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Indirect Prediction of Herd Life in Guernsey Dairy Cattle

J. Cruickshank,* K. A. Weigel,*
M. R. Dentine,* and B. W. Kirkpatrick†
*Department of Dairy Science and
†Department of Animal Sciences,
University of Wisconsin-Madison 53706

ABSTRACT

Production and type data were used to investigate the relationships of these traits with herd life data in US Guernsey cows that calved from 1985 through 1990. Two definitions of herd life were used: actual days from birth to disposal (true herd life) and herd life adjusted for milk production (functional herd life). Genetic parameters were calculated with data from cows that had an opportunity to reach 84 mo of age (n = 18,725). Linear type traits were preadjusted for stage of lactation and age at classification. True herd life was preadjusted for age at first calving and for functional herd life, within herd-year quartile ranking for milk yield. The (co)variance components for true and functional herd life, milk, fat, protein, and 15 linear type traits were estimated with multiple-trait REML in an animal model. Heritability estimates for true and functional herd life were 0.12 for both traits. Estimated genetic correlations of herd life with body size traits were from –0.14 to –0.29, with feet and leg traits were from –0.10 to 0.06, and with udder traits were from –0.09 to 0.24. These correlation parameters were used for indirect prediction of herd life from available production and type information in Guernseys.
(**Key words:** Guernsey, herd life, heritability, type)

Abbreviation key: AGA = American Guernsey Association, **FHL** = functional herd life, **THL** = true herd life.

INTRODUCTION

Production per lactation and total number of lactations are the most important determinants of a cow's lifetime value. When a cow becomes unprofitable due to illness, injury, reproductive inefficiency, or low milk production, she is likely to be culled. Profitability and longevity have a high positive correlation (Weigel et al., 1995; Norman et al., 1996). Extended herd life is economically beneficial due to lower heifer replacement costs and a higher proportion of cows producing at a mature level (van Arendonk, 1991). Culling based on low milk production is often referred to as voluntary culling, and culling based on health or reproductive problems is termed involuntary culling. Farmers benefit from a preponderance of voluntary culling and a corresponding reduction in involuntary culling. Here, following the convention of Boldman et al. (1992) and Harris et al. (1992a), true herd life (**THL**) indicates a cow's lifespan (birth to disposal) in days, and functional herd life (**FHL**) represents a cow's THL adjusted for milk yield. Hence, FHL should reflect involuntary culling. In the USDA's 1996 National Animal Health Monitoring System dairy cattle survey, 77% of cows culled for slaughter were removed for reasons other than low production.

Genetic improvement of herd life is difficult to achieve. Heritability of herd life is low (Boldman et al., 1992; Harris et al., 1992a; Short and Lawlor, 1992; Settar and Weller, 1999), and one must wait for the animal or its relatives to leave the herd before obtaining a direct measurement. Ideally, one would combine culling data with indirect predictors that are more highly heritable and are measurable earlier in life. Linear type traits are relatively easy to measure, and such information is generally available in a cow's first lactation. Conformation traits are correlated with herd life to varying degrees, and, therefore, represent logical predictors (Foster et al., 1989; Rogers et al., 1989; Rogers et al., 1991; Boldman et al., 1992; Short and Lawlor, 1992; VanRaden and Wiggans, 1995). Other traits, particularly those relating to cow health and reproduction, would also be useful, but these data are often more difficult to obtain. Indirect information, such as type data, can be used to enhance direct evaluation of longevity (Weigel et al., 1998).

Inclusion of longevity in the selection goal can yield economic benefits for producers (Allaire and Gibson, 1992; VanRaden and Wiggans, 1995). The American Guernsey Association (**AGA**; Reynoldsburg, OH) has used an FHL index based on 15 linear type traits since 1991. The AGA had included the FHL index in its over-

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Corresponding author: B. W. Kirkpatrick; e-mail: kirkpat@calshp.cals.wisc.edu.

all production type index with relative weights of 50% protein yield, 25% fat yield, and 25% FHL index (S. Johnson, personal communication). In 2001, the AGA changed the production type index so that protein, fat, and FHL are equally weighted. The original study that generated the weights for the FHL index utilized a sire model and data from cows born before 1987 (Harris et al., 1992a). At this time, the AGA does not utilize SCS or USDA's productive life information in their selection index.

