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GENETIC EVALUATION OF DAIRY CATTLE¹

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INTRODUCTION

Most researchers in dairy cattle breeding will agree that genetic evaluation programs are a means to an end rather than the solution to the genetic improvement of dairy cattle populations. Sire selection and consequently sire evaluation for most traits is paramount to breed improvement.

Tunisia developed plans to improve its' national production of milk in the 1960s. Purebred Friesians were first imported from the Netherlands in 1970 and later from the United States. Today there are approximately 80,000 purebred dairy cows and heifers (1976 to 1984) have been increasing at a rate of 4,670 cows per year. The national dairy herd is divided between small farms of less than 10 cows and large farms with more than 100 cows. Djemali et al. (1989) identified season and age at calving, as well as length of lactation as important sources of variation in milk yield records of Holstein cattle under North African conditions. Adjustment factors for age and length of lactation are being developed to standardize the comparison of production by different aged cattle across herds. It seems appropriate that Tunisia consider developing a national genetic evaluation program for dairy cattle so it can make the best use of its' resources in native and imported dairy cattle for genetic improvement.

The purpose of this article is to review the basic concepts of sire evaluation and then show how an evaluation of sires, dams and young animals can be accomplished by using an animal model. An example evaluation of dairy cattle is presented and used to illustrate the type of information wanted. A brief history of two programs now in progress is presented. There is no unique animal model for all species and traits. Each program reviewed applies different animal models, however the generality of concepts and general flexibility of the evaluation procedure are clearly visible by comparison of

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different programs. Genetic improvement within these programs is used to show the impact of genetic evaluations on genetic improvement within a breeding population. The following section on basic concepts in sire evaluation was adapted from Williams (1980).

Basics

"The purpose of a sire evaluation program is to enhance the effectiveness of sire selection in the breeding programs of all beef breeders. The justification of such a program is the many creative breeding programs being conducted by breeders. All that is needed to tie several breeding programs into a national sire evaluation program is a means of accurately comparing the breeding values of all sires. The accuracy and intensity of sire selection, as well as the genetic variation available (the product of the three composite selection response per generation) will be increased over what can be achieved by even the largest breeding herds separately. The problem then is one of developing a program whereby a large number of sires can be fairly compared on their transmitting ability for traits of economic importance."

The problem reduces to one of comparison. My bull is better! The obvious question is, better than what? Over time dairy cattle breeders have developed procedures to make comparisons among bulls. Subjective evaluation of physical appearance has been replaced by more objective progeny tests over a large number of herds. The important aspect is to predict future progeny performance from the sample of progeny information currently available.

Table 1. Simple illustration of sire evaluation for milk yield (kg).

Sires	Herd		Sire Averages
	1	2	
Reference Sire	4000 (10) ^a	3900 (10)	3950 (20)
Sire A	4100 (10)		4100 (10)
Sire B		4050 (10)	4050 (10)
Herd Average	4050 (20)	3975 (20)	

^a } Number in parentheses are the number of progeny from comparable dams and given equal treatment within each herd.

The analysis procedure used to calculate PREDICTED TRANSMITTING ABILITY

(PTA) involves no magic, just algebra and arithmetic. To demonstrate the procedure, the PTA for each sire in Table 1 will be calculated. The simple sire averages rank the sires A, B, and RS, but this is not satisfactory because sires A and B were not compared in the same herd and the herds differ by 75 kg. Within herds, sire A has progeny 100 kg superior to the reference sire, while sire B has progeny 150 kg superior to the same reference sire. This comparison uses the progeny of the reference sire as the control to eliminate management group differences (i.e., herd-year-seasons) between sire A and B. The best ranking of sires is B, A, and RS.

Table 2. Sire progeny averages as a difference from the herd average.

Sires	Herd		Weighted Sire Progeny Average ^a
	1	2	
Reference Sire	-50 (10) ^b	-75 (10)	-1250 (20)
Sire A	50 (10)		500 (10)
Sire B		75 (10)	750 (10)

^aWeighted by number of progeny.

^b() Numbers in parentheses are the number of progeny.

The basic data in the analysis are the sire progeny averages within herds, expressed as a difference from the herd average, the number of progeny in each average, and the total number of progeny in each herd. There are four differences, each of which is free of herd differences. Each sire progeny average from Table 1 is expressed as a difference from the herd average. These differences are in Table 2. Two of these differences concern the RS and one each exists for sires A and B. Weighting these differences by the number of progeny and collecting the two for the RS gives the weighted sire progeny average. These three numbers contain all the information concerning each sire, so next they need to be used to PREDICT future progeny based on the available progeny. A way to do this is to consider the composition of each of these numerical values in terms of the PTA's. For sire A, the 10 times 50 kg has

$$10 \text{ times } PTA_A = 10 \text{ times } (10 \text{ times } PTA_A + 10 \text{ times } PTA_{BS}) / 20$$

which equals $+5 \text{ times } PTA_A = 5 \text{ times } PTA_{BS}$. Doing the same for each of the sires yields three equations with three unknowns, PTA_{BS} , PTA_A , and PTA_B , as follows:

$$\begin{array}{lll} BS: & (10+15) \times PTA_{BS} & - 5 \times PTA_A & - 5 \times PTA_B & = & -1250 \\ A: & - 5 \times PTA_{BS} & (5+15) \times PTA_A & & & = & +500 \\ B: & & - 5 \times PTA_{BS} & (5+15) \times PTA_B & = & -750 \end{array}$$

