National genetic improvement programs for dairy cattle in the United States

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NATIONAL GENETIC IMPROVEMENT PROGRAMS FOR DAIRY CATTLE IN THE UNITED STATES

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ABSTRACT

Rate of genetic improvement for milk yield has been increasing in recent years. Cows born in 1986 were about 135 kg superior in breeding value for milk yield to those born in 1985. Over 2.2 million cows contribute new data to genetic evaluations for production traits annually. These evaluations are computed with an animal model that provides best linear unbiased predictions of transmitting abilities for milk, fat, and protein yields and fat and protein percentages. The model includes effects of management group, permanent environment, herd-sire interaction, and animal genetic merit. Unknown-parent groups represent the genetic merit of base populations defined by birth year and sex. Type appraisal data are collected by breed associations and are evaluated with a sire model. Holstein cow evaluations are computed using scores from all appraisals and a multitrait model; evaluations for other breeds are computed using all appraisal scores, a repeatability model, and a single-trait system. Dystocia data are collected by individual AI organizations and dairy records processing centers; they are analyzed by a categorical-trait sire model at Iowa State University with support from the National Association of Animal Breeders. The AI organizations have been extremely important in increasing rate of genetic progress by increasing numbers of young bulls sampled, increasing selection intensity of bull dams through multiple ovulation and embryo transfer, and shortening generation interval through the use of younger cows and some virgin heifers as bull dams. International sales have made an important contribution to financing AI programs. Future evaluations may include additional traits such as mastitis resistance, longevity, and fertility and may be computed more frequently. Additional factors may also be considered in the models.

Key Words: Dairy Cattle, Genetic Improvement, Genetic Evaluation, Sire Sampling


Introduction

Genetic improvement programs have been applied to dairy cattle for many years. Because the selection objective usually was limited solely to increased production, a system for recording production already existed and the physiological ability of a single dairy bull to sire many progeny enabled superior bulls to have large effects, dairy cattle were early beneficiaries from these programs. Progressively more sophisticated procedures have been applied to the evaluation of bulls and to the collection of data. The improvement in evaluation procedures has accompanied changes in production tech-
nology and breeding structure. Since 1978, AI organizations have more than doubled the number of bulls in their young sire sampling programs (Lawlor and Short, 1990). Embryo transfer (ET) has nearly assured that a bull calf will result from a planned mating and has enabled cows to achieve evaluations with reliabilities as high as those for some proven bulls.

A history of national evaluation procedures and the current state of dairy cattle improvement programs is reviewed, including the traits being evaluated, methods of predicting genetic values, application of genetic information by the industry, challenges, and future directions. Primary emphasis is on production traits, but type traits and dystocia also are discussed briefly.

**History**

**Production.** A dairy cattle improvement program was initiated in the United States in 1906 (Murrill, 1985; Voelker, 1985) and has been the basis since then for collecting the data necessary for national genetic improvement of production traits. Originally called Cow Testing Associations and later Dairy Herd Improvement Associations, this record keeping program for production testing today is known as the National Cooperative Dairy Herd Improvement Program (NCDHIP). The purpose of NCDHIP is to provide production and management information to dairy producers and cooperating industry and research organizations so that the U.S. dairy population can be improved on cow, herd, breed, and national levels.

Development of sire evaluation procedures is described by Norman (1986). In the 1930s, yield of a bull’s daughters was compared with yield of their dams. Although this daughter-dam comparison procedure did not account for variation in the environment between the time of the dam’s and daughter’s production, it did account for the merit of the dam. The herdmate comparison replaced the daughter-dam comparison in 1961. The herdmate comparison appropriately accounted for the environment but did not fully account for genetic differences among herds or for the merit of mates of bulls. In 1974, the national genetic evaluation system was revised to consider the merit of the sires of herdmates, thereby accounting for genetic trend. A fixed genetic base was instituted to simplify comparisons across generations. This Modified Contemporary Comparison (MCC) was an approximation of a BLUP sire model. The disadvantages of the MCC were that it did not account for merit of the mates of bulls and that it ignored information from progeny of females and sons of bulls. In 1989, an animal model was implemented that permitted simultaneous evaluation of cows and bulls and consideration of all relationships (Wiggans and VanRad, 1989).

