Maize Genetics Cooperation • Stock Center

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

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32,112 seed samples have been supplied in response to 277 requests for 2008. These include 76 requests received from 23 foreign countries. Popular stock requests include the NAM RIL populations, Hi-II lines, *ig1* lines, Stock 6 haploid-inducing lines, male sterile cytoplasms, transposable element lines, Maize Inflorescence Project EMS lines, and Chromatin stocks.

Approximately 7.2 acres of nursery were grown this summer at the Crop Sciences Research & Education Center located at the University of Illinois. Despite frequent heavy rains during the first part of spring, we managed to plant our crossing nurseries on schedule. Smaller than normal stands were observed in parts of the field that were covered with standing water for a day or two. By mid-June, more seasonable rainfall patterns were established and we had a normal pollination season without the need for supplemental irrigation. Moderate temperatures and low plant stress during and following pollination resulted in excellent yields.

Special plantings were made of several categories of stocks:

1. Plantings were made of donated stocks from the collections of David Braun (*tdy1* and *tdy2* alleles), James Brewbaker (Hi27 near-isogenic mutant lines), Kelly Dawe (abnormal chromosome 10 deficiencies) Patrice Dubois (*phyB1 phyB2* lines), Jerry Kermicle (various *r1* alleles), Gerry Neuffer (recent EMS-induced mutants), the North Central Regional Plant Introduction Station (*r1-cherry* accessions from tribal maize), Ron Okagaki (EMS-induced *wx1* alleles and *Spm* change-of-state mutations), Peter Rogowsky (embryo-lethal mutants), Mark Settles (*vp10* and *vp15* alleles), Margaret Smith (male sterile cytoplasm lines), and others. The dominant *amylose extender1* mutant *Ae1-5180::Mu1* came off patent this year and we have increased it and made it publicly available as well. We expect to receive additional accessions of stocks from maize geneticists within the upcoming year.

2. We conducted allelism tests of several categories of mutants with similar phenotype or chromosome location. We identified additional alleles of *pink scutelum1, viviparous5, lazy1, chlorophyll1*, *white3*, and *pale yellow9*. In 2009, we plan to test additional members of the viviparous and pale endosperm classes of mutants. In this manner, we hope to incorporate more stocks from our vast collection of unplaced, uncharacterized mutants into the main collection.

3. 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.

4. We further characterized the *Enr* (*Fcu*) system of *r1* aleurone color enhancers and published a paper on the results. We are continuing attempts to transposon tag *Enr1* using one of Tom Brutnell's transposed *Ac* lines. We are collecting and characterizing additional alleles of *Enr1* and other *r1* aleurone color enhancers and inhibitors.

5. Samples of 2,004 phenotype–only stocks were sent to the National Center for Genetic Resources Preservation in Fort Collins, Colorado for back-up. Selected samples from the main collection not yet sent were also pulled and sent this year. These represent 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.

6. Two acres were devoted to the propagation of the large collection of cytological variants, including A-A translocation stocks and inversions. Additional translocations received from W. R. Findley and Don Robertson marked with *wx1* were checked with linkage tests to confirm the chromosome arms involved. For those where we found no linkage, all sources were discarded. We were also able to add another useful *wx1* marked translocation from Susan Gabay-Laughnan in which the chromosome arms involved have been confirmed. These changes were all entered into MaizeGDB in 2008.

7. Stocks produced from the NSF project "Regulation of Maize Inflorescence Architecture" (see: https://www.fastlane.nsf.gov/servlet/showaward?award=0110189) were grown again this summer. Approximately 250 families of M2 materials that were produced in 2006 and 2007 were grown to increase seed supplies and recover previously observed mutations. Also, 1553 families of 2006 and 2007 M2 EMS materials were grown for adult plant observation; the materials observed include B73 and Mo17 inbred lines and the B73xMo17 hybrid. Visitors from 5 different institutes traveled to Illinois to walk these fields and found many new mutant phenotypes that will be added to the project database.

