56th EAAP meeting, 5-8 June, 2005, Uppsala, Sweden,
Cattle & Genetics Commissions, Session CG2.1

International Trends in Recording and Genetic Evaluation of Functional traits in Dairy Cattle

T. Mark, J.H. Jakobsen, H. Jorjani, W.F. Fikse and J. Philipsson
Interbull Centre, SLU, Box 7023, 750 07 Uppsala, Sweden

Summary

Functional traits have become increasingly important in the dairy cattle industry due to increased costs of production relative to milk prices. This has instigated recording of functional traits to be used for both management and breeding purposes. Although economic values differ between countries, the emphasis for functional relative to production traits have increased throughout the western world during past decades. The Scandinavian countries have traditionally recorded and performed genetic evaluation for a broad range of functional traits, but in recent years, many other countries have also implemented genetic evaluation for udder health, fertility, longevity and calving traits. International genetic evaluations are available or being investigated for these traits due to the increased trait availability and demand for such services. Across country genetic correlations are high for most trait groups, but further trait harmonisations could lead to better international evaluations. Modern and more cost effective recording devices give new opportunities of directly or indirectly measuring functional traits, especially in nucleus herd selection schemes, although it is a challenge to maintain emphasis on low heritability traits in such systems. Increasingly sophisticated genetic test-day models also provide useful information for management purposes. Locomotion, feed efficiency and metabolic stress measures are important traits that are currently not widely considered for genetic evaluation, but may be so in future.

Introduction and aim

The dairy industry is rapidly changing, as is the society as a whole. Economic circumstances are changing while the information and technological opportunities are increasing. Dairy cattle breeding is an increasingly international business. The genetic exchange of embryos, livestock and especially semen between countries is significant and is increasing. For example, the proportion of Holstein bulls sired by a foreign sire have increased from 36 percent for bulls born in 1980 to 65 percent for bulls born in 2000 (Interbull pedigree file, May 2005). The international selection of bulls requires international genetic evaluation, so the bulls can be accurately compared across countries.

The relative emphasis of dairy cattle breeding objectives has gradually shifted from production traits to functional traits during the past couple of decades (Miglior et al., 2005) and many countries now have genetic evaluation in place for important functional traits such as health, fertility, longevity and calving traits (Mark, 2004). Functional traits are defined as those characters of an animal that increase efficiency not by higher outputs of products but by reduced costs (Groen et al., 1997). The aim of this paper is to summarise international trends in genetic evaluation of functional traits. In order to speculate about the future of dairy cattle breeding, we will also briefly summarise some trends in international dairy cattle breeding structures and recording practices, as they constitute important prerequisites for future developments of breeding programmes.

Direct selection emphasis required to avoid unfavourable genetic trends

The genetic level for protein yield has increased noticeably during the past two decades for both the Holstein and Ayrshire breed (Fig. 1). These figures represent the trends in the global cow population relative to Swedish production circumstances, since bull breeding values were weighted according to the total number of daughters across all countries participating in the international genetic evaluation.

Since the late 1980’s, the genetic levels have deteriorated slightly for clinical mastitis and direct longevity for the Holstein breed (on the Swedish scale). This suggests that the selection emphasis on these traits have not fully counterbalanced the negative indirect effect of selection for increased production.

The genetic levels of clinical mastitis and direct longevity for the Ayrshire breed show a different trend than for the Holstein breed. Here the genetic levels for both of the functional traits increase slightly (except for longevity in the last year, but the average longevity breeding value in year 2000 is based on an incomplete batch of bulls). The majority of Ayrshire cattle are from the Nordic countries (77 percent), whereas most Holstein cattle come from non-Nordic countries (92 percent). This may explain the breed differences observed in Figure 1, i.e. selection indexes in Nordic countries have put relatively high emphasis on functional traits for many years.

