lings were pale-green and when self-pollinated these plants gave ears with all pale kernels.

New designations have been assigned to these alleles and they have been placed in the main collection. Stocks with this same phenotype that were found to complement *w3* will be tested for allelism with other stocks linked to pale endosperm.

Previous designation	allelism test with *w3*	New designation	MGCSC: stock number
5902D *w-vp*-84-5020-4*	3 positive	*w3-84-5020-4*	211I
5902F *pale-y*-84-5032-21*	3 positive	*w3-84-5032-21*	211J
5903G *pale-y-vp*-85-3385-34*	2 positive	*w3-85-3385-34*	211K
5903J *y-vp*-85-3572-30*	3 positive	*w3-85-3572-30*	211L
5904D *vp*-86-1407-15*	3 positive	*w3-86-1407-15*	211M
5905L *y-vp*-88-89-3563-33*	3 positive	*w3-88-89-3563-33*	211N
5906P *y-vp*-73-2656*	3 positive	*w3-73-2656*	211O
5908H *vp*-8111*	5 positive	*w3-8111*	211P
5909L *y-vp*-84-13*	3 positive	*w3-84-13*	211Q
5910H *pale-y*-84-5082-33*	6 positive	*w3-84-5082-33*	212E
5910L *pale-y*-85-3006-30*	3 positive	*w3-85-3006-30*	212F
5910N *pale-y*-85-3010-40*	3 positive	*w3-85-3010-40*	212G
5911C *lw*-85-3076-28*	2 positive	*w3-85-3076-28*	212H
5911D *pale-y*-85-3087-29*	2 positive	*w3-85-3087-29*	212I
5911H *lw*-86-87-1828-7*	3 positive	*w3-86-87-1828-7*	212J
5911O *pale-y*-90-3220-1*	3 positive	*w3-90-3220-1*	212K
5911P *pale-y*-90-3220-26*	3 positive	*w3-90-3220-26*	212L
5911Q *lw*-89-90-3609-5*	3 positive	*w3-89-90-3609-5*	212M
5912I *y-pg*-85-3044-34*	2 positive	*w3-85-3044-34*	212N
5912N *y-pg*-86-87-1723-27*	3 positive	*w3-86-87-1723-27*	212O
6109G *y-l*-8910 Briggs*	3 positive	*w3-8910*	212P

Mapping data for *enr* factors on chromosome 2

--Stinard, PS

Dominant alleles at the *enr* (*Enhancement of r1*) loci intensify aleurone color conferred by certain pale and near-colorless *r1* haplotypes (Stinard, Kermicle, and Sachs 2009, J. Hered., in press. Electronic version doi: 10.1093/jhered/esn091 http://jhered.oxfordjournals.org/cgi/content/full/esn091). Two *enr* loci, *enr1* and *enr2*, are linked to each other and map to chromosome 2. A third locus, *enr3*, is not linked to the other two.

We report four point linkage data for the *enr1 enr2* combinations *enr1-m594 Enr2-6117a* and *enr1-m694 Enr2-694* with respect to *fl1* and *v4* (Tables 1 and 2) and three point linkage data for *Enr1-628* with respect to *fl1* and *v4* (Table 3). We also report three point linkage data for the partially characterized *enr* factors *Enr*-459A* and *Enr*-459B* (Stinard, MNL 81:33-35, 2007) with respect to *fl1* and *v4* (Tables 4 and 5).

The linkage testcrosses were performed as indicated in the tables. All lines were homozygous for the pale *r1* reporter haplotype *R1-r(Venezuela559-PI302355)*. Kernels from the testcross ears were separated into purple (Enr) vs. pale (enr) vs. sectored (enr-m) as appropriate, and starchy (Fl) vs. floury (fl) classes, planted in a cold sand bench, and the resulting seedlings scored for green (V) vs. virescent (v). Linkage values were calculated according to Coe (Pp. 189-197 in Maize Handbook, M. Freeling and V. Walbot eds., New York: Springer-Verlag, 1994). The segregation of two enhancers (*enr1-m* and *Enr2*) in the four point linkage tests (Tables 1 and 2) presented a special problem in that the presence of the *Enr2* allele prevented the scoring for *enr1* vs. *enr1-m* in the purple kernel classes. Therefore, four point linkage data were calculated from *enr2* classes only, and three point linkage data for *fl1 enr2 v4* were calculated from total data.

