this chemical, which reportedly hastens date of flowering in pineapple, were applied as foliar spray to the maize single cross WF9 X 38-11, beginning at the 3 leaf stage, and repeated at 4 day intervals thereafter for 3, 6, 9, and 12 successive treatments. No important effects on either date of flowering or growth habit were noticeable.

However, one seed soaking treatment was made in addition to the foliar sprays. Seeds soaked over night in an .6% aqueous solution of beta-hydroxyethylhydrazine germinated more slowly than the controls, and growth was further drastically retarded after emergence. The treated seedlings became somewhat chlorotic, and made almost no progress for about 10 days. Normal growth then gradually resumed, and the plants flowered in a vigorous manner. A net delay in anthesis of about 14 days was obtained. A reduction in plant height of 2-3 feet occurred. Treated seeds experienced 40% mortality from this rate of treatment, with mortality occurring as both failure to emerge, and as post emergence dying.

Although only one rate of seed soaking treatment was attempted, the results obtained make it seem reasonable that lower rates of this chemical would be worth investigating as a possible means of obviating the costly and hazardous process of split planting in the production of some commercial maize hybrids.

3. Another source of id. (indeterminant growth habit).

A row of selfed maize was found to be segregating 7 indeterminant to 21 normal during the past season. Indeterminant plants were still vegetative as of Nov. 1, no inflorescences having been initiated. As yet, no photoperiodism studies have been made, or tests for allelism with the id recently studied by W. C. Galinat.

4. A cytological survey of some "problem" restorer lines of maize.

Using the "Eckhardt" system for introducing the "F" pollen restoring gene(s), it has been the writer's experience (Maize News Letter 1956 pp. 160-161.) that 10 to 15% of maize inbred lines show normal restoration in the F_1 and BC_1 recovery generation after crossing with a restorer source with "T" sterile cytoplasm. However, these exceptional "problem" lines show either merely partial or no restoration in the later back cross generations. Since such lines are by necessity quite exceptional, at least in their "T" cytoplasm restoring characteristics, it was thought worth while to investigate the possibility that the behavior of such lines might relate to cytologically detectable differences or abnormalities. The following F_1 crosses between restorer sources and "problem" lines were investigated: Ky21 X S134, K55 X S134, Ky21 X S139, K55 X S139, I153 X W22, K55 X W22, I153 X 159, I153 X Oh51a, and K55 X Oh51a.

No irregularities in chromosome morphology, pachytene pairing, diakinesis, anaphase I, anaphase II, or pollen grain formation were noted.

This may be considered as negative evidence in favor of the precept that the unusual behavior of these lines as noted relates purely to "genetic" causes.

Donald L. Shaver

IOWA STATE COLLEGE
Ames, Iowa
Department of Agronomy

1. A popcorn fertility restorer.

An inbred line of popcorn (W41) isolated from a strain of the White Rice variety obtained from Dr. Oliver E. Nelson of Purdue University appears to be equally as good as either T x 127C or K 55 in restoring fertility to the Texas type of cytoplasmic male sterility.

The fertility restoring ability of this inbred is indicated by the following comparisons with K 55 and T x 127C. The segregation for fertility restoration of F_2 as well as single crosses with non-restorer inbreds when crossed on cytoplasmic male sterile stocks is also shown.

Cross	Fertile plants	Sterile plants
Male sterile x K 55	22	0
Male sterile x T x 127C	92*	0
Male sterile x 41	144	0
(Male sterile x 41) F_2	43	16
Male sterile x (41 x non-restorers)	58	47

* Six of these plants in an early planting appeared to be only partially fertile.

W. I. Thomas

IOWA STATE COLLEGE
Ames, Iowa
Department of Agronomy
and
UNIVERSITY OF WISCONSIN
Madison, Wisconsin

1. Studies on the inheritance of resistance to corn leaf rust

Puccinia sorghi Schw.

It was reported in the 1955 Corn Genetic Newsletter that greenhouse seedling inoculations on 165 lines of corn showing field resistance revealed that 25 strains possessed protoplasmic resistance to one or more biotypes of the pathogen. A table included in the report indicated that resistance in each of B38, K148 Cuzco and GG208 was due to a dominant allele at a single locus. The following table shows the reaction of these strains to 11 cultures of Puccinia sorghi.

Reactions to 11 cultures of Puccinia sorghi

Source of resistance	901@	904	908	917	921	922	926	927	928	929	930
B38	0;	0;	0;	0;	0;	0;	0;	3	0;	0;	0;
K148	1-	1-	3	1-	1-	1-	1-	3	1-	1-	1-
GG208	1-	1-	1-	1-	0;	1-	1-	1-	1-	1-	3
Cuzco	0;	0;	0;	0;	0;	0;	0;	0;	0;	0;	0;

This table shows that these strains have different genotypes for resistance. It is necessary to know how many genes for resistance each source has and the number of loci involved among the four strains. Some

preliminary information on these points has been obtained by studying the reactions of backcrosses and F_2 progenies of various single crosses to relatively pure rust cultures and to mixtures of cultures. The following mixtures were used:

A - 901a, 904, 917, 921, 922, 926, 928, 929 and 930.
B - 901a, 904, 908, 917, 921, 922, 926, 928, 929 and 930.
C - 901a, 904, 908, 917, 922, 926, 927, 928 and 929.
D - 901a, 904, 908, 917, 922, 926, 928 and 929.
E - 901a, 904, 917, 922, 926, 928, 929 and 930.
F - 901a, 904, 908, 917, 921, 922, 926, 927, 928, 929 and 930.

Several of the progenies studied had as one parent inbred line B14 or M14 both of which give a susceptible reaction to all 11 rust cultures listed above. The following table shows the results of the greenhouse seedling inoculations.

Cross	Pathogen	Number of plants observed Res.	Susc.	Hypothetical Expectations	X^2 Value	P Value
(M14 x K148)F_2-1	Mixture A	76	21	3:1	0.581	0.50-0.30
(M14 x K148) x M14-1	"	46	50	1:1	0.167	0.70-0.50
" -2	"	51	42	1:1	0.872	0.50-0.30
" -3	"	49	48	1:1	0.010	0.95-0.90
(B14 x K148)F_2-1	"	69	29	3:1	1.102	0.30-0.20
" -2	"	74	21	3:1	0.425	0.70-0.50
(M14 x GG208)F_2-1	Mixture C	77	22	3:1	0.407	0.70-0.50
(M14 x GG208) x M14-1	"	49	49	1:1	0	1.00
" -2	"	37	54	1:1	3.176	0.10-0.05
(B14 x GG208)F_2-1	"	69	29	3:1	1.102	0.30-0.20
(M14 x GG208)F_2-1	Mixture D	77	18	3:1	1.856	0.20-0.10
(M14 x GG208) x M14-3	"	49	46	1:1	0.095	0.80-0.70
(B14 x GG208)F_2-2	"	72	26	3:1	0.122	0.80-0.70
(B14 x Cuzco)F_2-1	Mixture F	69	23	3:1	0	1.00
(GG208 x Cuzco)F_2-1	901a	89	1	all resistant		
" -2	901a	83	0	"	"	
(K148 x GG208)F_2-1	901a	101	0	"	"	
" -2	901a	98	0	"	"	
(B38 x K148)F_2-1	901a	90	0	"	"	
(K148 x B38)F_2-1	901a	92	0	"	"	
(GG208 x B38)F_2-1	901a	96	0	"	"	

All progenies involving susceptible and resistant parents have observed counts which fit a one factor pair hypothesis for rust resistance. The F_2 progenies of K148 x GG208 and GG208 x Cuzco when inoculated with race 901a gave only resistant reactions. (The one susceptible plant in GG208 x Cuzco may have been due to a seed mixture). This suggests that among these resistant strains the same locus is involved in conditioning resistance to 901a. Also, F_2 progenies of GG208 x B38 and B38 x K148 have all plants resistant to 901a thus placing the allele in B38 for resistance to 901a in this same series. The F_2 of K148 x B38 inoculated by mixture A gave only resistant reactions so that the resistance to 10 rust cultures by B38 may be due to one factor pair. Since the results of resistant x susceptible progenies indicate that a single gene in each source conditions resistance to several races, it is possible that we have an allelic series of four dominant genes.

Although the results discussed above suggest the presence of an allelic series, other observations create some doubts. The F_2 of K148 x GG208 inoculated with culture 908 to which K148 is susceptible gave (75) 0; to (24) x type. (The x type is a mixture of 3- and 1- or 0;). If culture 908 was not pure but contained spores to which K148 is resistant then this reaction is as expected. The F_2 of K148 x GG208 inoculated with mixture C containing 908 and 927 to which K148 is susceptible gave (76) 0; and (23) x type. Seedlings carrying alleles from K148 would have 1- and 3-type pustules or x type reaction. The F_2 of K148 x GG208 inoculated by culture 930 to which GG208 is susceptible gave (53) 0;, (25) x mostly 0; and (21) 3-. However, when this same F_2 progeny was inoculated by mixture A containing culture 930 the observations were (57) 0; and (43) 1- with few 3- pustules. The F_2 of B38 x K148 with mixture B gave (56) 0; to (42) x and with mixture E gave (64) 0; (27) x mostly 0; and (12) x mostly 3-. It should be emphasized that it is difficult to establish and maintain pure biotypes of the pathogen and to work with mixtures involving many races. Some readings may be due to such things as contamination, failure of some virulent spores to infect, or perhaps spore competition or even antibiosis. It is also possible that modifying factors may be present and/or genotype-environment interactions occur. Several F_3 analyses using single rust cultures recently established as clonal lines from single urediospores are being made either to confirm an allelic series among these four sources of resistance or to determine whether some more complicated segregations which can not be detected in F_2 progenies may be present.

W. A. Russell
A. L. Hooker

THE JOHN INNES HORTICULTURAL INSTITUTION
Hertford, England

The races of maize found in the West Indies have been described and discussed by W. L. Brown (Trop. Agric. 1953). It has been known since the pioneer work of Alfred Russell Wallace that island life presents special evolutionary features. Hence the maize races of the West Indian islands afford the geneticist interested in the scientific basis of the evolution and selection in cultivated plants, an opportunity of testing a number of hypotheses.

For instance, in the West Indies it is possible that gradual inbreeding has been accompanied by selection for general plant vigour: although the races are comparatively more inbred than usual for open-pollinated maize varieties found elsewhere, their vitality complex, so named by Harland, is undiminished. If the foundation of a race has depended on a limited number of parents then the amount of variation later released will be limited.

A preliminary examination of the genetics of these populations indicates that they may have been derived by methods involving closer inbreeding than is normally the case in open pollinated species.

G. Haskell
W. Williams

UNIVERSITY OF MINNESOTA
St. Paul 1, Minnesota
Department of Agronomy and Plant Genetics

1. A population study in the northwestern corner of Minnesota.

Four recommended hybrids with relative maturities of 80 days or less were tested in the A.E.S. 100 area of Minnesota at population rates ranging from fourteen thousand to twenty-four thousand plant per acre.

	I	II	III	IV	V	VI
Approximate Population	14,000	16,000	18,000	20,000	22,000	24,000
Rate in 36" Rows	2/25"	2/21½"	3/29"	2/17½"	3/24"	2/14½"
Avg. yield Bu./Acre	82	88	87	95	94	102
Moisture % at Harvest	17.7	17.9	18.6	17.6	18.4	18.0

The largest population continued to show a substantial increase in yield but the populations associated with three plants per hill yielded lower than expected from those populations involving two plants per hill. The moisture percentage at harvest was quite variable.

R. H. Peterson

2. The inheritance and linkage relationships of factors controlling a long mesocotyl type.

A study is under way to determine the mode of inheritance and linkage relationships of factors controlling the long mesocotyl type common to Indian corns from the Southwest. A stock averaging 24 mm (from germ face to first node) was crossed to nine inbreds (direct extractions from a number of open-pollinated varieties) and a set of chromosomal interchanges. The agronomic possibilities of this trait are being considered.

A. Forrest Troyer

3. Location of fertility restorer genes A and B in inbreds A293 and K55 using translocation stocks with $Wf9^t$ as a tester.

This study was initiated to determine the number of and locations of the fertility restorer genes in inbreds A293 and K55. Fertile segregates of $Wf9^t$ x ($B164^t$ x A293) $A286_2$ - 2 and $Wf9^t$ x ($Tx61^t$ x K55) $A286_2$ - 4 were crossed with 28 different translocations involving all arms of the chromosomes. The fertile plants with translocations from these crosses were crossed onto $Wf9^t$. A linkage study will be made in 1957.

Based on work of other investigators, it was hypothesized that the fertility restoration in these inbreds was the function of 2 complementary genes. The expected phenotypic ratios for the hypothesis are as follows:

[($Wf9^t$ x A293) $A286_2$-2] AaBb x aaBB (TRANSLOCATION STOCKS)

↓

	AaBb + AaBB	+	aaBB + aaBb
	Fertile-use		sterile-discard
($Wf9^t$) aabb x AaBb ⟶	1 AaBb	+	1 Aabb + 1 aaBb + 1 aabb*
	Fertile		Sterile
($Wf9^t$) aabb x AaBB ⟶	2 AaBb	+	2 aaBb
	Fertile		Sterile

* Data to be used for recombination test for B.

Fertile and sterile classes should consist of equal number of normal and semi-sterile plants where no linkage exists between the restorer genes and the translocation breakpoints.

Frank M. Remley

4. Linkage studies between a fertility restorer gene and genetic markers both in the presence and absence of translocations.

A recombination figure of 28% was obtained for the A293 fertility restorer gene and translocation 1-3 (5982-2) which has breaks in the short arm of chromosome one and about .66 of the distance out in the long arm of chromosome three. A recombination value of 5.4% was obtained between the A293 fertility restorer gene and translocation 1-3 (5883-1) which has breaks in the short arm of chromosome one and about .65 of the distance out on the short arm of chromosome three. These data indicated that the A293 fertility restorer gene is in the short arm of chromosome one. However allelic tests with other sources of fertility restoration which have been located in chromosome three have led to further studies.

The A293 source of fertility restoration has been crossed with several genes in chromosomes one and three which include in various combinations: sr, zb_4, br, d_1, Rg, ts_4, na and lg_2. The recombination results will be obtained in the summer of 1957.

A test is being made to determine if one or both of the translocations reduce crossing over in regions adjacent to the break positions. Crosses were made between plants which were heterozygous for both the fertility restorer gene and the translocation and various combinations of the genes previously mentioned. Crosses were also made with plants which did not have the translocation. Testcrosses were made by selecting plants which had both the translocation and the fertility restorer gene and backcrossing them to the appropriate recessive genetic stock. Whenever possible these crosses were made reciprocally. Testcrosses were also made with plants in the same row which did not contain the translocation so a comparison can be made of the effect of the presence of the translocation on the recombination between the fertility restorer gene and the various genetic markers. As the frequency of plants with both the fertility restorer gene and the 1-3 (5883-1) translocation was very low some crosses were also made onto sterile plants so the recombination percentages between the translocation and the genetic markers may be measured. These results will be obtained in the summer of 1957.

Duane B. Linden

5. Comparative performance of inbred lines and their testcross progenies at different populations per acre.

Thirty-two inbred lines of corn were planted at five different populations per acre in the A.E.S. 600 zone of Minnesota.

Rows 40 ins. apart.					
Approximate population:	12000	16000	20000	24000	28000
Rate and distance within rows:	2/26 ins.	2/20 ins.	2/16 ins.	2/13 ins.	2/11 ins.

Another trial containing the testcross progenies of twenty of these inbreds, resulting from testcrosses onto two double cross hybrids, was grown at two population levels, 16000 and 20000 plants per acre, with two replications at each of four locations all in the A.E.S. 600 zone of Minnesota.

Rows 40 ins. apart.		
Approximate population:	16000	20000
Rate and distance within rows:	2/20 ins.	alternating 2 and 3/20 ins.

Notes were taken on the dates of tassel emergence, pollen shedding and silking, plant height and ear height, and the number of good ears, bad ears and dropped ears on the inbred trial and the testcross trial grown at Waseca.

From these results it is intended to find the effects of population level on these characters of the inbreds and their testcross progenies. Also a study of the correlations between the performances of the inbreds and the testcrosses will be made to find if there is any relationship between the two.

Preliminary results from the inbred trial show a wide range of kernel moisture percentage at harvest time; there seems to be a tendency, as would be expected, for the higher populations to give higher moisture content, i.e. high population levels tend to delay maturity. Tassel emergence, pollen shedding and silking dates are all delayed with increase in population level.

A detailed analysis of all results is at present being prepared.

J. C. Sprang

6. Progress report on the big ring.

A ring of eight was observed in 3 plants out of 17 progeny from the cross of the F_1 of permanant rings of six (2-4b+2-3d x 2-4b+4-8a) x a standard normal. As predicted on pages 55 and 56 of the 1955 Maize News Letter, two rings of four were observed in the F_1 plants.

At the present time it appears to be possible by an extension of the method to produce combinations of big rings at will, once the component rings of six are available. After the permanent rings of six have been produced by a crossover in the differential segment of the F_1 of a cross between two translocations with breaks on a common chromosome, the larger rings are produced by the segregation of translocated chromosomes from crosses between the component smaller rings.

L. Inman

7. Striate-asynaptic stock.

The striate-asynaptic stock, originally under Emerson's #28-569 and carried along for several years at Minnesota, has been examined cytologically. Pollen sterile plants had 10 II and normal pairing. Seed-set on these plants was normal. This stock is apparently carrying a male sterile and does not contain the as gene.

O. F. Miller

8. Location of na_2.

The following data confirm last year's results (News Letter 1956). This gene is in chromosome 5 as shown by the following F_2 data:

Pr Na_2	Pr na_2	pr Na_2	pr na_2	(-)Aleur. Na_2	(-)Aleur. na_2	total
90	10	12	7	86	28	119
180	27	36	32	--	--	275

segregating c and r. p = 27.45% I2.72

Gertrud Joachim
C. R. Burnham

9. Crossing over in reciprocal crosses.

In chromosome 2, the fl - v_4 region showed much higher recombination in the ♂, the other regions only slightly higher.

	♀	♂
lg-gl	14.91 ± 1.81	17.53 ± 1.89
gl-fl	28.02 ± 2.28	31.60 ± 2.31
fl-v_4	12.60 ± 1.68	27.41 ± 2.22
N	389	405

10. Location of Y in chromosome 6.

A stock homozygous for T 5-6c, (break in short arm of 6 adjacent to the centromere) showed 14.5 ± 1.2% recombination between Y and Pl. Therefore Y as well as Pl are in the long arm. This new chromosome (65) is not attached to the nucleolus. The lower recombination (the normal value is 31) might conceivably be the result of the substitution of a short arm in which crossing over is higher than in the short arm of 6 normally present.

11. Big ring.

Some progress has been made in building other permanent rings of 6. Those now available are 2-4b+2-3d, 2-4b+4-8a, 8-9b+ 8-10a, and 1-7 (4405-2) + 5-7 (5179-9).

