

IV. MAIZE GENETICS COOPERATION STOCK CENTER



Maize Genetics Cooperation • Stock Center

USDA/ARS/MWA - Soybean/Maize Germplasm, Pathology & Genetics Research Unit

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3865 seed samples have been supplied in response to 292 requests, for 2006. A total of 82 requests were received from 24 foreign countries. More than 90% of our requests were received by electronic mail or through our on-line order form. Popular stock requests include the IBM RIL mapping populations, Hi-II lines, *ig1* lines, Stock 6 haploid-inducing lines, male sterile cytoplasm, transposable element lines, Maize Gene Discovery Project lines, and Chromatin stocks.

Approximately 11.2 acres of nursery were grown this summer at the Crop Sciences Research & Education Center located at the University of Illinois. Favorable weather in the early spring allowed the timely planting of our first crossing nursery. However, cool, rainy weather hindered germination and emergence in our early plantings, resulting in reduced stands and necessitating the replanting of a few lines. Rainfall was adequate, but like last year, redwing blackbirds started feeding on our second crossing nursery. As soon as we noticed this, we irrigated our second field, which seemed to reduce feeding. Subsequent rainfall seemed to solve the problem, and few rows were lost. Growing conditions were generally good, and supplemental irrigation was not necessary. Moderate temperatures and low plant stress resulted in a good pollination season.

Special plantings were made of several categories of stocks:

1. In the 'Phenotype Only' collection, we have made available an additional 48 stocks in 2006. This low number is due to the reduced stand of our second crossing nursery in 2005. We are still working on 119 phenotype-only stocks from the large collection sent to us by Gerry Neuffer in 1996 and 1997.

2. Plantings were also made from donated stocks from the collections of Alice Barkan (photosynthetic mutants), Ed Coe (*pg15*, *o16*, and *v29* alleles), Jerry Kermicle (various *r1* alleles), Robert Lambert (defective kernel mutants), Rob Martienssen (MTM material), Gerry Neuffer (recent EMS-induced mutants), the North Central Regional Plant Introduction Station (brown midrib and anther ear traits that were found in various PI accessions), Ron Phillips (mutants in various inbred backgrounds), Pat Schnable (*rth1*), Margaret Smith (male sterile cytoplasm lines), and others. We expect to receive additional accessions of stocks from maize geneticists within the upcoming year.

3. We conducted allelism tests of several categories of mutants with similar phenotype or chromosome location. We identified additional alleles of *albescens1*, *Factor Cuna (Fcu)*, *glossy1*, *defective kernel5*, *collapsed2*, *pink scutellum1*, *viviparous5*, *viviparous9*, and *pale yellow9*. We plan to test additional members of the viviparous, spotted leaf, and pale endosperm classes of mutants. In this manner, we hope to move more stocks from our vast collection of unplaced uncharacterized mutants into the main collection.

4. Occasionally, requestors bring to our attention stocks that do not carry the traits they are purported to carry. We devote field space each year to analyzing these stocks, fixing or enhancing those we can, and soliciting replacements from researchers for those we can't. In those rare instances in which a particular variation or combination of variations cannot be recovered, we modify our catalog to reflect this.

5. We further characterized the *Fcu* system of *r1* aleurone color enhancers. We are working on linkage stocks to refine the map position of *Fcu* alleles using visible kernel and seedling markers on Chromosome 2, and we continued a series of crosses to transposon tag *Fcu* using one of Tom Brutnell's transposed *Ac* lines. We are collecting and characterizing additional alleles of *Fcu* and other *r1* aleurone color enhancers and inhibitors.

6. Two acres were devoted to the propagation of the large collection of cytological variants, including A-A translocation stocks and inversions. In this collection is a series of *waxy1*-marked translocations that are used for mapping unplaced mutants. Over the years, pedigree and classification problems arose during the propagation of these stocks. We have completed testing on these stocks and can now supply good sources proven by linkage tests to include the correct translocated chromosomes. Additional translocations we have received from W. R. Findley and Don Robertson marked with *wx1* are being checked by linkage tests as we did for the main series of *waxy1*-marked translocations. Some of these may replace ones from the main collection that were found to be bad.

7. Stocks produced from the NSF project "Regulation of Maize Inflorescence Architecture" (see: <https://www.fastlane.nsf.gov/servlet/showaward?award=0110189>) were grown this summer. Families that were observed in 2005 to segregate mutations were

selected to be increased in the nursery. These increases help to confirm the presence of the mutation and maintain adequate seed stock to fill future requests. These mutants are being added to our phenotype-only collection.

We continue to grow a winter nursery of 0.5 acres at the Illinois Crop Improvement Association's facilities in Juana Díaz, Puerto Rico. We had an excellent winter crop last year, and all indications are that the crop will perform well this year. We plan to continue growing our winter nurseries at this location.

We have received 579 additional EMS lines from various inbred backgrounds produced by Dr. Gerry Neuffer (Regulation of Inflorescence Architecture in Maize project). There are sufficient seed for all of these for distribution. We have also received an additional four lines from the Functional Genomics of Maize Chromatin project (see: <https://www.fastlane.nsf.gov/servlet/showaward?award=0421619>) from Karen McGinnis.

