Conventional breeding programmes and genetic resistance to animal diseases

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Summary
The power of selection is illustrated by the increase in the average annual yield of dairy cows in Sweden in kg fat-corrected milk from 2,500 kg in the year 1900 to 8,200 kg in 1997. More than a half of this improvement has a genetic origin. The breeding goal for dairy cattle has successively been broadened to cover traits other than production. The prerequisites for a successful breeding programme and the consequences of the process are presented in this article. The dramatic improvement of the reproduction techniques and statistical tools for genetic evaluation of breeding stock and selection, which have occurred during the last 50 years, is also discussed. The factors which affect the genetic gain are described in detail to demonstrate the possibility of making genetic gains in traits reflecting disease resistance.

The Swedish procedure of disease recording and the procedures for genetic evaluation of fitness traits, such as disease resistance and female fertility, are described. The existence and consequences of negative genetic correlations between production and fitness traits are dealt with, as is the procedure for multi-trait selection. An illustration of methods for performing multi-trait selection in real life, and the consequences of such selection in an envisaged Nordic selection scheme, are given. Finally, the authors review the present genetic trends for fitness traits of dairy cows in Sweden.

Keywords
Bovines - Breeding programmes - Daughter fertility - Disease resistance - Genetic correlations - Genetic gain - Mastitis - Milk - Production - Selection - Sweden - Total merit index.

Introduction
In breeding plans for domestic species used for food production, efficiency in the yield of egg, meat, milk, etc. has been given the highest priority for obvious reasons. Continuously conducted breeding programmes will lead to an accumulation of genetic gains, which usually make such programmes quite profitable.

Although production traits are given the highest priority, breeding objectives generally include also health and reproductive traits. However, these traits often have somewhat different genetic characteristics and are sometimes difficult to register in recording schemes, and therefore must be given special consideration when designing breeding programmes. As health and reproductive efficiency is gaining in importance from both an economical and an ethical point of view, it is essential that breeding programmes consider animal welfare aspects.

Conventional breeding programmes for domestic animals which include genetic resistance to diseases are most commonly found in dairy cattle breeding. The recent reports by the International Bull Evaluation Service (Interbull) illustrate the extensive efforts in many countries to refine procedures for recording disease resistance, calving performance, fertility, persistency and longevity and to incorporate these traits in the selection procedures (7, 8).
The changes in yield illustrate the efficiency of the selection procedures applied in the past. In Table I, the development of the yield in fat-corrected milk (FCM) is shown for milk recorded cows in Sweden. The phenotypic change illustrated in the Table is the effect of improved environment and genetic capacity. Analyses reveal that somewhat more than a half of the improvement has a genetic origin.

<table>
<thead>
<tr>
<th>Year</th>
<th>Yield limit (kg) fat-corrected milk per cow</th>
<th>Number of years taken for 1,000 kg increase</th>
</tr>
</thead>
<tbody>
<tr>
<td>1900</td>
<td>2,500</td>
<td>-</td>
</tr>
<tr>
<td>1945</td>
<td>3,500</td>
<td>45</td>
</tr>
<tr>
<td>1962</td>
<td>4,500</td>
<td>17</td>
</tr>
<tr>
<td>1976</td>
<td>5,500</td>
<td>14</td>
</tr>
<tr>
<td>1985</td>
<td>6,500</td>
<td>9</td>
</tr>
<tr>
<td>1993</td>
<td>7,500</td>
<td>8</td>
</tr>
</tbody>
</table>

The time taken to elevate the yield by 1,000 kg has been reduced from 45 years for the first interval to eight years for the latest interval. In 1997, the yield amounted to 8,209 kg per cow per year. The Table illustrates the power of selection to change the cow in the desired direction. The present challenge is to formulate the breeding goal for the first decades of the third millennium with a view on past developments and continuous application of relevant new scientific findings.

