

Genetic and Phenotypic Parameters for Production and Stayability in British Friesian-Holstein Cattle

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RECORDS from daughters of 480 British Friesian-Holstein sires in England and Wales were used to estimate variance and covariance components of production traits in the first lactation and stayability. A restricted Maximum Likelihood algorithm was used.

Heritabilities were 0.24, 0.23 and 0.22 for milk, fat and protein yields, respectively. The heritability estimates for stayability defined as either the number of lactations completed up to the 5th lactation or the survival up to a complete 2nd and 3rd lactation were 0.02.

Genetic and phenotypic correlations between milk production and stayability ranged from 0.31 to 0.42 and from 0.15 to 0.17, respectively.

Selection for stayability would not be effective due to its low heritability. However, sire selected for high milk in first lactation would lead to an increase in length of herd life.

Stayability or longevity is the survival rate of a sire's daughters to a specific age given that they have the opportunity to reach that age. Stayability may have an important bearing on economic return on investment in the dairy cattle and on their lifetime production (Freeman, 1981; Gill and Allaire, 1976; Hoque and Hodges, 1980; Hudson and Van Vleck, 1981).

Heritability estimates of stayability vary (Hoque and Hodges, 1980; Hudson and Van Vleck, 1981; Miller, Van Vleck and Henderson, 1967; Parker, Bayley, Fohrman and Plowman, 1960; Robertson and Barker, 1966) probably due to the choice of different measures of longevity and to the limited number of observations used in estimation. The relationship between first lactation production and stayability was found to be positively correlated in most investigations (e.g. Hinks, 1966; Robertson and Barker, 1966; De Lorenzo and Everett, 1982).

This paper presents a study of genetic and phenotypic parameters of milk production and stayability in British Friesian-Holstein cattle to investigate the importance of longevity in selection.

Material and Methods

Records of first lactation production on daughters of British Friesian-Holstein sires were obtained from the Milk Marketing Board of England and Wales (MMB). Complete lactations comprised 305-day records. The average age at first calving was 32 mo. Daughters of test sires (bulls) were considered from the MMB's Dairy Progeny Testing Scheme (DPTS) in the years 1970 through 1973. Each cow had the opportunity to have at least five lactations. Data were split into two sets according to years of sire testing, 1970 & 71 as set 1 and 1972 & 73 as set 2. Sires with no effective daughter numbers after absorption of herd - year - season of calving (HYS), were eliminated. The number of sires actually used in this study was 480. The data structure is given in Table 1.

Stayability is defined in three ways, first the number of lactation completed up the 5th lactation (NLC), the second the survival up to a complete 2nd lactation (S1) and the third as survival up to a complete 3rd lactation (S2). In S1 and S2, stayability was scored as one for cows alive up to the respective completed lactation and zero otherwise. Any cow left a herd for any reason was considered culled because of the absence of disposal reasons.

Seasons were defined as December to March, April to July and August to November according to MMB classification. HYS for stayability was assigned according to the date at first calving of every cow in the same manner as production.

The data of all traits were adjusted for age at first calving using constants which were obtained from least squares solutions assuming a mixed model with HYS absorbed and age at calving as a linear regression using the programme of Harvey (1977).

Restricted Maximum Likelihood (REML) algorithm (Patterson and Thompson, 1971 and K. Meyer, Personal communication, 1983) was used to estimate variance and covariance components between and within sires for each trait using the following model

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

where : Y_{ijk} = individual record ; μ = overall mean ; H_i = fixed effect of i th HYS ; S_j = effect of i th sire ; and e_{ijk} = residual error. Three rounds of iteration were carried out in estimating heritabilities and their standard errors for each trait in every data set. Maximum difference convergences were below 0.1% for the sire and 0.01% for within sire components.

Estimates of variance and covariance components between and within sires were pooled over the two sets of data weighted by their respective degrees of freedom (Table 1).

Genetic and phenotypic correlations were estimated from variance and covariance components before the iteration. Standard errors of genetic correlations were calculated using the formula given by Falconer (1981).

