re_2 (reduced endosperm) chromosome 5. Eyster '31.

re_4 (reduced endosperm). Chromosome 4.

Rs_1 (rough sheath - dominant). Hadjinov.

rs_2 (rough sheath - recessive). Hadjinov.

Rw_1, etc. (row number genes). Tavcar.

si_2 (silky) (si_2 and si_3 are duplicate genes). Fraser.

si_3 (silky). Fraser.

su^{am} (an allelomorph of su). Mangelsdorf.

w_{12} (white seedling). Chromosome 4. Lindstrom.

ws_3 (white sheath). Rhoades.

yf (yellow flecked leaves). Chromosome 9. Eyster.

zg_2 (siz zag stalk). Chromosome 6. Singh.

Please add these to the list in the maize letter of January 23, 1933. We would appreciate it if you would notify us of any mistakes, oversights, etc. Notify this office of any new symbols you may wish to use before publishing so that we can help avoid duplication of symbols.

5. Linkage data from 3 point back crosses :-

Genetic constitution	Regions 0	1	2	1, 2	Total
$\frac{+\ +\ +}{pr\ ys\ v_2}$ *	79 - 70 : 149	20 - 15 : 35 : 15.8%	42 - 33 : 75 : 30.8%	6 - 1 : 7	266
$\frac{bm_1\ +\ +}{+\ pr\ ys}$	81 - 87 : 167	13 - 21 : 34 : 16.8%	6 - 5 : 11 : 6.1%	1 - 1 : 2	214
$\frac{+\ +\ +}{bm_1\ pr\ ys}$ (also seg. v_2 3:1)	118 - 79 : 197	21 - 21 : 42 : 17.8%	11 - 10 : 21 : 9.8%	0 - 5 : 5	265
$\frac{+\ +\ Ch}{bm_1\ yg_1\ ch}$ No linkage:	61 - 45 : 106	39 - 52 : 91 : 46%	59 - 54 : 103 : 49%	43 - 44 : 87	387
$\frac{+\ T5\text{-}7a\ bn}{gl_1\ +\ Bn}$	36 - 40 : 76	6 - 1 : 7 : 10.5%	2 - 8 : 10 : 12.6%	0 - 2 : 2	95 (bn-gl_1 18%)
$\frac{T5\text{-}7a\ +\ +}{+\ gl_1\ v_5}$	142 - 72 : 214	30 - 51 : 81 : 25.5%	12 - 31 : 43 : 14.5%	5 - 2 : 7 : 2.0%	345
$\frac{+\ +\ T5\text{-}7a}{ra\ gl_1\ +}$	107 - 74 : 181	4 - 3 : 7 : 4.0%	39 - 42 : 81 : 31.0%	3 - 1 : 4	273
$\frac{T_1\text{-}7\ +\ +}{+\ gl_1\ ij}$	292 - 201 : 493	6 - 7 : 13 : 2.6%	20 - 25 : 45 : 8.3%	1 - 0 : 1	552

* v_2 classification was not entirely satisfactory.

Burnham.

6. Notes on the above data :-

The linkage of T4-5a with yg_1 is the first found for yg_1. If it is in chromosome 5 it must be out in region where v_2 is or even nearer the end. Of course it may be in chromosome 4. The break in each chromosome was near the subterminal knob. The data on chromosome 7 are mostly from interchanges. In T5-7a both breaks were near the subterminal knobs, while in T1-7 the break in 7 was on the long arm not far from the spindle fiber insertion. The data indicate that Bn is out toward the end of the long arm, with ra near the break in 1-7 and gl_1 in between. Vp_2 apparently is on the bm_1 side of pr. Burnham.

E. G. Anderson

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

March 23, 1937

To Maize Geneticists:-

The information in this letter was contributed by a number of individuals, and has been organized into the following divisions:

I. General news items.
II. Collective publication of linkages.
III. Seed stocks grown in 1936.
IV. Seed stocks received for propagation in 1937.
V. List of genes not in Co-op.
VI. Tests of inbred strains for disease resistance.

Most of these reports are given almost verbatim but are not put in quotation marks because in numerous instances they have been somewhat condensed.

I. General News Items

Maize Genetics Cooperation, Ithaca, N. Y. -

1. Backcross data show that Hadjinov's barren stalk (ba_x) is allelomorphic to ba_2.

2. Seed received from L. C. Raymond, Quebec, labelled "Sweet Brittle", produced plants with brittle stalks and leaves. These plants differed from brittle stalk (bk_1. Wiggans, unpub.) in that they were normal size, and greenhouse tests show that "Sweet Brittle" and bk_1 are not alleles.

