GENETIC IMPROVEMENT FOR MILK TRAITS OF GERMAN HOLSTEINS THROUGH SELECTION INDICES

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ABSTRACT

Total of 20500 normal first lactation of German Friesian cows from 23 herds sired by 1003 bulls, were used to estimate the genetic and phenotypic parameters of 1st milk yield (MY), 1st fat yield (FY) and 1st protein yield (PY). Analysis was carried out using a mixed model including year and season of calving and the herd as fixed effects, age at first calving as a covariate and sires as a random effect. Least squares means were, 6096, 253 and 201, kg for MY, FY and PY, respectively. Heritability estimates were, 0.35 ± 0.02, 0.29 ± 0.02 and 0.29 ± 0.02 for the previous traits, respectively. All genetic and phenotypic correlations were positive and high (0.66 to 0.92). Four selection indices for improving milk traits were constructed including all combinations of two or three traits studied. The expected genetic change per generation ranged between 338 kg and 344 kg for MY, 4.11 kg and 10.81 kg for FY and 7.55 kg and 7.98 kg for PY. The maximum predicted genetic improvement in milk and protein yields were 344.18 kg and 7.98 kg per generation and achieved by I_3, while the highest predicted genetic response for fat yield gave by I_4 (10.81 kg). Index I_1 which included MY, FY and PY was the best (R_{IH}=0.66) and recommended for genetic improvement of German Friesian cows if the selection was exercised at the end of the first lactation.

Keywords: Genetic and Phenotypic Correlation, Heritability, Expected genetic change, Selection indices, and German Friesian cows.

INTRODUCTION

Since the beginning of last century the butterfat yield has been the most important production trait in European cattle breeding. Producers payment has been based on butterfat and the recording of fat percentage has been easy, accurate and inexpensive (Nelmann *et al.*, 1987). In recent years the importance of milk protein has increased rapidly. The improved standard of living and the modern consumers concern about their calorie intake has increased the demand for milk products with higher protein and lower fat content. Also, protein is very important in human nutrition and it is used in industrial value of the milk products. In addition, Anderson *et al.*(1978) and Kuipers and Shook (1980) reported additional genetic gain in milk yield when protein yield was included in the selection index. Ashmawy and Khalil (1990) concluded that genetic improvement for yield traits of cows might be achieved through milk traits selection based on reduced index including milk yield with either of fat or protein yield. Hazel *et al.* (1994) and Mrode, (1996) revealed that multiple-trait selection was more effective than independent culling level

or sequential selection. The purpose of this study were to (1) estimate the genetic and phenotypic variances and covariances for MY, FY and PY which were used for the construction of selection indices and (2) the selection indices.

MATERIALS AND METHODS

The data used in this study comprised 20500 normal first lactation records collected from 23 herds belonging to Vereinigte Informationssyteme Tierhaltung, (VIT), Verden Germany, spread over eighteen years from 1979 to 1996. Number of sires and average numbers of daughters per sire were 1003 and 19.30, respectively. Records less than 240 days or higher than 400 days of lactation length or those without registration for yields of milk, fat and protein were excluded. Cows were inseminated artificially (AI). Animals were kept loose under semi open sheds and were fed concentrate mixture with grassland. During summer and autumn months, concentrate were offered according to animal body weight and its milk production. During winter months cows were get conserved feed and supplemented with extra concentrate rations. El-Awady, (1998)) gave a detail of the material and management of those herds.

Data were analysed using the Mixed Model Least Squares and Maximum likelihood computer program, (LSMLMW of Harvey (1990). Heritability, genetic and phenotypic correlation were estimated according to the formula of Harvey (1990). Estimates of sire ($\sigma^2 s$) and residual ($\sigma^2 e$) components of variance and covariance were computed using the formula of Henderson (1953). The phenotypic and genetic variances and covariances are given in Table (1).

The estimates of genetic and phenotypic variance and covariance of MY, FY and PY were used for the construction of various selection indices using Henderson's modifications of Hazel's (1943) method as described by Karam *et al.* (1953) for improvement milk traits. The selection intensity for a trait was set to the unit.

Table (1) Phenotypic and genetic components of variances (diagonal) and covariances (below diagonal) for milk traits for first lactation.

