

GENETIC TRENDS IN ESTIMATED TRANSMITTING ABILITY FOR YIELD TRAITS OF SIRES BASED ON FIRST LACTATION

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ABSTRACT

A total of 10836 first lactation records German Friesian cows daughters of 781 sires, from 1979 to 1996 were used to study genetic progress achieved by predicted transmitting ability of sires (PTA) for 305 day milk yield (305dMY), milk fat (MF) and milk protein (MP). Data analyzed by using a multitrait REML with the animal model. Genetic variances were based on variation in estimated PTA values of individual sires. Also, regression methods to estimate the annual genetic progress were used. Heritabilities were 0.32, 0.36 and 0.31 for 305dMY, MF and MP, respectively. Genetic and phenotypic correlations among traits studied were positive and significant. PTA values for 305dMY ranged from -1984 to 1781 kg with average differences between sires of 3765 kg, as well as for MF ranged from -181.2 to 158.8 kg with average of 340 kg, and for MP ranged from -107.5 to 317.3 kg with average of 424.8 kg. Annual genetic change in the PTA for 305dMY, MF and MP averaged 222.11, 3.93 and 7.44 kg, respectively. The results indicated that the use of top ranking bulls on the basis of their PTA's for milk yield traits in breeding program will lead to noticeable genetic improvement in productivity of Friesian cows in Northern Germany.

Keywords: Heritability, Genetic, Phenotypic correlation, Genetic Trend, Predicted Transmitting Ability (PTA), Annual Genetic Change and German Friesian Cows.

INTRODUCTION

Genetic evaluations are key to producing improved animals and increasing profitability for the future. By monitoring the average predicted transmitting ability PTA's of cows and bulls born in each year, the genetic trend can be obtained. All PTAs' are estimates or alternatively predictions based on the available information. Estimation of genetic trends over time is problematic because of the difficulty to conduct experiments in uniform conditions over a period of several generations. So that changes in performance of selected population may reflect, in part, both environmental and genetical changes. Theoretically it is possible to simultaneously maintain a control population to remove the influence of environmental change (Hill, 1972), but this could prove expensive especially over a long period of time. A matter of fact milk yield is expressed only in females; therefore, selection of young bulls for sex-limited traits requires either selection by pedigree or indirect selection (Freeman, 1975). The most rapid genetic gain can be achieved by selecting and sampling young bulls, because younger animals are on average superior to the older animals. As genetic progress accelerates, the importance of young animals in breeding programmes increases. The purposes of the present research were to estimate (1)

phenotypic and genetic parameters for 305 day milk yield (305dMY), milk fat (MF) and milk protein (MP) and (2) additive genetic change for these traits in a herds of Friesian cattle raised in Northern Dutchland.

MATERIALS AND METHODS

Data on 10836 normal first lactation records of German Friesian cows daughters of 782 sires of milk, fat and protein yields were collected from 23 herds from 1979 to 1996. Data were supplied by VIT (Vereinigte Informationssysteme Tierhaltung), Verden, Germany. Cows without measurements on yields of milk, fat, and protein or with records less than 240d or greater than 400d length of lactation were deleted. Sires with 20 daughters or more were used. The originated data was 20500 first lactation records from 23 herds in one sub-region, so that the common variety farms as semi open sheds are presented. Editing data was extensive in order to have as many acceptable records as possible. The animals were fed on concentrates according the yielding with the grassland in summer and autumn. In the winter cows get concentrates and conserved feed.

Firstly, Estimation of non-genetic effects with mixed model of (Harvey, 1990) were used. The following mixed model was used:

$$Y_{ijklm} = \mu + h_i + s_{ij} + f_k + y_l + b_1(x-x') + b_2(x-x')^2 + e_{ijklm}$$

Where: μ = a population constant; h_i = the fixed effect of herd ($i = 1,2,\dots,23$); s_{ij} = the random effect of i^{th} sire within j^{th} herd; f_k = the fixed effect of season of calving ($k = 1,\dots,3$); y_l = the fixed effect of year of calving (1979 to 1996); b_1 and b_2 = the linear and quadratic regression coefficients of 305-dMY, MF and MP in kilograms on age at first calving in month; and e_{ijklm} = the random errors distributed as a normal distribution with zero mean and variance σ^2_e .