Following the scheme suggested by Inman, the following combinations are being produced: 1-9 X 1-7, 3-6 X 2-3, 9-10 X 2-9, 4-8 X 8-9, and 3-6 X 5-6.

A new series of crosses for producing rings of six which can be used for other purposes has been planned by Inman.

C. R. Burnham

12. Unlinked genes.

We have been unable to confirm by linkage tests with P, f, bm, the indication from T-Bla tests (News Letter 29: p. 51) that a crinkly-leaved dwarf is in chromosome 1.

X^2 tests for independence show:

silky tassel vs. colored and colorless aleurone (2 factors segregating) are associated, p = .02.
midget and Y vs. y in a culture segregating pale yellow - P = <.01.
gl_{11} no close association with py, Y y, mi,
gl_6 no close association with f, bm_2, Y y.
dwarf " " " with y ms.
fired " " " with su_2, Y, Pr-pr.

13. Effect of unequal chromatids on recovery of complementary cross-overs.

Translocations having unequal exchanged pieces and an interstitial segment of appreciable length are being tested for non-random segregation of crossover chromatids.

The first results are with T6-9b (6L.1 - 9S.37) in tests with Y sh Wx gl_{15}. The recovered complementary crossover classes are very unequal in the Wx - gl_{15}, Y - Wx and Wx - gl_{15} regions.

L. A. Snyder
C. R. Burnham

Those assisting in the above work are: L. L. Inman, O. L. Miller, and P. Yagyu.

MISSOURI BOTANICAL GARDEN
St. Louis 10, Missouri

1. Collection of North American Indian corn.

The collection of corn made by Collins, Kempton, Longley, and others for the Department of Agriculture which formed the basis of Longley's paper on chromosomes of North American Indian corn is now at the Missouri Botanical Garden. While the seed is no longer viable, the ears provide valuable information for people desiring to study the corn.

Hugh Cutler

NATIONAL INSTITUTE OF AGRICULTURAL SCIENCES
Hiratsuka, Japan

1. Characteristics of native races of maize in the orient.

Last year (in the 1956 Land and Crop of Nepal Himalaya 2: 373-530), a comprehensive survey of the morphological characteristics of oriental races was given in which the oriental races were classified into five types. They are (1) North American, (2) European, (3) Caribbean, (4) Persian, and (5) Aegean. This classification has been further re-examined by using other races of different sources from both the cytological and morphological view-points. Some evidence was obtained to support this classification.

Firstly, all of the flint races native to the southeastern region of the orient including Java and Siam were proved to be different from the five types described above, and they are called the "Javanese type". This is an intermediate form between the two types, Caribbean and Persian. In addition, plants in every race of this type are more vigorous than those of the latter two types. They may be described as follows: Plants tall and robust, late in maturity; stalk thick in diameter, with a lot of short internodes; tillers always lacking, but prop-roots prolific; tassels usually covered by upper leaves even when matured; tassel branches slender, delicate, and numerous (about 33 on the average), arising in a wide space on the main axis, and hanging down during anthesis; paired spikelets small and sparsely born in the node, shedding abundant pollen; ear placed very high on the stalk, small in size, conical in shape, light in weight, never exserted from the leaf-sheath during anthesis; row number 12 or 14, having no sterile tip; shank having a ribbed surface and enlarged node; husks few in number and flag leaves usually absent; kernels small in size, light in weight, spherical in shape, and orange in color; denting absent, and quality excellent.

Secondly, a karyotypic analysis of oriental maize of the six types was carried out with respect to difference in the number and position of chromosome knobs at mid-pachynema of meiosis in PMC. The karyotypic comparison is set forth in Table 1, where the abbreviations E, Af, Ad, C, Na, Np, Jv, and Jp correspond to the following types: "European flint" and "North American flint and dent" from northern Japan, "Aegean flint" from northern China and central Nepal, "Persian flint" from central Nepal, "Javanese flint" from Indonesia and "Caribbean flint" from southern Japan, respectively. As can be seen in this table, both the number and position of knob occurrence differ markedly in different types. In number, they are extremely variable ranging from nearly zero (E and Af) to nine (Jp), and their order is the following--$Jp > Jv \gg Np = Ad > Na = C \gg Af = E$. In position, some striking peculiarities also exist among them. The frequency of occurrence of a particular knob is not related to the overall frequency of knobs in that group. For instance, the average frequency of the terminal knob on the short arm of chromosome 9 is about 0.54 in Af or E, and 0.2 in Jp, although the former has the lowest average number of knobs and the latter has the highest number. The Continental races comprising Np, Na and C show the highest occurrence of knobbed chromosomes 9 in spite of the intermediate number (3 to 5) of total knobs. The Javanese races give an average of 0.3 for chromosome 9 knobs, being intermediate in frequency between the two types, Caribbean and Continental flint.

From these morphological and cytological findings, it may therefore be concluded that the present Javanese type could have arisen through hybridization between races of the Caribbean and Persian flint.

Table 1. Frequency of occurrence of chromosome knobs in 74 maize races.

Type of races	No. of races	1 S	1 L	2 S	2 L	3 S	3 L	4 S	4 L	5 S	5 L	6 S	6 L	7 S	7 L	8 S	8 L	9 S	9 L	10 S	10 L	Total
E	2	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	1	1	-	-	-	3
	av.	-	-	-	-	-	-	-	-	-	-	-	-	-	0.5	-	0.5	0.5	-	-	-	1.5
Af	12	-	-	-	-	-	-	-	-	-	1	-	4	-	3	-	1.5	7	0.5	-	-	17
	av.	-	-	-	-	-	-	-	-	-	0.1	-	0.3	-	0.3	-	0.1	0.6	0.1	-	-	1.3
Ad	5	-	-	1	3	-	2	1	1	-	2	-	7	-	3	-	3	1	1	-	-	25
	av.	-	-	0.2	0.6	-	0.4	0.2	0.2	-	0.4	-	1.4	-	0.6	-	0.6	0.2	0.2	-	-	5.0
C	8	1	-	-	1	-	2	-	3	-	1	-	5	-	1	-	7	4	3	-	-	28
	av.	0.1	-	-	0.1	-	0.3	-	0.4	-	0.1	-	0.6	-	0.1	-	0.9	0.5	0.4	-	-	3.5
Na	15	-	-	-	1	-	8	-	3	-	6	-	-	-	11.5	-	5.5	11	1.5	-	-	47.5
	av.	-	-	-	0.1	-	0.5	-	0.2	-	0.4	-	-	-	0.8	-	0.4	0.7	0.1	-	-	3.2
Np	13	-	-	-	6	-	8	-	5	-	10	-	6	1	7.5	-	9	11	2	-	-	65.5
	av.	-	-	-	0.5	-	0.6	-	0.4	-	0.8	-	0.5	0.1	6.0	-	0.7	0.9	0.2	-	-	5.0
Jv	6	-	2	-	4	-	4	-	5	-	6.5	-	9	-	5	-	7	2	2	-	-	46.5
	av.	-	0.3	-	0.7	-	0.7	-	0.8	-	1.1	-	1.5	-	0.9	-	1.2	0.3	0.3	-	-	7.8
Jp	15	1	2	3	14	-	10	-	7	-	12	-	32	1	13	-	25	3	8	-	-	130
	av.	0.1	0.1	0.2	0.9	-	0.7	-	0.5	-	0.8	-	2.1	0.1	0.9	-	1.7	0.2	0.5	-	-	8.7

2. Genic analysis of some mutant characters.

a. Giant plant (gi)

This simple Mendelian recessive mutant (gi) with white endosperm was crossed to a normal plant with yellow endosperm. The F_1 plant was normal as expected and the data on the segregation in 128 F_2 plants are listed in Table 2.

Table 2. Data on the segregation of the giant and yellow endosperm characters in the F_2 progeny.

Character	+	gi	Total
Y	59	22	81
y	44	3	47
Total	103	25	128

From this table, it seems highly probable that the two characters, giant and yellow endosperm, are linked in coupling phase ($x^2 = 7.856$). The present data indicate that yellow endosperm is caused by two or more genes. It is impossible to ascertain which of the genes governing yellow endosperm is linked with gi, although the gene gi may be on chromosome 6.

b. Recessive old gold stripe (og_r).

The phenotypic appearance of this mutant was exactly similar to that of the dominant old gold stripe reported by Lindstrom (1935). However, the genetic behavior differs as follows:

(i) The character is controlled by a recessive gene og_r, probably located on the right side of R in the linkage map (li-16-g-20-og_r) instead of to the left of g as was found for the dominant Og.

(ii) This character is considered to show cytoplasmic inheritance. Accordingly, the variegation appears not only in the homozygous recessive condition but also in the heterozygous F_1. The frequency of cytoplasmic transmission was low when the og_r stripe was used as the male parent, while it was high when used as the female parent. Consequently, the disturbance in segregation ratios was more pronounced in the latter case than in the former. In this stripe, the yellow variegation on the leaf-blade is most conspicuous in the upper leaves and in the flag leaves of the plant in the first generation of the homozygous og_r combination in the F_2 and backcross populations. On further selfing of the homozygous og_r plants, the appearance of striping shows a trend to decrease progressively. The striping usually disappears entirely in about the 6th or 7th generation of selfing, in spite of the homozygous recessive og_r constitution. Nevertheless, this apparently normal plant behaves genetically just like the homozygous og_r-stripe plant when crossed.

Table 3. Recombination percents of the three genes, og_r, g and li, on chromosome 10.

Phase	No. of fam.	Total plants	og_r-g	g-li	og_r-li
F_2 *	1	506	40.0	17.0	51.5
B *	1	206	53.7	16.5	60.2
F_2 1)	3	766	21.3	15.0	30.4
B 2)	4	1303	26.5	17.9	44.7
B 3)	5	852	25.6	17.7	43.3

* came from the female parent of the F_1 plants with the cytoplasmic stripe.

1) came from the F_1 normal plant without any striping.
2) indicates the use of the female heterozygous parent with the stripe.
3) indicates the use of the female heterozygous parent without the stripe.

T. Sutô

NORTH CAROLINA STATE COLLEGE
Raleigh, North Carolina
Department of Field Crops

1. The inheritance of resistance to brown spot of corn.

A study was designed to investigate the inheritance of brown spot of corn (Physoderma maydis). A susceptible inbred (NC7) was crossed with a resistant inbred (GT154) and the following generations derived for study: F_1, F_2, F_3, B_1, B_2, B_{11}, B_{12}, B_{22}. Individual plants were examined for brown spot symptoms and given a rating from 0 to 5; 0 being no symptoms and 5 being very badly infected. Data were collected at one location in 1954 and at each of two locations in 1955. The data were analysed using the methods proposed by Powers, Locke and Garrett 1950, and Powers, 1955.

It was found that four or more gene pairs differentiate the parents with respect to brown spot resistance. Several genetic models involving four loci and five loci, each defining the disease reaction of every genotype, were found which were compatible with the F_2 data obtained at each year-location. All of the models which were found to be compatible with the data involved epistasis; i.e., non-additivity between genotypes at certain of the loci. Further evidence of epistasis was

noted when the relative magnitude of the means of the various generations did not agree with the relative magnitude expected under the assumption of no epistasis.

The three genetic models involving five loci found to be compatible with the F_2 data collected at the three year-locations showed a consistent pattern of gene action, although the relative value of the genotypes varied, reflecting a genotype X environment interaction. Assuming these three models were correct, predictions were made concerning the disease reaction of single crosses relative to the disease reaction of their respective parental lines. This indicates that single crosses which are more resistant than either parent, and single crosses which are more susceptible than either parent are to be expected. Furthermore, a single cross more resistant than either parent and a single cross more susceptible than either parent may have one parental inbred in common.

Data obtained on various inbred lines and their single crosses in 1956 are in agreement with the expectations based on the five factor genetic models.

From the point of view of the plant breeder, these results indicate that the brown spot reaction of an inbred line is not a reliable indication of the reaction of single crosses involving that inbred, and the hybrid combinations themselves must be tested for brown spot resistance.

R. H. Moll
D. L. Thompson
P. H. Harvey
R. E. Comstock

OHIO AGRICULTURAL EXPERIMENT STATION
Wooster, Ohio

1. Studies on a mutable system involving chromosome 6.

A yellow mosaic kernel was found on an ear of a yy x YY cross. The resulting plant was selfed and yellow mosaic and white endosperms segregated. The yellow mosaic endosperms are characterized by a white background with yellow spots if the yellow area is small. The large yellow areas may be somewhat irregular in outline. Progeny from the selfed plant were grown and a recessive pale green character segregated. Some of the pale green plants possessed numerous mutant green areas on the pale green (or white) background. These plants in addition to being pale green also have a white sheath and somewhat banded white areas on the leaves. Classification of the pale green character in the seedling stage is good in the field but poor in the greenhouse. However, classification of the character in the mature plant is excellent both in the field and in the greenhouse. The mutable white allele has been designated as y^m and the mutable pale green allele as pg^m.

In crossover tests, $\underline{Y}\ \underline{Pg}/\underline{y}^m\ \underline{pg}^m \times \underline{y}^m\ \underline{pg}^m$, there was no crossing over between $\underline{y}^m$ and $\underline{pg}^m$ in tests involving 7944 plants. In some of these tests the female plants carried (either one or two) controlling elements and others had none. Two point tests gave approx. 35% crossing over between $\underline{y}$ and $\underline{su}_2$; crossing over between $\underline{y}^m$ and $\underline{su}_2$ was approx. 20%. Cytological studies provided no evidence for a chromosomal aberration. It seems possible that a rather large region on chromosome 6 may be involved. Spreading effect could be involved.

In preliminary tests the controlling elements failed to induce Ds action. Also, Ac did not induce $\underline{y}^m$ to mutate.

With respect to controlling elements, certain tests indicate the presence of two independent dominant controlling elements. One such test is presented below:

$\frac{\underline{Y}\ \underline{Pg}}{\underline{y}^m\ \underline{pg}^m}$ heterozygous for controlling elements $\times\ \underline{y}^m\ \underline{pg}^m$ no controlling elements

Endosperm Classification

Yellow	Yellow mosaic	White
190	130	35

Plant classification

	green	pale green	pale green mosaic	pale green
	171	34	77	24
Possible ratio	4	1	2	1

This and similar tests suggest that there are two dominant controlling elements one of which induces both $\underline{y}^m$ and $\underline{pg}^m$ to mutate and the other only induces $\underline{y}^m$ to mutate.

The controlling elements have been tentatively designated as $\underline{Ce}_1$ (controlling element) which induces both $\underline{y}^m$ and $\underline{pg}^m$ to mutate and $\underline{Ce}_2$ which induces $\underline{y}^m$ to mutate.

The time of mutation and mutation rates (number of mosaic areas per endosperm) vary for different plants. Dosage of controlling elements and perhaps dosage of the $\underline{y}^m\ \underline{pg}^m$ region as well affect mutation rates and ratios of yellow mosaic endosperms. Some tests indicate that the controlling elements do not affect the expression of normal $\underline{y}$. Tests relating to the above problems are in progress.

With respect to sectoring, no ear sectors of yellow mosaic endosperms have been found. However, ear sectors of germinal mutations (yellow endosperms) have occurred. In all cases except one, the plant grown from yellow endosperm germinal mutations (from ear sectors) have been green. In other words, $\underline{y}^m$ and $\underline{pg}^m$ mutated simultaneously to the dominant.

E. J. Dollinger

THE PENNSYLVANIA STATE UNIVERSITY
University Park, Pennsylvania
and
CALIFORNIA INSTITUTE OF TECHNOLOGY
Pasadena, California

1. Placement of seedling chlorophyll mutants.

Seventeen radiation-induced seedling chlorophyll mutants have been placed in appropriate linkage groups by utilizing endosperm-marked translocations as testers. Crosses between the mutants and an array of translocations were made at Cal Tech and the F_1 and F_2 populations were grown at Penn State.

The series of translocations used involved breaks near $\underline{Y}_1$ on chromosome 6, su on 4, or wx on 9; with breaks in different arms of all other chromosomes except 7. If clear-cut data indicated no linkage with any testers, the mutant was assumed to be on chromosome 7.

For each of the mutants the phenotype and number, the linkage group, and the translocation(s) with which each showed linkage are listed in the following table. Allelism tests have not been run on the two virescents and the two yellows which were placed in identical linkage groups.

Mutant Phenotype	Mutant Number	Linkage Group	Translocations which identified linkage group
(Pale green	8616	7	elimination)
Virescent	4873	3	3-9c
Virescent	5575	3	3-9c
Virescent	8623	4	4-9b
Virescent	8647	7	elimination (also linked to gl_1)
Virescent	8661	8	8-9d
White	8336	3	3-9c
White	8613	1	1-6c and 1-4d
White	8630	8	8-9a
White	8889	9	1-9c; 2-9b; 4-9b; 8-9d; 9-10b
White	9005	4	4-8a; 1-4a; 4-9(F-22)

Mutant Phenotype	Mutant Number	Linkage Group	Translocations which identified linkage group
White narrow leaf	8950	9	1-9c; 2-9b; 3-9c; 9-10b
White yellow	8721	10	9-10b
Yellow	8454	10	9-10b
Yellow	8793	10	9-10b
Yellow	8957	4	1-4a; 4-8a
Yellow	8954	3	3-9c

Dolores McHugh
J. E. Wright
E. G. Anderson

UNIVERSITY OF THE PHILIPPINES
College of Agriculture
Central Experiment Station
College, Laguna, Philippines

1. Reduction in grain yield from the F_1 to the F_2 of parental single crosses and double-cross hybrids.

In the 1955-56 dry season performance yield test of parental single crosses and double-cross hybrids and their respective F_2's at the U. P. College of Agriculture, College, Laguna, Philippines, the following results were obtained: (1) percentage decreases in the grain yield of the F_2 of five parental single crosses varied from 0.8 to 22.8 per cent, with a mean of 17.3 per cent and (2) percentage decreases in the grain yield of the F_2 of seven double-cross hybrids varied from 1.4 to 37.5 per cent, with a mean of 17.6 per cent. On the average, the F_2 yielded significantly lower than the F_1 in both the parental single crosses and the double-cross hybrids.

O. Q. Ballesteros
I. S. Santos
F. A. Aquilizan

2. Sweet corn in the Philippines.

In the performance trials for yield, agronomic characters, and quality of 13 varieities and hybrids of sweet corn, the top crosses of Hawaii Sweet x Golden Cross Bantam and Philippine Sweet x Golden Cross Bantam showed the best quality and were among the eight highest yielders, all of which yielded alike within the limits of statistical significance at the 1 per cent level. Sweet corn was preferred to glutinous or waxy corn by 80 per cent of the members of the panel.