We grew a winter nursery of 0.5 acres at the Illinois Crop Improvement Association's facilities in Juana Díaz, Puerto Rico in 2007/2008. We received a good increase of most lines. We did not have sufficient funds in our budget to grow a winter crop in Puerto Rico this year. Critical plantings of a few lines were made in the greenhouse, but the lack of a field grown winter crop represents a set-back to our program, not only because of the loss of a nursery generation, but also because it is easier to transfer mutations out of tropical backgrounds into Midwest adapted backgrounds under winter conditions.

We have received close to 5,000 of the Nested Association Mapping Recombinant Inbred Lines (NAM RILs) consisting of 25 populations, from the Molecular and Functional Diversity of the Maize Genome project (http://www.panzea.org/lit/germplasm.html). Complete sets of this material are available to those willing to increase and redistribute seeds to their company or institution; requests for subsets of this material will be available. There are also additional lines from the Functional Genomics of Maize Chromatin project (see: https://www.fastlane.nsf.gov/servlet/showaward?award=0421619); most of these are unconfirmed lines. The Maize TILLING Project (http://genome.purdue.edu/maizetilling/) has also donated an additional 1,712 lines to our current holdings.

Our IT Specialist 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. The tools are also used for our internal database (e.g., inventory, pedigrees and requests). A new pedigree-entry tool was developed that reduced pedigree data entry time significantly and other tools were rewritten or written from scratch to import many years of unentered pedigree information. A tool to generate field notes conveniently and easily was created and will be modified to also generate harvest tags. Our web site and all other services have been migrated to a new hardware/software arrangement, which is much more reliable and faster than the old setup. Maintenance continues on our web site (http://www.uiuc.edu/ph/www/maize).

The new greenhouse space in Urbana is being used for our third winter crop. The space has proven to be excellent for growing material that doesn't do well under our field conditions. Our new seed storage space presently has 803 seed storage drawers of the 1,584 the room will eventually hold (pending funding). Thanks to the help from the National Program Staff, we finally have enough new storage drawers to unpack and organize the approximately 36,000 Maize Targeted Mutagenesis (http://mtm.cshl.org/) lines we have held, up to now, in boxes in the aisles of our storage rooms.

Marty Sachs	Philip Stinard	Janet Day Jackson	Shane Zimmerman	Josh Tolbert
Director	Curator	Biol Res Tech (Plants)	Agric Sci Res Tech (Plants)	Information Tech Specialist

ADDITIONS TO OUR CATALOG OF STOCKS SINCE MNL82
(For a complete list of our stocks, see: http://maizegdb.org/cgi-bin/stockcatalog.cgi)

CHROMOSOME 1 MARKERS
106BA ts2 ^Hi27
107I P1-wr ^Hi27
110EA ad1 ^Hi27
111A bsd2-m1::Mu
115K bz2-s

CHROMOSOME 2 MARKERS
201FA ws3 ^Hi27
214JA sk1 fl1 ^Hi27

CHROMOSOME 4 MARKERS
405DA la1-R fl2 su1 ^Hi27
405DB la1-R fl2 ^Hi27
418FA o1 c2 ^Hi27

CHROMOSOME 5 MARKERS
510B Ae1-5180::Mu1
512A bt1-A
524E tdy2-R

CHROMOSOME 6 MARKERS
604AA y1-Guam
608N su2-ora3
616E tdy1-R

CHROMOSOME 7 MARKERS
703AA o2 v5 ^Hi27
704B o2-Tuxp
705BA sl1 ^Hi27
705BB sl1 sh2 ^Hi27
705DA bd1 ^Hi27
707FA y8 ^Hi27
707GA in1; A1 A2 C1 C2 Pr1 R1 ^Hi27

CHROMOSOME 9 MARKERS
901G Inr2-JD r1-g
903J emb2-8522
903K emb*-8516
903L emb*-g2422
903M bz1-m13CS-C
903N bz1-m13CS-E
906L wx1-EMS14
906M wx1-EMS17
906N wx1-EMS20
906O wx1-EMS28
906P wx1-EMS30
916CA bk2 ^Hi27