3. Backcross data show that Hadjinov's branched silkless (bd_x) is allelomorphic to Kempton's bd_1 (chrom. 7).

D. G. Langham

Cornell University, Ithaca, N. Y. -

1. Data sent by Anderson, with supplementary data of mine, show that sr (chrom. 1) is to the left of P, rather than between P and br as previously announced, and suggest that ts_2 is to the right of P. The following table includes the available data from three-point backcrosses:

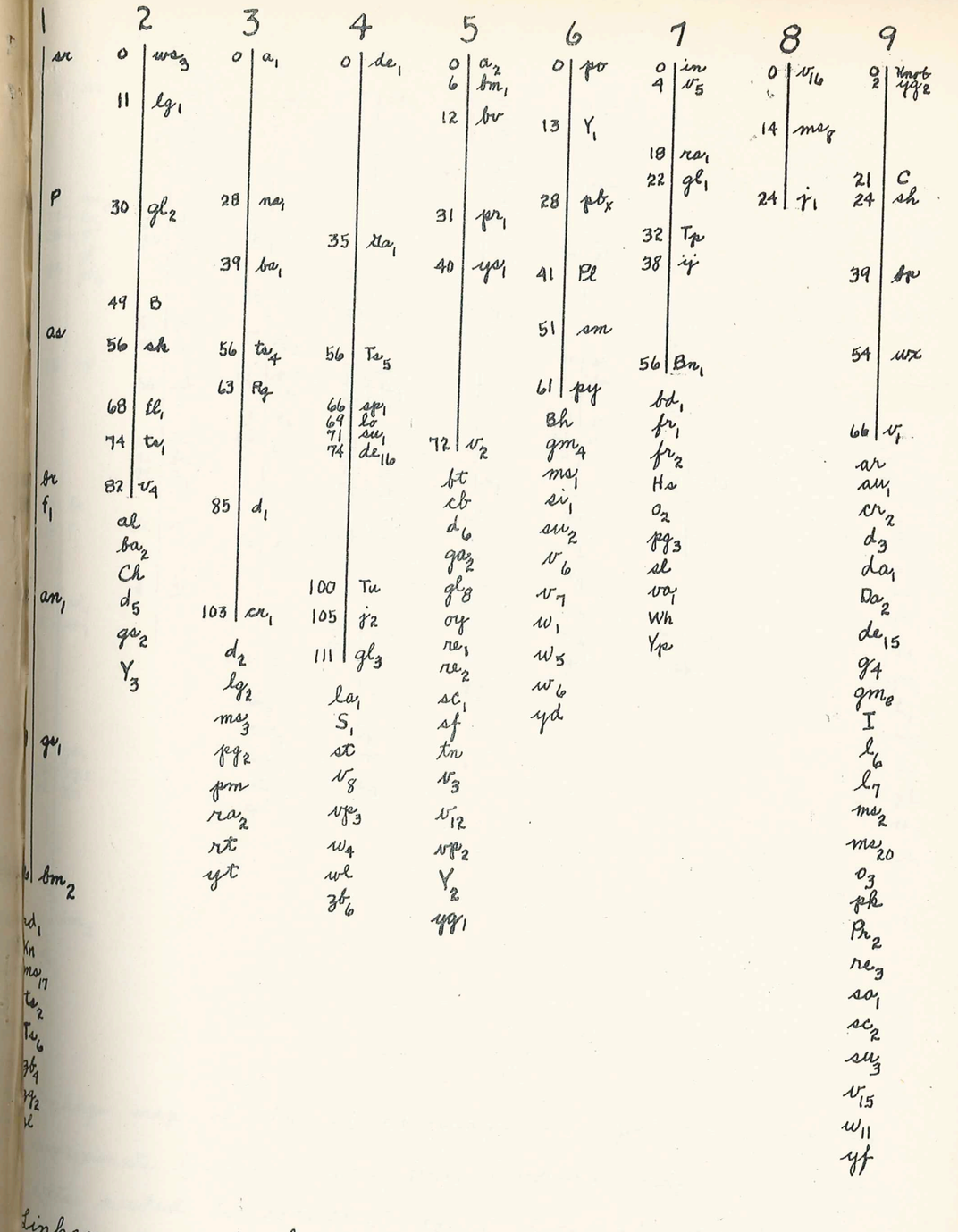
F_1 genotype	0	1	2	1,2	Total	Author
P + br / + T1-5b +	242	71 15.8%	108 24.1%	28 6.2%	449	Anderson
P + br / + T1-5c +	195	60 18.1%	58 17.5%	19 5.7%	332	Anderson
+ + T1-5b / sr P +	178	89 23.7%	88 23.5%	20 5.3%	375	Anderson

New Haven, Connecticut -

Pedigree	Date of Pollination	Erectness	No. plants	Smut plants	Smut ears	Good ears	Rust 1-10	Row No.	Notes
Co 206	8/15	/	13	0	0	9	1	14-16	fairly good
Co 208	8/13	/	15	0	0	13	6	12-14	slender, poorly filled
* Co 211	8/15	⌒	10	0	0	8	0	12	irregular rows, poorly filled
** Dr 276 A	8/21	/	19	0	0	14	5? all dead	12	sl. irr. rows, smooth dent
* WD 456 A2	8/20	/	16	0	0	13	2	20	good dent, vig., uniform, late
I 234	?	/	17	1	1	24	0	14-16	very good roots, 2 ears to stalk, sl. irregular rows
Co 214	?	/	8	0	0	10	0	16-18	irregular rows, poorly filled
** S 283	8/13	/	19	0	0	21	3	12	poorly filled
			17	0	0	17	0	12-16	reg. rows, well-filled, slender, green, good
Kvakan 6991	8/15	⌒	10	0	0	8	2	14-16	fair, early

* good ** very good

W. R. Singleton



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).