

GENETIC TRENDS IN BULL AND COW POPULATIONS BASED ON ESTIMATES
OF SIRES AND MATERNAL GRANDSIRE BREEDING VALUES (1)

LE PROGRES GENETIQUE DES POPULATIONS DES TAUREAUX ET
DES VACHES EN UTILISANT LES VALEURS GENETIQUES
DES PERES ET DES GRAND-PERES MATERNELS (2)

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INTRODUCTION

In most situations there is a need to check to what extent the predicted genetic progress according to a given breeding plan has been realized. Several methods for measuring the genetic change have been developed, and that proposed by Smith (1962) has been frequently used. This method measures how the sires of the cows in the population improve over time relative to known sires, whose genotypes are constant over time. Many assumptions have to be fulfilled and modifications have been suggested to overcome some of those, e.g. Syrstad (1974).

The mixed model technique developed by Henderson (1973) for sire and cow evaluation has opened new possibilities for a continuous check of the genetic progress. Several studies of genetic change have been made with the help of the new technique (Hintz et al., 1978; Kennedy & Moxley, 1975; Schaeffer et al. 1975). This method utilizes the estimated breeding values of the sires/cows to describe the genetic change in the population. The breeding values have to be unbiased and a correct ranking must be possible over years. As demonstrated in this report, the evaluated progress will refer to different subsets of the population depending on how the breeding values are utilized.

MATERIAL AND METHODS FOR ESTIMATION OF SIRES BREEDING VALUES

First-lactation yields of cows of Swedish Red and White (SRB) and Swedish Friesian (SLB) cattle were used to estimate their sires' breeding values for production of fat corrected milk. All daughters of AI-sires calving between January 1966 and February 1980 were used. A total of 590 000 SRB and 266 000 SLB cows representing 2 704 SRB sires and 814 SLB sires were available.

The mixed model used to evaluate the sires contained a fixed effect of herd-year-seasons, fixed effects of groups of sires and maternal grandsires (MGS) and random effects of sires and MGS within the corresponding groups. Grouping was according to year of birth of the sires and the additive relationship between sires was also utilized when setting up the mixed model equations. The predicted difference (PD) of a sire was obtained by adding the group and the sire solutions and is an estimate of one-half of the sires' additive genetic merit.

ESTIMATION OF GENETIC TRENDS

An estimate of the genetic level for each year's batch of AI-sires can easily be obtained by averaging their breeding values, where the breeding value is $2xPD$. The

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genetic trend among AI-sires is then the increase in average genetic level from one year to the next. If breeding values were available for each cow in the population, the genetic trend in the cow population could be estimated in the same way as for the sires. The accuracy is then dependent upon how much of the genetic differences between herd-year-seasons have been incorporated into the cows' breeding value.

As no such breeding values were estimated, an indirect method using the sires PD was used. A cow's genetic level (C_G) is made up of her sire's and dam's genotypes.

$$C_G = \frac{1}{2}S + \frac{1}{2}D = PD_S + \frac{1}{2}D$$

The dam's genetic level can be described by previous generations of sires (the cow's MGS etc.) and the genetic level of the cow is then:

$$C_G = PD_S + \frac{1}{2}PD_{MGS} + \frac{1}{4}PD_{MGG} + \frac{1}{8}PD_{MGGG} + \frac{1}{16}PD_{MGGGG} + \dots$$

This model ignores the selection practised among cow-dams within sire in each generation and it is also apparent that many generations of sires have to be traced to cover the complete genotype.

If only the sire's identity is known, the genetic change due to the sires of the cows can be estimated. The total genetic change is then twice as large if it is assumed that the progress among earlier generations of sires (MGG, MGGG, MGGGG etc.) is of the same size. The cow selection is also neglected. A better estimate can be obtained when also the identity and the PD of the cows MGS is known. If all generations of MGS are assumed to have the same genetic progress the genetic change can be measured by adding the trend due to sires and the trend due to MGS of the cow.

To calculate the trend in the total cow population would require that the sires' identity and PD is known for all cows in all lactations. In this study only first lactations were available, but as the first lactations from one year are the next year's second lactations, etc., the later lactations can be simulated. The percentage of cows in each lactation must be known and the culling of cows both within and across sires is ignored. If the genetic level due to sires' and MGS PD during four consecutive years is Y_1, Y_2, Y_3 and Y_4 and the percentage of cows in lactation 1-4 is p_1-p_4 , then the genetic level for 1-4th lactations in year 4 is $p_1 \cdot Y_4 + p_2 \cdot Y_3 + p_3 \cdot Y_2 + p_4 \cdot Y_1$.