CHROMOSOME 10 MARKERS
X03FA Inr1-JD r1-g
X12JA DfK10(L) R1
X237A r1-ch(Kokoma) Pl1
X237B R1-nj:st(n208)
X28EA Les3-NA781
X37A R1-r(spotted dilute2) Inr1-Dil wx1-m8::Spm-I8 Spm
X37B R1-r(spotted dilute2) K10-I Inr1-Dil Spm
X37C R1-r(spotted dilute2) Inr1-Dil wx1-m8::Spm-I8
X37D R1-Randolph

CHROMDB STOCKS
3201-34.1 T-MCG5065.033
3201-34.2 T-MCG5065.033
3201-34.3 T-MCG5065.049
3201-40.2 T-MCG5211.022
3201-41.1 T-MCG6123.017
3201-46 T-MCG3832.023
3201-47 T-MCG4322.006
3201-48 T-MCG4721.010
3201-49 T-MCG4963.024
3201-50 T-MCG4977.011
3201-51 T-MCG5071.014
3201-51.1 T-MCG5071.025
3201-52 T-MCG5641.016
3201-52.1 T-MCG5641.036
3201-53 T-MCG5825.005
3201-53.1 T-MCG5825.011
3201-54 T-MCG6082.002
3201-54.1 T-MCG6082.004
3201-54.2 T-MCG6082.018
3201-54.3 T-MCG6082.019

