

MAIZE GENETICS COOPERATION

NEWS LETTER

5

January 25, 1934

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

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To maize geneticists :-

The inventory of genetic stocks which comprises the bulk of this letter is, of course, not complete but it will serve as a basis for future and more extensive lists. We wish to thank those maize geneticists who have cooperated in making this inventory possible. Its value should be apparent to everyone. In a plant such as maize where it takes several years to build up a required stock for a certain experiment, it is essential that the list of existing stocks be kept up to date and be available so that the investigator can make use of these stocks.

No attempt has been made to credit the stocks to different investigators. Those stocks which are marked with an asterisk are those which have not been received here at Cornell. It by no means follows that those stocks which are not marked by an asterisk were synthesized here at Ithaca. In the past we have received so many stocks from different cooperators that an attempt to trace the origin of the different stocks seemed a hopeless task. So we have purposely avoided listing the origin of any of the stocks. This does not give the credit due those investigators who have spent a great deal of time in building up good genetic strains. In the future we shall try to remedy this condition.

In order that this laboratory may serve efficiently as a distributing center for genetic strains, we urge those of you who have the stocks marked by an asterisk to send a small amount of seed to us so that it can be increased for distribution.

At the Boston meetings a system of nomenclature was agreed upon by representatives of the Drosophila and maize groups. This proposed system, as it applies to maize, is submitted in this report for your consideration and your criticisms and suggestions are requested. It was agreed that the needs and requirements of maize and Drosophila genetics were so diverse that it would be unwise to attempt to formulate an identical system of nomenclature. Yet in the matter of symbolizing genes, designating translocations, deficiencies, etc., it was felt that a uniform system could be employed with advantage, and the symbols which are used in the proposed system were agreed upon by the representatives of the two groups.

It should be clearly understood that the proposed system is only tentative. It can and will be modified in any way that will make for a better and more useful system.

The proposed nomenclatorial system for maize is as follows:

1. The linkage groups will be designated by Arabic numerals. Group 1 will include those genes which lie in the longest of the monoploid set of 10 chromosomes, etc. The longest chromosome will be called chromosome 1 and the shortest chromosome 10. Arabic numerals will be used for both linkage groups and chromosomes since the Roman numerals are too cumbersome.
2. Whenever biliteral symbols are used the second letter shall not be dropped as a subscript. Italicize gene symbols.
3. Literal superscripts shall be used to represent different members of an allelomorphous series, e.g., R^r , R^g , r^r , r^g .
4. Numeral subscripts shall be used to represent different genes which give phenotypically similar effects, e.g., v_1 , v_2 , v_3 , etc.
5. The normal allelomorph of a mutant gene shall be designated by the use of the + sign as a superscript, e.g., the normal allelomorph of sugary (su) will be su^+ , and not Su or $+$. The plus sign alone may be used for normal allelomorphs in such genotypic formulae as $\frac{+}{su} \frac{+}{Tu}$, but these allelomorphs should be designated as indicated above when the formula is written as $su^+ Tu^+ / su Tu$.

This suggestion was made by the Drosophila group and we believe it meritorious. It enables one to tell whether the mutant gene is dominant or recessive to the normal or average condition. And, too, the normal gene is nothing more than an allelomorph of the mutant one.

6. The letter T (italicized) shall denote reciprocal translocations or segmental interchanges. $T(1-2)_1$ would represent the first case of a reciprocal translocation between chromosomes 1 and 2, $T(1-2)_2$ the second, etc. Numeral subscripts instead of literal ones are recommended to denote the different translocations. There are several objections for using a, b, c, etc. to denote the different translocations. When more than 26 different translocations involving the same two chromosomes are found we should be forced to use biliteral subscripts, such as aa, ab, ac, etc. The letters of the alphabet have in the past been used for symbolizing genes. For example, we have designated the different virescents as v_1 , v_2 , v_3 , etc., and not as v_a , v_b , v_c , etc.
7. The symbol Df (italicized) shall be used for Deficiency. For example, the first deficiency involving chromosome 10 will be represented as $Df 10_1$; the second as $Df 10_2$, etc.
8. The symbol In (italicized) shall stand for Inversion. An inversion involving chromosome 4 will be represented as $In 4_1$; the second one as $In 4_2$, etc.

