

## REQUIREMENTS AND USES OF EVALUATIONS FOR HEALTH AND REPRODUCTIVE TRAITS

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### SUMMARY

Dairy cattle breeding programs should consider selection for improved health traits although defining a breeding goal that includes health traits may be difficult. Considerable genetic variability exists for most health traits in dairy cattle. The underlying genetic variability for health traits may be larger than most estimates found in the literature because of incomplete and inconsistent data recording. Appropriate economic values for many health traits are substantial. Economic values should consider direct and indirect costs (including life cycle costs). Genetic standard deviations and economic values indicate that individual health traits may be 25% (or more) as important as yield in the breeding goal. Mammary, metabolic, and locomotive health traits are the most important. Reproductive traits exhibit genetic variation and some reproductive traits may have limited usefulness for selection. Clearly, genetic change in reproduction should be monitored in dairy cattle. The challenge for geneticists is to determine how to measure health and reproductive traits or correlated traits for optimum selection programs. Index weights for yield and health traits or correlated traits can be readily calculated if one assumes that multiple trait genetic evaluations are available for selection. Correlations among measured traits and breeding goal traits are especially important for proper index construction. Genetic markers have potential for improving health traits in dairy cattle, but the complexity of most diseases and lack of data will delay discovery of useful markers.

### INTRODUCTION

Dairy cattle breeding programs should focus on improving the economic efficiency of dairy cattle. Intense selection for increased yield, especially protein yield, is clearly justified. However, the importance of health and reproductive traits and the level of emphasis that should be placed on these traits in breeding programs is controversial. Some countries, e.g., Norway and Sweden, place considerable emphasis on health traits while other countries, e.g., United States, use indirect measures and place less emphasis on health traits compared to yield traits. Many factors impact the appropriate use of genetic evaluations for health and reproductive traits in breeding programs. Some key factors include the cost to measure a trait in a segment of the population, the genetic correlation between the measured trait and the underlying trait that needs to be changed (which could be 1.0), the genetic variability and economic value of the underlying trait, and the relationships among traits. Important traits should be included in an index with appropriate weights. Ideally, genetic evaluations should be calculated using a multiple trait approach and index weights calculated assuming multiple trait evaluations are to be used for selection. Some traits may not warrant selection pressure but are potentially useful in mating decisions, e.g., dystocia. Genetic markers will enhance our ability to alter health characteristics of dairy cattle in the future; genetic markers will not decrease the need for quantitative information.

**UNDERLYING GENETIC VARIABILITY, ECONOMIC VALUES  
AND POSSIBLE TRAITS FOR SELECTION**

Defining the breeding goal for a population is usually difficult because complete and accurate genetic information and economic values for the underlying traits of interest may not be available. However, characteristics that exhibit genetic variability and that impact the economics of dairy production or have social implications should be considered. Some characteristics that meet these criteria have limited importance and may be excluded from the breeding goal with little impact, e.g., color markings. Caution should be exercised when excluding traits from the breeding goal because some traits with minor importance could be important when considered in aggregate. The aggregate of these minor traits could have a substantial impact on the weights applied to the measured traits.

The underlying genetic standard deviation for the trait in the breeding goal and the net economic value per unit change in the trait are the best measures to compare the potential usefulness of changing a trait through selection. Net economic value should consider all input and output changes, timing of expression for the trait, social costs, and the impact of restrictions on output price from a finite market (Gibson, 1989).

The following sections present some of the most important traits for consideration in the breeding goal. The traits included in the discussion may not be exhaustive, but the major health and reproduction characteristics are addressed. Alternative trait definitions could also be appropriate. Definition of some traits on a continuous scale is difficult because appropriate economic values for the continuous scale are difficult to determine. Many health traits operate on a threshold model but are impacted by a continuum of underlying genetic control. In addition, some possible measures that might be useful for improving traits included in the breeding goal are briefly considered. Movement toward progeny test herds which are under more scrutiny and toward donor dam test herds may allow better recording and the use of new technologies for disease diagnosis in the future. Table 1 gives example genetic standard deviations and approximate net economic values under US circumstances for possible breeding goal traits.

**Table 1.** Genetic standard deviations (lactation basis) and approximate net economic values (US\$) under US circumstances for possible breeding goal traits.