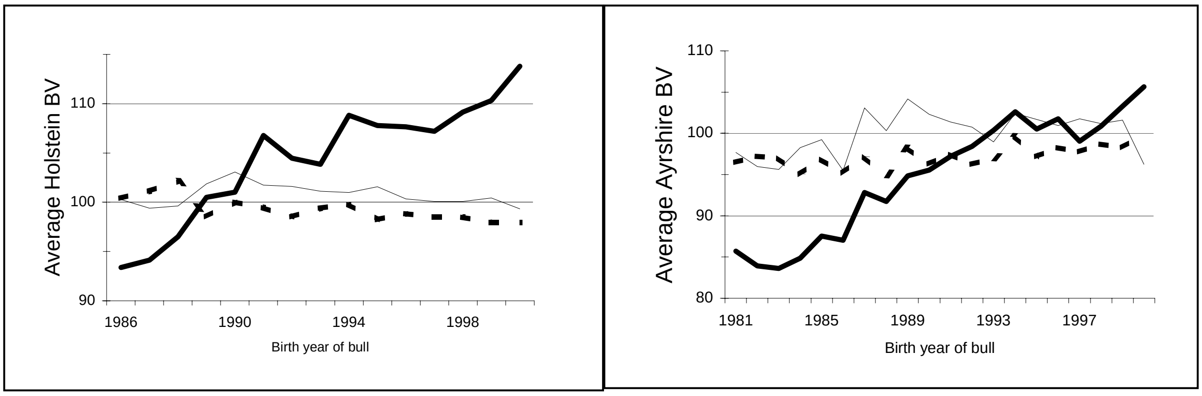

Figure 1. Estimated genetic trends in Holstein and Ayrshire cow populations for protein yield (thick-solid line), clinical mastitis (dotted line) and direct longevity (thin-solid line) on Swedish scales (weighted average of international bull breeding values from May 2005 Interbull evaluations; weighted by total number of daughters across all countries; high breeding values are favourable; all sets of breeding values are expressed with a base standard deviation of 10).

Due to genetic correlations less than unity among similar traits in different countries, it could be speculated that the genetic levels had increased more when only daughters in the concerned country were considered. The difference would then be greater for the two functional traits due to relatively lower across country genetic correlations than for protein yield. However, the genetic trends for the three traits shown in Figure 1 were similar when only daughters in Sweden were considered, except that yearly fluctuations were larger for both breeds.

The genetic levels for direct and maternal calving ease as well as stillbirth showed some fluctuations for the Holstein breed, but there was no clear direction of the trends. These fluctuations can be caused by extreme breeding values for a few very popular bulls. Maternal stillbirth showed a slightly unfavourable genetic trend for the Holstein breed since the early

1990's. Genetic trends based on international data are not available for female fertility, but Lindhé and Philipsson (2001) found a clear unfavourable genetic trend in female fertility for Swedish Holsteins and a slightly favourable genetic trend for Swedish Ayrshires. The negative genetic trends for Holsteins in Sweden occurred despite the relative high emphasis for these traits the Swedish selection index. This may partly be explained by the fact that about 75 percent of the sires of bulls with daughters in Sweden were first registered in a country other than Sweden (May 2005).

Antagonistic genetic association between production and many functional traits

Genetic correlations between production and functional traits are typically antagonistic, but at the same time moderate to low (e.g. Rauw et al., 1998). This allows for simultaneous improvement for both trait groups. However, undesirable genetic trends are expected for functional traits, if they are not included in the breeding goal. Table 1 shows examples of recent estimates of genetic correlations between production and functional traits. However, actual estimates vary for different populations, traits and studies.

Table 1. Examples of antagonistic genetic correlations between production and functional traits

Trait	Genetic Correlation	Reference
Clinical Mastitis	0.3	Carlén et al., 2004
Milk Somatic Cell	0.2	Carlén et al., 2004
Female Fertility	0.3	Roxström et al., 2001
Persistency	0.4	Jakobsen et al., 2002
Disease Resistance	0.5	Jakobsen et al., 2003

Large progeny groups important for low heritability traits

The number of progeny tested bulls has increased for the Holstein and Jersey breed, but decreased for the Ayrshire and Guernsey breed over the past couple of decades (Table 2). The number of daughters is positively correlated to the reliabilities of breeding values for a given trait and the median number of daughters reflects the reliability, which can be obtained for a "typical" bull. The median progeny group size varied across breeds, and to a lesser extent within breed, over the past two decades. Ayrshire bulls have higher median number of daughters than bulls from other breeds, which is likely due to the relatively high emphasis for functional traits in the Nordic countries.

