Genetic Analysis Of Body Condition Score With Milk Production Traits in Canadian Holsteins

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Introduction

Long term selection on increased milk production in dairy cows has led to selection for increased extent and duration of negative energy balance in early lactation, resulting in reduced health and fertility (Veerkamp et al. (2001); Heringstad et al. (2003)). Body condition score (BCS) is a subjective measure of available tissue reserves (Edmonson et al. (1989); Broster and Broster (1998)), and hence may be used to indicate energy balance of the dairy cow. If information on energy balance is taken into account in selection decisions, the indirect and unfavourable effect of increased milk production on health and fertility may be reduced (Koenen et al. (2001); Veerkamp et al. (2001)). In fact, studies have found that increased BCS is genetically favourably linked with health and fertility traits (Berry et al. (2003); Bastin et al. (2009); Neuenschwander et al. (2009)). It is first important to verify BCS heritability and the relationship of BCS among parities and with other traits of economical importance. The objective of this research was to estimate genetic parameters of BCS in the first three lactations, and to estimate genetic relationship of BCS with milk production traits in Canadian Holsteins.

Material and methods

Data. Body condition scores since 2001 were provided by Valacta, the milk recording agency of Québec, Canada. One or more BCS were available per cow per lactation (average of 2.5 records per cow for each parity before edits) and were taken on a scale from 1 (thin) to 5 (fat) (at increments of 0.25). The identification of the field staff taking each BCS was not recorded. Full pedigree records were provided by Canadian Dairy Network (Guelph, Canada). Several data edits at the herd and animal level were applied to eliminate erroneous data. Nine classes of age at calving for each parity and two seasons of calving (October-March and April-September) were defined.

Model. The model for each trait included a random herd-recording-date effect, fixed age-season of calving effects modeled using Legendre polynomials, random animal effects

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modeled using Legendre polynomials, permanent environmental (PE) effects modeled using Legendre polynomials, and a random residual error effect. Regression curves were modeled using Legendre polynomials of order 2 for BCS or order 4 for milk production traits. (Co)variance components were estimated using DMU software (Madsen and Jensen (2008)).

Multiple-lactation analysis. Only BCS data from the first three lactations were used. Parity 1, 2, and 3 records were treated as separate traits. Of the 498 herds remaining after edits, 196 complete herds were randomly selected for variance component estimation. A large limit for number of cows was chosen to ensure greater shared herd-scoring-date between parities. A total of 28,917 animals were included in the analysis (9,913 cows with BCS records + 19,004 pedigree animals).

Body condition score and milk production traits. Only first lactation data were used in this part of the study. Valacta data were merged with the test-day file provided by Canadian Dairy Network (Guelph, Canada), which included records on milk yield, fat percentage (fat%), protein percentage (pr%) and somatic cell count (SCC), collected since 1988. The SCC were log-transformed to SCS. Of the 445 herds remaining after edits, 98 complete herds were randomly selected to limit the number of cows with records to about 5,000. There were 15,681 animals included in the analysis (5,065 cows with own records + 10,616 pedigree animals).

Results and discussion

In the multiple-lactation analysis, the general trend across lactation for BCS for all 3 parities was an increase in genetic variability, a relatively constant PE variance and a resulting increase in heritability (Figure 1). The increase in genetic variance over time suggests that perhaps there are more genetic differences related to how well a cow recovers from the negative energy balance state. Similar trends occurred for BCS in the analysis with production traits, where daily heritability ranged from 0.30 at 45 DIM to 0.48 at 305 DIM. Berry et al. (2003b) also studied BCS using a random regression animal model, and found that the daily heritability ranged from 0.39 at the beginning of lactation to 0.51 at 105 DIM. For the multiple-lactation analysis, average daily heritabilities for BCS were 0.39, 0.44, and 0.33 for parity 1, 2, and 3. For the analysis including production traits, average daily heritabilities were 0.36, 0.54, 0.44, 0.52, and 0.17 for BCS, milk, fat%, pr%, and SCS, respectively. The phenotypic correlations between BCS records were: 0.87 between parity 1 and 2, 0.79 between parity 1 and 3, and 0.82 between parity 2 and 3 ($P<0.0001$). The average daily genetic correlations between BCS in different parities were: 0.92 between parity 1 and 2, 0.96 between parity 1 and 3, and 0.93 between parity 2 and 3. This suggests that the variation observed in BCS is controlled by similar genes for each of the first 3 lactations. Figure 2 shows the genetic correlations between BCS and production traits. Body condition score was positively genetically correlated with pr%, and negatively genetically correlated with milk yield and SCS. Body condition score did not seem to be genetically correlated with fat%. Genes associated with increased BCS in mid to late lactation were involved in lower milk production. This could have to do with genes involved in both replenishing tissue reserves and drying off in preparation for the next calving. Conversely, BCS was still moderately heritable at the beginning of lactation (Figure 1), when the genetic correlation with milk yield was closest to zero, and the strength of the genetic correlations with SCS and pr% were at their highest. It may be possible to select for BCS without a large negative impact on milk production, while reducing SCS and increasing pr%.

