

Genetic Analysis of Body Condition Score of Lactating Dutch Holstein and Red-and-White Heifers

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ABSTRACT

The aim of this study was to estimate phenotypic and genetic parameters for body condition scores (BCS) from the Dutch type classification system. Data included 108,809 Holstein (H) and 26,208 Red-and-White (R) heifers from 9701 herds that were scored once during lactation on a 1 to 9 scale (1 = emaciated and 9 = obese). Mean BCS for H and R data were 4.50 and 4.94, respectively. The BCS decreased as the percentage of Holstein genes increased. For both breeds, BCS after calving was about 5.6 and BCS was lowest around wk 11. For H heifers, mean BCS at drying off was about 0.8 lower than BCS at calving, whereas for R heifers BCS was at about the same level as at calving. Variance components were estimated using an animal model including the effects of herd × visit, classifier, age at calving, DIM, and genetic group. The random herd × visit effect explained about 10 to 15% of the phenotypic variation. Heritabilities ranged from 0.24 to 0.38, depending on breed and lactation period. Genetic correlations between BCS observations in bimonthly lactation periods were close to unity, especially for H. It was concluded that BCS data collected by type classifiers can well be used for genetic evaluation and that genetic variation between animals for BCS-change patterns is a small component of the overall variation in BCS.

(Key words: body condition score, energy balance, heritability, genetic correlation)

Abbreviation key: EB = energy balance, H = Dutch Holstein, R = Dutch Red-and-White.

INTRODUCTION

Energy balance (EB) in dairy cattle can be defined as the difference between energy intake and energy

requirements for milk yield and maintenance. The EB is mostly negative in early lactation (Berglund and Danel, 1987), which can result in a considerable mobilization of body adipose (Tamminga et al., 1997). Even though a negative EB is considered to be physiologically normal, size and duration of the negative EB are unfavorably related to health and fertility (Butler and Smith, 1989; Domecq et al., 1997b; Gearhart et al., 1990; Senatore et al., 1996; Villa-Godoy et al., 1988). Although no direct selection on EB is performed, size and duration of EB are affected indirectly by selection for milk yield. With selection for milk yield only, the correlated increase in feed intake is not large enough to cover the increased energy requirements (Gravert, 1985; Van Arendonk et al., 1991), implying that selection on yield alone is expected to increase the mobilization of body reserves in early lactation. This implication is supported by clear evidence from genetic correlations between yield and traits that indicate EB (Veerkamp, 1998) and by studies on groups with a high and low genetic merit for milk yield (Buckley et al., 2000). This unfavorable effect of selection on yield might be reduced when information on EB is considered when selection decisions are made (Veerkamp and Koenen, 1999).

Direct information on EB is not available mostly because of missing data on feed intake. However, BCS are already widely used as an indicator of the amount of stored energy reserves of a dairy cow (Broster and Broster, 1998; Edmonson et al., 1989; Wildman et al., 1982). Until now, BCS data have been used mostly for management purposes. These data can also be used for a genetic evaluation when a considerable genetic variation for BCS exists. The resulting EBV can then be used to improve EB by genetic selection. Information about large-scale data collection and on genetic evaluation for BCS is scarce (Gallo et al., 1999; Jones et al., 1999). In 1998, BCS was introduced in the Dutch type scoring system. Therefore, the objective of this study was to estimate phenotypic and genetic parameters for BCS from two Dutch dairy cattle breeds.

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MATERIALS AND METHODS

Data

Twenty experienced type classifiers of NRS collected BCS data for 156,755 lactating heifers from October 1998 through August 1999. These data were collected nationwide as part of the regular type classification scheme and included only animals with official herd-book registration. In scoring BCS, classifiers give most attention to the fatty tissue layer at the end of the spinous and transverse processes (loin area), the hip and the pinbones and the tailhead area, based on Lowman et al. (1976). For practical reasons, two modifications were used. First, classifiers scored on a 1 to 9 scale (1 = emaciated, 5 = average, and 9 = obese) in increments of 1, rather than on the more commonly used 1 to 5 scale, with increments of a quarter or half. This modification was used because the other linear type traits were already scored on the 1 to 9 scale. Secondly, only a visual assessment of the energy reserves was performed without palpating the cows to assess the amount of tissue under the skin.

