

BREEDING FOR FUNCTIONAL TRAITS IN HIGH YIELDING DAIRY COWS

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INTRODUCTION

The term “functional traits” describes a set of characteristics of animals whose effect on the economic efficiency of cows is through reduction of costs rather than increase of product output (Groen *et al.*, 1997). It replaced, and rightly so, the term “secondary traits”, which was still used as a session heading during the 5th WCGALP at Guelph. McDaniel (1994) chairing this session, pointed out that at the time experience with genetic evaluations of health, reproductive traits, herd life and others was still limited. One of the problems he saw was the low heritability of many of the traits, another one the incompleteness and inaccuracy of data on individual cows. In the meantime research on those traits has intensified (see, *e.g.*, the proceedings of the 6th WCGALP at Armidale). Even more significant, many data processing centres and breeding associations are nowadays routinely computing and publishing breeding value estimates even for such complicated traits (in a statistical sense) as herd life.

Partly this process was stimulated by an EU-sponsored Concerted Action, with participating scientists from all EU countries, the Czech Republic, Norway, Switzerland, Israel, Canada and INTERBULL. GIFT - the acronym stands for “genetic improvement of functional traits in cattle” - brought these people together to discuss issues of recording and genetic evaluation of functional traits and enhanced collaborative efforts and exchange of computer programs used for the genetic analysis of functional traits. Its main activities were a series of workshops held from spring 1997 to autumn 1999. The workshops were organised by subject areas (groups of similar traits), with a final workshop on breeding objectives and selection schemes. The proceedings of all workshops were published as Interbull Bulletins 12, 15, 18, 19, 21 and 23.

One of the obvious questions in current dairy cattle breeding is how to combine results from evaluations on production, functional traits and conformation. Different countries and organisations went different ways and some claim that their ways are more “balanced” than those of others. Starting from the theory of the optimal selection index, we will try to evaluate the effect of different digressions from the optimal index. We will use the index and breeding programme currently implemented in the Brown Swiss population of Austria as a reference point. From November 2002, a slightly modified index will be used in the joint evaluation system of Germany and Austria.

INDEX SELECTION

The optimal way of dealing with complex breeding objectives including several traits is index selection (Smith, 1936 ; Hazel, 1943). The derivation of a selection index involves decision of which traits are economically important, calculation of marginal gains for those traits, decision about traits to be recorded, calculation of phenotypic and genetic parameters related to the complete set of traits, and derivation of index weights based on all this information. Although the method was developed more than 60 years ago, it is still considered superior to all other

approaches of multiple trait selection. The probably most serious limitation of the method is that it implies use of correct population parameters (heritabilities and genetic correlations) for which only more or less good estimates exist (see Lin, 1978 ; Sales and Hill, 1976).

In dairy cattle breeding, indices are published and applied in almost all populations. Philipsson *et al.* (1994) presented an excellent review of the use of selection index methodology in dairy cattle. When compiling information for this presentation, we found it very difficult though, to find details on the rationale for choosing traits included in the index and methodology used for derivation of the index weights which would allow conclusions about how closely the indices actually in use agree with a selection index in the classical sense.

Decisions about traits in the breeding objective and traits recorded. In index selection, the breeding objective (total merit, aggregate genotype) is defined by a linear function of economically important traits. In theory, the decision about traits included in the aggregate genotype should only be driven by their economic importance under future conditions of production (Fewson, 1993). Recordability is not required as long as correlated traits which are more easily recorded are available. In dairy cattle, such a definition will include the traits related to products sold (milk yield, fat yield, protein yield, protein content, depending on the system of pricing), and traits affecting the cost of production (feed efficiency, health, fertility, longevity, etc.). In practice, when a selection index is defined by breeding organisations, economic weights are frequently only assumed for traits for which individual breeding value evaluations are available. The only exception from this rule is longevity, often assumed to be important but in many cases only selected for through conformation traits. Classical examples for important traits almost never defined explicitly in breeding objectives are feed efficiency or feed intake (Veerkamp, 1998). Another example is mastitis, which is only included into the aggregate genotype in Scandinavia, with an exceptionally high weight in Norway (Steine and Sehested, 1999). Scandinavian countries are actually recording mastitis incidence whereas most other countries use somatic cell count as an indicator trait but are actually putting the economic weight on somatic cell count (*e.g.*, VanRaden, 2000).

