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Selection Subindices for Improvement of Milk, Fat or Protein Yield in Holstein-Friesian Cows

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FIRST lactation milk records on 10314 Holstein-Friesian cows were used to estimate heritability of and genetic and phenotypic correlations between milk, fat and protein yields. Cows were daughters of 228 sires, each represented by at least 10 daughters. Restricted Maximum Likelihood procedure was used to estimate variance and covariance components between and within sires. A mixed model with a fixed effect of herd-year-seasons and a random effect of sires was used. Four selection subindices based on two or three variates (milk, fat and/or protein yield) were constructed to be used to improve just one trait (i.e. to select for milk or fat or protein yield). Selection subindices for milk yield based on milk with fat or with protein were from 98 to 100% as effective in selection as the three-variate subindex. Expected genetic gains for milk yield were from 196 to 200 kg per generation achieved by one standard deviation of selection differential on the subindex. Selection subindex without protein is nearly as effective as subindices that included protein. In the absence of fat or protein yields, selection based on milk yield resulted in decreasing milk yield by less than 5% as compared with the 3-variate subindex. Selection subindex based on milk and fat for improving fat yield is recommended. Using a selection subindex based on milk and fat yields for genetic improvement of protein yield resulted in a decrease of 0.4 kg in genetic gain of protein yield per generation (achieved by one standard deviation of selection differential) with a decrease of around 7% in the accuracy of selection as compared with the other subindices.

Key words : Holstein, Friesian cows, selection, milk fat and protein.

Breeding programs should emphasize important traits and reflect changes of the value of these traits due to the size of the market demand and changing the milk pricing system. Therefore, selection programs could differ not only between countries but also between breeders within a country. In countries with a big market for liquid milk, selection has been mainly on milk yield, whereas in countries which produce butter for export, the selection has been mainly on fat yield. However, breeder should place more emphasis on protein if their milk is used for cheese. Protein content of milk is also of increasing importance because of shifts of consumption patterns and changes of the relative cost of energy (Kennedy, 1982; Hillers, 1984). At the same time, the cost of evaluating protein in milk has decreased in the last 20 yr because of changes of testing procedures (Hillers, 1984) since the cost of evaluating a trait is also a variable that must be considered. Hillers (1984) cited that protein content is evaluated routinely for many cows in the Dairy Herd Improvement program (USA) at no additional cost to the breeders. For the improvement of a trait related to other traits, the most efficient procedure of using the available information is usually to construct a set of selection subindices (Henderson, 1963; Cunningham, and Mahon, 1977). Therefore, the objectives of this study were to construct several selection subindices for the improvement of just one trait milk, fat or protein yield of Holstein-Friesian cows and to compare the effectiveness of these subindices in selecting for that trait.

Material and Methods

Records of first lactation production on daughters of 228 Holstein-Friesian sires were supplied by the milk Marketing Board of England and Wales (MMB). They included 10314 305-days records of milk, fat and protein yields. Sires (bulls) entered the MMB's Dairy Progeny Testing Scheme (DPTS) in 1972 and 1973. Each sire was represented by at least 10 daughters. Seasons of calving were defined as December to March, April to July and August to November according to MMB classification. The numbers of effective daughters were determined and sires with zero effective daughters after absorption of herd-year-season of calving (HYS), were discarded.

Restricted Maximum Likelihood (REML) algorithm (Patterson and Thompson, 1971; Meyer, 1983) were used to estimate between and within sires components of variance and covariance for milk, fat and protein yields. The following mixed model was used :

$$Y_{ijk} = \mu + H_i + S_j + e_{ijk}$$

where : Y_{ijk} represents milk, fat or protein of the kth daughter of the jth sire in the ith herd-year-season of calving, μ represents the underlying population mean, H_i represents the fixed effect of the ith herd-year-season (absorbed), S_j represents the random effect of the th bull, and e_{ijk} represents the random residual component for the kth daughter of the jth bull in the ith herd-year-season.

The algorithm used an iterative solution scheme. Three rounds of iteration were carried out in estimating variance and covariance components between and within sires. Maximum difference convergences were below 0.1% for the sire component and below 0.01 for within sire component. Heritabilities and genetic and phenotypic correlations were estimated (Table 1) from variance and covariance components (Ashmawy and Khalil, submitted for publication).