The total data file was split into two files according to breed: either Holstein (**H**) or Dutch Red-and-White (**R**). Heifers in the H and R data file mainly originate from the Dutch-Friesian and Maas-Rijn-IJssel population, respectively, but have been upgraded with Holstein genes. In this study, the H and R population included 94 and 67% of Holstein genes, respectively.

Classifiers with <500 observations were removed from the data. Although classifiers were instructed to assume a standard deviation for BCS of 1.5, standard deviation within classifiers ranged from 1.1 to 1.8. To account for this heterogeneity, phenotypic observations were standardized to a standard deviation of 1.5 within classifiers. Furthermore, calving age had to be between 20 and 35 mo. Repeated observations on the same heifer, observations from herds with fewer than five records, and records on heifers scored after 305 DIM or from an unknown sire were removed. Finally, the H data file included 108,809 heifers from 7524 herds, and the R data file included 26,208 heifers from 2177 herds. Heifers in the H and R data were of 3632 and 963 sires, respectively; maximum number of daughters per sire was 9063 and 3370 for H and R data set, respectively.

Statistical Model

First, all observations for BCS were considered as observations on the same trait, i.e., it was assumed that genetic variance is constant during lactation and that genetic correlations among BCS in different lactation periods are unity.

The systematic effects of DIM and age at calving on BCS were modeled by polynomial regressions. For the regression on DIM, orthogonal Legendre polynomials (Amramowitz and Stegun, 1965) were used to reduce problems with high-order polynomials. As Legendre polynomials are only defined for variables in the range -1 to 1, DIM (1 to 305) were standardized to this range. The effects of age at calving and DIM on BCS were adequately described by a second- and fifth-order polynomials, respectively. Order of these polynomials was established by including parameters that differed significantly ($P < 0.01$) from zero. In the H data file, a sixth-order polynomial on DIM was still significant but explained little variation. Therefore, a fifth-order polynomial was used for both breeds.

Fixed effects and variance components were estimated with an animal model, including pedigree of the scored heifers that was traced for two generations. Parents with only one offspring in the data were treated as unknown parents to reduce computational efforts. The additive genetic relation matrix included 217,589 and 51,673 animals for H and R, respectively. Unknown parents in the pedigree were assigned to four genetic groups (Westell et al., 1988). These groups were defined according to the main breed composition (>50% Holstein-Friesian, >50% Dutch-Friesian, >50% Maas-Rijn-IJssel, and other breeds). The final model for BCS data is represented by:

$$\text{BCS}_{ijk} = \alpha_1 \text{age} + \alpha_2 \text{age}^2 + \sum_{n=1}^5 \beta_n t^n + \text{class}_i + hv_j + ani_k + e_{ijk} \quad (1)$$

where BCS_{ijk} is BCS; α_1 and α_2 are regression coefficients; age is age at first calving; β_n is regression coefficient for the Legendre polynomials; t is standardized DIM; class_i is fixed effect of classifier (20 levels); hv_j is random effect of herd \times visit (8529 and 2584 levels for H and R, respectively); ani_k = random effect of animal; and e_{ijk} is the random residual. Estimates for the fixed effects and variance components were obtained using REML (Gilmour et al., 1999).

Secondly, the assumption of the same genetic background across lactation periods is tested by estimating genetic parameters within five bimonthly lactation periods (mo 1 to 2, 3 to 4, 5 to 6, 7 to 8, and 9 to 10), followed by estimating the genetic correlations between lactation periods using model 1. As a complete multivariate analysis (five traits) posed large computational problems, genetic correlations were estimated in bivariate analyses. Within a bivariate analysis, estimates for the fixed effects were assumed to be the same for both traits.