Groen *et al.* (1997) tried to define a set of traits to be included in the breeding goal of dairy cattle (Table 1). They did not include longevity as a breeding goal trait as it was considered as a result from disposition for all the other traits measuring the success of a cow to survive both voluntary and involuntary culling. Only in case that a satisfactory decomposition of functional traits in the breeding goal is not possible, a “residual longevity” trait could be used as a measure of the general resistance for unrecorded disease.

Table 1. Breeding goal traits in dairy cattle breeding (Groen *et al.*, 1997)

	Production Traits		Functional traits		
Milk	carrier, fat, protein milk quality	Health	mastitis feet and legs	Calving ease	direct effects maternal effects
Beef	carcass weight/ growth lean meat yield meat quality	Fertility	other diseases showing heat pregnancy rate	Efficiency	stillbirth body weight feed intake capacity
		Milkability	milking speed behaviour		

Economic weights. Economic weights are necessary to determine the relative importance of the traits constituting the breeding objective. A host of literature on principles and methodology of deriving economic weights (or values) is available. Groen *et al.* (1997) and Dekkers and Gibson (1998) should be consulted for reviews related to dairy cattle breeding. For a more general review, see Goddard (1998). Weights for dairy cattle are usually derived via sets of profit functions or somewhat more complex “bioeconomic models” on the farm level. A herd model developed by Amer *et al.* (1994) for the comparison of overall economy of different cattle breeds was adapted and extended for derivation of economic values for the Austrian cattle breeds (Miesenberger, 1997 ; Miesenberger *et al.*, 1998). Core elements of the program are modules describing the age distribution of the herd based on different possible fates of cows, the production level in each lactation, using lactation curves according to Wood’s (1967) formula and a linear programming algorithm for selecting least cost rations on a daily basis.

Table 2. Economic weights (absolute and in genetic standard deviations) of the traits in the Austrian total merit index for Brown Swiss

Trait	Unit	Marginal gain €	s_A	Economic weight (s_A) €
Fat yield	kg	1.82	14.8	26.94
Protein yield	kg	2.83	9.8	27.73
Longevity	day	0.15	180	27.00
Persistency ^A	kg	6.60	0.66	4.36
Fertility paternal	%	1.60	5	8.00
Fertility maternal	%	1.60	5	8.00
Calving ease paternal	class	4.87	0.22	1.07
Calving ease maternal	class	4.87	0.22	1.07
Stillbirth paternal	%	1.38	2.5	3.45
Stillbirth maternal	%	1.38	2.5	3.45
Mastitis resistance	s_A	14.53	1	14.53

^A Persistency was calculated as standard deviation of test day yields (Sölkner and Fuchs, 1987)

s_A = additive genetic standard deviation

Table 2 presents the economic weights for the traits considered in the breeding objective, results were expressed per cow place and year. Comparing the lists of traits in Tables 1 and 2 we notice several differences. Milk carrier was not included because its calculated weight was very close to zero. Beef traits were excluded although there is evidence (Liinamo and Van Arendonk, 1999) that inclusion is economically sensible even in dairy populations. A rather large proportion of the functional traits considered by Groen *et al.* (1997) is represented in the list of economically important traits. Milkability (milking speed) will be included in a revised version of the index implemented in the joint German and Austrian evaluation from November 2002. Longevity was included as a breeding goal trait. To avoid double counting, effects of prolonged longevity resulting from increased fertility or reduced problems with calving ease were not counted when calculating the weights for those traits.

To be able to compare the relative economic importance of traits, they are usually expressed in terms of genetic standard deviations (see Table 2). When adding contributions from production and functional traits we arrive at relative weightings of 43.5 and 56.5 percent for the two groups of traits. According to our experience, breeders find it hard to accept that less than 50 percent of the total economic weight in a selection index are put on production. We would like to point out that the choice of scale that is very frequently used is somewhat arbitrary and misleading. The use of genetic standard deviations leads us to believe that the weights are proportional to response to selection because the heritabilities of the traits are taken care of. Response to selection depends on many more things as intensity of recording, timing of the availability of information (specifically important for longevity) and, most of all, genetic relations between traits. Table 3 gives the relative monetary responses to selection of the groups of traits found in a complex simulation of the Austrian breeding programme (Egger-Danner *et al.*, 1999). With the economic weights as described, most of the gain is still achieved for fat and protein yield. However, if functional traits were not included then, a loss rather than a gain would be expected for most of those traits (Egger-Danner *et al.*, 1999 ; Sölkner *et al.*, 2000).