**Type.** National type evaluations using a sire model were started by the U.S. Department of Agriculture (USDA) for Jerseys in 1978 (H. D. Norman, Anim. Improvement Progr. Lab., USDA-ARS, personal communication). This program was extended to Guernseys and Holsteins in 1979. Previously, breed associations had used daughter averages or a herdmate comparison system. In 1982, the Holstein Association initiated its own sire model evaluation system. Linear scoring of type appraisal traits on a 50-point scale was started in 1980 for Ayrshires, Jerseys, and Guernseys and was adopted later by other breed associations. Previously, animals were assigned to descriptive classes.

**Dystocia.** Research on dystocia evaluations began in 1972 (P. J. Berger, Iowa State Univ., personal communication). In 1977, the National Association of Animal Breeders (NAAB) began sponsoring evaluations for calving ease for Holsteins. Evaluations were computed across all AI organizations in 1980 so that interorganizational comparisons could be made. Scores for calving ease were analyzed by a BLUP sire model that included the inverse of the relationship matrix among sires until 1987. An ordered categorical analysis procedure that uses a threshold model was implemented in 1988. Reliability of each sire’s evaluation that includes pedigree information was added in 1989.

**Traits Evaluated**

**Production.** Through NCDHIP, milk yield data and milk samples are collected through monthly farm visits. Fat percentage, protein percentage, and somatic cell concentration are determined. Some experimental production testing plans with less frequent farm visits but more data collected automatically are being investigated. As of January 1, 1990, nearly
TABLE 1. COUNTS OF U.S. DAIRY CATTLE POPULATIONS FOR 1989

<table>
<thead>
<tr>
<th>Population</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total U.S. dairy population^a</td>
<td>10,130,000</td>
</tr>
<tr>
<td>All animals in National Cooperative Dairy</td>
<td></td>
</tr>
<tr>
<td>Herd Improvement Program (NCDHIP) test plans^b</td>
<td>4,654,094</td>
</tr>
<tr>
<td>All NCDHIP animals in supervised test plans^c</td>
<td>3,575,795</td>
</tr>
<tr>
<td>All NCDHIP animals with reported sire identification^d</td>
<td>2,263,767</td>
</tr>
<tr>
<td>Bulls with national genetic evaluations released for the first time^e</td>
<td>4,506</td>
</tr>
<tr>
<td>Young bulls sampled^f</td>
<td>1,631</td>
</tr>
<tr>
<td>Bulls in active AI service^f</td>
<td>686</td>
</tr>
</tbody>
</table>

^b As of January 1, 1990 (Wiggans, 1990).
^c Plans accepted for use in genetic evaluations.
^e Twice the number of bulls born in 1982 or later that met the requirement of at least 10 daughters with lactation records usable for calculation of genetic evaluations (Dickinsin, 1985) for the first time for January 1990 evaluations. This 6-mo period was not affected by new requirements for data that were instituted with the animal model.
^f Anim. Improvement Progr. Lab., USDA, unpublished data.

90% of samples were tested for protein concentration and almost 80% for somatic cell count (Anim. Improvement Progr. Lab., USDA, unpublished data). In addition to yield information, reproduction and management data also are collected. All these data are processed at one of nine regional dairy records processing centers (DRPC), and management reports are returned to producers. Semiannually, data are sent to USDA for use in calculating national genetic evaluations. The flow of NCDHIP production data is shown in Figure 1. Counts of U.S. dairy cattle populations in 1989 are given in Table 1.

Type. Type appraisal programs are administered by the breed associations. Participating herds are visited periodically, and appraisal information on all registered cows in the herd is collected. In addition to final score, 15 individual traits are scored by all breed associations: stature, strength, body depth, dairy character, thurl width, rump (pelvic) angle, foot angle, rear leg set, fore udder attachment, udder cleft (suspensory ligament), rear udder height, rear udder width, udder depth, teat placement, and teat length. Final score is the most important trait in selection programs. However, individual linear traits frequently are considered when deciding individual matings.

Dystocia. Calving difficulty scores are collected through cooperating AI organizations and more recently by the Midstates and Wisconsin DRPC. Member organizations of NAAB arrange for the collection of data from herds that have daughters of their bulls, primarily cooperating herds involved in the evaluation of young bulls.

