

Table 1

	Backcross	Br ₂ /-	br ₂ /br ₂	Total
1.	Br ₂ /Br ₂ x (br ₂ /br ₂ x TB-1a)(hypoploid plant)	26	0	26
2.	Br ₂ /br ₂ x " " "	37	28	65
3.	br ₂ /br ₂ x " " "	0	278	278*

*combined data from several families

The testcross data in table 2 were obtained by the use of reciprocal translocation stocks involving chromosome 1.

Table 2.

Translocation	Break Point	XY	xY	Xy	xy	Total	% Recomb.
1. T1-8	1S .39 8L .07	137	84	71	133	425	36.47
2. T1-6c	1S .25 6L .27	175	54	80	146	455	29.45**
3. T1-3	1 cent. 3 cent.	134	48	28	127	337	22.55**
4. T1-9	1L .19 9S .20	117	16	3	133	269	7.06**
5. T1-8	1L .22 8L .78	172	22	12	146	352	9.66**

X=translocation heterozygote;x=normal;Y=normal ht.;y=brachytic-2

** X² for independence P > .01

The data in table 2 again indicate that brachytic-2 is located in the long arm of chromosome 1.

Brachytic-1 dwarf is also located in the long arm of chromosome 1. The test for allelism of these two dwarf mutants is negative. The F₂ of these two dwarf mutants segregated 228 normal: 184 dwarf (X² for 2 9:7 ratio = .1368; P=.75-.50). Brachytic 1 and 2 should therefore be over 50 cross-over units apart in the long arm of chromosome 1.

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5. Frequency of seed set in an F₁ hybrid of *Tripsacum* and corn.

Well-established clonal divisions of the F₁ hybrid of *T. dactyloides* (3n=54) x *Zea mays* var. Puño (originally produced by Lois Farquharson) were allowed to open-pollinate in the nursery. Out of a total of 417 spikelets, 25 produced well developed seeds (6.0% seed-set). In hand pollinations, using corn as the male parent, 6 seeds were obtained from a total of 50 spikelets pollinated (12% seed-set). Nine of the 31 seeds germinated and two of these produced twin seedlings. The occurrence of twins indicates that the polyembryony of the *Tripsacum* parent was transmitted to the hybrid. The open-pollinated seedlings could be backcrosses to corn or *Tripsacum*, selfs, or apomicts. Cytological analysis of the plants is necessary to determine their chromosomal

Cross	No. of plants observed		Expected ratio	P value
	Res.	Susc.		
(W64A x LP) x W64A	30	29	1:1	0.80-0.90
Tx 325 x W37A F ₂	147	46	3:1	0.70-0.80
NC13 x W37A F ₂	150	45	3:1	0.50-0.70
(Field Data)				
B10 x GE440 F ₂	202	60	3:1	0.30-0.50
Oh41 x GE440 F ₂	187	68	3:1	0.50-0.70
B10 x LP F ₂	157	54	3:1	0.80-0.90
Oh41 x LP F ₂	186	63	3:1	0.90-0.95
(Oh07A x GE440) x Oh07A	92	97	1:1	0.70-0.80
(W22R x GE440) x W22R	97	110	1:1	0.30-0.50
(Oh07A x LP) x Oh07A	96	87	1:1	0.50-0.70
(W22R x LP) x W22R	102	98	1:1	0.70-0.80

a/ LP = Ladyfinger popcorn

To determine the relationship of the genes for resistance in the 3 resistant sources, the cross W37A x GE440 was advanced to the F₂ generation and the cross GE440 x Ladyfinger popcorn was crossed reciprocally with the susceptible hybrids Hy2 x Oh07 and WF9 x W22R as well as advanced to the F₂ generation. The genes in the 3 resistant sources appear to be identical, alleles, or very closely linked as indicated by the following data:

Cross	Number of plants in the greenhouse		Number of plants in the field	
	Res.	Susc.	Res.	Susc.
W37A x GE440	300	0		
GE440 x LP ^{a/} F ₂	110	0	297	0
(GE440 x LP) x (Hy2 x Oh07)	113	0	233	0
(Hy2 x Oh07) x (GE440 x LP)	112	0	240	0
(GE440 x LP) x (WF9 x W22R)	424	0	210	0
(WF9 x W22R) x (GE440 x LP)	109	0	229	0

a/ LP = Ladyfinger popcorn