Secondly, A Multi Trait Animal Model program (MTDFREML) of Boldman et al. (1995) was used to estimate the breeding values with Best Linear Unbiased Prediction (BLUP) methodology. The following linear animal model was used:

$$Y = X\beta + Z\mu + e$$

Where:

Y = a vector of observation for each trait,

X = the incidence matrix for fixed effects;

β = the vector of an overall mean and fixed effects of month and year of calving;

Z = the incidence matrix for random effects;

μ = the vector of random effects (animals additive genetic effects) associated with the incidence matrix Z ; and

e = the vector of random errors normally and independently distributed with zero mean and variance $(0, I\sigma^2_e)$.

The variance-covariance structure for the model was as follows:

$$V = \begin{bmatrix} a_1 \\ a_2 \\ a_3 \\ e_1 \\ e_2 \\ e_3 \end{bmatrix} = \begin{bmatrix} A\sigma^2 a_1 & \sigma a_1 a_2 & \sigma a_1 a_3 & 0 & 0 & 0 \\ \sigma a_2 a_1 & A\sigma^2 a_2 & \sigma a_2 a_3 & 0 & 0 & 0 \\ \sigma a_3 a_1 & \sigma a_3 a_2 & A\sigma^2 a_3 & 0 & 0 & 0 \\ 0 & 0 & 0 & In_1\sigma^2 e_1 & \sigma e_1 e_2 & \sigma e_1 e_3 \\ 0 & 0 & 0 & \sigma e_2 e_1 & In_2\sigma^2 e_2 & \sigma e_2 e_3 \\ 0 & 0 & 0 & \sigma e_3 e_1 & \sigma e_3 e_2 & In_3\sigma^2 e_3 \end{bmatrix}$$

Where:

A is the numerator relationship matrix,

$\sigma^2 a_1, \sigma^2 a_2, \sigma^2 a_3$ = the direct genetic variance for trait 1, 2 and 3,

$\sigma^2 e_1, \sigma^2 e_2, \sigma^2 e_3$ = the residual variance effects and

$\sigma a_i a_j$ = the direct genetic covariance items between any pair of the three traits studied.

To estimate heritability (h^2), the following equation were used:

$$h^2 = \sigma^2_a / (\sigma^2_a + \sigma^2_e)$$

Where:

σ^2_a = additive genetic variance; and σ^2_e = the random residual effect associated with each observation.

Genetic trends for different traits studied were obtained by estimating coefficients of regression the estimate of breeding values on years of birth.

For the p^{th} year, the average of sires transmitting abilities was

$$\sum_i n_{ip} \hat{s}_i / n.p'$$

where n_{ip} is the number of daughters of sire i born in the p^{th}

year, and s_i is the predicted transmitting ability of the i^{th} sire, (Canon and Munoz, 1991).

The accuracy of predicted breeding value for each individual was estimated according to Henderson (1975) as $r_{AA} = \sqrt{1 - d_j \alpha}$

Where r_{AA} = the accuracy of prediction of the i^{th} animals breeding value (animals with records) and animals transmitting ability (animals without records), d_j = the j^{th} diagonal element of inverse of the appropriate block coefficient matrix, and $\alpha = \sigma^2_e / \sigma^2_a$.

Table 1 Show, observations, means, minimum, maximum, standard deviations and coefficients of variation for milk, fat and protein yields.

Table (1) Summary of the data structure for yield traits for the first lactation.