Arthur M. Brunson
Jose D. Escarlos

PIONEER HI-BRED CORN COMPANY
Johnston, Iowa

1. Allelism of FR genes of inbreds which restore pollen fertility to $WF9^s$.

The inbreds KY21, BH2, CE1, JG3 and JG5 (all but KY21 are lines of the Pioneer Hi-Bred Corn Co.) restore pollen fertility to $WF9^s$, in such a way that all anthers appear normal, although only 60-90% of the pollen grains are "fertile" (plump, starch-filled). When these five lines were intercrossed in all possible combinations and the resulting F_1 hybrids crossed as male to $WF9^s$, 100% of the plants in each 3-way cross were fertile, as described above. This indicates that all 5 FR lines contain dominant forms of the same FR genes, with respect to $WF9^s$.

2. Further evidence for two complementary major genes for fertility restoration in T cytoplasm.

In the winter of 1956-57 five ear-progenies of the cross [(WF9^T x KY21)WF9] SK2 gave the following segregations:

Ear Number	Sterile Plants	Partially Fertile Plants	Fertile Plants
1	12	1	14
2	17	7	0
3	20	5	0
4	26	0	0
5	25	0	0

Each of the (WF9^T x KY21)WF9 plants used as female parent was fully pollen sterile. WF9^T x SK2 is pollen sterile. These results are in agreement with the postulated fertility restorer genotypes of: WF9 - aabb, SK2 - aaBB, and KY21 - AABB (postulated in Genetics, 1956, on the basis of backcross and three way cross data). According to this hypothesis, one in three crosses of SK2 to sterile plants of the backcross (WF9^T x KY21)WF9 should segregate 50% fully fertile to 50% sterile plants. The partially fertile plants presumably are due to interaction of minor genes (non-allelic with the two major fertility restorer genes) which can effect partial fertility restoration under some environmental conditions.

Donald N. Duvick

PURDUE UNIVERSITY
Lafayette, Indiana

1. Gametophyte factors in maize.

There are three alleles at the gametophyte locus on chromosome four in maize: Ga^s, Ga_1, and ga. The presence of other gametophyte factors in seven cross-sterile popcorn inbreds was tested for by examination of the F_2 progeny of crosses of these popcorns with various stocks marking the ten chromosomes of maize. If a gametophyte factor exists in a popcorn inbred and is linked to the locus of a marker gene, the proportion of the F_2 progeny homozygous for the marker gene is less than the expected 25%. This reduced percentage of marker type is caused by the competitive advantage of Ga gametes over ga gametes on heterozygous silk. Cross-sterile inbreds involved were 24-6 and 4501 of South American origin; 1001-52, a Hulless type; the Black Beauty, 4541; a Red popcorn, 4524; a Baby Golden type, 4513; and 401-127 from Minnesota Superb.

In the 1954 News Letter (28:38) the F_2 progeny of a cross between P51 (ga su/ga su) and 401-127 was reported to have resulted in approximately 25% sugary seed set, and it was suggested that there was no cross-sterile factor at the Ga_1 locus. This result was unexpected as all other cross-sterile inbreds so tested resulted in 12-16% sugary seed, and cross-sterility was attributed to the action of the Ga^s allele at the Ga_1 locus. Increased testing by selfing F_1 plants from the same seed which was used in obtaining the results reported in 1954 resulted in two homogenous classes, one with a mean at 22.8% sugary seed and the other with a mean at 19.1% sugary seed. The percent sugary seed in progeny of the cross (P51 X 24-6) X (P51 X 401-127) resulted in two homogeneous groups averaging 23.3 and 16.8% sugary seed. The progeny from the reciprocal cross averaged 24.0 and 17.4% sugary seed. There were on an average about 8-10 ears in each class. The 23.3 and 24.0 percentages were not significantly different from 25% but the 22.8% was. It would appear that the popcorn parent was heterozygous at the Ga_1 locus and the variation in percent sugary seed possibly due to modifying factors or to two allelic gametophyte factors of different competitive ability. All tests involving the F_2 progeny of P51 and a different source of 401-127 resulted in an average of 16.9% sugary seed indicating the presence of a gametophyte factor at the Ga_1 locus.

The F_2 progeny of crosses between bt stocks and 401-127 resulted in an average of 9.4% brittle seed. Analysis indicates that a gametophyte factor is present probably at the Ga_2 locus on chromosome five.

The cross-sterility reaction of 401-127 differs from that of other cross-sterile inbreds. Progeny of the cross ((Hy (ga/ga) X cross-sterile inbred) X cross-sterile inbred) usually result in half of the progeny which will set seed with ga pollen and half which will not. When 401-127 was tested no plants were obtained with a good seed set.

Because of the competitive advantage of Ga gametes over ga gametes all progeny of the cross (Hy X cross-sterile inbred) F_2 should be either Ga /Ga or Ga/ga and induce a full seed set when pollinated onto the cross-sterile parent. When 401-127 was involved not all F_2 plants, when acting as pollen parent, would induce a seed set on 401-127. Results from testing individual plants from the cross (Hy X 401-127) F_2 by pollinating onto 401-127 as the seed parent and by a ga/ga type as the pollen parent led to the formulation of a two factor genetic basis of cross-sterility. This hypothesis must be tested.

Inbreds tested must be divided into two groups on the basis of their behavior in F_2 progeny involving these inbreds crossed with a brittle stock. The first group involving 1001, 4524, and 4501 resulted in percentages of brittle seed not significantly different from 25%. Progeny from the second group segregated as follows:

Inbred	No. F_2 ears	% bt
24-6	1	25.4
	2	11.9
4513	8	21.7
	5	8.2
4541	4	25.2
	5	6.9

It appears that plants involved in these crosses were heterozygous for gametophyte factors at the Ga_2 locus. The inbred 4513, when tested, segregated with an average of 21.7% and 8.2% brittle seed and both classes were significantly less than 25%. This inbred might possess modifying factors, or two gametophyte factors at the locus each with a different competitive advantage over ga gametes. These results are of particular interest because these popcorns are long time inbreds.

In 401-127 there are uncertain indications of the presence of gametophyte factors on chromosome three linked to the dwarf locus, and on chromosome nine linked to the shrunken locus. Several other indications of the presence of gametophyte factors were found in 4541 linked with opaque, 4501 linked with shrunken, 4513 linked with waxy, and 24-6 linked with shrunken.

Leland R. House

2. A multifactorial r mottling system.

Further investigations have been made of the r mottling system reported in the 1954 News Letter. Evidence was given at that time which renders it unlikely that a mutable r is involved. Recent work shows the likelihood of a multifactorial system which is responsible for the development of aleurone color in a high percentage of cells of the

constitution $\underline{A}_1$, $\underline{A}_2$, $\underline{C}$, $\underline{r}$. This is reminiscent of the $\underline{r}$ blotchings reported by Mangelsdorf in the 1955 News Letter.

The original mottled stock was derived from a cross of P51 ($\underline{A}_1$, $\underline{A}_2$, $\underline{C}$, $\underline{r}$) x SA 24 ($\underline{A}_1$, $\underline{A}_2$, $\underline{C}$, $\underline{r}$). The F_1 had colorless aleurone; a small percentage of F_2 kernels showed faint to moderate mottling; by selection of the most deeply mottled kernels, one could obtain by the F_4 generation some plants which gave all deeply mottled kernels.

Table 1 gives the percentage of mottled kernels observed in various crosses and selfed progenies involving the mottled stock and the two parents from which it arose. It is apparent in reciprocal crosses that there is a greater percentage of mottled kernels when the mottled stock is the female parent than when it is the male parent (cf. lines 1 and 3, 4 and 6, 7 and 8, 12 and 14, 13 and 15.) This does not seem ascribable to a cytoplasmic influence since it makes no difference whether P51 or 24 was used as the female parent in such crosses as (51 x 24) x M and (24 x 51) x M (lines 14 and 15). It is assumed then that the reciprocal differences noted are due to dosage. Further, 24 seems to have a greater effect towards mottling than P51 (cf. lines 5 and 7, 6 and 8).

It is clear that plants of the mottled stock used as testers were of different genotypes since different percentages of mottled kernels resulted on some occasions when the same plant was used as a pollinator on several mottled plants (see Lines 12 and 13). In light of these differences between tester plants, it is not surprising that the data are variable.

A purely formal explanation can be advanced which gives rise to expected values (% mottled) which are not too incompatible with the observed values considering the complications added by tester plants of undefined genotypes. If one assumes: (1) that 7 loci are involved in the production of the mottled phenotype; (2) that all effective alleles at these loci have an equal weight of 1 and cumulative effect; (3) that all show a dosage effect; (4) that 24-6 has effective alleles at 4 of the 7 loci and P51 at the other 3 loci; (5) that the dosage necessary for the development of any mottling is 16, and higher dosages produce larger colored areas as well as more intense coloring; then the expected values for the various crosses are as listed in Table 1. Note that no attempt has been made to assume different weights for different loci, not has linkage been considered. Postulates of both types might offer possibilities of closer fits to observed data.

No germinal mutations to R have been observed in the mottled stocks which may be taken as evidence that the multifactorial system postulated is not causing $\underline{r}$ to mutate to $\underline{R}$ unless such events happen too late to take place in sporogenous tissue. Further, as Mangelsdorf noted in his $\underline{r}$ and $\underline{c}$ blotched stocks, the colored areas are not regular, nor do they show the same intensity of color.

Table 1. Comparison of observed % mottled and expected % mottled for various crosses.

	Pedigree	Observed % Mottled in 1956	Expected % Mottled
1.	P51 x M	0	0
2.	24 x M	0, 0, 4	0
3.	M x 51	100 (1 ear)	100
4.	M x 24	?	100
5.	(24 x M) x M	86, 90, 65, 78, 90, 83	87.5
6.	M x (24 x M)	100	100
7.	(51 x M) x M	80, 66, 65, 79, 64	62.5
8.	M x (51 x M)	99, 97, 89, 90, 86, 87, 98, 91, 99, 87	100
9.	M x (24 x M)	100	100
10.	P51 x 24	0	0
11.	24 x P51	0	0
12.	M x (51 x 24)	[1](48, 83), (65, 89) (95,90,80) (82,62), 85	94
13.	M x (24 x 51)	(68, 87) (63, 79), 89, 77, (69, 50)	94
14.	(51 x 24) x M	48, 52, 48, 50	50
15.	(24 x 51) x M	49, 59, 38	50
16.	51 x (51 x 24) or (24 x 51)	0	0
17.	(51 x 24) x 51	8, 2, 10, 3, 7, 4	6
18.	24 x (51 x 24) or (24 x 51)	0	0
19.	(51 x 24) x 24	4, 10, 4, 12, 9	6
20.	(P51 x 24) ♀	9, 7, 10, 5, 4, [2]7	4.5
21.	(P51 x M) ♀	38, 42, 38, 39, 47, 41, 37, 40, 36, 69	41
22.	(SA24 x M) ♀	61, 61, 60, 35, 26, 27, 27, 26	69

[1] Same pollinator used for data within parentheses.

[2] 1950 data.

An obvious possibility is that the multifactorial system is enabling or forcing r to become functional in some cells. We cannot, however, dismiss the possibility that the system acts to bypass the r locus, and the production of color has nothing to do with r.

Oliver E. Nelson, Jr.

3. A gene for iron chlorosis.

In the progeny of coop ear 54-613-1 (Oh 51A X "sh_3" pr selfed), four out of eleven plants were pale yellow striped and grew to approximately half the height of the normal sibs. One such plant was selfed and bred true in 1956. A complete nutrient solution including minor elements failed to bring about development of full green color in the greenhouse. Minor elements Ca, Mg, Fe, Mn, Cu, Zn, in combination with sulfate, phosphate, nitrate, and borate ions were added separately in excess. Not all possible combinations were tried. The Fe SO_4 treatment resulted in development of full green color whereas no other treatment was effective in overcoming the chlorosis.

J. M. Shively
H. H. Kramer

4. Interaction of endosperm genes.

Several new combinations of ha with su_2, du, and wx were synthesized and identified during the past year and showed some rather unusual interactions both with respect to the percent amylose in the starch and with respect to the temperature at which starch grains lose birefringence under polarized light. Data are given on page 120.

It appears that su_2 alone and with du and wx will reduce birefrengence end point temperature to about 55° C. Alone and in combination with su and su_2, ha raises the end point. Further the same genes, i.e. du and wx, which are lowered by su_2, also lower ha. The gene su which raises su_2 is also raised by ha.

With respect to amylose content, no combination with ha resulted in higher amylose than ha; su_2 combination with ha gave an unusually low value. The intermediate value of ha wx is of interest.

Gene Combination	% Amylose	Birefringence End Point, °C	Phenotype
Normal dent	27	68	Normal dent
du	38	69	dull dent
ha	61	89	tarnished dent
su	30	65	wrinkled
su_2	42	55	translucent, full
wx	0	68	opaque
du ha	58	70	translucent, full
du su	64	68	wrinkled
du su_2	48	56	translucent, full
du wx	0	70	opaque, shrunken
ha su	60	85	translucent, full
ha su_2	40	83	opaque
ha wx	15	72	opaque, shrunken
su su_2	56	66	wrinkled
su wx	0	67	wrinkled
su_2 wx	0	53	opaque

P. L. Pfahler
H. H. Kramer
R. L. Whistler

5. Recombination with Y and su_2 in T6-10b.

The interchange point in T6-10b is very close to Y. Repeated backcrossing of y^T/YN to a du su_2 stock since 1951 has finally resulted in a Semisterile YY su_2 su_2 plant. This will permit a test for linkage between su_2 and y in the homozygous translocation. If linkage is found, y will have been placed on the long arm of chromosome 6 distal to the translocation point. In the absence of linkage the position of y will remain uncertain.

6. Close linkage of y, ms-si, and rg on chromosome 6.

Material heterozygous for Yy, for a new "male sterile silky ear" mutant, and for a new recessive ragged leaf seedling mutant supplied by E. G. Anderson, who had located them on chromosome 6, was planted out.

Data from y si/Y Si selfed gave 48 Y Si: 1 Y si: 1 y Si: 39 y si for which recombination by maximum likelihood is 1.8%.

Preliminary germination tests from two selfed ears of y Rg/Y rg gave no ragged seedlings from 36 white kernels tested indicating close linkage of y with rg.

Herbert H. Kramer

7. Mutable su.

In 1955, a stock from Dr. McClintock carrying one Ds and one Ac was used as a pollinator on a sweet corn hybrid. From 500 outcrossed ears, about 1,000 endosperm mosaics were selected and planted in 1956. Out of approximately 500 selfed ears, two proved to be mutating su, Su, phenotype. It is hoped that a series of alleles can be isolated at the su locus.

N. K. Notani
Herbert H. Kramer

UNIVERSITY OF SÃO PAULO
Piracicaba, São Paulo, Brazil
Department of Cytology and Genetics

1. Comparative performance of some hybrids from Mexico, Colombia and Brasil.

During the season of 1955-56, an experiment in a 4 x 4 simple lattice with 4 replications, was carried out to test five three-way crosses of yellow dent corn from the Agricultural Program in Mexico for tropical regions, four double hybrids, of which three were orange flint (Rocol H-201, Rocol H-202, Rocol H-203), one white flint (Rocol H-251) two orange flint varieities (Eto and Peru 330), from the Agricultural Program in Colombia, three semi-dent double hybrids in distribution in our region and two synthetic varieties one being yellow dent (Pelotas) and one orange flint (Marilia). The Mexican hybrids used are experimental ones and were the best of some 300 in Mexico, according to Dr. Robert D. Osler. The pedigrees of these hybrids are as follows:

SR54

277 x 267	SLP28-2-1	x	(Cap. Amar. 76-4x Cap. 66-2-1)
289 x 267	Ver. 55-4-1	x	(")
275 x 268	Cap. Amar. 76-3	x	(SLP28-2-1-3-x Cap. 66-2-1)
284 x "	Cuba 23-7-1	x	(")
285 x "	Cuba 23-7-2	x	(")

Table 1. Performance of some hybrids and varieties from Mexico, Colombia and Brasil. Piracicaba, São Paulo - 1955-56.

Hybrid or Variety	Origin	Yield of grain		Relative Yield %	Grain Percentage	Moisture at Harvest %	Root Lodging %	Stalk Breaking %	Ears per Plant	Height of the Ear m
		Kg/ha	Bu/acre							
285 x 268	Mexico	6,494	103.90	174.5	87.26	22.5	-	2.5	0.99	1.90
275 x 268	Mexico	6,355	101.68	170.7	86.39	23.6	9.7	-	0.89	2.00
289 x 267	Mexico	5,888	94.21	158.2	86.40	21.8	12.4	1.7	0.97	1.90
284 x 268	Mexico	5,765	92.24	154.9	92.46	22.8	0.8	0.8	0.94	2.30
277 x 267	Mexico	5,500	88.00	147.8	88.42	21.5	1.6	0.8	0.85	2.10
Agroceres 7	Brasil	5,149	82.38	138.3	80.51	21.6	1.6	-	0.98	1.70
Agroceres 5	Brasil	5,055	80.88	135.8	83.46	21.2	4.1	0.8	1.02	1.90
Rocol H-201	Colombia	4,559	72.94	122.5	82.37	21.3	11.4	4.0	0.95	1.70
Rocol H-251	Colombia	4,281	68.50	115.0	79.33	21.9	9.0	4.8	0.85	1.90
I. A. H-4624	Brasil	3,722	59.55	100.0	86.77	20.0	8.1	1.6	0.82	1.70
Rocol H-202	Colombia	3,702	59.23	99.5	82.72	20.4	9.7	0.8	0.83	1.50
Rocol H-203	Colombia	3,640	58.24	97.8	84.43	20.2	2.5	1.6	0.89	1.70
Etº Amarillo	Colombia	3,439	55.02	92.4	78.90	21.0	7.2	4.0	0.75	1.80

The hybrids used from Colombia and from Brasil are already in distribution to farmers of each country.

This yield trial suffered through a very dry period during the flowering time. The varieties Pelotas, Marilia and Peru 330 had a very bad performance with yields below 2300 kg/ha. A summary of the data from the remaining entries (means from four replications) can be seen in Table 1.

All three Brasilian semi-dent double hybrids when compared with ordinary Brasilian field corns are very good under our conditions, and in another experiment carried out in 1954-55, in the same field, hybrid I.A. H-4624 yielded 4660 kg/ha, about 35% more than the mean of a group of 300 common yellow dent varieties from São Paulo (Maize Genetics Coop. News Letter 30: 129).

We can see the good performance of the Mexican hybrids and also of some Colombian ones. Mexican material was later than ours and the height of the ear and plant as a rule, was very high.

E. Paterniani

2. Further studies on adhesions of non-homologous centromeres and knobs.

In the 1955 News Letter data were presented on the frequency of adhesions of non-homologous centromeres at pachynema and also on the frequency of fusion of knobs on non-homologous chromosomes. Data were obtained from a strain of inbred Kys with structurally normal chromosomes and from a Kys strain homozygous for a 4-10 translocation. Additional data are now available from four different Kys strains each homozygous for a different reciprocal translocation. These studies have been confined to Kys lines because of the excellence of the pachytene preparations. Whether or not our conclusions as to the relative frequencies with which different chromosomes participate in non-homologous centromere and knob adhesions will hold for other strains is, of course, wholly conjectural.

