

NCR167 2006-7 Annual Report from the University of Wisconsin

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The corn breeding/genetics program at the University of Wisconsin involves research with both grain and silage germplasm. Our research 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 2006-7 are listed below:

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-testcross 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 2006 we evaluated 101 new S₂ and S₃ testcrosses with inbred LH244. In 2007, the 20 top-performing S₂ families will be recombined to create WQS C4.

GEM Quality Synthetic: In 2006, we continued our breeding effort for the GEM Quality Synthetic (GQS), developed from GEM breeding populations. 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 WQS, which is a non-Stiff Stalk breeding population. We will continue breeding GQS using the same S₂-testcross system used for WQS. In 2006, we evaluated 73 S₂ families crossed to W604S. In 2007, the 20 top-performing S₂ families will be recombined to create GQS C1.

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 also evaluated testcrosses involving 75+ inbreds from the GEM project and WQS for kernel hardness and vitreousness. We have also completed a QTL study of starch degradation using 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 B73o2 x CML161. B73o2 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. One-hundred and forty *o2* recombinant inbred lines have been evaluated for starch degradabilities in a ruminal *in situ* evaluation. We are in the process of completing the QTL mapping.

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 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. In 2006, we continued our evaluation of 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:

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

Collaborators:

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

Publications:

Krakowsky, M.D. M. Lee, and J.G. Coors. 2006. Quantitative trait loci for cell wall components in recombinant inbred lines of maize (*Zea mays* L.) II: Stalk tissue. *Theor. Appl. Gen.* 112: 717-726.

Coors, J.G. 2006. Who are Plant Breeders, What Do They Do, and Why? In K.R. Lamkey and M. Lee (eds) *Plant Breeding: The Arnel R. Hallauer International Symposium*. Blackwell Publishing, Ames, IA.