Items	Mean	SD	Minimum	Maximum	CV%
Yields, kg					
Milk	6322	1280	3301	10563	20.25
Fat	263	54	89	488	20.53
Protein	209	43	78	763	20.57
Observations					
Records, no.	10836				
Herd levels	23				
Year levels	17				
Seasons levels	3				
Animals in relationship matrix, no. A ⁻¹	11282				
Mixed model equations, no.	33978				
Simplex iteration carried out, no.	2266				

RESULTS AND DISCUSSION

(Co)variances and parameters

Estimates of genetic, phenotypic and environmental covariances for yields of milk, fat and protein are given in Table 2. However, genetic variances for milk and fat yields as proportions of the total variances were somewhat higher than protein yield, while the contrast trend was found for the environmental variances for protein yield as proportions of the total variance (Table 2). Consequently, for milk and fat yields, heritability estimates were higher than for protein yield, (0.32, 0.36 and 0.31 for milk, fat and protein yields, Table 3).

The present estimates are higher than those estimated by Hill et al., 1983, being 0.25, 0.24 and 0.21 for milk, fat and protein, respectively on British Holstein-Friesian cows. In addition, estimates obtained by Meyer, 1984 and Ashmawy and Khalil, 1990, were smaller than those estimates in this study. (0.25, 0.24 and 0.23 for milk, fat and protein yields, respectively). Hamed and Soliman, 1994, found that the estimates of h^2 for milk yield 0.43, fat yield 0.42 and protein yield 0.38. According to the moderate heritability estimates reported here, it can be concluded that the genetic improvement in milk production traits can be achieved through selective breeding program.

Table (2) Estimates of genetic and phenotypic (Co)variances for milk, fat and protein yields for the first lactation.

Yield traits	Genetic	Phenotypic	Environment
Variances, kg ²			
Milk (M)	2040.66	6359.88	4319.22
Fat (F)	1009.53	2827.18	1817.65
Protein (P)	698.65	2236.44	1537.78
Covariances, kg ²			
M x F	758.20	3545.85	2787.66
M x P	990.35	3558.65	2568.29
F x P	766.32	2435.59	1669.27

Table (3) Estimates of heritabilities, genetic, phenotypic and environmental correlations for yields of milk, fat and protein of the first lactation.

Yield traits	Parameters						
	h ²	r _G		r _P		r _E	
		(F)	(P)	(F)	(P)	(F)	(P)
Milk, (M)	0.32	0.53	0.83	0.84	0.94	0.99	1.00
Fat, (F)	0.36		0.91		0.97		1.00
Protein, (P)	0.31						

Estimates of heritability obtained in the present study are generally higher than those estimated by Manfredi et al., (1984), Lawlor (1984) and deJager and Kennedy (1987) with sire model. However, Cue et al., (1987), analysed Canadian data by sire model, found heritability estimates of 0.36 for milk and fat yields and 0.25 for protein yield. The present results are comparable with those estimated by Albuquerque et al., (1996), using animal model with two sets of California (CA) and New York (NY) data, being 0.30, 0.31 and 0.29 for milk, fat and protein, respectively in CA and 0.33, 0.35 and 0.30, respectively in NY. Those authors concluded that heritability estimates obtained with animal model vary, but most are higher than those obtained with sire models. In addition, Misztal et al., (1992), obtained much higher heritability estimates than those in the present study of 0.44, 0.42 and 0.40 for milk, fat and protein yields, respectively.

Genetic correlations between yield traits were positive and high. Estimates were 0.53 for milk and fat, 0.83 for milk and protein and 0.91 for fat and protein Table (3). The corresponding estimates except of between fat and protein of deJager and Kennedy, 1987 were 0.57, 0.82 and 0.66 respectively. This conclusion was similar to other workers (e.g. Ashmawy and Khalil, 1990; Soliman et al., 1990; Soliman and Khalil 1993; and Hamed and Soliman, 1994. In addition, Schutz et al., 1990 found smaller genetic correlation of milk and protein (0.50 to 0.62), also, milk and fat (0.20 to 0.28). Campos et al., (1994) estimated genetic association between MY and FY and MY and PY of 0.70 and 0.85, respectively.