Traits	Phenotypic components			Genetic components		
	MY	FY	PY	MY	FY	PY
MY, kg	893936			315484		
FY, kg	28112	1538		7897	452	
PY, kg	26193	948	900	8020	248	259

MY= milk yield, FY= Fat yield and PY= protein yield

The relative economic values used were 1:13:13 for MY, FY and PY, respectively, according to Vandepitte and Hazel (1977) and Dommerholt and Wilmink (1986). Four selection indices were constructed for improvement of milk production traits of Friesian cattle in Germany, I_1 (MY, FY and PY), I_2 (MY and FY), I_3 (MY and PY) and I_4 (FY and PY). The index value was calculated as:

$$I = b_1P_1 + b_2P_2 + \ldots\ldots + b_nP_n = \sum_{i=1}^{n} bipi$$

Where:

bi = partial regression coefficient, and

Pi = phenotypic value of traits

Regression coefficients (b) of all selection indices were estimated as:

$\underline{P}\,\underline{b} = \underline{G}\,\underline{a}$ or $\underline{b} = \underline{P}^{-1}\,\underline{G}\,\underline{a}$

Where:

$\underline{P}$ = the phenotypic variance-covariance matrix,

$\underline{G}$ = the genetic variance-covariance matrix,

$\underline{b}$ = vector of partial regression coefficients to be used in the index, and

$\underline{a}$ = vector of constants representing the relative economic values of yield traits and

P^{-1} = the inverse of phenotypic variance-covariance matrix

Values of partial regression coefficients and phenotypic variance-covariance matrix (P) were used to calculate values of index variance as $\sigma^2I = \underline{b}'\,\underline{P}\,\underline{b} = \underline{b}'\,\underline{G}\,\underline{a}$, where $\underline{b}'$ is the transpose of (b) vector of partial regression coefficients. Variance of the total aggregate genotypic value was estimated as $\sigma^2H = a'Ga$, where σ^2H, is the aggregate genotypic variance, and a' is the transpose of economic value column vector. Accuracy of the index (defined as correlation between variance of aggregate genotypic value and variance of the index value), was calculated as $R_{IH} = \sigma I/\sigma H$. The expected genetic gain (ΔG) for any one of the traits was calculated as $\Delta G = i\,R_{IH}\,\sigma I$, where i is the selection intensity, and for a trait was set to be the unit for only the purpose of comparisons, or calculated as according to Tabler and Touchberry (1955 & 1959), $\Delta G = \sigma I * i * B_{YI}$ where i is the selection intensity (assume selection differential as one standard deviation), B_{YI} is the regression of each trait in the index on the index value and calculated as $B_{YI} = \underline{b}'c_i / \underline{b}'\,\underline{P}\,\underline{b}$, where c_i is the i th column of G matrix.

To determine which trait and how many trait combine best into an index, relative efficiencies of the different selection indices were evaluated on the basis of the correlation of index with aggregate genotype (R_{IH}) and the efficiency (RE) of different indices relative to the original index (I_1).

RESULTS AND DISCUSSION

Least squares means

Means, standard deviations (SD) and coefficient of variations (CV%) for different traits are presented in table 2. Similarly, Swalve (1995) using another herd of Friesian cattle in Germany, found that means of milk, fat and protein yields were 6003, 251 and 199 kg, respectively. Coefficient of variations are ranged from 21 to 22%. The estimates of 20% for yield trait are reported by deJager and Kennedy (1987).

Ashmawy and Khalil (1990), Khalil and Soliman (1993) and Hamed and Soliman (1994), came to the same conclusion.

Table (2) Means, standard deviations (SD) and coefficients of variation (CV) for milk traits for first lactation

Traits	Means	S.D	CV%
MY, kg	6096	1258	21
FY, kg	253	55	22
PY, kg	201	42	21

No. of records and sires were 20500 and 1003, respectively with d.f of residual 19497

Genetic parameters:

Heritability estimates for milk, fat and protein yields were 0.35±0.02, 0.29±0.02 and 0.29±0.02, respectively (Table 3). The present estimates were slightly high compared with those estimated by Hill *et al.* 1983, being 0.25, 0.24 and 0.21 for milk, fat and protein yields, respectively on British Holstein-Friesian cows. In addition, estimates obtained by Meyer, 1984 and Ashmawy and Khalil, 1990, were nearly in agreement with the estimates in this study. (0.25 0.24 and 0.23 for milk, fat and protein yields, respectively). However, Hamed and Soliman, 1994, found that higher estimates of h^2 for milk yield 0.43, fat yield 0.42 and protein yield 0.38 with Fleckvieh cows in Austria. According to the moderate heritability estimates reported in the present investigation, it can be concluded that the genetic improvement in milk production traits can be achieved through selective breeding program.