TABLE 1. Estimates of heritability (on diagonal & underlined), and phenotypic (above diagonal) and genetic (below diagonal) correlations used in the construction of selection subindices.

Variate		X_1	X_2	X_3
Milk yield	(X_1)	$\underline{.25}$	.87	.94
Fat yield	(X_2)	.76	$\underline{.24}$	.89
Protein yield	(X_3)	.89	.80	$\underline{.23}$

Four cow selection subindices for each trait : milk, fat or protein yield were constructed using 2 or 3 variates (milk, fat and/or proteins yields). The selection subindex for a cow α will be of the form $I_\alpha = \Sigma b_i x'_i$ $i=1,2,3$ where x'_is are records on α and the b's are weighting factors (*i.e.* partial regression coefficients). A Fortran Selind Computer Program (Cunningham and Mahon, 1977) was used for construction of the subindices. The program required the following information :

P : a 3 × 3 matrix of phenotypic covariances of X— variates (milk, fat and protein yields).

G : a 3 × 1 matrix of genotypic covariances between the 3 variables in X— variates and Y— trait (milk, fat and protein yields).

C : a scalar matrix of genotypic variance of Y-trait.

Partial regression coefficients (b's) were estimated as $P^{-1}G$ where P^{-1} is the inverse of P. Variance of a subindex was $b'Pb$ where b' is the transpose of b, *i.e.* the transpose of the vector of partial regression coefficients. Correlation of a subindex and the trait was the square root of $(b'G/C_{ii})$. The value of each of the three variates (VX) in the subindex, *i.e.* the percent reduction in rate of genetic gain if variate is dropped from the subindex, can be obtained for the ith variate as :

$$VX = 100 - [\text{square root of } ((b'Pb - b_i^2/W_{ii}/b'Pb) * 100]$$

where W is a diagonal element of P^{-1}. The expected genetic gain in each trait (EG) equals to the selection intensity (i) times the square root of the variance of the subindex (σ_I), *i.e.* $EG = i\sigma_I$.

Results and Discussion

Partial regression coefficients of different selection subindices for the improvement of just one trait (*i.e.* milk, fat or protein yield), using all different combinations of two or three variates milk (x_1), fat (x_2) and/or protein (x_3) yields are presented in Table (2). The first subindex (I1) is designed to use the three variates while the others (reduced subindices) included only two variates as a criterion of selection.

Selection for milk yield

The following selection subindices for milk yield were constructed :

$$I1 = 0.5420\ x_1 - 2.9081\ x_2 - 6.9573\ x_3$$

$$I2 = 0.4047\ x_1 - 3.7102\ x_2$$

$$I3 = 0.5270\ x_1 - 8.5586\ x_3$$

$$I4 = -0.0407\ x_2 + 8.2406\ x_3$$

The standard deviation for the subindices ranged from 160 kg for I4 to200 kg for I1 (Table 2).

The correlation between the subindex and milk yield trait, r_{IG}, for I1 indicated that if the 3 variates are used in a subindex, the

TABLE 2. Selection subindices (T's), variances (σ^2_I), value of each variate (VX), **expected** genetic gain in each trait (EG), **correlation of subindex and each trait** (r_{IG}) and the **efficiency (RE) of the subindex relative to the first subindex.**

	I1		I2		I3		I4	
	b*	VX+	b	VX	b	VX	b	VX
For milk yield :								
1. Variates								
Milk (X_1)	0.5420	20.0	0.4047	27.1	0.5270	19.6		
Fat (X_2)	-2.9081	0.5	-3.7102	2.6			-0.0407	0.0
Protein (X_3)	-6.9573	2.1			-3.5586	4.2	8.2406	10.8
2. σ^2_I	40072		38400		39664		25663	
3. EG++ (kg)	200		196		199		160	
4. r_{IG}	0.56		0.55		0.56		0.45	
5. RE to I1	100		97.9		99.5		80.0	
For fat yield :								
1. Variates								
Milk (X_1)	0.0004	0.0	-0.0041	2.0	0.0039	1.4		
Fat (X_2)	0.4423	25.4	0.3828	25.2			0.4437	26.4
Protein (X_3)	-0.2299	1.9			0.1413	1.6	-0.2188	3.8
2. σ^2_I	49.3		47.5		27.5		49.3	
3. EG++ (kg)	7.0		6.9		5.2		7.0	
4. r_{IG}	0.55		0.54		0.41		0.55	
5. RE to I1	100		98.2		74.7		100	

TABLE 2. (Cont.).

