Genetic Parameters for Level and Change of Body Condition Score and Body Weight in Dairy Cows

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ABSTRACT

(Co)variance components for body condition score (BCS), body weight (BW), BCS change, BW change, and milk yield traits were estimated. The data analyzed included 6646 multiparous Holstein-Friesian cows with records for BCS, BW, and(or) milk yield at different stages of lactation from 74 dairy herds throughout Southern Ireland. Heritability estimates for BCS ranged from 0.27 to 0.37, while those for BCS change ranged from 0.02 to 0.10. Heritability estimates for BW records varied from 0.39 to 0.50, while heritabilities for BW change were similar to those observed for BCS change (0.03 to 0.09). The genetic correlations between BCS and BW at the same days in milk deviated little from 0.50, and the genetic correlations between BCS change and BW change over the same period ranged from 0.42 to 0.55. BCS and BW directly postpartum were both phenotypically and genetically negatively correlated with both BW change and BCS change in early lactation. The genetic correlations between BCS and milk yield were negative. The results of the present study show that animals that lose most BCS in early lactation tend to gain most BCS in late lactation, a trend also exhibited by BW.

(Key words: genetics, body weight, body condition score, dairy cow)

Abbreviation key: BW5, BW60, BW120, BW180 = BW on d 5, 60, 120, and 180 of lactation, respectively; BW60-5, BW120-60, BW180-120, BW180-5 = change in BW between the respective days; CS5, CS60, CS120, CS180, CS240 = BCS on d 5, 60, 120, 180, and 240 of lactation, respectively; CS60-5, CS120-60, CS180-120, CS240-180, CS240-5 = change in BCS between the respective days; Cum120, Cum180, Cum240 = cumu-

lative milk yields at d 120, 180, and 240 of lactation, respectively; HUKI = Holstein UK and Ireland, Milk60, Milk120, Milk180, Milk240 = milk test-day yields on d 60, 120, 180 and 240 of lactation, respectively; NAHF = North American Holstein-Friesian genetics.

INTRODUCTION

Body condition score is a quick, noninvasive, inexpensive, yet somewhat subjective means of estimating fat stores in dairy cows independent of the animal's frame size and BW (Waltner et al., 1993). It has long been recognized by many researchers (Wildman et al., 1982; Butler and Smith, 1989; Dimech et al., 1997a, 1997b) as a valuable tool in predicting the productive and reproductive performance in many domesticated animals. Its main practical advantage lies in its ability to allow the farmer to monitor and manage the nutritional status and health status of high producing cows during their productive cycle.

Body weight in dairy cows is affected by animal size (skeletal development), degree of fatness, and gut fill (Enevoldsen and Kristensen, 1997), all of which are dependent on the stage of pregnancy, stage of lactation, and age-dependent growth (Koenen et al., 1999). The BW profile of different strains of dairy cattle usually follow a similar pattern; there is a sharp fall in BW at parturition coinciding with the expulsion of the fetus and uterine contents; this is followed by a decline in BW due to the catabolism of body reserves to supply energy for milk production (Jones et al., 1999; Koenen et al., 1999; Buckley et al., 2000c), and there is a subsequent rise until the next parturition as new tissue reserves are built up (Bines, 1976) and the fetus begins to enlarge.

Heritability of BW has been estimated at 0.32 to 0.61 (Jensen et al., 1995; Koenen and Veerkamp, 1998; Veerkamp et al., 2000), while heritability estimates for BCS are 0.20 to 0.45 (Koenen and Veerkamp, 1998; Jones et al., 1999; Pryce et al., 2001; Veerkamp et al., 2001).

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Heritability estimates for BW change range from 0.10 to 0.34 (Veerkamp, 1998; Veerkamp et al., 2000), while heritability for change in BCS to wk 10 of lactation has been quoted as 0.09 (Pryce et al., 2001).

The correlations between BW and milk yield have not been consistent between studies (Tveit et al., 1991; Ahlborn and Dempfle, 1992; Veerkamp and Brotherstone, 1997). This may be attributed to variation in the correlations depending on the stage of lactation at which the BW measurements are taken (Veerkamp and Brotherstone, 1997). The variation in BW throughout lactation may be due to the genetic association between BCS and BW and the patterns of tissue mobilization, which differ throughout the lactation; therefore, covariances between milk yield and BW may also depend on stage of lactation (Veerkamp and Brotherstone, 1997). Mean BCS during lactation is correlated both genetically and phenotypically with production traits (Veerkamp and Brotherstone, 1997; Dechow et al., 2001; Veerkamp et al., 2001); slight, positive correlations between BCS at calving and production have also been reported (Dechow et al., 2001). Most researchers (Walton et al., 1993; Domecq et al., 1997b) stress the importance of the changes in both BW and BCS in deriving correlations with yield.

Very little is known about the genetics behind change in BCS and change in BW during the lactation, although genetic parameters are widely available for BCS and BW. Most estimates of genetic parameters for BCS and BW come from single measurements on related animals at different stages of the lactation. The objective of this study was to estimate the (co)variances of BCS, BW, BCS change, and BW change, and their correlations with yield traits using animals with several measurements during lactation.

