MAIZE GENETICS COOPERATION

NEWS LETTER

12

March 6, 1938

Department of Plant Breeding
Cornell University
Ithaca, N. Y.

Vol. 12

MAIZE GENETICS COÖPERATION
DEPARTMENT OF PLANT BREEDING
CORNELL UNIVERSITY
ITHACA, NEW YORK

November 17, 1937

To Maize Geneticists :-

Contributions of material for the annual Maize Genetics Cooperation news letter is hereby requested. Any new linkage data, methods, hypotheses, suggestions, or anything else that you think may be of interest to other maize workers will be incorporated in this news letter. Since it is desirable to have the information presented in a somewhat uniform system, it is suggested that you refer to some of the previous Co-op News Letters for ideas concerning the nature of your write-up. In order to be included in this News Letter your material must be received by the Co-op not later than January 15, 1938.

Several years ago when a number of maize geneticists found that they were unable to get their linkage data published in some of the leading journals, they conceived the idea of combining their relatively small papers into one larger paper and publishing collectively. This suggestion was approved by the Editor of Genetics, and the Secretary of the Maize Genetics Cooperation signified his willingness to collect the individual papers for the publication. But to date only one paper has been received by the Co-op. Perhaps the reason for this lack of response from maize workers has been due to some misunderstanding of the plan. With this possibility in mind, it may be advisable to quote from a recent letter to Dr. Dunn, Editor of GENETICS:

> "The Maize Genetics Cooperation circular letter does not constitute publication and none of the material in it may be quoted except by permission of the author. Much of the material in this Co-op News Letter is not complete, but rather is merely some ideas and indications which the men have obtained in their studies and are willing to pass on to other workers in this field to speed up progress with maize. Some of the material, however, is more complete and should be published so that it will be more readily available to other geneticists. This latter type of material will be included in the Co-op News Letter in the same form as in previous circular letters. But it will also be written up in a different manner to be included in the collective publication.

"The details of the method of handling the material in the proposed collective publication of linkage studies in maize will, of course, have to be worked out cooperatively between the publisher and the Maize Genetics Cooperation. During the several years that this idea of collective publication has been discussed among maize workers, the following plan has been formulated. Each cooperator who has linkage data which he considers useful and of permanent value to other geneticists, shall write a short paper in the same manner as he would if he were to publish independently. Then each of these papers will be sent to the Secretary of the Maize Genetics Cooperation, who will group them into one larger paper with an introduction, etc., and will serve as author of the collective paper. The important point is that each short paper will be an individual and separate unit within this larger paper, with the name and address of the author affixed to it. The Secretary of the Maize Genetics Cooperation shall be responsible for the organization and composition of the whole collective paper, but the respective authors of the 'unit papers' shall be responsible for their data. This means that any citation from the collective publication must include the name of the maize worker who furnished that particular data."

Dr. Dunn has written:

".......there is nothing in the policy of GENETICS to interfere with publication of maize linkage data in the form you suggest. Our numbers early in the year are likely to be the heaviest so May or July publication would fit our schedule best. Submission of the first paper in February would be most convenient for us."

It is suggested that you write your contribution to the News Letter <u>first</u>; then excerpt certain linkage data from it and write a separate papers(s) to be included in the collective publication. The particular data which you select for publication will appear in both the News Letter and the group publication. For further information concerning the general form of a linkage paper, see the Co-op News Letter of March 4, 1936, page 2; or March 23, 1937, page 15.

Sincerely yours,

D. G. Langham

D. G. Langham,
Secretary

MAIZE GENETICS COÖPERATION
DEPARTMENT OF PLANT BREEDING
CORNELL UNIVERSITY
ITHACA, NEW YORK

January 22, 1938

To Maize Geneticists :-

A number of maize geneticists have already sent in their items for the annual Co-op News Letter, and many of you probably have your contributions in the mail now. The final date for the receipt of material for this 1938 Letter is January 31st.

In the circular letter of November 17, 1937, I discussed the proposed collective publication of linkage data in such detail that the cardinal points were apparently lost in the shuffle. In brief, the plan is that linkage papers, any one of which in itself would not be sufficient for separate publication, will be sent to the Secretary of the Maize Genetics Cooperation who will group them in much the same manner as in BIOLOGICAL ABSTRACTS and send them to the Editor of GENETICS for publication. Each unit paper must be written as if it were to be published independently. No alterations or additions will be made by the Secretary of the Co-op.

In order to be included in this collective publication, your paper must be received by the Co-op not later than March 31, 1938.

Sincerely yours,

D. G. Langham

D. G. Langham

Vol. 12

MAIZE GENETICS COÖPERATION
DEPARTMENT OF PLANT BREEDING
CORNELL UNIVERSITY
ITHACA, NEW YORK

March 6, 1938

To Maize Geneticists:-

The material in this letter was obtained from many sources, and has been organized under the following heads:

I. General News Items.
II. Seed Stocks Grown in 1937.
III. Seed Stocks Received For Propagation in 1938.
IV. Miscellaneous Co-op Items.
V. Gene Index of all the Co-op letters.
VI. Chromosome Maps of Maize.
 A. Regular map: few genes, loci fairly definite.
 B. Working map: many genes, loci not well established.

Most of the information in this letter is given as it was received by the Co-op, but a few changes were made in some of the tables to conform to the accepted system of arrangement.

I. General News Items

University of Minnesota, St. Paul, Minn. -

1. Zebra seedling, zb_4, has been located in chromosome 1 by the following studies.

Genes	Phase	XY	Xy	xY	xy	Total	% Recomb.
Zb_4 Br	RS	448	142	152	12	754	31.1
Zb_4 F_1	RS	455	135	158	9	757	28.0
Zb_4 Bm_2	RS	487	103	144	23	757	46.0
Zb_4 P	CS	266	24	5	64	359	6.9

Progeny of 1 ear indicated that the P parent was heterozygous giving the following segregation:

CS	63	30	2	24	199	6.7

2. A culture of ra_2 received from Dr. Brink at Wisconsin proves to be similar to the one I have studied for many years. There is some variability in type of ear, some cultures showing rudimentary male flowers on the tips of some ears, irregularity of rows on the cob but no division of the cob as in ra_1. Other cultures have a divided cob on the tip of the ear but a solid cob at the base. Ra_1 can be separated from ra_2 in the F_2 of a cross.

H. K. Hayes

3. Virescent seedling. A virescent seedling in Minn. #13 corn was found to be linked with japonica and given the symbol $\underline{v}_{21}$. Rhoades (Co-op News Letter, March 23, 1937) has found $\underline{v}_{16}$ and $\underline{v}_{21}$ to be allelic after trisomic tests had placed $\underline{v}_{16}$ also in chromosome 8. Further linkage data of $\underline{j}_1$, $\underline{ms}_8$ and $\underline{v}_{16}$ are as follows:

Genes	Phase	XY	Xy	xY	xy	Total	% Recomb.
J_1 V_{16}	RB	82	565	542	71	1260	12.1
J_1 V_{16}	RS	354	149	154	4	661	16.9
J_1 Ms_8	CS	464	39	23	135	661	9.5
Ms_8 V_{16}	RS	337	150	171	3	661	13.9

The order of the genes appears to be j_1 - ms_8 - v_{16}.

4. Zebra striped. Emerson et al list five cases of zebra striping that have been reported. There are two types, one that is expressed in the seedling stage and which may completely disappear in partly grown plants. The type reported here was obtained from an inbred line of Del Maiz sweet corn furnished by J. D. Barnard of the Minnesota Valley Canning Company. The season in 1936 was very hot and dry. Germination of sugary seeds was much lower than normal. Zebra striping could not be classified until late summer when the weather was cooler. Classification was difficult in some cultures. The results given in the summary indicate $\underline{zb}_6$ is located in group 4.

Genes	Phase	XY	Xy	xY	xy	Total	% Recomb.
Zb_6 Tu	CS	410	64	64	90	628	23.3
Zb_6 Gl_3	RS	326	148	135	19	628	33.9
Tu Gl_3	RS	314	160	147	7	628	20.5
Zb_6 Su_1	CS	4227	259	175	361	5022	13.3

The order of the genes appears to be Su_1 - zb_6 - Tu - gl_3.

H. K. Hayes and M. S. Chang

University of Missouri, Columbia, Missouri -

1. Of the unknown glossies grown in 1937, tests were completed on one which was found to be different from the other ten and has been assigned the symbol $\underline{gl}_{11}$. This was an X-ray induced mutant. One of the ultra-violet induced glossies proved upon test to be $\underline{gl}_2$. Tests on three others have not been completed.

