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Single and Multi-Trait Selection for Lactation in Holstein-Friesian Cows

A.A. Ashmawy* and M.H. Khalil**

**Department of Animal Production, Faculty of Agriculture, Ain Shams University, Cairo, and **Department of Animal Production, Faculty of Agriculture at Moshtohor, Zagazig University, Banha Branch, Qalyoubia, Egypt.*

AN EVALUATION for cow productivity traits of British Holstein-Friesian cattle was carried out on 10314 first lactation records including 228 tested sires. Yields of 305-day milk, fat and protein were the traits examined. Restricted Maximum-Likelihood procedure was used to estimate variance and covariance components between and within sires. Analysis was carried out using a mixed model with a herd-year-season as a fixed effect and sires as a random effect. Heritabilities were 0.25, 0.24 and 0.23 for milk, fat and protein yields, respectively. Genetic and phenotypic correlations were positive and of high magnitude and ranged from 0.76 to 0.94. Single-trait selection for milk yield resulted in an expected increase of 4.4, 3.2 and 3.4 as a percentage of the overall mean of milk, fat and protein yields, respectively. Selection for fat yield compared with selection for milk yield resulted in —1.12, +0.93 and —0.29% of milk, fat and protein, respectively, while selection for protein yield resulted in —0.07, 0.0 and +0.29%. Therefore, selection for milk yield is more economic than selection for fat or for protein yield. Five indices of selection for improving yield traits of cows were constructed involving all combinations of two or three traits studied. Fat or protein yields did not contribute significantly to the different selection indices constructed while milk yield made a large contribution. Considerable genetic improvement for yield traits of cows might be achieved through multiple-trait selection based on reduced index including milk yield with either of fat yield or protein yield.

Key words : Holstein-Friesian cows, lactation, selection, single and multi-trait.

Pricing systems of milk, in recent years, depend not only on yield and fat content but also on protein percentage (Mbah and Hargrove, 1982; Dommerholt and Wilmink, 1986; de Jager and Kennedy, 1987) because of the importance of protein in human nutrition and for the industrial value of the milk products. However, genetic im-

provement of a certain milk trait using selection may affect the other traits, by increasing or decreasing, due to high genetic correlations between them. In this situation, the most efficient tool for several-traits selection, using the available information, is usually to construct a selection index (Hazel, 1943; Cunningham, 1969a&b).

The main objectives of this study were:

(1) to estimate the genetic and phenotypic parameters of first-lactation yield traits for Holstein-Friesian cows, and

(2) to evaluate and compare results of single and multiple yield-trait selection for milk, fat and/or protein.

Material and Methods

Data of 10314 first-lactation records were extracted from the files supplied by the Milk Marketing Board (MMB) of England and Wales on British Holstein-Friesian cows. Cows were daughters of 228 tested sires from the MMB's Dairy Progeny Testing Scheme (DPTS) in the years of 1972 and 1973. Each sire was represented by at least 10 daughters. Only 305-day first-lactation records were used. Abnormal lactation records affected by diseases or by disorders such as abortion were excluded. 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 eliminated. This yielded 228 DPTS sires, 4860 HYS subclasses and 5226 residual degrees of freedom.

Restricted Maximum Likelihood (REML) algorithm (Patterson and Thompson, 1971; Meyer, 1983) was used to obtain Best Linear Unbiased Prediction (BLUP) sire solution and to estimate between and within sire components of variances and covariances for milk traits (milk, fat and protein yields). The following mixed model was used :

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

where: Y_{ijk} = an individual record; μ = overall mean; H_i = fixed effect of the ith herd-year-season of calving subclasses (absorbed); S_j = random effect of the jth sire, and e_{ijk} = random error component associated with the individual record of the ijkth cow.

The algorithm used an iterative solution scheme. Three rounds of iteration were carried out in estimating heritabilities and their standard errors. Maximum difference convergences were below 0.1% for the sire component and below 0.01 % for within-sire component. Genetic and phenotypic correlations were estimated from variance and covariance components. Standard errors of genetic correlations were estimated approximately by the formula given in Falconer (1981). According to Falconer (1981), expected direct and correlated responses to selection for one trait were estimated as :

$$R = ih^2\sigma_p \quad \text{and} \quad CR = ih_x h_y r_g \sigma_{py}$$

where R = the direct response in selection for X trait, h^2 = the heritability estimate of X trait, σ_p is the standard deviation of phenotypic values, CR = the correlated response in Y trait, h_x and h_y are the square roots of heritability estimates of trait X and trait Y, respectively ; r_g is the genetic correlation between the two traits ; and σ_{py} is the standard deviation of phenotypic values of trait Y. The expected genetic changes in one generation were calculated assuming selection based on cow side. The intensity of selection for a trait was set to 1.0 for, only, the purpose of comparisons.

