

Maize Genetics Cooperation • Stock Center

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

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7,970 seed samples have been supplied in response to 458 requests for 2013. These include 178 requests received from 28 foreign countries. This was the third 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, *ig1* lines, Stock 6 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. Wet spring weather forced us to plant our crossing nurseries a couple of weeks later than we prefer, but excellent weather during the growing season allowed for a normal pollination season. There were sufficient stands for a good increase in most instances. Supplemental irrigation was required after the planting of our second crossing nursery in order to minimize bird damage, and again late in the season during a post-pollination dry spell. 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 Bong-Ho Choe (rlc1), Vicki Chandler (mop1, mop2, mop3, rmr1, and rmr2 alleles), Andrea Gallavotti (various inflorescence mutants), Inna Golubovskaya (mac1-Y211), Sarah Hake (kn1, Lgn1, Ts6, ifa1, mwp1, and ra2 alleles), Thomas Hartwig (na2, and url1 alleles), Jay Hollick (various B1 and Pl1 stocks), Don McCarty (vp8 alleles), Peter Rogowsky (ppr2263), Bao-Cai Tan (emb17), Clint Whipple (tasselsheath mutants), Mark Williams (clpp1-ys) and others. We expect to receive additional accessions of stocks from maize geneticists within the upcoming year.
- 2. We are continuing our attempts to recover instances of the lapsed y5 locus 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 vp5, te1, and oro1 loci. The isoprenoid biosynthesis mutant zb7 and the luteus seedling mutant l17 were found to be allelic to lw1.
- 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 450 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, 1,546 families of 2011 and

2012 EMS seed increase materials were grown for adult plant observation and 215 families were screened in sand benches for seedling traits; the materials observed include mutated A619, B73 and Mo17 inbred lines, A619xB73 and B73xMo17 hybrid, and various other inbred lines.

5. Critical plantings of a limited number of stocks were made in our greenhouse facilities. Current funding levels did not allow for a winter crop in Puerto Rico.

We currently have 8,849 UniformMu sequence indexed stocks, produced by the "Construction of comprehensive sequence indexed transposon resources for maize" project (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 (http://www.plantgdb.org/prj/AcDsTagging/).

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). Changing web standards and browser updates have caused considerable disruption with certain parts of the curation tools, but work on the tools continues. Moving to a more modern way of handling communication between various parts of the curation tools is the current major task. The harvest notes tool has been completed and this year's planting data was the first year to fully benefit from the harvest notes tool. Getting data from the pedigree records to harvest notes and finally into inventory is now streamlined, manual data entry has been reduced dramatically and data accuracy has improved. The family tree tool has been mostly integrated with the curation tool's pedigree pages and new features, like the ability to compare family trees for more than one pedigree at a time, are in the works. We work with MaizeGDB to make sure our tools continue to interoperate well with MaizeGDB's databases, plus offer suggestions on where to go in the future. Maintenance continues on our web site (http://www.illinois.edu/ph/www/maize).

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