Genetic Evaluation for Body Condition Score in the Walloon Region of Belgium

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Abstract

The objectives of this study were 1) the development of the genetic evaluation for body condition score (**BCS**) in the Walloon Region of Belgium using BCS data from the first three lactations, and 2) the development a method for expressing BCS breeding values as an indicator optimizing the genetic gain on fertility. Daily heritabilities for BCS ranged between 0.08 and 0.31 according to the number and the stage of lactation. Seven different options for expressing BCS breeding values were compared. Results indicated that BCS could be used as an indicator trait for improving fertility. Selecting for higher minimum genetic BCS averaged among the first 3 lactations would lead to a similar response to selection than selecting directly on PR. However negative impacts of selecting BCS on economically important traits other than fertility have also to be considered.

Introduction

Body Condition Score (**BCS**) assesses the stored energy reserves of the dairy cow and is therefore commonly used as an indicator of the extent and the duration of the postpartum negative energy balance (Roche *et al.*, 2009). A regular body condition scoring in a dairy herd is a valuable decision making tool to fine-tune feeding and manage fertility. Moreover the inclusion of BCS in selection programs has to be considered because of its relationships with economically important traits, especially fertility. However, target values for BCS vary across the lactation contrary to the most of the other traits such as milk yield for which a high value is desired. Currently, expression of breeding values for BCS is generally done as an average of the genetic effect for an animal across the entire lactation and does not take into account this specificity.

Bastin *et al.* (2007) reported the work done for the development of a genetic evaluation for BCS in the Walloon Region of Belgium using a two-trait (BCS and angularity) random regression model for first lactation. They indicated the interest of including angularity records to estimate BCS sire breeding values and improve their reliabilities. Based on this study, the Walloon Region of Belgium has been taking part to the international genetic evaluation for BCS performed by INTERBULL since September 2008.

This study had two main objectives: 1) extend the model currently used for the genetic evaluation to BCS data from the first three lactations, and 2) develop a method for expressing BCS breeding values as an indicator optimizing the genetic gain on fertility.

Materials and Methods

Data

Since April 2006, BCS has been monthly collected by milk recording agents (Walloon Breeding Association, Ciney, Belgium) in selected herds of the Walloon Region of Belgium. Holstein cows are given a BCS based on a nine-point scale (with unit increments) following the decision chart presented by Bastin *et al.* (2007). BCS were required to have been recorded between 5 and 365 days in milk (**DIM**) on lactating cows in parity 1 to 3. On average, 6 BCS records were available per cow per lactation. Angularity records were collected between 5 and 365 DIM for cows in parity 1. The final dataset included 30,081 BCS records in parity 1, 22,545 BCS records in parity 2, 15,102 BCS records in parity 3, 86,351 angularity records, 1364 herds, and 89,123 cows with records for at least one trait. A number of 7,213 cows had BCS records and 3,303 cows had both BCS and angularity records; and 521 cows had more than 1 angularity record for the first lactation.

For variance components estimation, cows were required to be born after 1996 and to come from one of the 86 herds including at least one cow with both BCS and angularity records. The variance components estimation dataset included 27,454 BCS records in parity 1, 20,576 BCS records in parity 2, 13,767 BCS records in parity 3, 7,088 angularity records, 9,842 cows with records for at least one trait, 6,553 cows with BCS records, and 3,235 cows with both BCS and angularity records.

Pedigree data were extracted from the database used of the official Walloon genetic evaluations and were limited to animals born after 1985 for the variance components estimation.

(Co)variance estimation and model

Based on the model presented by Bastin *et al.* (2007), the following four-trait model was used:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Q}(\mathbf{Ww} + \mathbf{Zp} + \mathbf{Za}) + \mathbf{e}$$

where:

- **y** was the vector of observations (BCS in lactation 1 (**BCS1**), BCS in lactation 2 (**BCS2**), BCS in lactation 3 (**BCS3**), and angularity in lactation 1),
- **β** was the vector of the following fixed effects: 1) class of 14 DIM x age at calving group, 2) herd x scoring date for BCS, and herd x date scored x classifier x classification system for angularity,
- **w** was the vector of BCS recorder random regression coefficients for BCS or the vector of classifier x classification system random regression coefficients for angularity,
- **p** was the vector of permanent environmental random regression coefficients,
- **a** was the vector of additive genetic random regression coefficients,
- **e** was the vector of random residuals,
- **X, W, Z** were incidence matrices,
- **Q** was the covariate matrix of second-order Legendre polynomials.