Five selection indices for improvement of yield traits of Holstein-Friesian cows (involving all combinations of two or three traits studied) were constructed using the general Fortran Computer Program cited by Cunningham (1977). The information required in constructing a cow genetic index were specified in the following four vectors and three matrices :

$\underline{y}$: a vector of additive genetic values for ith yield traits included in the aggregate genotypic value.

$\underline{a}$: a vector of constants representing the relative economic values of yield traits, assuming the relative economic values of milk: fat as 1 : 13 based on prices values for milk and milk butterfat cited from Dairy Facts and Figures (1986). According to

Dommerholt and Wilmink (1986), the protein value is almost the same as that of fat. Hence, the relative economic values for yields of milk, fat and protein were set to be 1 : 13 : 13. Several authors have concluded that the efficiency of an index is not very sensitive to changes in the economic weights. In this respect, Vandepitte and Hazel (1977) showed comparatively large changes (*e.g.* by a factor of 2) in economic weights may have small effects on selection efficiency. Moreover, it is possible that a certain degree of variation in relative economic weights will not change expected selection response very much (Lin, 1978).

$\underline{x}$: a vector of phenotypic measures for the $\underline{n}$ variables or sources of information to be included in the index (*i.e.* milk, fat and/or protein yields).

$\underline{b}$: a vector of weighting factors to be used in the index (*i.e.* partial regression coefficients).

P : a squared matrix of phenotypic variances-covariances of the three variables in jth variates.

G : a matrix of genotypic covariances between the $\underline{n}$ variables in jth variates and the ith traits in $\underline{y}$.

C : a squared matrix of genotypic variances-covariances of $\underline{y}$-traits.

The partial regression coefficients ($\underline{b}$'s) were computed as $\underline{b} = P^{-1}\underline{Ga}$ where P^{-1} is the inverse of P (in matrix notation). Percentages of total economic-genetic gain accounted for by gain in each ith trait was calculated according to Cunningham *et al.* (1970) as $[b'G_i/b'Ga]\ [a_i]\ (100)$, where a_i is the relative economic value of the ith trait. The correlation of the calculated index with the total aggregate genotype (r_{IH}) was estimated as $r_{IH} = b'Ga/a'Ca$

The contribution which each j variate makes to the genetic gain of the total genotype (*i.e.* percent reduction in rate of overall genetic gain if that variate is omitted) was calculated as $100 - [((b'Ga - (b^2/W_{jj}))/(b'Ga))\ (100)]^{1/2}$, where W_{jj} is the jth diagonal element of P^{-1}. The derivation of the method used to cal-

culate the value of each variate in an index is given by Cunningham (1969b) and Cunningham *et al.* (1970). The expected genetic change (ΔG) in any trait is the product of the standard deviation of the index (σ_I) multiplied by the intensity of selection (i) and regression of each trait on the index (b_{YI}), *i.e.* $\Delta G = (\sigma_I)\ (i)\ (b_{YI})$.

Results and Discussion

Means and coefficients of variation (CV) of first lactation milk, fat and protein yields are presented in Table (1). The CV were ranging between 22 to 23%. The estimates of 20% for yield traits were reported by de Jager and Kennedy (1987). The CV of fat yield was slightly high compared with those of milk and protein.

Genetic parameters

Heritability estimates for milk, fat and protein yields were 0.25, 0.24 and 0.23, respectively (Table 2). Similarly, Hill *et al.* (1983) reported a corresponding estimates of 0.25, 0.24 and 0.21, respectively on another set of data for the same breed. Another British study (Meyer, 1984) found a close estimates of 0.25 and 0.24 for milk and fat yields, respectively. According to the moderate heritability estimates reported herein, it can be concluded that the genetic improvement in milk-production traits can be achieved through selective breeding program.

Genetic correlations between yield traits were positive and high. The estimates were 0.76 for milk and fat, 0.89 for milk and protein and 0.80 for fat and protein (Table 2). The corresponding estimates of de Jager and Kennedy (1987) were 0.57, 0.82 and 0.66, respectively. High estimates of phenotypic correlations among yield traits (Table 2) were also observed (estimates ranged from 0.87 to 0.94). However, estimates of genetic and phenotypic correlations obtained herein agree closely with the corresponding literature averages reported by Meyer (1984) on another set of data for the same breed. As also noted by other investigators (Hargrove *et al.*, 1981; de Jager and Kennedy, 1987), phenotypic correlations were generally similar to the corresponding genetic correlations in directions and were higher in magnitudes.