The required progeny group size needed to obtain a specific reliability increases with decreasing heritability for a trait. Functional traits often have low heritabilities. Relatively large progeny group sizes are therefore needed to achieve reasonably high reliabilities. Results for milk yield and clinical mastitis from the May 2005 Interbull evaluation illustrate this. Milk yield and clinical mastitis in Sweden had a heritability of 0.33 and 0.03, respectively. The median reliability for international breeding values for bulls with daughters in Sweden was 74 percent on the Swedish clinical mastitis scale, whereas the median reliability for the Swedish milk yield scale was 95 percent. When all bulls in all participating countries are considered, the corresponding figures were 62 and 76 percent for the Swedish mastitis and milk yield scale, respectively. The latter figures depends to a large extend on the magnitude of across country genetic correlations as well as the reliability of national breeding values in foreign countries.

With decreasing cow numbers it can be difficult to ensure high reliabilities for a constant number of progeny tested bulls per year while maintaining selection intensity. In order to achieve this, some breeding programs might have to consider testing fewer bulls per year. Alternatively, investments to get better measurements of functional traits or indicators of functional traits can be made, or existing genetic evaluation models may be improved in order to utilize the available information better, and thus improve the reliabilities.

Table 2. Total number of bulls born between 1986 and 1999 with international genetic evaluation for milk yield in May 2005 and median number of daughters across all participating countries for six different breeds

	No. bulls						Median no. daughters					
Year	AYS	BSW	GUE	HOL	JER	SIM	AYS	BSW	GUE	HOL	JER	SIM
1986	631	383	43	4897	304	1340	187	110	57	92	81	91
1990	558	368	51	5559	317	1169	200	103	49	92	75	94
1994	477	398	42	6054	403	1163	206	92	52	100	84	89
1998	472	386	23	6344	396	1028	160	80	45	91	82	89
ALL	7775	5444	537	84365	5452	16836	186	93	52	94	79	90

From national to international genetic evaluation: some basics

Genetic evaluation is needed in order to select superior animals to breed the next generation of animals and thereby improve animal production. Genetic evaluations depend on the quality of performance data, pedigrees, the statistical model and software used to compute the evaluations. Therefore data quality assurance (e.g. Boichard et al., 1995; Klei et al., 2002; Thompson, 2001) is an important part of a genetic evaluation service, and all data considered in international genetic evaluations are required to meet specific quality standards (Fig. 2).

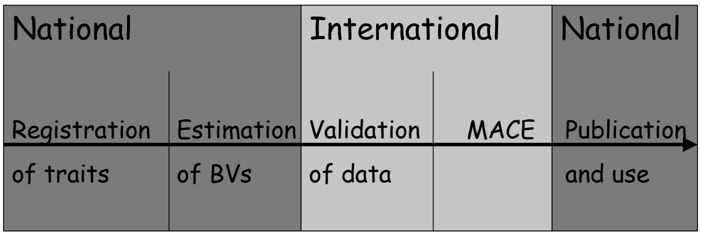

Figure 2. Illustration of the process from data recording to publication of international breeding values.

The results from a genetic evaluation are expressed relative to a specified group of animals and the results can be used to compare the genetic merit of the animals and ancestors, which are included in the evaluation. Animals evaluated in separate evaluations cannot be compared unless they are included in a subsequent meta-analysis.

Meta-analyses are necessary because it is not possible in practise to include raw data from all traits, all places and all times in the same evaluation. International genetic evaluations performed by Interbull are examples of a meta-analysis. International genetic evaluations are performed using the Multiple-trait Across Country Evaluations method (Schaeffer, 1994). This method considers deregressed national genetic evaluations free of all non-genetic and non-additive genetic effects as different, but correlated traits.