9. It was decided that there was, as yet, no need to formulate a system of nomenclature for duplications.

This office will do all that it can to enable you to secure any of the stocks listed in this letter but it should be remembered that in several cases the amount of seed is small and we may not be able to fill your request.

Sincerely yours,

M. M. Rhoades
B.

M. M. Rhoades

MMR:B

ENCLOSURES

Linkage group 1

- | | |
|--|---|
| 1. P br f ₁ bm ₂ | 13. $\frac{P + + an\ bm_2}{P\ br\ f_1 + bm_2} F_2$ |
| 2. p br f ₁ bm ₂ | 14. $\frac{p\ br\ f_1\ ad_1 +}{P\ br\ f_1 + bm_2} F_2$ |
| 3. $\frac{P}{+}$ br f ₁ bm ₂ | 15. $\frac{P\ br\ f_1\ an +}{P\ br\ f_1 + gs_1} F_2$ |
| 4. P an bm ₂ | 16. $\frac{P + + + + bm_2}{p\ ts_2\ br\ f_1\ an +} F_2$ |
| 5. p ad ₁ bm ₂ | 17. $\frac{P\ gl_{10}\ f_1\ an}{p + + an} F_2$ |
| 6. P gl ₁₀ f ₁ | 18. $\frac{P\ br\ f_1 + an}{p\ br\ f_1\ ad_1 +} F_2$ |
| 7. p br f ₁ ad ₁ * | 19. $\frac{p\ ts_2\ br\ f_1 + an}{p + br\ f_1\ ad_1 +} F_2$ |
| 8. p br ad ₁ * | 20. P sr |
| 9. f ₁ an may seg. bm ₂ * | |
| 10. p f ₁ bm ₂ * | |
| 11. ts ₂ f ₁ may seg. bm ₂ * | |
| 12. ts ₂ an may seg. f ₁ bm ₂ * | |

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Linkage group 2

- | | |
|--|---|
| 1. lg ₁ gl ₂ b v ₄ | 8. gl ₂ x sk F ₂ |
| 2. lg ₁ gl ₂ b v ₄ seg. ts ₁ * | 9. gl ₂ v ₄ seg. ts ₁ * |
| 3. fl v ₄ * | 10. gl ₂ fl v ₄ * |
| 4. lg ₁ B v ₄ | 11. gl ₂ fl |
| 5. lg ₁ b v ₄ | 12. lg ₁ v ₄ seg. ts ₁ * |
| 6. lg ₁ B ba ₂ seg. | 13. lg ₁ b sk v ₄ |
| 7. lg ₁ b ba ₂ seg. | 14. B sk |
| | 15. lg ₁ B seg. ts ₁ |

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Linkage group 3

- | | |
|--|---|
| 1. a_1 -na-ts ₄ | 10. a ₂ d ₁ -cr |
| 2. a_1 -ts ₄ | 11. lg ₂ -d ₁ |
| 3. $\frac{a_1 \text{ na } +}{+ + \text{ cr}}$ | 12. a_1 -lg ₂ |
| 4. $\frac{a_1 + d_1 \text{ cr}}{+ \text{ Rg } + +}$ | 13. a_1 -cr * |
| 5. a_1 -na-cr | 14. a_1 -Rg * |
| 6. a_1 -na-ts ₄ | 15. a_1 -ba ₁ |
| 7. $\frac{\text{cr } +}{+ \text{ pg}_2} \text{ F}_2 *$ | 16. cr ₁ -ms ₃ |
| 8. $\frac{a_1 \text{ ts}_4 +}{+ + \text{ cr}} \text{ F}_2 *$ | 17. pg ₂ -d ₁ seg. |
| 9. a_1 -na-ts ₄ -cr * | 18. $\frac{a \text{ ts}_4 +}{+ + \text{ ba}_1} \text{ F}_2$ |
| | 19. a_1 d ₂ |