The objectives of the present study were to estimate genetic parameters of production, type, and herd life traits in US Guernseys and to develop an updated FHL index that will more accurately reflect relationships between these traits in the contemporary US Guernsey population.

METHODS

Sire pedigree information was acquired from the USDA Animal Improvement Programs Laboratory; cow pedigree, production, and linear type data were acquired from the AGA. Cows were required to have a valid US sire, herd code, birth date, classification date, calving date, mature equivalent 305-d production records for milk, fat, and protein, and complete data for all 15 linear type traits. Final score was not considered in this analysis. Nonregistered (grade) cows, of which there were very few with complete records, were excluded. Cows were deleted from the data set if the termination code (1, 2, or 9) in their last lactation indicated abnormally long intervals (more than 75 d) between sample-day milk weights, if they were sold for dairy purposes, if testing was discontinued, or if there was an unknown reason for termination. For cows lacking a termination code, disposal date was assumed to be the final day of their last recorded lactation. Only cows with an opportunity to reach 7 yr (84 mo) of age by December 31, 1997 were included; 18,725 cows met this criterion. All cows still alive at 7 yr of age were assigned a maximum herd life value of 2555 d. Individuals were grouped into 60-d cohorts for age at first calving and age at classification; 30-d cohorts were used for stage of lactation at classification.

First lactation yield records and first recorded type appraisal records (from first or second lactation) were used. Due to small herd-year-season groups, season was considered separately in the model, and only two calving seasons, one starting in October and the other in April, were assigned. The within-herd quartile ranking based on mature equivalent milk production was determined for each cow's last known lactation, and this value was used to preadjust THL, thereby creating FHL. Use of a quartile rank rather than a smaller demarcation, such as deciles, was necessary due to small contemporary group size within herds.

Herd life values were preadjusted for age at first calving, and type scores were preadjusted for age and stage of lactation at classification for each cow. The adjustment factors were calculated with a single-trait BLUP animal model utilizing the JAA program of Misztal (1993). Herd-year of calving class, season of calving class, age, and stage of lactation at classification classes, and animal effects were included in the model for linear type traits. Age at first calving and animal effects were included in the model for FHL. Heritability and variance estimates from Harris et al. (1992b) were used in the adjustment calculations. These preadjustments were necessary, since the program used for analysis required a common model for every trait.

The following linear model was used for estimating genetic correlations between linear type traits, production traits, and longevity:

$$\mathbf{y}_{ijk} = \mathbf{hy}_i + \mathbf{s}_j + \mathbf{a}_k + \mathbf{e}_{ijk},$$

where $\mathbf{y}_{ijk}$ is a vector containing adjusted phenotypic observations for linear type, production, and herd life for cow k; $\mathbf{hy}_i$ is a vector containing the fixed effects for herd-year of calving class i; $\mathbf{s}_j$ is a vector containing the fixed effects for season of calving class j; $\mathbf{a}_k$ is a vector containing the random additive genetic effects for animal k; and $\mathbf{e}_{ijk}$ is a vector of random residuals. The following distributional assumptions were made: $\mathbf{a} \sim N(\mathbf{0}, \mathbf{A}\sigma_a^2)$, where $\mathbf{A}$ is the numerator relationship matrix among cows, and $\mathbf{e} \sim N(\mathbf{0}, \mathbf{I}\sigma_e^2)$, where $\mathbf{I}$ is the identity matrix. Eight genetic groups were formed based on year of birth of cows. The MTC program of Misztal (1994) was used.

To determine if there were intermediate optimum type scores with respect to herd life, a single-trait model for FHL incorporating only fixed effects was used to generate residuals. The residuals were used in calculating quadratic phenotypic regressions of FHL on each type trait individually. The resulting regression coefficients were applied to scores within two standard deviations of each trait mean to avoid anomalies at the extreme ends of the scale, where there were very few observations. Weights for indirect prediction of herd life from type traits were calculated using the procedure of Boldman et al. (1992).