Prediction Methods

Production. Production traits are evaluated genetically by USDA with an animal model (Wiggans et al., 1988; Wiggans and VanRadcn, 1989) that includes a fixed management group effect and random permanent environmental, herd-sire interaction, animal, and residual effects. The animal effect includes fixed unknown-parent groups that account for the base population. These groups are assigned by birth year and sex of animal and parent; for Holsteins, country of origin (United States or Canada) also is considered. This animal model is applied to milk, fat, and protein yields as single traits. Evaluations for component percentages are derived from yield evaluations. Computations for milk and fat are calculated at the same time because all milk records contain fat information. Protein computations are calculated similarly using milk and protein data from only those lactation records with protein reported.

Management groups are flexible in that the number of months encompassed is increased until at least five lactations are included. Separate groups are defined for first and later lactations. For Holsteins, separate groups also are defined for registered and grade cows. Animals registered with the Red and White Dairy Cattle Association are evaluated simultaneously with Holsteins and relative to the same genetic base.

The variance components for 305-d records scaled to a total variance of 1 are as follows: genetic, .25; herd-sire interaction, .14; permanent environment, .16; and residual, .45. These components result in a heritability of 25% and a repeatability of 55%. The residual variance is assumed to vary with the length of lactation.
Lactation length weights cause lactations with less than 305 d to receive less weight.

Type. Type traits for Holsteins are evaluated by the Holstein Association. A multitrait sire model is applied (VanRaden et al., 1990b). The correlations among the linear traits contribute to the accuracy of each other. Evaluations of cows are derived from evaluations of their sires. All classifications are used for cow evaluations, but only first classifications of daughters are used for sire evaluations. The model includes herd-classification round, herd-sire interaction, sire, and unknown-ancestor group. For other breeds (Ayrshire, Brown Swiss, Guernsey, Jersey, Milking Shorthorn, and Red and White), a sire model is applied by USDA (Norman et al., 1979). All scores are included, but correlations among traits are ignored. Information from the type and production analysis is combined into the Type-Production Index (TPI) for Holsteins or a Production-Type Index for other breeds.

Dystocia. Calving difficulty is evaluated with an ordered categorical analysis procedure that uses a threshold model (Djemali et al., 1987) at Iowa State University; the evaluation is supported by NAAB. The model includes herd-year, sex, parity, season, and sire effects. Observed categorical scores are assumed to reflect an underlying linear scale on which all effects are additive. Each sire’s evaluation is reported as the expected percentage of difficult births in heifers.

**Use of Genetic Information by Industry**

Information from genetic evaluations plays an important role in determining the value of animals, identifying bulls for heavy use, and planning the next generation of animals. Production and type evaluations are distributed to breeders and AI organizations in January and July; dystocia evaluations are distributed only in July. The AI centers use production and type evaluations to decide which bulls should be added and removed from the active lineup and to determine the price of semen. For cows with recent calving dates, a list of the top 1% for production is distributed. This list
identifies cows that may be of interest as bull dams, especially through ET. The Holstein Association distributes a list of the top 10,000 cows for TPI. Most young bulls (71% of the Holstein bulls born in 1988) are a result of ET because of the high likelihood of getting a bull calf from a planned mating; 44 of the top 100 TPI bulls resulted from ET (Lawlor and Short, 1990).

The rapid rate of improvement in milk yield of cows with records used to calculate national evaluations (Figure 2) indicates the success of the genetic improvement program for production. Cows born in 1986 were 135 kg superior in breeding value for milk yield to those born in 1985. Sire selection is the main engine for genetic improvement, as indicated by the substantially higher values for the average sire contribution to cows. Environmental trend was computed from first-lactation cows and represents environmental conditions 2 to 3 yr after the birth year. Environmental trend fluctuates; although it decreased for cows born from 1978 to 1981, there has been a steady increase in the last several years. The nearly 1,600 kg of genetic improvement since 1965 is considerably greater than the 700 kg of environmental improvement.

Genetic improvement in type has been steady. Because final scores are forced to average 80 for Holsteins (T. J. Lawlor, Holstein Assoc., personal communication), trend over time is not readily apparent. However, the average PTA for type for registered Holsteins increased by .66 from 1980 to 1986.

