

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

Testcross: *[Fl1 V4 Enr1-628 X fl1 v4 enr1] X fl1 v4 enr1*

Region	Phenotype	No.	Totals
0	Fl V Enr	425	
	fl v enr	465	890
1	Fl v enr	45	
	fl V Enr	71	116
2	Fl V enr	54	
	fl v Enr	51	105
1+2	Fl v Enr	3	
	fl V enr	8	11
Totals			1122

fl1 - v4 = 11.3 +/- 0.9 cM
v4 - enr1 = 10.3 +/- 0.9 cM

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

Testcross: *[Fl1 V4 Enr*-459A X fl1 v4 enr] X fl1 v4 enr*

Region	Phenotype	No.	Totals
0	Fl V Enr	734	
	fl v enr	768	1502
1	Fl v enr	121	
	fl V Enr	125	246
2	Fl V enr	108	
	fl v Enr	88	196
1+2	Fl v Enr	13	
	fl V enr	6	19
Totals			1963

fl1 - v4 = 13.5 +/- 0.8 cM
*v4 - enr** = 11.0 +/- 0.7 cM

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

Testcross: *[Fl1 Enr*-459B V4 X fl1 enr v4] X fl1 enr v4*

Region	Phenotype	No.	Totals
0	Fl Enr V	341	
	fl enr v	376	717
1	Fl enr v	24	
	fl Enr V	19	43
2	Fl Enr v	28	
	fl enr V	22	50
1+2	Fl enr V	3	
	fl Enr v	4	7
Totals			817

*fl1 - enr** = 6.1 +/- 0.8 cM
enr - v4* = 7.0 +/- 0.9 cM

v4 flank the centromere of chromosome 2; it is not presently known on which chromosome arm *enr2* resides.

The three point linkage data presented in Table 3 establish the following relationship: *fl1 - 11.3 - v4 - 10.3 - enr1*. The *fl1 - 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: *fl1 - 13.5 - v4 - 11.0 - Enr*-459A* (Table 4); and *fl1 - 6.1 - Enr*-459B - 7.0 - v4* (Table 5). The *fl1 - 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 located distal to the 3L breakpoint (3L.10) of TB-3La. Plants heterozygous for *w*-5787* were crossed to a line homozygous for *wx1 T3-9c* (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 *yel*-8630* with respect to *wx1 T3-9c* and *wx1 T3-9(8562)*.

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

Map distance *w*-5787 - wx1 T3-9c* = 32.1 +/- 2.0 cM
 Map distance *yel*-8630 - wx1 T3-9c* = 8.3 +/- 2.2 cM
 Map distance *yel*-8630 - wx1 T3-9(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 *wx1* and 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*.