MATERIALS AND METHODS

The study was made up of 74 spring-calving dairy herds (70 commercial and 4 research herds) in the south of Ireland, with a potential 6750 spring calving cows available for inclusion in the dataset. Herd size ranged from 30 to 240 cows. The key factors in herd selection were: 1) high standard of recording, 2) spring-calving herds, 3) at least the sire and maternal grand sire were known for the majority of cows in the herd, and 4) participating in A4 milk recording (once every 4 wk).

Pedigree Information

Of the cows available, 49% were herd book registered with Holstein UK and Ireland (HUKI). Four generations of ancestry on the paternal and maternal side were identified for 92 and 42% of these cows, respec-

Table 1. Number of cows available for analysis in the study.

	No. of cows
Potential spring calving cows	6750
Cows with BCS/BW	5815
Cows with >2 BCS/BW	5234
Cows with milk yield	6695
Cows with >1 test day yield	6528
Cows with BCS/BW and milk yield	5096

tively. For the remaining 51% of cows not registered with HUKI, their sire and maternal grand sire were obtained from Dairy Management Information System (Dairy-MIS; Crosse, 1986). Dairy-MIS is a recorder-based computerized system collecting detailed stock, farm inputs, production, and reproduction information on a monthly basis. For these herds, the paternal ancestry and maternal grand sire ancestry was provided by HUKI to the same level as for the pedigree cows.

The proportion of North American Holstein-Friesian genetics (NAHF) for each sire/maternal grand sire contained in the dataset was also provided by HUKI. The proportion of NAFH for the individual cows in the study was calculated as $0.5 \times \text{sire}$ plus $0.25 \times \text{maternal grand sire}$, assuming that maternal grand dams have zero NAFH. The proportion of NAFH was available for all sires in the dataset; however, it was only available for 50% of maternal grand sires and was assumed to be zero as these bulls were available pre-1980 and were not present in the dataset (Matt Winters, HUKI, personal communication). Holstein percentage in the present study varied from 0 to 75%. Average Holstein percentage was 48%. In Ireland, due to the continual importation of NAFH, the Holstein percentage of the dairy population is continually increasing (Buckley et al., 2000b). On this basis, it was assumed that by correcting for Holstein percentage, the need for genetic grouping of the pedigree would be minimized.

Data edits are summarized in Table 1. Within the edited dataset, there were 697 different sires with daughters. The number of daughters per sire ranged from 1 to 344, and the average was 9.5 daughters per sire. Daughters of the same sire were present on average in 2.7 different herds ranging from 1 to 43 herds. A total of 448 dams had more than one daughter in the dataset, with a maximum of four daughters with records per dam; 609 cows with records had daughters with records. A total of 4800 of the cows with records had identified maternal grandsires. The additive genetic relationship matrix included 14,272 animals.

BCS and BW Traits

Trained Teagasc personnel visited the farms up to nine times annually. Visits were carried out at two and

a half to four weekly intervals, with visits being more frequent in early lactation. During visits, all cows in the herd were recorded for BW and BCS. Body weight was recorded electronically, using a portable weighing scales and Winweigh software package. The scales were calibrated weekly against permanent scales in Moorepark Research Centre with cows and were calibrated again with known weights on arrival at each farm. BCS, recorded simultaneously using Winweigh software package was on a scale of 1 (thin) to 5 (fat) with increments of 0.25 (Lowman, 1976).

A total of 5815 cows from 61 herds had recorded spring calving dates and BCS and/or BW records. These data were further edited to include cows that had either greater than two BCS or BW observations between calving and 350 d postcalving; this reduced cow numbers to 5234 from 55 herds. After editing, there were on average 7.36 observations for BCS and 6.48 observations for BW for the animals from the commercial herds. The two numbers differed because only BCS was recorded on the last visit to each farm. A smoothing spline curve with four knot points was fitted to all the data for each cow separately using GENSTAT (Genstat 5, 1997) to model the effects of DIM on BCS and BW. The output facilitated the estimation of the level of both traits for specific DIM. This will account for different growth/BCS curves of differently aged animals. BCS and BW at d 5, 60, 120, 180 and BCS at d 240 (**BW5, BW60, BW120, BW180, CS5, CS60, CS120, CS180, CS240**) were considered to be traits of interest. To accept the estimates for BCS and BW at d 5, 60, 120, 180, and 240, criteria were set out such that an actual observation should have been recorded within an acceptable time range for the estimate to be considered accurate. Criteria set out for CS5 and BW5 were that an observation should have been recorded on the animal between d 5 and 35 of lactation. An interval range of 50 d was set around each trait for CS60, BW60, CS120, and BW120. For CS180 and BW180, the animal had to have an observation after 120 DIM, and a record after d 150 for CS240 to be accepted. Estimates deemed to be inaccurate based on these criteria were considered missing values and omitted from the analysis. Following this editing, cows had on average 3.85 BW predicted records and 4.78 BCS predicted records from a possible four and five records, respectively. BCS change and BW change were calculated as the difference between the traits of interest (where animals had an estimate for both test days).