All that has been done is to relate known values (i.e. progeny averages less herd averages) to what they are expected to contain (PTA's). Now solving these equations will give values of PTA's based on the information available. To predict future progeny, the equations have a value added to the lead diagonal that is a function of the heritability of the trait $[(4/\text{heritability})-1]$. This addition allows a unique solution and regresses the progeny difference for numbers and heritability not being perfect. For 25% heritability, the value is 15. Numerous ways exist to solve such a set of equations. (See Berger et al. (1989) and Mrosovsky and Diemala (1997) for a discussion of currently acceptable procedures.) With many sires involved the easiest one is iteration which involves a repetitive process of recalculating the PTA's using previous values until the values no longer change. The PTA's are as follows:

$$\begin{array}{ll} PTA_{BS} & = -41.67 \\ PTA_A & = 14.58 \\ PTA_B & = 27.08 \end{array}$$

These are the best estimates of Progeny Transmitting Ability in the future based on the available data. The values are regressed for progeny numbers available and for incomplete heritability. The raw differences were -50 and -75 for BS and +50 for A and +75 for B. Note that because the BS had 20 progeny the -41.67 is closer to the average of -37.5 than the 14.58 or 27.08 are to +50 or +75 because only 10 progeny were available for these two sires.

The sire evaluation in the example was based on progeny information.

There are other types of relative information in a population and it is important that breeders have an evaluation for all animals. In the decade from 1975 to 1985, the animal model has come to the forefront as the preferred method of conducting genetic evaluations.

The inverse of Wright's numerator relationship matrix (Henderson, 1973) enhanced the accuracy of genetic prediction. The relationship matrix provided the means of incorporating pedigree information in the analytical procedure and a method to account for genetic trend. Methods for Best Linear Unbiased Prediction (BLUP) of breeding values utilizing records of relatives as well as the individual's own record were described in 1976 (Henderson and Quass, 1976). Quass and Pollak (1980) published a paper describing an animal model that was less dependent on the assumptions about random mating of dams to sires and the absence of genetic trends in the population. There are earlier papers by C.R. Henderson (1976) which refer to an animal model, but the rapid development of advanced computing techniques led to more applications after 1980. Today the animal model is being applied in the beef (Renzette et al., 1988) and dairy (Wiggans et al., 1988) industries of the United States.

Animal Model Defined

Simply stated, the animal model is a simultaneous evaluation of cows and sires in which the genetic merit of all relatives plus the animal's own performance are used to estimate the animal's genetic merit. The concepts are similar to the basic sire evaluation, in that we are comparing differences among animals adjusted for environmental factors, but we are now able to make more use of existing information.

Animal Model for Dairy Sire and Cow Evaluations in the United States

The animal model provides an evaluation of sires as in the basic sire evaluation, but other animals are also being evaluated. These are the dams and cows without progeny in the population. Descriptions of information provided by the animal model are in Table 3.

The animal model being adopted for dairy sire and cow evaluation in the United States (Wiggans et al., 1988 and Cassel, 1988) is

$$Y = M + G + P + A + E$$

where

Y is a standardized yield (305d $\pm$ 2s, ME, common month of freshening) record.

M is the effect of management conditions specific to a given herd, year, and 2-month calving season (this is specific for registered, grade and first or later lactations).

G is the effect common to paternal half-sibs in a particular herd.

P is the permanent environmental effect that affects all lactations of a cow but is not transmissible to offspring.

A is the breeding value of the cow producing the record (genetic evaluations estimate half of this value, or the amount transmitted to offspring), and

E represents the portion of the yield record not explained by other terms in the model.

Table 1. Information possible by using an animal model.

Information	Description
Predicted transmitting ability (PTA)	One-half the breeding value; Predicted genetic superiority (inferiority) an animal will transmit to its offspring.
Predicted producing ability (PPA)	Prediction of a cow's relative performance in her own future lactations; the sum of predictions of breeding value, herd-sire effect and permanent environmental effect. Useful aid in making herd replacement and culling decisions.
Parent average (PA)	Average PTA of sire and dam. This is an indication of pedigree contribution.
Reliability (REL)	A measure of the amount of information in the evaluation.

Components of the animal model are illustrated using the milk yield records of 8 cows from a single herd as given in Table 4. The records were made over three year-seasons. Note that the three sires have no records. The PTA of sires is based on their progeny information. Likewise, dams D, E and F have no records. Their PTA is estimated by the records on their daughters. Some cows with records also have daughters in the herd, as do cows 21 and 22 in the example. The cows own records and records on her progeny are combined in an optimum way to help estimate her PTA. In addition, the records of the dam help to get a more accurate prediction of the transmitting ability for her daughters. That is, the PTA of a cow whose dam also has records is more accurate than the PTA of a cow whose dam has no records. The animal model combines this information in an optimum way to get the best linear unbiased predictor of the transmitting ability. It is the relationship among animals within a herd and across herds, through the multiple use of sires across herds, which makes it possible for us to combine these different sources of information.