In this study genetic trends were estimated for the population of AI-sires. By using the PD of the sires and MGS the genetic change due to the sires and MGS of first lactation cows was calculated. Therefrom the total genetic change was estimated based on only sires and on both sires and MGS of first lactation cows. A trend among cows in all lactations was also estimated.

RESULTS

Genetic trend among sires

The average breeding values for sires born during different years are shown in Table 1. These reflect the success in the bullsire and bulldam selection. There is a clear upward trend in both breeds, but there are also big fluctuations from one year to another, especially in the SLB breed, where there are fewer sires' progeny tested each year. Random variations, and varying genetic quality of bullsires and bulldams are probably the major reasons for the fluctuations. The reduction for the very last batch in both breeds occurred in three consecutive analyses and may be connected with the incompleteness and small progeny groups in the last batch. It is also apparent that the genetic trend among sires can be influenced to some extent by the mixed model used (Eriksson & Daneil, 1982). The number of daugh-

ters per sire and/or the genetic variances may also be of importance. In a study by Danell (1982) where the same sires were evaluated on both the total material and on each of three production levels of the same material, the trends among sires were different. The biggest trend was obtained when the total material was used.

Table 1. Average predicted difference (PD) for SRB and SLB sires born during different years in the period between 1960 and 1975

	Year of birth															
	1960	-61	-62	-63	-64	-65	-66	-67	-68	-69	-70	-71	-72	-73	-74	-75
SRB																
Number of sires	106	115	115	119	137	127	138	142	159	189	184	158	158	167	169	144
PD, \bar{x}	32	0	23	42	68	87	105	76	135	113	143	188	205	255	182	124
SLB																
Number of sires	38	29	30	42	27	32	30	53	35	54	47	44	50	59	53	50
PD, \bar{x}	16	-20	-22	31	49	12	-29	70	36	79	62	147	67	95	130	126

Genetic trends among cows

In Fig 1. the average PD of sires (line 1) and MGS (line 2) of first-lactation cows calving during different years have been plotted. The trend due to sires is different from the one due to MGS in both breeds. There is a time lag of about 4 years between a bull being a sire and becoming a maternal grandsire, so the increase in PD for MGS is displaced compared with that for sires. The upward trend for MGS is still apparent at the end of the study period when there is little increase in PD for sires. As a result of these differences the genetic trend estimated from only the sires PD (line 3) will be biased. It can also be seen in Fig. 1 that when the genetic trend is estimated from both the sires and MGS PD, the 4th line, the curve is smoother, than when the trend is estimated from only the sires PD (line 3). The fluctuations in the yearly average of PD of sires of first lactations cows are to some extent levelled out in the trend of the MGS, and are reduced even more when the contributions from both sires and MGS are added.

The genetic trend among all cows (line 5), finally, is the smoothest of them all. There the contributions from four generations of cows are added to get the genetic level for each year. Even here the decreasing progress during the end of the period among the sires of first lactation cows causes a decrease in the trend.

DISCUSSION AND CONCLUSIONS

The long generation intervals and the overlapping generations in dairy cattle breeding mean that it takes several decades before an equilibrium stage can be reached. Until then all attempts to measure the genetic trend in the cow population by using the sires' or the sires' and MGS breeding values will give biased results.

Another, maybe equally important reason preventing attainment of equilibrium is that the breeding plans are not constant over time. In Fig. 1 a rapid improvement of sires used to breed cows can be seen in both breeds followed by a period of no improvement. A change in the breeding policy from selecting sires for yield of FCM towards a multi-trait selection policy may have had some influence, but random variations in availability of good sires and failure in selecting the very best sires as bull and cowsires also play a part. The rapid increase at the beginning of the period also reflects the results of a more efficient way of using the best AI-sires, which was introduced in Sweden at that time. The nonlinearity in the genetic change has been pointed out in other reports, e.g. by Hintz et al. (1978).

It can also be predicted from gene-flow patterns (McClintock & Cunningham, 1974; Hill, 1974).