Milk Yield Traits

A total of 6695 cows from 74 herds had recorded spring calving dates and milk records. Test-day records

for each cow were obtained from the Irish Dairy Recording Co-operative. For inclusion in the analysis, each cow had to have at least two test-day milk records before 350 d postcalving; this reduced cow numbers to 6528 from 74 herds. Of these cows, 5096 had BCS and BW records included in the analysis. As with the BCS and BW traits, a smoothing spline with four knot points was fitted separately to each cow's individual milk test-day yields. This will account for differently shaped lactation curves for each animal. Observations within a range of 50 d around the estimates of milk test-day yields on d 60 (**Milk60**), milk test-day yields on d 120 (**Milk120**), and milk test-day yields on d 180 (**Milk180**) were accepted, while an interval of 80 d was accepted around milk test-day yields on d 240 (**Milk240**). As with the BCS and BW estimates, unaccepted estimates were treated as missing values and were not included in the analysis. Three cumulative milk yield traits (Cum120, Cum180, and Cum240) were also derived for each cow using the average of the test-day yields in increments of 30 d from d 60 to 120, d 60 to 180 and d 60 to 240, respectively. This average was then converted to a cumulative yield by multiplying the average of the test-day yields by the respective number of days. Cumulative yields were only included for a cow that had estimates for all 30-d interval test days included in the calculation of that cumulative yield. The 5096 cows that had both milk records, and BCS and BW observations had an average of 3.9 milk test-day records from a possible four and an average of 2.83 cumulative yield records from a possible three. Numbers of observations for milk production traits fell as the lactation progressed.

Data Analysis

A multivariate analysis for all 25 traits simultaneously was not computationally feasible. For this reason, we carried out a series of multivariate analyses in VCE (Neumaier and Groeneveld, 1998), and the remaining correlations were estimated with a series of bivariate analyses carried out in ASREML (Gilmour et al., 2001). Blocks within trait (e.g., CS5, CS60, CS120, CS180, and CS240) were analyzed together as one multivariate analysis. Following the analysis a 21×21 matrix was developed containing all the genetic correlations between the 21 traits (4 of the milk traits were not included in the correlation matrix). Due to the large matrix size, some eigenvalues were negative and were therefore made positive, and the correlation matrix recalculated using the eigenfunctions. In this new positive definite matrix, 85% of the correlations had changed by less than 0.05 and 95% of the correlations by less than 0.10. The SE, however, were not adjusted

since the change in correlations were so small and are thus likely to have little effect on the SE of the correlations. Therefore, estimates of those genetic correlations are presented. Herd-season groups were formed. Season was defined as month of calving. Herd-season groups with fewer than four cows had their records moved into an adjoining season group from the same herd to facilitate a more accurate estimate. The following linear animal model was used for the analysis of all traits:

$$Y_{ijklm} = \mu + h_j \times s_l + l_k + b_1Hol + b_2Hol^2 + a_i + e_{ijklm}$$

Where:

- Y_{ijklm} = Observation for each trait m on animal i in herd j ,
 μ = overall mean,
 $h_j \times s_l$ = fixed effect of herd j by month l of calving interaction ($jl = 196$),
 l_k = Fixed effect of lactation number ($k = 1, 2, 3, 4+$),
 $b_1Hol + b_2Hol^2$ = fixed effect of a quadratic polynomial regression on the percentage of North American Holstein-Friesian genes in animal i ,
 a_i = random animal effect,
 e_{ijklm} = random residual term,

The random animal and residual effects were assumed to be normally distributed with $\text{var}(a) = G$ and $\text{var}(e) = R$.

As changes in a trait are the differential between two measures, variances can be calculated using the variances and covariance between the two measures (e.g., the variance of CS60-5 may be calculated as the sum of the variances for CS5 and CS60 less twice the covariance between them). By calculating both the phenotypic and genetic variances for CS60-5, it is then possible to calculate the heritability of the trait.

RESULTS

As the proportion of NAHF increased, CS5 continually decreased while Cum240 continually increased. CS5 for animals of 0% NAHF was significantly higher than CS5 for animals with 75% NAHF, while Cum240 was significantly higher for the latter.

Variance Components

The mean, phenotypic, and genetic standard deviation and heritability for each of the 25 traits analyzed are presented in Table 2.

The heritabilities for BCS at different stages of lactation ranged from 0.27 at d 240 to 0.37 at d 60 (Table 3). Body weight had higher heritabilities than BCS, with values ranging from 0.39 to 0.50. The heritabilities of BCS change and BW change were lower than those observed for BCS and BW ranging from 0.02 to 0.10 and 0.03 to 0.09 for BCS change and BW change, respectively. The heritability of the change traits estimated by a univariate analysis were identical to those estimated from the (co)variances of the two traits involved in the calculation of the change trait. For both BCS change and BW change the heritability estimates were highest in early lactation. The heritability estimates for all of the milk yield traits were ranging from 0.19 to 0.29.

Correlations

BCS and BW. The phenotypic correlations between BCS at successive stages in lactation ranged from 0.64 to 0.89. The corresponding genetic correlations were all close to unity (0.83 to 0.95). However, as the interval between stages increased the genetic correlations decreased from 0.83 (CS5 with CS60) to 0.75 (CS5 with CS120) to 0.72 (CS5 with CS180), and rose again to 0.77 (CS5 with CS240). The standard errors for these correlations varied from 0.26 to 0.50. The phenotypic correlations between successive BW measures were 0.76 to 0.89. Genetic correlations between all BW test-day records remained close to unity (0.90 to 0.97). Both the phenotypic and the genetic correlations between level of BCS and BW at the same DIM deviated little from 0.50 (Table 3).

