

NCCC167 Missouri Station Report March 2006-February 2007

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Mission and Program Descriptions

Maize research at the in Columbia Missouri (USDA ARS and University of Missouri) is primarily genetic in nature. Although there is currently no active corn breeding program, several programs have applied projects that require large-scale field trials. These include Mike McMullen (USDA ARS), Sherry Flint-Garcia (USDA ARS), Bruce Hibbard (USDA ARS), and Georgia Davis (University of Missouri, Plant Sciences).

Mike McMullen investigates how selection has shaped molecular diversity in maize, and relates molecular diversity to functional phenotypic variation. As part of an NSF grant entitled "The Molecular and Functional Diversity of Maize," he has conducted SNP discovery on 4000 loci and, along with Jim Holland and Ed Buckler, has developed a 5000 recombinant inbred line mapping population derived from 25 inbred lines chosen to capture the greatest amount of genetic diversity. Subsequent Nested Association Mapping (NAM) will permit high-power and high-resolution genetic dissection of quantitative traits for maize.

Sherry Flint-Garcia utilizes the maize domestication model to identify genes of agronomic importance. Objectives include 1) examining the impact of artificial selection on kernel protein and amino acid composition; and 2) more broadly, diversifying the genetic base of maize by utilizing landraces and teosinte, the ancestor of maize. To accomplish these objectives, she is creating introgression (or NIL) libraries of a number of teosinte and landrace accessions in the B73 background.

Bruce Hibbard works on Western Corn Rootworm chemical ecology and host plant resistance, including 1) Identifying, developing and releasing corn germplasm with native resistance to the rootworm; 2) Determining the mechanism(s) of resistance and its inheritance; and 3) Investigating the biology, pest/ host interactions and chemical ecology of the rootworm, especially as they relate to resistance management.

Georgia Davis conducts functional genomics of biotic and abiotic stresses: 1) Fungal resistance in maize with emphasis on mechanisms and sources of resistance to *Aspergillus flavus* and aflatoxin production; 2) Insect resistance in maize, specifically fall armyworm and southwestern corn borer and their relationship to juvenility associated traits; and 3) Maize root architecture in relation to drought response.

Other active maize researchers in Columbia include: Jim Birchler (Biological Sciences), Ed Coe (professor emeritus), Karen Cone (Biological Sciences), Toni Kazic (Bioinformatics), Gerry Neuffer (professor emeritus), Kathy Newton (Biological Sciences), Henry Nguyen (Plant Sciences), Mel Oliver (Research Leader for the ARS Plant Genetics Research Unit), and Bill Wiebold (Plant Sciences).

2006 Program Highlights

Maize researchers at MU have been facing reductions in field space beginning last summer. Portions of South Farm (also known as Genetics Farm) have been repossessed by the University for the development of a research park. We are attempting to consolidate all maize programs at one of the two remaining facilities: Bradford Farm and Hinkson Bottom. Unfortunately, Hinkson Bottom is not large enough to accommodate everyone and still maintain a crop rotation with soybean. While Bradford Farm is large enough to accommodate us, they lack the structural facilities to store equipment and support the needs of the approximately 50 people that work the fields during peak pollination.

The Maize In Missouri website (www.maizeinmissouri.org) was launched in Fall 2006 to promote collaboration among maize researchers in Missouri. Reflective of our diverse research interests, our motto is "From DNA to the Field."

Specific Program Highlights:

Mike McMullen:

From sequencing a large number of candidate genes in panels of inbred lines and teosintes (progenitor of modern maize), we continue to identify genes that have experienced artificial selection. These genes are logical candidate genes for controlling agronomic traits and are being pursued for further study.

Sherry Flint-Garcia:

We are in the process of creating complete introgression libraries of 11 teosinte (*ssp parvliglumis*) accessions in the B73 background. This winter, BC4 seed was made for nine of the populations and selfing will begin this summer. We have also initiated introgression libraries from 17 landrace accessions, and currently have BC1 seed.

Bruce Hibbard:

Our corn rootworm native resistance breeding program includes collaborations with AgReliant Genetics, DowAgroSciences, Syngenta, the University of Illinois, the University of Missouri, USDA-ARS in Brookings, SD, and the University of J.J. Strossmeyer, in Osijek, Croatia. Since this trait has been difficult to identify and improve, we believe that large-scale collaborative efforts are the way that progress can be made.

Relevant Publications

Hibbard, B.E., D.B. Willmot, **S.A. Flint-Garcia**, and L.L. Darrah. 2007. Registration of the Maize Germplasm CRW3(S1)C6 with Resistance to Western Corn Rootworm. *Journal of Plant Registrations*. Accepted, *In press*.

Ivezic, M., J.J. Tollefson, E. Raspudic, I. Brkic, M. Brmez, and **B.E. Hibbard**. 2006. Evaluation of corn hybrids for tolerance to corn rootworm (*Diabrotica virgifera virgifera* LeConte) larval feeding. *Cereal Research Communications* 34:1101-1107.

Meyer, J.D.F., Snook, M.E., Houchins, K.E., Rector, B.G., Widstrom, N.W. and **McMullen, M.D.** Quantitative trait loci for maysin synthesis in maize (*Zea mays* L.) lines selected for high silk maysin content. *Theor. Appl. Genet.*, in press.

Morton, B.R., Vroh Bi, I., **McMullen, M.D.**, and Gaut, B.S. An analysis of neighboring nucleotide effects on SNPs in nuclear DNA from maize (*Zea mays* L.). *Genetics* 172:569-577. 2006.

Prischmann, D.A., K.E. Dashiell, D.J. Schneider, and **B.E. Hibbard**. 200X. Field screening maize germplasm for resistance and tolerance to western corn rootworms (Coleoptera: Chrysomelidae). *J. Appl. Entomol.* Accepted, *In Press*.

Vroh Bi, I., **McMullen, M.D.**, Sanchez-Villeda, H., Schroeder, S., Gardiner, J., Polacco, M., Soderlund, C., Wing, R., Fang, Z., and Coe, E.H. Jr. Single nucleotide polymorphisms and insertion-deletions for genetic markers and anchoring the maize fingerprint contig physical map. *Crop Sci.* 46:12-21. 2006.

Yim, Y.-S., Moak, P., Sanchez-Villeda, H., Musket, T., Close, P., Klein, P.E., Mullet, J.E., **McMullen, M.D.**, Fang, Z., Schaeffer, M.L., Gardiner, J.M., Coe, E.H. Jr., and Davis, G.L. 2007. A BAC pooling strategy combined with PCR-based screenings in a large, highly repetitive genome enables integration of the maize genetic and physical maps. *BMC Genomics* 8:47 (published online Feb 9).

Impact

Maize research at Missouri may be described as ranging from basic biology to applied quantitative trait analysis, hence our slogan "From DNA to the Field." Members of the four large-scale projects focus on trait dissection for corn rootworm, drought, insect, and disease resistance, all traits that impact maize production. All four projects also utilize diverse germplasm (inbred lines, landraces, and teosinte) to identify germplasm with novel alleles for trait improvement. Although Missouri does not have a corn breeding program per se, we are making great strides in understanding the genetic basis of traits of economic value while evaluating diverse germplasm that is critical for diversifying the genetic base of corn.