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Linkage group 4

- | | | |
|---|---|---|
| 1. su Tu gl ₃ | 9. $\frac{\text{su Ts}_5 +}{+ + \text{ j}_2} \text{ F}_2$ | |
| 2. su gl ₃ | 10. su j ₂ | |
| 3. su Tu | 11. Su j ₂ | |
| 4. su Ts ₅ | 12. su st * | |
| 5. $\frac{\text{su Ts}_5 +}{+ + \text{ w}_1} \text{ F}_2$ | 13. su Tu Ts ₅ * | |
| 6. $\frac{\text{su Tu } +}{+ + \text{ w}_1} \text{ F}_2$ | 14. F ₂ seg. su and vp ₃ | |
| 7. $\frac{\text{su gl}_3 +}{+ + \text{ w}_1} \text{ F}_2$ | 15. su la * | |
| 8. $\frac{\text{su Tu } +}{+ + \text{ j}_2} \text{ F}_2$ | 16. Tu la * | |
| | 17. $\frac{\text{su } +}{+ \text{ lo}}$ | 18. $\frac{\text{su lo}}{+ +}$ |
| | 19. $\frac{\text{su sp}}{+ +}$ | 20. $\frac{\text{su } +}{+ \text{ sp}}$ |

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Linkage group 5

- | | |
|-----------------------|-----------------------------------|
| 1. pr v_2 | 10. bt_1 bm_1 * |
| 2. pr v_3 | 11. ys_1 pr bm_1 * |
| 3. v_2 pr bm_1 | 12. ys_1 pr bm_1 seg. v_2 * |
| 4. pr bm_1 | 13. pr v_{12} bm_1 * |
| 5. ys_1 pr bt | 14. pr v_3 bm_1 * |
| 6. a_2 - bt_1 -pr | 15. ys pr v_3 * |
| 7. v_2 ys_1 pr * | 16. v_2 -bv |
| 8. pr bv bm_1 * | 17. pr v_{12} |
| 9. v_2 pr bv * | |

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Linkage group 6^x

- | | |
|-----------------|------------------|
| 1. y Pl py | 9. Y Bh Pl |
| 2. Y Pl py | 10. y pl sm |
| 3. y pl py | 11. y-si-pl seg. |
| 4. y Pl py | 12. v_7 -y-pl |
| 5. po y Pl * | 13. v_7 -Y-pl |
| 6. po Y Pl * | 14. v_6 -Y-pl |
| 7. po y pl * | 15. v_6 -Yy-pl |
| 8. sm Py py ⊗ * | |

^x Stocks carrying al are not listed since there is considerable doubt that al belongs in this linkage group.

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Linkage Group 7

- | | |
|--|--|
| 1. bn gl ₁ v ₅ | 9. ra sl |
| 2. Bn gl ₁ v ₅ | 10. Bn gl ₁ sl may seg. ra |
| 3. gl ₁ ij seg. fr ₁ and fr ₂ | 11. bn gl ₁ sl |
| 4. ra-gl ₁ -v ₅ | 12. gl ₁ v ₅ va ₁ * |
| 5. ra v ₅ | 13. in gl ₁ v ₅ seg. |
| 6. Bn gl ₁ ra * | 14. in ij |
| 7. $\frac{+ \text{ra} +}{\text{gl}_1 + \text{ij}} F_2 *$ | 15. in gl ₁ |
| 8. Wh gl ₁ | 16. gl ₁ ij |
| | 17. gl ₁ sl ra |

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Linkage group 8

1. $\frac{j +}{+ ms_8} F_2$

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Linkage Group 9

- | | |
|---|---|
| 1. yg_2 c sh wx | 11. g_4 sh ar |
| 2. c sh wx v_1 | 12. au_1 au_2 |
| 3. c sh v_{15} wx | 13. c sh wx d_3 seg. |
| 4. ARC wx homozygous terminal knob on 9 * | 14. yg_2 sh d_3 seg. |
| 5. c sh bp wx * | 15. sh l_6 |
| 6. ar pk sh * | 16. sh-wx- w_{11} F_2 |
| 7. c sh wx | 17. $\frac{c \text{ sh wx } au_1}{C \text{ sh Wx } au_1}$ F_2 |
| 8. da_1 au_1 au_2 sh | 18. da au_1 sh |
| 9. c sh wx w_{11} seg. | 19. I sh |
| 10. sh ms_2 | |