RESULTS AND DISCUSSION

Means and standard deviations of yield, type, and herd life were estimated for 18,725 cows with opportunity to reach 84 mo of age (Table 1). Linear type averages generally tend to the midpoint of the zero-to-50-

Table 1. Means, standard deviations, and estimated heritabilities of traits for Guernsey cows with opportunity to reach 84 mo of age.

Trait	Mean	SD	Heritability
Milk	6395.6[1]	1368.6	0.31
Fat	286.7	61.4	0.27
Protein	221.2	45.4	0.26
Stature	26.8	9.1	0.48
Strength	24.4	7.6	0.30
Body depth	26.7	7.4	0.33
Dairy form	27.7	7.9	0.27
Rump angle	27.3	7.4	0.35
Thurl width	25.5	7.0	0.27
Rear legs side view	27.2	7.8	0.13
Foot angle	23.8	7.5	0.12
Fore udder attachment	28.2	8.6	0.19
Rear udder height	29.0	7.5	0.23
Rear udder width	26.3	7.2	0.23
Udder cleft	26.8	6.0	0.17
Udder depth	34.0	7.8	0.31
Front teat placement	24.0	6.5	0.27
Teat length	21.3	6.7	0.34
THL	1823.8	616.1	
THL up to 84 months of age	1768.0	505.8	0.12
FHL up to 84 months of age	1770.2	500.8	0.12

[1]Production traits in kg, type traits in points, herd life traits in days.

point range, although udder depth (mean = 34.0) was noticeably closer to one extreme (deep). The average lifespan was 1824 d. When cows living longer than 84 mo were assigned a herd life value of 2555 d, the mean was 1768 d.

Estimates of heritability (Table 1) for yield traits were moderate (milk, 0.31; fat, 0.27; protein, 0.26). Heritabilities for structural and body size traits ranged from 0.12 (foot angle) to 0.48 (stature). Estimates of udder trait heritabilities ranged from 0.17 (udder cleft) to 0.34 (teat length). Estimates of type trait heritability were comparable to previously published values for Guernseys (Gengler et al., 1999; Harris et al., 1992b). Heritability of both true and functional herd life was estimated at 0.12. These values were higher than the herd life heritabilities found by Harris et al. (1992a), and higher than estimates in US Holsteins (Boldman et al., 1992; Short and Lawlor, 1992; Weigel et al., 1995), but similar to values found in Israeli Holsteins (Settar and Weller, 1999) and Swiss Brown cattle (Vukasinovic et al., 1995).

Both THL and FHL had moderately positive estimates of genetic correlations with first-lactation milk, fat, and protein yields (Table 2). All three body size traits (stature, strength, and body depth) had moderately negative estimates of genetic correlations with herd life traits. Dairy form appeared to be uncorrelated with THL and slightly negatively correlated with FHL. The structural traits of rump angle and rear leg set were estimated to have a rather small negative genetic correlation (roughly –0.10) with THL and FHL. However, thurl width had genetic correlations of –0.23 and –0.25 with THL and FHL, respectively. The estimated genetic correlation between herd life and foot angle was very small, as was the relationship between fore udder attachment and herd life, although both tended to be positive. Rear udder height showed a slightly negative estimated genetic correlation with herd life, as did teat placement. Genetic correlation of rear udder width and FHL or THL were nearly zero. Udder cleft showed higher estimates of genetic correlation with herd life (0.15), and the estimated genetic correlations between rear udder depth and herd life were the second highest of the udder traits (0.20 with THL, 0.24 with FHL). Estimates of genetic correlation between teat length and herd life, at –0.25 (THL) and –0.27 (FHL), were among the highest of all conformation traits. These genetic correlation values deviated widely from those calculated by Harris et al. (1992a). They also bear little similarity to type trait and longevity correlations for Jerseys (Rogers et al., 1991) or Holsteins (Short and Lawlor, 1992).

