3. Linkage data involving T1-5 interchanges.*

The backcross data from crosses with P br f bm_2, bm_1 pr ys yg or a_2 bm_1 pr v_2 have been summarized in Tables 1 and 2 as 3-point data for use in establishing the order of the breakpoints in relation to the marker genes. A few are from F_2 and a few are from an interchange homozygote. The breakpoints are based mainly on pachytene analyses (made by John T. Stout, with a few by Dr. Wm. Weinheimer), combined with observations on intercrosses and the original observations of Longley, 1961.

An interchange designated SL has the breakpoint in the short arm of 1 and the long arm of 5, etc.

Many of the complementary recombination classes deviate greatly from 1:1. The yg class is often deficient, but not as much so as the v_2 class. For chromosome 1, based on 384 plants from backcrosses of normal plants, the recombination values were: P-br = 46.6%, br-f = 4.7%, f-bm_2 = 41.9%. For chromosome 5, based on 1086 plants from backcrosses of normal plants, the recombination values were: bm-Pr = 14.5%, pr-ys = 12.7%, ys-yg = 33.3%. Based on 180 plants in the A_2 class: a_2-bm = 3.9%, bm-pr = 20.0%, pr-v_2 = 28.9%. If the same data are used, but the Pr-pr locus omitted, the recombination values in the A_2 class (175 plants) were: A_2-bm = 4.0%, A_2-v_2 = 37.7%; and in the a_2 class (227 plants) they were: a_2-bm = 14.5%, a_2-v_2 = 48.9%. The Bm:bm ratio was a perfect 1:1 and the V_2:v_2 ratio was 231:171, a large deviation from 1:1 but only slightly greater than that for A_2:a_2. No explanation is offered.

Chromosome 5 data for the interchanges

The 3-point data for the LL-3 heterozygote are not decisive, but the test for linkage in the homozygote shows that the breakpoint was not in the pr-ys-yg region. This places it in the bm-pr region.

The data from the SL-5 homozygote (breakpoint in 5 at L.19) show that bm and pr are no longer linked. Hence pr is distal to this breakpoint. The 3-point backcrosses for the heterozygote will be grown this summer. The LS-3 data are of some interest. The break is in the short arm but the order indicated in one test is A_2-bm-T, with a recombination

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Table 1

Linkage data involving the T1-5 interchanges and genetic markers in chromosome 5.
All are backcrosses unless marked otherwise.

	genotype	parental 0		recomb. in 1		recomb. in 2		recomb. in 1,2		total plants	% recomb. in 1	% recomb. in 2	% recomb. end markers	Code no.
1-5(044-10) L.05-S.83‡	no data													SS-1
1-5e S.08-S.16	$\frac{T + Pr}{+ bm\ pr}$	139	117	2	17	14	24	1	1	315	6.7	12.7	18.1	SS-2
1-5(8972) S.56-S.29‡	$\frac{T + Pr}{+ bm\ pr}$	57	46	1	5	12	20	-	1	142	4.9	23.2	26.8	SS-3
1-5(5525) S.66-S.52	$\frac{T + Pr}{+ bm\ pr}$	180	225	13	14	38	27	9	5	511	8.0	15.4	18.0	SS-4
"	$\frac{T\ A_2 +}{+\ a_2\ bm}$	37	43	2	14	1	7	-	-	103	17.1	9.7	20.5	"
1-5 i S.69-S.71	$\frac{T + Pr}{+ bm\ pr}$	119	123	23	22	11	13	8	8	327	18.7	12.2	21.1	SS-5
"	$\frac{T\ A_2 +}{+\ a_2\ bm}$	158	172	32	27	11	19	12	3	434	17.1	10.4	20.5	SS-5
1-5f L.09-L.20	$\frac{+\ T\ Pr}{bm + pr}$	149	176	1	0	6	7	1	0	340	0.6	4.1	4.1	LL-1
"	$\frac{T\ Pr + +}{T\ pr\ ys\ yg}$	15	21	7	2	4	7	8	1	65	27.7	30.8	30.8	"
"	$\frac{T\ Pr +}{T\ pr\ ys}$	17	32	10	5					64	23.4			"
1-5H L.09-L.50	no data													LL-2