The development of selection tools

**Milk recording and artificial insemination**

Modern breeding plans for dairy cattle depend to a large extent on technical and statistical tools which have been developed over the years. The oldest of these tools is milk recording, which celebrated its centennial in Sweden in 1997. Initially the amount of milk and fat percentage was recorded monthly, mainly as a management tool at farm level. In the 1960s, herd summaries and other calculations were taken over by computers and information from the milk records was integrated with artificial insemination (AI) statistics. This means that information has been accumulated on the birth date, pedigree, matings, calvings, yield and culling for all recorded cows since the 1960s as a basis for management and selection.

An integrated database which contains all information on each individual cow from various sources, including pedigree, production and reproduction data, is the most important register for a well-defined breeding programme. This can then easily be expanded to more traits, such as health, when such information is available.

Artificial insemination was introduced in the 1940s and developed fast. The main purpose of AI during the initial years of its use was to prevent and eradicate the venereal diseases which caused much harm at that time. The role of AI as a tool in the selection process was developed when the first procedures for progeny testing of bulls appeared. Although milk yield and other traits in the breeding goal can be recorded only in females, the bulls became the key animals in selection programmes, thanks to the reproductive capacity of the bulls that AI created.

**Frozen semen**

The deep-freezing and storing of semen developed by Polge (24) created possibilities for AI and dairy cattle breeding to become an international activity. On average, 2,000 semen doses per bull can be collected, deep-frozen and stored weekly. Individual bulls may produce much more. The deep-freezing procedure enables transportation of the semen around the world at low costs, and thus the use of semen at any time after collection. As a consequence, the best bulls in the world can be exploited heavily. Some bulls have already been used for more than one million inseminations. Another advantage of AI is the possibility to preserve semen for very long periods at low costs. Preservation of the existing genetic variation is thus possible parallel to selection which generates genetic change at a successively accelerated speed.

**Genetic evaluation methods**

The testing procedure generally adopted for genetic evaluation is annual progeny testing of a number of young
bulls, the best of which are selected for heavy use when the first crop of daughters (50 to 150 daughters) have completed their first lactation and have proved the superiority of their sires. The bulls are then 5 years old. The most appropriate design of such selection programmes was developed during the 1960s (28).

From a genetic point of view, the greatest advantage of the deep-freezing procedure is that it gives opportunities to conduct the selection of genetic material across broader areas than previously (i.e., countries and continents) depending on the quality and characteristics of the available genetic stocks. This exploitation is in turn dependent on the development of new statistical tools for analysis of animal records in order to identify the superior parents. Henderson developed the best linear unbiased prediction (BLUP) procedure, by means of which bulls of all ages can be compared (5). The next step was the introduction of the so-called relationship matrix, by means of which relationships between bulls can be used to improve the accuracy of the breeding value estimation. The further development of the BLUP procedure to include individual males and females across generations for genetic evaluations led to the so-called animal model.

**International genetic evaluations**

The BLUP procedure enables exploitation of the opportunities created by the international trade of semen to connect the genetic levels in different countries and to rank all bulls in the world on a common scale. An international body, Interbull, was officially formed in 1983 with headquarters at the Swedish University of Agricultural Sciences in Uppsala. In 1997, there were 35 member countries (usually represented by milk-recording or genetic evaluation organisations) from all continents. The main purpose of Interbull is to provide leadership in the communication, research and development of methods for comparison of genetic stock across member countries. In 1991, the Interbull Centre was formed for operational services including the routine international genetic evaluation of bulls (1). In 1997, more than 20 countries participated in this programme.

**Reproductive technologies**

Reproductive technologies have been developed by means of which the efficiency of the female reproduction has also been improved. Nicholas and Smith proposed selection procedures where embryo transfer (ET) played an important role (17). The procedure allowed heavier exploitation of the best females and a reduction of the generation interval. Applied breeding plans in which embryo transfer plays an important role can be found in many countries, especially in Europe and North America. The latest step in this development is in vitro embryo production. Breeding methods made possible by means of this procedure have been proposed by Woolliams and Wilmut (29), Kinghorn et al. (10) and De Boer and van Arendonk (2).