<u>Trait</u>	<u>Genetic Standard Deviation (GSD)</u>	<u>Net Economic Value Per Unit (\$) (NEV)</u>	<u>GSD*NEV(\$)</u>	<u>Value Relative To Yield</u>
Milk yield (mature)	650 kg	.14	91.00	1.00
Days open	6 days	1.50	9.00	.10
Clinical mastitis	.15 (0,1 trait)	150.00 or more	22.50	.25
Milking labor	.9 hours	8.00	7.20	.08
Ketosis	.06 (0,1 trait)	100.00 or more	6.00	.07
Milk fever	.08 (0,1 trait)	100.00 or more	8.00	.09
Displaced abomasums	.04 (0,1 trait)	100.00	4.00	.04
Laminitis	.10 (0,1 trait)	100.00 or more	10.00	.11

### Production traits

Genetic standard deviations for mature lactation milk yield are from 500 to 750 kg (Pearson et al., 1990). Genetic standard deviations for lactation protein yield are from 15 to 22 kg. Genetic standard deviations for fat yield are slightly higher than for protein. Lactose production is also under considerable genetic control (Pearson et al., 1990). Economic values for milk yield (with value of all components included) after adjustment for variable costs and to an actual yield basis (genetic standard deviations are on mature basis) are probably about \$12-\$15 (US) per 100 kg. Milk, fat, protein, and lactose can be easily measured in most dairy cattle populations. The ease of measurement along with the genetic variability and economic value make yield traits the most important traits for selection in most dairy cattle populations. The use of lactation records has been fruitful, but multiple trait genetic evaluations of test day records possibly could enhance dairy cattle improvement (Meyer et al., 1989). The importance of the yield traits relative to each other will differ across populations, but protein yield is clearly most important for most populations.

### Reproductive traits

The genetic standard deviation for days open is about 6 days with estimates ranging from 3-12 days (Hansen et al., 1983; Van Arendonk et al., 1989; Hayes et al., 1992). The economic value for days open may not be strictly linear, however, a linear value of approximately \$1.50 (US) per day may be appropriate (Groen and Vollema, 1993). Conception rate, cystic ovaries, retained placenta, age at puberty, and other reproductive measures also exhibit genetic variation (Philipsson, 1981; Freeman, 1984; Freeman, 1986; Lyons et al., 1991). Age at puberty may have little associated economic value since it is not limiting in most dairy breeds if calf and heifer nutrition are reasonable. Ovarian disease, conception rate and retained placenta are components of days open but they may have some additional economic value. Ovarian disease may be difficult to measure and record consistently on a large portion of the population in many countries. Conception rate and retained placenta incidence are likely to be more easily measured. Genetic evaluations for reproductive traits are possible with the wide-scale recording of reproductive performance for management decisions. Recording of reproductive diseases such as metritis and cystic ovaries will be of limited value unless this recording is accurate and consistent in critical segments of populations. The potential for genetic change in reproductive traits using the measures currently available is limited. However, due to an antagonistic genetic correlation between production and reproduction (Freeman, 1986), reproduction should not be ignored in breeding programs.

Dystocia or calving difficulty as a trait of the calf (direct trait) and as a trait of the cow (maternal trait) is under some genetic control (Thompson et al., 1981; Freeman, 1984). Unfortunately, an antagonistic genetic correlation exists between the two traits (Thompson et al., 1981). This correlation has lead geneticists to recommend non-random mating to reduce the likelihood of dystocia in heifers and to monitor genetic change in the populations with little direct selection for either trait. However, Dekkers (1993b) has suggested that combining selection and non-random mating would benefit the dairy industry.

### Udder health

Mastitis is the most costly disease in most dairy cattle populations. Both clinical and subclinical diseases are under some genetic control (Miller, 1984; Emanuelson, 1988; Emanuelson

et al., 1988; Shook, 1989). This implies genetic variability in the underlying resistance to intramammary infections. Studies involving clinical mastitis incidence where data are accurately and consistently recorded indicate heritabilities of .10 and higher for clinical incidence (Miller, 1984; Lin et al., 1989; Lyons et al., 1991). Heritabilities for somatic cell counts (SCC) in milk are also .10 or higher (Emanuelson, 1988; Shook, 1989). The genetic standard deviation for clinical mastitis on a non-incidence versus incidence (0 or 1) basis per lactation is around .15 if one assumes a heritability of .10 and a .30 incidence rate per lactation. The genetic standard deviation for clinical mastitis may be underestimated in many studies because of recording inconsistencies and recording of only veterinary treated cases. The genetic standard deviation for intramammary infections may be larger than for clinical incidence because of a higher frequency. However, many intramammary infections may have little economic impact other than reduced yield. Cost per lactation that involves at least one clinical episode is probably more than \$150 (US) (Rogers, 1993). This includes drug cost, extra labor cost, veterinary treatment cost, discarded milk value, and costs for premature culling (or death); no costs for reduced lactation milk yield are included other than discarded milk. Lower milk quality premiums from subclinical infections could make the total costs even higher. Premature culling costs (life cycle costs) are often underestimated when determining total costs of mastitis. The definition of mastitis used in the breeding goal may not be important as long as all costs of mastitis are appropriately considered.

