

Maize Genetics Cooperation • Stock Center

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

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5,511 seed samples have been supplied in response to 459 requests for 2014. These include 205 requests received from 26 foreign countries. This was the fourth record-breaking year in a row for requests, but only a bit higher than last year. Interest in reverse genetics tools, such as the UniformMu sequence indexed stocks, continues to grow. Presently, requests for UniformMu stocks represent more than 50% of our total requests. Other popular stock requests include the NAM RILs and other mapping populations, Hi-II lines, haploid-inducing lines, male sterile cytoplasms, kernel starch quality traits, plant architecture traits, and Maize Inflorescence Project EMS lines.

Approximately 6.0 acres of nursery were grown this summer at the Crop Sciences Research & Education Center located at the University of Illinois. Warm, dry spring weather allowed us to plant both of our crossing nurseries a timely manner, and excellent weather during the growing season allowed for a normal pollination season; no supplemental irrigation was required. There were sufficient stands for a good increase in amost all instances. Moderate temperatures and low plant stress resulted in excellent yields from most pollinations.

Special plantings were made of several categories of stocks:

- 1. Plantings were made of donated stocks from the collections of Ming-Tang Chang (an improved haploid inducer), Vicki Chandler (various b1 recombinant alleles), Prem Chourey (sus1, sh1, coe1, de18, and mn1 alleles), Candy Gardner (a novel pericarp pigment pattern trait from the GEM project), Brenda Hunter (opaque and floury mutants in a W64A inbred background), Dave Jackson (ct2 alleles), Jerry Kermicle (teosinte cytoplasms, Tcb1-s, and various r1 alleles), Kathy Newton (teosinte cytoplasms and mitochondrial mutator), Pat Schnable (gl13 alleles), Bao-Cai Tan (emp5, emb14, smk1, and why1-3), and others. We expect to receive additional accessions of stocks from maize geneticists within the upcoming year.
- 2. We are continuing to characterize enhancers of yellow endosperm color from PI accessions of orange endosperm tropical flints and are continuing collaborations to identify the specific gene products associated with previously uncharacterized (or incompletely characterized) white endosperm/albino seedling loci. Through tests of allelism, we have identified new alleles at the *lw1*, *lw2*, *te1*, *v30*, *vp9*, *w1*, *y1*, *y8*, and *y10* loci.
- 3. Due to lack of personnel, we continue to provide only bare-bones curation of the A-A translocation stocks that were previously maintained by Janet Day Jackson. We are continuing to grow up recent outcrosses of translocation stocks in our observation fields to score for male and female semisterility.
- 4. Stocks produced from the NSF project "Regulation of maize inflorescence architecture" (see: http://www.maizegdb.org/MIP/) were grown again this summer. Approximately 350 families of M2 materials that were produced between 2003 and 2007 were grown to increase seed supplies and recover previously observed mutations; this also included previously phenotyped families that had limited seed supplies. In addition, 2,060 families of 2012 and 2013 EMS seed increase materials were grown for adult plant observation and 282 families were screened in sand benches for seedling traits; the materials observed include mutated

A619, B73 and Mo17 inbred lines, Mo17xA632 and B73xMo17 hybrid, and various other inbred lines.

5. Critical plantings of a limited number of stocks were made in our greenhouse facilities.

We currently have 9,425 UniformMu sequence indexed stocks, produced by the "Construction of comprehensive sequence indexed transposon resources for maize" project (see: http://www.maizegdb.org/documentation/uniformmu). We have also recently received an additional 228 stocks from the "Genome-wide mutagenesis of maize using Ac/Ds transposons" project (see: http://acdstagging.org).

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). As web technology has changed over the years, the code for our tools has become somewhat outdated. Therefore, work has been initiated on a new implementation of the curation tools from the ground up. Working with MaizeGDB, plans are being worked out and testing is being conducted with an eye towards creating a single set of curation tools that will work well for both groups, re-working database organization, automating much more of the low-level data manipulation at the database level to make working with our data and creating new tools a much easier process, and overall applying what we've all learned over the past decade or so with our current tools to the next generation of tools for both groups. Maintenance continues on our web site (http://www.uiuc.edu/ph/www/maize).

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