Table 4. Representative sample of milk yield records (kg) for eight cows from a single herd.

Cow	Sire	Dam	Number of Records	Management Group		
				1	2	3
20	A	D	2	----	5897	6396
21	A	E	1	4513	----	----
22	A	F	3	4899	4791	4763
23	B	D	1	4608	----	----
24	B	21	2	----	4944	4445
25	B	E	2	4309	4536	----
26	C	F	1	5783	5443	5670
27	C	22	2	----	4990	5262

The PTA's for the three sires are: A=7, B=-52.1, and C=38.1 kg. For dams, the PTA's are: D=81.7, E=-67.7, and F=-2.7 kg (cows 21 and 22 are also dams but they appear as cows in the herd). Predicted values for all cows in the herd are in Table 5. The best ranking of cows is by their PTA. PTA is the relevant value for selection. If three of the eight cows are to be

retained as herd replacements than the three cows with above average PTA's are the best choices. PTA and PA results in some misranking of individual cows but these predicted values provide relevant management information. PTA and PA can also be used in the absence of a PTA for every cow.

Two genetic evaluation programs now in progress for beef and dairy cattle in the United States are reviewed in the next section. Evidence of genetic improvement is presented to show that records and people can make a difference.

Table 3. Predicted values (kg) for cows in example herd.

Cow	Predicted transmitting ability (PTA)	Predicted producing ability (PPA)	Parent average (PA)
20	129.5 (1) ^a	572.2 (1)	42.2 (1)
26	85.7 (2)	391.5 (2)	17.7 (2)
23	12.3 (3)	-132.8 (4)	15.8 (3)
27	-16.6 (4)	42.2 (3)	-6.8 (4)
22	-51.2 (5)	-210.6 (6)	-1.0 (5)
21	-69.5 (6)	-188.0 (5)	-13.5 (6)
24	-77.6 (7)	-134.6 (7)	-60.8 (8)
25	-91.7 (8)	-470.8 (8)	-59.9 (7)

^aNumbers in parentheses indicate ranking by respective predicted values.

Current programs

a. Genetic Prediction in the Angus breed

The American Angus Association initiated a sire evaluation program in the spring of 1972. Young breeder-owned bulls were progeny tested for performance in growth by requiring them to produce progeny in designed comparisons with designated reference sires (i.e. AI sires used across herds with a minimum number of progeny per herd). The first group of sires were reported in a summary in the fall of 1974. Expected Progeny Differences (i.e. values similar to PTA's in the sire evaluation example) were calculated using mixed model analysis procedures prescribed by the Beef Improvement Federation in their guidelines (BIF, 1981). Artificial insemination became more popular among beef breeders in the late 70's and this tended to increase the number of

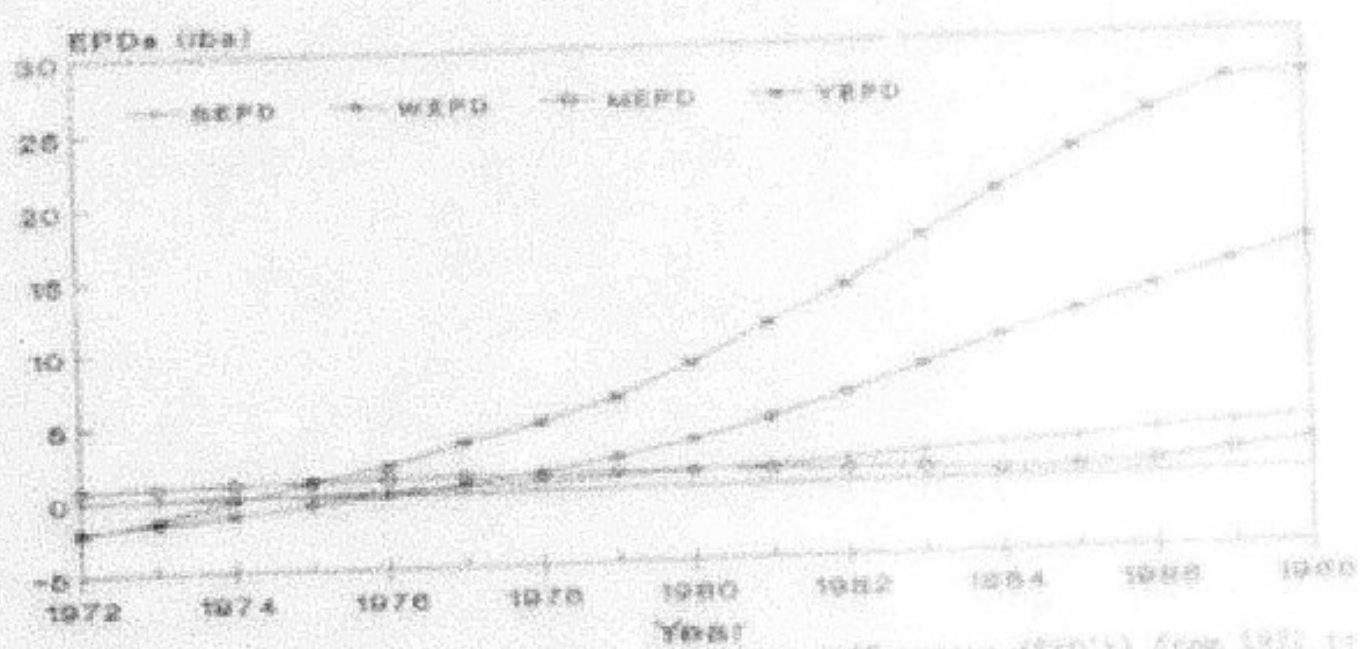


Figure 1. Genetic trends in expected progeny differences (EPD's) from 1972 to 1990 for BWPD-birth weight, WPD-weaning weight, MRPD-milk production, and YRPD-yearling weight (lbs). Kewenush et al. (1989).