UNPLACED GENES
U240F zn2-PI251887

MULTIPLE GENES
M341BA B1 C1-I pl1 ^Hi27
M341BB B1 C1 pl1 ^Hi27

RARE ISOZYME
3004-001 Mdh3-16; Mdh5-16
3004-003 Mdh1-5
3004-004 Mdh3-11.5
3004-005 Mdh1-9.2; Mdh3-n
3004-006 Mdh5-15; mmm1-1
3004-007 Mdh5-15.3
3004-008 Cat3-n
3004-009 Mdh1-.05; Mdh2-n; Mdh5-16.5
3004-010 Mdh1-10.5; Mdh2-n; Mdh3-n
3004-011 Mdh1-n; Mdh2-n; Mdh3-16
3004-012 Mdh1-1; Mdh2-n; Mdh3-n
3004-013 Cat3-6
3004-014 Mdh2-n; Cat3-14
3004-015 Mdh4-13; Mdh5-n
3004-016 Mdh1-n; Mdh2-7.4
3004-017 Mdh4-10.5; mmm1-1
3004-018 Mdh1-n; Mdh5-16.7
3004-019 Me1-VF
3004-020 Mdh1-n; Mdh3-n
3004-021 Mdh4-n; Mdh5-n
3004-022 Mdh4-n; Mdh5-12+; Cat3-9+
3004-023 Mdh4-n; Mdh5-12
3004-024 Cat3-n
3004-025 Mdh1-n; Mdh2-9.3; Cat3-n
3004-026 Mdh1-n; Mdh2-n; Me1-VF
3004-027 Mdh4-n; Mdh5-n
3004-028 Mdh4-13; Mdh5-n
3004-029 Mdh1-n; Mdh2-n; Mdh5-n
3004-030 Mdh1-.05; Mdh2-n; Mdh3-n; Gdh1-S
3004-031 Mdh1-n; Mdh2-n; Mdh5-n; Mdh4-D8.5
3004-032 Mdh1-n; Mdh2-n; Mdh3-16.9
3004-033 Mdh1-n; Mdh3-n; Mdh2-B6.1ap
3004-034 Pgd1-3.8; Ep1-6
3004-035 Est8-4.5
3004-036 Cat3-11
3004-037 Mdh1-n; Mdh2-4m
3004-038 Got1-8; Mdh1-n; Mdh2-n; Mdh4-12; Mdh5-16.7
3004-039 Mdh1-n; Mdh2-n; Mdh3-7.3
3004-040 Mdh1-n; Mdh2-n; Mdh3-18
3004-041 Mdh1-n; Mdh2-.2
3004-043 Mdh1-n; Mdh3-n
3004-044 Mdh1-n; Mdh2-n; Mdh4-8; Mdh5-16.7
3004-045 Mdh1-2.8; Mdh2-n
3004-046 Aco1-2; Aco2-6
3004-047 Dia2-4; Pgd1-3.8; Pgd2-n
3004-048 Dia2-6
3004-049 Mdh1-n; Mdh2-n; Mdh5-n; Mdh4-8
3004-051 Mdh1-n; Mdh3-n; Mdh2-6.1
3004-052 Mdh1-n; Mdh3-n; Mdh2-5.6
3004-053 Mdh1-6; Mdh2-n; Mdh3-n
3004-054 Mdh1-n; Mdh2-n; Mdh4-8; Mdh5-16.7
3004-055 Mdh1-n; Mdh2-n; Mdh3-16.8
3004-056 Mdh1-n; Mdh3-n; Mdh2-.03/n
3004-057 Adh1-2; Gdh-S; Amp3-6
3004-059 Mdh1-n; Mdh2-n; Mdh5-n; Mdh4-8.5; mmm1-1
3004-060 Got3-8; Pgd2-8; Est8-8
3004-061 Got3-8; Me1-VS; Mdh1-n; Mdh2-n
3004-062 Aco1-1; Mdh1-n; Mdh2-n; Mdh3-18
3004-063 Pgm2-12; Mdh5-16.4
3004-064 Adh1-2; Phi1-8; Amp3-6
3004-066 Amp1-6; Mdh4-16.7
3004-068 Me1-VS
3004-069 Amp1-6; Mdh4-16.7; Pgm1-5
3004-070 Hex2-6; Idh2-8; Mdh2-.03
3004-071 Idh1-4; Idh2-n
3004-072 Adh1-2; Phi1-8; Gdh1-S
3004-073 Mdh4-n; Mdh5-16.4
3004-074 Mdh1-.4; Mdh2-n; Mdh3-n
3004-075 Tpi4-8; Mdh3-16.9; Me1-VS; Got3-8
3004-076 Amp1-6; Mdh4-16.7; Ep1-12
3004-077 Amp1-6; Mhh4-16.7; Pgm1-5
3004-078 Mdh1-n; Mdh3-n; Mdh2-B5.6s
3004-079 Mdh1-.05; Mdh4-8; Mdh2-n; Mdh3-n; Mdh5-n
3004-080 Dia1-10; Dia2-6
3004-082 Tpi3-2; Mdh1-.65; Idh1-2; Tpi5-8; Aco1-1
3004-083 Acp4-1; Dia2-6; Gdh1-VS; Adh1-2; Phi1-8; Pgm1-18; mmm1-1; Mdh4-8.5
3004-084 Ak1-5; Pgd1-9; Est8-10; Hex2-6; Idh2-8; Mdh2-.03
3004-085 Ak1-5; Est8-10; Pdd1-9; Idh2-8; Mdh2-B.03; Hex2-6
3004-086 Pgd1-9; Ep1-10; Hex2-6; Idh2-8; Mdh2-.03; Adk1-5; Tpi3-2; Mdh1-.65; Idh1-2; Tpi5-8
3004-087 Phi1-8; Gdh1-VS; Dia2-6; Acp4-.5
3004-088 Mdh4-8.5; mmm1-1; Gdh1-VS; Dia2-6; Acp4-.5
3004-089 Mdh4-8.5; mmm-1; Pgm1-18; Adh1-2; Pgd1-8; Gdh1-VS; Dia2-6; Acp4-.5
3004-090 Cat3-5.5
3004-091 Tpi3-2; Est8-8; Mdh1-.65; Idh1-2
3004-093 Amp1-6; Mdh4-8.5; mmm-1; Dia2-6; Acp4-.5
3004-094 Tpi1-2; Tpi2-2; Tpi5-4
3004-095 Pgd2-10
3004-096 Pgm2-12; Amp3-7; Got2-10
3004-097 Cat3-5; Aco1-1; Tpi1-2
3004-098 Amp1-6; Mdh4-8.5; mmm1-1; Pgm1-18; Adh1-2; Phi1-8; Dia2-6; Acp4-5; Gdh seg
3004-099 Pgd1-9; Ep1-10; Hex2-6; Idh2-8; Mdh2-.03; Adk1-5; with Ep12
3004-100 Mdh2-.03; Mdh1-n; Mdh3-n; Mdh4-n; Mdh5-n
3004-101 Sad1-6; Glu1-16
3004-102 Dia1-10; Tpi2-2; Aco1-1; Cat3-5; su1; Tpi1-2
3004-103 Amp1-6; Mdh4-8.5; mmm1-1; Pgm1-18; Adh1-2; Phi1-8; Gdh1-S; Dia2-6; Acp4-5; Pgm2-12; Mdh5-16.4; Got3-2.... + see comment
3004-104 Mdh1-n; Mdh2-n
3004-105 Mdh4-8; Mdh5-n
3004-106 R12 check line