The estimated phenotypic correlation between yield traits and herd-life traits mirrored the estimated genetic correlation. For type traits, estimated phenotypic and genetic correlations with herd life were similar in direction, although the phenotypic correlations were generally smaller. Phenotypic and genetic correlations between THL and FHL were 1.00, as opposed to the lower values (0.92 and 0.97) of Harris et al. (1992a). In this study, THL and FHL were nearly equivalent traits, although due to the large proportion of very small herd-

Table 2. Estimates of genetic correlations (above diagonal) and phenotypic correlations (below diagonal) among yield, type, and herd life traits in Guernsey cows with opportunity to reach 84 mo of age.

	Milk	Fat	Prot	ST	SR	BD	DF	RA	TW	RL	FA	FU	UH	UW	UC	UD	TP	TL	THL	FHL
Milk[1]		0.72	0.90	0.22	0.24	0.22	0.78	0.04	0.28	0.01	0.08	−0.49	0.50	0.65	0.18	−0.51	−0.13	0.14	0.30	0.23
Fat	0.86		0.80	0.17	0.23	0.28	0.68	0.03	0.21	0.00	0.12	−0.50	0.33	0.50	0.10	−0.45	−0.07	0.03	0.30	0.26
Prot	0.94	0.91		0.24	0.24	0.24	0.76	0.08	0.28	0.05	0.06	−0.52	0.44	0.62	0.17	−0.49	−0.09	0.13	0.35	0.30
ST	0.24	0.19	0.22		0.70	0.58	0.59	0.12	0.72	−0.04	0.31	−0.17	0.39	0.42	0.15	−0.08	0.03	0.36	−0.26	−0.28
SR	0.20	0.18	0.21	0.56		0.87	0.50	−0.08	0.92	0.01	0.37	−0.19	0.19	0.46	0.20	−0.34	0.00	0.48	−0.27	−0.29
BD	0.23	0.22	0.23	0.49	0.71		0.58	−0.01	0.74	−0.09	0.32	−0.18	0.29	0.47	0.23	−0.44	0.02	0.37	−0.26	−0.29
DF	0.57	0.49	0.53	0.44	0.40	0.48		0.02	0.56	−0.04	0.20	−0.50	0.67	0.83	0.36	−0.58	0.08	0.29	0.00	−0.06
RA	0.05	0.03	0.05	0.12	0.02	0.04	0.05		−0.12	−0.16	−0.17	−0.19	−0.06	−0.12	−0.07	−0.07	0.02	0.01	−0.10	−0.11
TW	0.24	0.21	0.24	0.53	0.72	0.58	0.43	−0.01		0.03	0.42	−0.11	0.36	0.60	0.26	−0.26	0.04	0.50	−0.23	−0.25
RL	−0.01	−0.02	−0.02	−0.02	−0.09	−0.05	−0.01	0.01	−0.06		−0.44	−0.06	−0.11	0.00	−0.08	−0.06	0.09	−0.07	−0.10	−0.10
FA	0.07	0.07	0.09	0.16	0.23	0.16	0.16	−0.05	0.23	−0.18		0.15	0.18	0.27	0.15	0.01	−0.04	0.12	0.06	0.04
FU	−0.18	−0.13	−0.15	−0.05	0.03	−0.02	−0.13	−0.15	0.03	−0.07	0.12		0.06	−0.22	−0.13	0.76	0.17	−0.13	0.00	0.04
UH	0.33	0.26	0.30	0.28	0.23	0.26	0.54	−0.03	0.28	−0.08	0.16	0.15		0.81	0.39	−0.11	0.03	0.18	−0.03	−0.07
UW	0.44	0.37	0.41	0.33	0.38	0.38	0.66	−0.02	0.45	−0.08	0.19	0.04	0.69		0.42	−0.45	0.13	0.32	0.05	0.00
UC	0.16	0.13	0.15	0.10	0.14	0.16	0.27	−0.02	0.17	−0.02	0.10	0.07	0.30	0.31		−0.10	0.14	0.20	0.15	0.14
UD	−0.30	−0.22	−0.26	−0.09	−0.20	−0.28	−0.33	−0.09	−0.18	−0.03	0.03	0.46	−0.01	−0.20	0.05		0.09	−0.31	0.20	0.24
TP	0.03	0.04	0.04	0.05	0.09	0.10	0.14	−0.05	0.10	−0.01	0.10	0.21	0.18	0.19	0.23	0.13		−0.12	−0.03	−0.02
TL	0.12	0.07	0.11	0.23	0.22	0.19	0.20	0.01	0.23	0.00	0.08	−0.05	0.14	0.19	0.14	−0.14	−0.03		−0.25	−0.27
THL	0.26	0.28	0.29	−0.07	−0.02	−0.03	0.10	−0.04	−0.01	−0.05	0.04	0.07	0.08	0.09	0.06	0.09	0.05	−0.05		1.00
FHL	0.22	0.25	0.25	−0.08	−0.03	−0.04	0.07	−0.04	−0.02	−0.05	0.04	0.08	0.07	0.07	0.06	0.10	0.05	−0.05	1.00	