Table (3) Heritabilities (on diagonal), genetic correlations (above diagonal) and phenotypic correlation (below diagonal) for milk traits of first lactation.

Traits	Milk	Fat	Protein
Milk	0.35 ± 0.02	0.66	0.89
Fat	0.76	0.29 ± 0.02	0.72
Protein	0.92	0.81	0.29 ± 0.02

Standard errors of genetic correlations ranged from 0.01 to 0.03.

Genetic correlations between yield traits were positive and high. Estimates were 0.66 for milk and fat yields, 0.89 for milk and protein yields and 0.72 for fat and protein yields (Table 3). The corresponding estimates 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 between 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.

High estimates for phenotypic correlation among yield traits were obtained in the present study and ranged between 0.76 and 0.92 (Table 2). The phenotypic correlations were high than corresponding genetic correlation (El-Awady *et al.*, 2000).

Selection Index

Four selection indices were constructed (Table 4). The original selection indices (I_1) incorporating 1st lactation milk, fat and protein yields

was the best (R_{IH} = 0.66) and it was superior to other indices. When the decrease in R_{IH} by dropping a trait was considered, it became clear that in two traits selection, the maximum decrease in R_{IH} was observed in the first lactation index I_4 (Table 4). Furthermore, when two traits were combined, the best index (I_3) was the one comprising milk yield and protein yield (R_{IH}) = 0.60), since the expected genetic gain in first lactation milk yield increased by 344.18 kg/generation and the protein yield increased by 7.98 kg/generation.

The comparative study of various selection indices clarified that the selection index I_1 was the best and it was recommended for improving Friesian cattle in Germany, because it is very simple and easy to construct. The suggested index was:

I = 0.781 (First lactation milk yield) – 10.754 (First lactation Fat yield) + 4.835 (First lactation protein yield).

Table (4): Selection indices (I's), expected genetic gain (ΔG) per generation in each traits, correlation of index with aggregate genotype (R_{IH}) and the efficiency (RE) of different indices relative to the original index (I_1)*

Index	MY		FY		PY		R_{IH}	RE
	b	ΔG	b	ΔG	b	ΔG		
I_1	0.7809	338.68	-10.754	4.11	4.835	7.96	0.66	100
I_2	0.4378	328.81	0.9533	8.78			0.57	86
I_3	0.6711	344.18			-6.880	7.98	0.60	91
I_4			3.999	10.81	3.1116	7.55	0.52	79

* Selection intensity equal one.

Expected genetic gain per generation (ΔG) for MY, FY and PY are summarized in Table (4). The expected genetic change per generation ranged between 328.81 and 344.18 kg for MY, 4.11 and 10.81 kg for FY and 7.55 and 7.98 kg for PY Table (4). The maximum predicted genetic progress in milk and protein yields were 344.18 kg and 7.98 kg per generation and achieved by I_3, while the highest improvement for fat yield was achieved by using selection index I_4. The present results were consonantly with those obtained by Sivanadian *et al.* (1998) with Canadian dairy cattle, they reported that the expected genetic response per generation for milk, fat and protein yields, being, 305.44 kg, 9.28 kg and 9.83, kg, respectively. In addition, Amin *et al.* (1996), found the maximum genetic gain per generation for MY and FY were, 139.27 kg and 7.05 kg, respectively.

The accuracy of index I_1 which included all traits (MY, FY, and PY) was higher (0.66) compare with the other indices (I_2, I_3, and I_4). However, the fourth index (I_4) was the lowest in accuracy (0.52). Adding fat or protein yield in the I_2 or I_3 as demonstrated I_1, the accuracy of index increased by 13.64% and 9.09% for I_2 and I_3, respectively.