Direct measures of clinical mastitis may be useful for selection in populations where direct measurement is feasible. Somatic cell counts could be useful to select for reduced mastitis (Shook, 1989; Weller et al., 1992; Rogers, 1993; Schutz, 1994). Also, milk conductivity may have some potential as an indirect measure of mastitis. Perhaps future technologies will allow frequent testing for intramammary infections at a low cost. Even at moderate cost, some new technologies and accurate clinical or intramammary infection recording could be implemented in donor dam and progeny test herds. New technologies will provide new mechanisms for selection to improve udder health and will improve the understanding of genetic resistance to mastitis.

Udder edema, milking speed, and milking labor interact with udder health traits. Udder edema is heritable (Dentine and McDaniel, 1983) and could warrant selection pressure if recorded appropriately. Milking speed and milking labor are not strictly health traits, but they should be mentioned as possible traits for selection or mating because they are genetically correlated with measures of udder health (Blake and McDaniel, 1978; Miller, 1984; Seykora and McDaniel, 1986). These associations make selection for improved udder health and husbandry traits more complex. Selection for increased milking speed may not be warranted but mating to avoid extremes might be reasonable. Selection for reduced milking labor (labor involved with cow preparation, machine adjustment, and postmilking cow attention) or traits associated with milking machine suitability (independent of machine time) could be valuable in the future with increased automation of milking equipment. Rogers (1993) outlines possible genetic variability for current milking labor.

#### Metabolic and digestive diseases

Clinical ketosis or acetonemia occurs in about 2-12% of the lactations in dairy cattle and is dependent on many factors including genetics (Emanuelson, 1988; Lyons et al., 1991; Mantysaari et al., 1991; Simianer et al., 1991; Tveit et al., 1992). Ketosis is much more frequent in second and later lactations so expression of genetic variability will likely be greater in older cows. Most studies indicate very low heritabilities, but some studies perhaps with more complete data recording (Lyons et al., 1991; Mantysaari et al., 1991) found heritabilities near .10. Underlying

genetic variance is likely larger than most studies would indicate because of measurement error. The genetic standard deviation for ketosis on a non-incidence versus incidence (0 or 1) basis per lactation is around .06 if one assumes an underlying heritability of .10 and a .04 incidence rate per lactation. The average total cost per clinical occurrence including labor, veterinary care in some cases, treatment supplies, and life cycle costs (sometimes death) probably exceeds \$100 (US). Death losses alone could account for \$100 per clinical episode (assume 10% of clinical cows die and expected future net revenue including salvage is \$1000).

Milk fever or pronounced hypocalcemia has a similar frequency to ketosis in many populations. Clinical episodes requiring intervention occur in about 2-15% of the lactations and, like ketosis, episodes are more frequent in second or later lactation cows. Genetic variation for milk fever is similar in magnitude to the genetic variation for ketosis (Emanuelson, 1988; Lin et al., 1989; Lyons et al., 1991; Tveit et al., 1991). Heritability estimates in some studies may be lower than the underlying heritability because of incomplete recording. The underlying genetic standard deviation for milk fever on a non-incidence versus incidence (0 or 1) basis per lactation is around .08 if one assumes an underlying heritability of .10 and a .06 incidence rate per lactation. The average total cost per clinical occurrence is probably similar to ketosis. Life cycle costs including the risk of death and limited salvage value can be an important part of the total cost.

Displaced abomasums tend to have an impact on herd economics that is similar to ketosis and milk fever. However, veterinary costs may be higher and life cycle costs may be lower for displaced abomasums. The frequency of occurrence is low and the heritability may be around .10 (Lyons et al., 1991).

Lack of consistent, accurate, and complete recording prohibits direct selection on ketosis, milk fever and displaced abomasums in most populations. Indirect selection using metabolic markers may be helpful where recording is not possible on large segments of a population.

#### Locomotive traits

Locomotive traits impact reproductive performance, survival, salable milk, and labor needs. Genetic variation in hoof disorders is low to moderate (Distl et al., 1990). Laminitis, hoof injuries, abnormal claw growth, and skin disorders are the most prevalent problems. Lameness from hoof disorders clearly has a substantial impact on reproductive efficiency (Collick et al., 1989; Ward, 1990). Laminitis is perhaps the most important of the disorders. The underlying genetic standard deviation for laminitis on a non-incidence versus incidence (0 or 1) basis per lactation is around .10 if one assumes an underlying heritability of .20 and a .05 incidence rate per lactation (Distl et al., 1990). The average total cost per clinical occurrence not including reduced milk yield may be \$100 (US) or more. Reproductive costs (increased days open), treatment costs, labor costs and reduced survival are major contributors to the total cost. Hoof diseases are not recorded in many national populations, but some indirect measures (Distl et al., 1990; Rogers, 1993) may be helpful for selection.