Groups of age at calving were defined within lactation. Random effects were assumed to be normally distributed and residual variances were assumed to be independent and constant over the lactation. Variance components estimation was performed using EM-REML (Misztal, 2009). The initial variance matrices were those presented by Bastin *et al.* (2007). Daily heritabilities and daily genetic correlations among the 4 traits were calculated.

Breeding values definition

The model was solved using the final dataset and 9 BCS genetic solutions (3 Legendre coefficients for BCS1, BCS2, and BCS3) were obtained for each animal in the pedigree. These solutions were named $BCSi_{Lj}$ and represented the genetic solution of the j^{th} Legendre polynomial coefficient for BCS in lactation i. They were then combined to generate daily genetic values ($BCSi_k$, with k=1 to 305) for each animal in lactation 1 to 3 for every DIM between 1 and 305.

Based on these genetic solutions, 7 different options for expressing BCS breeding values were investigated and then compared. Reliabilities were estimated based on INTERBULL EDC computation. All options were defined as a high value is desirable to improve fertility.

The first option tested (**EBV$_1$**) previously used by Bastin *et al.* (2007) was basically the genetic solution for the constant Legendre coefficient in lactation 1: $BCS1_{L0}$.

The second option (**EBV$_2$**) was defined as the average BCS over DIM 1 to 305 and across first 3 lactations; EBV_2 was calculated using the following formula:

$$EBV2 = \frac{\left(\sum_{i=1,3}\sum_{j=1,3} q_{Lj} BCSi_{Lj}\right)}{3}$$

where q_{Li} was averaged j^{th} Legendre polynomial coefficient over DIM 1 to 305.

Option 3 (**EBV$_3$**) was defined as the minimum genetic BCS averaged among the first 3 lactations:

$$EBV3 = \frac{\left(\sum_{i=1,3} BCSi_{\min} \right)}{3}$$

where $BCSi_{min}$ was the lowest daily genetic solution between DIM 1 and 200 for BCS in lactation i; $BCSi_{min}$ was defined for each animal.

Option 4 (**EBV_4**) was defined as the genetic BCS postpartum loss averaged among the first 3 lactations:

$$EBV4 = -\frac{\left(\sum_{i=1,3} BCSi_{cal} - BCSi_{\min} \right)}{3}$$

where $BCSi_{cal}$ was the genetic solutions for DIM 1 for BCS in lactation i.

Option 5 (**EBV_5**) took into account both the genetic BCS postpartum loss and the time when it occurred:

$$EBV5 = -\frac{\left(\sum_{i=1,3} di_{\min} \left(BCSi_{cal} - BCSi_{\min} \right) \right)}{3}$$

where di_{min} was the dim when occurred the lowest daily genetic solutions for BCS in lactation i; di_{min} was defined for each animal.

Option 6 (**EBV_6**) was defined as the genetic BCS recovering from its lowest value to its value at 300 DIM:

$$EBV6 = -\frac{\left(\sum_{i=1,3} BCSi_{300} - BCSi_{\min} \right)}{3}.$$

Option 7 (**EBV_7**) combined both the genetic BCS recovering and the time needed for starting this recovering:

$$EBV7 = -\frac{\left(\sum_{i=1,3} di_{\min} \left(BCSi_{300} - BCSi_{\min} \right) \right)}{3}.$$

Afterwards EBV_1 to EBV_7 were standardized using as the genetic reference base the 1,272 cows with BCS records and born in 2005. Heritabilities were estimated for each option; variances for $BCS1_{min}$, $BCS2_{min}$, and $BCS3_{min}$ were assumed to be variances estimated for the averaged $d1_{min}$, $d2_{min}$, and $d3_{min}$, respectively. Averaged $d1_{min}$, $d2_{min}$, and $d3_{min}$ were estimated on cows with BCS records.