## Factors affecting genetic gain

The expected genetic improvement of traits selected for can be described by the following formula:

\[
\text{Genetic improvement per year in the trait selected for} = \frac{\text{Accuracy of selection} \times \text{Selection intensity} \times \text{Genetic variation}}{\text{Generation interval}}
\]

The 'accuracy of selection' is a function of the heritability of the trait in question and the different sources of information used (individual, parents, sibs, progenies). The 'selection intensity' is a function of the proportion of the population selected from the top phenotypic values as parents of the next generation. The amount of available 'genetic variation' is expressed as the genetic standard deviation. The 'generation interval' is the average time in years between the birth of the parents and the birth of the offspring that will replace their parents.

The genes are transmitted from one generation to the next by four paths, as follows:
- sire to son (ss)
- sire to daughter (sd)
- dam to son (ds)
- dam to daughter (dd).

The formula above is applied to each path and summarised to estimate the total gain.

The accuracy in selection, \( r_{1G} \), is of specific relevance in the discussion of genetic gain for low heritability traits, such as disease resistance and fertility. The heritability, \( h^2 \), denotes the ratio between the additive genetic and the phenotypic variance. For traits recorded on the candidate animal itself the accuracy, \( r_{1G} \), equals the square root of \( h^2 \), or \( h \). For low heritability traits the accuracy, and the resulting genetic gain, is low when records on the selection candidate are the only source of information available. When the heritability is 0.03 for instance, the value of \( r_{1G} \) is as low as 0.17. This value is much lower than the value of \( r_{1G} \) of 0.50, which is achieved at selection for milk yield based on records of individual cows, as the heritability is as high as \( h^2 = 0.25 \) for this trait.

However, the handicap in terms of a low heritability can be overcome if the selection is based on progeny group means in programmes where the size of the progeny groups is relatively large. In Figure 1, the magnitude of the accuracy of selection, \( r_{1G} \), is illustrated for traits recorded on daughter groups of varying sizes. When the size of the progeny group is small, \( r_{1G} \) is much smaller for low heritability traits than for traits with higher heritability, as is the case when the selection is based only on the performance of the candidate animal. However with increasing levels of \( n \) (the size of the progeny group), the difference in \( r_{1G} \) decreases. Thus, if selection for mastitis...
Disease traits in the breeding programme

Recording of diseases

A prerequisite for consideration of disease resistance in a breeding programme is that the diseases, or other traits closely related to these, are recorded accurately. Ideally, this should be done on the candidates for selection themselves. In the case of diseases which are solely governed by genetic factors, modern methods of DNA-typing may provide efficient means to distinguish between desired and undesired genotypes. Bovine leucocyte adhesion deficiency (BLAD) is an example of a recessive gene causing an immunodeficiency that is fatal to calves when expressed in its homozygous form. BLAD calves can be detected at an early stage of life by means of DNA analysis (9).

However, most traits affecting the health or culling of dairy cows are due to both genetic and environmental factors and the interaction between these. The genetic variation is mostly a result of the effects of many genes. Thus, most disease and fitness traits have a multifactorial background and the genetic part is of a polygenic nature. A general feature of fitness traits is that they show heterosis, i.e., positive effects of crossbreeding. This is why crossbreeding is used extensively in species where the reproduction rate plays an important role, as in pigs and poultry.

In dairy cattle, the most common reasons for culling cows are mastitis and fertility problems. Dystocia and stillbirths constitute serious problems in certain breeds. Foot and leg problems and metabolic diseases are also important but are more affected by the environment. In all cases, these disease and fitness traits have a multifactorial background and need to be recorded and analysed accordingly.

As the heritabilities are low in all these traits, the only efficient procedure for genetic evaluation is based on progeny testing of bulls, as indicated in Figure 1. A systematic recording of disease and fertility results in cows and survival rates of calves constitutes the necessary basis for the progeny testing procedure. Figure 2 illustrates the interactive parts of a breeding programme as described by Philipsson (20).