TABLE 1. Means, coefficients of variation (CV), phenotypic and genetic components of variances (on diagonal) and covariances (below diagonals) of yield traits for first lactation of Holstein-Friesian cows*.

Trait	Mean (kg)	CV (%)	Phenotypic component			Genetic component		
			M	F	P	M	F	P
Milk yield (M)	4295	22	436472			126103		
Fat yield (F)	162	23	13621	568		3406	161	
Protein yield (P)	138	22	12144	416	382	3132	101	99

* Number of lactation records was 10314.

TABLE 2. Estimates of heritability (on diagonal) and phenotypic (above diagonal) and genetic (below diagonal) correlations traits.*

Traits	M	F	P
Milk yield(M)	0.25 (0.042)	0.87	0.94
Fat yield(F)	0.76 (0.051)	0.24 (0.041)	0.89
Protein yield(P)	0.89 (0.025)	0.80 (0.044)	0.23 (0.040)

* Standard errors of estimates are given in parentheses adjacent to estimates.

TABLE 3. Expected direct (diagonal) and correlated response (off-diagonal) from one generation of selection of Holstein-Friesian cows for a single trait.*

Selected trait	Expected genetic response in yields (kg)		
	Milk	Fat	Protein
Milk yield	191	5.2	4.7
Fat yield	143	6.7	4.3
Protein yield	160	5.2	5.1

* Selection intensity equals 1.0.

Single-trait selection

The phenotypic and genetic variances and covariances given in Table (1) are used to estimate the response to selection for one trait in one generation of cow selection. The selection intensity was set to 1.0 for, only, the purpose of comparative study of different yield traits under the present study. Expected direct and correlated responses are given in Table (3). Direct selection on a single-trait resulted in higher advances, in the desired direction, for all traits. However, selection for any trait would result in correlated increase in the others. The expected direct response of fat yield was much higher by 31% than direct response of protein yield. It could be due to that genetic variation and heritability estimates for fat yield were high (Tables 1 and 2).

Selection for milk yield resulted in an increase of 191, 5.2 and 4.7 kg of milk, fat and protein, respectively. Responses per generation expressed as percentages of the overall mean were 4.4, 3.2 and 3.4, respectively. Selection for fat, compared with selection for milk, resulted in —1.12, +0.93 and —0.29% of milk, fat and protein, respectively as calculated from Table 3, while selection for protein yield resulted in —0.07, 0.0 and +0.29%. Therefore, selection for milk yield is more economic than selection for fat or for protein. Similarly, Kennedy (1982) and de Jager and Kennedy (1987) indicated that selection for any yield trait would tend to increase yields of other traits.

Multi-trait selection

For multi-trait selection, the following selection indices (Table 4) were constructed :

$$I1 = 0.5491 \times 1 + 3.0651 \times 2 - 5.7911 \times 3$$
$$I2 = 0.4348 \times 1 + 1.5651 \times 2$$
$$I3 = 0.5732 \times 1 - 3.2190 \times 3$$
$$I4 = 4.9569 \times 2 + 9.6046 \times 3$$
$$I5 = 0.3844 \times 2 + 0.1049 \times 3$$

Where : $\times 1$ = milk yield, $\times 2$ = fat yield and $\times 3$ = protein yield; all yields (in kg) are of 1st alctation. Indices I1, I2, I3 and I4 are used for the improvement of all traits while I5 is used for improving fat and protein yields only. The first index (I1) was considered the full index which included the three variates (*i.e.* milk, fat and protein yields) and was assumed to be the base of comparison while other indices (I2, ..., 15) are defined as reduced ones.

The contribution of each variate to the index can be measured as the percentage of reduction in the rate of genetic gain for aggregate genotype if that variate is omitted. The reduction percentages (VX) in rate of genetic progress for aggregate genotype given in Table (4) indicate that fat and protein yields contributes little to most selection indices constructed (I1, I2 and I4). Gjedrem (1972) reported that omitting one trait (using two traits instead of three traits) was always less efficient and in some situations, negative rather than positive responses might be obtained. The

TABLE 4. Selection indices (I) for milk traits of Holstein-Friesian cows, value of each X-variate in index (VX), percentage of total gain attributable to each trait ($\Delta\bar{H}$) and expected genetic change (kg) in each traits (ΔG).*

