Genetic and Phenotypic Parameters for Type and Production in Guernsey Dairy Cows[1]

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ABSTRACT

Heritabilities; genetic and phenotypic correlations for milk, fat, and protein production; and linear type traits were estimated from a sire model including sire relationships using multiple-trait REML. For the milk production traits, 68,109 first parity records were analyzed. Heritabilities ranged from .31 to .37, genetic correlations between the milk production traits ranged from .80 to .92, and phenotypic correlations ranged from .86 to .94. Linear type traits from 12,996 cows on 15 traits were used to estimate heritabilities and genetic and phenotypic correlations between linear type traits. The heritabilities ranged from .53 for stature to .09 for foot angle. Rear udder height and rear udder width had the highest positive genetic correlation (.85), whereas dairy form and udder depth had the highest negative genetic correlation (–.41). When the first parity production records were merged with type records for cows, 9867 records on 18 traits were obtained. Dairy form, rear udder height, and rear udder width had strong to moderate positive genetic correlations with the three production traits. Fore udder attachment and udder depth had moderate negative genetic correlations with the three milk production traits. These results suggest that selection for improvement of milk production will lead to correlated increases in dairy form, rear udder height, rear udder width, and udder depth and to correlated decreases in the strength of fore udder attachment.
(**Key words**: Guernsey, type, production, parameter estimation)

INTRODUCTION

Since 1980, the American Guernsey Association has been appraising Guernsey cows using a uniform linear functional type trait program. Similar programs have been implemented for North American Jersey, Holstein, Brown Swiss, and Ayrshire breeds. Currently, 15 type traits are scored on Guernsey cows: 6 traits broadly describe the body characteristics of the cow, 7 traits describe the udder, and 2 traits describe the feet and legs. The type traits are described with numerical scores on a 50-point scale beginning at 50. The distribution of the scores is close to normal (9), allowing continuous trait evaluation.

Relationships between individual type traits and type and production traits have been reported by Norman et al. (9, 10) for Guernsey cows and by Thompson et al. (13), Lawstuen et al. (6), Meyer et al. (8), and Foster et al. (5) for other breeds of dairy cattle. Norman et al. (9) used a sire model to analyze 8328 records on 13 type traits. Variances and covariances for the type traits were estimated by Henderson's method 3 (9). The highest heritability estimates were for stature (.44) and chest and body (.42); foot angle and rear legs side view had the lowest heritabilities of .06 and .13, respectively. Stature, chest and body, dairy character, rump width, and fore udder attachment were moderately to highly positively genetically correlated, whereas udder depth was negatively correlated with dairy character

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TABLE 1. Summary of the data structure for Guernsey production, type, and joint type and production analysis.

	Production	Linear type scores	Joint type and production
Records	68,109	12,996	9867
Sires	970	232	197
Levels of major fixed effect[1]	5119	1020	880
Levels of minor fixed effects			
Genetic groups	5	5	5
Age at first calving	8		
Month of calving	12		
Stage of lactation		11	
Age classification covariables		2	
Residual df	61,998	11,728	8786

[1]Herd years for production analysis and herd year classifier for type and joint analysis.

(−.42) and with rear legs side view (−.28). Generally, phenotypic correlations between the type traits were smaller in absolute value than were genetic correlations.

Norman et al. (10) analyzed 9984 records on 14 type traits and on mature equivalent 305-d milk and fat production. Genetic (co)variances were estimated by Henderson's method 3 (10). The heritability estimates for the type traits were lower than those reported by Norman et al. (9); pelvic angle (.33), stature (.26), and strength (.29) had the highest heritabilities, and foot angle (.11) had the lowest. Genetic and phenotypic correlations exhibited the same trends reported by Norman et al. (9). Of the type traits, dairy character was highly positively genetically correlated with milk production (.75) and moderately positively correlated with fat production (.53) (10). Foot angle, udder depth, thurl width, and fore udder attachment were negatively genetically correlated with both fat and milk production.

The objectives of this study were to examine genetic and phenotypic relationships by using large data sets for milk, fat, and protein production in the first parity of Guernsey cows among 15 linear type traits and among 15 linear type traits and the three production traits.