Dystocia evaluations have been successful in increasing the use of AI for heifers. Bulls can be selected so that the likelihood of a difficult calving is reduced. This opportunity to reduce calving difficulty and get herd replacements from heifers has been an effective incentive to accept the extra effort to use AI on heifers.

The U.S. dairy cattle industry is a leader internationally. Foreign sales of semen, em-
bryos and cattle have been an important source of income for U.S. breeders. In western Europe, the black-and-white populations have been largely transformed to the North American type. International markets rely heavily on genetic evaluations as a measure of value. Considerable effort is directed toward developing conversion formulas (Philipsson, 1987; Powell and Sieber, 1990; Rozzi et al., 1990) so that imported genetic material can be compared with that available locally.

All evaluations have an indication of their accuracy. The term “reliability,” the squared correlation between predicted and true genetic values, has been accepted generally. With the adoption of the animal model for production traits, contributions of all relatives to accuracy were included in the estimate. Previously, accuracy contributed to bulls by parents was not included. To simplify understanding by producers, the term “reliability” also was adopted for measurements of accuracy for the evaluation systems for type and dystocia.

Administration

National genetic improvement programs are decentralized in the United States. Dairy producers, breed associations, and AI organizations provide data on traits of interest; AI organizations and breeders sample young bulls; and USDA and other organizations compute genetic evaluations. Traits emphasized in selection are determined by the marketplace. Sire analysts attempt to predict future requirements so that bulls with the desired characteristics will be available to meet projected needs. Data collection for production traits is producer-financed, and the cost of collecting data and maintaining the DRPC is included in NCDHIP fees. Reports returned by the DRPC to NCDHIP participants are a major source of management information and have been shown to be a good investment (Everett et al., 1982). In addition to supplying pedigree and type data, breed organizations have an important role in promoting breed improvement and distributing genetic evaluations. The AI organizations are represented by NAAB, which reports availability status of bulls and identifies young bulls in progeny test programs in addition to collecting and evaluating dystocia data. All participants are represented on the NCDHIP Policy Board (Table 2), which sets policy on issues affecting dairy producers and their organizations.

Contribution by USDA is through the Animal Improvement Programs Laboratory (AIPL), part of the Agriculture Research Service. The primary mission of AIPL is development of improved genetic evaluation systems. The routine computation of national evaluations enables immediate implementation of research results and the maintenance of a current data base of production information, which is available to researchers in the United States and other countries.

Challenges

Genetic improvement programs are in a period of rapid change. Advances in computer capability enable adoption of sophisticated computational procedures. Advances in reproductive technology such as ET, which allows cows to have many progeny, create tremendous opportunities. Cloning may require recognition by evaluation systems that animals share a common genotype. Feed additives and injectable products such as bovine somatotropin (bST) can have large effects on yield and thus increase environmental diversity.

As the value of animals is tied more closely to their genetic estimates, the incentive increases to make certain animals seem as favorable as possible; consequently, the danger of unethical record keeping and biased evaluations also grows. In recent evaluations, many of the highest ranking bulls were not sampled through major AI sampling programs. Everett (Cornell Univ., personal communication) has

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### TABLE 2. VOTING MEMBERSHIPS OF NATIONAL COOPERATIVE DAIRY HERD IMPROVEMENT PROGRAM (NCDHIP) POLICY BOARD

<table>
<thead>
<tr>
<th>Cooperating group</th>
<th>No. of board members</th>
</tr>
</thead>
<tbody>
<tr>
<td>National Dairy Herd Improvement Association</td>
<td>5</td>
</tr>
<tr>
<td>Agricultural Research Service, U.S. Department of Agriculture</td>
<td>1</td>
</tr>
<tr>
<td>Extension Service, U.S. Department of Agriculture</td>
<td>1</td>
</tr>
<tr>
<td>Extension Committee on Organization and Policy</td>
<td>1</td>
</tr>
<tr>
<td>Extension Dairy Specialists for NCDHIP</td>
<td>2</td>
</tr>
<tr>
<td>National Association of Animal Breeders</td>
<td>1</td>
</tr>
<tr>
<td>Purebred Dairy Cattle Association</td>
<td>1</td>
</tr>
<tr>
<td>Total</td>
<td>12</td>
</tr>
</tbody>
</table>

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found that evaluations of breeder-proven bulls are more likely to decrease substantially when they have daughters from widespread use (second crop). A type-of-sampling classification has been adopted by NAAB so that semen purchasers will know which evaluations are subject to greater instability.