comparisons among sires. The first field data sire evaluation report was published in 1960 (Berger and Williams, 1960). Genetic trends in performance for growth were identified for the first time in a beef breed anywhere in the world. National sire evaluation and on-farm testing programs were adopted in 1965 in a national cattle evaluation with the adoption of an animal model in 1965 (Kewenush et al. 1989). It was generally accepted that unless national sire evaluation was merged with on-farm and ranch testing programs, genetic progress would be slow, particularly in commercial herds (Williams 1979, 1982) because commercial herds were not able to use AI. Today genetic values are computed for sires, dams and young animals (males and females) not yet producing progeny. Genetic values (either in the form of breeding values or expected progeny differences) are computed for direct growth and maternal ability for these traits that are externally influenced. Figure 1 shows the genetic improvement in the Angus breed since the beginning of the sire evaluation program. Genetic improvement within the Angus breed is testimony to the fact that beef breeders throughout the country were willing to accept the concepts of national cattle evaluation and they responded by making effective use of these concepts in their breeding programs.

Current Programs

5. Genetic Prediction in the United States Dairy Industry

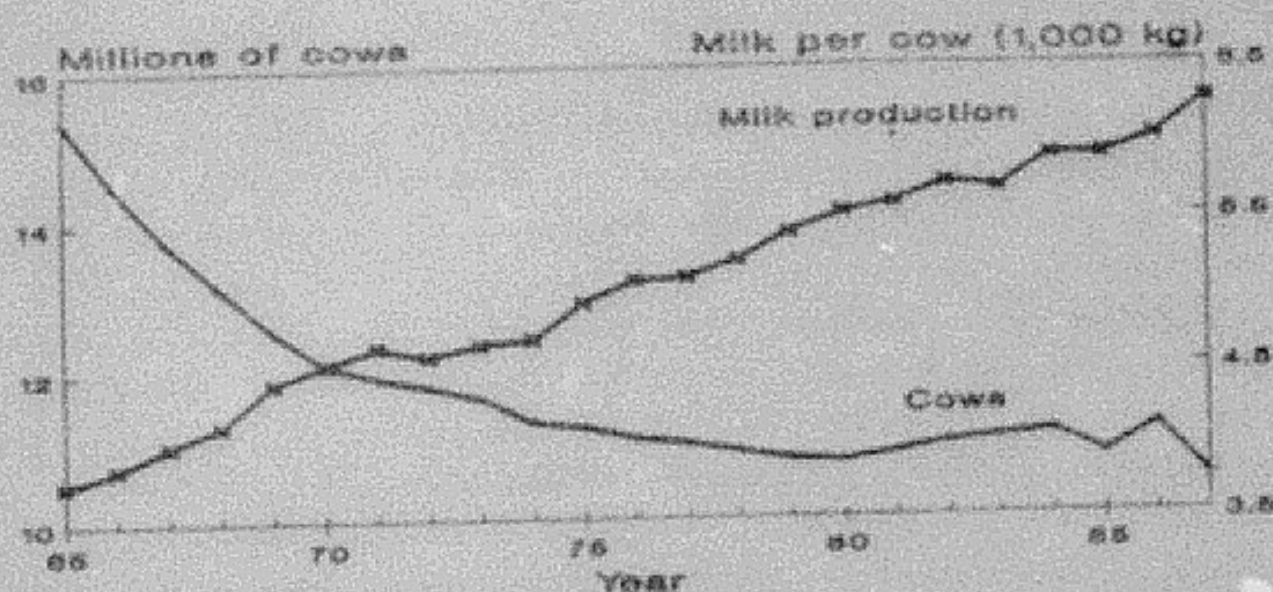
Milk production records are collected on a national scale and because of the management system, extensive use of artificial insemination resulted in spreading the daughters of many sires over herds. The United States Department of Agriculture (USDA) put this data together on a national basis and developed sire predicted differences (PD) for milk and fat yield. The USDA began evaluating the genetic merit of sires in 1933. The program has grown and become progressively more complicated. The Modified Contemporary Comparison (MCC) was implemented in 1974. The comparison of a particular sire was with the average bull whose daughters produced in the average dairy herd. The base or reference point was set in 1974 so that the sire of the average cow born in the base year would have a zero predicted difference. The base became known as PD74 and was updated to a new base (PD82) in 1984. The USDA implemented a new genetic evaluation program in July, 1989 based on procedures defined by the Animal Model (Wiggans et al. 1988). PD's are now published as PTA's.

The genetic base used in computing sire and cow evaluations was updated with implementation of the Animal Model. The change affected all genetic evaluations equally. Therefore, the change only affected the magnitude of the evaluations, not the ranking among animals.

