

Maize Diversification by Capturing Useful Alleles from Exotic Germplasm

**Candice A.C. Gardner,
USDA-ARS Plant Introduction Research Unit and
Department of Agronomy, Iowa State University**

Archeological, carbon-14 dating of maize specimens, and microsatellite evidence has provided strong support for domestication of maize 9,000 - 10,000 years ago from *Z. mays* ssp. *parviglumis* (Doebley, 1990) in southern Mexico (Matsuoka et. al., 2002). Since then, early and modern plant breeders have steadily capitalized on the amazing genetic diversity engine uniquely inherent to maize. Understanding of genetic architecture, mechanisms that underpin genetic improvement, and breeding methodologies continue to evolve.

Use of diverse plant genetic resources by dedicated individuals who understood their importance underpins crop improvement progress all over the world, regardless of crop. In the U.S., a group of dedicated individuals who were devoted to assembling and effectively utilizing maize genetic resources to address threats to crop production and improve productivity have had a major role in establishing maize as the world's number one crop today.

Exotic germplasm can be challenging to work with due to lack of adaptation, poor agronomics, and other issues. Fortunately, today we have access to environments and technologies that help us make crosses, effectively select progeny, and identify superior performance through high-throughput phenotyping or performance testing of huge numbers of progenies to enable rapid progress. We also have genomic and bioinformatic technologies that can help us characterize diversity at the sequence and allele level. When these are coupled with the insights and skills of multidisciplinary collaborators who focus on challenges associated with disease, pests, abiotic stress, software development and analytical capacity, unique germplasm is developed and progress results. Perhaps kernel composition is to be altered to enable more rapid digestion, slower digestion, higher energy yield, or other unique purpose; regardless of the challenge, genetic diversity is key to achieving objectives.

The maize collections of the U.S. National Plant Germplasm System and of CIMMT in Mexico are the most extensive repositories of maize genetic diversity in the world. The private sector, with its vast history of proprietary germplasm development, likely holds the most diverse collections of elite germplasm with current intellectual property protection. Details will be provided on the NPGS holdings and suggestions for their access.

Some examples of successful introgression programs will be discussed, historical and current. Double haploid line development from the GEM Project and identification of novel alleles for cell wall development will be discussed. Challenges to effective utilization will be examined.