Table 3. Relative “weights” of milk vs. fitness traits using different scales

	Scaling by s_A	Scaling by response to selection	Scaling by s_H
Production traits	43.5	83.3	68.4
Functional traits	56.5	16.7	31.6

s_A = additive genetic standard deviation s_H = standard deviation of herd means

As an aside, a third method of scaling is presented in Table 3. It investigates non-genetic ways of improvement. The standard deviation of herd means was taken as an indicator on how easy changes in a trait are achieved *via* changes in management. It shows that it is also not so easy to change functional traits by improvements in management, implying that genetics is still a viable route to take.

When comparing the relative weighting (based on genetic standard deviations) in different breeding programmes, Norway (Steine and Sehested, 1999) is probably using the index with the largest weight on functional traits, followed by many European countries and Canada. The weight on functional traits in the U.S. Holstein population (VanRaden, 2000) is comparatively low.

Genetic parameters. As pointed out above, availability of the correct genetic parameters is one of the limitations of the selection index. Estimation of a coherent set of parameters for a large number of traits involves a major effort in terms of computing time and personnel cost. A specific problem exists for correlation of longevity with other traits as no software is currently available that allows evaluation of the correlation including the complex nonlinear survival analysis model (Ducrocq and Sölkner, 1998) nowadays applied in many countries.

But even for more conventional traits computing power is still limiting when trying to fit multiple trait models with a large number of traits. Very often, persons responsible for running the routine evaluation turn to the very simple method of Calo *et al.* (1973) for which single trait

estimated breeding values and their reliabilities are needed as input. When the number of traits would get large, and genetic parameters were not estimated via a multiple trait model, care should be taken to check the matrices of phenotypic and genetic parameters for singularity. Use of ill-defined matrices in the selection index may yield ridiculous results. The matrix used in the Austrian index was constructed from literature values using a conservative approach “rounding” correlations towards zero. The matrix turned out to be positive definite so that no further procedure like bending (Hayes and Hill, 1981) was necessary.

Construction of index weights. Classical selection index theory weighs phenotypic information from different sources correctly and transforms it into breeding values. At the same time, it yields weights that allow combination of different traits. A set of index weights covers only one particular situation with regard to information provided (e.g. a fixed number of offspring for a bull or a fixed number of lactations per cow). It does not deal with the wealth of information from relatives different for almost all selection candidates. A multiple trait animal model including all traits of interest (such with economic weights and such contributing through correlations) takes care of the relationship structure and of the phenotypic and genetic (co)variance structure of the data. To retrieve the correct index from a multiple trait evaluation, it is only necessary to add up the products of individual breeding values and their respective economic weights. In real life we are dealing with estimated breeding values from single trait animal models or maybe from animal models combining a few traits. A procedure for approximating index weights that use estimated breeding values from single trait BLUP analyses as input was presented by Schneeberger *et al.* (1992). A modification of this procedure is used in the Austrian evaluation scheme. Alternative approximations are procedures as used in MACE (Multiple trait Across Country Evaluation; Schaeffer, 1994) where estimated breeding values are deregressed and “recycled” (see, e.g. Druet *et al.*, 1999). The approach currently closest to a real multiple trait evaluation was presented by Ducrocq *et al.* (2001). It involves a simple multi-trait prediction based on pre-adjusted records, eliminating environmental effects. The procedure is not very easy to implement and a comparison between the different approaches should be performed for decision support.

The current situation in many countries is that weights are not adjusted at all to take individual accuracies into account. Estimated breeding values from single trait analyses are multiplied by economic weights, ignoring the genetic correlation structure of traits. Also, indices are frequently only provided for bulls. This is not consistent as the ranking of all breeding individuals (e.g. for choice of bull dams) should be performed according to the breeding goal defined for the population. Extension to the female part of the population where the information content for individual estimates is much more variable calls for individual index weights as described above.