Index	Variates		
	Milk yield (×1)	Fat yield (×2)	Protein yield (×3)
I1 :			
b	0.5491	3.0651	—5.7911
VX	7.4	0.5	0.6
$\Delta\bar{H}$	22.3	18.3	59.4
ΔG	191.2	5.5	4.5
I2 :			
b	0.4348	1.5651	
VX	10.7	0.2	
$\Delta\bar{H}$	58.7	22.0	19.3
ΔG	188.0	5.9	4.7
I3 :			
b	0.5732		—3.2190
VX	0.2		8.4
$\Delta\bar{H}$	60.7	20.6	18.7
ΔG	194.2	5.1	4.6
I4 :			
b		4.9569	9.6046
VX		1.6	4.1
$\Delta\bar{H}$	52.9	25.9	21.2
ΔG	157.6	5.9	4.9
I5 :			
b		0.3844	0.1049
VX		7.2	0.4
$\Delta\bar{H}$		59.6	40.4
ΔG		6.6	4.5

*b : values of the coefficients of the index (i.e. partial regresion coefficients).

VX : percentage reduction in rate of genetic gain for aggregate genetype if variate is omitted.

ΔG : Expected genetic change in each trait achieved by one standard deviation on the index.

low contribution of milk yield variate in I3 (Table 4) may be due to the high genetic correlation between milk and protein and due to the high economic value of protein as compared with milk.

The expected genetic change (ΔG) in any trait achieved by the index is the genetic standard deviation for the trait multiplied by the correlation coefficient of the index and the genetic value for such trait, assuming selection intensity of one as mentioned before. All the indices provided relatively large increase in yields of milk, fat and protein. The genetic improvement (ΔG) ranged between 157.6 and 194.2 kg for milk, between 5.1 and 6.6 kg for fat and between 4.5 and 4.9 kg for protein. A relatively large difference is noticed for milk yield (36.6 kg of milk vs 1.5 kg of fat and vs 0.4 kg of protein). Therefore, it could be stated that considerable genetic improvement for cow productivity might be achieved through selection for milk yield. However, there were little difference in ΔG of milk traits between each pair of I1, I2 and I3. Using I4, as a criterion of selection for fat and protein, resulted in an increase of 157.6 kg as an indirect response for milk yeld, as compared with 191 kg for I1. The difference was 0.78% as a percentage of the overall mean. Similarly, the differences in fat and protein yields were 0.25 and 0.29%, respectively, in favor of I4. Therefore, ΔG in milk yield was high from using the reduced indices (I2 or I3) as compared to I4 and I5, de Jager and Kennedy (1987) reported that selection with equal values for fat and protein yields would result in lower response in milk but higher responses in fat and protein in a descending order.

The value, in economic units, of the genetic gain (kg) in aggregate genotype achieved by one standard deviation on the index are presented in Table (5). The first index (I1) which included all the variables would result in slight increase in the value of the genetic gain over I2 and I3 and relatively high increase compared with 14 or 15 ((149) (1) + (6.6) (13) + 4.5) (13) = 293.3)).

Correlation coefficients ($r_{I\times}$) between each index constructed and each trait (milk, fat and protein) in the aggregate genotype are presented in Table (5). Higher correlations between each index and milk yield compared to those for fat and protein were observed. However, all the coefficients ranged between 0.40 to 0.55. These moderate or high sizes of correlations between each index and milk

traits indicate that selection per generation on any cow index would actually lead to a moderate (or may be a high) genetic increase in the yield traits of Holstein-Friesian cows. Therefore, cow indices and sire evaluation based on cow indices (Kennedy, 1982) would lead to a moderate (or substantial) increase in yield traits.

The chief measure of the utility of an index is based on its correlation with the aggregate genotype, r_{IH}, where the genetic response to selection is proportional to this correlation. Correlation coefficients of indices with total genotypes were around 0.5 (Table 5). However, The fourth index (I4) was the lowest in accuracy. Adding protein (or fat) yield in the index 12 (or 13), as demonstrated by I1, the accuracy of index increased by 1.9%. While adding milk yield to the index I4, the accuracy increased by 8.2%. 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 thus have to be considered in estimating accuracy. de Jager and Kennedy (1987) reported that including protein in the index increased the accuracy of sire breeding value.

TABLE 5. Standard deviations (σ_I) for selection indices constructed, correlation of index with total genotype (r_{IH}), correlation of index with each individual trait (r_{IX}) and the relative efficiency (RE) of the index.