The present study shows higher genetic, phenotypic and environmental correlations between fat and protein yields comparison with correlations between both milk and fat yields or milk and protein yields (Table 3). Albuquerque et al., (1995) reported that genetic, phenotypic and environmental correlations were largest between milk and protein (0.84, 0.93 and 0.96) followed by correlations for fat and protein (0.87, 0.83 and 0.86). The same trend was observed by Dong et al., (1988), Misztal et al., (1992); and Visscher and Thompson (1992) with the animal models analysis. Generally, High estimates for phenotypic and environmental correlations among yield traits were obtained in the present study and ranged between 0.84 and 1.00 Table (3). Phenotypic correlations were high than corresponding genetic correlation (El-Awady et al., 2000).

PTA's and Annual genetic change

Predicted transmitting ability of sires (PTA's) and accuracies of milk, fat and protein yields for first lactation are in Table (4). Number of daughters per sire ranged from 20 to 1034. Estimates of PTA as deviation from mean ranged from -1984 to 1781 kg for milk yield, from -181.2 to 158.8 kg for fat yield and from -107.5 to 317.3 kg for protein yield, with an average being, 3765 kg, 340 kg and 424.8 kg, respectively. Predicted transmitting ability obtained from the present study were larger than those obtained by Schneeberger et al., 1982; Abubakar et al., 1986. However, McAllister et al., 1990 with Holsteins in Canada found that average PTA for first lactation yields of milk, fat and protein were -197 to 838 kg, -14 to 39 kg and -11 to 31 kg, respectively. In addition Abubakar et al., 1986 evaluated 1442 sires of Holsteins by best linear unbiased prediction procedures for first lactation and reported that sire value for milk ranged from -340 to 359 kg.

Table (4) Predicted minimum (Min), maximum (Max), standard error (SE) and range of sire transmitting ability (PTA) for the first lactation milk, fat and protein yields.

Yield traits	Min ± SE	Max ± SE	Range	Average accuracy
Milk	-1984±253	1781±292	3765	87%
Fat	-181.2±18.8	158.8±16.8	340.0	76%
Protein	-107.5±17.6	317.3±20.6	424.8	81%

The present estimates showed large genetic differences between sires for different traits studied, indicate the high potential for rapid genetic improvement in milk, fat and protein yields through selection. The accuracy of sire PTA value for yield traits studied was high, this may be due to higher number of daughters per sires.

The Annual genetic progress for milk, fat and protein yields are given in Table (5). The genetic progress for milk, fat and protein yields was greater for the period from 1985 to 1990, being 315.00, 7.75 and 10.30 kg, respectively, than the overall genetic gain, being 222.11, 3.93 and 7.44 kg, respectively. Van Tassel and Van Vleck, 1991 reported genetic gain of 60.8 kg for milk for Holstein sires of bulls (SB) from 1955 to 1973. In addition, Nizamani and Berger, 1996 with Jersey cows, found that genetic response for milk, fat and protein yields was greater from 1982 to 1986 at 232.0, 6.0 and 4.9kg, respectively, than the overall genetic response at 91.7, 3.4 and 2.6 kg, respectively. Because the genetic progress for milk, fat and protein yields were greater for the period from 1985 to 1990 than the progress achieved for the period from 1979 to 1990, these results suggest that the use of high ranking bulls on the basis of their PTA's in the breeding program through AI will lead to high genetic improvements in these herds. Burnside et al., 1992 found a higher trend for milk, fat and protein yields of Italian Holsteins from 1985 to 1988 and a lower overall trend. In additional, our results are in close agreement with these estimated by Jamrozik et al., 1997, who reported that the PTA's for milk and protein yields were, 210 and 6.93 kg, respectively.

Table (5) Estimates of annual genetic change (kg/year) and its (standard errors) for milk, fat and protein yields.