BCS change and BW change. The phenotypic and genetic correlations between BCS change at various stages of lactation and for BW change at various stages of lactation are presented in Tables 4 and 5, respectively. There was a moderate phenotypic association between BCS change in early to mid-lactation as indicated by CS60-5, CS120-60, and CS180-120 with BCS change from d 5 to 240 of lactation (0.25 to 0.51) (Table 4), while the genetic correlations over the same measurement periods ranged from 0.38 to 0.58 (Table 5). The genetic correlations between BCS change in periods before d 180 with CS240-180 were all negative. Figure 1 shows the effect of selecting for a greater loss in BCS to d 60 of lactation on BCS change in later lactation. Those animals that lose most BCS in early lactation continue to do so until d 180 of lactation, after which it is these animals that gain most BCS. The trend of a moderate genetic correlation between BCS change in early lactation with BCS change over the whole lactation was also noticeable for BW change; however, the restoration of lost BW (BW60-5) occurred earlier in lactation (120 to 180 DIM); the SE for BW change were

Table 2. Number of observations, mean, genetic SD (σ_g) phenotypic SD (σ_p), heritabilities (h^2) and estimated SE of h^2 for a range of body condition score, body weight and milk yield traits.

Trait ¹	No. Obs	Mean	σ_g	σ_p	h^2	SE of h^2
CS5 (BCS units $\times 100$)	5066	301.1	22.3	41.3	0.29	0.046
CS60 (BCS units $\times 100$)	5165	283.1	18.6	30.6	0.37	0.047
CS120 (BCS units $\times 100$)	4928	286.0	15.6	26.0	0.36	0.050
CS180 (BCS units $\times 100$)	4995	288.3	14.2	26.5	0.29	0.047
CS240 (BCS units $\times 100$)	4808	290.0	14.4	27.9	0.27	0.048
CS60-5 (BCS units $\times 100$)	5013	-18.2	9.5	31.8	0.09	0.032
CS120-60 (BCS units $\times 100$)	4883	2.7	6.0	19.2	0.10	0.033
CS180-120 (BCS units $\times 100$)	4794	2.1	2.3	18.5	0.02	0.016
CS240-180 (BCS units $\times 100$)	4808	1.3	2.6	16.4	0.03	0.020
CS240-5 (BCS units $\times 100$)	4668	-11.2	11.1	40.9	0.07	0.030
BW5 (kg)	5021	534.4	32.6	52.5	0.39	0.050
BW60 (kg)	5172	534.4	30.1	43.8	0.47	0.051
BW120 (kg)	4933	552.9	31.1	44.0	0.50	0.051
BW180 (kg)	4988	569.9	33.8	48.7	0.48	0.053
BW60-5 (kg)	4976	0.0	8.0	34.3	0.05	0.023
BW120-60 (kg)	4893	18.3	6.0	20.6	0.09	0.028
BW180-120 (kg)	4803	16.8	3.9	23.4	0.03	0.017
BW180-5 (kg)	4799	35.7	9.3	42.9	0.05	0.022
Cum120M (kg)	6352	3189	201	397	0.29	0.053
Cum180M (kg)	6211	4383	285	539	0.28	0.052
Cum240M (kg)	5735	5265	356	656	0.26	0.053
60Milk (kg)	6368	28.5	1.7	3.8	0.19	0.037
120Milk (kg)	6479	24.5	1.6	3.3	0.24	0.040
180Milk (kg)	6367	19.7	1.5	3.0	0.26	0.041
240Milk (kg)	5959	14.1	1.3	3.0	0.19	0.037

¹CS5, CS60, CS120, CS180, CS240 = BCS on d 5, 60, 120, 180 and 240 of lactation, respectively; CS60-5, CS120-60, CS180-120, CS240-180, CS240-5 = change in BCS between the respective test days; BW5, BW60, BW120, BW180 = BW on d 5, 60, 120, and 180 of lactation, respectively; BW60-5, BW120-60, BW180-120, BW180-5 = change in BW between the respective test days; Cum120, Cum180, Cum240 = cumulative milk yields at d 120, 180, and 240 of lactation, respectively; Milk60, Milk120, Milk180, Milk240 = milk test-day yields on d 60, 120, 180, and 240 of lactation, respectively.

higher than for BCS change. Changes in BCS were moderately phenotypically (0.21 to 0.44) and more strongly genetically correlated (0.42 to 0.55) with changes in BW over the same period (Table 3).

The phenotypic correlations between the BCS and BW traits with the BCS change and BW change traits are shown in Table 6. A similar table showing the genetic correlations is presented in Table 7. The phenotypic correlations between CS5 and all of the BCS change traits were negative, as were the genetic correlations between CS5 and the BCS change traits, with the exception of that with CS240-180. BCS in mid- to late lactation was poorly genetically correlated with CS60-

5. The SE for the correlations involving CS180-120 were all high due to both a lower number of observations and a lower heritability for CS180-120 than most other traits. Phenotypic and genetic correlations between BW and BW change showed similar trends to the correlations between BCS and BCS change.