MATERIALS AND METHODS

Production Data

Data were extracted from files of the USDA Animal Improvement Programs Laboratory. The records consisted of first parity lactation information on milk, fat, and protein production for registered and grade daughters of Guernsey sires. Data editing consisted of the removal of cows with an age at first calving greater than 40 mo. All cows were required to have both mature equivalent 305-d records for milk, fat, and protein production and sires with a US registration number. Sires were required to have 10 or more progeny in two or more herds. Data are summarized in Table 1.

The linear model for multiple-trait analysis was

$$y_{tijklmn} = hy_{ti} + m_{tj} + a_{tk} + g_{tl} + s_{tlm} + e_{tijklmn} \quad [1]$$

where

$y_{tijklmn}$ is the record for trait t (t = milk, milk fat, and protein production) on daughter n of sire m in group l, age at calving k, calving in month j, in herd year i;

hy_{ti} is the fixed effect for herd year i for trait t;

m_{tj} is the fixed effect for month of calving j (j = 1,. . .,12) for trait t;

a_{tk} is the fixed effect for age at first calving k for trait t;

g_{tl} is the fixed effect for genetic group l for trait t;

s_{tlm} is the random effect for sire m in genetic group l for trait t; and

$e_{tijklmn}$ is the the random residual.

In matrix notation,

$$y = (I_t \otimes X)b + (I_t \otimes Z)s + e$$

with

$$E\begin{bmatrix} y \\ s \\ e \end{bmatrix} = \begin{bmatrix} (I_t \otimes X)b \\ 0 \\ 0 \end{bmatrix},$$

$$\text{Var}\begin{bmatrix} y \\ s \\ e \end{bmatrix} = \begin{bmatrix} V & ZA \otimes G & R \otimes I_c \\ AZ' \otimes G & G \otimes A & 0 \\ R \otimes I_c & 0 & R \otimes I_c \end{bmatrix}$$

and

$$V = G \otimes ZAZ' + R \otimes I_c$$

where

- y is the vector of the records containing milk, fat, and protein;
- X and Z are incidence matrices containing zeros and ones relating fixed and random effects to records, respectively;
- s is the vector of random sire effects;
- e is the vector of the random residuals;
- A is the numerator relationship matrix;
- G is the genetic covariance matrix between the t traits;
- R is the error covariance matrix between the t traits;
- t is the number of traits;
- c is the number of cows with records on each of t traits; and
- $\otimes$ is the direct product operator (12).

The relationship matrix was computed using sires and maternal grandsires of the sires in the data by the method outlined by Quaas (11). Sires of sires or maternal grand sires with no daughters with production records and fewer than two relationship ties were excluded from the relationship matrix. The sires were assigned to five genetic groups by birth year in 5-yr intervals; the first interval was birth year less than or equal to 1965. Age at calving was assigned to eight 60-d intervals; the first parity interval was less or equal to d 720.

Linear Type Data

Data were from the American Guernsey Association linear type program. The records consisted of information on 15 linear type traits. Data editing removed cows without a US registration number for the sire. Cows were required to have all 15 linear type traits recorded and DIM when scored within 0 to 350 d. For cows with multiple records for type scores, only the first records were used. Sires were required to have 10 or more progeny in two or more herds. The data are summarized in Table 1.

The linear model for analysis was

$$y_{tijklmn} = hyc_{tik} + st_{tj} + \beta_{t1}(a_{tijklmn} - \bar{a}) + \beta_{t2}(a_{tijklmn} - \bar{a})^2 + g_{tl} + s_{tlm} + e_{tijklmn} \quad [2]$$

where

- $y_{tijklmn}$ is the record for linear type trait t (t = 1,. . .,15) on daughter n of sire m in group 1, classifier k, stage of lactation j, in herd year i;
- hyc_{tik} is the fixed effect for herd year i of freshening when classified for t trait by classifier k;
- st_{tj} is the fixed effect for stage of lactation j (j = 1,. . .,11) for trait t;
- g_{tl} is the fixed effect for genetic group 1 for trait t;
- s_{tlm} is the random effect for sire m in genetic group 1 for trait t;
- $a_{tijklmn}$ is the age at classification associated with $y_{tijklmn}$;
- $\bar{a}$ is the average age at classification;
- β_{t1} and β_{t2} are the linear and quadratic regression coefficients, respectively; and
- $e_{tijklmn}$ is the random residual.

