NCR167 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. 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. Current projects receiving the most attention in 2001 are listed below:

Selection Methodology and Genetic Variation:

Double cross improvement: Selection schemes designed to improve the cross between two populations are known as reciprocal recurrent selection (RRS). W577 was originally a double-cross hybrid [(W64A x A295)(Oh43 x W374R)] introduced by the Wisconsin corn-breeding program in 1963. Six cycles of full-sib RRS have now been completed using the F_2 of two parental single crosses as the initial A and B populations. Preliminary results show that the A x B population crosses have increased grain yield over cycles of RRS, but the per se performance of both the A or B populations have not improved. The objectives of the ongoing research are: 1) to compare genetic variation within and between the A and B parental populations at cycle 0 and cycle 6, 2) to determine direct and indirect responses to selection after six cycles, 3) to estimate inbreeding depression within the A and B parental populations, and 4) to compare estimates of genetic variation within and between the A and B parental populations using both phenotypic measures and molecular markers (SSRs). Phenotypic data is being obtained from a set of experiments conducted in two locations over two years (2001 and 2002).

Long-term selection for prolificacy: The Golden Glow maize population has been selected for 29 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. We are conducting a quantitative trait locus (QTL) analysis of 194 F_3 families derived from the cross of the inbred line A679 and a single S_1 plant developed from a highly prolific plant from cycle 23 in order to 1) to identify molecular genetic markers linked to chromosomal regions that influence the number of ears per plant and associated morphological traits, 2) to determine whether *tb1* (*teosinte branched1*) or similar genes influencing tillering in maize (e.g., *tillered1* - *tlr1* and *tillered2* - *tlr2*) are associated with QTLs influencing prolificacy and associated morphological changes, and 3) to evaluate epistatic interactions between chromosomal regions that influence the number of ears per plant and related morphological traits.

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, specifically designed to produce high-quality inbreds for use as parents for silage hybrids. The WQS synthetic is continuously improved using a S_2-topcross recurrent selection breeding method, and inbreds derived from succeeding cycles of improvement will be developed to the S_6 stage and released (See http://uwsilagebreeding.agronomy.wisc.edu). We finished a two-year evaluation of two cycles of selection, and are releasing WQS C2 in 2002. The nutritional improvements characteristic of WQS C2 are low neutral detergent fiber (NDF), high in vitro true digestibility (IVTD), high NDF digestibility (NDFD, and low lignin concentration. In fact, the lignin concentration is equal to or lower than the *brown-midrib3* (*bm3*) check hybrid used in our evaluations. A large number of inbreds are under development from the first two cycles of selection in WQS.

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 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).

Digestion Kinetics of Silage Germplasm: We are evaluating the extent of genetic variation for digestion kinetic components of maize silage, and also determining whether there is potential for prediction of kinetic components by NIRS. Digestion kinetics are assessed in time-course digestion studies where rate and extent of digestion can be estimated. We have not seen much genetic variation for digestion kinetics components to date, but we are continuing to refine techniques and to examine a broader array of germplasm.

Personnel:

James G. Coors	Project Leader
Dustin T. Eilert	Senior Research Specialist
Patrick J. Flannery	Research Program Manager
Natalia de Leon Gatti	Ph.D. student (prolificacy)
Eduardo Graterol	Ph.D. student (double-cross improvement)
Ben Justen	M.S. student (digestion kinetics)
Travis Frey	M.S. student (through 6/02, WQS evaluation/kinetics)
Luciano Nass	Visiting Scientist