Table 3. Phenotypic and genetic correlations between BCS with BW at the same DIM and BCS change with BW change over the same period and estimated SE of the genetic correlations.

DIM	Phenotypic	Genetic	SE of r_g
5	0.55	0.50	0.077
60	0.51	0.46	0.070
120	0.46	0.35	0.080
180	0.40	0.45	0.084
60-5	0.44	0.48	0.219
120-60	0.31	0.55	0.186
180-120	0.21	0.42	0.492

Figure 1. Effect of selecting on body condition score (BCS) loss between d 5 and 60 of one (●), two (■), or three (▲) genetic standard deviations, on BCS change throughout lactation relative to the mean (◆). Included also on the vertical bars is one genetic standard deviations of the mean BCS curve.

Table 4. Phenotypic correlations between BCS change at different stages of lactation (below diagonal) and BW change at different stages of lactation (above diagonal).

DIM	60-5	120-60	180-120	240-180	180-5
60-5		-0.15	0.06		0.72
120-60	0.00		-0.06		0.33
180-120	-0.04	-0.04			0.52
240-180	-0.04	-0.24	0.25		
240-5	0.51	0.25	0.27	0.22	

Correlations with milk yield. The phenotypic correlations between CS5 and milk production were all close to zero (Table 8), while the phenotypic correlations between all other BCS traits and milk yield traits were all negative and ranged from -0.21 to -0.10. BCS in mid- to late lactation showed moderate negative genetic correlations with milk yield (-0.40 to -0.22).

The phenotypic correlations between BCS change in early lactation with milk yield were all negative. However, BCS change in late lactation was not phenotypically correlated with milk yield. CS60-5 had a weak negative genetic correlation with Milk60 (-0.11) and also with Cum240 (-0.17); both correlations were not significantly different from zero.

The phenotypic correlations and genetic correlations between BW and BW change with the milk yield traits are given in Tables 8 and 9, respectively. All phenotypic correlations between BW and milk yield were either positive and low or close to zero (-0.01 to 0.20). There was a trend for BW during lactation to be positively genetically correlated with milk production in early lactation. The phenotypic correlations between BW change and milk production were all weak and negative.

DISCUSSION

The objective of this study was to estimate the genetic parameters for BCS and BW related traits. No other study with the same objective had such a large number of cows with both BCS and BW records measured repeatedly on the same animal throughout lactation.

Table 5. Genetic correlations and estimated SE¹ between BCS change at different stages of lactation (below diagonal) and BW change at different stages of lactation (above diagonal).

DIM	60-5	120-60	180-120	240-180	180-5
60-5		0.16*	-0.47*		0.64**
120-60	0.26***		0.11*		0.74*
180-120	0.26**	0.38*			0.10*
240-180	-0.37**	-0.61**	-0.56***		
240-5	0.58***	0.54***	0.38*	-0.34**	

¹***SE < 0.10.

**SE < 0.20.

*SE < 0.30.

However, estimates of variance components within a population may be subjected to bias by not accounting for selection among older cows and progeny tested sires. A consequence of selection would be a change in gene frequencies within a population, resulting, for example, in a reduction in genetic variances (Falconer, 1989). Therefore, variance components estimated without accounting for selection within a population may lead to biased genetic variances for selected traits or other correlated traits. Hofer (1998), in his review of variance component estimation, recommended that all data on which selection decisions were based and all pedigree data should be included in the analysis. It is not practical to include all data on which selection decisions were based in analysis, as most selection takes place in other countries. Another alternative would be to include only daughters from progeny-tested sires in the analysis. However, given the limited use of progeny testing in Ireland, and the difficulty of recording BW and BCS, it was not feasible to restrict the data to daughters of progeny tested sires. In the study of Brotherstone (1994) proven sires were added as fixed effects to improve the connectedness of the data, while randomly used sires were used to estimate the between-sire variance components. Selection in the data is, however, a common issue for all studies focusing on traits that are relatively difficult to measure, i.e., using data from experimental herds or collecting data in farms. The dataset in this study consisted of 74 different farms, which is large compared with most other studies measuring BCS and BW repeatedly on the same animals, and the farms were a good representative sample of the whole population.

Body weights observed in this study were similar to those reported by Buckley et al. (2000a) in an Irish research herd, and also by Koenen and Veerkamp (1998). Observed BCS in the present study tended to be higher than that observed by Buckley et al. (2000a) and Koenen and Veerkamp (1998); the present phenotypic SD for CS5 was about twice as high as the latter study. The observed BCS pattern, i.e., that all animals lost BCS after calving and by d 240 of lactation had still not regained lost condition) was similar in all studies. The drop in BCS directly postpartum was more pronounced in the present study than that reported by Koenen and Veerkamp (1998) but was similar to that observed by Buckley et al. (2000c). A likely explanation for the more pronounced drop in BCS to d 60 in the present study as compared to that observed by Koenen and Veerkamp (1998) was the probable difference in feed quality available to the cows in early lactation. The average metabolizable energy value for grass silage offered immediately postcalving across the 55 herds was 10.47 MJ/kg DM compared with a TMR in the

Table 6. Phenotypic correlations between BCS and BW traits¹ at different stages of lactation with BCS change and BW change at different stages of lactation.