In a previous report it was stated that somewhere along the line gl$_6$ and gl$_8$ had been confused and the present stocks of these are identical. Since the symbol gl$_8$ has been used in print for the glossy on the 5th chromosome, this designation has been retained and a new glossy assigned the symbol gl$_6$.

2. Glossy 7 has been tested with j$_1$ ms$_8$ with no indication of linkage:

Genes	Phase	XY	Xy	xY	xy	Total	% Recomb.
Gl$_7$ J$_1$	CS	159	22	40	9	230	43
Gl$_7$ Ms$_8$	CS	148	23	51	8	230	50

3. The inheritance of yellow endosperm color is more complex than has been generally believed. Evidence is available for the presence of at least one gene in addition to Y$_1$ and Y$_3$ which is concerned with the presence or absence of yellow endosperm pigment. Ratios of 3:1, 9:7, 15:1, 45:19 and others possibly more complex have been obtained.

The yellow scutellum gene sy is able to produce its effect in the presence of y$_1$y$_1$, but in the presence of other recessive whites the development of pigment (carotin) is completely suppressed. The factor or factors involved have not been completely identified.

G. F. Sprague

John Innes Horticultural Institution, London, England -

1. Experiments on the inheritance of quantitative characters commenced by Dr. Brieger were continued during the summers of 1936 and 1937. The ultimate aim is to produce varieties of sweet corn which are early enough for the English climate and yet satisfactory in yield. In a comparison of F$_1$ families and their parents it was found that the application of a pseudo-factorial method of analysis (Yates, 1936) is not warranted for field trials with maize. The efficiency of the experiment when treated as a 3 x 3 x 3 pseudo-factorial arrangement was about 60% of that when treated as a simple randomised block lay-out.

C. D. R. Dawson

Connecticut Agricultural Experiment Station, New Haven, Conn. -

1. The evidence so far obtained indicates that mosaics in maize are due to losses or rearrangements of chromosome fragments rather than to somatic crossing over as Stern finds for Drosephila. Paired mosaics involving different chromosomes have been found for nearly all of the easily identified endosperm characters. In seeds heterozygous for C and Pr the following results have been obtained:

	White Spots	Red Spots	Red and White Paired Spots
Number	8409	1061	37
Ratio	227	29	1

These figures indicate a more or less random exchange between the 60 chromosome arms in this triploid tissue.

The secondary paired mosaics (twin spots within the dark part of primary twin spots) can not be accounted for by somatic crossing over but are understandable on the basis of translocation followed by further breaking at other places. Variegated waxy tissue in areas that have previously lost the C gene show an unstable condition that would not be expected from somatic crossing over. Similar variegation has been found involving C, Pr, and Su.

In seeds resulting from the pollination of C wx by c Wx light and dark aleurone twin spots were found indicating a shift of one C allele. If this resulted from an exchange of homologous segments the endosperm underlying the dark part of the twin spot should be waxy. In many such twin spots examined no waxy areas were found.

D. F. Jones

Agricultural Experiment Station, College Station, Texas -

1. The most important development in Texas during the past year is the discovery that the essential differences between Zea and Euchlaena are not due to numerous genes scattered at random over all the chromosomes as we first thought, but are due to four chromosome segments which are transmitted in inheritance in almost the same manner as single genes. The fact that these segments all carry genes similar to those possessed by Tripsacum, and the simultaneous discovery that short segments of the chromatin are interchanged between Zea and Tripsacum in hybrids of these two genera, has led us to the conclusion that teosinte is nothing more than maize with several translocation segments from Tripsacum superimposed upon the maize germplasm; the product of a natural hybrid between Zea and Tripsacum.

Two of these translocation segments have been located by linkage studies. They occur at opposite ends of chromosome 4 and both show linkage with Su and Tu. These translocation segments from Tripsacum are probably the cause of the unpaired terminal segments which Longley has observed in his cytological studies of the hybrid of maize and teosinte. We have verified his observations on the occurrence of these segments but we are not yet certain that they occur in every case on the chromosomes which he has designated.

The differences between the various kinds of teosinte which have been collected in Guatemala and Mexico may be attributed partly to the differences in the maize to which these translocations segments have been added, and partly to a loss of portions of one or more segments as the result of repeated hybridization with maize.

These new facts reopen the entire question of the origin of maize. With teosinte as a recent development out of the picture, it is reasonable to assume that maize originated from pod corn, which in the homozygous condition is frequently a perfect flowered plant similar to the Andropogonae, and which has the essential characteristics of a plant adapted to survival in the wild. The place of origin was probably in South America, either in Peru or Bolivia.

We suspect that the crossing of South American types of maize with Tripsacum to produce the new genus Euchlaena, has also resulted in some new types of maize previously not in existence, such as the pointed pop corns and the long slender flint and flour corns, neither of which are known in Peru or Bolivia. If this is the case most of our North American maize varieties, with the possible exception of the Southern Gourd-seed types, carry Tripsacum genes in their germplasm. It is possible that the knobs which many of our North American corn exhibit on the chromosomes have been received from Tripsacum via Euchlaena, in which case we are quite likely to find some South American varieties which are lacking in knobs.

These hypotheses suggest a number of genetic and cytological tests which will keep us well occupied for a number of years. We are having some difficulty in locating viable seed of Bolivian and Peruvian maize and if any of the readers of this letter have such seed available we should appreciate receiving some of it.

P. C. Mangelsdorf and R. G. Reeves

<u>Iowa State College, Ames, Iowa</u> -

1. The following linkage data were obtained from the backcross:

$$\frac{+ \quad + \quad Kn \quad +}{br \quad f_1 \quad + \quad bm_2} \times br\ f_1\ kn\ bm_2$$

<u>0</u>	<u>1</u>	<u>2</u>	<u>3</u>	<u>1,2</u>	<u>1,3</u>	<u>2,3</u>	<u>1,2,3</u>
165 182	14 4	50 50	47 52	7 10	1 2	16 32	6 2
347	18	100	99	17	3	48	8
	2.8%	15.6%	15.5%	2.7%	0.5%	7.5%	1.3%

Recombination percentages: br-f_1 7.2, br-Kn 26.1, br-bm_2 35.2, f_1-Kn 27.0, Kn-bm_2 24.1.

These data do not agree completely with the present accepted location of <u>br</u> and <u>f_1</u>. On the basis of these data <u>Kn</u> is located closer to <u>br</u> than to <u>f_1</u> but it must be between <u>f_1</u> and <u>bm_2</u>. After more extensive tests in 1937 the writer is doubtful that homozygous knotted plants can be distinguished from the heterozygous plants.

2. A tall late type of plant with about 50 per cent more nodes than the normal was discovered among the plants from an F_2 selfed

ear from the Krug variety. Plants of this type were crossed with several normal stocks in 1936 and the F_1 progenies were grown in 1937. All of the F_1 plants were normal. A similar type was found in 1936 among the plants from another F_2 selfed ear from the Krug variety.

A. A. Bryan

California Institute of Technology, Pasadena, Calif. -

1. Correlation between cytology and map position in chrom. 1.

	Cytological Position	Linkage Map Position
T1-2c	S .7	near sr
T1-9c	S .6	near P
T1-2b	S .4	P ± 1.5
T1-6c	S .3	P - 7.6 - T - br
T1-3a	S .25	P - 17.3 - T - br
T1-9a		P - 20.0 - T - 34 - br
T1-5b		P - 25.6 - T - 32.4 - br
T1-5c		P - 24.2 - T - 27.8 - br
T1-6b	L .25	P - 39.0 - T - 3.8 - br
T1-6a	L .2	br - 13.4 - T
T1-3d		near br
T1-7c	L .3	near br (± 2.7)
T1-7a	L .4	near br
T1-10a	L .4	near br
T1-7b	L .6	near br
T1-9b	L .6	br ± 7.0
T1-2a		near ad and an
T1-5a		br - 9.7 - T - 39. - bm_2
T1-4a		br - 20. - T - 45. - bm_2
T1-7d	L .8	br - 34.7 - T - 18. - bm_2

2. Chocolate. In the distal part of long arm of chrom. 2. Homozygous long inversion gave the linkage order:

lg_1-44-v_4-32-B-25-Ch

As the inversion includes about 4/5th of the long arm, <u>Ch</u> must be very near the end.

