

Evaluation and Methods

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Introduction

The ultimate goal of animal selection is to create a new generation of animals that are superior to the current population. 'Superior' is interpreted broadly to include functionality of animals, cost reduction of production, consumer perception and quality of products. These factors contribute to overall sustainability and long-term economic profitability of animal production. An essential element of selection is a genetic evaluation system for the detection of superior animals to be used to produce future generations. Current genetic evaluations that use phenotypic records and advanced statistical methods allow the separation of genetic and environmental effects. These traditional methods are complemented by DNA-based technologies that attempt to detect genetic superiority on a molecular level.

Genetic evaluation systems are highly complex and involve the collection of data from thousands of farms, determination of milk characteristics in laboratories, processing and storage of data in regional computing centres, and application of advanced statistical procedures to estimate genetic merit. Genetic evaluations are widely distributed and are the primary determiner of the value of semen and embryos. Internationally, bull evaluations are combined across country so that each country has a single national ranking of all bulls worldwide. Selection decisions on farms and by artificial insemination organizations are highly dependent on that genetic information.

Aspects of genetic selection that stretch from basic data collection including identification (ID) systems, traits recorded and evaluated, and characteristics of current and future evaluation systems to new DNA-based technologies are discussed below.

Identification Systems

Accurate genetic evaluation systems require knowledge and use of relationships among animals. An ID system is needed to record performance and pedigree information. Initially, breed associations

were responsible for recording of pedigrees in herd books. Later, milk recording agencies also recorded pedigrees. ID standards of identification are defined by the International Committee for Animal Recording (ICAR). Historically, ear tags, neck chains, tattoos, leg bands and brands have been used to identify animals. For cattle recorded by breed associations, sketches or pictures have been used also. More recently, electronic ID has been introduced. Some work has been done on implanting ID, but ear tag and neck chain mounting are the most common methods. Some of the interest in improving ID systems has been in the area of food safety in providing a trace back to the farm of origin for meat production.

Identification systems may be within farm, countrywide or international. Recently, an international system of ID has been adopted where a three-character country code is included with a 12-digit number. Breed and sex codes may also be part of the ID system and in some cases are required for uniqueness, particularly for ID from preexisting systems. With the acceptance of the country code as part of the ID, countries no longer have to assign a local ID to a foreign bull when his semen is used in that country.

The international ID system, as implemented in most countries, assigns a number to an animal at birth. This number stays with the animal and is used in milk recording and breed association herd books. In some countries, this number is centrally managed and stored in a national database.

Milk Recording

Production records are the foundation of evaluation systems for dairy cattle. International standards of milk recording are defined by ICAR. The historical standard has been to record the milk production of each cow once per month, and these daily yields are used to estimate lactation yields. The standard lactation measure has been the yield for the 10-month (305-day) period following calving. Most systems require that a representative of the milk recording agency (supervisor) conducts the on-farm recording, which contributes to the authenticity of the data. Milk samples may be collected which are then analysed in a laboratory to obtain fat and protein percentages, somatic cell counts and, in some cases, additional traits such as urea and lactose levels.

Owing to recent increases in herd size, a reduction in support by governments and economic pressure on dairy producers, alternatives to traditional milk recording plans have been developed to reduce the costs. One popular approach has been to record only one milking on a particular test day. The interval

between milkings is recorded to determine what portion of the daily yield is represented by the milking measured. This reduced method of recording is called an AM-PM plan because the milking recorded is typically at alternating times (AM or PM). Another approach has been to allow longer intervals between recordings. In some countries, a supervisor is not used; the owner or an employee records all the information. Greater flexibility has also been allowed in scheduling the frequency and type of tests (supervised or not) and frequency of laboratory analysis of milk samples. Electronic milk meters can record the milk yield at every milking. A common method of integrating these data into the current milk recording system is to report the average yield for a period of 5 to 10 days as the yield on test day. Future enhancements may allow collection of yields on every milking.