With implementation of the Animal Model, the base was defined by the cow population rather than by sires. The new base was set so the breeding values of all cows born in 1985 averaged zero. Approximately 50% of the cows evaluated in July, 1989 were expected to be above zero with the Animal Model. The bases (separate for each trait and breed) will be changed or updated about every five years and labeled according to the year in which they are implemented.

The number of dairy cows in the United States has declined since 1965 but at the same time production per cow has been increasing, as in Figure 2. This translates into more efficient production and a greater return to dairy producers, but consumers also benefit, because dairy products are cheaper.

Profitability (income minus expenses) in daughters of high versus average Holstein sires selected for milk yield of daughters was reported by



92% fewer COWS, 108 times more MILK
Herd size: 24 in 1940, 72 in 1978

Figure 2. The decline in number of cows (+) and increase in production per cow (*) from 1965 to 1987.

Bertrand et al. (1985). Daughters of high Predicted Difference Milk sires had 49% higher semen costs, 1% fewer breedings, and less than 1% more reproductive examinations. They had 9% more respiratory costs, 6% more

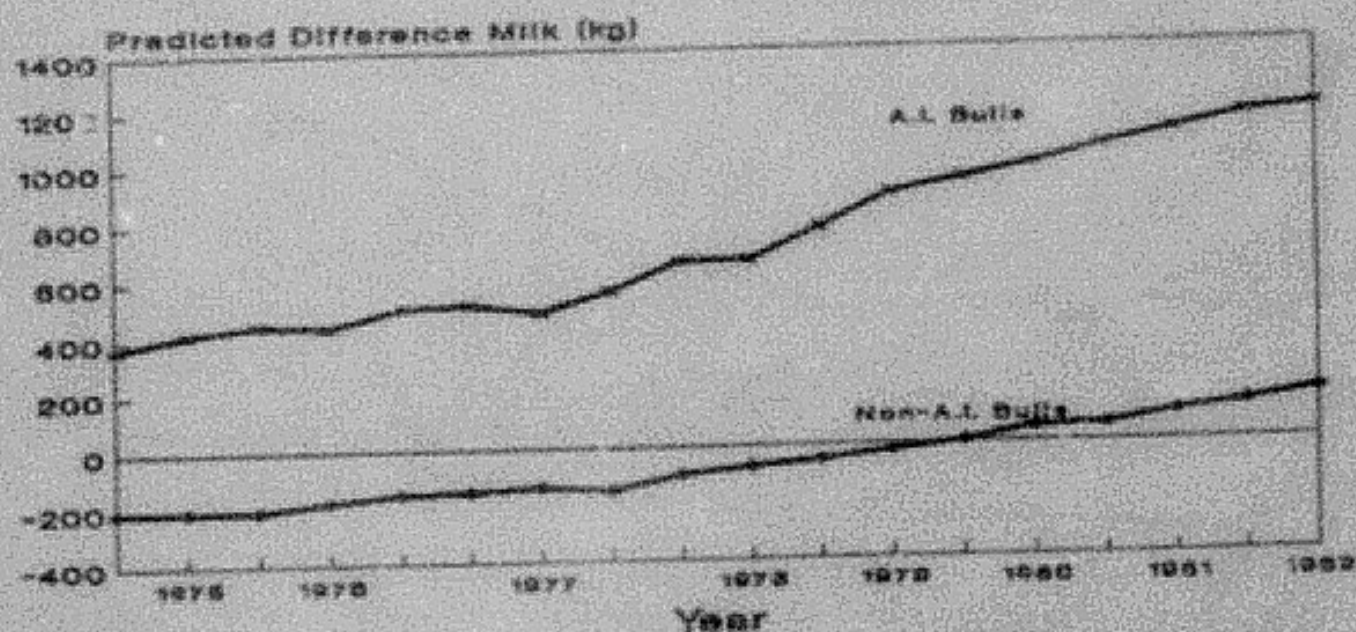


Figure 3. Comparison of average predicted difference milk (kg) for A.I. bulls (+) and non-A.I. bulls (*) in the Holstein breed summarized by the U.S.D.A. from 1974 to 1982 (Miller, 1982).

digestive costs, and 8% more skin and skeletal costs. Daughters of high Predicted Difference Milk sires produced 18% more milk, had 1% more mammary costs, and 42% more discarded milk costs. Disregarding breeding costs, they had 21% higher health costs. Including breeding costs, total health costs were 32% higher. With 9% increased feed costs, they netted 16% more lifetime profit and 18% more profit per day of life.

Size selection has been effective and we can continue to make genetic improvement. Figures 3 and 4 compare the average PD of A.I. bulls with non-A.I. bulls from 1974 to 1982 in the Holstein breed (see Wiggans et al. 1988 for more recent trends in all breeds of dairy cattle within the United States). The A.I. bulls are improving at a faster rate than non-A.I. bulls because of the greater intensity of selection. Primary emphasis in selection has been on milk yield (Figure 3) but fat yield has also increased (Figure 4) due to the high positive genetic correlation between the two traits.