When the decrease in R_{IH} value by dropping a trait was considered, it became clear that the decrease in R_{IH} (0.66) was maximum (21.21%) when 1st lactation milk yield as a main important trait was dropped from selection index I_1 (Index 4 Table4). Whereas the minimum decrease (9.09) in R_{IH} was

noticed when 1st lactation fat yield was dropped from the same index I_1. While the decrease in R_{IH} ,being 13.64% when 1st lactation protein yield as a trait was dropped from the original index I_1. These results clarified the importance of adding fat yield or protein yield or both of them to the milk yield in the index, since it will be lead to considerable important of R_{IH} value of such as selection index.

Similarly, Ashmawy and Khalil (1990) found that, adding protein or fat yield in the index increased the accuracy of selection index by 1.9%. Smith (1983) concluded that any loss in accuracy of an index is affected mainly by both the genetic and phenotypic correlations among traits included in the index and therefore the genetic correlations tend to have the more important role in affecting the accuracy, while the phenotypic correlations have a further effect and they have to be considered in estimating accuracy. deJager and Kennedy (1987) concluded that, including protein in the index increased the accuracy of sire breeding value.

Figures of relative efficiency (RE) given in table 4, showed that of all the selection indices developed I_2 and I_3 that the highest efficiency (86 and 91%, respectively) relative to the full index I_1. Therefore I_2 or I_3 which incorporated milk yield and fat or protein yield are considered the best criteria, from an economic and protocol view point, of selection for genetic improvement of yield traits of Friesian cows. The present results indicated that genetic improvement for yield traits of cows could be achieved through multiple trait selection based on reduced index including milk yield with either of fat yield or protein yield.

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التحسين الوراثى لصفات إنتاج اللبن فى الهولشتين الألمانى عن طريق الأدلة الإنتخابية

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تم استخدام ٢٠٥٠٠ سجل حليب للموسم الأول لأبقار الهولشتين الألمانى لعدد ١٠٠٣ أب من ٢٣ قطيع وذلك لتقدير المعايير الوراثية والمظهرية لمحصول اللبن، محصول الدهن، محصول البروتين فى موسم الحليب الأول و عمل التوليفات المختلفة من الأدلة الإنتخابية لهذه الصفات. ولقد استخدم النموذج الخطى المختلط والمشتمل على تأثير كل من سنة وموسم الولادة والقطيع كعوامل ثابتة والعمر عند أول ولادة كعامل مستقل وتأثير الطلوقة كعامل عشوائى. و كانت النتائج كالتالى:

١- بلغ متوسط محصول اللبن والدهن والبروتين فى الموسم الأول ٦٠٩٦، ٢٥٣ و ٢٠١ كجم على التوالى.

٢- كانت تقديرات المكافئ الوراثى ٠,٣٥±٠,٠٢، ٠,٢٩±٠,٠٢، ٠,٢٩±٠,٠٢ لمحصول اللبن، الدهن والبروتين فى الموسم الأول على الترتيب.

٣- جميع قيم الارتباطات الوراثية والمظهرية كانت موجبة ومرتفعة وتراوحت من ٠,٦٦ إلى ٠,٩٢.

٤- تم تكوين أربع أدلة انتخابية لتحسين صفات اللبن وراثيا فى الهولشتين الألمانى باستخدام الثلاث صفات المدروسة.

٥- تراوحت قيم التحسين الوراثى المتوقع فى الجيل لمحصول اللبن من ٣٣٨,١٦ إلى ٣٤٤,١٨ كجم ولمحصول الدهن من ٤,١١ الى ١٠,٨١ كجم ولمحصول البروتين من ٧,٥٥ الى ٧,٩٨ كجم.

٦- أعلى تحسين وراثى متوقع فى الجيل فى محصول اللبن والبروتين تم الحصول علية من الدليل الإنتخابى الثالث بينما تم الحصول على أعلى تحسين وراثى متوقع لمحصول الدهن من الدليل الإنتخابى الرابع.

٧- ينصح باستخدام الدليل الأول (كفاءة الدليل =٠,٦٦) والذى يشتمل على الثلاث صفات المدروسة كوسيلة فعالة للتحسين الوراثى فى صفات إنتاج اللبن فى أبقار الهولشتين الألمانى وذلك فى حالة إذا ما أجرى الإنتخاب فى نهاية الموسم الأول.