

NCR-167 Minnesota Station Report

March 2004 – February 2005

Rex Bernardo
Department of Agronomy and Plant Genetics
University of Minnesota, St. Paul, MN

Mission and Program Description

My mission at the University of Minnesota is (i) to conduct research that is meaningful to corn breeders and (ii) to educate future plant breeders. My research focuses on developing methods for gene discovery with plant breeding data; elucidating the nature of genetic variation for quantitative traits; and enhancing germplasm adapted to the northern U.S. corn belt. My work involves theoretical research, computer simulation, molecular marker analysis, or field experimentation. I advise graduate students, serve on graduate committees, and teach two graduate courses and one undergraduate course.

Program Highlights

- Martin Arbelbide and I found that corn BC₁ populations need not be random mated prior to the development of inbreds (Crop Sci. 44: 401-404).
- Jennifer Taller and I identified *Cateto* as a most suitable exotic population for improving Northern corn hybrids (Crop Sci. 44:1444-1449): this population combines high mean performance and a large genetic distance from Northern corn germplasm.
- Jianming Yu and I found that for corn grain yield, the rate of loss in genetic variance due to inbred recycling is not as fast as expected (Crop Sci. 44: 405-410).
- Jianming Yu and I found that metabolic control analysis, a biologically-meaningful model that nicely describes the behavior of genes in a metabolic pathway, is also a mechanism that can account for the conservation of genetic variance during advanced cycle breeding (Theor. Appl. Genet. 108: 1614-1619).
- Studies to discover genes for quantitative traits have used significance levels ranging from 0.0001 to 0.05. I found that if a significance level of 5% is used in gene discovery, the probability that a putative gene turns out to be false can be as high as 80% (Theor. Appl. Genet. 109: 419-424). This research has led to the general recommendation that very stringent significance levels be used in gene discovery.
- Bertrand Parrisieux and I successfully used *in silico* mapping methodology to discover DNA fingerprints for smut resistance, grain moisture, and plant height in corn (Theor. Appl. Genet. 109: 508-514). Most notably, a marker on chromosome 8 was consistently associated with resistance to common smut; no other markers on this chromosome showed a significant association with corn smut. This work represents the first successful exploitation, for gene discovery, of large-scale phenotypic, pedigree, and genomic databases in a plant breeding program.

- We continued to conduct the Minnesota corn maturity tests. The testing program comprised nearly 700 hybrids and 12 locations, with each hybrid being tested at three locations in its declared maturity zone.
- From August to December 2004, I was on sabbatical leave as a visiting scientist at the Institut National de la Recherche Agronomique (INRA) near Paris, France. I conducted research with Dr. Alain Charcosset on the usefulness of gene information in marker-assisted recurrent selection.
- I hosted the NCR-167 meetings on 21-22 February 2005 at the University of Minnesota.

Publications

1. Arbelvide, M., and R. Bernardo. 2004. Random mating before selfing in maize BC₁ populations. *Crop Sci.* 44: 401-404.
2. Yu, J., and R. Bernardo. 2004. Changes in genetic variances during advanced cycle breeding in maize. *Crop Sci.* 44: 405-410.
3. Taller, J.M., and R. Bernardo. 2004. Diverse adapted populations for improving northern maize inbreds. *Crop Sci.* 44:1444-1449.
4. Yu, J., and R. Bernardo. 2004. Metabolic control analysis as a mechanism that conserves genetic variance during advanced cycle breeding. *Theor. Appl. Genet.* 108: 1614-1619.
5. Bernardo, R. 2004. What proportion of declared QTL in plants are false? *Theor. Appl. Genet.* 109: 419-424.
6. Parisseaux, B., and R. Bernardo. 2004. In silico mapping of quantitative trait loci in maize. *Theor. Appl. Genet.* 109: 508-514.

Plans for Next Year

- Publish work on the usefulness of gene information in marker-assisted recurrent selection.
- Conduct research on optimizing the number and fitness of selected individuals in recurrent selection.
- Conduct field studies on potential uses of dwarf corn. Unlike normal corn hybrids, dwarf corn grows only 1.5m tall, matures in only 65 days, and can be solid seeded like small grains. It has potential uses as a forage crop or grain crop and may be a useful component in crop rotation patterns.

Impact

The University of Minnesota corn genetics and breeding program leads to new information on useful genes (e.g., for smut resistance) and novel breeding methodologies (e.g., with DNA fingerprints), and explores nonconventional forms (i.e., dwarf corn) of Minnesota's major crop.