E. G. Anderson

3. Ms_{20}. Backcross tests with the following chromosome alterations show no obvious linkage:

Inversion of chrom. 2 (near <u>B</u> and beyond <u>v_4</u>)

T2-4b (2 near <u>v_4</u>, 4 beyond <u>gl_3</u>)

T2-3c (2 near <u>sk</u>, 3 near <u>d_1</u>)

T4-8a (4 near <u>su</u>, 8 near spindle attachment)

4. Correlation between cytology and map position in chromosome 2.

	Cytological Position	Linkage Map Position
T2-3a		near lg
T2-6b	S .75	B ± 2.2
T2-9a	S .65	B - 2.7 - T - 23.7 - v_4
T1-2b	S .6(?)	B - 5.3 - T - 30.9 - v_4
T2-3c		B - 6.0 - T - 28.0 - v_4
T2-3d		B - 13.3 - T - 12.4 - v_4
T2-4d		B - 18.0 - T - 6.0 - v_4
T2-9b	S .1	B - 22.5 - T - 7.2 - v_4
T2-5a	L .1	B - 25.0 - T - 7.0 - v_4
T2-7b	L .25	B - 28.2 - T - 4.6 - v_4
T2-10a	L .2	B - 36.5 - T - 6.0 - v_4
T2-6c	L .3	v_4 ± 1.1
T2-7a	L .3	v_4 ± 1
T2-4a	L .3+	v_4 ± 1
T2-7c	L .3	v_4 ± 1.6
T2-5b		v_4 ± 5.3
T2-4b	L .6+	v_4 ± 7.7
T2-4c		v_4 ± 35.0 - T

I. M. Clokey and E. G. Anderson

5. Linkage of sb. Slit blade is probably not on chromosome 6 where first reported:

Genes	Phase	XY	Xy	xY	xy	Total	% Recomb.
Y_1 Sb	RS	930	249	306	84	1569	50
Pl Sb	RS	478	135	154	49	816	48
Su_2 Sb	RS	896	265	340	68	1569	43
Py Sb	RS	1165	328	352	68	1913	50

The Y was not certainly, but probably, Y_1. In any case, sb is not between Y_1 and py.

6. Sb is not on chromosome 2.

Genes	Phase	XY	Xy	xY	xy	Total	% Recomb.
Lg_1 Sb	RS	288	95	76	35	494	50
Gl_2 Sb	RS	288	92	78	36	494	50

sb x trisome 2:

	Sb	sb
Culture 1	6	3
Culture 2	187	63
Culture 3	126	20
	319	86

If $\underline{sb}$ were on chromosome 2 there should be about 30 $\underline{sb}$ plants; if on some other chromosome, about 100.

Notes: $\underline{Sb}$ is generally readily classifiable, though quite variable. Many of the plants are fully fertile. Usually the ratio is about as expected, though in two of my cultures the ratio was about 8:1 (F_2 seed). This was not due to lethalness of $\underline{sb}$, for nearly all of the seeds grew. In $\underline{A}$ $\underline{B}$ $\underline{Pl}$ plants the slitting of the blades seemed less developed than in green plants.

J. Shafer

University of Wisconsin, Madison, Wisconsin -

1. Linkage of $\underline{ra}_2$.

Genes	Phase	XY	Xy	xY	xy	Total	% Recomb.
Cr_1 Ra_2	RB	14	26	22	3	65	26.1

This is further evidence indicating that the $\underline{ra}_2$ locus may be near that of $\underline{d}_1$.

R. A. Brink

Arlington Experiment Farm, Arlington, Virginia -

1. The dominant $\underline{Dt}$ gene has been reported (1936) to produce dots of aleurone color on $\underline{a}_1$-tester seeds. The nature of the interaction between $\underline{Dt}$ and $\underline{a}_1$ was unknown at that time. It has now been established that $\underline{Dt}$ causes $\underline{a}_1$ to become unstable and to mutate at a rate thousands of times greater than normal. Mutations of $\underline{a}_1$ in the presence of $\underline{Dt}$ can be detected in aleurone, husks, and leaves i.e. plant color, and pericarp tissue. Recessive $\underline{a}_1$ mutates to the $\underline{A}_1$ allele a thousand times as frequently as to the $\underline{a}_1^p$ allele. There is no chromosome abnormality present in the $\underline{Dt}$ line. The $\underline{a}_1$ gene is in chromosome 3 while $\underline{Dt}$ may belong to chromosome 9. Mutations of $\underline{a}_1$ to $\underline{A}_1$ or $\underline{a}_1^p$ occur late in development in all tissues. It is not possible, at least by the writer, to reconcile these data with any of the hypotheses advanced by Schultz, Stern or Patterson to explain variegation. They seem, however, to agree with Demerec's conception of increased mutability being caused by a chemical or physiological condition produced in the cell. Recessive $\underline{a}_1$ is highly stable in the presence of $\underline{dt}$. The $\underline{Dt}$ gene is specific in its effect on $\underline{a}_1$. No other recessive locus including $\underline{a}_2$, $\underline{c}$, $\underline{r}$, $\underline{lg}_1$, $\underline{wx}$ and $\underline{su}$ is affected. A dominant modifying gene reducing the frequency or rate of mutation has been isolated. There is some evidence of a recessive gene affecting the time of mutation.

2. The following data on the location of $\underline{ws}_3$ show the order to be as follows:

ws_3	lg_1	gl_2	B
0	11	30	49

These four genes are all located in the short arm of chromosome 2 and if the $\underline{R}^g$ or $\underline{r}^g$ alleles are used with $\underline{B}$ all of them can be classified in the seedling stage.

	ws_3 lg_1 + - 415	ws_3 lg_1 gl_2 - 16
$\frac{ws_3 lg_1 +}{+ + gl_2}$ selfed	+ + gl_2 - 525	+ + + - 1068
	ws_3 + gl_2 - 24	ws_3 + + - 90
	+ lg_1 + - 99	+ lg_1 gl_2 - 4

Total = 2241

$ws_3 - lg_1 = 11\%$ $ws_3 - gl_2 = 27\%$ $lg_1 - gl_2 = 19\%$

3. Trisomic tests show $\underline{v}_{10}$ is in chromosome 6. Since $\underline{v}_{10}$ gave 43% recombination with Y_1 it will fall near the end of either the long or short arm. Tests with py will be made this spring.

4. Preliminary results indicate that the pollen tube is not parasitic but is dependent for its growth in the silk upon the starch stored in the pollen grain.

5. There is a highly significant increase in crossing over in the A_2-Bt and Bm_1-Pr regions of chromosome 5 in microsporocytes as compared with megasporocytes. In a "low" line there was 7.6% recombination between A_2-Bt in the female gametes contrasted with 12.2% in the male gametes. Similar differences between the frequency of crossing over in the two sexes is the explanation of the inexplicable difference found by the writer (1936) in crossing over for the Bm_1-Pr region in plants hyperploid for the short arm of chromosome 5 as compared with diploid sibs. The hyperploid individuals had been used as the male parent while the diploid sibs had been used as the female.

M. M. Rhoades

Cornell University, Ithaca, New York -

1. In the News Letter of March 23, 1937, pp. 1, 2, it was shown by means of three-point tests involving the genes sr, P, and br and the translocations T1-5a and T1-5c, that the order of the genes is sr - P - br with the translocation breaks between P and br. Backcross data from 476 individuals were also presented suggesting that ts_2 is between P and what was then called T1-10b but now designated T1-2c.