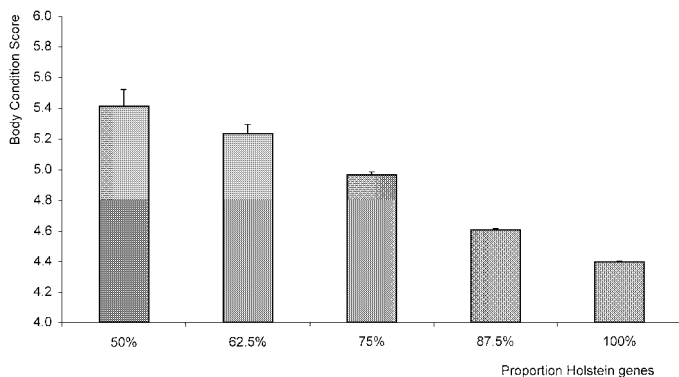


Figure 1. Mean BCS for Holstein heifers by proportion of Holstein genes.

RESULTS

Phenotypic Means

Unadjusted phenotypic means for H and R heifers were 4.50 ± 1.55 and 4.94 ± 1.51 , respectively. The difference between breeds is illustrated by unadjusted phenotypic BCS means for breed groups including ≥ 500 heifers. In the H data, BCS decreased as percentage of Holstein genes increased (Figure 1). In the R data, BCS increased as percentage of Maas-Rijn-IJssel genes increased (Figure 2).

The regression on age at calving showed for both breeds that BCS increased as calving age increased: mean BCS of heifers calving at the maximum age (35 mo) was about 0.6 higher than of heifers calving at the minimum age (20 mo).

The effect of DIM on BCS is illustrated in Figure 3 by unadjusted weekly means for BCS and the fitted polynomial regression from model 1. The unadjusted means were based on 26 to 3486 scored heifers per lactation week; especially in the first and last lactation

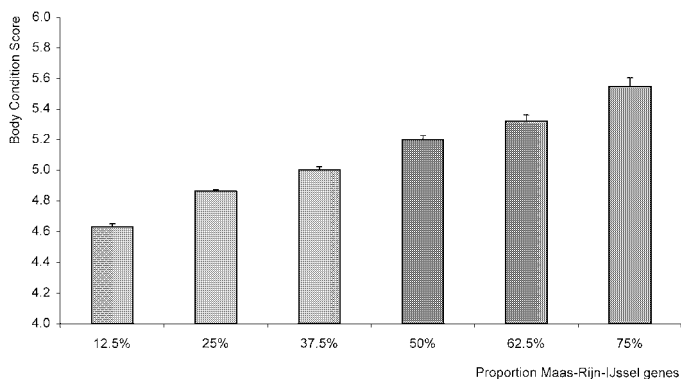


Figure 2. Mean BCS for Red-and-White heifers by proportion of Maas-Rijn-IJssel genes.

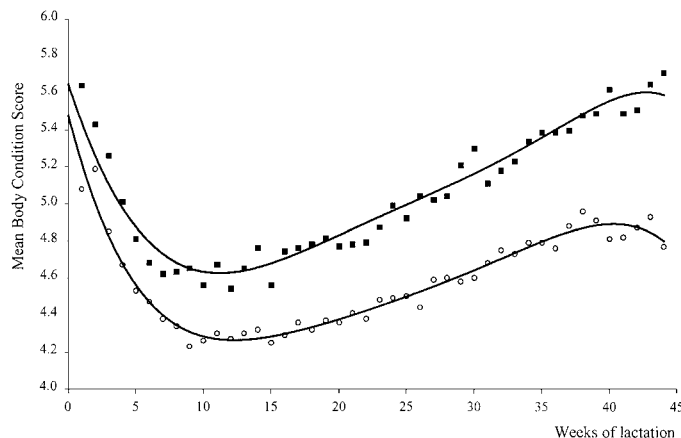


Figure 3. Unadjusted means and lactation effects estimated by a fifth-order polynomial for BCS of Holstein (O) and Red-and-White (■) heifers during first 44 wk of lactation.

