levels of constitutive resistance in the laboratory were significantly related to the amount of damage that was sustained by lines in the field, as shown in Figure 3 (Likelihood ratio test: deviance=1.267, df=7, P=0.033).

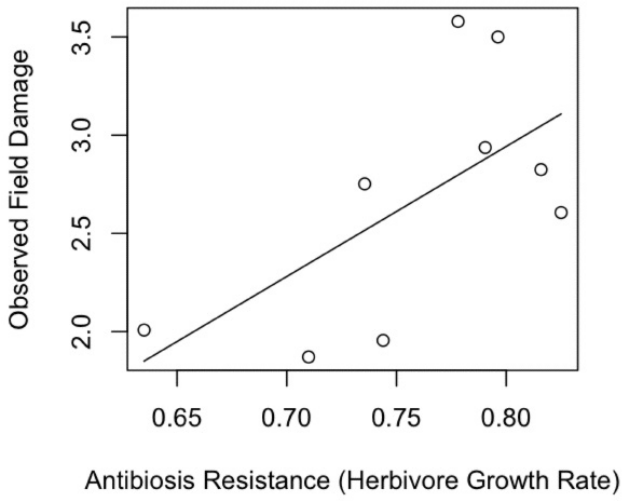

Figure 3. The relationship between average damage index values and average antibiosis resistance (as measured by herbivore growth rates) for the chosen subset of nine lines. Antibiosis resistance demonstrated a significant linear relationship with observed damage levels according to a likelihood ratio test (deviance=1.267, df=7, P=0.033).

The concordance between the patterns of resistance observed in the field versus laboratory suggests that constitutive antibiosis resistance expressed by the lines is important for deterring leaf damage. To the extent that this relationship holds up, these types of herbivore growth rate bioassays may provide an efficient method to pre-screen germplasm for resistance prior to more extensive field trials. Despite the fact that our observations of damage in the field were predicted by laboratory measures of resistance, follow-up studies will still be needed in order to confirm whether levels of resistance in these lines are stably expressed across seasons, locations, and developmental stages. This study confirms our suspicion that these maize diversity lines could be used to learn more about the genetic basis of herbivore resistance and the effect of genetic variation in plant defense on ecological dynamics.

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Allelism testing of miscellaneous stocks in the Maize COOP phenotype only collection

--Jackson, JD; Harper, C

This report summarizes allele testing of miscellaneous stocks characterized by phenotype only in the Maize Genetics COOP Stock Center collection. Crosses were made between known heterozygotes if possible. Ears were shelled and planted in sand benches to score seedlings for the appropriate phenotypes. Plants from the lazy crosses were scored in the field at maturity. Proposed new designations have been assigned to these alleles. These stocks have been increased and placed on our stocklist. It is expected that with further sorting and allelism testing of mutations characterized by phenotype only, additional alleles of characterized mutants will be discovered and placed in the main collection.

POSITIVE TESTS:

previous designation	allelism test with *spt1*	new designation	MGCSC: stock number
spt-92-3239-53*	positive: (+ / *spt1-N464*) x (+ / *spt**)	*spt1-92-3239-53*	226J

previous designation	allelism test with *oro1*	new designation	MGCSC: stock number
oro-85-3087-3*	positive: (+ / *oro1-6474*) x (+ / *oro**)	*oro1-85-3087-3*	616C
oro-88-89-3550-32*	positive: (+ / *oro1-6474*) x (+ / *oro**)	*oro1-88-89-3550-32*	616D

previous designation	allelism test with *la1*	new designation	MGCSC: stock number
la-05HI-RnjxW22GN-333*	positive: (+/*la1*) x *la**	*la1-05HI-RnjxW22GN-333*	406E
la-MTM4659*	positive: (+/*la1*) x *la**	*la1-MTM4659*	406F

New alleles of *chlorophyll1* found in lemon white endosperm stocks in the Maize COOP phenotype-only collection

--Jackson, JD

This report summarizes allele testing of lemon-white endosperm stocks characterized only by phenotype in the Maize Genetics COOP Stock Center collection. Here pale kernels linked to pale-green or albino seedlings characterized all stocks. Many had previously given negative results in tests with *vp*9, *w3* and *y9*. The *cl1 Clm1-3* stock used in crosses here carries a dominant modifier of *cl1* that allows for viable green plants, making crosses with a homozygous stock possible. Crosses were made as follows: [+/*lw**]@ X *cl1 Clm1-3* or +//+/*lw** X *cl1 Clm1-3*. Ears were scored for the segregation of pale yellow 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 *cl1 Clm3* will be tested for allelism with other stocks linked to pale endosperm.

Previous designation	allelism test with *w3*	New designation	MGCS stock number
5705F *pale- y*-87-88-2679-1*	4 positive	*cl1-87-88-2679-1*	306H
5908Q *y-vp*-1982-1*	3 positive	*cl1-1982-1*	306I
5910M *pale-y*-85-3007-40*	3 positive	*cl1-85-3007-40*	306J
5912P *lw-y-pg*-1998-4*	5 positive	*cl1-1998-4*	306K

New alleles of *white3* found in viviparous stocks in the Maize COOP phenotype only collection

--Jackson, JD

This report summarizes allele testing of various viviparous and lemon-white endosperm stocks characterized only by phenotype in the Maize Genetics COOP Stock Center collection. Here pale kernels linked to pale or albino seedlings characterized all stocks. Many had previously given negative results in tests with *vp*9 and *y*9. The *w3-y11* stock used in crosses here is homozygous viable. Crosses were made as follows: [+/*vp**]@ X *w3-y11* and +//+/vp* X *w3-y11*. Ears were scored for the segregation of pale yellow kernels. In most cases, pale-yellow kernels were selected from positive allele test ears and planted in the field for observation. Seed-

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