Centromere adhesions occurred in nearly 75% of the cells observed. The kinds and frequencies of non-homologous centromere associations are given in Table 1. In those PMC with centromere adhesions the most frequently observed cells were those where two pairs only were so associated. Next in frequency were PMC where four of the 10 pairs were involved but the associations were 2 by 2--i.e., two pairs had adhered centromeres as did two other pairs in the same microsporocyte. Much less frequent were those cells with 3 cases of centromere adhesions with two chromosome pairs involved in each fusion. Occasionally a cell was found with one adhesion involving the centromeres from three chromosome pairs. Rarest of all were cells with two adhesions, one involving two and the other three chromosome pairs.

Table 1. Frequencies of different kinds of centromere adhesions at pachynema in normal KYS strains and in five different homozygous translocations (3-9, 4-6, 4-9, 4-10 and 5-6) with KYS background.

No. of adhesions per cell	No. of bivalents involved	Normal KYS		Homozygous 3-9 Translocation		Homozygous 4-6 Translocation	
		Cells recorded		Cells recorded		Cells recorded	
		No.	%	No.	%	No.	%
1	2	148	50.9	129	67.9	132	63.5
2	4	125	42.9	53	27.9	67	32.2
3	6	10	3.4	4	2.1	5	2.4
1	3	5	1.7	1	0.5	4	1.9
2	5	3	1.1	3	1.6	-	-
		291	100.0	190	100.0	208	100.0

No. of adhesions per cell	No. of bivalents involved	Homozygous 4-9 Translocation		Homozygous 4-10 Translocation		Homozygous 5-6 Translocation	
		Cells recorded		Cells recorded		Cells recorded	
		No.	%	No.	%	No.	%
1	2	114	62.6	76	42.2	127	63.2
2	4	60	33.0	89	49.4	67	33.3
3	6	5	2.7	8	4.4	3	1.5
1	3	2	1.1	5	2.8	3	1.5
2	5	1	0.6	2	1.1	1	0.5
		182	100.0	180	100.0	201	100.0

The average pachytene lengths of the 6 Kys strains studied are given in Table 2. The data for the structurally normal Kys line are from 6 well-spread figures at mid-pachynema where there was no obvious distortion by unequal stretching. The measurements for the homozygous 4-10 translocation are from 4 cells. Pachytene lengths for the remaining four homozygous translocation lines were each from 8 good figures. The total lengths and arm ratios found for Kys chromosomes agree well with the average values reported by Longley (1938) for different strains of maize but some differences exist. The greatest discrepancy found is that for chromosome 1 where our data give a long : short arm ratio of 1.1:1 while Longley reported a ratio of 1.3:1.

Involvement of the different chromosome pairs is clearly not at random but in general appears to be related to their relative pachytene lengths. Using the data in Table 2 (page 126), the expected number of centromere adhesions are given in Table 3 (page 128) on the hypothesis that the frequency with which the centromere of a specific chromosome pair adheres to other centromeres is a function of its relative pachytene length. Considering the normal Kys strain, the high chi-square value for the total of the 10 pairs appears to invalidate this hypothesis but a closer inspection shows that the only significant individual difference is for chromosome 5 and that for the remaining nine chromosomes there is a close relationship between pachytene length and frequency of centromere adhesion. The anomalous behavior of chromosome 5 is apparent also in the five translocation strains where the observed number of adhesions it undergoes is consistently higher than expected.

A check on the validity of this hypothesis is afforded by the data from the five translocation strains where the relative length of certain chromosomes has been drastically changed. If the frequency of centromere adhesions is a function of relative chromosome length then the translocated chromosomes whose lengths have been modified should show differences in adhesion frequencies. This is precisely what was observed with only two exceptions. In the homozygous 4-6 translocation, chromosome 6^4 had fewer adhesions than expected on the basis of its relative length and in the 4-9 homozygous translocation the 4^9 pair had significantly more adhesions than the calculated number. In general, however, the data are consistent with the hypothesis that the frequency of centromere adhesions depends in some unknown fashion upon the relative pachytene lengths.

The data on non-homologous knob associations given in the 1955 News Letter have been extended by observations on the 4 additional strains mentioned above. As was found previously, the larger knobs on chromosomes 5 and 7 are involved more frequently than the smaller knobs. The heterochromatic satellite located on the 4^6 chromosome in the homozygous T4-6 stock occasionally fused with other knobs although in its usual position such association has not been observed. Multiple knob associations occurred in less than 1% of the total number of cells recorded.

Table 2. Lengths in micra and arm ratios of inbred KYS chromosomes and those of five homozygous translocations in comparison with Longley's data.

	Normal KYS				Homozygous 3-9 Translocation				
Chrom.	S	L	Total length	Arm ratio	Chrom.	S	L	Total length	Arm ratio
1	40.17	45.73	85.90	1.1:1	1	39.42	47.45	86.87	1.2:1
2	31.52	34.46	67.98	1.2:1	2	32.40	36.00	68.40	1.1:1
3	20.39	40.17	60.56	2.0:1	3^9	22.29	26.01	48.30	1.2:1
4	22.25	35.23	57.48	1.6:1	4	22.68	34.02	56.70	1.5:1
5	29.05	31.52	60.57	1.1:1	5	29.72	31.95	61.67	1.1:1
6	11.74	36.46	48.20	3.1:1	6	11.11	34.09	45.20	3.1:1
7	11.12	33.37	44.49	3.0:1	7	11.15	34.08	45.33	3.1:1
8	11.12	35.23	46.35	3.2:1	8	10.41	34.97	45.38	3.3:1
9	14.21	27.19	41.40	1.9:1	9^3	12.63	42.35	54.98	2.4:1
10	9.27	25.96	35.23	2.8:1	10	9.12	26.60	35.72	2.9:1
Σ	200.84	347.32	548.16	-	Σ	200.93	347.62	548.55	-

Homozygous 4-9 Translocation					Homozygous 4-10 Translocation				
Chrom.	S	L	Total length	ratio	Chrom.	S	L	Total length	ratio
1	39.04	46.36	85.40	1.2:1	1	40.58	45.90	86.48	1.1:1
2	32.45	36.66	69.11	1.1:1	2	31.06	39.66	70.72	1.3:1
3	20.22	39.18	59.40	1.9:1	3	21.08	41.82	62.90	2.0:1
4^9	17.70	36.02	53.72	2.0:1	4^{10}	12.24	22.10*	34.34	1.8:1
5	28.01	32.89	60.90	1.2:1	5	27.08	33.54	60.62	1.2:1
6	12.46	35.98	48.44	2.9:1	6	11.78	34.68	46.46	2.9:1
7	12.01	34.13	46.14	2.8:1	7	13.14	32.86	46.00	2.5:1
8	11.07	35.80	46.87	3.2:1	8	10.66	34.00	44.66	3.2:1
9^4	13.27	26.54	39.81	2.0:1	9	12.46	25.16	37.62	2.0:1
10	9.48	25.91	35.39	2.7:1	10^4	11.44	45.78	57.22	4.0:1
Σ	195.71	349.47	545.18	-	Σ	191.52	355.50	547.02	-

* It should be noted that the long arm of the 4^{10} chromosome is the short arm of chromosome 4.

Table 2. Cont'd.

Homozygous 4-6 Translocation					Chromosome Atlas (after Longley)				
Chrom.	S	L	Total length	ratio	Chrom.	S	L	Total length	ratio
1	39.05	44.96	84.01	1.1:1	1	35.87	46.52	82.39	1.3:1
2	31.90	38.91	70.81	1.2:1	2	29.51	36.97	66.48	1.2:1
3	20.35	41.66	62.01	2.0:1	3	20.51	41.49	62.00	2.0:1
46	12.51	26.67	39.18	2.1:1	4	22.47	36.31	58.78	1.6:1
5	28.18	33.00	61.18	1.2:1	5	27.37	32.45	59.82	1.1:1
64	22.82	39.74	62.56	1.7:1	6	11.91	36.82	48.73	3.1:1
7	12.40	32.47	44.87	2.6:1	7	12.44	34.34	46.78	2.8:1
8	11.00	33.82	44.82	3.1:1	8	11.26	36.22	47.48	3.2:1
9	14.01	27.62	41.63	2.0:1	9	15.21	28.03	43.24	1.8:1
10	9.26	26.22	35.48	2.8:1	10	9.81	27.12	36.93	2.8:1
Σ	201.48	345.07	546.55	-	Σ	196.36	356.27	552.63	-

Homozygous 5-6 Translocation				
Chrom.	S	L	Total length	ratio
1	38.64	46.48	85.12	1.2:1
2	31.30	36.12	67.42	1.2:1
3	20.46	40.92	61.38	2.0:1
4	21.45	35.75	57.20	1.7:1
56	31.91	37.93	69.84	1.2:1
65	6.02	34.92	40.94	5.8:1
7	11.50	34.00	45.50	3.0:1
8	11.90	34.30	46.20	2.9:1
9	13.24	27.09	40.33	2.0:1
10	8.82	26.46	35.28	3.0:1
Σ	195.24	353.97	549.21	-

Table 3. Comparisons of the observed frequencies of centromere adhesions with the expected frequencies calculated on basis of chromosome length.

Normal KYS				Homozygous 3-9 Translocation				Homozygous 4-6 Translocation			
Chrom.	ob.	exp.	x^2	Chrom.	ob.	exp.	x^2	Chrom.	ob.	exp.	x^2
1	87	105.3	3.18	1	72	86.9	2.55	1	74	89.8	2.78
2	69	83.3	2.45	2	52	68.7	4.06*	2	64	75.7	1.81
3	71	74.3	0.15	39	59	48.5	2.27	3	65	66.2	0.02
4	75	70.5	0.29	4	63	56.9	0.65	46	51	41.9	1.98
5	112	74.3	19.13**	5	85	61.9	8.62**	5	92	65.4	10.82**
6	50	59.1	1.40	6	42	45.3	0.24	64	48	66.8	5.30*
7	67	54.5	2.87	7	47	45.4	0.06	7	56	47.9	1.37
8	63	56.7	0.68	8	56	45.5	2.42	8	57	47.9	1.73
9	43	50.8	1.98	93	50	55.1	0.47	9	46	44.5	0.06
10	35	43.2	1.56	10	24	35.8	3.89*	10	31	37.9	1.26
Σ	672	672.0	33.69**	Σ	550	549.6	25.23**	Σ	584	584.0	22.36**

Homozygous 4-9 Translocation				Homozygous 4-10 Translocation				Homozygous 5-6 Translocation			
Chrom.	ob.	exp.	x^2	Chrom.	ob.	exp.	x^2	Chrom.	ob.	exp.	x^2
1	69	76.4	0.72	1	81	96.2	2.37	1	82	90.8	0.85
2	50	61.9	2.29	2	64	78.6	2.71	2	64	71.9	0.87
3	45	53.1	1.24	3	59	69.9	1.70	3	68	65.5	0.10
49	64	48.1	5.26*	410	44	38.2	0.88	4	67	61.1	0.57
5	81	54.5	12.89**	5	100	67.4	15.77**	56	95	74.5	5.64*
6	31	43.4	3.54	6	45	51.6	0.84	65	32	43.7	3.13
7	43	41.3	0.07	7	56	51.1	0.50	7	54	48.5	0.62
8	52	42.0	2.38	8	52	49.6	0.12	8	59	49.3	1.91
94	30	35.6	0.88	9	37	41.8	0.55	9	36	43.1	1.17
10	23	31.7	2.39	104	70	63.6	0.64	10	29	37.6	1.97
Σ	488	488.0	31.66**	Σ	608	608.0	26.08**	Σ	586	586.0	16.83

Two clear cases of knob and centromere adhesion were found. These involved the knob on 5 with the centromeres of 4^6 and 7 and the satellite on the 5^6 chromosome with the 6^5 centromere. Although hypotheses to account for the non-randomness of knob associations could be presented, none have been adequately tested.

José do Amaral Gurgel

SYRACUSE UNIVERSITY
Syracuse, New York

1. Orange variegated pericarp.

Orange variegated pericarp is one of the relatively rare mutants arising in variegated pericarp stocks. The mutant P allele responsible for this phenotype affects both pericarp and cob color. Orange variegated pericarp shows (1) self colored stripes similar to those of variegated pericarp and (2) a homogeneous orange-red ground color between these stripes, rather than colorless as in ordinary variegated. The cob exhibits only a slight flush of color, with occasional larger flecks of red. The allele associated with this mutant phenotype is designated P^{ovov}. The present studies indicate that P^{ovov} is composed of the gene, P^{rr}, and a transposable element similar to the Modulator (Mp) of the P^{vv} allele. The transposable element is designated Mp'. The orange variegated allele has been isolated from eight different Wisconsin P^{vv} stocks. In all cases tested, the mutant allele "activates" Dissociation (Ds).

The mutational pattern and the mutational spectrum of P^{ovov} are similar to those of P^{vv}. The phenotype of the ears produced by plants grown from kernels on orange variegated ears is, for the most part, the same as that of the parent ear both in the frequency of the self colored striping and in the shade of ground color. A low percentage of ears (2 to 3% in stocks graded to inbred W22R) exhibit a markedly lower frequency of striping and a lighter shade of ground color. This class is referred to as "orange light variegated" and is due to the presence of a transposed Mp' in the genome in addition to the P^{ovov} allele. Self red ears occur with about the same frequency as orange light variegated ears in these families.

Twinned sectors of orange light variegated and self red pericarp have been observed on heterozygous orange medium variegated ears (P^{ovov}/P^{wr}). Five twin spots with a minimum number of three kernels in either sector have been further tested. The phenotypes of the progeny ears were in accord with the expected types. Each of these plants was tested for the ability to activate Ds. All plants in the control families (orange medium variegated sibs) and in the families representing

the orange light variegated twin components exhibiting an orange variegated phenotype induced Ds breakage events. None of the white pericarp red cob (P^{wr}) plants activated Ds. Plants with self red ears in two only of the five families representing the red components of the twinned sectors activated Ds. This is in accord with Brink's findings for the red component of twin spots in ordinary variegated pericarp.

The frequency of stripes involving one-fourth or more of the abgerminal side of the kernel in orange variegated and standard variegated proved to be statistically different. The mean grade of the ground color of the orange light variegated ears was lighter than that of the corresponding orange medium variegated class in each of four groups tested.

The Ds breakage pattern induced by orange medium variegateds representing two of the P^{ovov} alleles was compared to that induced by the medium variegateds from the stocks in which these alleles arose. The kernels on the mature ears were scored for the presence of (1) early breaks, represented by colorless sectors involving one-eighth or more of the aleurone in the otherwise colored kernel (other colorless sectors also occurred on these kernels) and (2) very late breaks only, represented by colorless aleurone sectors in which no more than about six aleurone cells were included in any of the sectors on the kernel. No attempt was made to compare the frequency of these breakage events on individual kernels. A highly significant difference in the number of kernels exhibiting only very late breaks is obtained for one of the P^{ovov} alleles compared to the P^{vv} control. The data for the early breaks in this group are not consistent.

In two tests no difference is found, in one test the difference is barely significant at the 5% level, and in one test a highly significant difference is obtained. In the comparison of the other P^{ovov} allele with its P^{vv} control, no differences are found for either early or very late breakage events. This latter group was difficult to classify because of the presence of a pronounced R-mottling in the aleurone pigmentation, and so the data, especially for the very late events, are not reliable. Further tests are being made.

The mutation to P^{ovov} could be (1) a mutation of the P^{rr} gene, (2) a mutation of the Mp element, and (3) a change in the relationship of the two components of the allele. The present results indicate that the P^{ovov} allele is significantly different from P^{vv} in the pattern of early somatic mutations to self red. According to the Modulator hypothesis, these mutations are the result of the loss in somatic tissue of Mp from the P locus, allowing the pigment-producing capacity of this gene to be expressed. The P^{ovov} phenotype also differs from the P^{vv} phenotype in the presence of the ground color. Both the demonstrated response of the ground color to an increase in the number of Mp's in the genome and the linear regression of the shade of the ground color on the frequency of the somatic striping support the conclusion that this component of the orange variegated phenotype as well as the conspicuous striping is a Mp' function. It is believed that the loss of

Mp' from the P locus in a high proportion of the cells late in the development of the pericarp is the basis of the ground color. Variations in shade are due to varying proportions of the two kinds of cells, self red and colorless. The lower frequency of self colored striping and the lighter shade of ground color in the orange light variegated phenotype indicate that the frequency of all somatic mutations is decreased at all stages in the development of the pericarp. The mutation to P^{ovov} is interpreted to be due to a mutation of the Mp component of the P^{vv} allele to Mp'. The results of the comparison of the time of Ds breakage events induced by P^{vv} and P^{ovov}, though not conclusive, support this hypothesis.

F. A. Valentine

TENNESSEE AGRICULTURAL EXPERIMENT STATION
Knoxville, Tennessee
and
U. S. DEPARTMENT OF AGRICULTURE
Beltsville, Maryland

1. Recovered strains of inbred 33-16.

In the 1954 Newsletter (P 19) a report was made of the availability of strains of 33-16 in which the cytoplasmic contribution to male sterility had been eliminated through backcrossing.

Five recovered strains of 33-16 have been maintained through backcrossing by the Kentucky strain of 33-16 following the initial crosses on K64 and CI.43 as female parents and four recovered strains have been maintained by backcrossing with the Beltsville strain of 33-16, following initial crosses on K64 and Ky39 as female parents.

Crosses involving these recovered strains and original 33-16 (Kentucky strain) as seed parents by Ky 27 x CI.61, CI.43 x CI.61, K63, Mo2RF, Ky27, CI.43, and CI.61 as male parents were grown at Knoxville and Crossville, Tenn., Beltsville, Md., and Huntsdale, Mo., in 1956 and the amount of pollen sterility determined. The only pollen sterility observed occurred in test crosses with the original 33-16 as seed parent, indicating that the cytoplasmic contribution to sterility has been completely eliminated from the recovered strains.

Single crosses between the recovered strains and original 33-16 (Kentucky strain) as seed parents and K55, K64, N72 and Ky49 as male parents were compared for yield at Crossville, Tenn., Lexington, Ky, and Huntsdale, Mo., in 1956. Considering the average yields on all four testers, there were no significant differences in yield between any of the recovered strains and original 33-16 at any of the locations. Also

the recovered strains were equal to or better than original 33-16 in all important agronomic characters, except that original 33-16 produced more ears per plant in Tennessee. The data indicate that any of the recovered strains may be substituted for original 33-16 in crosses to eliminate the possibility of pollen sterility without lowering the performance of the hybrid.

Visual comparisons of the 33-16 recoveries indicate distinct phenotypic differences between the recoveries backcrossed to the Kentucky strain of 33-16 and those backcrossed to the Beltsville strain. Recoveries involving both the Kentucky and Beltsville strains are available to interested breeders. It is suggested that breeders interested in 33-16 having normal cytoplasm obtain a strain from each of the writers for comparison. These may then be further backcrossed by their own 33-16 if this seems desirable.

Seed of the recovered strains may be obtained from the writers at the Tennessee Agricultural Experiment Station and Plant Industry Station, Beltsville, Maryland, respectively.