Table 1. Four point linkage data for *fl1 Enr2-6117a v4 enr1-m594*.

Testcross: [*Fl1 Enr2-6117a V4 enr1-m594* X *fl1 enr2 v4 enr1*] X *fl1 enr2 v4 enr1*

Region	Phenotype	No.	enr2 class
0	fl enr2 v enr1	550	550
0; 3	Fl Enr2 V; enr1 or enr1-m	663	
1; 1 + 3	fl Enr2 V; enr1 or enr1-m	63	
1	Fl enr2 v enr1	54	54
2	fl enr2 V enr1-m	74	74
2; 2 + 3	Fl Enr2 v; enr1 or enr1-m	72	
3	fl enr2 v enr1-m	71	71
1 + 2; 1 + 2 + 3	fl Enr2 v; enr1 or enr1-m	5	
1 + 2	Fl enr2 V enr1-m	5	5
1 + 3	Fl enr2 v enr1-m	6	6
2 + 3	fl enr2 V enr1	4	4
1 + 2 + 3	Fl enr2 V enr1	0	0
Total (n)		1567	764

enr2 data: *fl1 - enr2* = 8.5 +/- 1.1 cM
enr2 - v4 = 10.9 +/- 1.1 cM
v4 - enr1 = 10.6 +/- 1.1 cM
Total data: *fl1 - enr2* = 8.5 +/- 0.7 cM
enr2 - v4 = 10.2 +/- 0.8 cM

Table 2. Four point linkage data for *fl1 Enr2-694 v4 enr1-m694*.

Testcross: [*Fl1 Enr2-694 V4 enr1-m694* X *fl1 enr2 v4 enr1*] X *fl1 enr2 v4 enr1*

Region	Phenotype	No.	enr2 class
0	fl enr2 v enr1	310	310
0; 3	Fl Enr2 V; enr1 or enr1-m	330	
1; 1 + 3	fl Enr2 V; enr1 or enr1-m	34	
1	Fl enr2 v enr1	28	28
2	fl enr2 V enr1-m	32	32
2; 2 + 3	Fl Enr2 v; enr1 or enr1-m	37	
3	fl enr2 v enr1-m	35	35
1 + 2; 1 + 2 + 3	fl Enr2 v; enr1 or enr1-m	13	
1 + 2	Fl enr2 V enr1-m	13	13
1 + 3	Fl enr2 v enr1-m	1	1
2 + 3	fl enr2 V enr1	6	6
1 + 2 + 3	Fl enr2 V enr1	5	5
Total (n)		844	430

enr2 data: *fl1 - enr2* = 10.9 +/- 1.5 cM
enr2 - v4 = 13.0 +/- 1.6 cM
v4 - enr1 = 10.9 +/- 1.5 cM
Total data: *fl1 - enr2* = 11.1 +/- 1.1 cM
enr2 - v4 = 12.6 +/- 1.1 cM

The four point linkage data presented in Tables 1 and 2 establish the gene order *fl1 enr2 v4 enr1* and the linkage values (*fl1* – 8.5 – *enr2* – 10.2 – *v4* – 10.6 – *enr1* and *fl1* – 11.1 – *enr2* – 12.6 – *v4* – 10.9 – *enr1*) are fairly consistent with each other and with previously reported data (*fl1* – 6.2 – *enr2* – 7.8 – *v4* – 10.3 – *enr1*; Stinard, Kermicle, and Sachs, 2009), although the *fl1* – *v4* interval is extended in the present data (18.7 cM and 23.7 cM vs. 14.0 cM reported in Stinard, Kermicle, and Sachs). The *v4* – *enr1* values (10.6 cM, 10.9 cM, and 10.3 cM) are remarkably similar. Differences in the *fl1* – *v4* interval could be due to the fact that the *enr1* and *enr2* alleles used in the two different tests are from different sources and genetic backgrounds (although they have been partially introgressed into W22). It may also be significant that *fl1* and

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
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 – 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*.