Trait ¹	CS60-5	CS120-60	CS180-120	CS240-180	CS240-5	BW60-5	BW120-60	BW180-120	BW180-5
CS5	-0.68	-0.40	-0.15	-0.03	-0.77	-0.38	-0.15	-0.05	-0.39
CS60	0.12	-0.54	-0.24	-0.09	-0.31	-0.05	-0.15	-0.05	-0.15
CS120	0.13	0.11	-0.32	-0.29	-0.13	0.04	0.05	-0.05	0.02
CS180	0.08	0.05	0.40	-0.15	0.16	0.07	0.11	0.10	0.13
CS240	0.05	-0.10	0.46	0.47	0.34	0.01	0.08	0.09	0.10
BW5	-0.29	-0.28	-0.10	-0.03	-0.39	-0.56	-0.09	-0.04	-0.50
BW60	0.00	-0.20	-0.11	-0.06	-0.17	0.11	-0.21	-0.02	-0.03
BW120	0.02	-0.07	-0.76	-0.06	-0.08	0.04	0.25	-0.07	0.10
BW180	0.02	-0.07	0.03	-0.04	-0.02	0.03	0.17	0.43	0.35

¹BW5, BW60, BW120, BW180 = BW on d 5, 60, 120, and 180 of lactation, respectively; BW60-5, BW120-60, BW180-120, BW180-5 = change in BW between the respective test days; CS5, CS60, CS120, CS180, CS240 = BCS on d 5, 60, 120, 180, and 240 of lactation, respectively; CS60-5, CS120-60, CS180-120, CS240-180, CS240-5 = change in BCS between the respective test days.

Langhill study. This is likely to induce higher BCS catabolism postpartum as reported by Pryce et al. (2001) for selected animals on different diets.

BCS and BW

The heritability of BCS in the present study ranged from 0.27 to 0.37 and is similar to many studies (Koenen and Veerkamp, 1998; Jones et al., 1999; Koenen et al., 2001). The heritabilities were higher than those reported by Dechow et al. (2001); however, they followed a similar pattern, namely, the highest heritability for BCS occurred when mean BCS was at its lowest (d 60 in the present study). The trend of highest heritability when BCS is lowest was also noticed by Koenen et al. (2001). This indicates that in early lactation when BCS of the cows tends to be at its lowest point, the animal's BCS is less influenced by differences in management practices.

Heritabilities of BW at different stages ranged from 0.39 to 0.50 and were similar to those in other studies

(Veerkamp and Brotherstone, 1997) but were somewhat lower than those reported by Koenen and Veerkamp (1998). The present BW heritability estimates were higher than those estimated by Ahlborn and Dempfle (1992) from field data in New Zealand. Unlike the present study, body weight in the New Zealand study was assessed subjectively, and this is likely to affect accuracy as indicated by the low repeatability of subjective scores (Ahlborn and Dempfle, 1992). The heritability of BW5 estimated in the present study (0.39) was very similar to the value reported by Jensen et al. (1995) on the second day of lactation, and that estimated by Veerkamp and Brotherstone (1997).

The genetic correlations between successive measurements of BCS were close to unity and agreed with several other studies (Koenen and Veerkamp, 1998; Dechow et al., 2001; Koenen et al., 2001). The trend of decreasing correlations as the interval between measurements increases was also found. The increase in the genetic correlation between CS5 and CS240 is an indication that animals have a genetically predeter-

Table 7. Genetic correlations between BCS and BW traits¹ at different stages of lactation with BCS change and BW change at different stages of lactation.

Trait ¹	CS60-5	CS120-60	CS180-120	CS240-180	CS240-5	BW60-5	BW120-60	BW180-120	BW180-5
CS5	-0.51**	-0.72***	-0.42+	0.47*	-0.74**	-0.56**	-0.11**	0.01*	-0.53**
CS60	-0.03**	-0.70***	-0.30+	0.31*	-0.41**	-0.33**	-0.03**	0.17*	-0.21*
CS120	0.01**	-0.54**	-0.26+	0.17*	-0.33**	-0.22**	0.07**	0.14*	-0.08*
CS180	0.11**	-0.52**	-0.24+	0.13*	-0.26**	-0.23**	0.18**	0.16*	-0.02*
CS240	0.00**	-0.56**	-0.29+	0.35*	-0.29**	-0.20**	0.15**	-0.01*	-0.09*
BW5	-0.23**	-0.51**	0.36+	0.27*	-0.27**	-0.43**	0.13**	0.27*	-0.10*
BW60	-0.08**	-0.45**	0.45+	0.27*	-0.07**	-0.17**	0.17**	0.20*	0.09*
BW120	-0.07**	-0.36**	0.52+	0.21*	-0.01**	-0.14**	0.28**	0.20*	0.20**
BW180	0.00**	-0.38**	0.46+	0.12*	-0.05**	-0.26**	0.32**	0.35**	0.18**

¹BW5, BW60, BW120, BW180 = BW on d 5, 60, 120, and 180 of lactation, respectively; BW60-5, BW120-60, BW180-120, BW180-5 = change in BW between the respective test days; CS5, CS60, CS120, CS180, CS240 = BCS on d 5, 60, 120, 180, and 240 of lactation, respectively; CS60-5, CS120-60, CS180-120, CS240-180, CS240-5 = change in BCS between the respective test days.