L. M. Josephson
M. T. Jenkins

2. Stability of 33-16 sterile cytoplasm.

In a previous publication (Em. Jour. Exp. Agric. 23: 1-10, 1955) the writer reported on the behavior of various inbred lines to Texas sterile cytoplasm and that carried in inbred 33-16. The latter type, designated "J" type sterile cytoplasm, was incorporated into inbred Ky27. This line has remained completely sterile through nine generations of backcrossing. The two types of cytoplasm can be differentiated by the reaction of the following inbreds:

Inbred	T cytoplasm	J cytoplasm
Ky21	Fertile	Fertile
R7	Fertile	Fertile
A14 (South Africa)	Fertile	Fertile
Ky39	Sterile	Fertile
Ky39xKy21	Seg.	Fertile
K55	Fertile	Sterile
K64	Seg.	Sterile
K63	Fertile	Sterile
R6	Fertile	Sterile
K6	Fertile	Sterile
Ky122	Fertile	Sterile
E184 (South Africa)	Fertile	Sterile

Other lines that act as fertility restorers to T sterile cytoplasm have been crossed on J sterile cytoplasm and will be grown in 1957 to determine if lines other than Ky21, R7 and A14 will restore fertility to both types. Studies are also being made to determine the inheritance of the fertility restorers to J cytoplasm and also to determine whether the restoring ability of the three lines common to both types of sterile cytoplasm is due to the same or to different genes.

The J type sterile cytoplasm has now been transferred to inbred K55 and has remained stable through five generations of backcrossing. Since inbred K64 does not restore J cytoplasm it will be possible to produce hybrid U. S. 523W by the male sterile method. Inbreds Ky27 and Ky49 used in the pollen parent single cross of this hybrid are also being converted to fertility restorers using Ky21 and A14 as sources of restorer genes.

3. Male sterile restorers in varieties.

A number of open-pollinated varieties utilized in the breeding program in Tennessee were tested for restoring ability to cytoplasmic pollen sterility. The varieties were crossed with inbred T111 in which Texas sterile cytoplasm has been incorporated. Varieties Jellicorse, Rockdale and Salisbury White are good potential sources for restoring genes to Texas sterile cytoplasm.

Variety	No. of Plants	Fertile %	Part. Fertile %	Part. Sterile %	Sterile %
Jellicorse (W)	37	40.5	2.7	8.1	48.7
Rockdale (W)	34	23.5	17.6	11.8	47.1
Neal Paymaster (W)	39	5.1	2.6	7.7	84.6
T61 (Y) Synthetic	40	0	0	0	100.0
Bechino Hickory King (South Africa) (W)	31	0	6.4	0	93.6
Salisbury White (S. Rhod.)	43	20.9	0	4.6	74.5
Teko Yellow (South Africa)	25	0	4.0	0	96.0

L. M. Josephson

UNION OF SOUTH AFRICA
College of Agriculture
Potchefstroom, Union of South Africa

1. Maize stalk-borer resistance.

The first-generation larvae of maize stalk-borer (Calamistis fusca, Hmpsn.) generally emerge prior to tasseling and feed in the whorl of leaves prior to burrowing through the stalk to the base of the plant where they pupate. In this respect, the insect is similar to European corn borer. The second and succeeding generations generally feed in the ears causing a type of damage similar to corn earworm. Prior to complete maturity the borers migrate to the base of the plant for overwintering. The average annual loss due to the ravages of this insect has been assessed at about 10 percent. Little apparent success has accrued from selection for resistance.

Data collected on infestation and degree of damage of ears in single cross yield trials and inbred tests during 1953-54 was used as a basis for classifying resistant and susceptible inbreds. In addition to obtaining the percentage of ears infested, the infested ears were scored as to the average percent of grain destroyed per ear. The product of these figures provided the actual grain loss per sample. The inbreds and crosses between them were compared under heavy natural infestations.

The resistant lines selected for testing during 1954-55 were all flint types, while the susceptible lines were soft dents; e.g., Hy and 38-11. The infestation in the plants as well as in the ears was obtained in these tests. A highly significant r of + .71 (N = 24) between plant and ear infestation indicated that resistance was not due entirely to the type of grain.

The lines selected for testing during the 1955-56 season consisted entirely of similar dent types, and here also a highly significant r of + .72 (N = 21) between ear and plant infestation suggested that plant resistance is closely associated with ear resistance. The slight dominance of resistance to ear damage in 1954-55 was not apparent in the dent types tested during 1955-56 indicating that resistance to ear damage is due in part to the hard flint grain type.

The data given in the following table shows that the percentage infestation in both plants and ears and the degree of ear damage to maize stalk borer is controlled genetically and that classification of ears for infestation and degree of damage is a reliable guide to plant resistance. Studies on inheritance of resistance to this insect are now under way.

	1954-55			1955-56	
	Plant infestation, 74 days	Ear infestation	Total damage in ear	Plant infestation, 126 days	Ear infestation
	%	%	%	%	%
R inbreds	47.3	17.4	0.46	-	-
S inbreds	70.1	38.9	1.20	-	-
R X R	53.5	26.8	0.85	32.4	13.4
R X S	60.7	28.9	1.01	39.4	20.9
S X S	78.1	61.7	3.44	50.8	30.1

B. Stead

UNITED STATES DEPARTMENT OF AGRICULTURE
Beltsville, Maryland
and
UNIVERSITY OF FLORIDA
Everglades Experiment Station
Belle Glade, Florida

1. Breeding tests for blight resistance.

Inbred lines resistant to the leaf blight caused by Helminthosporium turcicum differ greatly in their usefulness as sources of blight resistance. Experiments to evaluate the comparative breeding potential of resistant inbred lines have been in progress for several years. The general procedure has been to cross the resistant lines with one or more susceptible testers, advance the crosses to the F_2 generation, grow these populations under a heavy blight epidemic, make individual blight ratings on the F_2 plants, and compare the distributions of these F_2 blight scores.

An experiment involving 16 resistant inbred lines and the three susceptible testers R4, Tr and 187-2 was grown at Belle Glade, Florida last spring. The resistant lines, the mean blight scores of the F_1 and F_2 plants of the crosses involving them and the percentage of F_2 plants with "0" blight ratings are listed in table 1. The tests suggest that CI.90A and GAL440 are superior to the other tested lines as breeding sources of resistance.

Table 1. Summary of the blight reaction of 16 resistant lines in crosses with 3 susceptible testers.

Resistant lines	Mean Blight Scores		Percent of F_2 plants rated "0"
	F_1's	F_2's	
CI.28A	1.84	2.07	0
CI.81A	2.15	2.68	0
CI.84A	2.01	2.61	.3
CI.86A	1.80	1.90	.8
CI.87	1.95	2.31	0
CI.88A	2.22	2.09	.4
CI.90A	1.63	1.67	3.3
CI.91A	2.34	2.73	0
GAL440	1.23	1.67	1.7
GE259	2.13	2.38	.1
GA199	1.84	1.91	.4
B3478	1.80	2.00	0
Np3197-3	1.89	2.11	.6
Lg2323	1.85	2.21	.3
B3372	2.24	2.52	.1
Ba4032	1.67	1.94	.1

Merle T. Jenkins
Alice L. Robert

UNITED STATES DEPARTMENT OF AGRICULTURE
and
UNIVERSITY OF MISSOURI
Department of Field Crops
Columbia, Missouri

1. Test of doubleness at C locus.

Three of the cases in the test for crossover-separable components in C^i, reported last year, proved to be contaminations. Tests are not yet complete on the fourth, and new cases obtained this year are still to be tested. The accumulated data are as follows:

Cross: + C^i +/yg C sh X yg c sh, B.C. to c

Class	Examined	Plants	Per Plant	Colored	Test of
C^i sh	193,050	508	380	1 sh	I c
yg C^i +	423,600	1,411	300	3 Sh,1 sh	c I
Grand T	616,650	1,919	681	5	I C, C I

Tentative maximum map distances for C to I have been calculated for each of the four assumed structures:

1. I C: Four possible cases. 0.0013 map units maximum.
2. C I: One possible case. 0.00032 map units maximum.
3. I c: One possible case. 0.064 map units maximum.
4. c I: One possible case. 0.097 map units maximum.

An additional test for the fourth constitution was obtained through the use of a terminal deficiency. Deficiency to C^i is approximately two units, providing a much more efficient marker than yg. Plants of constitution Def C^i +/C sh were used as pollen parent on c sh, and colorless Sh were selected. These crossover plants were then backcrossed to c. In 75 plants, averaging over 300 gametes per plant, no colored exceptions were found. Combining these data with the numbers in the standard test, a maximum C-I distance for structure c I of 0.079 units can be derived.

2. Spontaneous mutation of C^i.

For C^i X c, 422,513 gametes have yielded only 6 possible cases of mutation to C; these have not yet been tested for confirmation. All are from C^i/c individuals, in the crossover tests above. For C^i X C, a large-scale test in detassel plot last summer gave the following (1955 data is included for cumulative total):

Year	Whole Seed Self Color	Whole Seed Variegated	Variegated Sector	Colored Pits	Colored Scutellum	Diffuse Color	Total
1955	0	3	0	0	0	0	11,970
1956	6	82	19	12	4	4	797,400
	6	85	19	12	4	4	809,370

Of the six whole-seed-self-color cases, four are unusually small, and could be deficiencies for C^i. The other two are normal in size. The three variegated cases from 1955 have been tested; two had non-corresponding embryo, and the other was deficient for Yg. This type of kernel, of which 5 have now been analyzed, clearly arises from terminal breaks and breakage-fusion-bridge cycles. Thus no more than 6 mutation cases were obtained (7.4 per million), and perhaps as few as 2 can be valid (2.5 per million).

3. Anthocyanin synthesis and intensifier.

The bronze-metallic sheen in the pericarp of in in kernels, reported in News Letter 29: 7, 1955, is probably the effect called "brassy" by Fraser in the original description of in. Various combinations of in with other aleurone factors have been checked for this effect:

	Constitution	Pericarp Sheen
(A_1 A_2 Bz_1 C R)	Pr in	yes
	pr in	occasional
	a_1 Pr in	yes
	a_1 pr in	occasional
	a_2 Pr in	yes
	bz_1 Pr in	yes
	c Pr in	no
	C^i Pr in	no
	r Pr in	no

These interactions can be interpreted simply as indicating that C and R actions precede the effects of in, assuming that a diffusible substance is produced in excess in in kernels, and that this substance develops into a brown pigment (not anthocyanin) when it enters the pericarp. It is suggested that C and R are essential for the production of this substance.

A logical construction for the sequence of action, using the available information, is (C, R); In; A_1; (Bz_1, A_2). The position of Pr is not clear, but probably preceding A_2, at least.

4. High-haploid line.

Further data on frequency in self progenies of the two sources of stock 6 (see News Letter 30: 98, 1956) were obtained this year:

Stock 6 Selfs

Year	Haploids	Total	% Haploids
1955	15	760	1.97**
1956	36	1,184	3.04
Both years	51	1,944	2.62**

(Hap. X sib) Selfs

1955	35	1,222	2.86
1956	156	4,540	3.44
Both years	191	5,762	3.31
Grand Total	242	7,706	3.14

** Highly sign. diff. from grand total.

The effect of background is still not clear, but may be slight (note 1956 data alone).

Outcross tests clearly show a high frequency of maternal haploid parthenogenesis, but not of the same magnitude as in self progenies:

Stock 6 (R^g) X R^r

Year	Haploids	Total	% Haploids
1955	6	1,085	0.55
1956	186	21,196	0.88
Both years	192	22,281	0.86

The percentage above may be a little below the true frequency, as it has been found that stock 6 occasionally shows a weak R^r expression. For R^r X stock 6, however, no difficulty in classification was experienced:

R^r X stock 6

R^g haploids	Total
0	6,946

No sperm-derived haploids were found. Haploid androgenesis probably does not contribute significantly to the high percentage of haploids in selfs.

A very high frequency of heterofertilization occurs in the line, and may be associated with the production of haploids.

5. Test for non-homologous crossing-over in translocation heterozygotes.

The test reported last year is negative. The single case proved to be spurious.

6. Ds and sticky.

Cross:

$$\frac{c\ sh\ wx}{c\ +\ +}\ ,\ \frac{+}{st}\ ,\ ac\ X\ \frac{C\ +\ +\ Ds}{c\ +\ +}\ ,\ \frac{+}{st}\ ,\ ac$$

compared with:

$$\frac{c\ sh\ wx}{c\ +\ +}\ ,\ \frac{+}{st}\quad X\ \frac{C\ +\ +}{c\ +\ +}\ ,\ \frac{+}{st}$$

No cases of activation of Ds by st were found in 1,818 kernels, where 1/16 are observable for concurrent losses of C Sh Wx on st kernels. Thus st does not carry Ac, and its effect of increasing stickiness in chromosomes does not result in massive activation. Whether this may be significant to the concept of Ds as consisting of modified heterochromatin is difficult to judge, but should be considered, in view of the "sticky" property of heterochromatin.

On one ear of the control cross, unusually strong st expression (pitted kernels) was found. Here, there were numerous non-concurrent losses of C and Wx, demonstrating clearly that st can result in endosperm mosaics.

7. High-amylose factors.

The ha gene reported by Kramer, and the ha_m gene (to be designated ha_2) both interact strongly with wx, giving highly collapsed kernels, variably translucent, very similar to bt_1 kernels. The effect of ha_1 is much greater than that of ha_2; in fact ha_1 wx kernels have a small amount of blue-staining starch, while ha_2 wx kernels do not. This property of ha_1 wx is similar to that reported for ae wx (News Letter 26: 5, 1952). The phenotypic effect of ha wx combinations suggests that new ha factors might best be sought on a waxy background, where their effects are easily distinguished phenotypically.

Using this interaction, the linkage of ha_1 with chromosome 5 has been confirmed, where wx T5-9c/Wx ha_1 X wx ha_1 shows very few collapsed kernels (4-5%). Linkage of ha_2 with chromosome 10 is also clear. Chromosomes 1, 2, 3, 4, 5, 6, and 8 show independence ratios with waxy translocations, but wx T9-10b/Wx ha_2 X wx ha_2 shows the following:

	Normal	Waxy	Tarnished	Collapsed
ear 1	(1)	53	(60)	1
ear 2	(5)	140	(122)	2
	(6)	193	(182)	3

9/384 = 2.3% crossing over, wx-ha_2, across translocation. Anderson (Genetics, 1938) reports wx-T as 5.7 units. The Ha Wx and ha Wx kernels are difficult to distinguish with certainty.

E. H. Coe, Jr.

8. Allelism and mutability of anther-ear 6923.

The an_{6923} mutant discussed last year has been tested and found allelic to an_1, as suggested (News Letter 30: 100, 1956). Since it is also allelic to $bz_2{}^m$, which responds to Ac (or M), a test of the

mutability of $\underline{an}_{6923}$ has been carried out. In the cross $+\ bz_2/6923$; M m X + +/6923; m, 3/8 are stable bz, and 1/8 are mutable. Thus the bronze "component" of $\underline{an}_{6923}$ is not mutable.

E. H. Coe, Jr.
M. G. Nuffer

9. A crossover analysis of some mutable alleles of A_1.

An experiment has been conducted to determine whether crossing over immediately adjacent to a mutable locus can change its state of mutability (in the absence of a mutator factor) or can remove that unknown agent which according to the prevailing view of mutable loci, is suppressing the dominant allele to give the mutable recessive effect. Only those crossovers that occur immediately adjacent to the mutable locus can be expected to give the answer to this question. It is possible to make such a test using the A_1 locus because of its compound nature and because of the closeness of the sh_2 marker. The experiment was designed as follows: Plants of $\underline{\alpha\ a\ sh}/\underline{a^m\ Sh}$, dt, ac were crossed by a^s sh, Dt Dt, ac pollen and the ears produced were examined for recombinants and unusual seed types. The following diagram shows the possible types of crossovers:

	Pairing type	Reg	Crossover type
A.	$\underline{\alpha\ {}^{1}\ a\ {}^{2}\ sh}$ / $\underline{a^m \quad Sh}$	1	$\alpha\ a^m\ Sh$
		2	$\alpha\ a\ Sh$
		2	$a^m\ sh$
		1	$a\ sh$
B.	$\underline{\alpha\ {}^{1}\ a\ {}^{2}\ sh}$ / $\underline{a^m \quad Sh}$	1	$\alpha - Sh$
		2	$\alpha\ a\ Sh$
		2	$a^m\ sh$
		1	$a^m\ a\ sh$

Four different mutable alleles and one stable allele were used. Two were Dt responding, a^{m}-1:Cache and a^{m}-1:D5 and one was stable, a^s. These have had a complete test. The other two were Ac responding alleles, a^{m-3} and a^{m-4}. They have had only a preliminary test. The a in the α a sh segment is the standard dottable a found by Emerson.

The data listed in table 1 indicate that the Dt responding alleles pair with either α or a as expected. The occurrence of $\alpha\ a^m$ Sh cases proves pairing type A while the α - Sh and a^m a sh cases prove type B. The only unusual crossover type found was a single colored non-shrunken case which had normal A phenotype and proved to have brown pericarp. It is not known, however, whether this pericarp is dominant or recessive. If it turns out to be dominant this would be an α A Sh case or the type expected from a crossover removal of an agent suppressing A phenotype.

Table 1. Frequency of crossovers from type cross α a sh/a^m Sh, dt, ac X a^s sh, Dt.

Ear parent	Total number	α a^m Sh	α a Sh	α - Sh	a^m sh	a sh	a^m a sh	Trisomic	A Sh
α - a sh/a^m - 1:Cache	15,163	1	2	4	6	--	--	4	0
α - a/a^m - 1:D5	12,733	3	6	8	5	--	1	5	1
α a sh/a^s	42,120	--	13	27	--	3	--	6	0
Cases not yet tested									
α a sh/a^{m-3}	131,448	1	17	14	--	23	--	--	0
α a sh/a^{m-4}	40,507	4	20	7	--	18	--	--	1

Trisomics: A number of the supposedly dilute dotted non-shrunken seeds turned out on test to be trisomics. The number was not extremely high but they were easily obtained because the experimental design was ideally suited for picking up such cases since they resemble two of the crossover types (α a^m Sh and α a Sh) that we were looking for.

a^m-a-sh segment: This unique combination of two Dt responding alleles on the same segment is recognized only when the Dt gene induces the more mutable of the two (a^m) to mutate to a^s leaving a sector of a^s a tissue that permits the expression of the less mutable of the two original alleles (a). There are perhaps several others among the a^m sh class which will not be recognized until further tests are made.