The use of laptop computers by milk recording supervisors is widespread for on-farm collection of data. These computers can perform preliminary validation to identify errors for immediate correction. Management information such as cows to breed or cows to dry-off may be available for the owner on test day. On farms with their own computer systems, production records can be calculated and maintained on site. Data can then be exchanged with regional computing centres, which provide assistance to users and act as a back-up site for the herd's data. Milk recording agencies are increasingly involved in providing extended services to farmers in support of the management of the dairy herds. Regional computing centres assemble yield and laboratory data and compute lactation information.

Traits

Production

Yields of milk, fat and protein are the major determinants of income to dairy producers and are included in nearly all evaluation systems. Milk and fat yields have been part of milk recording since it began in the early 1900s; widespread recording of protein yield began in most countries in the late 1970s. If milk is used primarily for fluid consumption, component information may not be collected.

Type

Visual appraisals of cows for conformation (type) traits have been collected for many years. A programme to collect appraisal information on a categorical scale began in 1929 for US Holsteins and in 1922 in Canada. In most countries, conformation traits are scored on a linear scale and include udder,

locomotion and other body traits. Scoring is usually done by breed association personnel or classifiers. Recent research efforts have focused on using type traits to select for increased profitability through increased herd-life, greater disease resistance or as an indicator of maintenance cost.

Fitness

Longevity, or herd-life, is an important trait from an economic point of view. This trait is usually determined from milk recording data. Somatic cell score is a logarithmic representation of the somatic cell count and is used as an indicator of udder health. Other traits that are measured and evaluated in various countries include health and disease resistance, fertility, calving ease, still births, body weight, feed intake, milking speed and temperament.

Genetic Evaluation

The goal of a genetic evaluation system is to calculate genetic merit and rank animals to enable selection decisions to be made for genetic improvement. There have been many developments in both national and international genetic evaluation systems over the last 60 years. Evaluation systems have evolved in complexity and become more accurate in estimating genetic differences as statistical techniques and computing power have improved.

Methodology

An early method for genetic evaluation of dairy bulls was a daughter-dam comparison. With this method the difference in yield between a bull's daughter and its dam was assumed to have resulted from the genetics of the bull; that is, the effect of differences in environment was not considered. The daughter-dam comparison was followed by the herd-mate comparison, which accounted for the effect of environment by comparing animals in the same herd that calved during the same season. These animals were called a contemporary group or herd-mates and the method was often referred to as contemporary comparison. The selection index theory was used to obtain sire genetic evaluation by regressing these herd-mate deviations towards the expected value of the sire. The herd-mate comparison did not account for genetic differences between herds and the genetic contribution from the parents of the contemporaries. The best linear unbiased prediction procedure or an equivalent (modified contemporary comparison), which enabled the joint estimation of phenotypic deviations and genetic values, overcame this limitation. Also, relationships among cows through their

sires (and later maternal grandsires in some countries) were accounted for with a sire model, thereby combining the genetic accounting of the daughter-dam comparison and the environmental accounting of the herd-mate comparison.

Today, nearly all major dairy countries use an animal model. An animal model allows for accounting of all relationships among animals and results in simultaneous evaluation of cows and bulls. An animal's evaluation is a function of the evaluations of its parents and its progeny, as well as its own records. Other relatives affect its evaluation through either parents or progeny. Because the system is simultaneous, information from one animal can affect the evaluations of others.

In Australia, New Zealand and the northeastern United States, deviations of yield on individual test days are combined to create a lactation measure. This test day model allows a more accurate accounting for the effects of environment because the effects of specific test days are estimated. The test day model uses the test day yields as input instead of the lactation yields. A recent advance in test day models is to allow for genetic differences by test day. In Canada, a lactation curve is fit for each cow and lactation through random regression effects. This approach provides genetic evaluations of persistency. Other countries have adopted or are working on some form of a test day model.

Evaluation Models

Evaluation systems differ by country, reflecting differences in the structure of data and the dairy industry. Some of the ways in which systems differ include calculation of lactation records, parameter estimates, accounting for age, definition of environmental groups, definition of unknown parent groups, accounting for inbreeding and heterosis due to crossbreds from different breeds, and reporting scale for evaluations.