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Linkage Group 10

- | | |
|-----------------------|--|
| 1. r g_1 | 7. pg_1 g_1 r seg. |
| 2. r g_1 nl_1 | 8. pg_1 l_2 seg. |
| 3. R g_1 nl_1 | 9. g_1 l_4 seg. |
| 4. R g_1 | 10. d_7 r g_1 seg. |
| 5. g_1 li | 11. r tester stock which does not carry the inhibitor of the mottling allelomorph. |
| 6. l_2 r g_1 seg. | 12. g_1 -r mottled |

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Multiple combinations involving two or more groups

A ₁ C-sh-wx r-g Pr	a ₁ r ^r C B-lg Y-pl pr j
A ₁ C-sh-wx r-g pr	a ₁ R C lg y pr j in Su
A ₁ C-sh-wx R-g Pr	a ₁ R c-wx Bb-lg Y-pl pr su
A ₁ C-sh-wx R-g pr	a ₁ R c-sh-wx B-lg Yy-Pl Pr su
A ₁ C-sh-wx R-g-nl Pr	a ₁ R ^g C pr Y in b pl *
A ₁ B-lg Y-Pl su-Tu	A ₁ c R ^g -g pr In Su su Y-pl
A ₁ B-lg Y-Pl Su-Tu	b-lg bm ₂ j may seg.
A ₁ B-lg y-Pl Su-Tu	cr ts ₂ d ₁
A ₁ B-lg y-Pl su-Tu	pr gl ₁ -v ₅
A ₁ B-lg y-Pl su-Tu+	pr lg in
A ₁ + + y-+ su-+-gl ₃ F ₁	lg gl ₁ -v ₅
BB-Lg lg Su-tu Yy-Pl pl wx *	pr in-gl ₁
Bb-lg Su su-tu Yy-Pl pl wx *	pr in-ij
BB-Lg lg su-Tu tu Yy-pl Wx wx *	pr-bm ₁ an *
Bb-Lg lg su-Tu tu Yy-pl Wx wx *	pr f ₁ -(Br br)-(Bm ₂ bm ₂) *
b-Lg lg su-tu y-pl wx *	pr lg-gl ₂ -b F ₂ *
a ₁ pr in wx y C R ^g Su su	pr ts ₄ *
a ₁ B Pl C R Pr Y	pr a ₁ -na-ts ₄ C R *
A ₁ -cr C R ^g pr su y-pl b-lg j	pr-bm ₁ su Tu tu *
a ₁ B-lg Y-Pl Pr C R	pr-bm ₁ y *
A ₁ B-lg y-pl Pr C R S	pr gl ₁ -ra *
A ₁ B Y-Pl Pr C R Su	pr-bm ₁ sh-wx *
A ₁ -cr C? r ^r -g pr in-Bn bn	pr-bm ₁ wx *
Su su y-pl b-lg bm ₂	pr-bm ₁ sh-wx su *
may seg. ts ₂ d ₁ j	pr-bm ₁ -v ₃ wx F ₂ *
A Cc R ^g pr In in Su su y-pl	bm ₁ -yg ₁ wx *
b-lg bm ₂ j v? may seg.	A R c-sh-wx pr-bm ₁ -v ₂ *
gl ₁ d ₁ cr ts ₂	A R C-sh-wx-v ₁ pr *
A ₁ R ^g c-Sh sh-wx pr in su y P ^{VV}	