10. Grouped crossovers.

In examining the ears for the above described experiment it was noted that a number of examples of a sector that included two or more crossovers were found. In one case for example, three α a Sh crossovers were found in a single row within the distance of six seeds. Their order on the ear was α a Sh, a^m Sh, α a Sh, a^m Sh, a^m Sh, and α a Sh. The crossovers have double underlining. This same ear had two α a Sh cases on the other side of the ear which were separated by one non-crossover seed. The possibility of contamination has been excluded for these cases and since there were no mutator factors such as Dt or Ac present it is very unlikely that they arose by mutation. Several cases, as yet unconfirmed, of complementary crossover types in pairs have been observed, for example α a Sh and a^m sh. There also was found in the progeny from the α a sh/a^s Sh material, one case of three a^s sh seeds in a single sector. Their order on the ear was α a sh, a^s sh, α a sh, a^s sh, a^s Sh, a^s sh, and α a sh. A total of 341,421 seeds have been examined and at most 450 crossover cases have been found (later confirmation tests will give an accurate figure). Thirty-six of these were found in 17 sectors of two or more essentially adjacent seeds. This suggests something more than coincidence. Among the possibilities being investigated are somatic crossing over and a pre-disposition to high frequency of crossing over in certain sectors of the developing ear.

M. G. Nuffer

11. High amylose starch.

It was reported in the Maize Genetics News Letter #30 that the cross between ha_1 and one of the Missouri high amylose strains (ha_m 123) gave an amylose content of 27%, indicating the two factors were not allelic. When grown in Missouri, ha_1 and ha_m 123 gave amylose contents of 49% and 37%, respectively. Selected samples of kernels from the F_3 ears gave amylose contents from 60% to slightly more than 70%. It is possible

strains with higher amylose contents will be found in this or in later generations. The amylose was determined by potentiometric titration with iodine at the Northern Regional Utilization Branch, Peoria, Illinois.

M. S. Zuber
C. O. Grogan

UNIVERSITY OF WISCONSIN
Madison, Wisconsin
Department of Genetics

1. Distribution of transposed Modulator.

Modulator (Mp), the element postulated by Brink and Nilan as responsible for the suppression of P^{rr} (red pericarp, red cob) action to give the P^{vv} (variegated pericarp, variegated cob) allele, frequently undergoes transpostion from the P locus. A transposed-Modulator (tr-Mp) when present in the genome with an unaltered P^{vv} allele ($\overline{P^{rr}Mp}$) gives the light variegated phenotype.

An experiment was designed to study the distribution of these transposed Modulators. Independent transpositions of Mp (new mutations from medium variegated to light variegated) were collected, and the linkage relations of tr-Mp then studied.

It was found that tr-Mp could occupy positions both linked and non-linked to the P locus. Cases were observed in which tr-Mp showed linkage to reciprocal translocations marking chromosomes 4 and 5, and 5 and 9. In the majority of cases, however, tr-Mp shows some degree of linkage with the P locus on the first chromosome. Among 67 independent transpositions of Mp from the P locus, 64 per cent of the new positions were linked to the P locus. This percentage is much higher than would be expected if moves were at random. The frequency with which tr-Mp occupies any given position on chromosome 1 increases sharply as the distance from the P locus decreases. Modulator, after becoming transposed from the P locus, often undergoes further transposition. Limited data were obtained suggesting that tr-Mp is less likely to undergo secondary moves if the position first held is close to the P locus.

2. Cytological positions of reciprocal translocations involving chromosome 1 and linkage with the P locus.

During the course of an experiment in which various reciprocal translocations were used as markers, the data given below were collected showing the linkage between the P locus and several reciprocal

translocations involving chromosome 1. The cytological designations are those given by Anderson and Longley in the 1956 Maize Genetics Co-op. News Letter.

Trans-location	Total indiv.	Cytological determination	% c.o. with P
1-2b	767	1S.43 2S.36	5.0
1-2c	384	1S.77 2L.33	33.9
1-2d	822	1S.78 2L.56	20.9
1-3a	839	1S.19 3L.14	10.1
1-3d	235	1L.67 3S.81	11.1
1-3i	152	1L.68 3S.30	39.5
1-4a	248	1L.51 4S.69	41.5
1-4b	2103	1S.55 4L.83	7.3
1-4h	460	1S.94 4L.52	35.9
1-5b	6150	1S.17 5L.10	21.8
1-5i	7248	1S.71 5S.74	17.2
1-6c	649	1S.25 6L.27	7.7
1-8b	1209	1L.59 8L.82	45.3
1-10g	859	1S.80 10L.21	19.1

Nancy Worner van Schaik*

* Present address: 112 Wenning Street
Pretoria, Union of South Africa.

3. The neutral effect of a heterochromatic knob on variegated pericarp.

A variegated pericarp stock was crossed to a strain heterozygous for a large heterochromatic knob (K) closely linked with R on chromosome 10, as shown below. (The knobbed stock was obtained from M. M. Rhoades.)

$$P^{vv}P^{vv}\ rk/rk \times P^{ww}P^{ww}\ RK/rk \longrightarrow \begin{cases} P^{vv}P^{ww}\ RK/rk & \text{(purple, knobbed)} \\ P^{vv}P^{ww}\ rk/rk & \text{(colorless, no knob)} \end{cases}$$

The plants reared from the kernels with colored aleurone were hand pollinated with II pollen to inhibit aleurone pigmentation in order to facilitate scoring for variegated pericarp, and the colorless kernels were allowed to open pollinate.

The pattern of variegation on the two classes of ears was then compared. The ears were lined up side by side and examined for any gross differences in the variegation pattern. A detailed examination of individual kernels was not made. There were 83 variegated ears carrying

knobbed chromosome 10 and 106 not carrying it. No difference in variegated pericarp pattern was observed. It would appear that either the heterochromatic knob does not have an effect on variegated pericarp, or that the effect is too small to be resolved by the technique used.

R. Bruce Ashman

4. Directed and specific genetic changes in an R^r allele occurring regularly in certain heterozygotes.

An R^r allele which has been in the writer's cultures for several years without showing any other unusual property has been found recently to change regularly and specifically to forms with decreased aleurone pigment-producing action in heterozygotes with stippled (R^{st}), light stippled (R^{stL})--a mutant from R^{st}, and marbled (R^{mb}). The changes in the case of R^{st} and R^{stL} have been shown to be heritable; that with R^{mb} remains to be tested in this respect. More or less marked reversion of the respective modified R^r's toward the standard level of R^r pigment-producing action occurs in homozygous R^rR^r plants extracted by selfing the three kinds of heterozygotes. In heterozygotes with certain r^r alleles, on the other hand, a modified R^r appears either not to revert, or to revert less rapidly and regularly.

The various R alleles in question had been incorporated previously into inbred W22, and so were on a uniform and relatively homozygous background when tested. The various endosperm phenotypes were scored in the Rrr form following testcrosses to two other inbred lines, 4Co63 (r^gr^g) and W23 (r^gr^g). A predetermined aleurone area on each kernel, approximately 12 mm^2, was scanned for pigmentation under a binocular microscope at 27X magnification, using a 20 x 20 reticule.

The initial body of experimental data, based on testcrosses on the 4Co63 r^rr^r line, are summarized in the accompanying chart. The symbol R' is used to designate the modified form of R^r arising in R^rR^{st} heterozygotes.

The results presented in the chart, supplemented by those from more recent experiments, may be summarized as follows:

1. All the R^r male gametes formed by R^rR^{st} plants are changed to the R' form, which gives lightly mottled, rather than standard darkly mottled, kernels in testcrosses on r^rr^r.

2. The R' condition subsequently is transmitted by $R'r^r$ ♂♂ through the sporophyte, and reappears in the succeeding generation. It is now known that this holds for a second generation of R'r plants also. R' is transmitted through the ♀ gametophyte also.

(a) Initial testcrosses with 4Co63 rr♀♀ of sibs from R^rR^{st}, selfed, in the W22 inbred line.

P_1	Testcross	Testcross Kernels: Embryo Genotype	Endosperm Genotype	Endosperm Phenotype
W22 R R^{st} Selfed	RR → [rr♀ x RR♂] →	Rr (1)	Rrr	Dark mottled
	RR^{st} → [rr♀ x RR^{st}♂] →	R'r (2)	R'rr	Light mottled
		$R^{st}r$ (3)	$R^{st}rr$	Stippled
	$R^{st}R^{st}$ → [rr♀ x $R^{st}R^{st}$♂] →	$R^{st}r$ (4)	$R^{st}rr$	Stippled

(b) Progeny of the above F_1 testcross kernels (1-4)

	Endosperm (colored kernels only) Genotype	Phenotype
4Co63 rr♀ x F_1 Rr (1) ♂	Rrr	Dark mottled
4Co63 rr♀ x F_1 R'r (2) ♂	R'rr	Light mottled
4Co63 rr♀ x F_1 $R^{st}r$ (3) ♂	$R^{st}rr$	Stippled
4Co63 rr♀ x F_1 $R^{st}r$ (4) ♂	$R^{st}rr$	Stippled
F_1 Rr (1) selfed →	RRR	Self colored
	RRr	Self colored
	Rrr	Dark mottled
F_1 R'r (2) selfed →	R'R'R'	Self colored
	R'R'r	Self colored
	R'rr	Light mottled
F_1 $R^{st}r$ (3 or 4) selfed →	$R^{st}R^{st}R^{st}$	Stippled
	$R^{st}R^{st}r$	Stippled
	$R^{st}rr$	Stippled
F_1 Rr (1) ♀ x rr ♂ →	RRr	Self colored
F_1 R'r (2) ♀ x rr ♂ →	R'R'r	Self colored
F_1 $R^{st}r$ (3 or 4) ♀ x rr ♂ →	$R^{st}R^{st}r$	Stippled

(Plant color symbols are omitted. The 4Co63 inbred line is $\underline{r}^r\underline{r}^r$.)

3. Most of the kernels on selfed ears borne by $\underline{R}'\underline{R}'$ individuals extracted from $\underline{R}^r\underline{R}^{st}$ plants by selfing are fully pigmented, but an occasional seed is darkly mottled.

4. Pollen from these $\underline{R}'\underline{R}'$ homozygotes results in darkly mottled kernels when used on 4Co63 $\underline{r}^r\underline{r}^r$ plants. This shows that $\underline{R}'$ reverts toward the standard level of pigment-producing action in such homozygotes.

5. Reversion of $\underline{R}'$ toward standard $\underline{R}^r$ in $\underline{R}'\underline{R}'$ homozygotes, however, is only partial. This point could not be definitely established in the test matings on 4Co63 because the $\underline{R}'\underline{r}^r\underline{r}^r$ kernels resulting were about as darkly mottled as those formed when this $\underline{r}^r\underline{r}^r$ strain is pollinated by standard $\underline{R}^r\underline{R}^r$. Repetition of the test matings, using a different inbred line, W23 $\underline{r}^g\underline{r}^g$, as the pistillate parent, clearly demonstrated, however, that the $\underline{R}'$ allele in extracted homozygotes, although showing pronounced reversion toward standard $\underline{R}^r$, was still sub-standard in pigment-producing action. Evidently the 4Co63 strain has a much lower threshold for aleurone pigmentation than the W23 inbred.

6. The $\underline{R}'\underline{R}'\underline{R}'$ and $\underline{R}'\underline{R}'\underline{r}^r$ endosperms produced on selfing $\underline{R}'\underline{r}^r$ plants are self-colored, whereas the $\underline{R}'\underline{r}^r\underline{r}^r$ class is weakly pigmented. This suggests that two (or three) $\underline{R}'$ alleles in a nucleus promote reversion toward the standard $\underline{R}^r$ condition. There is little that can be said at present, however, concerning the reversion process, except that it occurs regularly under certain circumstances.

7. No regular change in the $\underline{R}^{st}$ allele has been detected thus far in $\underline{R}^r\underline{R}^{st}$ heterozygotes. The same is true for the $\underline{R}^{stL}$ and $\underline{R}^{mb}$ alleles in $\underline{R}^r$ heterozygotes.

8. $\underline{R}'$ male gametes again are regularly produced by F_1 hybrids between $\underline{R}'\underline{R}'$ and $\underline{R}^{st}\underline{R}^{st}$ plants extracted from $\underline{R}^r\underline{R}^{st}$ individuals by selfing.

9. The influence of $\underline{R}^{st}$ on the plant color component of the $\underline{R}^r$ allele in $\underline{R}^r\underline{R}^{st}$ heterozygotes currently is under study. If there is any effect on plant color it is of a much lower order of magnitude than that in the aleurone.

10. Seventeen unrelated $\underline{rr}$ inbred lines have been tested for expression of the $\underline{R}'$ phenotype after pollination with $\underline{R}^r\underline{R}^{st}$, using standard $\underline{R}^r\underline{R}^r$ as the control. All the lines regularly showed the change.

11. The light stippled allele ($\underline{R}^{stL}$) uniformly produces a more extreme effect on $\underline{R}^r$ than $\underline{R}^{st}$ in heterozygotes. The modified $\underline{R}^r$ allele in this case is termed $\underline{R}''$.

12. Similarly, $\underline{R}^{mb}$ markedly reduces the pigment-producing potential of $\underline{R}^r$ in $\underline{R}^r\underline{R}^{mb}$ heterozygotes.

13. $\underline{R}^r$ is stable in heterozygotes with $\underline{r}^r$ and $\underline{r}^g$ in the two cases thus far tested.

14. The differences in aleurone pigmentation resulting when pollen from $\underline{R}^r\underline{R}^{st}$, $\underline{R}^r\underline{R}^{stL}$, and $\underline{R}^r\underline{R}^{mb}$ plants is used in testcrosses on $\underline{rr}$ individuals shows that the changes induced in $\underline{R}^r$ in these respective heterozygotes not only are directed but are specific also.

15. The kernels on selfed R"R" ears (plants derived from $\underline{R}^r\underline{R}^{stL}$ by selfing) vary in pigmentation from self color to rather light mottling. Pollen from such R"R" plants used in matings both with 4Co63 $\underline{r}^r\underline{r}^r$ and W23 $\underline{r}^g\underline{r}^g$ results in a higher proportion of colorless kernels than is given by R'R' pollen (R'R' plants derived from $\underline{R}^r\underline{R}^{st}$ by selfing). This is further evidence for (a) transmission of the modified R's through both male and female gametophytes and (b) specificity of the effects of $\underline{R}^{st}$ and $\underline{R}^{stL}$ in $\underline{R}^r$ heterozygotes.

16. A few self-colored mutants from $\underline{R}^{st}$ either were not altered in pigment-producing potential, or only slightly, in heterozygotes with $\underline{R}^{st}$. This material has not yet been scored quantitatively.

17. Similarly, such self-colored mutants in heterozygotes with $\underline{R}^r$ have little, or possibly no, effect on the determinative action of $\underline{R}^r$. In this case also detailed measurements of pigmentation have not yet been made.

18. The changes in $\underline{R}^r$ action arising in heterozygotes with $\underline{R}^{st}$, $\underline{R}^{stL}$, and $\underline{R}^{mb}$ cannot be explained in terms of any of the known kinds of plasmids. The possibility has not yet been excluded, however, that a novel type of pollen-transmitted plasmid is involved.

R. A. Brink

UNIVERSITY OF ZAGREB
Institute of Plant Breeding and Genetics
Zagreb, Yugoslavia

1. Numbers of chromosomes and knobs in some inbred lines from native varieties of Zea mays var. rostrata.

From the native varieties of Zea mays rostrata which are cultivated at the coast of the northern part of the Yugoslav Adriatic Sea, some inbred lines have been developed and the number of chromosomes and of the knobs on the chromosomes studied, using typical rostrata lines. Although the varieties of rostrata type are grown by the farmers on small fields surrounded by flint maize /n = 10 chromosomes and 2-3 knobs/ the mentioned inbreds have n = 10 + 1 to 10 + 3 chromosomes and

11 to 20 knobs. From the cytogenetical analysis of the Zea mays rostrata x Zea mays indurata it can be concluded that there must be a linkage between rostrata type of kernels and a high number of knobs and perhaps also B chromosomes.

Inbred No.	Chromosome number	Knob number
318	10 + 1	12
332	10 + 2	18
335	10 + 2	16
336	10 + 2	16
341	10 + 1	14
343	10 + 2	16
351	10 + 2	14
353	10 + 1	12
354	10 + 3	20
355	10 + 3	18
356	10 + 2	16
358	10 + 3	18
360	10 + 2	15
364	10 + 1	13
366	10 + 2	17

There are variations between the inbreds as well as between the sporocytes of the same plant with respect to chromosomes and knob number.

2. Cytoplasmic male sterility due to grafting of embryos.

Hundreds of grafts of embryos from white kernels to embryos of yellow kernels have been made. For this purpose germinated kernels have been used. The upper part of the embryo of white kernels has been transplanted to the lower part of the embryo of yellow kernels. The latter embryo has been left in the endosperm. The grafts have been wrapped in paraffin. From some hundreds of grafts only two plants have developed and these were cytoplasmic male sterile.

A. Tavčar

III. REPORT ON MAIZE COOPERATIVE

Adequate supplies of improved stocks of most of this project's original collection of genetic traits are now available. A partial conversion of all stocks to the inbred lines M14, W23, and Oh51A is under way. In most cases increases from F_2 segregants have been obtained, and further crosses to the respective inbred lines have been made.

With stabilization of seed supplies now largely accomplished, increased attention is being given to further necessary activities of the project. Among these is the development of improved multiple tester combinations incorporating useful new genetic markers. This in turn is dependent upon the chromosome placement and mapping of the considerable collection of unplaced genes that have accumulated during recent years. Extensive work in chromosome placement and mapping is in progress making use of multiple genetic testers, trisomics, A-B translocations, and chromosome rearrangements.

A large number of traits have been added to the collection during the past year. Most of these are as yet untested and must be checked for allelism with similar known traits. Approximately one hundred clear-cut traits have been obtained from commercial hybrid corn companies in the Midwest. In addition, during the past season 220 maize introductions from the collection maintained at the Plant Introduction Station, Ames, Iowa were grown at Urbana. Most of these represent collections of open-pollinated sources from Canada or from Midwest or Southwest United States. In our plantings each accession was thinned to 45 plants. Observations were made on these plantings during the growing season and a number of mature plant traits noted. Dr. E. R. Leng of the Agronomy Department took agronomic notes on the plantings and made several crosses of each accession to a tester stock to determine general combining ability. It is planned that some of these will be placed in yield tests next year. In addition, each accession was routinely self-pollinated to uncover recessive traits. A total of 4466 selfed ears were obtained. These have been checked for kernel and ear traits and are being tested in the greenhouse for seedling traits. Assistance in running seedling tests of this material is gratefully acknowledged to Dr. Peter Peterson, Iowa State College, Dr. Arnold Wellwood, Ontario Agricultural College, Mr. David Walden, Cornell University, and Mr. Janson Buchert, Connecticut Agricultural Experiment Station. Of the total of 3293 selfed ears from 140 accessions which were tested here, perhaps one-fifth segregated either kernel or seedling traits. When adjustments are made for multiple occurrence of similar traits within a given accession and for those traits not genetically useful, the number of potentially valuable new traits is considerably diminished, though still sizable.