Recording of functional traits is a prerequisite for genetic evaluation

Accurate data recording and storage of data are prerequisites for any genetic evaluation. Databases and recording schemes are most often characterised by national policies and country borders. In several cases different schemes and databases are kept for different regions within a country. In the future, across country databases will be beneficial as joint national genetic evaluations evolve. However, the difficulty to implement cross-national identification systems is an important constraint, which needs to be effectively addressed.

The first union of farmers for recording and collection of milk production data started in Denmark in 1895. The aim was to use this information for future phenotypic selection. Recordings of the functional traits were initiated much later and started with a systematic recording of conformation and artificial insemination data. Later, health data from veterinary services were computerised and integrated in the national databases of the Scandinavian countries. Absence of recordings of the functional traits has been, and still is, a bottleneck for national genetic evaluations in some countries.

The Scandinavian countries have a unique position in registration and collection of information about functional traits. Veterinary treatments are regularly recorded. In a few cases the farmers can also record a disease incidence. Information about calvings (date, size of calf and stillbirth information) is recorded by the farmer and submitted to a central database, as is the culling date of the cow, as part of the milk-recording schemes. This information can be used for genetic evaluations of calving and longevity traits. Information about artificial inseminations (AI) is recorded by the AI-technician or by the farmer and can also be used for national genetic evaluation for fertility traits. It is advantageous to store all information in one central database as it eases the matching of data from different sources.

Classifiers record a large number of conformation traits. Conformation traits are useful indicators for many functional traits due to early registration, moderate to high heritabilities and genetic correlations with certain functional traits. Recently, classifiers in many countries have started to record locomotion and body condition score.

Use the information for multiple purposes

It is a substantial, but important, task to make sure all relevant collected data are being made available for systematic evaluation. The recorded information can and should be used for several purposes (Fig. 3). A central database, which integrates data from several sources, is especially advantageous in such cases. Increasingly sophisticated genetic models can also provide useful information for management purposes. Such information can be more useful than traditional management lists, because the separate sources of variation of the traits are better described when environmental and genetic effects are considered simultaneously.

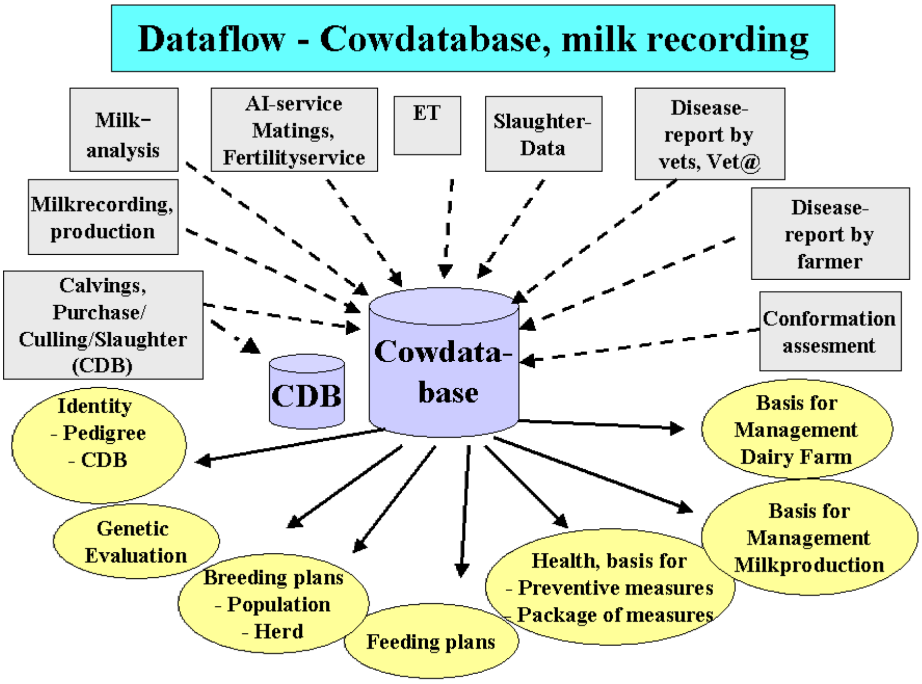

Figure 3. Illustration of information flow to and from a central cow database (from Philipsson et al., 2003)

The application of test-day models in animal breeding makes solutions from the genetic evaluation particularly interesting for management purposes, since the different effects can be monitored on a daily basis, although typically with some delay since genetic evaluations are usually not performed continuously. Mayeres et al. (2002) showed a nice example of how small changes in the modelling of fixed effects in a test-day model can increase the usefulness of solutions for fixed effects, while solutions for genetic effects were essentially unchanged. The farmer will be stimulated to record information when this information is used to create current and projected key-figures which can be used for management purposes.