CYTOPLASMIC-STERILE/RESTORER
C437A A619 (N); mito-N
C437B A619 (C); cms-C
C437C A619 (S); cms-S
C437D A632 (N); mito-N Rf3 rfC
C437E A632 (C) Sterile; cms-C Rf3 rfC
C437F A632 (S) Restored; cms-S Rf3 rfC
C437G A634 (N); mito-N Rf3 rfC

C437H A634 (C) Sterile; cms-C Rf3 rfC
C437I A634 (S) Restored; cms-S Rf3 rfC
C437J Hi27 (C) Sterile; cms-C rfC
C437JA Hi27 (N); mito-N rfC
C437K B73 (C) Sterile; cms-C rf3 rfC
C437L B73 (S) Sterile; cms-S rf3 rfC
C437M H95 (N); mito-N Rf3 RfC
C437N H95 (C) Restored; cms-C Rf3 RfC
C437O H95 (S) Restored; cms-S Rf3 RfC
C437P K55 (C) Restored; cms-C rf3 RfC
C437Q K55 (S) Sterile; cms-S rf3 RfC
C437R KYS (C) Sterile; cms-C rf3 rfC
C437S KYS (S) Sterile; cms-S rf3 rfC
C437T Ky21 (C) Restored; cms-C Rf3 RfC
C437U Ky21 (S) Restored; cms-S Rf3 RfC
C537A M14 (N); mito-N rf3 RfC
C537B M14 (C) Restored; cms-C rf3 RfC
C537C M14 (S) Sterile; cms-S rf3 RfC
C537D NY821LE (N); mito-N
C537E NY821LE (C); cms-C
C537F NY821LE (S); cms-S
C537G Oh43 (N); mito-N
C537H Oh43 (C); cms-C
C537I Oh43 (S); cms-S
C537J Oh45 (N); mito-N Rf3 RfC
C537K Oh45 (C) Restored; cms-C Rf3 RfC
C537L Oh45 (S) Restored; cms-S Rf3 RfC
C537M Oh51A (N); mito-N rf3 rfC
C537N Oh51A (C) Sterile; cms-C rf3 rfC
C537O Oh51A (S) Sterile; cms-S rf3 rfC
C537P Tr (C) Sterile; cms-C Rf3 rfC
C537Q Va26 (N); mito-N
C537R Va26 (C); cms-C
C537S Va26 (S); cms-S
C537T Va58 (N); mito-N Rf3 rfC
C537U Va58 (C) Sterile; cms-C Rf3 rfC
C537V Va58 (S) Restored; cms-S Rf3 rfC
C637A W23 (C); cms-C
C637B W23 (S); cms-S
C637C W64A (N); mito-N rf3 RfC
C637D W64A (C) Restored; cms-C rf3 RfC
C637E W64A (S) Sterile; cms-S rf3 RfC
C637F 38-11 (C); cms-C
C637G 38-11 (S); cms-S