	I1		I2		I3		I4	
	b*	VX+	b	VX	b	VX	b	VX
For protein yield :								
1. Variates								
Milk (X_1)	0.0002	0.0	0.0065	10.7	—0.0003	0.0		
Fat (X_2)	—0.0598	0.8	0.0230	0.2			—0.0592	0.8
Protein (X_3)	0.3190	7.0			0.2694	6.4	0.3237	17.0
2. σ^2_I	26.1		22.5		25.7		26.1	
3. EG++ (kg)	5.1		4.7		5.1		5.1	
4. r_{IG}	0.51		0.48		0.51		0.51	
5. RE to I1	100		92.8		99.2		100	

*b Values are the partial regression coefficients of the subindex.

\+ Values of each X— variate in subindex (= percentage reduction in rate of genetic gain for trait if variate is omitted).

++ The value of the genetic gain in each trait achieved by one standard deviation on the subinder.

genetic value for milk yield of a cow can be estimated as 56% as accurately as it would be if the additive genotype of each cow were completely known. Selection subindices based on milk yield with fat yield (I2) or with protein yield (I3) were from 98 to 100% (Table 2) as efficient as the three variates subindex (I1) in estimating the genetic value for milk.

Estimates of expected genetic gain in milk yield ranged from 196 to 200 kg per generation achieved by one standard deviation on the subindex (Table 2). Selection without protein is nearly as efficient as selection including protein. This is in close agreement with the findings of Anderson *et al.* (1978), Kuipers and Shook (1980) and Mbah and Hargrove (1982). They reported that the extra cost of protein testing might not be recoverable by the extra value of genetic gain from selection based on an index including protein. However, protein content is now evaluated routinely for many cows in the Dairy Herd Improvement program with no additional cost to the breeders (Hillers, 1984).

The fourth subindex including fat and protein yields is considered the poorest one for the improvement of milk yield. It resulted in an about 20% decrease in the expected gain as well as in accuracy compared with I1.

As expected, the contribution of milk yield in each subindex was higher than protein and fat yields in a descending order. If milk yield was dropped from any subindex, genetic progress would be reduced by 19.6 to 27.1%. The corresponding values ranged from 2.1 to 10.8% for protein yield and from 0 to 2.6% for fat yield.

Expected direct response in milk yield was 191 kg as reported by Ashmawy and Khalil (submitted for publication) while the maximum expected gain achieved using a 3-variate subindex was 200 kg with an increase of less than 5%. This implies that, in countries with no information on protein or fat yield, a subindex containing only milk yield as a criterion for selection is recommended in practice with little compromise in gain assuming similar phenotypic and genetic parameters.

Selection for fat yield

The following selection subindices for fat yield were obtained :

$$\begin{aligned}
I1 &= 0.0004\ x_1 + 0.4423\ x_2 - 0.2299\ x_3 \\
I2 &= -0.0041\ x_1 + 0.3828\ x_2 \\
I3 &= 0.0049\ x_1 + 0.1413\ x_3 \\
I4 &= 0.4437\ x_2 - 0.2188\ x_3
\end{aligned}$$

with standard devations ranging from 5.2 to 7.0 kg (Table 2).

The percent reduction in rate of genetic gain for the genotype of fat yield if they were dropped from the subindex is shown in Table (2). The value of the fat variate was around 25% in different subindices constructed. The corresponding values were 1.6 to 3.8% for protein yield and 0 to 2% for milk yield. Khalil and Soliman (1989) indicated that milk yield contributed little to the subindices used to select for fat yield. The higher values for protein yield might be due to the higher genetic correlation between fat and protein yields than that between fat and milk yields (0.80 vs. 0.76, Table 1).

A comparison of the r_{IG}'s estimates for selection subindices. constructed (Table 2) shows that the breeding value of a cow for fat yield can be estimated as 34% more accurately when using I1, I2 or I4 as compared to using I3. However, efficiency of selection is dependent on genetic correlation more than phenotypic correlations among variates (Smith, 1983).