***SE < 0.10.

**SE < 0.20.

*SE < 0.30.

+SE < 0.50.

Table 8. Phenotypic correlations between BCS traits, BW traits, and milk yield traits.¹

Trait ¹	Milk60	Milk240	Cum240
CS5	0.06	0.00	0.04
CS60	-0.10	-0.10	-0.12
CS120	-0.20	-0.13	-0.21
CS180	-0.21	-0.14	-0.21
CS240	-0.18	-0.16	-0.19
CS60-5	-0.18	-0.10	-0.17
CS120-60	-0.11	-0.01	-0.09
CS180-120	0.00	0.01	0.03
CS240-180	0.05	-0.04	0.03
CS240-5	-0.17	-0.11	-0.17
BW5	0.20	0.04	0.17
BW60	0.17	0.02	0.14
BW120	0.12	0.01	0.11
BW180	0.09	-0.01	0.09
BW60-5	-0.10	-0.04	-0.09
BW120-60	-0.11	-0.01	-0.05
BW180-120	-0.03	-0.02	-0.01
BW180-5	-0.16	-0.05	-0.11

¹CS5, CS60, CS120, CS180, CS240 = BCS on d 5, 60, 120, 180, and 240 of lactation, respectively; CS60-5, CS120-60, CS180-120, CS240-180, CS240-5 = change in BCS between the respective test days; BW5, BW60, BW120, BW180 = BW on d 5, 60, 120, and 180 of lactation, respectively; BW60-5, BW120-60, BW180-120, BW180-5 = change in BW between the respective test days; Cum240 = cumulative milk yield at d 240 of lactation; Milk60, Milk240 = milk test-day yields on d 60 and 240 of lactation, respectively.

Table 9. Genetic correlations between BCS traits, BW traits, and milk yield traits, and the estimated SE of the correlations.¹

Trait ¹	Milk60	Milk240	Cum240
CS5	-0.16**	-0.14**	-0.13**
CS60	-0.23**	-0.22**	-0.28**
CS120	-0.40**	-0.22**	-0.39**
CS180	-0.34**	-0.22**	-0.36**
CS240	-0.23**	-0.35**	-0.31**
CS60-5	-0.11*	-0.04*	-0.17**
CS120-60	-0.05**	0.21*	0.01*
CS180-120	0.37+	0.23+	0.41+
CS240-180	0.12*	-0.39**	-0.09+
CS240-5	0.08*	-0.07**	-0.04**
BW5	0.22**	-0.14**	0.09**
BW60	0.32**	-0.10**	0.17**
BW120	0.34**	-0.11**	0.18***
BW180	0.31**	-0.14**	0.07**
BW60-5	0.21*	0.33*	0.29*
BW120-60	-0.04*	0.08*	0.03*
BW180-120	0.10*	0.03*	-0.01+
BW180-5	0.14*	0.29*	0.18*

¹CS5, CS60, CS120, CS180, CS240 = BCS on day 5, 60, 120, 180, and 240 of lactation, respectively; CS60-5, CS120-60, CS180-120, CS240-180, CS240-5 = change in BCS between the respective test days; BW5, BW60, BW120, BW180 = BW on d 5, 60, 120, and 180 of lactation, respectively; BW60-5, BW120-60, BW180-120, BW180-5 = change in BW between the respective test days; Cum240 = cumulative milk yield at d 240 of lactation; Milk60, Milk240 = milk test day yields on d 60 and 240 of lactation, respectively.

***SE < 0.10.

**SE < 0.15.

*SE < 0.30.

+SE < 0.40.

mined BCS that they strive to achieve. It is hypothesized that this correlation would have been higher if BCS data were available later than d 240 of lactation.

The correlations between BCS and BW in Table 3 show that variation in BCS throughout the lactation accounts for about quarter of the phenotypic and genetic variation in BW throughout the lactation. This is slightly lower than the genetic correlation of 0.67 between mean BCS and mean BW reported by Veerkamp and Brotherstone (1997). These correlations indicate that some breeding indices pursuing a reduction in BW, to increase animal efficiency, may also lead to reducing the animal's BCS. This problem may be overcome by including BCS in the index.

Correlations Between BCS Change and BW Change

The negative genetic correlations between BCS change in early to mid-lactation with BCS change in late lactation indicate that those cows that lose most BCS in early lactation gain most BCS in late lactation (Figure 1). The moderate to strong correlations between both BCS change and BW change in early lactation with BCS change and BW change over the whole period of lactation studied may be due to the part-whole relationship between the traits since change over the whole lactation will include change that occurred earlier in lactation.