More and more countries conduct genetic evaluation of functional traits

Many functional traits have non-Gaussian statistical properties, which make it more challenging to develop appropriate genetic evaluations for these traits. In spite of this, many countries use relatively simple genetic evaluation models (e.g. linear sire models). However, survival analyses are being used to evaluate longevity for about half of the countries in Interbull longevity evaluations. Similarly, three countries apply threshold models for analyses of calving traits. Random regression models are frequently used to infer longitudinal breeding values for milk somatic cell and in a few cases also milking speed.

The dissemination of genetic evaluations for different trait groups in 31 Interbull member countries was recently reviewed by Mark (2004), and up to date details can be found at www.interbull.org. Since the results by Mark (2004) were compiled (2003-08-25), four, three and two countries introduced national genetic evaluations for longevity, milk somatic cell and calving traits, respectively, while the number of countries with evaluations for other main trait groups remained constant in this time period (Table 3). However, information on traits currently not considered for international genetic evaluations might not have been reported. The higher increase for longevity may be explained by the recent introduction of international genetic evaluations for this trait. A similar trend was seen for udder health traits, when Interbull launched international genetic evaluations for this trait in 2001.

Table 3. Trends in dissemination of genetic evaluations for different main trait groups

Trait group	No. countries with at least one evaluation (08-2003)[1]	No. countries with at least one evaluation (05-2005)
Dairy Production	31	31
Health	19	21
Longevity	14	18
Calving	14	16
Female Fertility	14	14
Workability	13	13
Efficiency	2	2

[1] From Mark (2004); status for 31 Interbull member countries

Across country genetic correlations partly reflect degree of trait harmonisation

Across country genetic correlations are high for most trait groups (Table 4), but further trait harmonisations in national recording and genetic evaluations could lead to more comparable and precise international evaluations. However, across country correlations are relatively low for direct longevity, which may be due to different culling reasons and ways of measuring longevity in different countries.

Table 4. Weighted[1] average, standard deviation (SD) and range in estimated[2] genetic correlations (r_G) across different Holstein populations for selected traits

Trait	#Populations	Mean r_G	SD of r_G	Range of r_G
Protein yield	27	0.85	0.05	0.19
SCC	23	0.89	0.05	0.23
Clinical mastitis	4	0.85	0.07	0.18
Longevity	18	0.70	0.16	0.66
Direct calving ease	12	0.76	0.15	0.83
Maternal calving ease	11	0.76	0.17	0.70
Direct stillbirth	7	0.71	0.14	0.47
Maternal stillbirth	7	0.77	0.22	0.99
Non-return rate (cows)	3	0.61	0.18	0.36
Days open / calving interval	4	0.90	0.02	0.05
Body condition score	2	0.86	-	-

[1] Weighted by number of bulls with evaluations in both of the concerned countries

[2] Estimated genetic correlations from Interbull March 2005 test evaluations (except for fertility and body condition where estimates were taken from ongoing pilot investigations)

Changing structure of dairy industries affects possibility for genetic evaluation

The structure of the dairy production has major implications for opportunities and design of genetic evaluations. For example, countries with large, relatively homogeneous herds and frequent use of artificial insemination have better possibilities of adjusting for non-genetic effects.

The structure and rate of structural changes of national dairy herds are diverse and depend largely on national subsidies, legislation, climate and other production circumstances. According to the International Farm Comparison Network report by Hemme et al. (2004), more than 70 percent of dairy cows in the U.S., Oceania, Argentina and a few European countries (Denmark, the U.K., Ireland, the Netherlands, Estonia and the Check Republic) are in herds of more than 50 cows, while less than 10 percent of the cows are in herds with more than 50 cows in Switzerland, Austria, Norway, Finland, Poland and India. The rapid decrease in number of farms in North America and many European countries has been compensated by increased herd sizes and increased production per cow. The structural changes have been less in countries such as Norway, Switzerland and Austria, which significantly subsidise their farming sector.