The first efforts to create a national computerised recording system for animal disease diagnoses in Sweden began in 1971, and the present compulsory system, whereby all veterinary treatments are recorded, commenced in 1984. The records include the identity of the cows and are integrated in the milk recording system. Lindhå et al. have described the recording system (12). The first genetic analyses of these data were made by Philipsson et al. (21). Later reports have been given by Emanuelson et al. (4) and Koenen et al. (11).
Fig. 2
Interactive parts of a breeding programme

**Genetic evaluation for mastitis resistance**

There are several possibilities for the consideration of mastitis resistance in selection. The systematic recording of clinical cases of mastitis is the most important way to evaluate the sires accurately for resistance to mastitis among their daughters. However, only the Nordic countries have so far developed systems to register clinical cases of diseases. Alternatively, selection must be based on closely related traits. The most important means of detecting mastitis resistance found to date involves the use of somatic cell counts (SCC).

Screening tests of SCC in milk for the detection of clinical and sub-clinical mastitis cases in individual herds started in the late 1970s and the practice was later expanded to include SCC-recording on individual cows. The SCC records on individual cows are also integrated in the milk recording system. The first results from genetic analyses of these data were published by Emanuelson et al. (4).

The present procedure for calculating the breeding values for dairy bulls in Sweden with regard to mastitis resistance began in 1985. The recorded frequency of clinical cases occurring in the female offspring of each bull is used together with SCC during a period starting 10 days before the first parturition to 150 days after the first calving. The SCC value of the individual cow equals the mean during the period mentioned, expressed as a logarithm (base = 10) of 10,000 units of cells. The heritabilities used are 0.02 for clinical mastitis and 0.08 for the SCC. The genetic correlation used between these two traits is 0.7. The breeding values of the bulls are then calculated following the BLUP procedure. Relative breeding values are given with 100 as a mean and the range from 76 to 117. High breeding values indicate low frequencies.

Many countries have now developed national genetic evaluation systems for SCC. In the Netherlands, De Jong and Lansbergen have constructed direct and indirect indices for selection for udder health (3). Traits used for indirect selection were somatic cell count, milking speed and linear udder traits. From the index calculations it was concluded that indirect selection based on clinical mastitis resulted in the same genetic progress as direct selection. However, combining direct and indirect selection gave 15% higher response, which is in accordance with the study in Sweden.

Fertility, stillbirths and 'other diseases'

When milk recording data with all pedigree and calving information are integrated with AI and health data, as in the system in Sweden, further opportunities for the evaluation and selection of bulls exist.

Female fertility is considered by combining the information about the number of inseminations required per serviced heifer, first- and second-calvers with number of days open in the first and the second lactations, into a fertility index. The genetic variation among daughter groups has proved to be surprisingly large, as shown in Table II.

Stillbirths are defined as calves born dead or dying within 24 hours of birth. The fate of the calf at birth is regularly reported, together with other perinatal observations, in the milk recording system. Problems at calving exist mainly at the first parturition, and therefore the genetic evaluations in Sweden consider only the results of the first parity.

Bulls are evaluated both as sires of calves and as sires of first-calvers, as the fertility trait is clearly dependent on the effects of both the calf and the dam.

Diseases other than mastitis that are treated by veterinarians are not evaluated individually because the frequencies of occurrence are low. However, analyses have shown that the combined frequency of all treatments, except mastitis, also had a considerable genetic variation. They are thus evaluated together.
The disease panorama (as measured by statistics on veterinary treatments) for dairy cattle in Sweden is dominated by mastitis as the most frequent diagnosis. According to statistics for the period 1995-1996, 19.2 veterinary mastitis diagnoses are recorded per 100 ended or broken lactations. There is a persistent difference between the two main breeds. The figure for the Swedish Red and White breed amounted to 17.5, compared to 21.6 for the Swedish Holstein breed. During the last decade, the general level has remained very stable following an earlier rise to this level. The second most frequent diagnosis is paresis (4.0%), followed by retained placenta (3.4%) and ketosis (2.7%).