Linkage tests during the past summer indicated that *at* and *si* are very closely linked to *Y_1*. *Ms_1* and the new trait "ms-si" were previously found to be very close to *Y_1*. In view of the similar phenotypes of all

four of these separately described traits, possible allelism is being checked. Intercrosses of $\underline{bt}_2$ (Chromosome 4) and Singleton's "bt_4" indicate allelism. The trait $\underline{h}$ (soft starch) and a mutable pale-green have been found to be closely linked. Neither trait is located. The trait Kn, which is ordinarily classified in the mature plant stage by characteristic "knotting" of the vascular bundles, may also be classified with fair accuracy at much earlier stages by a broadening and thickening of the midrib adjacent to the ligule. In this respect, the homozygote appears more extreme than the heterozygote.

Requests for genetic stocks should be sent to the Botany Department, University of Illinois. Many combinations of traits not specifically listed in the accompanying catalogue of stocks are available or may be readily derived. In the case of multiple chromosome testers, for example, various combinations having fewer traits than those listed are available and will usually be more vigorous. Also, traits such as aleurone color, plant color, pericarp color, y, wx, su, etc., are widespread in the stocks and may often be obtained in specific desired combinations with a wide variety of other traits. Following is a listing of Cooperative stocks:

Chromosome 1

ad_1 bm_2; seg p^{RR}, Kn
an_1 bm_2; seg sr, p^{RR}, br_1, gs_1
as
br_1 f_1 bm_2; seg p^{RR}, an_1, gs_1
br_1 f_1 bm_2; seg p^{WW}, an_1, gs_1
Hm
Kn
lw_1
necrotic 8147-31
(pCR)
(pCW)
p^{mo}
(por)
p^{RR} ad_1 an_1
p^{RR} ad_1 bm_2
p^{RR} an_1 bm_2; seg br_1, ad_1
p^{RR} an_1 gs_1 bm_2
p^{RR} gs_1 bm_2; seg br_1, f_1, an_1
p^{VV}
p^{WR}; seg ad_1, an_1 (coupling)
p^{WR} bm_2
p^{WR} gs_1 bm_2
p^{WW} br_1 f_1 bm_2
p^{WW} hm br_1 f_1
sr p^{WR} an_1 bm_2
sr zb_4 p^{WW}
seg ts_2 p^{WW} bm_2; may seg zb_4 (coupling)

Chromosome 1 (Cont'd)

Ts_6
Vg
vp_5
vp_8
zb_4 ms_{17} PWW
zb_4 PWW bm_2
zb_4 PWW br_1
zb_4 PWW br_1 bm_2
zb_4 ts_2; seg PWW

Chromosome 2

al lg_1
al lg_1 gl_2 B sk
al lg_1 gl_2 b sk
ba_2
fl_1
lg_1 gl_2 B
lg_1 gl_2 b
lg_1 gl_2 b fl_1 v_4
lg_1 gl_2 gs_2 b v_4
lg_1 gl_2 gs_2 b v_4 Ch; may seg sk
lg_1 gl_2 B sk v_4
lg_1 gl_2 b sk v_4
lg_1 gl_2 B v_4
lg_1 gl_2 b v_4
lg_1 gl_2 b v_4 Ch; may seg sk
lg_1 gs_2 v_4
seg ts_1 v_4 (coupling); may seg lg_1, gl_2
ws_3 lg_1 gl_2 B
ws_3 lg_1 gl_2 b
ws_3 lg_1 gl_2 b fl_1 v_4; A_1 A_2 C R

Chromosome 3

A_1 ga_7; A_2 C R
a_1 et; A_2 C R Dt
a_1 sh_2; A_2 C R Dt
a_1 sh_2; A_2 C R dt
a_1 sh_2 et; A_2 C R Dt
A^{d-31}; A_2 C R
a^P et; A_2 C R Dt
a_{x-1}; A_2 C R
a_{x-3}; A_2 C R
a_{x-3} et; A_2 C R
ba_1
Cg

Chromosome 3 (Cont'd)

(cr$_1$) ts$_4$ na$_1$
d$_1$
d$_1$ gl$_6$
d$_1$ lg$_2$
d$_1$ Lg$_3$
d$_1$ pg$_2$
d$_1$ Rg
d$_1$ ts$_4$ lg$_2$
d$_2$
g$_2$
gl$_6$
gl$_6$ lg$_2$ a$_1$ et; A$_2$ C R Dt
gl$_6$ Lg$_3$
gl$_6$ Rg
gl$_6$ v$_{17}$
Lg$_3$
ms$_3$
pg$_2$
pm
ra$_2$
ra$_2$ lg$_2$ pm
ra$_2$ pm
Rg
rt; A$_1$ A$_2$ C R
sh$_2$
ts$_4$ na$_1$
vp$_1$

Chromosome 4

bm$_3$
bt$_2$
de(7 or 16?)
Ga$_1$ Su$_1$
ga$_1$ su$_1$
gl$_3$
j$_2$
la su$_1$ gl$_3$
la su$_1$ Tu gl$_3$
lo Su$_1$
lo su$_1$
lw$_4$; lw$_3$
o$_1$
sp$_1$ Su$_1$
sp$_1$ su$_1$
st
su$_1$^{am}

Chromosome 4 (Cont'd)

su$_1$ bm$_3$
su$_1$ gl$_3$
su$_1$ gl$_4$
su$_1$ j2 gl$_3$
su$_1$ Tu
su$_1$ Tu gl$_3$
su$_1$ zb$_6$
su$_1$ zb$_6$ gl$_3$
Ts$_5$
Ts$_5$ su$_1$
Tu gl$_3$
v$_8$

Chromosome 5

a$_2$ pr; A$_1$ C R
a$_2$ bm$_1$ pr v$_2$; A$_1$ C R
a$_2$ bt$_1$ pr; A$_1$ C R
bm$_1$ bt$_1$ bv$_1$ pr; (a$_1$) A$_2$ C R
bm$_1$ pr; A$_1$ A$_2$ C R
bm$_1$ pr ys$_1$; seg v$_2$; A$_1$ A$_2$ C R
bm$_1$ yg$_1$
bt$_1$
bt$_1$ pr; A$_1$ A$_2$ C R
Ga Bt$_1$
ga bt$_1$
gl$_5$
gl$_8$
gl$_{17}$ a$_2$ bt$_1$ v$_2$; A$_1$ C R
gl$_{17}$ v$_2$
intensifier of pr closely linked to bt$_1$
lw$_2$
lw$_3$; lw$_4$
na$_2$
pr; A$_1$ A$_2$ C R
shfl = "sh$_4$"
tn
v$_3$ pr; A$_1$ A$_2$ C R
v$_{12}$
vp$_2$ gl$_8$
vp$_2$ pr; A$_1$ A$_2$ C R
vp$_7$
vp$_7$ pr; A$_1$ A$_2$ C R

Chromosome 6

pb_4
po y
Y at si
y at si
Y L_{10}
y l_{10}
y ms(1)
y pg_{11} pl; A_1 A_2 C R wx pg_{12}
Y Pl; A_1 A_2 b P^{RR}
y pl Bh; A_1 A_2 B sh_1 wx
y Pl; seg luteus on chrom 6; A_1 A_2 b
Y Pl sm py; A_1 A_2 b P^{RR}
Y pl; seg w_1
y Pl; seg w_1; A_1 A_2 b P^{RR}
y pl; seg w_1
y; seg w_1, luteus on chrom 6; carries P^{RR}
y su_2
"male sterile-silky"
"orobanche" (seedling)
"ragged" (seedling)
"white-8522" (seedling)
"white-8896" (seedling)

Chromosome 7

Bn_1
gl_1 sl Bn_1
gl_1; y A_1 A_2 C R pr
gl_1; Y wx A_1 A_2 C R Pr
Hs
ij
in; pr A_1 A_2 C R
o_2
o_2 gl_1 sl Bn_1
o_2 ra_1 gl_1
o_2 v_5 ra_1 gl_1
o_2 v_5 ra_1 gl_1; seg Hs
ra_1 gl_1
Tp_1
v_5 gl_1 Tp_1
va_1
vp_9 gl_1; wx

Chromosome 8

mn
v_{16} ms8 j_1
v_{16} ms_8 j_1; l_1
"necrotic-6697" (seedling)
"sienna-7748" (seedling)

Chromosome 9

au_1 au_2
Bf_1
bk_2
bk_2 Wc
bm_4
c sh_1 wx; y A_1 A_2 R b Pl
c sh_1 wx gl_4(Coop); A_1 A_2 R
c sh_1 wx gl_{15}; A_1 A_2 R
c wx; y A_1 A_2 R b Pl
c wx bk_2; A_1 A_2 R
Dt_1 (See Chromosome 3 stocks)
gl_{10}
I wx; A_1 A_2 R Pr B pl
I wx; A_1 A_2 R pr B pl
l_7
ms_2
ms_2 sh_1; A_1 A_2 C R
ms_{20}
sh_1 wx d_3
sh_1 wx l_7
sh_1 wx pg_{12}; y A_1 A_2 B pl pg_{11}
sh_1 wx v_1
wx^a
wx ar
wx Bf_1
wx da_1; A_1 A_2 C R
wx g_4
wx l_6
wx pg_{12}; y A_1 A_2 B pl pg_{11}

Chromosome 10

a_3 g_1 R; A_1 A_2 C b pl
bf_2
du_1
g_1
g_1 l_2
g_1 rg; A_1 A_2 C
gl_9

Chromosome 10 (Cont'd)

l_1; v_{16} ms_8 j_1
li g_1 R; A_1 A_2 C
li g_1 r; A_1 A_2 C
li g_1 r; A_1 A_2 C; carries abnormal 10
nl_1 g_1 R; A_1 A_2 C
Og R; A_1 A_2 C B Pl; may carry B chromosomes
R^{mb}; A_1 A_2 C
R^{nj}; A_1 A_2 C
R^{st}; A_1 A_2 C
v_{18}
w_2
zn
"oil yellow" (seedling)
"Waseca stripe" (plant)

Stocks of unplaced genes

an_2
bk_1
cl
de_{17}
du_2
dv
dy
fl_2
gl_{11}
gl_{12}
gl_{13}
gl_{14}
gl_{16}
gl_g
h
ms_5
ms_6
ms_7
ms_9
ms_{10}
ms_{11}
ms_{12}
ms_{13}
ms_{14}
Mt
New starchy
ra_3
Rs_1
rs_2
"sh_5"

Stocks of unplaced genes (Cont'd)

Ts_3
tw_1
tw_2
$v13$
$v17$
va_2
$vp6$
wa
ws_1 ws_2
zb_1
zb_2
zb_3

Multiple gene stocks

(A_1 A_2 C R) Pr
" Pr wx
" Pr wx y
" Pr wx Y gl_1
" pr
" pr wx
" pr wx y
" pr su_1
" Pr B Pl; seg Og; may carry B chromosomes
A_1 A_2 C Rg Pr B pl lg_1 fl_1 y
(A_1 A_2 c R Pr) su_1
" y wx
" y sh_1 wx
(A_1 A_2 C r Pr) su_1
" su_1 y g_1
" y wx
" y sh_1 wx
bm_2 lg_1 a_1 su_1 pr Y gl_1 j_1 wx g_1
colored scutellum
lg_1 su_1 bm_1 y gl_1 j_1
su_1 y wx a_1 A_2 C Rg pr
wx lg_1 gl_2 b v_4
y su_1 ra_1 gl_1
y wx gl_1

Popcorns useful in studies of Ga factors

Amber Pearl
Black Beauty
Hulless
Ladyfinger

Popcorns useful in studies of Ga factors (Cont'd)

Ohio Yellow
Red
South American
Supergold

Exotics and varieties

Argentine Popcorn
Black Mexican Sweet Corn (without B chromosomes)
Black Mexican Sweet Corn (with B chromosomes)
Gourdseed
Maiz chapolote
Papago Flour Corn
Parker's Flint
Strawberry Popcorn
Tama Flint
Tom Thumb Popcorn
Zapaluta chica

Primary trisomics

Stocks of trisomics 3, 4, 5, 6, 7, 8, 9, and 10 are available. Stocks of trisomics 1 and 2 are not yet represented in the collection. An effort is being made to mark the trisomics genetically as an aid in selecting trisomic plants. Various procedures are being used, depending upon the markers available in each instance. In most cases, the relative effectiveness of alternative procedures remains to be tested. Among the procedures being tested are the use of closely-linked markers, dosage effects of alleles, and multiple allelic series. The latter method is especially valuable in the cases of chromosomes 3 and 10 where multiple allelic series are available at the A_1 and R loci. In the former case, pale kernels with dots are being selected from the cross $a^p\ a^m\ a^{st}$ X a^{st} Dt. In the case of trisomic 10, kernels with both R^{nj} and R^{st} phenotype are selected from the cross $R^{nj}\ R^{st}\ r$ X r. Trisomic 9 plants of the constitution Wx Wx wx may be recognized by the ratio of Wx : wx pollen.

Chromosome rearrangements

A selected group of inversions and reciprocal translocations, whose breakpoints mark most of the regions of the ten chromosomes, is being maintained primarily for use in determining the chromosome locations of new traits. Two inversions, Inv 2a and Inv 9a are included. In all cases, the rearrangements are marked with closely-linked endosperm or

seedling traits. Most of the translocations are closely linked to wx, the remainder being linked to su_1, y, gl_1, gl_2, or lg_1. The list is as follows:

Inversions

lg_1 or gl_2 Inv 2a (also available with Ch)
wx Inv 9a

Reciprocal translocations

wx 1-9c
wx 1-9 4995-5
wx 2-9b
wx 3-9c
wx 3-9 5775-1
wx 4-9b
wx 4-9 5657-2
wx 4-9g
wx 5-9a
wx 5-9c
wx 5-9 4817-7
wx 5-9 5614-3
wx 6-9a
wx, y 6-9b
wx 6-9 4505-4
wx 6-9 4778-9
wx 7-9a
wx or gl_1 7-9 4363-1
wx 8-9d
wx 8-9 6673-6
wx 9-10b
su 1-4a (also available with P^{RR})
su 1-4d (also available with P^{RR})
su 4-5j
su, y 4-6a
su 4-8a
su, R 4-10b
y 1-6c (also available with P^{RR})
gl_2 2-3c
gl_2 2-3 5304-3
gl_2 2-6b
gl_2, R 2-10b
gl_1 6-7 4545-5

Stocks of A-B chromosome translocations

B-1a	1L .2	Proximal to Hm
B-1b	1S .05	
B-3a	3L .1	
B-4a	4S .25	Proximal to su_1
B-7b	7L .3	Proximal to ra_1
B-9b	9S .4	Between C and wx; close to wx
B-10a	10L .35	Proximal to g_1

Earl B. Patterson

IV. RECENT MAIZE PUBLICATIONS

Agble, W. K. The inheritance of maturity as measured by time of silking; and other character associations in Zea mays. Diss. Abstr. 15: 924. 1955. Abstr.

Alexander, D. E. The genetic induction of autotetraploidy: A proposal for its use in corn breeding. Agron. J. 49: 40-44. 1957.

Alldridge, N. A. and W. G. Whaley. The pattern of respiration and carbohydrate level in germinating maize. Plant Physiology Supplement 31: 33. 1956. Abstr.

Anderson, E. G. The application of chromosomal techniques to maize improvement. Brookhaven Symp. Biol. 9: 23-37. 1956.

Andrew, R. H. Some associations of sweet corn yield with climate and maturity. Agronomy Abstracts p. 76. 1956.

_____, F. P. Ferwerda, and A. M. Strommen. Maturation and yield of corn as influenced by climate and production technique. Agron. Jour. 48: 231-236. 1956.

Avila, A. Study on the content of carotene and tryptophane in commercial maizes. Rev. invest. agric. B. Aires 6: 417-423. 1952.

Baker, R. From lines to commercial corn. Proc. 10th Ann. Hybrid Corn Industry-Research Conference 10: 14-17. 1955.

Ball, H. J. Effect of insecticides on corn root growth. J. Econ. Entom. 49: 230-232. 1956.

_____. Corn rootworm control for surface-planted and listed corn. J. Econ. Entom. 49: 709. 1956.

Ballesteros, O. Q., I. S. Santos and F. A. Aquilizan. Reduction in grain yield from the F_1 to the F_2 of parental single crosses and double-cross hybrids. Philippine Agriculturist. In press.

Beevers, H. Intermediates of the pentose pathway as respiratory substrates. Plant Physiology 31: 339-346. 1956.

Bianchi, A. Defective endosperm mutants from maize-teosinte derivatives. Records of the Genetics Society of America. 25: 634. 1956. Abstr.

_____. Defective caryopsis factors from maize-teosinte derivatives. I. Origin, description and segregation. Genetica Agraria 7: 1-38. 1957.

Bianchi, A. and A. Bottazzi. Meccanismi genetici nel tempo di fioritura in un incrocio di Zea mays. Genetica Agraria 5: 213-228. 1955.

Blackwood, M. The inheritance of B chromosomes in Zea mays. Heredity 10: 353-366. 1956.

Blanco Gonzalez, M., A. S. Veiguinha, and J. L. Blanco Gonzalez. Selection of maize lines with sweet stems and the yield of their hybrids, in relation to the dual use of the grain and plants. Results of studies made from 1951 to 1954. Agron. lusit. 17: 61-86. 1955.

Boothroyd, C. W., H. J. Otto, and J. M. Barnes. Stalk rot of corn in New York, 1954. U. S. D. A. Plant Disease Reporter 39: 380. 1955.

Briggle, L. W. Interaction of cytoplasm and genes in male-sterile corn crosses involving two inbred lines. Agron. J. 48: 569-573. 1956.

_____. A comparison of cytoplasmic-genotypic interactions in a group of cytoplasmic male sterile corn types. Iowa St. Coll. J. Sci. 29: 385-386. 1955. Abstr.

Brink, R. A. A regularly reversible change in determinative action of the R locus in maize. Records of the Genetics Society of America 25: 636. 1956. Abstr.

_____. Effect on endosperm phenotype in maize of heterozygosity at the R locus in the staminate parent. Science 123: 672. 1956. Abstr.

_____. A genetic change associated with the R locus in maize which is directed and potentially reversible. Genetics 41: 872-890. 1956.

Brunson, A. M. and J. D. Escarlos. Sweet corn in the Philippines. Philippine Agriculturist 39(9).

Burnham, C. R. Chromosomal interchanges in plants. Bot. Rev. 22: 419-552. 1956.

Campbell, A. D. Electrophoretic analyses of protein fractions extracted from an inbred and a hybrid variety of corn. Diss. Abstr. 16: 442-443. 1956. Abstr.

Catcheside, D. G. Double reduction and numerical non-disjunction in tetraploid maize. Heredity 10: 205-218. 1956.

_____. The genetics of B chromosomes in maize. Heredity 10: 345-352. 1956.

Clark, J. A. Collection, preservation and utilization of indigenous strains of maize. Econ. Bot. 10: 194-200. 1956.

Cleland, R. E. Report of the committee on preservation of indigenous strains of maize. Proc. 3rd Ann. Meeting Agr. Res. Inst. Nat. Acad. Sci.-Nat. Res. Counc. 1954: 36-37 and Proc. 4th Ann. Meeting 1955: 28.

