parent is heritable. In the following, 2698 ($\underline{a_2}$ $\underline{B}$ $\underline{Pl}$ $\underline{R^r}$), stock 6, their F_1, backcrosses to 6 and selfs of backcrosses are compared in maternal haploid frequencies when outcrossed to $\underline{gl_1}$. In the "segregating" progenies only $\underline{R^r}$ $\underline{B}$ $\underline{Pl}$ plants were tested. Haploids were verified by root-tip chromosome checks.

Male	No. plants Tested	No. Seedlings	No. Haploids	% Haploids
2698	3	1298	2	0.15
6	5	1531	35	2.29
F_1	4	3109	13	0.42
F_1 x 6	9	3694	44	1.19
(F_1 x 6) self	9	3611	46	1.27

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3. Chromosome 9 linkage.

The following table includes new data, sums of new data with those reported last year, and one correction, indicated by an asterisk:

Genes X Y	Phase	XY	Xy	xY	xy	Total	Recomb.
Ar Bk_2	RS	355	200	188	2	745	10
Ar Ms_2	RS	328	167	144	0	639	<8
Ar Wx	CS	1214	87	67	310	1678	10
Bf Bk_2	CS	126	34	22	8	190	46
	RS	288	81	112	17	498	41
Bf Bm_4	RS	249	120	129	0	498	<9
Bk_2 Bm_4	CS	752	196	218	80	1246	45
Bk_2 Gl_{15}	CS	209	7	17	41	274	9
Bk_2 V	RB	2	47	37	6	92	9
Bk_2 Wx	RB	6	43	36	7	92	14
	CS	367	39	49	72	527	20
	RS	688	269	316	15	1268	23
Bz Sh	CB	1025	19	21	974	2039	2
Bz V	CB	771	260	240	713	1984	25
Bz Wx	CB	887	157	136	859	2039	14
D3 Wx	CB	67	7	5	63	142	8
	CS	964	57	125	208	1354	14
$Gl_{15}Ms_2$	RS	271	128	80	0	479	<11
Gl_{15}Wx	CB	170	12	14	187	383	7*
Ms_2 Pg_{12}	RS	359	142	206	0	707	<8
Ms_2 Wx	RS	1235	488	645	0	2368	<4
Pg_{12}Wx	CS	797	44	31	209	1081	7
V Wx	CB	913	146	146	891	2096	14

It should be pointed out that Bf_1 is treated as recessive in the above, since it is classified only in the seedling stage.

Data from the following 3-point tests are included above.

F_1	Parental	Reg.1	Reg.2	1 - 2	Total
wx v + + + bk	36 42 78	1 5 6 6.5%	6 1 7 7.6%	1 0 1 1.1%	92
+ + + sh bz wx	870 840 1710	19 17 36 1.8%	155 134 289 14.2%	2 2 4 0.2%	2039
+ + + sh wx d_3	58 48 106	15 9 24 16.9%	5 5 10 7.0%	2 0 2 1.4%	142

The following 4-point test is also included:

F_1	Parental	Reg. 1	Reg. 2	Reg. 3	1-2	1-3	2-3	1-2-3	Total
+ + + + sh bz wx v	747 676 1423	15 11 26 1.3%	141 109 250 12.6%	111 125 236 11.9%	2 2 4 0.2%	4 6 10 0.5%	13 22 35 1.8%	0 0 0	1984
		sh-bz 2.0	bz-wx 14.6	wx-v 14.2					

No improvements in the map can be made over the one presented last year; with further refinement of the data, the 6 clustered factors appear to be still more tightly disposed in relation; in fact the order of factors between Wx and Bk_2 is entirely open, and will remain so until double mutants and backcross data are obtained for Ar, D_3, Gl_{15}, Ms_2, Pg_{12}, and V. These are all very nearly the same distance from Wx (4-14 units); all overlap in their 5% probability limits on the map.

Tests for inclusion of some of these factors between the break points of translocations 1-9a and 1-9c, in which a plant heterozygous for the two translocations will produce a female-transmissible deficiency between the break points on the long arm of the ninth chromosome, have been carried out. The test consists in crossing the 1-9a/1-9c heterozygote by the recessive. Turcotte (Maize Newsletter 30:164, 1956) has reported that Ar is included in the deficiency. This has been confirmed. Tests of d_3, gl_{15} and $+/ms_2$ were negative. Tests of pg_{12} were also negative, but since this is a duplicate factor system there is no assurance that positive results would have been obtained, even if the deficiency included pg_{12}.

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