The indicator trait somatic cell score is used for selection against mastitis in the Austrian index. No other indicator traits are used, i.e. conformation is not at all included in the index at the current stage.

The role of conformation traits. Conformation traits constitute an important part of most selection indices in dairy cattle. The usual rationale is that certain conformation traits have an effect on culling rate and are therefore (early) indicators for longevity (Boettcher *et al.*, 1997). In the index selection system, they may therefore be used either as indicators for individual

functional traits like feet and leg problems or udder health, according to the approach of Groen *et al.* (1997) or as indicator traits for the composite trait longevity. The latter approach has been followed by some countries (e.g., Brotherstone *et al.*, 1998). The estimated genetic correlation coefficients between some of the conformation traits and longevity are moderate. For the Brown Swiss population of Austria, we found the highest correlations (estimated by the method of Calo *et al.*, 1973) for udder depth (0.44), udder overall score (0.40), feet and legs overall score (0.35), suspensory ligament (0.20), teat length (0.18) and hock quality (0.14). Using these traits as indicators for longevity using the modified Schneeberger *et al.* (1992) approach, we found that accuracies increase by roughly 5 percentage points when the accuracy of evaluation for longevity alone was between 0.3 and 0.4 and by 2-3 percentage points when the longevity accuracy was between 0.5 and 0.6.

Inclusion of conformation traits to modify evaluations for longevity is methodologically correct. Including conformation with an economic weight (as done in many countries) is incorrect when the economic weights were derived on the level of a production farm. Sölkner *et al.* (2000) showed that putting 10 percent of the total weight on conformation leads to a loss of 4 percent in total merit whereas putting 30 percent results in a loss of 32 percent of economic merit within a specified breeding programme.

SELECTION FOR FUNCTIONAL TRAITS IN LOW INPUT ENVIRONMENTS

All that has been written above refers to a situation where recording and data transfer systems are well developed, animal model BLUP is standard and the educational level of the farmers is high enough to cope with a wealth of information presented in figures. Although the situation in developing countries is quite different, the appropriate breeding goal is probably even more complex (Baker and Rege, 1994). Longevity under adverse conditions is definitely a trait of high interest and in addition to the traits already mentioned, pre- and postweaning survival rates are important traits to be considered in an index. Some general comments on breeding goals in low input environments are provided by Amer *et al.* (1998) and Sölkner *et al.* (1998).

THE PROMISE OF MAS

The last decade has seen the emergence of molecular genetics as a tool in practical animal breeding. The search for QTL (quantitative trait loci) in dairy cattle has originally concentrated on production traits (Georges *et al.* 1995). The potential utility of QTL of large effect is considered to be higher for traits of low heritability and search for QTL for functional traits has started (Zhang *et al.*, 1998 ; Reinsch *et al.*, 1998 ; Heyen *et al.*, 1999 ; Schrooten *et al.*, 2000 ; Ashwell *et al.*, 2001). Putative QTL have been found for somatic cell count and, less convincing, herd life. The search for loci affecting functional traits will continue, using full genome scans for yet untyped populations, confirmation studies and fine mapping for loci of interest according to previous studies. It is likely that for traits with low heritability, QTL effects are also rather small but this has to be seen. In the near future, utilisation of QTL in marker assisted selection will probably be by within family selection, *i.e.* preselection of full sib bull calves entering the progeny testing system (Mackinnon and Georges, 1997).

As we are dealing with an extremely complex breeding goal in dairy cattle, it is likely that selection based on phenotypic data will still provide the bulk of genetic progress made.

CONCLUSIONS

The tools for selecting for production *and* functional traits are available in most countries with populations of high-yielding dairy cows. These tools are recording schemes for traits of economic importance, genetic evaluation procedures based on the animal model and index selection theory. Depending on the number of functional traits included in a breeding scheme, the relative economic importance of production vs. functional traits varies from 70:30 to 30:70. In any of these schemes, monetary selection response will still come for a large part from production traits because genetic parameters favour fat and protein yields (high heritability, high positive genetic correlation). Model calculations show that without inclusion of functional traits in an index, most of them will deteriorate while small positive responses may be expected under selection for an index. Marker assisted selection may gain some importance in the future but most of the selection response will still be provided by appropriate use of phenotypic data.

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