Records of the past summer presented below show that T1-2c is to the left of P very near sr, that ts_2 is to the left of P with ms_{17} presumably to the left of ts_2, and that T1-3a and T1-9c are probably to the right of P. The data are as follows:

Genes	Phase	XY	Xy	xY	xy	Total	% Recomb.
Sr T1-2c	CB	151	1	1	144	297	0.7

F_1 genotype	0	1	2	1, 2	Total
$\frac{ts_2\ P\ +}{+\ \ +\ \ T1\text{-}5b}$	76 93 169	1 2 3 1.4%	17 22 39 13.7%	0 0 0	211
$\frac{ms_{17}\ P\ +}{+\ \ +\ \ T1\text{-}5b}$	26 25 51	3 2 5 5.7%	15 13 28 32.2%	2 1 3 3.4%	87
$\frac{ts_2\ P\ +}{+\ \ +\ \ T1\text{-}3a}$	106 140 246	3 1 4 1.3%	29 36 65 20.6%	0 0 0	315
$\frac{ms_{17}\ P\ +}{+\ \ +\ \ T1\text{-}3a}$	54 33 87	2 0 2 2.0%	7 5 12 11.9%	0 0 0	101
$\frac{sr\ P\ +}{+\ \ +\ \ T1\text{-}9c}$	38 32 70	24 17 41 35.0%	0 5 5 4.3%	0 1 1 0.9%	117
From '37 News Letter	97 167	24 65 26.4%	5 10 4.1%	3 4 1.6%	129 246
$\frac{T1\text{-}2c\ +\ P}{+\ \ ts_2\ \ +}$	156 138 294	51 29 80	2 1 3	0 0 0	377
$\frac{+\ \ ts_2\ \ P}{T1\text{-}2c\ +\ +}$	204 276 480 774	50 49 99 179 18.7%	3 0 3 6 0.6%	0 1 1 1 0.1%	583 960
From '37 News Letter	401 1175	70 249 17.4%	5 11 0.8%	0 1 0.1%	476 1436
$\frac{+\ \ ms_{17}\ \ P}{T1\text{-}2c\ +\ +}$	152 157 309	29 31 60 15.7%	3 5 8 2.0%	0 4 4 1.0%	381

Two of the cultures reported above involving T1-2c with B of chromosome 2 and P and ts_2 of chromosome 1, gave the following data from $\frac{B\ \ T1\text{-}2c\ \ +\ \ P}{+\ \ +\ \ ts_2\ \ +}$

0	1	2	3	1,2	1,3	2,3	1,2,3	Total
122 111 233	27 34 61 16.2%	30 21 51 13.5%	2 0 2 0.5%	8 21 29 7.7%	1 0 1 0.3%	0 0 0 0	0 0 0 0	377

One of these cultures also segregated lg_1 as in F_2. Using only lg_1 plants, the records for $\frac{lg_1\ \ B\ \ T1\text{-}2c\ \ +\ \ P}{+\ \ +\ \ +\ \ ts_2\ \ +}$ are:

0	1	2	3	4	1,2	1,3	2,3	1,2,3	Total
28	15	12	10	0	6	3	1	4	79
	19.0%	15.2%	12.7%	-	7.6%	3.8%	1.3%	5.1%	

One of the cultures reported above to show close linkage between T1-2c and sr also involved B of chromosome 2 but no marker other than sr of chromosome 1. The data are:

F_1 genotype	0	1	2	1,2	Total
B T1-2c + / + + sr	63 44	28 9	0 0	0 0	
	107	37	0	0	144
		25.7%	0	0	

Since no crossover between T1-2c and sr appeared in this culture, the orientation of these two markers with respect to the rest of chromosome 1 cannot be told.

2. Among 2052 F_2 plants of crosses of ad_1 with an_1, no double recessive appeared, but F_3 cultures from 220 F_2 an_1 and ad_1 plants indicated a crossover value of 4.1% (Linkage Summary, 1935, p. 32). Backcross cultures of last summer gave the following results:

Genes	Phase	XY	Xy	xY	xy	Total	% Recomb.
Ad_1 An_1	CB	247	7	10	199	463	
Ad_1 An_1	RB	4	36	31	1	72	
						535	4.1

R. A. Emerson

3. Chromosome 7.

F_1 genotype	0	1	2	1,2	Total
in + + / + v_5 gl_1	880	30	99	8	1017
		3.4%	11.3%	0.9%	

in - 4.3 - v_5 - 12.2 - gl_1

F_1 genotype	0	1	2	1,2	Total
in gl_1 + / + + ij	81	12	23	7	123
		9.8%	18.7%	5.7%	

in - 15.5 - gl_1 - 24.4 - ij

A number of seedlings in the latter cross were destroyed by mice in early stages. Counts are not dependable for distances but they are consistent with the order in the first cross.

A. C. Fraser

4. Doubling the number of chromosomes in yellow corn increased the carotinoid content 43 per cent as determined by chemical analysis of 2N and 4N stocks having a common origin. The volume of the endosperm cells of the tetraploid was more than 3.5 times as great as that of the diploid. Thus the individual endosperm cells of the tetraploid contained more than 5 times as much carotinoid as did those of the diploid and in terms of gene concentration within the endosperm tissue the amount of carotinoid was increased 2.5 times as a result of chromosome doubling. Chemical analyses by D. B. Hand.

5. The following results have been obtained to date on haploid frequencies in seedling progenies from untreated and x-rayed (1500 r-units) pollen:

	N	2N	N/1000
From untreated pollen	66	126,308	.53/1000
From x-rayed pollen	31	24,619	1.25/1000

The haploids were identified with the aid of recessive seedling genes, stomate examination and root-tip chromosome counts.

L. F. Randolph

6. The following characters have appeared in inbred lines:

co -Corrugated leaf. Raised striations of tissue in seedling and mature leaves. Classification good. Viability normal.

bk_x-Brittle stalk. Similar to brittle stalk-1. Classification good. Viability normal.

de_a-Defective endosperm. Seed similar to de_1.

de_b-Defective endosperm. Seed similar to de_1.

de_c-Defective endosperm. May be a new sugary. Classification good. Viability good in germinator, but hasn't been tested under field conditions.

f_x- Fine stripe. Plant striped in seedling stage and throughout development. Classification good. Viability normal.

Pu_x-Purple plumule. Similar to Pu_1.

w_x- White seedling. Similar to w_1.

ws_x-White sheath. Similar to ws_3.

R. G. Wiggans

7. White seedling-1 (w_1) has been known to be loosely linked with the $\underline{Y_1}$ gene of the sixth chromosome (Linkage Summary, 1935). To place $\underline{w_1}$ more accurately in the chromosome seedling counts were made of the F_2 cross between $\underline{w_1}$ and pigmy (py). Seeds were taken from the Co-op stocks. The results indicate a very close linkage between <u>py</u> and $\underline{w_1}$.

Genes	Phase	XY	Xy	xY	xy	Total	% Recomb.
Py W_1	RS	867	416	443	0	1726	4.8(if one xy)

G. A. Lebedeff

8. Segregation in autotetraploid maize. To determine the nature of segregation of some genes in autotetraploid maize, backcrosses were made involving the genes B(plant color booster) and Su(sugary endosperm).

Cross	B	b	No. of Plants	Ratio
BBbb x bbbb	437	135	572	3.25 : 1

Some difficulty was encountered in classifying the progeny of the backcross, sun red (BBbb) x green (bbbb), since there was a great deal of variation in degree of coloration. Some plants were distinctly sun red, others resembled dilute sun red, while still others showed a tinge of color on and around the ligules. Undoubtedly errors were made in classification, there being an excess of green plants. However, the backcross ratio approaches 3.67 : 1. Since the type of segregation is a function of cross over distance between the gene locus and the spindle fiber attachment region, this would indicate that the gene B is located fifty or more units from the spindle fiber attachment region and that chromatid segregation had occurred.

Cross	Su	su	No. of plants	Ratio
Su Su su su x su su su su	2877	645	3522	4.46 : 1
su su su su x Su Su su su	369	87	456	4.24 : 1
	3246	732	3978	4.43 : 1

There was no difficulty in classifying sugary segregates in a backcross of autotetraploids. The ratio of 4.43 Su : 1 su indicates that this gene has segregated on a basis intermediate between the random distribution of four chromosomes and random distribution of eight chromatids, and suggests that the gene Su is located about 20 cross over units from the spindle fiber attachment region.

H. E. Fischer

9. It has been observed by many investigators that the F_1 ears of maize-teosinte hybrids are 4-rowed (paired spikelets, two-ranked). This indicates that the paired spikelet condition

of the maize ear is dominant to the single spikelets of teosinte. Collins and Kempton, 1920, showed that in an F_2 population, paired and single spikelets segregated 3:1. Data obtained by the writer in the summer of 1937 have confirmed their findings.

It has not been pointed out, however, that the two-ranked condition of teosinte, which appears in the F_1 of maize-teosinte hybrids, segregates as a unit character in the F_2 population. The combined 3:1 segregation of the dominant two-ranked condition of teosinte (as contrasted with the many-ranked condition of maize) and the 3:1 segregation of paired vs single spikelets, gave a 9:3:3:1 ratio, indicating that these two genes are independent of each other. This independence makes possible the combination of the recessive many-ranked condition of maize with the recessive single spikelets of teosinte, giving two kinds of ears: some with an even number of rows and others with an odd number of rows. Thus, 3-, 4-, and 5-rowed ears with single spikelets have been found. With paired spikelets these would presumably have been 6-, 8-, and 10-rowed ears, respectively.

10. Preliminary F_2 and reciprocal backcross data on maize-teosinte hybrids indicate that response to short-day may be due to one, or a few, genetic factors.

