Overview of Dairy Cattle Breeding

A.S. Leaflet R1893

A. E. Freeman, Distinguished Professor Emeritus of Agriculture; and P. J. Berger, Professor of Animal Science

Summary and Implications
The overall objectives of dairy cattle breeding research are to generate new knowledge and to provide this information to breeders in Iowa and the nation. We are attempting to accomplish this by developing new knowledge that will be of value in the future and also have information that can be provided to the breeding industry to answer present-day problems. Because more than 70% of the dairy cattle in the United States are bred artificially, our work will have more impact if it can eventually be applied through the artificial insemination (AI) industry and breed associations. A great deal of research and groundwork needs to be done before research can be applied on an industry-wide basis.

Introduction
Education of undergraduate and graduate students is central to our service to the people of Iowa, the United States, and the world. We participate in undergraduate teaching and our breeding group has total responsibility for graduate education in animal breeding and genetics in this department. We have three specializations under the Animal Breeding PhD degree: quantitative genetics, molecular genetics, and immunogenetics. Within each of these specializations students take about the same courses and they work on one or more research topics on the species of their choice. We have had students that worked in dairy breeding that have been in all three specializations, but by far most have worked in quantitative genetics. The Animal Breeding group has reorganized the complete graduate curriculum in 1999 – 2000. We considered what we had been teaching and what we thought should be taught, then reordered the material into logical sequences for courses and now we are teaching these courses. Some revision may be necessary over time, but we feel good about the courses and their content. We also are teaching a beginning animal breeding course over the Iowa Communications Network (ICN) to people in the state.

Materials
Personnel
People working totally or in part in dairy breeding are as follows:
Dr. A. E. Freeman, Professor (Emeritus)
Dr. P. J. Berger, Professor
Joe Detrick, Superintendent Ankeny Dairy
Mary Healey, Systems Specialist I
Donna Watson, Clerk III
The following are graduate students, where they are from, and the topic of their research:
James Johanson—graduate student, South Dakota, Health and fertility of Holstein cattle selected for high and average yield;

James Koltes—graduate student, Wisconsin, A directed search for quantitative trait loci affecting perinatal survival in Holstein cattle;
Daniele Marcomin—visiting scientist, Italy, Estimates of genetic trend for yield traits of the registered Brown Cattle population reared in Italian Trentino Alto Adige region.
Gustavo Gutierrez—graduate student, La Molina University, Peru, Genetic factors influencing reproductive health of Holstein cattle selected for high and average fat plus protein.

Facilities
We are fortunate to have the herd at Ankeny to use for research and where experience managing the herd has often pointed out problems that lead to research projects. Calving problems experienced in the herd led to research that eventually resulted in the calving ease evaluations that are now distributed around the world. Another example is how to use type scores to predict herd life. Our initial work relating type scores to herd life was augmented by UDSA–AIPL, where the sire evaluations are computed, and the result is now known as Predicted Transmitting Ability for Productive Life.

Much of our work and the work of our graduate students requires the use of computers. As the science of dairy breeding progresses, problems become more complex. The increased complexity is in nearly every task that we undertake. For example, when Dr. Berger started computing sire evaluation for ease of birth, he was using approximately 69,782 records, and now he is using 5,488,365 records. Another area where there is an increasing need for more computer "power" is in finding whether differences in the DNA that molecular biologists discover can be associated with traits of economic importance. After some of these markers are found to be useful, we need to determine how to use them in practical breeding programs, and we need to determine whether the gain in economic traits will more than offset the costs.
We have three high-performance DEC Alpha work stations that greatly increases our computing power and allows availability of the workstations when we need them. These workstations can be linked together to use as parallel processors. This is done by writing programs that can be divided into two parts with one section running on each processor and the other section running on the second processor. The results are combined after the two programs have run on both processors. Sometimes, programs have to run through the processors many times to get the results needed. This greatly reduces the time needed to get the final results. This computing power is needed to investigate the gains that can be expected by using marker-assisted selection. Another example is to develop methods to determine the maximum gain that can be made using marker-assisted selection. Then these methods will have to be tested to determine in which breeding programs and mating plans they can be used most efficiently.