#### Longevity, herd life, culling, and lifetime performance

Longevity, herd life, culling or lifetime performance can be used in defining breeding goals (Rogers and McDaniel, 1989; Strandberg, 1990), but utilization of the individual components (health, management/husbandry, and yield traits) that impact these measures may allow a more refined approach to establishing total merit indexes. If individual components are included in the definition of a breeding goal, life cycle costs must be considered because in many cases these life

cycle costs could be larger than the direct costs. If longevity, herd life, culling or lifetime performance are included in the breeding goal, genetic parameters (especially genetic correlations) between lifetime measures and yield must be handled appropriately (Dekkers, 1993a). Measures of longevity, herd life, culling, and type characteristics can be used as selection criteria; these measures are considered by Dekkers (1994). Some of these measures will be useful for selection in most populations.

#### FACILITATING GENETIC CHANGE IN BREEDING GOAL TRAITS

Directional genetic change in the breeding goal traits will only occur if selection is practiced on the breeding goal trait or if selection is practiced on a correlated trait. For many traits it may be too costly or difficult to directly measure the trait as it is defined in the breeding goal; it may be easier to measure a correlated trait or a trait with a slightly different definition. Multiple trait selection utilizing a combination of traits that are included in the breeding goal and correlated traits is likely to result in optimum breeding programs for many countries. The weights applied to these correlated traits will depend on: the correlation between the measured trait and the underlying trait that needs to be changed, the genetic variability and economic value of the underlying trait, and the relationships among the traits. Multiple trait genetic evaluations would be most desirable for use in calculating total merit for individuals. The appropriate index vector (b) to combine multiple trait genetic evaluations for the measured traits is (P.M. Van Raden, personal communication 1993):

$$b = a_m + a_n G_{nm} G_{mm}^{-1}$$

where,

$a_m$  is the vector of economic values for measured traits included in the breeding goal  
 $a_n$  is the vector of economic values for non-measured traits included in the breeding goal  
 $G_{nm}$  is the genetic covariance matrix between the non-measured and measured traits  
 $G_{mm}$  is the genetic variance/covariance matrix between the measured traits.

The index weights (b-values) for the measured traits can be standardized for comparison by multiplying by the genetic standard deviation of the measured trait. If the traits included in the selection criteria are defined as they are in the breeding goal and only measured traits are included in the breeding goal, the index weights for multiple trait genetic evaluations are the net economic values for the breeding goal traits. If the traits included in the selection criteria have a genetic correlation of 1.0 with the breeding goal trait, the index weights multiplied by the genetic standard deviation of the measured trait will equal the product of the genetic standard deviation and the net economic value of the breeding goal trait they represent. However, in many cases the measured traits have a genetic correlation with the breeding goal trait of less than 1.0, e.g., genetic correlation between somatic cell counts in milk and mastitis.

Economic values and genetic parameters must be known for calculation of selection indexes. When economic values and parameters are not known with certainty (the usual case), sensitivity analyses can be used to evaluate the impact of incorrect parameters. Genetic covariances between measured traits and breeding goal traits may be especially critical for deriving appropriate weights for measured traits. Economic values for breeding goal traits often

differ among populations. In some cases economic values may not be linear, but approximating with linear values may be very acceptable. Inaccurate estimates of economic values under many circumstances may make additional refinement to account for nonlinear economic values trivial.

#### GENETIC MARKERS

The use of genetic markers for improving health and fertility traits in dairy cattle has been reviewed briefly by Solbu and Steine (1990) and Freeman and Lindberg (1993). Physiological and DNA markers for disease resistance were thoroughly discussed at the 4th World Congress on Genetics Applied to Livestock Production. Major discoveries for improving health of dairy cattle have not been made, but some useful markers may be discovered in the near future. The Bovine Lymphocyte Antigen (BoLa) complex is being investigated at many locations. Some alleles within the BoLa complex may be more desirable than others (Solbu and Lie, 1990; Weigel et al., 1990), but their usefulness for selection is currently limited. Inconsistent identification of the most desirable alleles may reflect the complexity of most diseases and hint that single genes with major importance for complex diseases may be rare. Genetic variability in immune competence, especially at the time around parturition, may eventually be useful for selection (Freeman and Lindberg, 1993).

Dentine (1990) outlined the general principles involved in using markers for selection. Markers may be most useful for selection within major families. Major genes with direct effect may be useful across families. Recording of disease incidence and quantifying disease resistance to identify and exploit genetic markers will always be necessary. Markers may be relatively more useful for disease traits than production traits because disease incidence is difficult to measure in some populations. In addition, heritabilities are lower for disease traits than for production traits. More studies are needed that will capitalize on improved molecular biological techniques before the usefulness of genetic markers can be accurately assessed.

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