Item	Index				
	I1	I2	I3	I4	I5
σ_I+	321.8	320.1	320.2	298.0	144.3
r_{IH}	0.53	0.52	0.52	0.49	0.51
r_{IX1}	0.54	0.53	0.55	0.44	
r_{IX2}	0.44	0.43	0.49	0.47	0.52
r_{IX3}	0.45	0.48	0.46	0.49	0.45
RE to I1	100.0	98.1	98.1	92.4	96.2

+ This is the value, in economic units, of the genetic gain (kg) in aggregate genotype achieved by one standard deviation on the index.

Figures of relative efficiency (RE) given in Table (5) showed that of all the selection indices developed, I2 and I3 had the highest efficiency (98.1%) relative to the full index (I1). Therefore, I2 or I3 which incorporated milk yield and fat or protein yield are considered the best criteria, from an economic and practical viewpoint, of selection for the genetic improvement of yield traits of Holstein-Friesian cows. In this respect, Smith (1983) stated that the main factors controlling the efficiency of index selection are largely determined by the values of the factors ah^2, the product of the economic weight (per standard deviation) and the heritability of each trait, *i.e.* if one trait dominates the index (for instance milk yield herein), the efficiency will not be sensitive to changes in the economic weight of the other traits, but will be sensitive to the loss or reversal (to negative values) or weights for the originally important trait. Van Vleck (1978) and Kennedy (1982) indicated that including milk, fat and protein yields in the evaluation of dairy cattle offer little in economic advantage over milk and fat measures even if the price system of milk depends on protein yield besides milk and fat. Mbah and Hargrove (1982) found that selection indices without protein yield is nearly as effective as selection indices that include protein. They also stated that selection indices based on milk and fat yields only were 91 to 100% as effective as the indices included the three variates. de Jager and Kennedy (1987) found that expected selection responses for most traits were similar to responses of selection based on an index which did not include protein.

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الانتخاب لصفة أو لعدة صفات للادرار فى ابقار الهولستين فريزيان

عبد الحليم أنيس عشماوى * وماهـر حسب النبى خليل **

* كلية الزراعة ـ جامعة عين شمس ـ القاهرة

** وكلية الزراعة بمشتهر ـ جامعة الزقازيق ـ فرع بنها ـ القليوبية ـ مصر .

تم تقييم انتاجية ابقار الهولستين فريزيان البريطانية باستخدام بيانات الموسم الاول من الادرار لعدد ١٠٣١٤ بقرة (بنات ٢٢٨ طلوقة) وكانت الصفات المستخدمة هى محصول اللبن والدهن والبروتين خلال موسم حليب طولة ٣٠٥ يوما . استخدمت طريقة دالة الامكان الاعظم المقيدة لتقدير التباينات والتغايرات بين وداخل الطلائق لتلك الصفات . تم تحليل البيانات باستخدام نموذج يحتوى على تأثير ثابت (قطيع ـ سنة ـ موسم) بالاضافة الى الطلائق كتأثير عشوائى .

كانت قيم المكافىء الورائى لمحصول اللبن والدهن والبروتين هى ٢٥ر ، ٢٤ر ، ٢٣ر ، على التوالى وكانت معاملات الارتباط الورائى والمظهرى بين الصفات موجبة وذات قيم عالية حيث تراوحت بين ٧٦ر، الى ٩٤ ر، يؤدى الانتخاب لصفة محصول اللبن الى زيادة متوقعة فى محصول اللبن والدهن والبروتين مقدارها ٤ر٤ ، ٣ر٢ ، ٣ر٤ كنسبة مئوية من متوسط تلك الصفات على التوالى . ادى الانتخاب لمحصول الدهن بالمقارنة للانتخاب لمحصول اللبن الى عائد مقداره ـ ١٢ر١ ، + ٩٣ر٠ و ـ ٢٩ر٠ ٪ لمحصول اللبن والدهن والبروتين على التوالى بينما ادى الانتخاب لمحصول البروتين الى ـ ٠٧ر ، صفر ، + ٢٩ر٠٪ وعلى هذا فان الانتخاب لمحصول اللبن يكون اكثر اقتصادا من الانتخاب لمحصول الدهن أو البروتين .

استخرجت خمسة ادلة للانتخاب بفرض تحسين صفات اللبن للابقار حيث اشتملت الادلة على ثلاثة متغيرات أو متغيرين . كانت مساهمة كل من محصول الدهن أو البروتين ضئيلة بينما كانت المساهمة لمحصول اللبن كبيرة فى ادلة الانتخاب المستخرجة . يمكن تحقيق تحسينا وراثيا ملموسا لصفات اللبن للابقار من خلال استخدام دليل انتخابى يشتمل على محصول اللبن مع أى من محصول الدهن أو محصول البروتين .