11. New characters.

gc_2 - Glucostacious-2. Seedlings pale green in very early stages. Then brown blotches appear and the plants die. Chrom. unknown.

cz_x - Cuzcoid. Plant too late to shed pollen under field conditions at Ithaca.

la_t - Lazy teosinte. Similar to la_1 in maize. Has not been tested for allelism.

D. G. Langham

II. Seed Stocks Grown, 1937

1. Testers.

Chromosome 1:

p ad_1 seg. an_1

P/ + f_1 bm_2 seg. br

(p ad_1 x p ad_1 an_1)self

sr an_1 bm_2

br f_1 bm_2 x (Kn x br f_1 bm_2)

Chromosome 2:

lg_1 gl_2 B ts_1 v_4 A Pl x lg_1 +/gl_2 B +/ts_1 v_4 A Pl

lg_1 b gs_2 V_4/? Gl_2/? x Inbred II

lg_1 Gl_2/? b v_4 gs_2 x Inbred I

Chromosome 2 (con't):

Inbred x lg_1 gl_2 b v_4 A pl	b gs_2 lg_1
lg_1 gl_2 b v_4 A_1 Y	trisome #2

Chromosome 3:

a_1 lg_2 Dt/?	a_1 na cr gl_1 v_5 Y
a_1 Dt/?	a_1 Dt/? seg. lg_2
a_1 +/na +/lg_2 +/ts_4 x a_1 na +/lg_2 +/ts_2	
a_1 lg_2 d_1 x A_1 lg_2 d_1 ts_4	A_1 lg_2 +/d_1 x A_1 lg_2 ts_4 d_1
a_1 lg_2 ra_2	a_1 lg_2 Dt/? y_1 seg. na
a_1 yt seg. na	na ts_4 x na +/ts_4
a_1 ts_4 +/na Dt/? x a_1 +/ts_4 na Dt/?	Trisome #3

Chromosome 4:

(su_1 x d_H) x (Tu su_1 x d_H)	(gl_3 x su_1 j_2)self
su^{am} du	(Ga x su_1)self
(+/w_4 +/su_1)self	(su_1 gl_3 x wl)self
(Ts_5 su_1 x wl)self	(Ts_5 su_1 x la su_1)self
(Ts_5 su_1 x la) x la su_1	Trisome #4

Chromosome 5:

Homo. A_1 C R a_2 bt bv pr_1	Homo. A_1 C R a_2 bt bv pr_1 seg. v_2
v_2 a_2 A_1 C R b pl	Homo. A_1 C R A_2 bt bv pr_1
Trisome #5	

Chromosome 6:

Pl sm +/py A b x Pl py A b	Pl sm x pb_x(Lebedeff)
Y_1 Pl sm seg. py	

Chromosome 7:

Inbred x ra_1 gl_1 ij bl_x	ra_1 gl_1 ij x bd_1
ra_1 gl_1 ij x gl_1 ij fr_1 +/fr_2	ra_1 gl_1 ij
v_5 gl_1 Tp seg. ra_1 tp	(bd_1 x gl_1 ij) x gl_1 ij bd_1
ra_1 gl_1 v_5 x Tp gl_1 v_5	Trisome #7

Chromosome 8:

v_{16} ms_8 j_1 x (ms_8 j_1 x v_{16})

ms_8 x ms_8/+

ms_8 j_1 x ms_8/+ j_1

Trisome #8

Chromosome 9:

Inbred I x g_4 wx

g_4 wx x (gl_4 x yg_2 c sh wx)

au_1 au_2 sh

wx da ar sa_1

Trisome #9

Inbred I x ar wx

c sh wx bp

ms_2 x ms_2/+

(gl_4 x yg_2 c sh wx)self

Chromosome 10:

r zb_5 seg. nl_1

Og/+ Y P^{wr}

Inbred x OgOg

r A_1 C y_1 seg. g_1

l_1 seg. w_1

Og Og

seg. l_1

Trisome #10

2. Miscellaneous

U. S. 204 (Inbred I)

Inbred I x bm_3

A_1 C R Pl B Y_1 a_2

g_2 A_1 b Pl

seg. v_{12}

v_{13}

va_2 x va_2/+

wa x wa/+

ms_5 x ms_5/+

ms_6 x ms_6/+

ms_7 x ms_7/+

ms_9 x ms_9/+

ms_{10} x ms_{10}/+

ms_{12} x ms_{12}/+

West Branch (Inbred II)

seg. hf

Kn A_1 +/b Pl x A_1 +/b Pl

A_1 C R A_2 Pr_1

(bm_3 x yg_3)self

A_1 C R A_2 pr_1 i

Vg/+ x vg

an_2 x Inbred

+/na_2 x na_2

r pr_1 x A_1 C R^{st} B

A_1B pl R^{st} x r pr_1

+/bk_1 x bk_2

(+/bk_1)self

+/de +/mi x de mi

ms_{13} x $ms_{13}/+$

ms_{14} x $ms_{14}/+$

ms_{37} x $ms_{37}/+$

ms_{39} x $ms_{39}/+$

ms_{42} x $ms_{42}/+$

v_{12} x v_{12} pr_1

seg. gl_{10}

(sb x A_1 b pl $+/y_1$ su_2)sib

y_1 su_2 seg sb

pb_4

S_x

sy

Pc_x

Ch/? seg. gl_1

$Ts_3/+$ $v_4/+$ x Rg/+

$Ts_3/+$ $v_4/+$ x R g_1 C sh wx

$+/an_2$ x $+/an_2$

Inbred x mi

Wc Y_1

f_x(Wiggans)

de_a "

de_b "

de_c "

co "

ws_x "

Chlorophyll types-

Yellowish green

rather lt. green

medium to lt. green

dark green

nl_2

gc_2

Seed stocks from Australia grown by Shafer in Calif. for the Co-op:

3 different stocks of yellow-striped seedling.

5 different stocks of virescent seedling.

crinkly.

3. Stocks too late to mature at Ithaca.

From Krug:

brown pericarp
branched ear
seg. dwarf
oily spots
seg. mealy
variegated pericarp
ragged
seg. zebra seedling
crinkly

black pericarp
seg. tassel seed
bract in tassel
seg. defective endosperm
rolled leaf
semi-dwarf
striped leaves
ms x ms/+
zebra leaves

From Mangelsdorf

mottled dwarf

seg. vp_x

4. No germination.

$sr\ an_1\ bm_2$

$da\ au_1\ au_2\ sh$

$ms_4 \times ms_4/+$

$ms_{27} \times ms_{27}/+$

$J_{33a} \times A\ c\ R\ sh\ wx\ B\ Pl$

$+/v_{15} \times +/v_{15}$

$ms_{15} \times ms_{15}/+$

$g_4\ ar\ sa_1\ pk_1$

III. Seed Stocks Received For Propagation in 1938

1. J. Shafer, Ithaca, N. Y.:-
   v_{19}
   T 1-2b x T 1-2b
   T 2-4b

2. R. A. Brink, Madison, Wisconsin:-
   $(pm \times lg_2\ d_1)$ sib

   $(A_1\ pm \times a_1\ lg_2)$ sib

3. J. H. Kempton, Washington, D. C.:-
   fs

4. A. Tavcar, Zagreb, Jugoslavia:-
   Hs

5. M. M. Rhoades, Arlington, Virginia:-
   $(ws_3\ lg_1\ B\ A_1\ pl \times gl_2) \times (ws_3\ lg_1\ b\ A_1\ pl \times gl_2)$

6. W. R. Singleton, New Haven, Connecticut:-
   ra_2?

   $su_1 \times +/lo$

   v_5?

   yellow x yellow

   $zb_x\ f \times ys$

   $+/ba_x$

   $gl_3\ v_4 \times lg_1\ gl_2\ b\ v_4\ r^g ACYSu$

   ys_x (7 cultures)

7. R. G. Wiggans, Ithaca, N. Y.:-
   de_c

   f_x

   Pu_x

IV. Miscellaneous Co-op Items

1. Seed stock inventory. In March, 1937, an inventory of the genetic seed stocks in the Co-op collection showed that 148 of the genes reported in the Linkage Summary, 1935, were not in the seed trays here. A list of those 148 genes was included in the News Letter, March 23, '37, and several maize geneticists responded by sending in 16 genetic stocks.

In January, 1938, personal requests were sent to each of the 25 geneticists who, collectively, had first reported the remaining 132 stocks. We have learned that about 75% of those genes have been lost due to inviability of seed stocks.