Unfavourable genetic correlations between milk yield and health and fertility traits

The magnitude of the genetic correlations between yield on one side and fitness traits included in the selection goal on the other side are decisive for the effects of selection procedures, which include disease resistance and other fitness traits, as illustrated by Philipsson et al. (22). In Table III, recent estimates are given for the two main dairy breeds in Sweden. Daughter fertility includes the number of inseminations performed and a score for heat intensity behind the first three pregnancies and the interval between the calving and the first insemination in the first and the second lactation. The heritability for female fertility is estimated to be 0.05.

Table III
Genetic correlations among traits in Swedish dairy cattle based on progeny testing results (15)
All traits were recorded in the first lactation. High indices indicate low disease frequencies

<table>
<thead>
<tr>
<th>Traits</th>
<th>SRB</th>
<th>SLB Swedish sires and</th>
<th>SLB Holstein sires</th>
</tr>
</thead>
<tbody>
<tr>
<td>Protein (kg)-daughter fertility</td>
<td>-0.29</td>
<td>-0.21</td>
<td>-0.38</td>
</tr>
<tr>
<td>Protein (kg)-mastitis index</td>
<td>-0.13</td>
<td>-0.32</td>
<td>-0.20</td>
</tr>
<tr>
<td>Protein (kg)-other diseases index</td>
<td>-0.25</td>
<td>-0.18</td>
<td>-0.32</td>
</tr>
<tr>
<td>Daughter fertility-mastitis index</td>
<td>0.14</td>
<td>0.06</td>
<td>0.03</td>
</tr>
<tr>
<td>Mastitis index-other diseases index</td>
<td>0.41</td>
<td>0.31</td>
<td>0.26</td>
</tr>
</tbody>
</table>

SRB: Swedish Red and White breed
SLB: Swedish Black and White Holstein breed

The figures in the Table reveal that the genetic correlations are far from universal but vary from one population to the next. Yield of protein is negatively correlated with daughter fertility as well as with resistance to mastitis and 'other diseases'. The mastitis index is based on clinical mastitis diagnoses and SCC. The coefficients of correlation range from -0.1 to -0.4. There appears to be a connection between the magnitude of the genetic correlation and the general level of the fitness trait. Mastitis is a greater problem among SLB cows of pure Swedish origin, while daughter fertility is more of a problem among cows with Holstein pedigree, which seems to be reflected in the genetic correlations.

There is a positive genetic correlation between resistance for mastitis and the index for other diseases. This may reflect the fact that one diagnosis is a risk factor for a subsequent diagnosis in the same disease or for other diagnoses (Oltenacu and Lindhé [19]). The genetic correlation between daughter fertility and mastitis is close to zero. The figures in Table III coincide neatly with similar Dutch (Hoekstra et al. [6]), Danish (Nielsen et al. [18]) and Lund and Jensen [16]), Norwegian (Simianer et al. [27]) and Finnish studies (Pösö and Mäntysaari [25, 26]).

The negative genetic correlations illustrated in Table III mean that unidirectional selection for yield without consideration of female fertility and mastitis resistance or any trait correlated with these (udder conformation is positively correlated with mastitis resistance) will result in a deterioration in these fitness traits. The present negative trend found for female fertility in the Holstein populations (6, 13) is an illustration of the effects of such negative genetic correlations.

Multi-trait selection for total merit

Selection for many traits, simultaneously with consideration of the relative economic importance of different traits, their heritabilities and the genetic correlations between all traits considered, is possible by means of a selection index. Each trait is given an economic weight which reflects its importance for the net return of production. This 'economic' weight may also include ethical values and animal welfare aspects. The selection index procedure allows the following:

a) selection of individuals for a given trait using records on themselves and/or on relatives, and

b) selection of individuals for several traits considered simultaneously, using records on themselves and/or on relatives

so that the total economic gain from the expected genetic progress is maximised.

One obvious consequence if many traits are considered simultaneously is that the gain in the first trait considered is reduced when more traits are added to the breeding goal. This reduction is even greater when the added traits are negatively correlated with the primary one. If female fertility and mastitis are included in an index together with yield, the gain in yield is reduced in comparison with unidirectional selection for
yield. The magnitude of the negative genetic correlations and the relative economic weights for the fitness traits decide how severe the reductions in yield will be. However, the use of a total merit index (TMI) maximises the net return. If the economic weights for the fitness traits are high enough, these traits can be improved parallel to yield. Philipsson et al. have shown that the value of the improvement of female fertility and disease resistance is higher than the loss in production (22).