week numbers of observations were small. Average BCS at calving was about 5.6 for both breeds. Decrease in BCS was largest during the first lactation weeks. Days in milk with minimum BCS and the magnitude of BCS loss were derived from the fitted polynomial regression. In both data sets, BCS was at minimum at wk 11. Average BCS loss was greater for H (1.2) than for R (1.0). After reaching minimum BCS, BCS increased gradually until the end of lactation. At the end of the 305-d lactation period, mean BCS of H heifers was substantially lower than BCS at calving, whereas mean BCS of R heifers was at about the same level as at calving.

Variance Components

Estimated variance components and heritabilities for BCS across lactation periods are in Table 1. Between-herd variance accounted for 10 to 15% of the total variance; e.g., for H heifers 95% of the herd \times visit solutions were between -0.98 and 0.98 . Heritability was higher for H (0.38) than for R (0.30).

Unadjusted means and estimates for the variance components and heritabilities for BCS within bi-monthly lactation periods are given in Table 2. Unadjusted standard deviations for BCS tended to increase slightly with later lactation periods. Heritability estimates within lactation periods ranged from 0.23 to 0.37. Heritability was lowest in the first period and highest in the second period. Estimates for the genetic correlations between BCS observations in different lactation periods are in Table 3. Genetic correlations between BCS in different lactation periods were close to unity, especially in the H data. In the R data, genetic correlations tended to decrease slightly as period between ob-

Table 1. Number of observations, means \pm SD, herd variance (σ_{hv}^2), genetic variance (σ_a^2), residual variance (σ_e^2), and heritability for BCS in Holstein and Red-and-White heifers.

Data file	n	X \pm SD	σ_{hv}^2	σ_a^2	σ_e^2	h^2
Holstein	108,809	4.50 \pm 1.55	0.241	0.864	1.160	0.38 \pm 0.02
Red-and-White	26,208	4.94 \pm 1.51	0.287	0.665	1.235	0.30 \pm 0.03

servations increased. The high correlations indicated that the genetic variation in BCS changes during lactation is limited.

DISCUSSION

The aim of this study was to estimate phenotypic and genetic parameters for BCS data from a field-recording scheme. As heifers can be scored at all moments in lactation, adequate adjustments for DIM are needed when field data are used for a genetic evaluation. The estimated loss in BCS in this study is in line with results of Ruegg and Milton (1995) and Domecq et al. (1997b). However, several other studies reported lower estimates. For UK Holstein heifers, Jones et al. (1999) found an average BCS loss of only 0.4. On a five-point scale, both Waltner et al. (1993) and Gallo et al. (1996) reported a BCS loss of about 0.3, whereas Ruegg and Milton (1995) estimated a BCS loss of 0.7. The higher estimate for BCS loss in this study might be related to the use of a fifth-order polynomial to model the effect of DIM, whereas Gallo et al. (1996) and Jones et al. (1999) used cubic polynomials. When cubic polynomials were fitted to our data, predicted BCS agreed well with observed BCS in mid and late lactation but not in early lactation. Evaluation of the residuals showed that BCS was systematically underestimated in early lactation, which resulted in an underestimated BCS loss.

The higher BCS loss of H heifers (1.2) compared with R heifers (1.0) might also be related to the higher production level of H. On a national level, the average milk yield of H cows was about 1000 kg higher compared with R cows (8003 vs. 6975 kg; NRS, 1998). Positive relations between BCS loss and production level have been reported (Domecq et al., 1997a; Gallo et al., 1996; Ruegg and Milton, 1995; Waltner et al., 1993).

The moment with minimum BCS was about wk 11 after calving in our study, which was later than estimates in the literature for the time of maximum milk yield and minimum BW (Berglund and Danell, 1987; Gravert, 1985; Wood et al., 1980), which might suggest that changes in BCS do not fully reflect changes in EB.