TABLE 1. Data Structure

| Set | Number of DPTS ¹ sires | Number of records | Number of HYS ² | Residual Degrees of freedom |
|-------------|-----------------------------------|-------------------|----------------------------|-----------------------------|
| 1 (1970&71) | 252 | 10698 | 4751 | 5695 |
| 2(1972&73) | 228 | 10314 | 4860 | 5226 |
| Total | 480 | 21012 | 9611 | 10921 |

¹Dairy Progeny Testing Scheme

²Herd-Year-Season

Results and Discussion

Means, estimates of variance components and heritability for all traits under study are presented in Table 2. Heritabilities were near 0.25 for milk, fat and protein yields. The present findings were similar to those reported by Hill, Edwards, Ahmed and Thompson (1983) on a similar data set of British Friesian-Holstein Cattle.

The estimates of heritability for stayability defined as NLC was small (0.022) and nonsignificant, in agreement with Parker *et al.* (1960). The estimate of 0.06 was reported by Robertson and Barker (1966). Heritability estimates for survival up to a complete 2nd lactation and up to 3rd lactation were found to be 0.021 and 0.022 respectively, in agreement with the estimates of Robertson and Barker (1966) for Friesian in Britain and Holstein-Friesian in U.S.A. The heritability estimate of S1 was smaller than the estimates for S2, as was theoretically expected since the proportions of survival up to the 2nd and the 3rd lactations were 0.70 and 0.49, respectively, and variance of binomial traits such as stayability increases as the proportion of each category approaches 0.5.

Estimates of genetic correlations between milk yield and each of stayability defined as NLC and S2 were 0.42 (Table 3), rather higher than that of 0.31 between the former trait and S1. Genetic correlation estimates between each of fat and protein yields and stayability followed the same pattern as those between milk yield and stayability (Table 3). The positive genetic and phenotypic correlation between milk yield and stayability as indicated in Table 3 are in agreement with many reports (*e.g.* Hudson and Van Vleck 1981).

TABLE 2. Estimates of means, variance components and heritabilities

| | Milk yield (kg) | Fat yield (kg) | Protein yield (kg) | NLC ⁺ | SI ⁺⁺ | S2 ⁺⁺⁺ |
|---|--------------------|-------------------|-----------------------|------------------|-------------------|-------------------|
| Set 1 : | | | | | | |
| Sire variance | 27256 | 34.62 | 22.24 | 0.001879 | 0 ⁺⁺⁺⁺ | 0.000229 |
| Error variance | 409767 | 555.71 | 371.03 | 1.53121 | 0.152686 | 0.168605 |
| Set 2 : | | | | | | |
| Sire variance | 23391 | 27.99 | 18.06 | 0.016435 | 0.001431 | 0.001619 |
| Error variance | 369919 | 494.17 | 330.77 | 1.88511 | 0.137981 | 0.183087 |
| Pooled estimates: | | | | | | |
| Mean | 4160 | 156.8 | 133.7 | 2.77 | 0.70 | 0.49 |
| Sire variance | 25227 | 31.14 | 20.05 | 0.009522 | 0.000751 | 0.000959 |
| Error variance | 388987 | 523.62 | 350.04 | 1.715759 | 0.145018 | 0.176157 |
| h ($\times 100$) | 24.4 | 22.5 | 21.7 | 2.2 | 2.1 | 2.2 |
| s.e. _b ² ($\times 100$) | 2.9 | 2.8 | 2.7 | 1.5 | 1.2 | 1.5 |

⁺ number of lactations completed up to the fifth lactation.
⁺⁺ survival up to the second lactation.
⁺⁺⁺ survival up to the third lactation.
⁺⁺⁺⁺ analysis would converge to negative value.