In Table IV, the calculation of a TMI from the estimated breeding values of a number of traits is illustrated for a bull of the Swedish Red and White breed.

**Table IV**

<table>
<thead>
<tr>
<th>Trait</th>
<th>Relative breeding value</th>
<th>Weight of deviation from 100</th>
<th>Contribution to the total merit index</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Production</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Protein (kg)</td>
<td>108</td>
<td>1.00</td>
<td>+8.0</td>
</tr>
<tr>
<td>Daily gain</td>
<td>99</td>
<td>0.50</td>
<td>-0.5</td>
</tr>
<tr>
<td><strong>Fitness traits</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Daughter fertility</td>
<td>106</td>
<td>0.30</td>
<td>+1.8</td>
</tr>
<tr>
<td>Stillbirths-sire effect</td>
<td>98</td>
<td>0.10</td>
<td>-0.2</td>
</tr>
<tr>
<td>Stillbirths-maternal effect</td>
<td>99</td>
<td>0.10</td>
<td>-0.1</td>
</tr>
<tr>
<td>Mastitis resistance</td>
<td>116</td>
<td>0.30</td>
<td>+4.8</td>
</tr>
<tr>
<td>Other diseases</td>
<td>111</td>
<td>0.15</td>
<td>+1.7</td>
</tr>
<tr>
<td><strong>Conformation</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Body</td>
<td>96</td>
<td>0.10</td>
<td>-0.4</td>
</tr>
<tr>
<td>Legs</td>
<td>98</td>
<td>0.20</td>
<td>-0.4</td>
</tr>
<tr>
<td>Udder composite</td>
<td>106</td>
<td>0.50</td>
<td>+3.0</td>
</tr>
<tr>
<td>Temperament</td>
<td>105</td>
<td>0.15</td>
<td>+0.8</td>
</tr>
<tr>
<td><strong>Total merit index</strong></td>
<td></td>
<td></td>
<td>+18</td>
</tr>
</tbody>
</table>

The bull chosen to illustrate the operation of the TMI currently used in Sweden has an unusual health profile, with the relative breeding values of 116 for mastitis resistance and 111 for other diseases. The fact that the contribution of the production traits constitutes less than half of the value of the TMI is rather uncommon: normally this contribution is 70% to 80%. The TMI per se is the basis for the selection of bulls as sires of the bulls and the cows of the next generation, but the individual farmer has the choice to select bulls according to his preferred 'profile'. Many of the bull sires in the SLB-breeding programme are imported from North America, the Netherlands and France. One handicap in this work is the lack of breeding values for all the fitness traits described above and of TMI for these bulls. Efforts are now made to use the available breeding values for fitness traits in the countries mentioned and to rank the bulls in those countries, with respect to the Swedish breeding goal for domestic purposes.

**An envisaged breeding plan for the Nordic red breeds**

Lindhé and Philipsson estimated the genetic progress in different traits from alternative breeding plans for the Nordic red breeds under the assumption of a total integration of the breeding activities in the Nordic countries (14). The population comprised 700,000 cows. In the model simulation, the traits in the breeding goal and their economic weights coincide with those used in Sweden. In Table V the expected total genetic gain, expressed in index units, is given together with the expected genetic gain for the main fitness traits. The proportion of young bull inseminations in the population was 20% and 40% respectively, and the size of the progeny groups varied from 75 to 150 daughters.

