Table 3. Three point linkage data for fl1 v4 Enr1-628.
Testcross: [F11 V4 Enr1-628 X fl1 v4 enr1] X f11 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 | FI V enr | 54 |  |
|  | fl v Enr | 51 | 105 |
| $1+2$ |  |  |  |
|  | Fl v Enr | 3 |  |
|  | fl V enr | 8 | 11 |
| Totals |  |  |  |

fl1-v4 = $11.3+/-0.9 \mathrm{cM}$
$v 4-e n r 1=10.3+/-0.9 \mathrm{cM}$
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 | 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 |

fl1 $-v 4=13.5+/-0.8 \mathrm{cM}$
$v 4-e n r^{*}=11.0+/-0.7 \mathrm{cM}$
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 |  |  |  |

fl1 - enr* $=6.1+/-0.8 \mathrm{cM}$
$e n r^{*}-v 4=7.0+1-0.9 \mathrm{cM}$
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 f11 - v4 interval is shorter in this test, but the v 4 - 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 f11-6.1-Enr*-459B-7.0-v4 (Table 5). The f11 - 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 $2(15 \mathrm{cM}$; 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 $w^{\star-5787}$ and yel*-8630

--Stinard, PS; Jackson, JD
We report F2 linkage data for the 3L seedling lethal mutants $w^{*}-5787$ and $y$ ye $l^{*}-8630$ 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 $w \times 1$ 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 $w x 1$ 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 |
| :--- | :--- | :--- | :--- | :--- | :---: |
| $w^{*}-5787$ | wx1 T3-9c | 1130 | 464 | 390 | 43 |
| yel*-8630 | wx1 T3-9c | 1076 | 497 | 463 | 3 |
| yel*-8630 | wx1 T3-9(8562) | 407 | 169 | 105 | 26 |

Map distance $w^{*}-5787-w x 1$ T3-9c $=32.1+/-2.0 \mathrm{cM}$
Map distance yel* ${ }^{*} 8630-w x 1$ T3-9c $=8.3+/-2.2 \mathrm{cM}$
Map distance yel*-8630 - wx1 T3-9(8562) $=42.7+/-3.0 \mathrm{cM}$
Linkage of wx1 with chromosome 3 markers in crossings involving 3-9 translocations is dependent upon the linkage of $w \times 1$ 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 $w \times 1$ of 8.3 cM ), and that $w^{*}$-5787 is located farther out on the long arm of chromosome 3 (separation between $w^{*}-5787$ and $w \times 1$ of 32.1 cM ).

## $d 4$ is allelic to d1

--Stinard, PS
The Maize Genetics Stock Center recently received a stock of the andromonoecious dwarf plant mutant $d 4$ from Ron Phillips of the University of Minnesota. $d 4$ 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 $d 4$ with the andromonoecious dwarfs $d 1, d 3, d 5$, and an1 and found it to be allelic to $d 1$. We renamed the mutant allele we received from Ron Phillips d1-4.