lg-gl₂-b wx F₂ *
 a₁-ts₄ lg gl₂ F₂ *
 a₁-na-ts₄ C-R B Pl F₂ *
 bm₂ cr *
 bm₂ lg₁ g₁ *
 Ch j su *
 su-gl₃ lg₁-v₄ *
 a₁ B Pl c-sh-wx pr su-gl₃ *
 a₁ B Pl c-sh-wx P^v su-Tu *
 A c R pr lg₁ g₁ Su y Bn
 br-li seg. bd (branched silkless)
 g₁-li wx seg. bd.
 cr li gi
 ra g₁-li lg
 A B Pl li lg₁ f₁
 lg₁ g₁ f₁
 lg₁ ad-f₁
 ra₁ g₁ lg₁ br
 wx lg₁ gl₁
 cr ra₁ f₁
 a₁ r C pr wx y Bn ? *
 a₁ C r pr wx y Bn ?
 a₁ C R^g pr in y wx Su su
 A C r^g sh wx y pr Su su
 a C R^g pr Y pl in b
 A C R pr su Tu tu gl₃
 a₁ P sh-wx su lg-b f₁
 a₁ p sh-wx Su lg-b f₁

A B pl lg ts₁ F₂
 A C R b pl pr v₂
 A C R pr-bm₁ wx may seg. v₂
 A C R lg-B-v₄ pr bv Yy-pl F₂
 A C r j Y
 a₁-na-cr Y-pl gl₁-v₅
 a₁-na-cr Y-pl b-lg gl₁-v₅
 a₁-na b-lg Y-pl
 a₁-na-cr b-lg Y-pl
 a₁-Na na-Ts₄ ts₄ b-lg g₁
 a₁-na b-lg Y-pl gl₁-v₅
 A C R Pr gl₁-ra *
 A C R so₁ so₂
 Aa Rr-g₁ B Pl su
 #2 trisome
 #3 "
 #5 "
 #6 "
 #7 "
 #8 "
 #9 "
 #10 "
 A C (Rr)? Pr (Bb)? pl Yy
 tetraploid
 A C r^g b pl y Su tetraploid
 a₁ C R pr y Su
 A₁ c R Pr y Su
 A₁ C r pr y su *
 A₁ C R pr y

A₁ C R pr sh

A₁ B pl lg₁ y

A₁ c R sh wx b pl y

Three inbred strains of Leaming selfed for 29 years. *

Strain resistant to physiological forms 1 and 3 of Puccinia sorghi.

Strain susceptible to physiological forms 1 and 3 of P. sorghi.

Strain resistant to physiological form 1 but susceptible to physiological form 3 of P. sorghi.

List of reciprocal translocations at Cal. Tech.

<u>Pedigree No.</u>	<u>Chromosomes involved</u>
A 11	1- 7
A 12	1- 3
A 13	4- 9
A 14	4- 5
A 15	3-10
A 16	8-10
A 17	2- 7
A 18	3-10
A 19	2- 3
A 20	5-10
A 21	5- 8
A 22	8-10
A 23	6-10
A 24	1- 5
A 25	2- 7
A 26	3-10
A 27	3- 7
A 28	3- 5
A 29	1- 2
A 30	3- 6
A 31	3- 9
A 32	1- 5
A 33	2- 6
A 35	1- 9
A 36	4- 6
A 37	4- 6
A 38	3- 8
A 40	1- 5
A 41	2- 6
A 42	2- 4
A 43	1- 9

<u>Pedigree No.</u>	<u>Chromosomes involved</u>
A 52	3- 5
A 58	1- 3
A 61	4-10
A 62	8-10
A 64	1-10
A 66	4- 5
A 69	2- 7
A 70	4- 6
A 73	1- 7
A 74	1- 3
A 75	2- 5
A 76	2- 9
A 77	1- 9
A 78	2- 8
A 79	4- 9
A 80	2- 6
A 83	8- 9
A 84	8-10
A 85	4-10
A 87	1- 3
A 88	2- 4
A 90	2- 3
A 94	9-10
A101	2- 4
A103	1- 7
A111	6- 8
A118	2- 3
A119	6- 9
A122	1- 4
A129	2- 4
A133	3-10
A136	5- 7
A137	4- 7
C & A 125	3- 6
A & C 6452	5- 6
A & C 6460	2- 9
A & C 6462	4- 5
A & C 6465	3- 9
A & C 6466	1-10
A & C 6467	4- 8
A & C 6468	3- 5
A & C 6470	6- 9
A & C 6471	2- 6
A & C 6472	4- 5
A & C 6473	2-10
A & C 6474	3- 7
A & C 6475	5- 7
A & C 6477	3- 8