**Table V**

<table>
<thead>
<tr>
<th>Progeny group size</th>
<th>Young bulls = 20%</th>
<th>Young bulls = 40%</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>75</td>
<td>150</td>
</tr>
<tr>
<td>Total merit</td>
<td>1.49</td>
<td>1.47</td>
</tr>
<tr>
<td>Protein yield</td>
<td>1.51</td>
<td>1.45</td>
</tr>
<tr>
<td>Daughter fertility</td>
<td>-0.20</td>
<td>-0.14</td>
</tr>
<tr>
<td>Mastitis resistance</td>
<td>0.13</td>
<td>0.16</td>
</tr>
<tr>
<td>Other diseases</td>
<td>-0.18</td>
<td>-0.13</td>
</tr>
<tr>
<td>Stillbirths</td>
<td>0.16</td>
<td>0.19</td>
</tr>
</tbody>
</table>

The figures in Table V illustrate the importance of having relatively large progeny groups, and consequently a relatively high proportion of young bull inseminations, for the total genetic gain and for the absolute and relative gain in the fitness traits. Other conclusions from that study were as follows:

a) An integrated Nordic breeding plan is approximately 10% more efficient, as measured by total genetic gain, than an isolated Swedish breeding plan with the same breeding goal.

b) With the genetic correlations with yield of protein, which have been used in the study and which coincide with the situation in the Swedish SRB breed, the genetic change is negative for daughter fertility. The relative economic weight for daughter fertility has to be elevated if a positive development is to be achieved.

c) If the economic weights for daughter fertility and mastitis are doubled from 0.3 to 0.6, the annual genetic gain in daughter fertility changes from -0.13 (the right column in the table) to +0.18, and the gain in mastitis increases from 0.18 to 0.49. The reduction in gain in protein yield is 19% (or from 1.52 to 1.22 index units). To reach a zero change in daughter...
fertility, the weight was estimated to be 0.42. The gain in protein yield is then reduced by 3.7%.

d) A high proportion of the bull dams should be selected from the youngest age group, thus making use of good daughters of the best sires for their total merit.

Actual genetic trends

In a study of the applied breeding policy in the period 1981 to 1992 and its genetic effects in the two mentioned dairy breeds in Sweden, Lindhé et al. estimated the genetic gain in yield of milk and protein, daughter fertility and disease resistance by the use of proof trends for sires of bulls and sires of cows (13). As the BLUP procedure for breeding value estimation ranks bulls of all ages on the same scale, genetic trends can be estimated by the trends in the breeding values of the bulls used. For yield of protein, the figure for SRB amounted to 1.28 index units per year. For daughter fertility, the figure was -0.10, and for mastitis, 0.01. Trend studies up to 1995 confirm the sign and relative magnitude of these figures, though they also reveal a somewhat accelerated speed in the genetic gain during the latest years. The trend figures show that the present selection procedure keeps the level of female fertility and mastitis rather stable, in spite of the negative genetic correlations between yield and these traits. The challenge for the future is to initiate a positive trend for these fitness traits parallel to the improvement in yield. A prerequisite for such a development is that more countries include health and fertility traits in their evaluation and selection programmes, as so many bulls – especially bull sires – are used internationally nowadays.

Conclusion

Conventional progeny testing of bulls is still the main procedure in dairy cattle breeding and will remain so in the foreseeable future. Fitness traits, such as disease resistance and female fertility, are low heritability traits. If selection had been employed based on the phenotype of the candidates for selection themselves, the expected genetic change in the fitness traits would have been negligible. However, when progeny testing is used with large daughter groups (> 100), the accuracy of the breeding values for bulls allows genetic gains in fitness traits to be achieved. Figure 2 illustrates the organisational requirements for a successful inclusion of the fitness traits in the running breeding plans.

Despite the unfavourable genetic correlations found between yield on one side and daughter fertility and mastitis resistance on the other, it has been possible to keep the level of these traits relatively stable. The challenge for the future is to create a genetic improvement in the fitness traits parallel to continued improvements in yield. The tools are available. However, as breeding programmes have become international for most breeds, it seems important that fertility and health traits, as in the Nordic countries, receive more attention in the selection of dairy bulls on a global scale.