**Future Directions**

Recent developments in computer capacity and programming strategy may be used to generate evaluations more often (Wiggans and VanRaden, 1990). Increased frequency of evaluation should assist in shortening the generation interval slightly by enabling earlier decisions on young bulls. A system presently being developed to identify errors and inconsistencies in incoming data on a monthly basis. This monthly editing will allow for early correction and will support more frequent evaluations.

Genetic evaluations can be improved through adoption of a more appropriate model or through improvements in the data (VanRaden, 1990). Recent studies (Boldman and Freeman, 1990; Dong and Mao, 1990) demonstrated that genetic and residual variance continue to vary by herd and over time. This heterogeneous variance could be accommodated in the animal model if the appropriate variances were known. The problem is in estimating them with consideration of the small herd-year group size that frequently will be encountered. One case for which heterogeneous variance can be accommodated relatively easily is for incomplete records. VanRaden et al. (1990a) found that genetic variance for records in progress is substantially less than for completed records. A method of expanding the incomplete records about the management group mean is planned to stabilize the genetic variance.

A practical method of accounting for inbreeding in large populations has been developed (VanRaden, 1990; VanRaden et al., 1990a). This concept can be extended to include heterosis by assuming a non-zero level of inbreeding in the foundation breeds being crossed.

Improvements in data may be even more important. With preferential treatment and the use of all relationships, positively correlated genetic and environmental effects could lead to bias that accumulates over time. If the quality of data deteriorates, establishing certified progeny test herds and extending the degree of data validation imposed may be necessary to determine whether data are reliable.

New technologies may fundamentally change the practice of genetic improvement. Marker-assisted selection holds the promise of evaluating the quantitative trait value of segments of the chromosome (Soller, 1990). The use of cloning halts genetic progress in the clone itself; therefore, methods to retain adaptability and generate improved clones must be developed. Special treatments such as bST may change the environment for expression of production traits, and rankings of animals could change. If such an environment became commonplace, then selection would need to be directed toward genetic improvement for production in the bST environment.

The economic merit of animals is not determined solely by the traits currently evaluated. Traits such as reproductive fitness, longevity, and disease resistance clearly affect profit. Economic indexes that combine evaluations of economically important traits offer the possibility of selection for more profitable animals, not merely for ones that produce more (Van Arendonk and Brascamp, 1990). Efficiency of production must consider costs as well as revenue. Many traits that may be added to routine evaluation systems are ones that affect cost and fitness, such as somatic cell concentration as an indicator of mastitis, longevity, and body weight. For dairy cattle, the primary interest in milk yield has made single-trait selection extremely effective in improving profitability. However, appropriate consideration of other economically important traits should result in more rapid improvement of economic productivity.

Interest and investment in nucleus herd schemes as a way to increase the rate of genetic improvement have been considerable. The pioneering work of Nicholas and Smith (1983) showed that more rapid rates of increase are possible. In the United States, the primary application of these concepts has been to reduce the average age of bull dams, thereby reducing the generation interval. Earlier use of the latest crop of proven bulls on the dam side is made possible through the use of virgin heifers as bull dams. Average age of Holstein dams decreased from 81.9 mo in 1981 to 60.8 mo in 1987 (Lawlor and Short, 1990). No national nucleus herd scheme has been under-
taken in the United States, perhaps because of the investment and organization required.

Adoption of animal models is planned for type evaluations. For dystocia, routine collection of data through NCDHIP could increase the amount of information available and simplify its collection.

Implications

The effectiveness of genetic improvement programs for dairy cattle in the United States results from cooperation of dairy producers, artificial insemination organizations, breed associations, and government and research agencies. These groups provide functional data recording programs, accurate evaluation methods, and large, effective progeny testing schemes. Evaluation procedures have been adapted and must continue to be modified to adjust to changing conditions. Since 1975, genetic trend has been substantial and environmental trend small. Biotechnology has made modern breeding programs possible and offers the possibility of further substantial changes in animal breeding methods.

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