Table 1. (continued)

	genotype	parental 0		recomb. in 1		recomb. in 2		recomb. in 1,2		total plants	% recomb. in 1	% recomb. in 2	% recomb. end markers	Code no.
1-5c L.44-L.34	$\frac{T + +}{+ ys\ yg}$	92	40	1	13	42	30	6	10	234	12.8	41.9	36.8	LL-3
"	$\frac{pr\ T +}{Pr + ys}$	76	82	3	8	6	16	0	2	193	6.7	12.4	17.1	"
1-5a L.58-L.45	$\frac{+ T +}{bm + ys}$	65	49	3	7	3	3	1	0	131	8.4	5.3	12.2	LL-4
1-5(7267) L.92-L.82‡	$\frac{+ T +}{ys + yg}$	95	50	33	6	5	16	10	6	221	24.9	16.7	27.1	LL-5
1-5(8782) S.02-L.01	$\frac{T + Pr}{+ bm\ pr}$	131	110	2	3	10	7	1	2	266	3.0	7.5	8.3	SL-1
1-5b S.09-L.05	$\frac{T + +}{+ ys\ yg}$	69	47	5	30	46	22	3	14	267	19.8	32.2	38.6	SL-2
1-5(7219) S.15-L.33	$\frac{T\ Pr +}{+ pr\ ys}$	122	125	1	3	3	2	1	1	258	2.3	2.7	3.5	SL-3
"	$\frac{T\ Pr +}{+ pr\ v_2}$*	62			7		33		3	105	9.5	34.3	38.1	"
"	$\frac{+\ T\ Pr}{bm + pr}$	125	127	0	0	1	4	0	1	258	0.4	2.3	1.9	"
"	$\frac{T + +}{T\ ys\ yg}$**F_2									32	32.3			"
1-5(6899) S.37-L.11	$\frac{T\ Pr +}{+ pr\ ys}$	106	114	4	11	8	13	1	2	259	6.9	9.3	13.9	SL-4
"	$\frac{A_2 + T}{a_2\ bm +}$	143	245	4	24	39	6	4	6	471	8.1	11.7	15.5	"

Table 1. (continued)

	genotype	parental 0		recomb. in 1		recomb. in 2		recomb. in 1,2		total plants	% recomb. in 1	% recomb. in 2	% recomb. end markers	Code no.
"	$\frac{T\ Pr\ +\ +}{T\ pr\ ys\ yg}$ **F_2									92	16.7	18.0		"
1-5(4613) S.78-L.19	$\frac{T\ +\ Pr\ +}{T\ bm\ pr\ ys}$	48	44	37	52	5	5	9	11	211	51.7	14.2		SL-5
1-5(5045) S.94-L.45	$\frac{Pr\ T\ +}{pr\ +\ ys}$	238	282	4	2	6	32	4	0	568	1.8	7.5	7.7	SL-6
"	$\frac{+\ Pr\ T}{bm\ pr\ +}$	239	311	3	3	5	0	2	5	568	2.3	2.1	1.9	"
1-5(6197) L.02-S.01	$\frac{T\ +\ Pr}{+\ bm\ pr}$	164	131	10	2	11	17	1	1	337	4.1	8.9	11.9	LS-1
1-5(043-15) L.10-S.42	no data													LS-2
1-5(6401) L.16-S.19	$\frac{T\ +\ Pr}{+\ bm\ pr}$	55	82	3	-	-	2	2	-	144	3.5	2.8	3.5	LS-3
"	$\frac{A_2\ +\ T}{a_2\ bm\ +}$	129	123	4	5	4	6	0	0	271	3.3	3.7	7.0	"
1-5(070-12) L.34-S.62	no data													LS-4
1-5(7212) L.44-S.21	$\frac{T\ +\ Pr}{+\ bm\ pr}$	160	157	1	4	7	12	2	1	344	2.3	6.4	7.0	LS-5
"	$\frac{A_2\ T\ +}{a_2\ +\ bm}$	64	62	8	1	-	1	1	1	138	8.0	2.2	7.2	"
1-5(4597) L.51-S.44	$\frac{T\ +\ Pr}{+\ bm\ pr}$	114	114	4	10	12	17	-	-	271	5.2	10.7	10.7	LS-6