RECOMBINANT INBRED
NAM5000 Full set of 5,000 NAM RILs (we presently have 4,835 of these RILs)
Subpopulations of NAM RILs
NAM-Z001 B73 x B97 NAM RILs
NAM-Z002 B73 X CML103 NAM RILs
NAM-Z003 B73 X CML228 NAM RILs
NAM-Z004 B73 X CML247 NAM RILs
NAM-Z005 B73 X CML277 NAM RILs
NAM-Z006 B73 X CML322 NAM RILs
NAM-Z007 B73 X CML333 NAM RILs
NAM-Z008 B73 X CML52 NAM RILs
NAM-Z009 B73 X CML69 NAM RILs
NAM-Z010 B73 X Hp301 NAM RILs
NAM-Z011 B73 X Il14H NAM RILs
NAM-Z012 B73 X Ki11 NAM RILs
NAM-Z013 B73 X Ki3 NAM RILs
NAM-Z014 B73 X Ky21 NAM RILs
NAM-Z015 B73 X M162W NAM RILs
NAM-Z016 B73 X M37W NAM RILs
NAM-Z018 B73 X Mo18W NAM RILs
NAM-Z019 B73 X MS71 NAM RILs
NAM-Z020 B73 X NC350 NAM RILs
NAM-Z021 B73 X NC358 NAM RILs
NAM-Z022 B73 X Oh43 NAM RILs
NAM-Z023 B73 X Oh7B NAM RILs
NAM-Z024 B73 X P39 NAM RILs
NAM-Z025 B73 X Tx303 NAM RILs
NAM-Z026 B73 X Tzi8 NAM RILs

INVERSION
I943D Inv7c (7L.34; 7L.52)

RECIPROCAL TRANSLOCATIONS (wx1 AND WX1 MARKED)
wx24D T8-9(043-6) (8L.17; 9S.34); wx1

STOCKS CHARACTERIZED ONLY BY PHENOTYPE
adherent leaf
3610L ad*-N1945

albino seedling
4510O v*-N1867
6212P w*-92-2440-2

bleached leaf
3612E blh*-N2237

brown kernel
3606H bnk*-N1519C

brown midrib
5803M bm*-PI586725

brown pericarp
5805C bp*-Lima94

collapsed endosperm
3703H de*-N978
4104R cp*-N2376

compressed top
3708P cmpt*-N2378
3912N wrt*-N2384

defective kernel
3703H de*-N978
3704G de*-N1069A

dwarf plant
4406D d*-N2249A
4407F D*-N2468
5505C d*-PI184286

green striped leaf
4009I gs*-N720D

lemon white
5911R lw*-92-1253-80
5911S lw*-92-3240-53
5912Q lw*-RJL

miniature kernel
138-32 mn*-MTM4714; lp*-MTM4714
138-38 mn*-MTM4752; wrk*-MTM4752
238-50 mn*-MTM5888
3807U mn*-N904C
438-45 mn*-MTM16089
438-48 mn*-MTM16165
538-18 mn*-MTM16702

necrotic leaf
4101IA nec*-N249A

opaque endosperm
3904I o*-N1100

patched leaf
4105G ptc*-N888B

reduced pollen fertility
138-40A lp*-MTM4887

rough kernel
3806Q rgh*-N1412

semidwarf
4408L Sdw*-N2433

short plant
4407O Py*-N983

small kernel
4003N smk*-N1238A
4004H smk*-N1946

spotted leaf
4107T spt*-N1620B

streaked leaf
3709G stk*-N208A

striped leaf
6005G str*-Morrow
6009A Og*-65-563

tassel seed
5807M ts*-Ames 17676

virescent seedling
4511K v*-N2250B

white luteus seedling
4108G wl*-N56
4510O v*-N1867

white stripe leaf (japonica-like)
4011J j*-N358B
6005M j*-92-1259-92

wrinkled kernel
138-37C wrk*-MTM4751

Additionally, we received 1,712 stocks from the Maize TILLING project and additional stocks from other maize genome projects.