

NCR167 2005-6 Annual Report from the University of Wisconsin

James G. Coors, Professor
Department of Agronomy

The corn breeding/genetics program at the University of Wisconsin involves research with both grain and silage germplasm. The more basic research focuses on selection methodology and genetic variation for grain yield and related agronomic traits. The more applied breeding work focuses on germplasm and technology development for improving yield and nutritional quality of silage corn, as well as creating suitable germplasm for energy biofeedstock development. Current projects receiving the most attention in 2005-6 are listed below:

Selection Methodology and Genetic Variation:

Long-term selection for prolificacy: The Golden Glow maize population has been selected for 33 cycles for increased prolificacy at the University of Wisconsin. During selection for increased number of ears per plant, it was noticed that morphology of prolific plants from later generations seemed quite different from that of the typical plant of the original Golden Glow. The increase in number of ears per plant has been accompanied by a reactivation of axillary meristems at multiple nodes of the main stalk, as well as an increase in lateral branch length and an increase in number of tillers per plant. It appears that *tb1* (*teosinte branched1*) or similar genes influencing tillering in maize (e.g., *tillered1 - tlr1* and *tillered2 - tlr2*) are associated with prolificacy and associated morphological changes.

Germplasm and Technology Development for Improved Yield and Nutritional Value for Silage:

Wisconsin Quality Synthetic: The UW corn breeding program has unique germplasm, the Wisconsin Quality Synthetic (WQS), specifically designed to produce high-quality inbreds for use as parents for silage hybrids. The WQS synthetic is continuously improved using a S₂-topcross recurrent selection breeding method, and inbreds derived from succeeding cycles of improvement will be developed to the S₆ stage and released (See <http://www.silagebreeding.agronomy.wisc.edu/>). The nutritional improvements characteristic of WQS germplasm are low neutral detergent fiber (NDF), high in vitro true digestibility (IVTD), high NDF digestibility (NDFD), and low lignin concentration. We are in the fourth cycle of selection, and in 2005 we created approximately 150 new S₂ testcrosses with inbred LH244 for evaluation in 2006.

GEM Quality Synthetic: In 2005, we continued our new breeding effort for the GEM Quality Synthetic (GQS), developed from GEM breeding populations CUBA164:S1517, CUBA164:S15, and CUBA117:S1520. Since GQS is approximately 75% Stiff Stalk, inbred lines from GQS may well produce silage hybrids with high forage yield as well as superior nutritional quality when crossed to inbred lines from our Wisconsin Quality Synthetic, which is a non-Stiff Stalk breeding population. We will continue breeding GQS using the same S₂-testcross system used for WQS. In 2005, we visually screened

approximately 200 S₁ GQS families in the nursery and in a separate stress trial. We will cross the surviving S₂ families (~100) to W604S in our 2005/6 winter nursery. These crosses will be evaluated for silage potential in 2006. In our inbred breeding nursery in 2005, we made additional self-pollinations and selection for approximately 300 advanced families derived from GEM breeding crosses.

Near-Infrared Spectroscopy (NIRS): We have developed and updated a useful set of broad-based NIRS prediction equations for predicting four measures of nutritive value of corn silage; NDF, IVTD, starch, and protein. IVNDFD can then be obtained as a function of NDF and IVTD. These NIRS equations, which are based on trials conducted throughout Wisconsin starting in 1991, are now routinely used by the UW corn breeding program as well as the corn hybrid evaluation program (conducted by Dr. J. Lauer, UW Agronomy - Corn Extension).

Starch Utilization by Ruminants: The primary aim of this research is to improve the utilization of corn grain and silage by dairy cattle through evaluation of starch and endosperm characteristics that influence ruminal starch degradation and the development of corn hybrids with increased starch digestibility. We are using near-isogenic lines for *fl2* and *o2* genes in the Oh43 and W64A inbred backgrounds. These genes may produce a less dense endosperm than normal, which may influence starch degradability. We are also evaluating testcrosses involving 75+ inbreds from the GEM project and WQS for kernel hardness and vitreousness. A subset of these testcrosses are being evaluated for *in vivo* starch degradability. We have also initiated a QTL study of starch degradation. This study uses genetic materials that have been developed by Dr. Javier Betran, Texas A & M University for a study of kernel hardness (flint versus dent) and pest resistance (*Aspergillus flavus*). These materials include 140 recombinant inbred lines (RILs), which are inbred lines derived from the cross B73*o2* x CML161. B73*o2* is a soft-kernel inbred line expressing the *o2* mutation. CML161 also contains the *o2* mutation, but CML161 was selected during its development for hard, vitreous kernels as part of CIMMYT's Quality Protein Maize project. The grain of the RILs spans a wide range of vitreousness, but, importantly, all lines are homozygous for the *o2* mutation, and most still express elevated lysine concentration. One-hundred and forty *o2* recombinant inbred lines will be evaluated for starch degradabilities in a ruminal *in situ* evaluation.

Biofeedstock Development:

This project addresses needs for corn stover feedstock development through an integrated multidisciplinary approach. The collaboration includes Iowa State University, the University of Wisconsin, the University of Pennsylvania, the USDA Dairy Forage Research Center, and the USDA Corn Insect and Crop Genetics Research Unit along with several industry partners. Research teams are focused on plant breeding and crop physiology, harvest and storage technologies, and systems integration. The overall goal is to develop productive, efficient, and sustainable strategies for stover biomass as a primary feedstock. The overall objectives of this project are to: 1) develop innovative harvesting and storage technologies to efficiently and economically move maize stover from the field to the factory gate; 2) identify genetic varieties of maize with specific

properties attractive for biobased industries and initiate a breeding program to enhance those properties; and 3) evaluate and optimize these systems for economic and environmental sustainability. Specific maize breeding targets include lignin and cellulose metabolism for their impacts on fiber quality and hydrolysis characteristics; silica, sulfur, and phosphorous content for their impact on downstream processing and thermochemical conversion; and yield and distribution of maize biomass among stover constituents with respect to densification and conversion characteristics. In 2005, we evaluated 50 hybrids from a variety of sources for ethanol production potential and demonstrated that there are significant genotypic differences among hybrids for most characteristics related to ethanol production potential.

Current Personnel:

| | |
|---------------------|---|
| James G. Coors | Project Leader |
| Dustin T. Eilert | Senior Research Specialist |
| Patrick J. Flannery | Research Program Manager |
| Ntjapa Lebaka | Ph.D. student (starch degradability) |
| John Goeser | M.S. student (starch and fiber degradability) |
| Aaron Lorenz | Ph.D. student (biofeedstock development) |

Collaborators:

Randy Shaver, Dept. of Dairy Science, UW
Joe Lauer, Dept. of Agronomy, UW
Mike Blanco, USDA-ARS, ISU
Kendall Lamkey, ISU
Javier Betran, TAMU

Publications:

de Leon, N., J.G. Coors, S. M. Kaeppler, and G.J.M. Rosa. 2005. Genetic control of prolificacy and related traits in the Golden Glow maize population: I. Phenotypic evaluation. *Crop Sci.* 45:1361-1369.

de Leon, N., J.G. Coors, and S.M. Kaeppler. 2005. Genetic control of prolificacy and related traits in the Golden Glow maize population: II. Genotypic analysis. *Crop Sci.* 45:1370-1378.

Krakowsky, M.D. M. Lee, and J.G. Coors. 2005. Quantitative trait loci for cell wall components in recombinant inbred lines of maize (*Zea mays* L.) I: Stalk tissue. *Theor. Appl. Gen.* 111:337-346.