The variances and the expectations for Model [2] have the same form as those for Model [1] with the appropriate vectors and matrices. The sires were assigned to genetic group by birth in 5-yr intervals, resulting in five genetic groups. Stage of lactation was assigned in 30-d intervals.

Linear Type and Production Data

The first parity production and type records were merged to analyze genetic and phenotypic correlations between type and production. The production records were preadjusted for age at calving and month of calving using the solutions from Model [1] in addition to the prior adjustment to 305-d mature equivalent basis. The linear type records were preadjusted for stage of lactation and age at classification using the solutions from Model [2] to obtain equal incidence matrices so that a canonical transformation could be used for (co)variance estimation. Sires were required to have 10 or more progeny in two or more herds for both the type and production records.

The linear model for analysis was

$$y_{tijkl} = hyc_{ti} + g_{tj} + s_{tjk} + e_{tijkl}$$

where

y_{tijkl} is the record for linear type or production trait t (t = 1,. . .,18) on daughter l of sire k in group j, in herd year classifier subclass i;

hyc_{ti} is the fixed effect for herd year classifier i of freshening for trait t;

g_{tj} is the fixed effect for genetic group j for trait t;

s_{tjk} is the random effect for sire k in genetic group j for trait t; and

e_{tijkl} is the random residual.

The variances and the expectations for Model [3] have the same form as those for Model [1] with the appropriate vectors and matrices. The sires were assigned to five genetic groups by birth year.

All analyses were carried out using REML. A review of this method and a discussion of its properties are given by Thompson (14). For Models [1] and [2], a multiple-trait expectation-maximization algorithm described by Meyer (7) was used. All fixed effects were absorbed, and, because traits had identical design matrices, a canonical transformation and tridiagonalization of the coefficient matrix could be used. Solutions for the fixed effects, except herd-year, were obtained by backsolving. The standard errors for heritability estimates are approximate lower bounds for large samples (7). For Model [3], a multiple-trait expectation-maximization algorithm for sire models using canonical transformation as described by VanRaden (15) was applied. For all analyses, convergence was assumed when the change of each (co)variance estimate was smaller than .001% between rounds.

RESULTS AND DISCUSSION

Unadjusted means and standard deviations, heritabilities, sire variances, and error variances for the production traits from Model [1] are in Table 2. Means and standard deviations for first parity milk and fat are in close agreement with estimates reported by Norman et al. (10). Milk, fat, and protein means and standard deviations were slightly greater than those given by Schutz (1988, personal communication) for Minnesota Guernseys. Heritability estimates for milk and fat were greater than those reported by Norman et al. (10). These

TABLE 2. Unadjusted means and standard deviations, heritability estimates with approximate standard errors[1], sire variance estimates (σ_s^2), and error variance estimates (σ_e^2) for type traits.

Trait	Mean	SD	h^2	SE	σ_s^2	σ_e^2
	(kg)				(kg^2)	
Milk	5736	1290	.37	.03	106,880	1,033,918
Fat	261	56.7	.32	.02	156.1	1797.2
Protein	200	43.7	.31	.02	95.5	1133.3

[1]Standard errors approximate lower bounds for large samples (7).

TABLE 3. Genetic (above diagonal) and phenotypic correlations between Guernsey production traits.

Trait	Milk	Fat	Protein
Milk		.80	.92
Fat	.86		.89
Protein	.94	.90	

heritabilities were comparable with recent heritability estimates reported for other North American dairy breeds such as Holsteins (2, 3, 4, 16) and Jerseys (10).

Genetic and phenotypic correlations between production traits from Model [1] are in Table 3. The estimated genetic and phenotypic covariance matrices between production traits are positive definite. The phenotypic correlations were higher than the corresponding genetic correlations; the highest phenotypic and genetic correlations were between milk and protein production, and the lowest were between milk and fat production. These results agree with estimates reported by Norman et al. (10) for milk and fat production traits and were consistent with estimates reported for other dairy breeds (2).