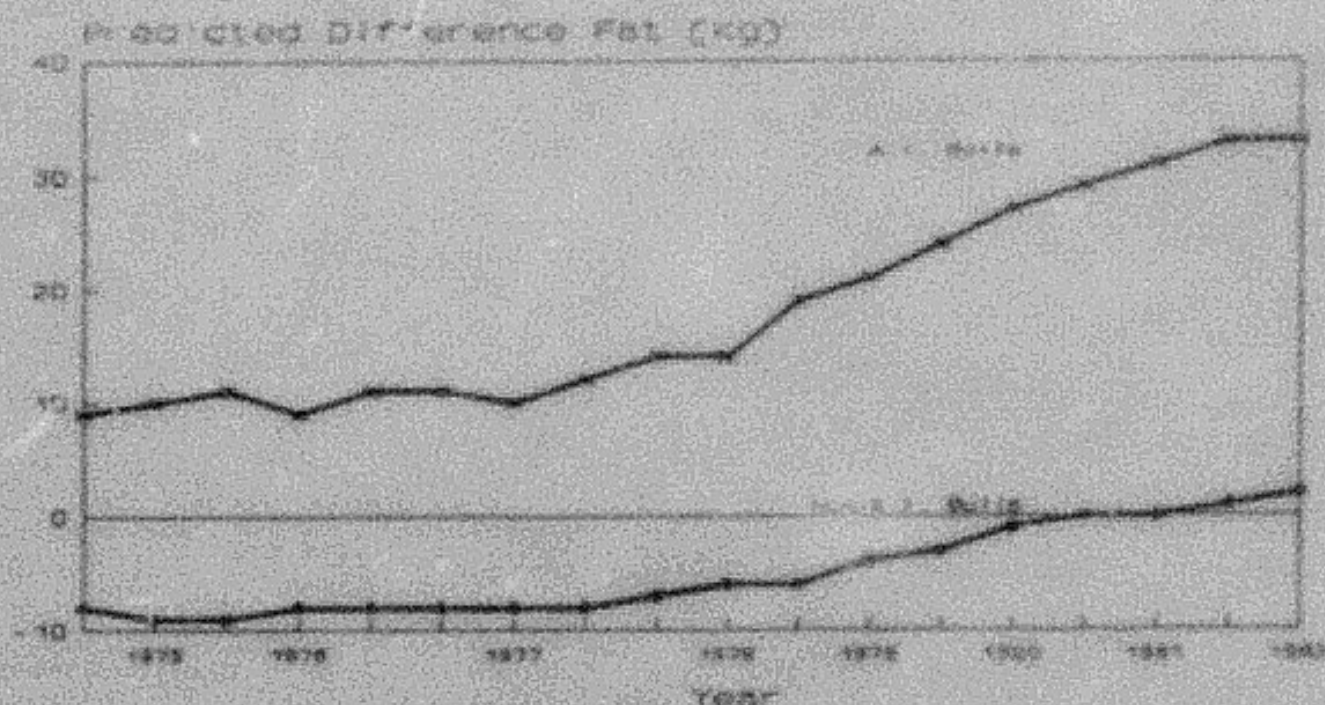


Figure 4. Comparison of average predicted difference fat (kg) for A.I. bulls (+) and non-A.I. bulls (*) in the Holstein breed summarized by the U.S.D.A. from 1974 to 1982 (Miller, 1982).

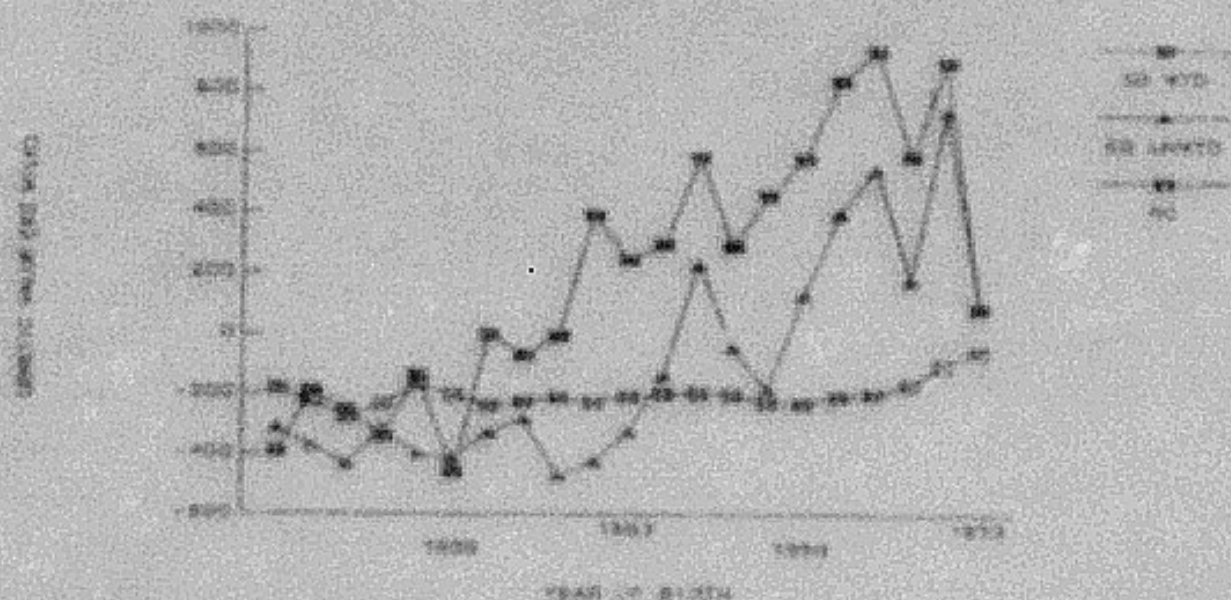


Figure 5. Average genetic values of sires of bulls weighted (SBWTD) and unweighted (SBUSWTD) by number of sons by year of birth of sire compared to average genetic values of registered cows (RC) born in the same year (VanTassell and VanVleck, 1967).