Genetic progress in different sub-sets of the population cannot differ in the long run. However, when measured during a relatively short time period as in this study, the trends obviously are different. It is therefore necessary to restrict the application of an estimated change to well defined situations. In particular, the estimates of genetic trends obtained from only the breeding value of the sire of the 1st lactation cows can give a very biased picture of what is happening in the total cow population (cf. lines 3 and 5 in Fig. 1). It seems therefore that a better model, e.g. built on gene-flow technique, would be necessary to be able to estimate the genetic change in the cow population on the basis of the PD of sires of all first lactation cows.

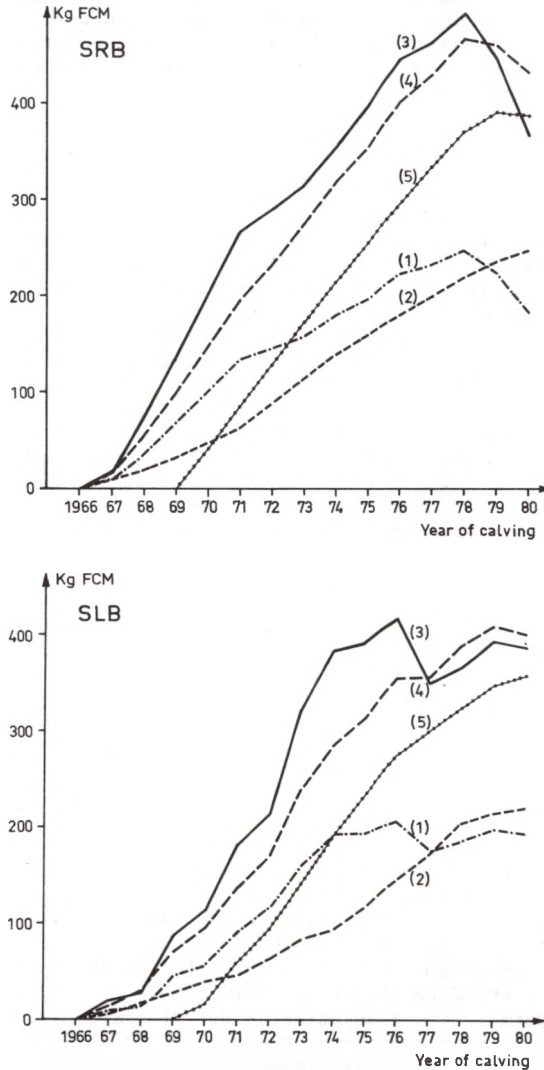


Fig. 1. Average PD of sires (1) and MGS (2) of 1st lactation cows. Genetic trend among 1st lactation cows estimated from 2xPD of sires (3) and from PD of sires and MGS (4). Line (5) is the genetic trend among cows in all lactations. The first year have been set to zero in all cases.

SUMMARY

The genetic trends for milk production in two Swedish dairy breeds were estimated using breeding values (BLUP) of the sires. Trends were estimated in the populations of sires, first lactation cows and all cows. Using only the sires breeding value to estimate the trend among the first lactation cows gives a biased estimate if previous generations of sires have a different genetic trend. The difference was demonstrated by utilizing both the sire and the maternal grandsire of the cow. The trend in the total cow population was based on yearly genetic levels which were estimated by pooling the genetic contribution from lactations of different parities. Since the genetic trend estimates for each of the three populations were different, it is concluded that the application of a specific estimate must be restricted to a carefully defined population

RESUME

Le progrès génétique de la production laitière des races bovines Suédoises a été estimé en utilisant les valeurs génétiques (BLUP) des géniteurs. Les taux de progrès ont été estimés pour les populations des géniteurs, des vaches en 1ère lactation et de toutes les vaches. L'utilisation de la valeur génétique des père seulement pour estimer le progrès des filles en 1ère lactation produit une estimation biaisée si le progrès causé par des générations antérieures des géniteurs est différent. La différence a été démontrée en utilisant l'information sur tant le père que le grand-père maternel de la vache. Une estimation du progrès génétique de la population entière des vaches a été obtenue en prenant la contribution de chaque lactation pour estimer le niveau génétique de chaque année. Puisque tous ces taux de progrès génétique ont été trouvés différents, c'est important à définir à quelle partie de la population s'adresse une telle estimation.

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