An evaluation model is a representation of the factors that affect the trait, including the genetic merit of the animal, the factor of primary interest. A typical model is:

$$y = b + f + a + p + e$$

where y = observed value, b = contemporary or herd-mate group effect, f = other known environmental effects (e.g. age), a = animal genetic effect, p = permanent environmental effect and e = unexplained residual (error). A contemporary group is composed of animals subjected to the same environmental influences; for milk production, this is the same herd

and season of calving. The permanent environmental effect is an estimate of the similarity among repeated records of an animal that is not due to genetics. The effects are classified into fixed and random effects. Random effects include the residual, animal genetic and permanent environmental effects. These effects are assumed to have some distribution of values. Solutions for random effects have the desirable property that they are regressed towards their expected values. The expected values of p and e are typically 0, and for a , it is the average of the evaluations of parents. This regression means that only as information accumulates for an animal can its evaluation deviate substantially from the parental average. Without this characteristic, the most extreme evaluations would usually be for animals with the least data.

The classification of an effect as fixed or random is not always clear. The contemporary group is assumed to be a random effect in some systems that have very small contemporary group sizes. This assumption allows these small groups to be included, but may result in biases in the genetic evaluations. For random effects, the covariances or relationships among observations can be specified. For instance, observations on the same animal, or related animals, are obviously not independent. These relationships are specified by adding the inverse of the covariance matrix to the systems of equations for each random effect. Typically, p and e have diagonal (co)variance matrices. This means that the residuals of all observations are considered uncorrelated, and that there are no nongenetic covariances among animals. For the genetic effect, the relationship matrix (A) specifies the covariances among animals. The inverse of this matrix can be constructed, using remarkably simple rules, from a list of animals and their parents. This matrix connects animals with their parents and progeny so that information on one animal affects evaluations of all relatives.

Ancestors are traced to the point where parents of an animal are unknown, or do not provide connections to observations or other animals. These animals are replaced by unknown parent groups. Typically, they are defined to reflect known reasons for genetic differences which may include year of birth, sex and country or breed of origin. These unknown parent groups improve the accuracy of evaluations by accounting for genetic differences in the origins of current animals.

The equations for most evaluation systems are solved through iteration. In iteration, the solution for one effect is updated using the earlier solutions for all other effects. All the solutions are updated during one round of iteration. In some cases, hundreds of rounds of iteration are required to meet the

convergence criterion. Convergence occurs when the changes in solutions from one round to the next are no longer significant. Many stopping criteria could be used such as the largest relative difference, or the mean squared relative differences. For this very common method, squared differences are collected during a round and summed; when the ratio of that sum to the sum of squared solutions falls below a specified threshold, convergence is declared. The value selected is affected by the numerical accuracy possible of the computer. A value of 1×10^{-8} is reasonable.

An advance in evaluation systems is multitrait analysis. Multitrait systems provide evaluations for several traits simultaneously, allowing the information from one trait to contribute to the accuracy of the evaluations of other traits. The covariances among the traits determine the degree of this influence. In a multitrait analysis, an animal may receive an evaluation for a trait that was not recorded on that animal. For example, if a herd does not have its milk component concentrations determined, in a multitrait analysis cows in that herd could still be evaluated for fat and protein yields based on the correlations of those traits with milk yield.

Multitrait analysis is desirable in that it may account for selection. When traits are positively correlated, selection for one trait results in genetic progress in the other trait even if the second trait was not recorded. To avoid bias, an evaluation system must include the data that were used in making selection decisions.

A common application of multitrait analysis is in evaluation of linear type traits. Where all traits are observed on all animals, a canonical transformation is used to create uncorrelated traits, which are then evaluated separately. The reverse transformation is then applied to the solutions to achieve the same result as would have been achieved with the much more computationally demanding multitrait analysis. Recently, a technique was developed that allows a canonical transformation to be applied even when values are missing.