Change in BCS

It has been suggested (Wildman et al., 1982) that the change in BCS throughout the lactation may be a more important trait affecting cow performance than the level of BCS. Since the difference between the genetic values of the BCS traits used to calculate BCS change will be smaller than the phenotypic differences and thus the genetic variance of BCS change will be proportionally smaller than the corresponding phenotypic variance, a lower heritability is expected for BCS change. In the present study the heritability for BCS change ranged from 0.02 to 0.10. This agrees with the heritability of 0.09 estimated by Pryce et al. (2001) for change in BCS to wk 10 of lactation. Also, our heritability estimate of 0.09 for CS60-5 is identical to that of Gallo et al. (2001) calculated based on the (co)variances of BCS to d 75 of lactation and BCS from d 76 to 130 of lactation. It is worthwhile noting that with a heritability of 0.09 for CS60-5, there is indeed some scope for improvement in this trait. It also showed one of the highest genetic variance of the BCS change traits analyzed in this study. The low heritability for BCS change in the present study may also be a consequence of mea-

suring BCS in quarter units. For CS60-5 the phenotypic SD was 0.32 BCS units and, therefore, about 95% of the animals will be either gaining or losing less than 0.6 of a BCS unit. Thus, a large measurement error is expected when using quarter scores at each period and this will reduce the heritability for these traits.

We are unaware of any trial-based literature documenting the genetic correlations between BCS and BCS change, but the negative phenotypic correlations (Table 6) agree with observations made from field data (Garnsworthy, 1988). The phenotypic correlations in the present study suggest that cows that are fatter immediately postcalving tend to lose more condition to d 240; this suggestion is also supported by the high genetic correlation. The results also showed that the level of BCS recorded in mid- to late lactation is a poor genetic indicator of early BCS loss (CS60-5), which is the BCS change trait that is arguably phenotypically the most important for animal fertility (Butler and Smith, 1989; Domezq et al., 1997a). Thus by selecting for CS60-5, changes in the genetic level of BCS in mid- to late lactation are unlikely to occur, although selection for increased BCS loss to d 60 is likely to increase CS5, due to the moderate genetic correlation (-0.51). However, such a high correlation may be due to the part-whole relationship between the two traits since CS60-5 is calculated from CS5. This part-whole relationship indicates that most of the variation in loss is due to CS5 rather than CS60, since the genetic correlation between CS60-5 and CS60 is low (-0.03 ; $SE = 0.16$). The genetic correlation between CS5 and CS60-5 is important since it may provide a more practical option of selection for reduced BCS loss in early lactation than having to record BCS twice on each animal.

Change in BW

Body weight change throughout lactation had a lower heritability than BW throughout lactation and, therefore improvement through selection may prove to be slow. Similar to BCS change, the low heritability for BW change may be an artifact of using a difference between two traits. The difference in genetic variance between two traits will be smaller than the phenotypic difference, which will result in a proportionally larger phenotypic variance for the change trait and thus a lower heritability. Our estimate of 0.05 for BW change from d 5 to 60 was considerably lower than that of 0.28 over a similar time period in heifers estimated by Lee et al. (1992). One reason for difference is that the 1266 heifers in the latter study were reared with the same management and were fed to yield during lactation. This is likely to reduce phenotypic variance for BW change and, thereby, increase the observed heritability

for the trait. Another reason may be that Lee et al. (1992) may have used more frequent weight measurements in their calculations of weight at a particular DIM.

It is not surprising that cows with high CS5 tended to lose BW to d 60, since they also lose BCS and both traits are correlated. The genetic correlation between BW5 and BW60-5 of -0.43 is similar to the -0.41 estimated by Tveit et al. (1991) for similar traits, and indicates that heavier animals at d 5 tended to lose most BW postpartum.

Correlations with Milk Production

Phenotypically, neither BCS directly postpartum nor BCS change had any influence on milk production. This is in contrast with previously published negative correlations (Garnsworthy, 1988; Waltner et al., 1993). Cows that are genetically superior milk producers tend to have genetically lower BCS in late lactation, which agrees with previous observations (Veerkamp and Brotherstone, 1997; Dechow et al., 2001). A reduced BCS for higher yielding cows is expected since many studies have shown a lower BCS in animals selected for high milk yield (Pryce et al., 2001), and also since the increase in intake associated with selection for yield is expected to cater for less than 50% of the extra milk produced (van Arendonk et al., 1991).

Body weight throughout lactation had a moderate positive genetic correlation with Milk60 (0.22 to 0.34). The genetic correlations between BW and milk production had comparable correlations with milk yield as those reported in the literature using mean BW as a trait (Veerkamp, 1998).

It can be concluded from the present study that BCS and BW are genetically correlated, as are BCS change and BW change in early to mid- lactation. Cows that lose most BCS before d 60 of lactation continue to lose most to d 180, after which these animals replenish the most. The study also shows that BCS change and BW change traits have a low heritability. As a result, improvement through selection in these traits may prove slow. However, due to the genetic associations between BCS, BW, BCS change, and BW change, improvements in BCS change and BW change in early lactation are achievable through suitable inclusion of any of the BCS and/or BW traits in a selection index. Before the inclusion of these traits in a breeding index can be recommended, the correlations between these traits and those of fertility and health of the dairy cow must first be established.

The high SE of the genetic correlations observed in this study, especially involving the change traits, may indicate the use of more suitable methods (e.g., random

regression models and covariance functions) to fit the data. However, we first thought it necessary to use conventional methods to analyze these traits, which can later be used for comparisons with other methods.

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