This study found considerable heritabilities for BCS data from the Dutch type classification scheme based on only visual assessment of BCS. These heritabilities are slightly higher than literature estimates for field data. Heritability estimates for Holstein heifers from the UK ranged from 0.20 to 0.28 (Jones et al., 1999). For Italian-Friesian cows, a heritability of 0.29 was reported (Gallo et al., 1999).

The high genetic correlations between BCS observations from different lactation periods agree with earlier estimates. Koenen and Veerkamp (1998) found very high genetic correlations (0.84 to 1.00) between BCS observations of heifers during the first 26 wk of lactation. Dechow et al. (1999) found genetic correlations >0.90 for BCS data from different lactation moments. Estimates from Jones et al. (1999) were somewhat lower: genetic correlations among BCS observations in different months ranged from 0.63 to 1.00 (on average 0.89). Gallo et al. (1999) found genetic correlations between lactation periods in the range from 0.70 to 0.97. The small changes in genetic variances across lactation periods and the high genetic correlations imply that BCS scores from various lactation periods are genetically similar and that genetic variation among animals for BCS changes during lactation is limited. In practice, this means that BCS observations from all lactation periods can be used in a similar way when the aim is to produce EBV for mean BCS during first lactation.

This study showed that EBV for BCS can easily be obtained from the regular type scoring system, e.g., in

Table 2. Number of observations, mean \pm SD, herd variance (σ_{hv}^2), genetic variance (σ_a^2), error variance (σ_e^2), and heritability¹ for BCS in different lactation periods in Holstein and Red-and-White data file.

Month	Holstein						Red-and-White					
	n	X \pm SD	σ_{hv}^2	σ_a^2	σ_e^2	h^2	n	X \pm SD	σ_{hv}^2	σ_a^2	σ_e^2	h^2
1 to 2	18,209	4.48 \pm 1.54	0.300	0.601	1.226	0.28	4418	4.80 \pm 1.45	0.333	0.455	1.186	0.23
3 to 4	29,348	4.31 \pm 1.50	0.229	0.827	1.159	0.37	6968	4.69 \pm 1.46	0.230	0.657	1.192	0.32
5 to 6	26,941	4.43 \pm 1.52	0.284	0.725	1.253	0.32	6467	4.86 \pm 1.50	0.343	0.528	1.312	0.24
7 to 8	22,826	4.68 \pm 1.56	0.312	0.755	1.287	0.32	5774	5.22 \pm 1.52	0.363	0.603	1.284	0.27
9 to 10	11,485	4.87 \pm 1.61	0.420	0.729	1.342	0.29	2581	5.48 \pm 1.54	0.370	0.626	1.316	0.27

¹Standard errors of the heritabilities ranged from 0.03 to 0.05 for Holstein and from 0.05 to 0.07 for Red-and-White.

Table 3. Genetic correlations between BCS in different lactation periods in the Holstein and Red-and-White dataset.

Month	Holstein					Red-and-White				
	1 to 2	3 to 4	5 to 6	7 to 8	9 to 10	1 to 2	3 to 4	5 to 6	7 to 8	9 to 10
1 to 2	...	0.99	0.99	0.97	0.99	...	0.98	0.94	0.90	0.87
3 to 4		...	1.00	1.00	1.00		...	1.00	0.93	0.88
5 to 6			...	0.99	0.97			...	0.89	0.86
7 to 8				...	1.00				...	1.00
9 to 10				

the Dutch situation, the accuracy of an EBV for BCS of young sires based on 60 scored daughters is about 0.90 to 0.95. Although BCS has no explicit economic value, it might provide additional genetic information on traits that relate to EB such as milk production, feed intake, health, and fertility. The optimal use of a EBV for BCS in combination with EBV for other traits therefore largely depends on the genetic relationships with these traits. For example, Pryce et al. (2000) found a clear genetic correlation between BCS and calving interval and suggested the use of BCS data as a tool to improve fertility. However, as knowledge on most of these relationships is still scarce, further studies are needed before the optimal breeding strategy including genetic information on BCS can be established.

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