2. Assignment of linkage groups. One of the topics discussed at a special meeting of maize geneticists at the A A A S meetings in Indianapolis, was the problem of linking workable genes and developing more desirable tester stocks. This is an important question because there are more than 50 suitable genes that haven't been linked and some of the chromosomes are poorly marked.

The plan previously outlined for linking new genes has not been fundamentally changed, but it may well be reviewed here. Each of the ten linkage groups in maize has been assigned to one, or more, cooperator who is charged with testing unplaced characters with his particular chromosome and building up suitable tester stocks. The following assignments have been made:

Chromosome 1. Emerson.
Chromosome 2. Rhoades and Clokey.
Chromosome 3. Brink and Woodworth.
Chromosome 4. Singleton and Brunson.
Chromosome 5. Burnham.
Chromosome 6. Stadler and Lebedeff.
Chromosome 7. Jenkins and Fraser.
Chromosome 8. Sprague and Perry.
Chromosome 9. Eyster and Shafer.
Chromosome 10. Lindstrom, Wentz, and Bryan.

When a new gene is found, a few seeds involving it should be sent to the secretary of the Maize Genetics Cooperation who will grow them in an increase block and obtain a liberal supply of seed for the central repository. Then the secretary will send a few seeds to each of the above geneticists who will test for linkage in his particular chromosome.

This system has been devised not to limit the number of workers who are trying to link new genes, but rather to insure the linkage of every workable gene.

3. More vigorous genetic stocks. During the summers of 1935 and 1936, a number of maize geneticists tested a group of inbred strains for disease resistance and general desirability. The two inbreds, U.S. #204 and West Branch Sweepstakes, seemed best suited to Ithaca conditions and have been selected for use in the Co-op. They have been designated as Inbred I and Inbred II, respectively, and are being used in crosses with weak genetic stocks to increase vigor and, by repeated backcrossing of the segregates to the

inbreds, to obtain a more nearly homozygous chromosome complement. Later, the segregates from each inbred line may be crossed to get hybrid vigor.

Last summer 17 genetic stocks were crossed with both Inbred I and Inbred II.

4. Linkage maps. The linkage maps attached to this Letter were prepared from the data in the Linkage Summary and the data which appeared in the Co-op News Letters since the Linkage Summary was published.

Sincerely yours,

D. G. Langham

D. G. Langham
Secretary

V. Gene Index of Co-op News Letters

This gene index of the Co-op News Letters was made so that the information in the Letters which might be of value in connection with linkage studies could be more readily found. It includes mainly those genes about which some statement of linkage has been made in the Letters, and does not include those that are merely mentioned without any supplementary information. John Shafer.

a_1:

1-25-34, p. 5
(January 25, 1934, page 5)
11-24-34, pp. 13, 18, 11
1-23-33, pp. 3, 6
3-6-35, p. 3
3-4-36, pp. 7, 10, 11
3-23-37, pp. 8, 13, 14
3-6-38, pp. 8, 15

a_2:

12-18-33, p. 5
1-25-34, p. 6
11-24-34, pp. 2, 14
1-23-33, p. 6
3-4-36, pp. 7, 17
3-6-38, pp. 9, 15

a_3:

11-24-34, p. 10

ad_1:

1-23-33, p. 6
1-25-34, p. 4
3-6-35, pp. 3, 15
3-4-36, p. 9
3-6-38, pp. 6, 11, 14

ad_2 (= ad_1):

3-6-35, p. 3

ad_2 (first called ad_3):

3-6-35, pp. 3, 15

ad_3 (now ad_2)

3-6-35, p. 3

ag (=ij):

12-18-33, p. 6
9-13-34, p. 8
1-23-33, p. 6

al:

12-18-33, pp. 3, 5
1-23-33, pp. 3, 6
3-6-35, pp. 3, 5
3-4-36, pp. 15, 16
3-23-37, pp. 8, 15

an:

1-25-34, p. 4
11-24-34, p. 5
1-23-33, p. 6
3-6-35, p. 1
3-36-38, pp. 6, 11, 14

ar_a:

9-13-34, p. 2

ar:

12-18-33, p. 2
1-25-34, p. 8
1-23-33, p. 3
3-6-38, p. 16

as:

1-23-33, p. 6

an_1:

12-18-33, p. 2
1-25-34, p. 8
1-23-33, p. 3
3-6-38, p. 16

an_2:

1-25-34, p. 8
3-6-38, p. 16

B:

12-18-33, p. 6
1-25-34, p. 4
11-24-34, p. 5
1-23-33, pp. 3, 6
3-6-35, pp. 1, 3, 4
3-4-36, pp. 11, 15
3-23-37, pp. 14, 15
3-6-38, pp. 6,7,8,10,11,13,14

ba_1:

1-25-34, p. 5
11-24-34, p. 13
1-23-33, p. 3

ba_2:

1-25-34, p. 4
1-23-33, p. 6
3-23-37, p. 1

bd:

9-13-34, pp. 6, 8
11-24-34, p. 10
3-4-36, pp. 7, 16
3-23-37, pp. 1, 9
3-6-38, p. 15

be (=bd):

9-13-34, p. 8

Bh:

1-25-34, p. 6
1-23-33, p. 6

bk_1:

3-23-37, p. 1

bm_1:

12-18-33, pp. 2, 5
1-25-34, p. 6
11-24-34, pp. 2, 4, 5, 6, 7
1-23-33, pp. 3,6

bm_1 (con't.):

3-6-35, pp. 1, 4, 9, 10, 11
3-4-36, pp. 3, 7
3-6-38, p. 9

bm_2:

1-25-34, p. 4
11-24-34, p. 5
1-23-33, pp. 3, 6
3-6-35, pp. 1, 3
3-4-36, p. 10
3-23-37, pp. 3, 5
3-6-38, pp. 1, 5, 6, 14

bm_3:

12-18-33, p. 5
11-24-34, p. 6

Bn_1:

1-25-34, p. 7
11-24-34, pp. 6, 7
1-23-33, pp. 3, 7
3-4-36, p. 7

bn_2:

9-13-34, p. 8

bp:

1-25-34, p. 8
1-23-33, p. 7
3-6-38, p. 16

br:

1-25-34, p. 4
11-24-34, p. 5
1-23-33, pp. 3, 7
3-6-35, p. 3
3-4-36, p. 10
3-23-37, pp. 1, 2, 5
3-6-38, pp. 1,5,6,9,14

bt_1:

12-18-33, pp. 3, 5
1-25-34, p. 6
11-24-34, pp. 2, 4, 4, 6
1-23-33, p. 7
3-6-35, p. 3

g_1:

1-25-34, p. 8
11-24-34, pp. 5, 10
1-23-33, pp. 3, 8
3-6-35, p. 4
3-4-36, pp. 8, 9, 11, 16
3-23-37, pp. 6, 8, 9
3-6-38, p. 16

g_2:

12-18-33, p. 5
11-24-34, p. 6
3-23-37, p. 14

g_3:

1-23-33, p. 8

g_4:

1-23-33, p. 8
1-25-34, p. 8
3-6-38, p. 16

Ga_1:

1-23-33, p. 8
3-6-38, p. 15

ga_2:

3-4-36, p. 14

gl_b:

9-13-34, p. 3

gl_c:

9-13-34, p. 3

gl_d:

9-13-34, p. 3

gl_1:

1-23-33, pp. 3, 9
12-18-33, pp. 2, 5
1-25-34, p. 7

gl_1 (con't.):

11-24-34, pp. 5, 7, 14
3-6-35, p. 1
3-4-36, pp. 3, 9, 16
3-23-37, pp. 4, 9
3-6-38, pp. 11, 15

gl_2:

1-23-33, pp. 3, 9
1-25-34, p. 4
3-6-35, p. 1
3-4-36, p. 15
3-23-37, p. 8
3-6-38, pp. 7, 8, 9, 14

gl_3:

1-23-33, pp. 3, 9
12-18-33, p. 5
1-25-34, p. 10
3-6-35, p. 1
3-23-37, pp. 6, 10
3-6-38, pp. 2, 6, 15

gl_4:

12-18-33, p. 6
1-23-33, p. 9
3-23-37, p. 10
3-6-38, p. 16

gl_6(= old gl_8):

3-23-37, pp. 9, 10
3-6-38, p. 3

gl_6 (new)

3-6-38, p. 3

gl_7

3-6-38, p. 3

gl_8:

3-6-35, p. 2
3-23-37, p. 9
3-6-38, p. 3

sf:

3-6-35, p. 11

sh:

1-23-33, pp. 3, 13
12-18-33, pp. 2, 6
1-25-34, p. 8
3-6-35, pp. 12, 13
3-23-37, p. 7
3-6-38, p. 16

si:

1-25-34, p. 6
1-23-33, p. 13

sk:

1-23-33, p. 13
1-25-34, p. 4
3-6-38, p. 6

sl:

1-23-33, p. 13
1-25-34, p. 7

sm:

1-23-33, p. 13
1-25-34, p. 6
11-24-34, p. 14
3-6-35, p. 4
3-4-36, p. 9
3-6-38, p. 15

so_1:

12-18-33, p. 6

sp_1:

1-23-33, p. 13
12-18-33, p. 4
1-25-34, p. 5
11-24-34, p. 8
9-13-34, p. 8
3-6-35, p. 1

sp_2:

11-24-34, p. 2

sp_2 (con't.)