The possibilities for data recording depend, among other factors, on the intensity of the production system. Also, in some countries legislation has promoted recording of some traits, which would otherwise be difficult to record. For example, veterinary treatments must be recorded in Scandinavia. Intensive production systems often involve more record keeping and are to some extent associated with higher costs of production. The cost of production varies substantially across and within country. In Asia (India, Pakistan), South America (Argentina, Brazil) and Oceania (Australia, New Zealand) it is much cheaper to produce milk compared with Europe (Hemme et al., 2004). In these regions the total milk production has increased over the past decade, while the total milk production in countries with milk quota (Europe, Canada) has been constant and the production in former centrally planned countries has declined. Extensive dairy production systems (e.g. Ireland, parts of Australia and especially in New Zealand) are favoured by mild climates, which allow for grazing during almost all months of the year and relatively inexpensive housing facilities.

Modern technology gives new recording opportunities

The use of information technologies and automatic recording devises in dairy cattle herds are expected to increase in the future as herd sizes and labour costs increase, new or cheaper recording technologies and data-handling tools emerge. Today automatic milking systems (AMS) and automatic milk metering devices are becoming more widely used; at least in the north-western European countries where labour costs are relatively high. AMS allows daily measures of milk characteristics such as conductivity, temperature and oestrus indicators. Automated registrations also allow for automatic transfer of data from the equipment to a central database, which can reduce the number of erroneous recordings and ease the recording for especially the farmer.

Variables that can be measured automatically during milking are milk yield, electrical conductivity of milk, milking speed, milk temperature, the cow's activity during milking and body weight (de Mol, 2000). Although it is possible to record feed intake it is usually not practiced, except in some experimental herds. However, this may change as automatic milking systems become more common. Some AMS can record the intake of concentrates when cows are automatically fed during milking.

Milk progesterone level can be used as an indicator of the cow's oestrus, but currently needs to be analysed off the farm (in a laboratory). The same is the case with somatic cell count and bacteriological measures of the milk. However, in-line measurements of progesterone may be feasible in the future (Tang et al., 1998).

More advanced and expensive recording technologies may be used in nucleus herds, but have limited use in most commercial herds. However, missing records on some animals are not uncommon phenomena for many traits, but some information is better than no information, especially since nucleus herds tend to have elite animals, which are of highest interest for breeding purposes.

Large-scale recordings of clinical disorders have so far been limited to the Scandinavian countries, but initiatives to record clinical mastitis are under way in the Netherlands, France, and Canada (Holstein International, 2005). Large modern herds increasingly rely on own registrations for management purposes. American research studies have demonstrated that such farmer registrations (e.g. of clinical disorders) can be collected and used for genetic evaluation purposes (Zwald et al., 2004).

Functional traits – the next generation

Table 5 summarises some traits, which have been investigated in research projects or may be so in the near future. Genetic evaluation for persistency has become feasible with the development of test-day models for production traits. Persistency has a direct value in itself (Dekkers et al., 1998) and is favourable correlated to health (Jakobsen et al., 2003) and female fertility traits (Muir et al., 2004).

Physiological measures seem to offer valuable opportunities to improve genetic evaluations for female fertility (e.g. Darwash et al., 1997; Royal et al., 2002). Body condition score (BCS) can also be used as an indicator for female fertility (e.g. Dechow et al., 2004) as well as udder health and resistance to other diseases (Lassen et al., 2003). Research suggests that repeated measures increase the value of BCS or ultrasound (Dechow et al., 2002; Banos et al., 2005; Sloniewski et al., 2004), e.g. the cow’s ability to mobilize energy from body reserves can be measured with repeated observations. However, repeated body condition scores are usually not available, since animals are often only classified once during their lifetime. Repeated measures may be recorded in nucleus herds, and body weight of lactating cows can also be measured routinely in some milking parlours.

