

NCR-167 Minnesota Station Report

March 2005 – February 2006

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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

- Jianming Yu, Martin Arbelbide, and I examined the power and false discovery rate in mapping quantitative trait loci (QTL) from plant breeding data in hybrid crops (*Theor. Appl. Genet.* 110: 1061-1067). We found that the power to detect QTL was highest and the frequency of falsely declared QTL was lowest when the trait was controlled by few QTL and the population size was large. These are the same conditions for successful QTL mapping in designed mapping populations.
- Dindo Tabanao and I found that in maize populations created by crossing different numbers of parents, the amount of genetic variance was in excess of what was predicted from a simple (i.e., additive) genetic model (*Crop Sci.* 45: 2301-2306). These results implied that nonadditive effects in elite maize inbreds help maintain genetic variation in small populations and that the use of multiple parents may help sustain genetic variability in inbred-recycling programs.
- Alain Charcosset and I explored the usefulness of gene information in marker-assisted recurrent selection in maize (*Crop Sci.* 46: in press). We found that it was generally advantageous to exploit only the QTL with large effects and ignore those with small effects, even if the locations of all QTL were known. We speculated that a combination of approaches would be needed to exploit information on markers for QTL themselves, markers linked to QTL, and unknown QTL.
- Martin Arbelbide, Jianming Yu, and I found that although mixed-model QTL mapping was useful in self-pollinated crops, the approach was more useful in hybrid crops than in self-pollinated crops (*Theor. Appl. Genet.*, in press). We speculated that this was due to exploiting two sides of the pedigree in hybrid crops but only one pedigree in self-pollinated crops. Martin Arbelbide and I used this mixed-model QTL mapping methodology to detect markers associated with kernel hardness and dough strength in bread wheat (*Theor. Appl. Genet.*, in press). The results were consistent with previously reported markers and QTLs associated with these two traits, thereby providing empirical validation for the procedure.
- Alain Charcosset, Laurence Moreau, and I studied the number of fitness of selected candidates in recurrent selection (*Crop Sci.*, tentatively accepted). In this research we discovered a rule-of-thumb: The number of individuals or families selected in each generation of recurrent selection should be

roughly equal to the total number of generations for which selection will be conducted. Whether this rule-of-thumb becomes useful in practice remains to be seen, as breeders find it difficult specify in advance how long a recurrent selection program will be conducted. Furthermore, we propose a simple method (which we called “Better Half”) for optimizing the number of progenies contributed by selected parents to the next generation.

- Craig Sheaffer and I conducted dwarf corn trials in Saint Paul and Rosemount, MN in summer 2005. We compared an open-pollinated dwarf corn population with the earliest commercial hybrids we could find in Minnesota. Dwarf corn had a higher harvest index than conventional corn but had only 60% of the yields of conventional corn. This latter result was expected because the dwarf corn was an open-pollinated population rather than a hybrid, and it matured about 10-15 days earlier than conventional corn.
- 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. In 2003, Minnesota state law was amended, however, so that the maturity tests (and the major source of graduate-student funding for our program) will be discontinued after 2006.

Publications

1. Yu, J., M. Arbelbide, and R. Bernardo. 2005. Power of in silico QTL mapping from phenotypic, pedigree, and marker data in a hybrid breeding program. *Theor. Appl. Genet.* 110: 1061-1067.
2. Tabanao, D.A., and R. Bernardo. 2005. Genetic variation in maize breeding populations with different numbers of parents. *Crop Sci.* 45: 2301-2306.
3. Arbelbide, M., J. Yu, and R. Bernardo. 2006. Power of mixed-model QTL mapping from phenotypic, marker, and pedigree data in self-pollinated crops. *Theor. Appl. Genet.* DOI: 10.1007/s00122-005-0189-7
4. Arbelbide, M., and R. Bernardo. 2006. Mixed-model QTL mapping for kernel hardness and dough strength in bread wheat. *Theor. Appl. Genet.* DOI: 10.1007/s00122-005-0190-1
5. Bernardo, R., and A. Charcosset. 2006. Usefulness of gene information in marker-assisted recurrent selection: A simulation appraisal. *Crop Sci.* (in press)

Plans for Next Year

- Conduct studies on combining marker-assisted recurrent selection and double haploidy as a means of quickly obtaining superior corn inbreds.
- Continue to explore the usefulness and breeding potential of dwarf corn.
- Compare corn performance in conventional and organic environments. These studies aim to answer the question of whether it is necessary to specifically breed for organic environments, or whether the corn germplasm that does best in conventional environments will also tend to do best in organic production.

- Explore corn as a potential sugar crop for food and bioenergy (e.g., ethanol) uses.

Impact

The University of Minnesota corn genetics and breeding program can be described as “Breeding nonconventional corn by conventional ways and conventional corn by nonconventional ways.” Nonconventional forms of Minnesota’s major crop can lead to food and bioenergy benefits (i.e., high-sugar corn) as well as feed and environmental benefits (i.e., dwarf corn). Nonconventional ways of breeding corn (i.e., with DNA fingerprints and double haploids) can further enhance per-year increases in corn productivity.