Categorical Analyses

A linear model is a powerful tool for analysing data; however, some data are not linear. If the trait is recorded as an assignment to a category, a linear model is not appropriate, and a categorical analysis is used instead. The results are interpreted as the probability of being a member of a particular class or category. Conceptually, the observed classes are located on an underlying linear scale. An ordering of the classifications is assumed, but the difference between

consecutive classes is not specified. In the United States, an ordered categorical analysis is applied to calving difficulty scores (also known as calving ease or dystocia), and the evaluation is reported as the expected percentage of difficult calvings. Calving difficulty is reported on a scale of 1 to 5, with 1 being no difficulty and 5 being extreme difficulty.

Survival Analyses

Longevity data pose additional problems. Records from animals that have reached the end of their productive lives (realized records) and from animals that are still alive and producing (censored records) both contribute information on longevity. Advanced statistical techniques based on survival analysis can be used where the survival of an animal is modelled using a proportional hazard function.

Heterogeneous Variance Adjustment

The accuracy of an evaluation is determined by how well the model represents the data. The random effects in the model represent the variability remaining after the fixed effects have been removed. If the actual genetic variance is different in various subsets of the data and the model does not account for this, the resulting evaluations will not be optimal. If a bull's daughters were primarily in herds with low genetic variance, he probably would not receive a very high evaluation even if he really had the best genetics. To account for differences in variance, the data can be adjusted, or the model can be designed to reflect the data better. To adjust the data, an estimate of the variance within each contemporary group is needed. This variance may be approximated from the phenotypic variance. Other factors such as herd size, year and region may also contribute to the estimate. By multiplying the record or deviation from an appropriate average by a factor, the genetic variance is adjusted to a common value. Adjustment can be carried out before evaluations or as part of the evaluation system.

Genetic Base

Genetic evaluation systems allow selection candidates to be compared. They do not provide absolute estimates of genetic ability. To simplify presentation, a group of animals is selected as the reference group (i.e. base) and their evaluations are forced to average zero. The evaluations of all animals are expressed relative to this group. The current base in the United States is the average of cows born in 1995. This base group is changed every 5 years. Some countries change their base every year; this is called a rolling base. With an animal model, cows and bulls are

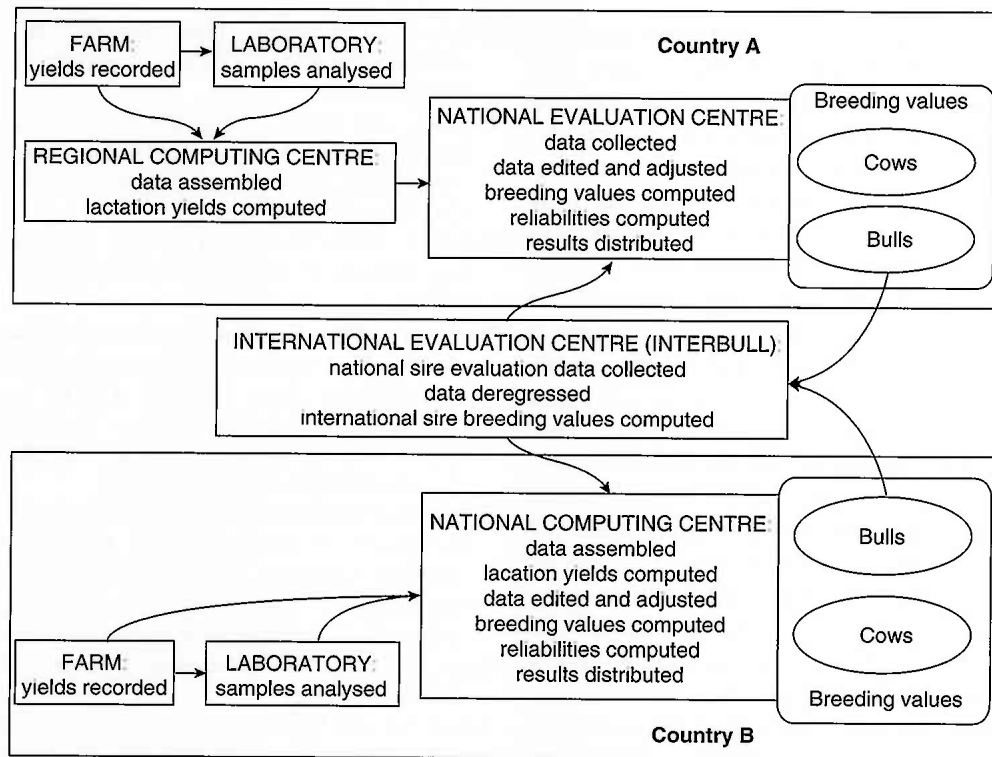


Figure 1 Flow of data through a genetic evaluation system (nationally and internationally).