Unadjusted means, standard deviations, heritabilities, sire variances, and error variances for the linear type traits from Model [2] are in Table 4. For most of the linear type traits, the means were slightly greater than 75, the median of the scale. The unadjusted standard deviations ranged from 6.08 to 9.06. The heritabilities ranged from .53 for stature to .09 for foot angle. Stature, body depth, rump width, and teat length had heritabilities greater than .30, whereas foot angle, rear legs side view, fore udder attachment, and udder cleft had heritabilities smaller than .15. These heritabilities are comparable with estimates from Norman et al. (10), except for the heritability for stature, which is considerably greater (.53 vs. .26). However, high heritabilities for stature have been reported in Guernseys (9) and in Holsteins (1, 5, 13).

Genetic and phenotypic correlations between the linear type traits from Model [2] are in Table 5. The estimated genetic and phenotypic covariance matrices between the linear type traits are positive definite. Stature, strength, body depth, thurl width, and rear udder width seem to be strongly genetically correlated in the positive direction. The phenotypic correlations between these traits are lower. Within the udder traits, fore udder attachment, rear udder height, rear udder width, and front teat placement were positively genetically and phenotypically correlated; the highest genetic correlation was between rear udder

TABLE 4. Unadjusted means and standard deviations, heritability estimates with approximate standard errors[1], sire variance estimates (σ_s^2), and error variance estimates (σ_e^2) for type traits.

Trait	Direction[2]	Mean	SD	h^2	SE	σ_s^2	σ_e^2
Stature	Tall	78.3	8.63	.53	.06	8.55	55.52
Strength	Strong	76.9	7.69	.26	.04	2.81	40.39
Dairy form	Excellent dairy character	79.5	8.02	.25	.04	3.40	50.68
Foot angle	Steep angle	72.8	6.95	.09	.02	.89	37.64
Rear legs side view	Sickle hocked	78.9	7.35	.12	.03	1.48	46.79
Body depth	Deep body	79.1	7.68	.31	.05	3.35	40.51
Rump width	Wide	77.2	7.21	.31	.05	3.74	43.90
Thurl width	Wide	77.5	7.18	.29	.04	2.78	35.05
Fore udder attachment	Tight	77.2	8.48	.12	.03	1.94	61.19
Rear udder height	High	80.4	6.94	.28	.04	3.04	39.67
Rear udder width	Wide	76.6	6.74	.21	.04	1.98	35.44
Udder depth	Shallow	80.9	9.06	.26	.04	3.16	44.87
Udder cleft	Extreme cleft	77.5	5.92	.14	.03	1.20	31.99
Front teat placement	Close placement	73.3	6.41	.23	.04	2.11	35.07
Teat length	Long	72.3	6.08	.32	.05	2.36	27.05

[1]Standard errors approximate lower bounds for large samples (7).

[2]Direction of the largest score (i.e., 100 = tall).

TABLE 5. Genetic (above diagonal) and phenotypic correlations between Guernsey type traits.

Trait	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1 Stature		.72	.65	.29	–.05	.71	.22	.76	.01	.52	.62	–.15	.12	.04	.32
2 Strength	.53		.36	.57	–.07	.80	.06	.95	.03	.22	.50	–.30	.13	.03	.52
3 Dairy form	.43	.32		.12	.08	.52	.04	.50	–.14	.76	.80	–.41	.37	.22	.22
4 Foot angle	.16	.23	.13		–.37	.47	.12	.53	–.04	–.12	.13	–.20	.13	.12	.31
5 Rear legs side view	–.02	–.13	.00	–.23		–.10	–.34	–.04	–.07	–.05	.04	–.13	–.16	.25	–.40
6 Body depth	.49	.67	.45	.16	–.06		.14	.78	.13	.37	.50	–.35	.20	.21	.35
7 Rump width	.15	.04	.05	–.04	–.02	.06		.05	–.17	–.03	–.02	–.26	.04	.13	.15
8 Thurl width	.53	.77	.36	.23	–.11	.57	.00		.07	.35	.62	–.24	.18	.05	.54
9 Fore udder attachment	–.01	.08	–.07	.14	–.07	.03	–.15	.10		.38	.21	.54	–.05	.20	.05
10 Rear udder height	.28	.18	.48	.13	–.07	.22	–.03	.22	.27		.85	–.01	.33	.03	.23
11 Rear udder width	.35	.39	.58	.16	–.09	.37	.00	.45	.15	.62		–.24	.35	.14	.33
12 Udder depth	–.08	–.16	–.29	.05	–.03	–.25	–.11	–.12	.41	.10	–.09		–.03	.03	–.35
13 Udder cleft	.09	.11	.26	.09	–.03	.14	–.02	.13	.11	.30	.31	.10		.16	.04
14 From teat placement	.05	.10	.16	.11	–.01	.13	–.06	.11	.24	.20	.24	.17	.29		–.07
15 Teat length	.22	.20	.18	.05	–.03	.18	.04	.22	–.01	.12	.19	–.15	.10	.00	