Table 1. (continued)

	genotype	parental 0		recomb. in 1		recomb. in 2		recomb. in 1,2		total plants	% recomb. in 1	% recomb. in 2	% recomb. end markers	Code no.
"	$\frac{T\ A_2 +}{+\ a_2\ bm}$	132	144	4	22	3	6	12	2	325	12.3	7.1	10.8	"
1-5g L.56-S.78	$\frac{T + Pr}{+\ bm\ pr}$	115	88	45	45	25	19	8	10	355	30.4	17.5	37.7	LS-7
1-5(8041) L.80-S.10	$\frac{T + Pr}{+\ bm\ pr}$	343	432	6	5	42	28	9	3	868	2.6	9.4	9.3	LS-8

‡ - breakpoints are those reported by Longley, 1961

* - A_2 data only

** - F_2 data only

Table 2

Linkage data involving T1-5 interchanges and genetic markers in chromosome 1

	genotype	parental 0		recomb. in 1		recomb. in 2		recomb. in 1,2		total plants	% recomb. in 1	% recomb. in 2	% recomb. end markers	Code no.
1-5e S.08-S.16	+ T + / P + br	8	10	3	2	3	3	0	5	34	29.4	32.4	32.4*	SS-2
1-5(5525) S.66-S.52	T + + / + P br	28	17	2	9	14	24	4	1	99	16.2	43.4	49.5	SS-4
1-5i S.69-S.71	T + + / + P br	42	21	4	7	11	22	5	2	114	15.8	35.1	38.6	SS-5
1-5a L.58-L.45	+ + T / br f +	86	70	4	2	4	6	0	2	174	4.6	6.9	9.2	LL-4
1-5b S.09-L.05	T + + / + br bm	11	9	0	7	9	10	0	1	47	17.0	42.6	55.3	SL-2
1-5(6899) S.37-L.11	T + + / + P br	30	29	1	7	18	25	2	3	115	11.3	41.7	44.3	SL-4
1-5(4613) S.78-L.19	T + + / + P br	25	29	3	3	13	30	4	2	109	11.0	44.9	44.9*	SL-5
1-5(5045) S.94-L.45	T + + / + P br	17	15	10	5	10	10	6	6	79	34.2	40.5	44.3	SL-6
1-5(7212) L.44-S.21	T + + / + br bm	41	53	0	3	30	52	2	0	181	2.8	46.4	47.0	LS-5
1-5(4597) L.51-S.44	T + + / + br bm	55	50	5	3	29	23	3	6	174	9.8	35.1	34.5	LS-6
1-5g L.56-S.78	T + + / + br bm	32	33	1	5	20	22	0	2	115	7.0	38.3	41.7	LS-7
1-5(8041) L.80-S.10	+ T + / br + bm	8	4	4	5	1	2	1	0	25	40.0	16.0	48.0	LS-8

value of 3.7 for bm-T. The other test is non-discriminatory. The bm marker is known to be in the short arm, very close genetically to the centromere. If it is a centromere marker, then this order shows the interchange is SL and not LS. The diakinesis observations from the intercrosses indicate this interchange is either SL or LS. The pr marker is at about 5L.3, ys is distal to SL-6 at 5L.45, yg is distal to LL-5 at 5L.82.

The data for chromosome 1 markers are based on relatively small numbers.

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4. A stain for pollen sterility determinations.*

A simple staining technique can be used for efficient and accurate recording of pollen sterility. Certain advantages result from the use of a gel-like mixture prepared as follows:

1 gm of agar is dissolved in 50 ml of distilled water and boiled for 3 minutes.

6 ml of strong I_2KI is added to the agar (0.3 gm I_2 and 1.0 gm KI in 100 cc H_2O).

14 ml of 1N HCl is added.

Allow to cool and mix well.

Pollen forced from the anther into the substance will stain immediately. Mixing the pollen well before placing a cover glass (one-third size) over it insures random dispersal of grains for predetermined sweeps of the slide. Differential dispersion of aborted and viable grains to the edges of the cover glass does not take place. The gel also prevents subsequent movement of grains on the slide during the counting. Three sweeps will usually constitute over 500 counted grains in a minimal amount of time. The mixture maintains its gel and staining properties for long periods of time at room temperature, even though the color of the mixture fades.

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