The correlated response to selection on pregnancy rate (**PR**) using the different options were calculated and compared to the response to selection expected while selecting directly on PR. The expected response R_{PR} to selection on pregnancy rate was computed using the following formula (Falconer and Mackay, 1996):

$$R_{PR} = ih_{PR}^2 \sigma_{PR}$$

where i was the selection intensity (set to 1); h_{PR}^2 was the heritability of PR and was 0.039; and σ_{PR} was the phenotypic standard deviation of PR and was 25.26. The correlated response (CR_{PR}) in PR as a result of selection on BCS was estimated using the following formula (Falconer and Mackay, 1996):

$$CR_{PR} = ih_{PR} h_{EBV_k} r_{PRxEBV_k} \sigma_{PR}$$

where h_{PR} was the square root of the heritability of PR; h_{EBV_k} was the square root of the heritability of EBV_k; r_{PRxEBV_k} was the correlation between the PR breeding values and EBV_k. Responses to selection were estimated for the 13,376 Walloon cows born after 2004 and presenting reliability for V€G ≥ 0.30 and reliability for BCS ≥ 0.30.

Correlations between the different options and the breeding values of the economically important traits were estimated. The economically important traits were: milk, fat and protein yields; somatic cell count (**SCS**); longevity; and the Walloon economic indexes: V€L (partial economic index milk), V€T (partial economic index type), V€F (partial economic index functionality), and V€G (global economic index which is the sum of V€L, V€T, and V€F).

Finally Spearman and Pearson correlations among EBV_1 to EBV_7 were estimated for the 769 bulls with BCS reliability ≥ 0.30.

Results and Discussion

Heritabilities and genetic correlations

Daily heritabilities for BCS ranged between 0.08 and 0.31 according to the number and the stage of lactation (Figure 1). BCS heritability increased with the number of lactation. They increased from 5 to 200 DIM and then decreased until 305 DIM. These heritabilities were lower than estimates obtained by Berry *et al.* (2003) on a similar data set (repeated BCS records collected by trained staff) with a random regression animal model; their estimates ranged from 0.39 to 0.51. Daily heritabilities for angularity were between 0.13 and 0.18.

Genetic correlations among BCS1, BCS2 and BCS3 ranged between 0.64 and 0.88 (Figure 2). It indicated that BCS over the parities is not exactly the same trait. Genetic correlations between BCS and angularity were negative and ranged between -0.81 and -0.46. Estimates for parity 1 were similar to previous results (Bastin *et al.,* 2007).

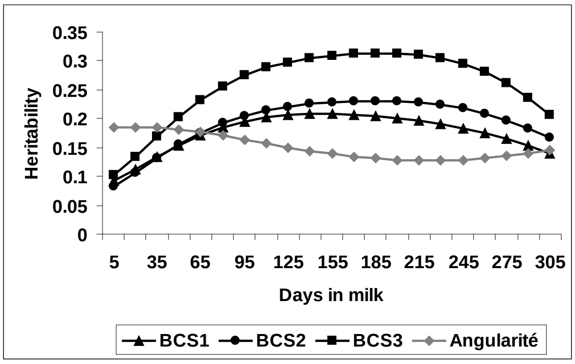

Figure 1. Daily heritabilities of angularity and BCS across days in milk.

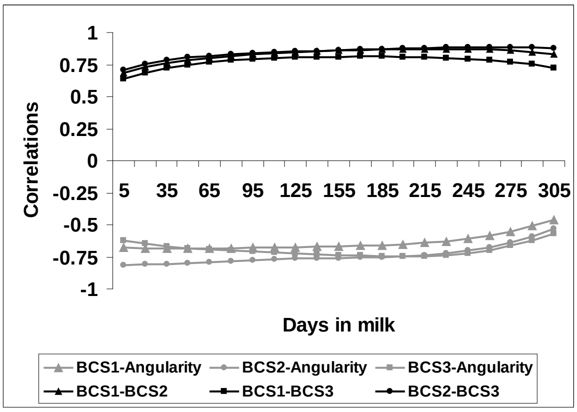

Figure 2. Daily genetic correlations among BCS1, BCS2, BCS3, and angularity across days in milk.

Table 1 shows heritabilities of EBV_1 to EBV_7. Except for EBV_1 which presented low heritability (0.185), estimates were moderate: from 0.344 for EBV_4 to 0.412 for EBV_7.