[1]Milk = Milk yield, Fat = fat yield, Prot = protein yield, ST = stature, SR = strength, BD = body depth, DF = dairy form, RA = rump angle, TW = thurl width, RL = rear legs side view, FA = foot angle, FU = fore udder attachment, UH = rear udder height, UW = rear udder width, UC = udder cleft, UD = udder depth, TP = front teat placement, TL = teat length, THL = true herd life, FHL = functional herd life.

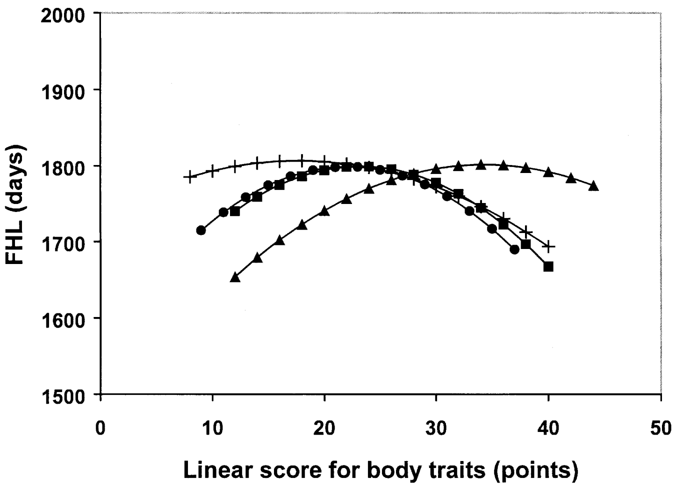

Figure 1. Quadratic relationships between functional herd life (FHL) and the individual linear type traits of stature (+), strength (●), body depth (■), and dairy form (▲) for Guernsey cows with the opportunity to reach 84 mo of age. The ranges (zero to 50 points) of the trait descriptions are: short to tall for stature, frail to strong for strength, shallow to deep for body depth, and tight rib to open rib for dairy form.

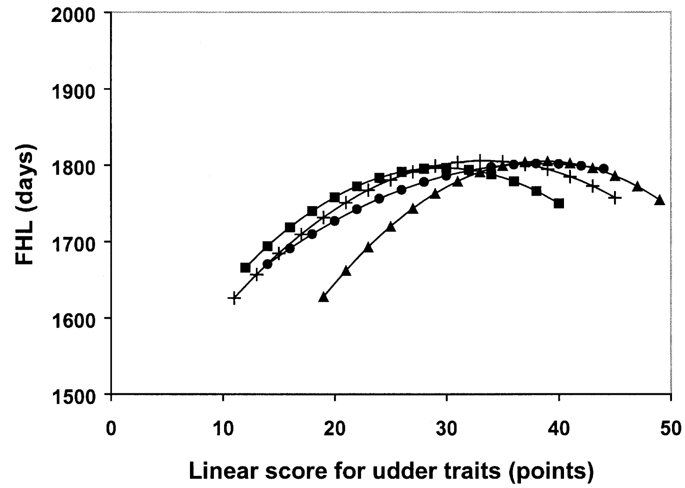

Figure 3. Quadratic relationships between functional herd life (FHL) and the individual linear type traits of fore udder attachment (+), rear udder height (●), rear udder width (■), and udder depth (▲) for Guersey cows with the opportunity to reach 84 mo of age. The ranges (zero to 50 points) of the trait descriptions are: loose to strong for fore udder attachment, low to high for rear udder height, narrow to wide for rear udder width, and deep to shallow for udder depth.