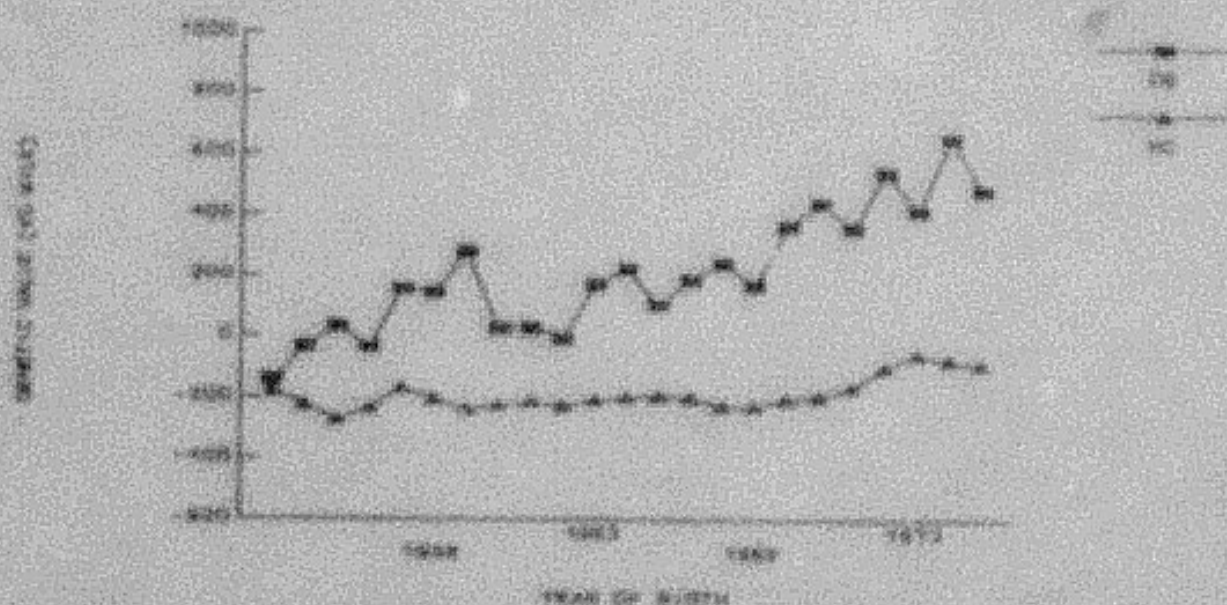


Figure 6. Average genetic values of dams of bulls (DB) by year of birth of dams compared to average genetic values of registered cows (RC) born in the same year (VanTassell and VanVleck, 1967).

Sire and cow selection can lead to genetic improvement within a population. Sire selection is more effective in making change because of the greater intensity of selection, particularly through A.I. The four paths of selection leading to genetic improvement are illustrated in Figures 5 to 8. The paths of selection are: 1) sires of bulls, 2) dams of bulls, 3) sires of cows, and 4) dams of cows. The data are genetic values from an Animal Model analysis of records from dairy herds in the Northeastern United States. The analysis was conducted by Westell and VanVleck (1987) but the values in the figures were reported by VanTassell and VanVleck (1987). Figure 5 compares the genetic values of sires of bulls (weighted and unweighted by number of sons) to the genetic value of all registered cows. Sire selection became effective after 1964 (SB H&WTD). The weighting by number of sons shows that better bulls were being used to produce sons in A.I. by as early as 1958 (SB WTD). Figure 6 compares the genetic values of dams of bulls with registered cows. The rate of improvement was less than for sires of bulls (Figure 5) but the better cows were clearly being used to produce sons in A.I. Figure 7 compares the genetic values of sires of cows (weighted and unweighted by the number of daughters) with the genetic value of all registered cows. The trends are more variable and lower in magnitude than in Figures 5 and 6.