Year of Calving	Traits		
	Milk, kg	Fat, kg	Protein, kg
1979	-1377.94	57.87	-54.19
1980	-925.28	38.86	-30.35
1981	-861.37	36.81	-28.25
1982	-841.10	35.32	-27.59
1983	-232.49	9.76	-7.63
1984	365.08	15.33	11.97
1985	-21.29	0.89	-0.69
1986	-659.66	27.71	-21.64
1987	-194.73	8.18	-6.39
1988	265.44	11.15	8.71
1989	1084.03	45.53	35.56
1990	1044.53	43.85	34.24
1991	2147.68	90.17	70.42
1992	1262.92	53.00	41.39
1993	1555.46	65.33	51.04
1994	2189.40	91.94	71.79
1995	2112.21	88.70	69.27
1996	2544.85	106.88	83.41
b's			
(1)	308.96 ± 69.21	-8.61 ± 2.91	11.40 ± 2.66
(2)	314.87 ± 86.11	7.75 ± 3.49	10.30 ± 1.43
(3)	147.60 ± 107.58	6.21 ± 4.53	4.84 ± 3.54
(4)	189.45 ± 30.04	-1.29 ± 1.60	6.56 ± 1.01
(5)	222.11 ± 76.09	3.93 ± 1.09	7.44 ± 0.64

b's = annual genetic change per kilograms of milk, fat and protein yields.

(1) = annual genetic change from 1979 to 1984; (2) = annual genetic change from 1985 to 1990; (3) = annual genetic change from 1991 to 1996; (4) = annual genetic change from 1979 to 1990 and (5) = overall mean of annual genetic change from 1979 to 1996.

CONCLUSION

The present study concluded that the annual genetic gain in milk yield was high as compared with the annual genetic progress in either fat or protein yield, which indicated that the selection of high yielding cows for the 305 days milk yield will be associated with the improvement in the corresponding fat and protein yield. Thus considerable genetic progress in milk, fat and protein yields could be achieved in Friesian cows in Germany by using the top ranking bulls in the breeding program.

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الاتجاهات الوراثية لصفات إنتاج اللبن عن طريق تقدير المقدرة العبورية
للطلائق على أساس الموسم الأول للإدرار
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تم استخدام ١٠٨٣٦ سجل حليب للموسم الأول لعدد ٧٨١ أب في الفترة من ١٩٧٩ وحتى ١٩٩٦ بشمال ألمانيا وذلك لدراسة الاتجاهات الوراثية عن طريق تقدير المقدرة العبورية للطلائق. قدر المكافئ الوراثي لكل من إنتاج اللبن في ٣٠٥ يوم ، إنتاج الدهن ، إنتاج البروتين بـ ٣٢ ، ٣٦ و ٣١ ، على التوالي. كانت الارتباطات الوراثية والمظهرية موجبة ومعنوية.

تم تقدير القيمة العبورية للطلائق والتي لديها ٢٠ بنت فأكثر بطريقه أفضل انحدار خطي غير متحيز (BLUP). تراوحت القيمة العبورية للطلائق في الموسم الأول لصفه إنتاج اللبن من -١٩٨٤ إلى ١٧٨١ كجم بمتوسط ٣٧٦٥ كجم و لصفه إنتاج الدهن من -١٨١,٢ إلى ١٥٨,٨ كجم بمتوسط ٣٤٠ كجم و لصفه إنتاج البروتين من -١٠٧,٥ إلى ٣١٧,٣ كجم بمتوسط ٤٢٤,٨ كجم.

قدر التغير الوراثي السنوي للطلائق لكل من صفه إنتاج اللبن في ٣٠٥ يوماً وإنتاج الدهن وإنتاج البروتين بـ ٢٢٢,١١ ، ٣,٩٣ و ٧,٤٤ كجم على التوالي. وقد أوضحت نتائج هذه الدراسة ان استخدام الطلائق عالية الكفاءة الوراثية على أساس مقدرتها العبورية لصفات إنتاج اللبن والدهن والبروتين في برنامج التربية سوف يؤدي إلى تحسين وراثي ملحوظ في إنتاجية أبقار الفريزيان بشمال ألمانيا.