year-season groups, the adjustment of THL by within-herd milk production was somewhat coarse. More precise assessment of relative milk production may have resulted in a clearer differentiation between THL and FHL.

Each of the 15 linear type traits for Guernseys has a possible range of 1 to 50 points. Figures 1, 2, 3, and 4 show the relationship between the individual type traits and FHL. All 15 traits show a significant association with FHL for linear and quadratic regression coefficients ($P < 0.0001$), except teat length ($P < 0.05$ for linear value). These data contrast with the findings of Foster et al. (1989), who found a significant association with herd life for only seven traits in Holsteins. The

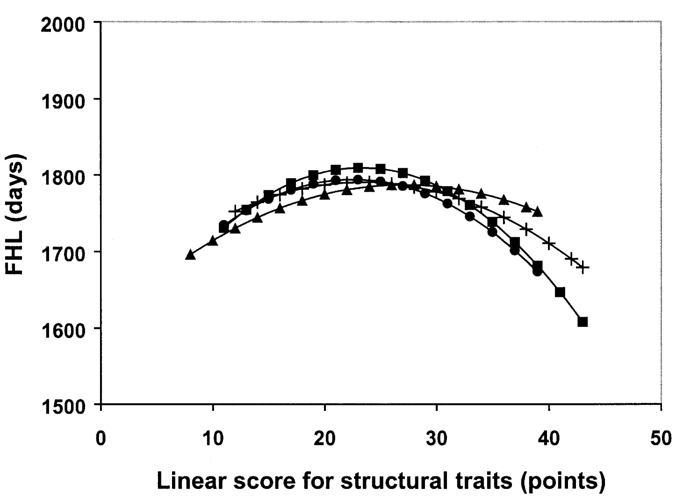

Figure 2. Quadratic relationships between functional herd life (FHL) and the individual linear type traits of rump angle (+), thurl width (●), rear legs side view (■), and foot angle (▲) for Guernsey cows with the opportunity to reach 84 mo of age. The ranges (zero to 50 points) of the trait descriptions are: high pins to sloped for rump angle, narrow to wide for thurl width, posty to sickle for rear legs side view, and low to steep for foot angle.

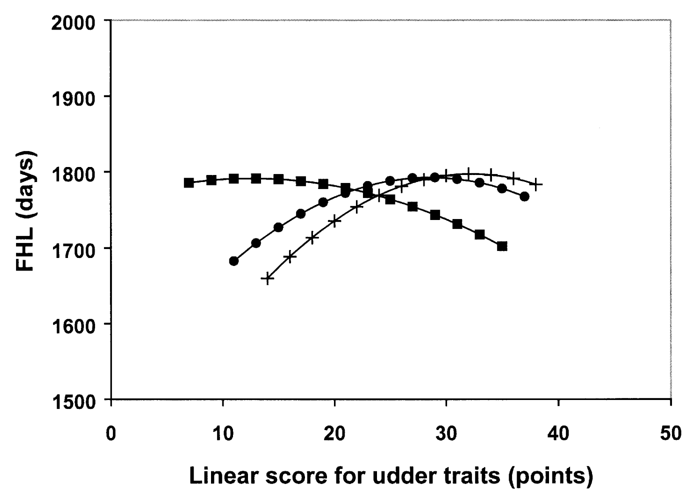

Figure 4. Quadratic relationships between functional herd life (FHL) and the individual linear type traits of udder cleft (+), front teat placement (●), and teat length (■) for Guersey cows with the opportunity to reach 84 mo of age. The ranges (zero to 50 points) of the trait descriptions are: weak to strong for udder cleft, wide to close for front teat placement, and short to long for teat length.