The expected genetic gain in fat yield for I1, I2 or I4 was 7 kg compared with 5 kg for I3 (Table 2). Accordingly it appears that a subindex (I2) which includes milk and fat yields is recommended for the improvement of fat yield.

Selection for protein yield

The following selection subindices for protein yield were constructed (Table 2) :

$$\begin{aligned}
I1 &= 0.0002\ x_1 - 0.0598\ x_2 + 0.3190\ x_3 \\
I2 &= 0.0065\ x_1 + 0.0230\ x_2 \\
I3 &= -0.0003\ x_1 + 0.2694\ x_3 \\
I4 &= - 0.0592\ x_2 + 0.3237\ x_3
\end{aligned}$$

Standard deviations for these subindices constructed ranged from 4.7 to 5.1 kg.

Genetic progress would be reduced by 6 to 17% if protein yield was dropped from the subindex. The corresponding values were from 0 to 10.7% for milk yield, and were from 0.2 to 0.8% for fat yield.

Correlation coefficints (r_{IG}'s) between a subindex and protein trait yield were 0.48 for I2 and 0.51 for the other subindices.

Expected genetic gain in protein yield was 5.1 kg when using I1, I3 or I4 compared with 4.7 kg when using I2. However, it is doubtful whether the increase of 0.4 kg in genetic gain of protein yield per generation achieved by one standard deviation of selection differential with only 7% increase in the accuracy (Table 2) are enough justification to recommend the use in practice of either I1, I3 or I4 over I2 including milk and fat yields. Using protein in the subindex for selecting for protein yield is depended on the economics of its estimating in the milk (Mbah and Hargrove, 1982; Hillers, 1984).

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ادلة انتخاب جزئية لتحسين كمية اللبن أو الدهن أو البروتين فى ابقار هولستين – فريزيان

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اجريت هذه الدراسة باستخدام بيانات ١٠٣١٤ موسم حليب اول لابقار هولستين فريزيان وذلك لتقدير المكافىء الوراثى والارتباطات الوراثية والمظهرية بين كمية اللبن والدهن والبروتين . وهذه الابقار هى بنات ٢٢٨ طلوقة وكان لكل طلوقة ١٠ بنات على الاقل .

استخدمت طريقة دالة الامكان الاعظم المقيدة لتقدير مكونات التباين والتغاير بين وداخل الطلائق . استخدم نموذج رياضى يحتوى على التأثير الثابت للقطيع – سنة – موسم وضع . والتأثير العشوائى للطلائق .

استخرجت ٤ ادلة جزئية لانتخاب صفة واحدة فقط اما اللبن أو الدهن أو البروتين باستخدام متغيرين أو ثلاثة متغيرات من كمية اللبن ، الدهن و (أو) البروتين . كانت كفاءة الادلة الجزئية للانتخاب لكمية اللبن والتى اعتمدت على كمية اللبن والدهن أو كمية اللبن مع البروتين يمثل ٩٨ الى ١٠٠٪ كما لو استخدم دليل يعتمد على الثلاث متغيرات . تراوحت كمية التحسين الوراثية المتوقعة لكمية اللبن بين ١٩٦ الى ٢٠٠ كجم لكل جيل على اعتبار ان شدة الانتخاب مقدارها الواحد الصحيح والتى استخدمت كاساس للمقارنة فقط . اما كفاءة ادلة الانتخاب الجزئية المحتوية على البروتين فكانت كالتى بدونه . وفى غياب كمية الدهن أو البروتين فان الانتخاب باستخدام كمية اللبن فقط يؤدى الى خفض فى كمية التحسين الوراثى المتوقعة بما لايزيد عن ٥٪ بالمقارنة بدليل يحتوى على الثلاث متغيرات .

وبالنسبة للتحسين الوراثى فى كمية الدهن فيوصى باستخدام ادلة انتخاب جزئية معتمدة على كمية اللبن وكمية الدهن . وللتحسين الوراثى فى كمية البروتين فان دليل انتخاب جزئى محتويا على كمية اللبن والدهن يؤدى الى خفض فى كمية التحسين الوراثى المتوقعة فى البروتين مقدارها ٤ر٠ كجم فى الجيل مع اعتبار ان شدة الانتخاب مقدارها الواحد الصحيح مع نقص فى دقة التقدير تقدر بحوالى ٧ ٪ مقارنة ببقية ادلة الانتخاب الجزئية .