No measures are available to directly measure feed utilization efficiency under practical farm conditions. However, the quantities of feed eaten and used for milk production and maintenance can be measured or predicted with sufficient accuracy and simultaneous consideration of all these traits can be used to improve feed efficiency (Veerkamp, 1998).

Indicator traits (e.g. conformation and milk somatic cell) will continue to be valuable, because of low heritabilities and late expression of important functional traits. It should be underlined, though, that these indicator traits should be analysed simultaneously with direct observations of the traits of interest. As regards conformation traits it should be observed that positive scores for the trait group dairyness, angularity etc are clearly negatively associated with health and fertility, and should be seriously re-evaluated by the breed societies (Rogers et al., 1999), if they haven’t been so already.

Molecular genetic information can be used to identify underlying genetic regulations of the traits and thereby help to discover suitable physiological indicators for important functional traits. Today, research in molecular genetic have started to focus more on analyses of micro-array data to investigate the effects of several single genes simultaneously. For functional traits such an approach is desirable, since several genes affect the majority of these traits.

Table 5. Examples of traits, which are currently not frequently considered for genetic evaluation, but may be so in the future

Trait	Value	Recording possibility	Heritability
Persistency[1]	Higher ratio of roughage to concentrates; favourably correlated with health	Milk production test-day records required	0.2
Body condition score	Amount of energy reserves at given time, positively correlated to health, fertility and beef production	Classifiers	0.2
Feed efficiency, Productivity (production per metabolic weight)	Affects costs directly and substantially	Intake of concentrates if fed separately; expensive; not sufficient; e.g. bull test stations; body weight of cows	0.4
Clinical disorders	Very costly (direct veterinary costs and reduced production)	Veterinarians or farmers	<0.1
Conductivity	Correlated with udder health	Online; frequent measures; requires hi-tech parlour	0.3
Locomotion	Important in grazing and free stall systems; correlated to longevity	Classifiers; moderate space and time consuming	0.1
Activity (milking)	Milking temperament	Electronically in hi-tech milking parlour or by farmer	0.1
Activity (general)	Indicate oestrus	Pedometer	
Temperature (milk)	Indicate fever or oestrus	Online; requires hi-tech parlour	
Progesterone profiles	Correlated to fertility	Expensive; limited use	0.2

Interbull meets demands for international comparisons of more functional traits

In the mid 1990's, dairy producers were limited to information about production traits in order to select foreign bulls and to compare foreign and domestic bulls for selection purposes. In May 2001, the first international genetic evaluation for clinical mastitis and milk somatic cell was launched (Mark et al., 2002), which marked a significant shift in focus for the international selection of bulls towards functional traits. Since then, direct longevity, direct and maternal calving ease and direct and maternal stillbirth have been added to the Interbull services. In the future, more functional traits are expected to be added to the portfolio (Table 6).

International genetic evaluations for female fertility are currently being investigated and a routine service is expected to be a reality within the coming couple of years. Milking speed and temperament are widely considered in different countries and we expect that international genetic evaluations could relatively easily be developed for these traits. Persistency within lactation is an important trait and many countries have begun to evaluate this trait after introducing test-day models for production traits. However, the possibilities for genetic improvement of this trait along all other traits of the breeding goal still needs to be demonstrated, and no demand has been expressed for international genetic evaluations for persistency.

Table 6. Year of realised or possible future onset of international genetic evaluations for different traits

Main trait group	Number of sub-traits	Year of onset of international genetic evaluation
Dairy production	3	1994
Conformation	19-20	1999
Udder health	2	2001
Longevity	1	2004
Calving	4	2005
Female fertility[1]	3-6	>2005
Workability	2	>2005
Locomotion	1	>2006
Body condition	1	>2006

[1] Research ongoing

Concluding remarks

International genetic evaluations are now available for the most important traits, except for female fertility, which is expected to commence next year. However, even then, the declaration of total genetic merit of dairy cows can still be made more complete. The methods for genetic evaluation of functional traits can be improved to utilise the available data optimally. Furthermore, several new traits seem to offer valuable potentials to improve the profitability of dairy productions worldwide.

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