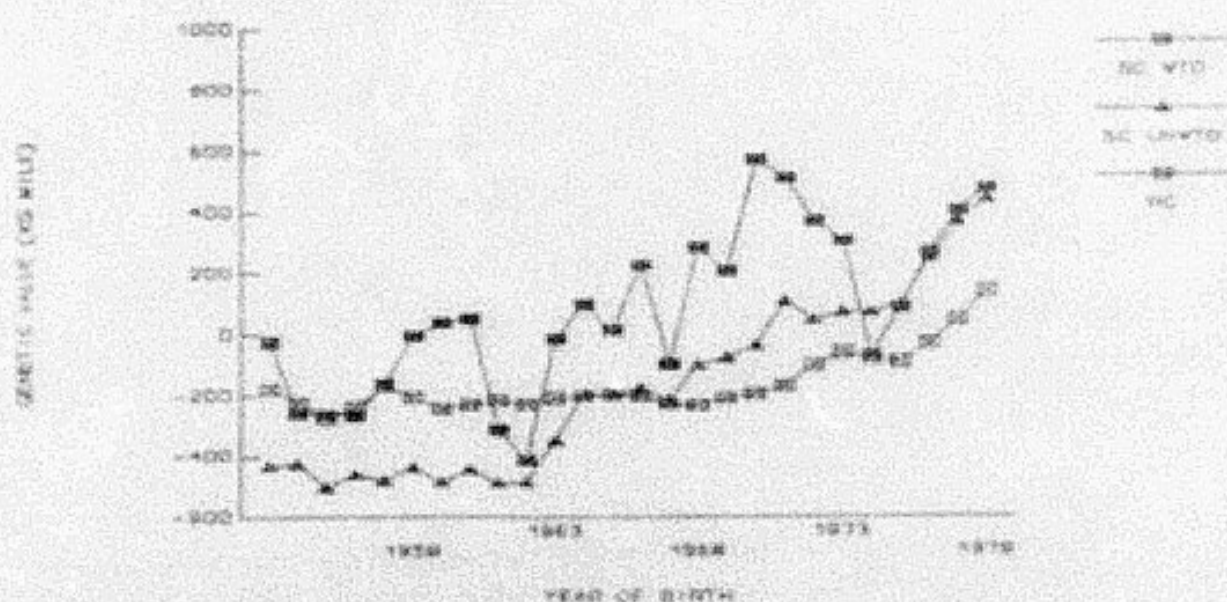


Figure 7. Average genetic values for sires of all cows weighted (SCWTD) and unweighted (SCUWTD) by number of daughters by year of birth of sires compared to average genetic value of registered cows (RC) born in the same year (VanTassell and VanVleck, 1987).

This indicates the influence of traits other than milk yield in the selection of sires to produce replacement heifers (cows). Figure 8 compares the average genetic values of dams used to produce replacement heifers with the average genetic value of all cows. The trend here is less than in the previous three figures and there was little difference between the average genetic value of dams and all cows. This was expected because of the lower intensity of selection possible with selection of dams to produce heifer replacements.

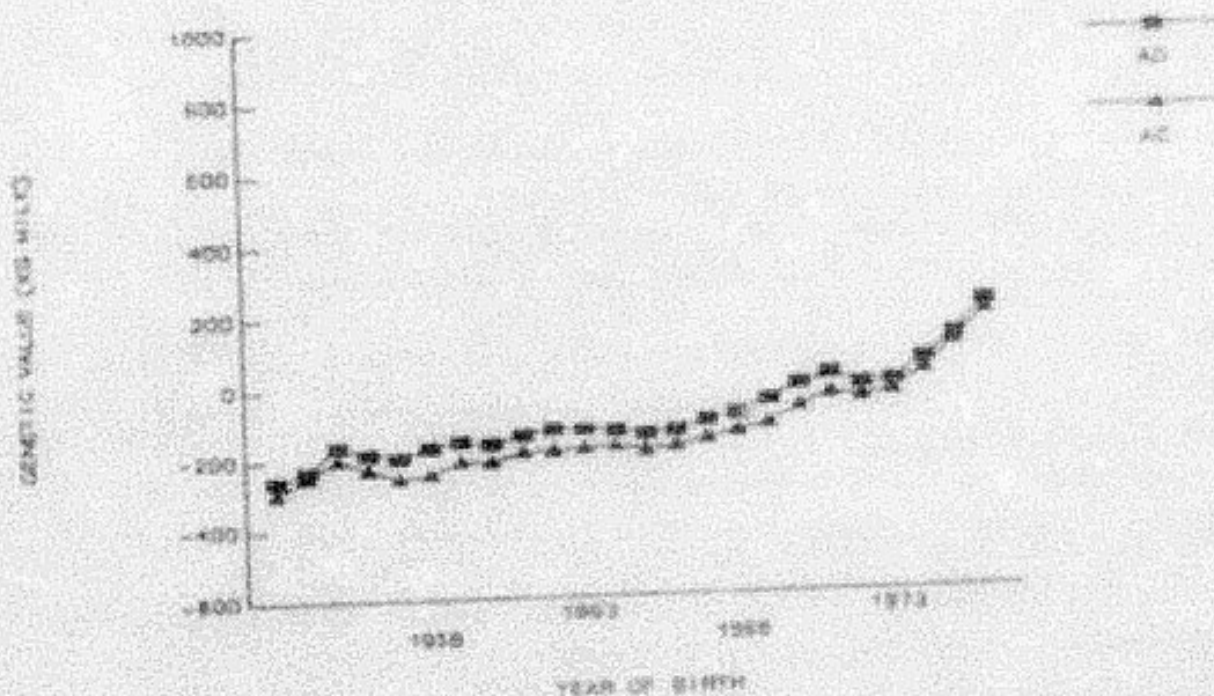


Figure 8. Average genetic values of all dams (AD) by year of birth compared to average genetic values of all cows (AC) born in the same year (VanTassell and VanVleck, 1987).

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