height and rear udder width. The highest negative genetic and phenotypic correlations were between dairy form and udder depth.

Genetic and phenotypic correlations between linear type traits and milk, fat, and protein production from Model [3] are in Table 6. Dairy form had the highest genetic and phenotypic correlations; the three production traits agreed with results from Norman et al. (10). Rear udder height and rear udder width were moderately genetically and phenotypically correlated with the three production traits. This would be expected because rear udder height and width appear to be strongly genetically correlated with dairy form and with each other. Negative genetic and phenotypic correlations existed between udder depth, fore udder attachment, and rear legs side view and production traits. Selection for milk production in Guernseys is likely to increase the udder dimension—height and width—and to weaken depth and to weaken fore udder attachment. There was little difference between the phenotypic correlation estimates among the type traits from Model [3] compared with those from Model [2]. Differences were observed when comparing genetic correlations estimates among the type traits from Model [3] with those from Model [2]. Most of the differences were small, except for the estimates of genetic correlations among udder depth and udder cleft (–.42), fore udder attachment and body depth (.43), and strength and dairy form (.65). These differences could be due to accounting for the covariances between type and production in Model [3] or analyzing fewer records with Model [3].

CONCLUSIONS

The (co)variance estimates are similar to estimates from previous studies. As expected, the correlations between protein production and type traits were similar to those between type traits and milk and fat production. Although these estimates should be useful in multiple-trait animal evaluation and in studying selection responses in multiple traits, further investigation is required in at least two areas. First, primary selection for the improvement of milk traits should lead to correlated increases in scores for dairy form, rear udder height, and rear udder width. Traits such as udder depth and fore udder attachment may deteriorate as result of selection for the im-

TABLE 6. Phenotypic and genetic correlations between Guernsey type and production traits.

	Phenotypic correlations			Genetic correlations		
Trait	Milk	Fat	Protein	Milk	Fat	Protein
Stature	.25	.18	.23	.30	.13	.20
Strength	.19	.16	.20	.19	−.03	.05
Dairy form	.59	.49	.55	.83	.61	.76
Foot angle	.05	.06	.06	−.10	.05	−.04
Rear legs side view	.00	−.01	−.01	.09	−.02	.03
Body depth	.23	.20	.21	.27	.07	.11
Rump width	.05	.05	.06	−.02	.13	.10
Thurl width	.22	.17	.21	.21	−.06	.05
Fore udder attachment	−.13	−.10	−.12	−.22	−.33	−.26
Rear udder height	.30	.23	.26	.58	.34	.54
Rear udder width	.40	.32	.38	.60	.33	.52
Udder depth	−.30	−.22	−.27	−.44	−.35	−.36
Udder cleft	.15	.13	.13	.29	.25	.28
Front teat placement	.03	.02	.02	−.04	−.10	−.13
Teat length	.14	.09	.12	.11	−.07	.04

provement of milk traits. Thus, methods for the development of breeding goals accounting for the correlations between type and production traits are required to maximize the producer's net income accrued from genetic improvement. Second, selection on linear type traits may improve the functionality and the longevity of the animal for dairy production. Investigation into genetic and phenotypic associations between type traits and longevity is required.

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