Comparison among EBV_1 to EBV_7

The expected response to selection, under the hypothesis that selection intensity was equal to 1, for PR was 0.985%. The correlated responses in the same trait as a result of selection for higher EBV_1 to EBV_7 are presented in Table 1 and vary between 0.638% (EBV_1) and 0.981% (EBV_3). Given these results, using BCS as an indicator trait for better fertility performances has to be considered. Furthermore, selecting for higher EBV_3 for improving the PR would lead to a similar response to selection than selecting directly on PR.

Table 1. Heritabilities of EBV1 to EBV7 and correlated response to selection on PR while selecting on EBV_1 to EBV_7.

	Heritabilities	CR_{PR} (%)
EBV_1	0.185	0.638
EBV_2	0.375	0.929
EBV_3	0.416	0.981
EBV_4	0.344	0.843
EBV_5	0.350	0.807
EBV_6	0.406	0.662
EBV_7	0.412	0.838

Previous studies indicated that BCS is not only genetically related to fertility but also to health and production (Dechow *et al.,* 2001; Pryce *et al.,* 2001; Berry *et al.,* 2003; Lassen *et al.,* 2003). Therefore EBV_1 to EBV_7 were also compared based on their correlations with the breeding values of economically important traits (Table 2). Results indicated that, except for EBV_6 and EBV_7, correlations with breeding values of economically important traits other than fertility were generally negative and ranged between -0.39 and 0.00. Therefore, selection for improved BCS would have a relatively low negative impact on production, SCS and longevity. Negative correlations with V€T is mainly explained by the negative relationship between BCS and dairy character. Finally correlations with V€G ranged between -0.26 and 0.00.

Table 2. Correlations between EBV_1 to EBV_7 and breeding values of the economically important traits.

	EBV_1	EBV_2	EBV_3	EBV_4	EBV_5	EBV_6	EBV_7
Milk yield	-0.11	-0.14	-0.13	-0.16	-0.17	0.03	-0.05
Fat yield	-0.16	-0.18	-0.18	-0.20	-0.22	0.08	0.00
Protein yield	-0.02	-0.05	-0.04	-0.08	-0.10	0.14	0.06
SCS	-0.01	-0.01	-0.01	-0.01	0.00	-0.09	-0.08
Longevity	-0.18	-0.18	-0.18	-0.16	-0.17	-0.03	-0.08
Pregnancy rate	0.30	0.30	0.31	0.29	0.27	0.21	0.26
V€L	-0.05	-0.06	-0.06	-0.10	-0.12	0.16	0.08
V€T	-0.38	-0.39	-0.39	-0.34	-0.32	-0.31	-0.36
V€F	-0.14	-0.14	-0.14	-0.13	-0.13	-0.01	-0.04
V€G	-0.23	-0.25	-0.25	-0.25	-0.26	0.00	-0.09

Table 3. Pearson (above the diagonal) and Spearman (below the diagonal) correlations among EBV_1 to EBV_7.

	EBV_1	EBV_2	EBV_3	EBV_4	EBV_5	EBV_6	EBV_7
EBV_1		0.97	0.97	0.87	0.86	0.66	0.82
EBV_2	0.97		0.99	0.91	0.90	0.65	0.82
EBV_3	0.97	0.99		0.93	0.91	0.68	0.84
EBV_4	0.88	0.95	0.95		0.99	0.63	0.82
EBV_5	0.87	0.93	0.94	0.99		0.58	0.78
EBV_6	0.65	0.65	0.67	0.62	0.57		0.93
EBV_7	0.82	0.84	0.85	0.81	0.77	0.92	

Pearson and Spearman correlations were estimated among EBV_1 to EBV_7 for 769 bulls (Table 3). Results indicated that EBV_1, EBV_2 and EBV_3 are closely related. As they were both indicators of BCS postpartum loss, EBV4 and EBV5 were highly correlated. Moreover EBV_6 was not clearly related to others, except to EBV_7.

Conclusion

Based on genetic solutions obtained from the model using BCS data of the first three parities, different options for expressing BCS EBV were investigated and compared. Results indicated that BCS could be used as an indicator trait for improving fertility. Selecting for higher EBV_3 for improving PR would lead to a similar response to selection than selecting directly on PR. However negative impacts of selecting for BCS on economically important traits other than fertility have also to be considered; therefore EBV_7 could be a good compromise for improving fertility while limiting deleterious effects on V€G.

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