TABLE 3. Estimates of genetic and phenotypic correlations among traits⁺

| | M | F | P | NLC | SI | S2 |
|----------------------------|------|------------|------------|------------|------------|------------|
| Milk yield (M) | | 0.79(0.03) | 0.87(0.03) | 0.42(0.17) | 0.31(0.17) | 0.42(0.17) |
| Fat yield (F) | 0.86 | | 0.83(0.03) | 0.42(0.17) | 0.39(0.16) | 0.41(0.17) |
| Protein Yield (P). | 0.94 | 0.89 | | 0.49(0.16) | 0.31(0.19) | 0.47(0.16) |
| NLC | 0.17 | 0.16 | 0.17 | | 0.70(0.23) | 0.89(0.10) |
| SI | 0.15 | 0.15 | 0.16 | 0.68 | | 0.53(0.32) |
| S2 | 0.15 | 0.13 | 0.14 | 0.84 | 0.57 | |

⁺ Phenotypic correlations below diagonal, genetic correlations (\pm se) above.
NLC : number of lactations completed up to the fifth lactation.
SI : survival up to the second lactation.
S2 : survival up to the third lactation.

The reason for this positive relationship may be that the proportion of cows culled for low production is the largest source of culling (Van Vleck and Norman, 1972). Genetic correlations between production traits and stayability in general were similar to those obtained by De Lorenzo and Everett (1982) which ranged from 0.24 to 0.47. Genetic correlations reported by Robertson and Barker (1966) were 0.67 to 0.79.

The genetic correlations between NLC and each of S1 and S2 were positive and high being in agreement with Hudson and Van Vleck (1981). Although the estimate of the genetic correlation between NLC and S1 was lower than that between NLC and S2, the latter may be considered as a less useful measure of stayability than S1. Using S1, the sires can be evaluated at younger age and thus increasing the annual genetic gain by reducing the length of generation interval.

The effect of selection for milk yield could mask the true value of stayability evaluation, as described by Hoque and Hodges (1980). However, selection for herd life allows selection of more offspring of the better producing animals and increases the net profit for the dairymen.

Due to the low heritability of stayability, individual selection for that trait would not increase herd life as much as the indirect selection for it through production. However, using estimates shown in Tables 2 and 3, sire selection on herd life could increase herd life more than the indirect selection through milk production (1.23 times) when selection intensities are equal in both cases and the sire family size was 45. Hoque and Hodges (1980) reported the ratio between progress in the two selection procedures as 1.27 vs 1.23 obtained in the present study.

To predict stayability using milk yield in the first lactation the regression of the breeding value of stayability defined as S1, S2 and NLC on the breeding value of milk yield were estimated as 1.1×10^{-4} , 1.6×10^{-4} and 4.6×10^{-5} units of stayability per kilogram of milk.

So, selecting 0.01 from the sires under study based on milk yield would result, for instance, in an increase of approximately 4% in survivability of cows up to the second lactation (the sire family size was 45).

Thus, it may be concluded that evaluation of young tested sires should be based on selection for high milk production in the first lactation of their daughters. This will also lead to an increase in stayability defined as the length of herd life.

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المعالم الوراثية والمظهرية للإنتاج والحياة الانتاجية في ماشية هولستين - فريزيان البريطانية

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استخدمت سجلات بنات ٤٨٠ طلوقة هولستين - فريزيان البريطانية لتقدير التباين والتغاير للصفات الانتاجية في الموسم الأول والحياة الانتاجية . كانت قيم المكافئ الوراثي ٢٤ر ، ٢٣ر ، ٢٢ر لكل من محصول اللبن والدهن والبروتين على التوالي . بينما كان المكافئ الوراثي للحياة الانتاجية حيث عرفت على أنها عدد مواسم الحليب الكاملة حتى نهاية الموسم الخامس والبقاء حتى الموسم الثاني وحتى الموسم الثالث يساوي ٠٢ر . الارتباط الوراثي والمظهري بين إنتاج اللبن والحياة الانتاجية يتراوح بين ٣١ر الى ٤٢ر وبين ١٥ر الى ١٧ر على الترتيب .
قد لا يكون للانتخاب للحياة الانتاجية تأثير نتيجة انخفاض مكانتها الوراثي .
وعلى كل حال فان انتخاب الطلائق للإنتاج العالي من اللبن في الموسم الأول سوف يؤدي الى زيادة في طول الحياة الانتاجية .