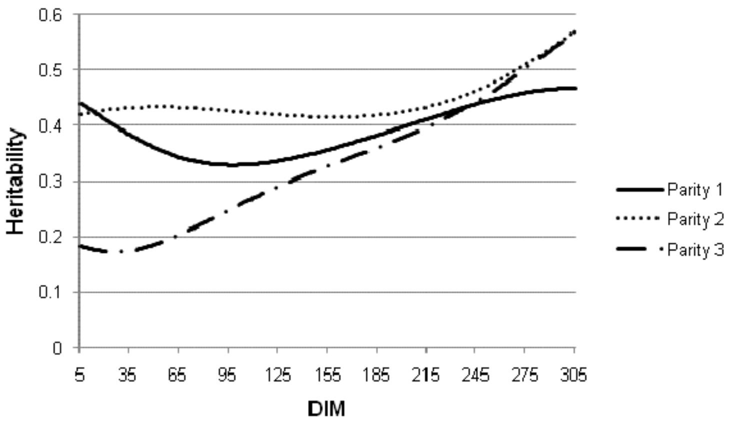

Figure 1: Estimates of daily heritabilities of BCS for first, second, and third parity Holstein cows across days in milk (DIM)

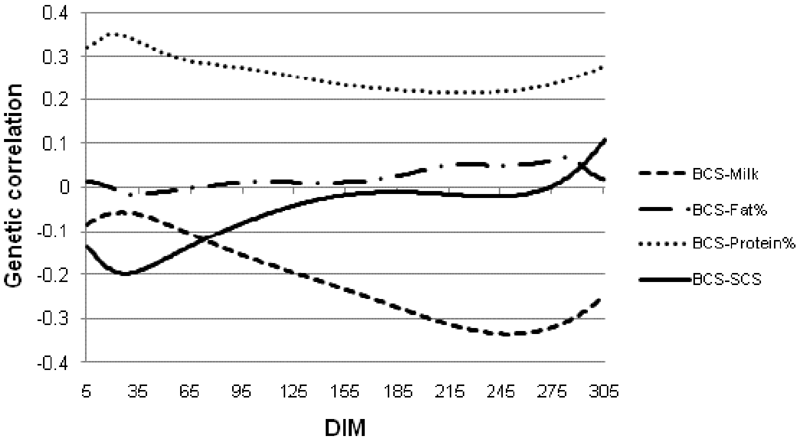

Figure 2: Genetic correlations between BCS and the production traits

Conclusion

Body condition score was highly phenotypically and genetically correlated among parities. This could suggest that a similar group of genes may control the trait over time in various parities, and that first lactation EBV should be a good indicator of BCS performance in later parities. Primiparous cows that had a genetically higher BCS tended to produce less milk, with a greater protein percentage and reduced SCS. Body condition score was not as strongly genetically correlated with milk yield at the beginning of lactation, while the genetic correlations between BCS and pr% and SCS were at their strongest during this period. Body condition score was not genetically correlated with fat%. Past studies have found that increased BCS is genetically favourably linked with health and fertility traits, and the results of this study suggest that BCS is moderately heritable and may be selected for without a large negative impact on milk production. Therefore, BCS shows potential for use in improving health and fertility status of dairy cattle.

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