Analysis of Herd Life in Guernsey Dairy Cattle[1]

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ABSTRACT

Heritabilities and genetic and phenotypic correlations for 48- and 72-mo herd life were estimated with multiple-trait REML from sire models incorporating sire relationships. Two traits were defined for 48- and 72-mo herd life, true herd life and functional herd life, which were adjusted for milk production prior to culling. Heritabilities for 48- and 72-mo herd-life traits were low, ranging from .02 to .07; genetic correlations among herd-life traits ranged from .82 to .95, and phenotypic correlations ranged from .80 to .97. Genetic correlations between the herd-life traits and first lactation milk, fat, and protein production ranged from .37 to .81. Genetic correlations were lower between functional herd life and milk, fat, and protein production than among true herd life and these same variables. Multiple-trait REML from sire models, which included sire relationships, was used to estimate genetic and phenotypic correlations between 48-mo true or 48-mo functional herd life and linear type traits for registered Guernsey cattle. The genetic correlations were used to compute weights for indirect prediction of true and functional herd-life transmitting abilities from linear type traits transmitting abilities. The predictions are equivalent to multiple-trait BLUP with no observations for herd life.

(**Key words**: Guernsey, herd life, genetics, linear type traits)

Abbreviation key: FHL = functional herd life, **ME305** = mature equivalent 305-d, **MME** = mixed model equations, **THL** = true herd life.

INTRODUCTION

Longevity, or a cow's productive life in a herd, has been measured in terms of several traits, e.g., number of lactations, age at disposal, stayability, and survival scores (5, 14, 15, 16). The economic importance of longevity has been well documented (1, 10, 19, 27).

Direct selection for longevity in dairy cattle is limited by the time required to accumulate sufficient data to estimate sire breeding values accurately (24). Direct selection is hampered further by low heritabilities on the observed scale (5, 15). Several studies found moderate to high genetic relationships between longevity and milk production traits (4, 5, 8, 15, 28). These relationships appear to be due partly to voluntary culling for low production. Therefore, if longevity is to be incorporated into dairy cattle breeding objectives, the characteristic should be redefined in terms of involuntary culling (6, 7). Ducrocq et al. (6, 7) defined two herd-life traits: true herd life (THL), or total longevity, and functional herd life (FHL), a measure of herd life when cows are subject to involuntary culling only. Genetic relationships between type and longevity have been reported (2, 20, 21, 23). Much of the work on longevity has been confined to the Holstein and Jersey breeds. The objectives of this study were 1) to investigate the genetics of THL and

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FHL and the relationships among them, 2) to investigate linear type traits and first lactation milk production in Guernsey cows, and 3) to derive prediction equations for indirect selection for 48-mo THL and FHL.

MATERIALS AND METHODS

Herd-Life Data

Production data were extracted from USDA Animal Improvement Programs files. The records consisted of registered and grade daughters of Guernsey sires that had left the herd or had an opportunity to survive to 48 or 72 mo. The criteria given by Foster et al. (9) and by Boldman et al. (2) were used to determine whether a cow had left the herd. Cows were assigned the number of days that they remained in the herd from birth; if they were still in the herd at 48 or 72 mo, they were assigned a herd life of 1464 or 2196 d from birth, respectively. The 72-mo herd-life data were a subset of the 48-mo data. Data for cows with an age at first calving greater than 40 mo were removed. All cows were required to have mature equivalent 305-d (ME305) records for milk, fat, and protein production and to have sires with a US registration number. Milk, fat, and protein production was used to compute a measure of FHL. Sires were required to have 10 or more progeny in two or more herds. Data consisted of 39,910 records on daughters of 563 sires for 48 mo and 21,453 records on daughters of 353 sires for 72 mo. The linear model for THL analysis was

$$y_{ijklm} = hy_i + a_j + g_k + s_{kl} + e_{ijklm} \quad [1]$$

where

y_{ijklm} = the record for THL on daughter m of sire l in group k, age at first calving j, in herd birth year i;
hy_i = the fixed effect for herd birth year i;
a_j = the fixed effect for age at first calving j;
g_k = the fixed effect for genetic group k;
s_{kl} = the random effect for sire l in genetic group k; and
e_{ijklm} = the random residual.

The relationship matrix included sires of the sires and maternal grandsires of the sires and was computed from the method outlined by Quaas (18). Sires of sires or maternal grandsires with no production records and fewer than two relatives were excluded from the relationship matrix. The sires were assigned to one of five genetic groups by birth year in 5-yr intervals; the first interval was before or in 1965. Age at first calving was assigned to one of eight 60-d intervals; the first parity interval was before or on d 720.

Values for THL reflect both voluntary and involuntary culling. To estimate FHL, Ducrocq et al. (7) used a cow's last lactation production prior to culling. In our study, linear and quadratic covariables—a cow's standardized milk, fat, and protein production records—were included in Model [1] to obtain a measure of FHL. Production records were standardized as follows:

$$z_{ijk} = \frac{y_{ijk} - \bar{x}_{jk}}{\sigma_{jk}}$$

where

z_{ijk} = the standardization of production record for cow i, trait j (j = milk, fat, or protein) in herd-year k;
y_{ijk} = the last ME305 record for trait j of a cow i in herd-year k if the cow was culled before 48- or 72-mo, or if the record began immediately before 48- or 72-mo of age and the cow remained in the herd after 48- or 72-mo of age;
$\bar{x}_{jk}$ = the mean ME305 production of all cows in herd-year k for trait j; and
σ_{jk} = the standard deviation for trait j in herd-year k.

For standardization of production records, at least 5 cows per herd-year were used to estimate herd-year standard deviations (12).

Genetic and phenotypic covariances among 48-mo THL and FHL and 72-mo THL and FHL were estimated using a multiple-trait model similar to Model [1], except that the effects were nested within traits. Both 48- and 72-mo FHL were preadjusted for estimates of the linear and quadratic covariables for standardized milk, fat, and protein production to