3-4-36, p. 8
3-23-37, p. 8

sr:

1-25-34, p. 4
1-23-33, p. 13
3-4-36, p. 10
3-23-37, pp. 1, 2, 3, 5
3-6-38, pp. 6, 9, 10, 11, 14

$st_?$:

3-6-35, p. 12

st:

1-23-33, p. 13
1-25-34, p. 5

su_1:

1-23-33, pp. 3, 13
12-18-33, pp. 3, 4, 5, 6
1-25-34, p. 5
11-24-34, pp. 8, 9, 10
9-13-34, p. 9
3-6-35, pp. 1, 2, 3, 11
3-23-37, pp. 5, 6, 13, 14
3-6-38, pp. 2,4,6,13,15

su_2:

12-18-33, p. 6
3-6-35, p. 11
3-23-37, p. 15
3-6-38, p. 7

su_3:

3-6-35, pp. 11, 12

sy:

3-6-38, p. 3

th (=sr):

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3-23-37, p. 3

T1-9c:

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3-4-36, p. 10
3-23-37, p. 2
3-6-38, pp. 6, 9, 10

T1-10a:

3-6-35, pp. 3, 4
3-4-36, pp. 10, 11
3-6-38, p. 6

T1-10b(see 1-2c):

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3-23-37, p. 2
3-6-38, p. 9

T2-3a:

3-6-38, p. 7

T2-3b:

3-4-36, p. 10

T2-3c:

3-6-35, p. 3
3-4-36, pp. 10, 11
3-23-37, p. 5
3-6-38, pp. 6, 7

T2-3d:

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3-6-38, p. 7

T2-4a:

3-4-36, p. 11
3-6-38, p. 7

T2-4b:

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3-4-36, p. 11
3-23-37, p. 6
3-6-38, pp. 6, 7

T2-4c:

3-6-35, p. 3
3-4-36, p. 11
3-6-38, p. 7

T2-4d:

3-6-35, p. 3
3-4-36, p. 11
3-23-37, p. 6
3-6-38, p. 7

T2-5a:

3-6-38, p. 7

T2-5b:

3-6-35, p. 4
3-4-36, p. 11
3-6-38, p. 7

T2-6b:

3-4-36, p. 11
3-6-38, p. 7

T2-6c:

3-6-38, p. 7

T2-6d:

3-6-35, p. 4

T2-7a:

3-6-35, p. 4
3-4-36, p. 11
3-6-38, p. 7

T2-7b:

3-6-35, p. 4
3-4-36, p. 11
3-6-38, p. 7

T2-7c:

3-6-35, p. 4
3-4-36, p. 11
3-6-38, p. 7

T2-9a:

3-4-36, pp. 10, 11
3-6-38, p. 7

T2-9b:

3-4-36, pp. 10, 11
3-6-38, p. 7

T3-5b:

3-6-35, p. 3
3-4-36, p. 10

T3-5c:

3-6-35, p. 3
3-4-36, p. 10

T3-6a:

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T3-7a:

3-6-35, p. 4
3-4-36, pp. 10, 16

T3-7b:

3-6-35, pp. 3, 4
3-4-36, p. 10
3-23-37, p. 5

T3-8a:

3-6-35, p. 4
3-4-36, p. 10
3-23-37, p. 6

T3-8b:

3-6-35, p. 4
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T3-9a:

3-6-35, pp. 3, 4
3-4-36, p. 10

T3-9b:

3-6-35, p. 3

T3-10a:

3-6-35, pp. 3, 4
3-4-36, pp. 10, 11

T3-10b:

3-6-35, p. 4
3-4-36, pp. 10, 11

T3-10c:

3-6-35, p. 4
3-4-36, p. 11

T4-5a:

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T4-5d:

3-6-35, pp. 3, 4

T4-6a:

3-6-35, pp. 3, 4

T4-6b:

3-6-35, pp. 3, 4
3-23-37, p. 6

T4-6c:

3-6-35, p. 3

T4-9a:

3-6-35, pp. 3, 4
3-6-36, p. 10

T4-9b:

3-4-36, p. 10
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T4-10a:

3-6-35, p. 3

T4-10b:

3-6-35, pp. 3, 4
3-4-36, p. 11

T5-7a:

11-24-34, pp. 6, 7

T5-7c:

3-4-36, p. 17

w_4(=$v_{12?}$):

11-24-34, p. 10
3-4-36, p. 3
3-23-37, pp. 6, 15

w_5:

1-23-33, p. 15

w_6:

1-23-33, p. 15

w_{11}:

1-23-33, p. 15
1-25-34, p. 8

w_{12}:

9-13-34, p. 9

Wh:

1-23-33, p. 15
1-25-34, p. 7

wl:

1-23-33, p. 15
1-25-34, p. 5
11-24-34, p. 8
3-6-35, p. 1
3-6-38, p. 15

ws_3:

11-24-34, p. 2
3-6-35, p. 2
3-23-37, pp. 7, 8
3-6-38, pp. 8, 9

wx:

1-23-33, pp. 3, 15
12-18-33, pp. 2, 6
1-25-34, p. 8
9-13-34, p. 8
3-6-35, pp. 4, 12, 13, 14
3-4-36, pp. 3, 10, 11
3-23-37, pp. 7, 10, 11, 14
3-6-38, p. 16

xn_1:

1-23-33, p. 15

Y_x(=Y_3):

3-6-35, pp. 3, 5, 14
3-4-36, p. 16

Y_1:

1-23-33, pp. 3, 16
12-18-33, p. 6
1-25-34, p. 6
3-6-35, pp. 4, 5, 14
3-4-36, p. 9
3-23-37, pp. 2, 15
3-6-38, pp. 3, 7, 9, 15

Y_4:

3-4-36, p. 9

yd:

1-23-33, p. 16
12-18-33, p. 4

yf:

12-18-33, p. 6
9-13-34, p. 9

$yg_?$:

3-6-35, p. 14

yg_a:

9-13-34, p. 3

yg_1:

1-23-33, p. 16
11-24-34, pp. 6, 7
3-6-35, p. 11
3-4-36, p. 3

yg_2(=v_{14}):

1-23-33, pp. 3, 16
12-18-33, p. 2
1-25-34, p. 8
3-6-35, p. 14
3-6-38, p. 16

yg_3:

12-18-33, p. 5

ys_1:

1-23-33, pp. 3, 16
12-18-33, p. 5
1-25-34, p. 6
11-24-34, pp. 2, 6, 7
3-4-36, p. 7

ys_2:

1-23-33, p. 16

yt:

1-23-33, p. 16
3-6-38, p. 15

zb_4:

3-6-38, p. 1

zb_5:

11-24-34, p. 1
3-6-38, p. 16

zb_6:

3-6-38, p. 2

z $(=zg_1)$:

1-23-33, p. 16
3-6-35, pp. 3, 12

$zg_1(=zg_2)$:

1-23-33, p. 16
3-6-35, pp. 3, 12?