evaluated simultaneously, and their evaluations are comparable. The selection pressure on bulls used in artificial insemination is much greater than that for cows; therefore the bulls in widespread use generally have higher evaluations than do cows. In a few countries, cow evaluations are presented relative to a base different from that for bulls.

International Evaluation

Because of the extensive marketing of semen and embryos internationally there is an interest in the international comparison of bulls. The Interbull Centre, in Uppsala, Sweden, combines bull evaluations from participating countries to generate rankings that include the bulls from those countries. These rankings are reported on each country's national evaluation scale. This multitrait, across-country evaluation (MACE) allows correlations to be less than one between performance in different countries; therefore the rankings may not be the same in different countries. The MACE procedure was first used in 1994; before then, conversion equations were used. Bulls can be compared if there is a link between countries. The most obvious link is when the same bull is used in two or more countries. Sons of bulls can also help link their sires across countries. The Interbull centre also conducts research into improving international evaluation systems, promoting harmonization and finding ways to extend the procedure to

other nonproduction traits. Figure 1 illustrates the flow of information from the farm through national evaluation systems and on to the Interbull Centre.

Control of Inbreeding

An important consideration in selection is the control of inbreeding. Even breeds with large populations such as Holstein have in reality very small effective population sizes (below 100). They are experiencing a loss of genetic variation and show annual increases of percentage of inbreeding of about 0.2. Inbreeding is a consequence of selection. Its rate of increase can be minimized by accounting for potential inbreeding when making mating decisions. Inbreeding depression may have its greatest economic effect on fitness traits such as fertility. Reduced fertility with increased inbreeding may result from an increase in matings that generate homozygous lethal or sublethal genotypes.

Selection Based on DNA Technology

Yield of milk and its components and most other economically important traits are affected by many genes as well as environmental factors. With the advances in DNA technology, genes that affect these traits are being discovered; such genes are called quantitative trait loci (QTL) or economic trait loci

(ETL). Evaluation systems can be adapted to estimate the effect of the various alleles of these genes and improve accuracy of evaluations by using that information. Some QTL will probably be found to be known genes linked to important biological functions.

Some QTL have been identified or mapped by linkage to genetic markers. DNA tests for genotype at these loci provide additional information on the genetic value of bulls and cows and could lead to more accurate selection. This genotype information is most useful early in the life of animals and for traits that are otherwise difficult to select for or for genes that show nonadditive gene action because mass selection techniques are not as effective in these cases.

Computer simulations of herds from nucleus breeding schemes have shown that using tests for markers linked to QTL could increase the rate of genetic gain by up to 20%. With traditional progeny testing programmes, however, the benefit is less. Many years will pass before the maximum benefit from markers is achieved because the initial data are used to establish linkages. Over the long term, the benefit from markers declines because the linked QTL becomes fixed (all animals in the population have the favourable allele) and so the markers are no longer useful. In the very long term, selection using markers may even achieve less progress than that not using markers. When QTL can be identified without using markers, genetic progress will be faster and marker-assisted selection easier to implement because data to establish linkage will not be needed. DNA tests are currently used to detect carriers of some genetic diseases such as deficiency of uridine monophosphate synthase (DUMPS) and bovine leucocyte adhesion deficiency (BLAD) (*see Genetic Defects in Cattle*).

See also: **Genetic Defects in Cattle. Genetic Selection:** Concepts; Economic Indices for Genetic Evaluation. **Genetics, Cattle Genomics. Genetics, International Flow of Genes. Mating Management:** Artificial Insemination, Utilization. **Phenotypic Selection.**

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Economic Indices for Genetic Evaluation

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Introduction

Optimal selection decisions in dairy cattle breeding should be determined by genetic and economic