Clem, M. A., C. C. Mosier, and G. F. Sprague. Simplified punched card procedures for predicting double cross performance. Agron. J. 48: 319-320. 1956.

Cockerham, C. C. Analysis of quantitative gene action. Brookhaven Symp. Biol. 9: 53-68. 1956.

Comstock, R. E. Theory of quantitative genetics: Synthesis. Cold Spring Harbor Symp. Quant. Biol. 20: 93-102. 1955.

_____ and H. F. Robinson. Findings relative to reciprocal recurrent selection. Proc. Int. Genetics Symp. in Tokyo and Kyoto, Japan. 1956.

Crane, P. Factors affecting resistance to Pythium seedling blight of maize incited by Pythium ultimum. Agron. J. 48: 365-368. 1956.

Curtis, J. J., A. M. Brunson, J. E. Hubbard, and F. R. Earle. Effect of the pollen parent on oil content of the corn kernel. Agron. J. 48: 551-555. 1956.

Dios, R. and G. Dios. Content of macro- and micro-nutrients in the grain of some maize hybrids cultivated in Galicia. An. Edafol. Fisiol. Veg. 15: 231-252. 1956.

Duvick, D. N. Allelism and comparative genetics of fertility restoration of cytoplasmically pollen sterile maize. Genetics 41: 544-565. 1956.

Edwardson, J. R. Cytoplasmic male-sterility. Bot. Rev. 22: 696-738. 1956.

Ellis, B. G., C. J. Knauss, and F. W. Smith. Nutrient content of corn as related to fertilizer application and soil fertility. Agron. J. 48: 455-460. 1956.

Emmerling, M. H. Unequal crossing over between elements of the R complex in Zea mays. Records of the Genetics Society of America 25: 641. 1956. Abstr.

Everett, H. L., R. G. Wiggans, and H. J. Otto. An Adapted field corn hybrid produced the easy way. Farm research 22: 2. 1956.

Faberge, A. C. The analysis of induced chromosome aberrations by maize endosperm phenotypes. Z. indukt. Abstamm.- u. VererbLehre 87: 392-420. 1956.

_____. Forecasting the rate of induced marker loss for maize endosperm. Records of the Genetics Society of America 25: 642. 1956. Abstr.

Ferwerda, F. P. Monoploids as a starting point for homozygous lines in maize. Erfelijkh. i. Prakt. 16: 5-6. 1955.

Fleming, A. A., T. H. Rogers and T. A. Bancroft. Field plot technique with hybrid corn under Alabama conditions. Agron. J. 49: 1-4. 1957.

Floyd, E. H. and L. D. Newsom. Protection of stored corn with lindane-impregnated sawdust. J. Econ. Entom. 49: 753-756. 1956.

Fradkin, C. W. and R. A. Brink. Effect of modulator on the frequency of endosperm mosaics in maize. Amer. Jour. Bot. 43: 267-273. 1956.

_____ and _____. Crossing over in maize in the presence of the transposable factors Activator and Modulator. Genetics 41: 901-907. 1956.

Freeman, W. H. Evaluating hybrids in the south. Proc. 10th Ann. Hybrid Corn Industry-Research Conference 10: 24-31. 1955.

French, O. C., R. G. Wiggans, H. L. Everett, and R. B. Musgrave. Researchers study ear corn storage. Farm Research 21: 14. 1955.

Genter, C. F., Eheart, J. F. and Linkous, W. N. Effects of location, hybrid, fertilizer and rate of planting on the oil and protein contents of corn grain. Agron. J. 48: 63-67. 1956.

Gingrich, J. R. and M. B. Russell. Effect of soil moisture tension and oxygen concentration on the growth of corn roots. Agron. J. 48: 517-521. 1956.

Gopinath, D. M. and C. R. Burnham. A cytogenetic study in maize of deficiency-duplication produced by crossing interchanges involving the same chromosomes. Genetics 41: 382-395. 1956.

Gosi, L. Il Mais della varieta culturale "Precoce di Bagnolo". Genetica Agraria 5: 1-44. 1955.

Grogan, C. O. Detasseling responses in corn. Agron. J. 48: 247-249. 1956.

_____ and M. S. Zuber. Missouri Hybrid Popcorn Yield Trials. Univ. of Mo. Coll. of Agric. Exp. Sta. Bul. 671. 1956.

Grogan, C. O. and M. S. Zuber. A comparative study of topcross tester parents of maize. Agron. J. 49: 68-72. 1957.

Haines, R. G. Evidence of lindane translocation in corn plants. J. Econ. Entom. 49: 563-564. 1956.

Harada, K., M. Murakami, A. Fukushima and M. Nakazima. Studies on the breeding of forage crops. I. Studies on intergeneric hybridization between Zea and Coix. Saikyo Daigaku Gakujutsu Hokoku, Nogaku/Sci. Rep. Saikyo Univ., Agric. 6: 139-145. 1954.

Harvey, P. H., D. L. Thompson, and T. T. Hebert. Reaction of inbred lines of corn to brown spot. Plant Dis. Reptr. 39: 973-976. 1955.

Haskell, G. Internode patterns, adaptation and the origins of sweetcorn. Genetica 28: 308-344. 1956.

Haynes, J. L. and J. D. Sayre. Response of corn to within-row competition. Agron. J. 48: 362-365. 1956.

Hoen, K. and R. H. Andrew. Osmotic value of germinating corn. Agronomy Abstracts p. 78. 1956.

Hooker, A. L. Correlation of resistance to eight Pythium species in seedling corn. Phytopath. 46: 175-176. 1956.

_____. Association of resistance to several seedling, root, stalk and ear diseases in corn. Phytopath. 46: 379-384. 1956.

Horner, E. S., Fred H. Hull, W. H. Chapman, and H. W. Lundy. Progress report on recurrent selection for specific combining ability in corn. Proceedings Southern Agricultural Workers, Louisville, 52: 36-37. 1955.

Hume, A. W., V. A. Dirks and D. B. Shank. Date and rate of corn planting. So. Dak. Agr. Expt. Sta. Bull. 455. 1956.

Jones, D. F. Genic and cytoplasmic control of pollen abortion in maize. Brookhaven Symp. Biol. 9: 101-113. 1956.

Jugenheimer, R. W. Hybrid maize and sorghum in the Punjab of India. Ill. Agr. Exp. Sta. Mimeo. 1956.

_____ and A. F. Troyer. Experimental corn hybrids tested in 1955. Ill. Agr. Exp. Sta. Bul. 597. 1956.

_____ and K. E. Williams. Experimental corn hybrids tested in 1956. Ill. Agr. Exp. Sta. Bul. 606. 1957.

Kay, R. E. and B. O. Phinney. Plastid changes in the early seedling leaves of Zea mays L. Plant Physiology 31: 226-230. 1956.

_____ and _____. The control of plastid pigment formation by a virescent gene, pale-yellow-1, of maize. Plant Physiology 31: 415-419. 1956.

Konzak, C. F. and W. R. Singleton. The effects of thermal-neutron radiation on mutation of endosperm loci in maize. Proc. Nat. Acad. Sci. 42: 78-83. 1956.

_____ and _____. The mutation of linked maize endosperm loci induced by thermal-neutron, x-, gamma, and ultraviolet radiation. Proc. Nat. Acad. Sci. 42: 239-244. 1956.

Kramer, H. H., R. L. Whistler and E. G. Anderson. A new gene interaction in the endosperm of maize. Agron. J. 48: 170-172. 1956.

Lang, A. L., J. W. Pendleton and G. H. Dungan. Influence of population and nitrogen levels on yield and protein and oil contents of nine corn hybrids. Agron. J. 48: 284-289. 1956.

Leone, I. A., E. Brennan and R. H. Daines. Atmospheric fluoride: its uptake and distribution in tomato and corn plants. Plant Physiology 31: 329-333. 1956.

Longley, A. E. The origin of diminutive B-type chromosomes in maize. Amer. Jour. Bot. 43: 18-21. 1956.

Lonnquist, J. H. and D. P. McGill. Performance of corn synthetics in advanced generations of synthesis and after two cycles of recurrent selection. Agron. J. 48: 249-253. 1956.

Manrique Chavez, A. and A. Grobman. Duration of receptivity of the pistillate spikelets in maize and the factors that affect it. Agronomia, Lima 20: 50-58. 1955.

Mazoti, L. B. Spontaneous hereditary variation in maize. Rev. invest. Agric. B. Aires 6: 1-27. 1952.

Mehrotra, H. N. Inheritance of foliage leaf number in maize. Diss. Abstr. 15: 315-317. 1955. Abstr.

Mesa Bernal, D. Where did maize originate? V. and VI. Agric. trop. 11: 941-946 and 12: 87-90. 1956.

_____. Geological, archeological and botanical information on the origin of maize. Agric. trop. 12: 229-240. 1956.

Mesa Bernal, D. The origin of maize in Mexico and Guatemala. Agric. trop. 12: 287-298. 1956.

Morgan, D. T. Asynapsis and plasmodial microsporocytes in maize following x-irradiation of the pollen. Jour. Hered. 47: 269-274. 1956.

Moschini, E. Water consumption and root system of maize. Ann. Fac. Agr. Pisa 16: 209-230. 1955.

Nakamura, N. and S. Tate. Estimation of the number and values of the genes determining combining ability in maize and of the heritability of combining ability. Jap. J. Breeding 6: 46050. 1956.

Neal, N. P. and J. R. Davis. Seed viability of corn inbred lines as influenced by age and condition of storage. Agron. J. 48: 383-384. 1956.

Nelson, R. R. Resistance to the stunt nematode in corn. Plant Dis. Reptr. 40: 635-639. 1956.

Newlin, O. J. Inheritance of fertility restoration in cytoplasmic male-sterile Zea mays. Diss. Abstr. 15: 1478. 1955.

Otto, H. J. and H. L. Everett. Influence of nitrogen and potassium fertilization on the incidence of stalk rot of corn. Agron. Jour. 48: 301-305. 1956.

Penny, L. H. and F. F. Dicke. Inheritance of resistance in corn to leaf feeding of the European corn borer. Agron. J. 48: 200-203. 1956.

Pfahler, P. L., H. H. Kramer and R. L. Whistler. Effect of genes on birefringence end-point temperature of starch grains in maize. Science 125: 441-442. 1957.

Phinney, B. O. Biochemical mutants in maize: Dwarfism and its reversal with gibberellins. Plant Physiology Supplement 31: 20. 1956. Abstr.

_____. Growth response of single-gene dwarf mutants in maize to gibberellic acid. Proc. Nat. Acad. Sci. 42: 185-188. 1956.

Picklum, W. E. Histological and cytological changes in the maize embryo during germination. Iowa St. Coll. J. Sci. 29: 479-480. 1955. Abstr.

Pirovano, A. Effects of competition between pollen of dominant and recessive types in hybrid maize. Ann. Sper. Agr. 10: 539-543. 1956.

Rahman, O. and A. H. Brown. Some phenotypic effects of single gene mutations on respiratory characteristics of maize leaf tissue. Plant Physiology 31: 408-410. 1956.

Rhoades, M. M. Lewis John Stadler. Genetics 41: 1-3. 1956.

Richardson, D. L. The analysis of a compound locus in maize as revealed by genic instability. Diss. Abstr. 16: 220-221. 1956. Abstr.

Robinson, H. F. and R. E. Comstock. Analysis of genetic variability in corn with reference to probable effects of selection. Cold Spring Harbor Symp. Quant. Biol. 20: 127-136. 1955.

_____, _____, A. Khalil and P. H. Harvey. Dominance versus over-dominance in heterosis: evidence from crosses between open-pollinated varieties of maize. Amer. Nat. 90: 127-132. 1956.

Robinson, R. G. and R. S. Dunham. Spray placement in corn after layby. Agron. J. 48: 35-37. 1956.

Rossman, E. C. The stand problem. Proc. 10th Ann. Hybrid Corn Industry-Research Conference 10: 18-23. 1955.

Rubis, D. D. Inheritance of resistance in corn to the European corn borer and to diplodia stalk rot. Iowa St. Coll. J. Sci. 29: 489-490. 1955. Abstr.

Russell, M. B. and R. E. Danielson. Time and depth patterns of water use by corn. Agron. J. 48: 163-166. 1956.

Sayed Galal Sayed. Heterosis in corn; and the role of photosynthesis in the development of Puccinia sorghi Schw. Diss. Abstr. 16: 216. 1956. Abstr.

Schuler, J. F. and G. F. Sprague. Natural mutations in inbred lines of maize and their heterotic effect. II. Comparisons of mother line vs. mutant when outcrossed to unrelated inbreds. Genetics 41: 281-291. 1956.

Schwartz, D. Studies on crossing over in maize and Drosophia. Oak Ridge Symposium on genetic recombination. J. Cell Comp. Physiol. 45: Suppl. 2: 171-188. 1955.

_____ and C. E. Bay. Further studies on the reversal in the seedling height curve at very high levels of ionizing radiations. Amer. Nat. 90: 323-326. 1956.

Shams-ul-Islam Khan. Theoretical aspects of crossing over in T 5-6c in corn, Zea mays L. Cellule 56: 309-327. 1954.

_____. Effect of temperature on crossing over in heterozygous T 5-6c with homozygous inversion in chromosome 5 in maize. Cytologia, Tokyo 20: 150-156. 1955.

Shams-ul-Islam Khan. Effect of temperature on crossing over in heterozygous T 5-6c with normal chromosome 5 in maize. Beitr. Biol. Pfl. 32: 171-183. 1956.

Silva, J. B. Vieira da. Leaf blight and yield in S_1 inbreds of two varieties of maize. S. Afr. J. Sci. 52: 226. 1956.

Singleton, W. R. Mutation breeding. Proc. 10th Ann. Hybrid Corn Industry-Research Conference 10: 32-40. 1955.

Sirks, M. J. A genetical puzzle. Acta bot. neerl. 4: 471-473. 1955.

Smith, R. C. Movement of phosphate into the xylem of corn roots. Plant Physiology Supplement 31: 6. 1956. Abstr.

Sprague, G. F. Problems in the estimation and utilization of genetic variability. C.S.H.S.Q.B. 20: 87-93. 1955.

_____. Replication versus location. Proc. 10th Ann. Hybrid Corn Industry-Research Conference 10: 10-13. 1955.

_____. Corn genetics. Proceedings of the fourth annual meeting of the Agricultural Research Institute. Nat. Acad. Sci.-Nat. Res. Counc. 1955: 60-65.

Stadler, J. K. An analysis of instability at the R locus in maize. Diss. Abstr. 16: 435-436. 1956. Abstr.

Stadler, L. J. and M. H. Emmerling. Relation of unequal crossing over to the interdependence of R^r elements (P) and (S). Genetics 41: 124-137. 1956.

Stein, O. L. The rates of leaf initiation in two dwarfing genes, dwarf-1 and brachytic-2 in Zea mays L. Diss. Abstr. 15: 325-326. 1955. Abstr.

Stowe, B. B., K. V. Thimann and N. P. Kefford. Further studies of some plant indoles and auxins by paper chromatography. Plant Physiology 31: 162-164. 1956.

Stringfield, G. H. Introduction to "techniques in evaluating hybrids". Proc. 10th Ann. Hybrid Corn Industry-Research Conference 10: 7-9. 1955.

Sutô, T. A list of genes in maize (Japanese). Handbook of Genetics (Jap.) 200-225. 1956.

_____ and Y. Yoshida. Characteristics of oriental maize. Land and Crops of Nepal Himalaya 2: 373-530. 1956.

Tavčar, A. Heritable proliferation of tassels, a viviparism in Zea mays L., and its cytological basis. Caryologia Vol. Suppl. 1954.

_____. Methods of breeding hybrid maize in Yugoslavia. Agronomski Glasnik. 1955.

_____. Heterosis in theory and practice. Soc. scientiarum nat. Croatica. 1955.

_____. Somatic mutation of endosperm from indentata to indurata in Zea mays L. and the mode of inheritance. Soc. scientiarum nat. Croatica. 1955.

_____. Combining ability of some Yugoslav inbred lines of maize. Plant Production, Zagreb. 1956.

Thomas, W. Effect of plant population and rates of fertilizer nitrogen on average weight of ears and yield of corn in the south. Agron. J. 48: 228-231. 1956.

_____ and I. J. Johnson. Inheritance of pollen restoration and transmission of cytoplasmic sterility in popcorn. Agron. J. 48: 472-475. 1956.

Urano, K. Studies on the diagnosis of relationships between maize strains using the precipitin reaction. I. On the precipitin reaction between inbred lines of maize. Proc. Crop Sci. Soc. Japan 24: 4-7. 1955.

_____ and K. Odogiri. Studies on the diagnosis of relationships between maize strains using the precipitin reaction. II. On protein constitution in relation to serum reaction. Proc. Crop Sci. Soc. Japan. 24: 7-8. 1955.

_____, Y. Tanaka and S. Kiyosawa. Genecological studies on maize. II. On varietal differences in the content of growth hormone in the maize coleoptile. Proc. Crop Sci. Soc. Japan 23: 110-115. 1954.

Wallace, H. A. Public and private contributions to hybrid corn--past and future. Proc. 10th Ann. Hybrid Corn Industry-Research Conference 10: 107-115. 1955.

_____ and W. L. Brown. Corn and its early fathers. Mich. State Univ. Press 1956.

Warren, L. O. Behavior of Angoumois grain moth on several strains of corn at two moisture levels. J. Econ. Entom. 49: 316-319. 1956.

Waterhouse, W. L. Australian rust studies. XIV. Investigations of rust of maize caused by Puccinia sorghi Schw. Proc. Linn. Soc. NSW 80: 138-141. 1955.

Wellwood, A. A. and L. F. Randolph. Inheritance of differences in pachytene chromosome configuration in maize. Amer. Jour. Bot. 44.

West, C. A. and B. O. Phinney. Properties of gibberellin-like factors from extracts of higher plants. Plant Physiology Supplement 31: 20. 1956. Abstr.

Whiteley, J. R. Cross incompatability in maize. Iowa St. Coll. J. Sci. 29: 530-531. 1955. Abstr.

Wood, D. R. and R. A. Brink. Frequency of somatic mutation to self color in maize plants homozygous and heterozygous for variegated pericarp. Proc. Nat. Acad. Sci. 42: 514-518. 1956.

Zuber, M. S. and W. L. Decker. Effects of 1954 drought on corn. Univ. of Mo. Coll. of Agric. Res. Bul. 604. 1956.

_____ and C. O. Grogan. Hybrid seed corn production. Mo. Agric. Exp. Sta. Bul. 674. 1956.

_____ and _____. Corn hybrids for Missouri. Mo. Agric. Exp. Sta. Bul. 673. 1956.

_____ and _____. Rates of planting studies of corn. Univ. of Mo. Coll. of Agric. Res. Bul. 610. 1956.

_____ and _____. Missouri hybrid corn yield trials for 1956. Mo. Agric. Exp. Sta. Bul. 682. 1956.