$zg_2(= zg_3)$:

11-24-34, p. 1
9-13-34, p. 9

zg_3:

3-6-35, p. 3

zl:

1-23-33, p. 16
11-24-34, p. 3

1

0 sr
28 P
53 as
80 br
85 f_1
102 an_1
129 gs_1
156 bm_2

ad_1, Kn, ms_{17}, ts_2, Ts_6, zb_4, zn_2, zl

2

0 ws_3
11 lg_1
30 gl_2
49 B
56 sk
68 fl_1
74 ts_1
82 v_4

al, ba_2, Ch, d_5, gs_2, Y_3

3

0 a_1
28 na_1
39 ba_1
56 ts_4
63 Rg
85 d_1
103 cr_1

d_2, lg_2, ms_3, pg_2, pm, ra_2, rt, yt

4

0 de_1
35 Ga_1
56 Ts_5
66 sp_1
69 lo
71 su_1
74 de_{16}
100 Tu
105 j2
111 gl_3

la_1, S_1, st, v_8, vp_3, w_4, wl, zb_6

5

0 a_2
6 bm_1
12 bv
31 pr_1
40 ys_1
72 v_2

bt, cb, d_6, ga_2, gl_8, oy, re_1, re_2, sc_1, sf, tn, v_3, v_{12}, vp_2, Y_2, yg_1

6

0 po
13 Y_1
28 pb_x
41 Pl
51 sm
61 py

Bh, gm_4, ms_1, si_1, su_2, v_6, v_7, w_1, w_5, w_6, yd

7

0 in
4 v_5
18 ra_1
22 gl_1
32 Tp
38 ij
56 Bn_1

bd_1, fr_1, fr_2, Hs, o_2, pg_3, sl, va_1, Wh, Yp

8

0 v_{16}
14 ms_8
24 j_1

9

0 Wmb
2 yg_2
21 C
24 sh
39 bp
54 wx
66 v_1

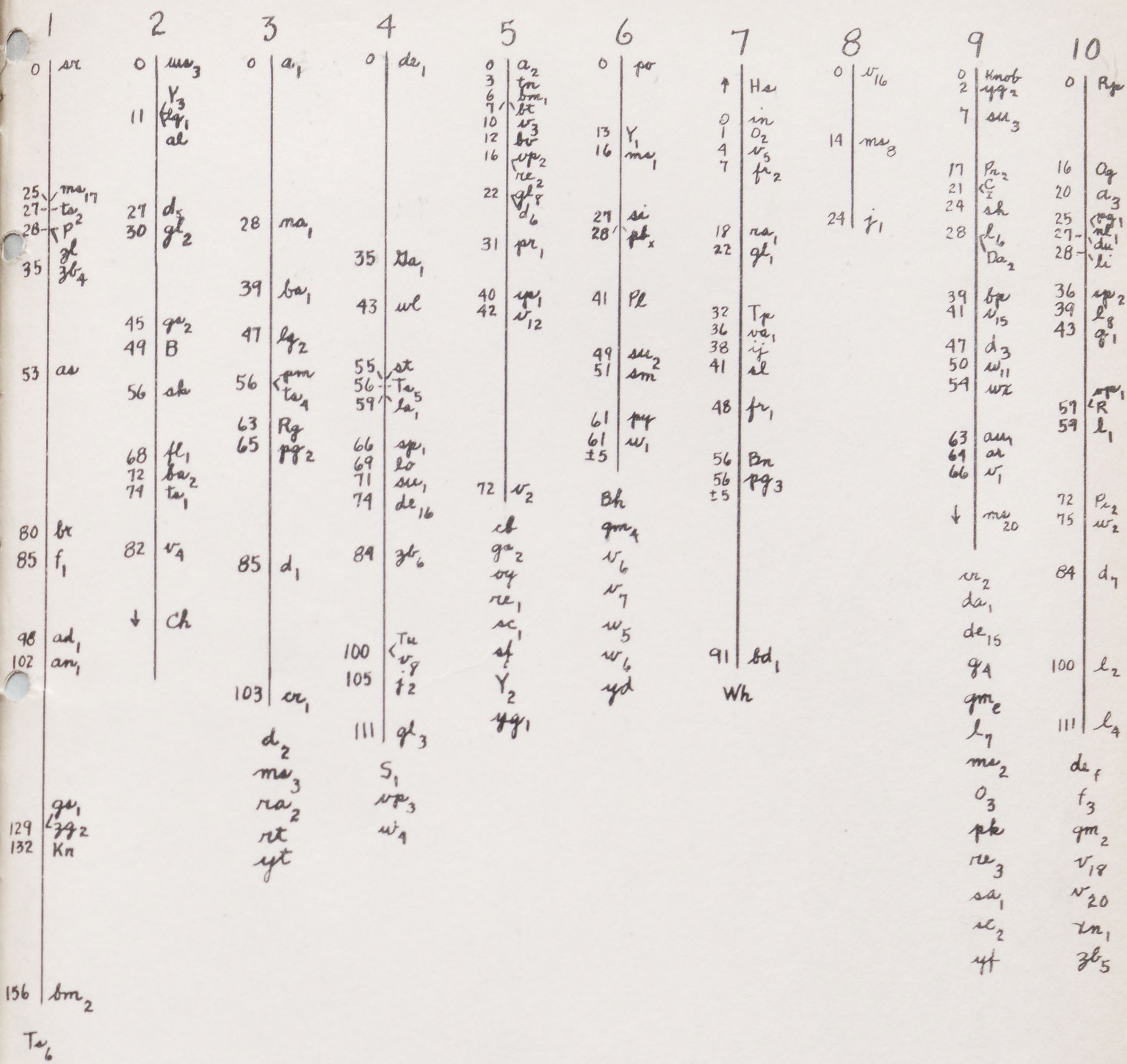
ar, au_1, cr_2, d_3, da_1, Da_2, de_{15}, g_4, gm_8, I, l_6, l_7, ms_2, ms_{20}, o_3, pk, Pr_2, re_3, sa_1, sc_2, su_3, v_{15}, w_{11}, yf

10

0 Rp
28 li
43 g_1
57 R
84 d_7

a_3, de_4, du, f_3, gm_2, l_1, l_2, l_4, l_8, nl_1, Og, Pc_2, pg_1, sp_2, v_{18}, v_{20}, vp_1, w_2, xn_1, zb_5

Linkage map of the ten chromosomes of Zea mays showing the loci of those genes whose position can be determined with reasonable certainty.



Linkage map of the ten chromosomes of Zea mays showing the approximate loci of many genes. (Working map. More 3-point tests needed to establish exact loci of genes).

1

- 0 sr
- 28 P
- 53 as
- 80 br
- 85 f_1
- 102 an_1
- 129 gs_1
- 156 bm_2

ad_1, Kn, ms_{17}, ts_2, Ts_6, zb_4, zp_2, zl

2

- 0 ws_3
- 11 lg_1
- 30 gl_2
- 49 B
- 56 sk
- 68 fl_1
- 74 ts_1
- 82 v_4

al, ba_2, Ch, d_5, gs_2, Y_3

3

- 0 a_1
- 28 na_1
- 39 ba_1
- 56 ts_4
- 63 Rg
- 85 d_1
- 103 cr_1

d_2, lg_2, ms_3, pg_2, pm, ra_2, rt, yt

4

- 0 de_1
- 35 Ga_1
- 56 Ts_5
- 66 sp_1
- 69 lo
- 71 su_1
- 74 de_{16}
- 100 Tu
- 105 j_2
- 111 gl_3

la_1, S_1, st, v_8, vp_3, w_4, wl, zb_6

5

- 0 a_2
- 6 bm_1
- 12 bv
- 31 pr_1
- 40 ys_1
- 72 v_2

bt, cb, d_6, ga_2, gl_8, oy, re_1, re_2, sc_1, sf, tn, v_3, v_{12}, vp_2, Y_2, yg_1

6

- 0 po
- 13 Y_1
- 28 pb_x
- 41 Pl
- 51 sm
- 61 py

Bh, gm_4, ms_1, si_1, su_2, v_6, v_7, w_1, w_5, w_6, yd

7

- 0 in
- 4 v_5
- 18 ra_1
- 22 gl_1
- 32 Tp
- 38 ij
- 56 Bn_1

bd_1, fr_1, fr_2, Hs, o_2, pg_3, sl, va_1, Wh, Yp

8

- 0 v_{16}
- 14 ms_8
- 24 j_1

9

- 0 Knob
- 2 yg_2
- 21 C
- 24 sh
- 39 bp
- 54 wx
- 66 v_1

ar, au_1, cr_2, d_3, da_1, Da_2, de_{15}, g_4, gm_8, I, l_6, l_7, ms_2, ms_{20}, o_3, pk, Pr_2, re_3, sa_1, sc_2, su_3, v_{15}, w_{11}, yf

10

- 0 Rp
- 28 li
- 43 g_1
- 57 R
- 84 d_7

a_3, de_4, du, f_3, gm_2, l_1, l_2, l_4, l_8, nl_1, Og, Pc_2, pg_1, sp_2, v_{18}, v_{20}, vp_1, w_2, xn_1, zb_5

Linkage map of the ten chromosomes of Zea mays showing the loci of those genes whose position can be determined with reasonable certainty.