Table 3. Three point linkage data for fl1 v4 Enr1-628.

Region	Phenotype	No.	Totals
0	FI V Enr	425	
	fl v enr	465	890
1	Fl v enr	45	
	fl V Enr	71	116
2	FI V enr	54	
	fl v Enr	51	105
1+2	Fl v Enr	3	
	fl V enr	8	11
Totals			1122
f 1 - v4 = 11.3 + / -	0.9 cM		

Testcross: [FI1 V4 Enr1-628 X fl1 v4 enr1] X fl1 v4 enr1

v4 – enr1 = 10.3 +/- 0.9 cM

Table 4. Three point linkage data for fl1 v4 Enr*-459A.

Testcross:	[FI1 V4 Enr*-459A X fl1 v4 enr] X fl1 v4	enr
		· · · ·
Dogion	Phonotypo	No

Region	тпепотуре	NU.	101813
0	FI V Enr	734	
	fl v enr	768	1502
1	Fl v enr	121	
	fl V Enr	125	246
2	FI V enr	108	
	fl v Enr	88	196
1+2	Fl v Enr	13	
	fl V enr	6	19
Totals			1963
f/1 - v4 = 13.5 + -0.8 c	N		

Totala

 $v4 - enr^* = 11.0 + -0.7$ cM

Table 5. Three point linkage data for fl1 Enr*-459B v4.

Testcross: [FI1 Enr*-459B V4 X fl1 enr v4] X fl1 enr v4

Region	Phenotype	No.	Totals
0	FI Enr V	341	
	fl enr v	376	717
1	Fl enr v	24	
	fl Enr V	19	43
2	FI Enr v	28	
	fl enr V	22	50
1+2	FI enr V	3	
	fl Enr v	4	7
Totals			817
$fl1 - enr^* = 6.1 + - 0.8 c$	M		

 $enr^* - v4 = 7.0 + -0.9 \text{ cM}$

v4 flank the centromere of chromosome 2; it is not presently known on which chromosome arm *enr*² resides.

The three point linkage data presented in Table 3 establish the following relationship: f/1 - 11.3 - v4 - 10.3 - enr1. The f/1 - v4 interval is shorter in this test, but the v4 - enr1 interval is similar to other reported data.

For the partially characterized *enr* factors *Enr*-459A* and *Enr*-459B*, the following linkage order and distances (in centiMorgans) were established: f/1 - 13.5 - v4 - 11.0 - Enr*-459A (Table 4); and f/1 - 6.1 - Enr*-459B - 7.0 - v4 (Table 5). The f/1 - v4 distances established by these tests (13.5 cM and 13.1 cM, respectively) agree with each other and are close to that reported on the 1993 genetic map of chromosome 2 (15 cM; Neuffer et al., Mutants of Maize, Cold Spring Harbor Laboratory Press, 1997).

The gene order established by these two tests taken together, *fl1* $Enr^*-459B v4 Enr^*-459A$, as well as the map distances, are consistent with those of *enr1* and *enr2* (Stinard, Kermicle, and Sachs 2009; and this report). It is likely that Enr^*-459A and Enr^*-459B are alleles of *enr1* and *enr2*, respectively. Direct mapping tests of Enr^*-459A with *enr1* and *Enr^*-459B* with *enr2* are in progress.

Two point linkage data for 3L mutants w*-5787 and yel*-8630 --Stinard, PS; Jackson, JD

We report F2 linkage data for the 3L seedling lethal mutants w^* -5787 and yel^* -8630 with respect to wx1-marked A-A translocations. Both mutants are uncovered by TB-3La and therefore lo-

tions. Both mutants are uncovered by TB-3La and therefore located distal to the 3L breakpoint (3L.10) of TB-3La. Plants heterozygous for w^* -5787 were crossed to a line homozygous for wx1T3-9c (breakpoints 3L.09; 9L.12). F1 kernels were planted in our summer nursery and the resulting plants self-pollinated. F2 kernels from the selfed ears were separated into starchy (Wx) and waxy (wx) classes, planted in a sand bench, and the resulting seedlings scored for green (W) vs. albino (w). Roughly half the ears segregated for albino seedlings and the data from those ears were pooled and are summarized in Table 1. A similar crossing scheme was used to map *yel*-8630* with respect to *wx1* T3-9c and *wx1* T3-9(8562) (breakpoints 3L.65; 9L.22). Linkage distances were calculated according to the product method (Immer, Genetics 15:81-98, 1930) and are summarized in Table 1.

Table 1. F2 linkage data for w*-5787 with respect to wx1 T3-9c and ye/*-8630 with respect to wx1 T3-9c and wx1 T3-9(8562).

mutant	translocation	Wx W	Wx w	wx W	WX W
w*-5787	wx1 T3-9c	1130	464	390	43
ye/*-8630	wx1 T3-9c	1076	497	463	3
yel*-8630	wx1 T3-9(8562)	407	169	105	26

Map distance w*-5787 - wx1 T3-9c = 32.1 +/- 2.0 cM Map distance ye/*-8630 - wx1 T3-9c = 8.3 +/- 2.2 cM

Map distance ye/=8630 - wx713-9(8562) = 42.7 +/- 3.0 cM

Linkage of wx1 with chromosome 3 markers in crossings involving 3-9 translocations is dependent upon the linkage of wx1and the chromosome 3 markers with the 3-9 cytological breakpoints. The only data that are directly comparable are those involving the same translocation, in this case T3-9c. We conclude that yel^*-8630 is located relatively close, but distal to the 3L.09 breakpoint (separation between yel^*-8630 and wx1 of 8.3 cM), and that w^*-5787 is located farther out on the long arm of chromosome 3 (separation between w^*-5787 and wx1 of 32.1 cM).

d4 is allelic to d1

--Stinard, PS

The Maize Genetics Stock Center recently received a stock of the andromonoecious dwarf plant mutant d4 from Ron Phillips of the University of Minnesota. d4 was first reported by Suttle (Cornell Univ. Ph.D. Dissertation, 1924) and appears in Emerson, Beadle, and Fraser's (1935) gene list, but no further information appears in the literature. We figured that it was found to be allelic to some other better characterized dwarf mutant and disappeared from the literature for that reason, but could find no report of allelism. We conducted tests of allelism of d4 with the andromonoecious dwarfs d1, d3, d5, and an1 and found it to be allelic to d1. We renamed the mutant allele we received from Ron Phillips d1-4.