The 579 lines from Gerry Neuffer's EMS material that were screened for ear and kernel mutations in the lab, were planted in observation fields on the University of Illinois Crop Science Research facility for observation of seedling and adult plant mutations during our annual mutant hunt. In addition to these lines, 2300 lines of MTM material from Rob Martienssen (<http://mtm.cshl.edu>) were also planted this year to be observed for new adult mutant phenotypes. Unfortunately, the MTM material was apparently extremely susceptible to the cool damp conditions that we had during the few weeks after planting, and therefore had extremely poor stands and was subsequently plowed under. We plan to have another mutant hunt next summer.

Our IT specialist, Josh Tolbert, has continued to make updates and improvements to our curation tools, which are used to maintain data for our collection. These tools input our public stock data directly into MaizeGDB, to give maize scientists access to up-to-date information about our collection. They are also used for our internal database (e.g., inventory, pedigrees, requests). Development of new tools is underway to improve the efficiency of the input processes for pedigree information, and creation of forms required for planting and harvest information. Our web site has also been updated (<http://www.uiuc.edu/ph/www/maize>).

Samples of 1239 stocks were sent to the National Center for Genetic Resources Preservation in Fort Collins, Colorado for back up. These represent new stocks that had not been previously backed up. Our new inventory system has made selecting ears to be sent and producing a packing list to accompany them a much more efficient procedure.

The new greenhouse space in Urbana has been completed and is being used this winter. Our new seed storage space (which will double our capacity) is presently being built.

Marty Sachs
Director

Philip Stinard
Curator

Janet Day Jackson
Biol Res Tech (Plants)

Shane Zimmerman
Agric Sci Res Tech (Plants)

Josh Tolbert
Information Tech Specialist

ADDITIONS TO OUR CATALOG OF STOCKS SINCE MNL80
(For a complete list of our stocks, see: <http://maizegdb.org/cgi-bin/stockcatalog.cgi>)

CHROMOSOME 1 MARKERS

116B bz2-m::Ds; Ac2
116BA bz2-m::Ds; Ac2-strong
128DB pg15-N495B

CHROMOSOME 2 MARKERS

213K w3-N1907

CHROMOSOME 4 MARKERS

402G tga1

CHROMOSOME 5 MARKERS

504H v36-N1835
520L nec3-85-3457-40

CHROMOSOME 7 MARKERS

704K gl1-N1845

CHROMOSOME 8 MARKERS

804F elm1-ref

CHROMOSOME 10 MARKERS

X02M Oy1-N1460
X06G Og*-Catlin-yel
X17G R1-r(standard)
X27KA v29-N1224C

CHROMDB STOCKS

3201-22.1 T-MCG4291.007
3201-28.2 T-MCG5297.020
3201-42 T-MCG3832.001
3201-43 T-MCG4585.005
3201-43.1 T-MCG4585.009
3201-44 T-MCG6071.022
3201-45 T-MCG6432.027
3201-45.1 T-MCG6432.034
3201-45.2 T-MCG6432.046

UNPLACED GENES

U139J d4

TETRAPLOID

N108B Autotetraploid; Oh43

CYTOPLASMIC-STERILE / RESTORER

CX36E Wf9 (C) Sterile; cms-C rf1
rf2 rf3 rfC

TOOLKIT

T3301-56 Ac-im; r1-sc:m3::Ds

INVERSION

I543E Inv5e (5S.21; 5L.75)

PHENOTYPE ONLY

adherent leaf

3608L ad*-N247A
3610O ad*-N2507

anther ear

5802CA an*-PI595561

bleached leaf

3612G blh*-N2325

collapsed endosperm

3602G cp*-N1225B

defective kernel

3706E de*-N1234A
3706EA de*-N1222A

discolored kernel

3605Q dsc*-N1362

etched endosperm

3804M et*-N1344
3804Q et*-N1941

germless

3807LA gm*-N2485B

luteus yellow seedling

3810J l*-N1229B
3811A l*-N1879

miniature kernel

338-02 mn*-MTM5910
438-05 mn*-MTM11139

necrotic leaf

6106K nec*-91g-6045-25

opaque endosperm

3904F o*-N1071
3906D o*-N1246A
3906M o*-N1350A
3907A o*-N1354
3907E o*-N1360

pale green seedling

4301H pg*-N760A
4304L pg*-N2404

shrunk kernel

4006P sh*-N1307C
4007K sh*-NA695

small kernel

4004D smk*-N1432

spotted leaf

4107M spt*-N474A
4107O spt*-N537A

stiff leaf

4010L stf*-N227A

virescent seedling

4506P v*-N688A
4510H v*-N1395B
4511M v*-N2286B

white stripe leaf

3512F whv*-N2288

yellow streak leaf

3812P Ysk*-N2324

yellow stripe leaf

6005L yel-str*-W23