Table 3. Standardized weights for predicting functional herd life from linear type traits in Guernseys derived from cows with opportunity to reach 84 mo of age.

Trait	Weight
Stature	–0.51
Strength	–0.21
Body depth	0.18
Dairy form	0.59
Rump angle	0.00
Thurl width	–0.16
Rear legs side view	–0.08
Foot angle	0.06
Fore udder attachment	–0.31
Rear udder height	–0.88
Rear udder width	0.94
Udder cleft	0.07
Udder depth	1.08
Front teat placement	–0.18
Teat length	–0.05

local slope at the mean approximated the general direction of the relationship. Some traits, such as strength and body depth, showed a clearly intermediate optimum for FHL. Other traits displayed more of a plateau toward one end of the scale and a decrease towards the other end. Stature and dairy form were two such traits; short and moderately sized cows appeared to have an average life expectancy, while tall cows were culled at younger ages. This apparent relationship is supported by the report of increased longevity in Holsteins selected for smaller stature (Hansen et al., 1999). Tightly-ribbed cows would be expected to have lower FHL values than moderately open- and very open-ribbed cows. Cows with medium and higher rear udder heights would be expected to have longer FHL than cows with low rear udders. Short to moderate teat length also corresponded with higher FHL values compared with cows with longer teats.

Table 3 displays weights for predicting FHL, calculated from cows with opportunity to reach 84 mo of age. These weights can be considered partial genetic regression coefficients and have been adjusted to a standard variance for all type traits. These weights can be applied, as a set, to type PTA values of a Guernsey animal to create an index that reflects that animal's genetic potential for longevity. All 15 type traits contributed to this FHL index. Reducing the number of type traits by eliminating those that least influence herd life can minimize problems arising from multicollinearity among highly correlated traits (Weigel et al., 1998). However, considering that this index ultimately will be used by dairy producers, and that all 15 type traits are routinely assessed, no effort was made to decrease the number of FHL index components. The maximum R^2 value was 0.50. For the weights calculated for THL (not shown), the R^2 value was 0.91. It is not surprising that the R^2 value for THL was larger than for FHL, because prediction of THL includes yield traits that are very influential. It should be noted that these R^2 values are probably overestimated. Error that arises in the genetic correlation matrix due to too many traits and too few animals tends to inflate the R^2 values (Visscher, 1994).

This analysis utilized only data from registered Guernsey cows, due to a lack of sufficient data from grade Guernseys. Significant differences in genetic correlations of various type traits with herd life between registered and nonregistered Holsteins have been observed (Dentine et al., 1987; Short and Lawlor, 1992), although estimates of correlations between registered and grade Jerseys showed little difference (Rogers et al., 1991). Also not considered in this study were differences in the relationships between herd life and type traits in different management systems, which have been documented in Holsteins (Burke and Funk, 1993). Consideration of health traits, such as mastitis incidence as estimated by SCS, and reproductive traits, such as days open, would improve the accuracy and enhance the value of FHL estimation. Unfortunately, reliable reproductive data are less readily available than linear type scores, and SCS data have not yet been incorporated into selection indexes used by the AGA. USDA generates PTA values for productive life, a trait that incorporates milk, fat, and protein yields; SCS; and udder, body size, and feet and leg composites, in addition to direct information from longevity data. The calculation of productive life uses the type heritability estimates of Jerseys for all non-Holstein breeds, and uses Holstein genetic correlations of PL with yield, type, and SCS. Productive life, as currently calculated, may not be very appropriate for use by Guernsey breeders.

CONCLUSIONS

The estimated herd-life heritability, albeit moderately low, suggests that selection for herd life could yield observable results. Estimated correlations between linear type traits and herd life were low to moderate, but these traits still make up a substantial portion of herd life variance. At this time, a type-based predictive index for FHL serves the purposes of the AGA, as the results are included in a production-oriented selection index. The AGA implemented the new FHL index in August 2001.

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