Programmes de sélection classiques appliqués à la résistance génétique aux maladies animales

B. Lindhé & J. Philipsson

Résumé

En Suède, la production annuelle de lait par vache est passée de 2 500 kg en 1900 à 8 200 kg en 1997 (en kg de lait corrigé en matière grasse). Plus de la moitié de cette augmentation est due à la sélection génétique, ce qui témoigne du rôle croissant joué par les techniques génétiques. Les techniques de sélection ont été ensuite appliquées à d'autres caractères génétiques que ceux liés à la production de lait. Les auteurs examinent les conditions préalables d'un bon programme de sélection ainsi que les conséquences de cette pratique. Ils font le point sur les techniques de reproduction et les outils statistiques applicables lors de l'évaluation et la sélection génétiques des animaux reproducteurs, techniques qui ont considérablement progressé au cours des cinquante dernières années. Les
facteurs qui sont à l'origine de l'amélioration génétique sont décrits en détail, afin de montrer les applications potentielles de cette technique à la sélection d'animaux résistants aux maladies.

Les auteurs décrivent également le système suédois de déclaration des maladies et les méthodes appliquées en Suède pour l'évaluation génétique des caractères d'adaptation (fitness traits), tels que la résistance aux maladies et les caractères héréditaires de fertilité des femelles. L'hypothèse de corrélations génétiques négatives entre les caractères de la production laitière et ceux de l'adaptation est ensuite examinée et évaluée, puis les auteurs décrivent les procédés permettant la sélection de plusieurs caractères à la fois. Cette dernière méthode est illustrée par un exemple de sélection multi-caractères réalisée en conditions réelles ; les auteurs soulignent les conséquences qu'une telle méthode pourrait avoir dans le programme de sélection actuellement à l'étude dans les pays scandinaves. Enfin, ils indiquent les tendances qui prévalent actuellement en Suède dans le cadre de la sélection génétique des caractères de l'adaptation chez les vaches laitières.

Mots-clés
Amélioration génétique — Bovins — Corrélations génétiques — Fertilité héréditaires des femelles — Indice de qualité totale — Lait — Mammite — Production — Programmes de sélection génétique — Résistance aux maladies — Sélection — Suède.

Programas convencionales para la selección de rasgos de resistencia genética a las enfermedades animales

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Resumen
El incremento que ha experimentado en este siglo la producción anual media de las vacas lecheras de Suecia (de 2.500 kg en 1900 a 8.200 kg en 1997, en kg de leche rectificada en materias grasas) ilustra de manera elocuente el potencial de los métodos de selección. Más de la mitad de dicho incremento es de origen genético. Los objetivos de la selección del ganado lechero se han visto progresivamente ampliados para dar cabida, además de los rasgos ligados al rendimiento, a caracteres de otro tipo. Los autores exponen los requisitos previos que deben cumplirse para que un programa de cría tenga éxito, así como las consecuencias de un tal proceso. Se evoca asimismo el espectacular progreso que han conocido en los últimos 50 años las técnicas de reproducción y las herramientas estadísticas para la selección y la evaluación genética del ganado reproductor. Se describen también detalladamente los factores que influyen en la ganancia genética, a fin de demostrar que pueden obtenerse ganancias genéticas en rasgos ligados a la resistencia a la enfermedad.

Se exponen además los procedimientos aplicados en Suecia al registro de enfermedades y a la evaluación genética de los rasgos de aptitud (fitness), como la resistencia a la enfermedad o la fertilidad de las hembras. Se considerarán igualmente la existencia y las consecuencias de correlaciones genéticas negativas entre rasgos de rendimiento y rasgos de aptitud, así como el procedimiento utilizado para realizar selecciones múltiples (selección simultánea de diversos rasgos). Se ofrece un ejemplo real que ilustra los métodos de
selección múltiple, y se describen los efectos que tendría este tipo de selección sobre un programa de selección previsto en los países escandinavos. Los autores repasan, por último, las tendencias de la genética en Suecia en lo que concierne a la selección de rasgos de aptitud en vacas lecheras.

**Palabras clave**
Bovinos - Correlaciones genéticas - Fertilidad de la progenie - Ganancia genética - Índice de idoneidad total - Leche - Mastitis - Producción - Programas de selección - Resistencia a la enfermedad - Selección - Suecia.

### References


