Multi-Variate Genetic Evaluations of Body Condition and Milk Production in Dairy Cows

Haja N. Kadarmideen
Statistical Animal Genetics Group, Institute of Animal Science,
Swiss Federal Institute of Technology (ETH), Zurich CH 8092, Switzerland

Abstract: Bivariate (BV) analysis of Body condition score (BCS) jointly with milk yield was investigated as a method for BCS genetic evaluation and compared to univariate (UV) analysis of BCS records, adjusted or unadjusted for milk yield (n = 38 930). Additionally, milk yield was analysed with and without adjusting milk yield for BCS. An animal model with additive genetic and permanent environmental effects was fitted to data and analysed by REML. For BCS, the range of heritability (h^2) was 0.21 - 0.26, which was similar to milk yield, showing the potential for genetic improvement. The magnitude of h^2 and $ó_{pe}^2$ was smaller for adjusted than unadjusted BCS data for milk yield. Similar results were found for milk yield, with or without adjustment for BCS. This reduction in the genetic variation is a result of removing the differences in milk yield level / BCS. The UV and BV methods differed greatly when sire in data had small progeny group size (n=10). The BV analysis produced higher heritabilities and wider range and good accuracy of estimated breeding values for BCS showing that genetic response to selection is likely to be higher when it is based on multi-trait evaluations. Based on this result, a bivariate or multi-trait genetic evaluation with milk yield is recommended for BCS.

Key words: Kadarmideen dairy cattle, Bivariate evaluations, Body condition score, Milk production

Introduction

Functional traits in dairy cattle such as disease resistance, regularity of estrous cycle, conception success to inseminations and feed efficiency are economically important traits. The efficiency/profit of milk production would be reduced by continued selection for milk production due to antagonistic genetic correlations of milk yield with functional traits (Kadarmideen *et al.* 2000 and 2003). Body condition scoring (BCS) is a management technique used by breeders to judge the amount of body fat and indirectly asses the energy status in cattle (Wildmann *et al.* 1982). BCS has favorable genetic correlations with many functional traits and hence could be used as an indicator trait for, for example, fertility (Veerkamp *et al.* 2001, Pryce *et al.*, 2001 and Kadarmideen and Wegmann, 2003) and for health, longevity and fertility (Kadarmideen 2004, Neuenschwander *et al.* 2004) in dairy cows. In view of these findings, many countries are interested in regular BCS as a part of type classification and genetic evaluations in Holsteins as well as in other breeds.

Genetic correlation between BCS and milk yield is unfavourable and range from -0.17 to -0.50 (Pryce *et al.*, 2001, Kadarmideen 2004). Farmers may have been selecting for genetically thin animals (which partition energy towards milk production more often than towards maintenance) via selection on genetic and/or phenotypic merit for milk yield in early lactations. This selection: a). could determine presence or absence of BCS data in later lactations and b). may lead to lower averages of BCS data in later parities (i.e., high frequency of genetically thin cows in later parities). On the other hand, good body fat reserves may influence how much milk cow produces by being able to partition available energy for milk versus maintenance requirements; this means that true genetic merit for milk yield should be estimated after correcting for body fat reserves.

Failing to address these issues would lead to inaccurate and biased genetic evaluations for BCS as well as milk production. To account for such biological mechanisms and selection policies, one should include milk yield as a covariate in BCS analysis or BCS as covariate in milk yield analysis. The 'covariate' option, however, can only correct BCS with respect to differences in milk yield level of cows or milk yield with respect to body condition of cows. A two-trait analysis of BCS with milk yield as a genetically/biologically related trait is a different approach which aims to improve accuracy of genetic evaluations for both traits involved by reducing variances of prediction error of estimated breeding values (Schaeffer, 1984) and provide breeding values for animals that are not recorded for a particular trait. In fact, Kadarmideen *et al.* (2003) showed that bias and differences in sire evaluations/rankings for fertility exist if only single-trait fertility analysis is performed, instead of multiple trait genetic analysis of fertility trait with milk yield and recommended multiple trait evaluations. In fact, increase in accuracy, wide-spread breeding values and reductions in bias are usually expected from multi-trait genetic evaluations, according to the theory (Schaeffer, 1984 and Henderson, 1984). However, it would be important to quantify (to know how much) benefit that is expected from two-trait analyses, so that it could be decided whether or not to make this computationally demanding multi-trait genetic evaluations as a routine, in practice.

Main objectives of this study were (i) to perform single-trait genetic evaluations of BCS with and without milk yield as a covariate and (ii) to perform two-trait analysis of BCS with milk yield as a correlated trait and (iii) to compare estimated genetic parameters and genetic evaluations such as best linear biased predictor (BLUP) or estimated breeding values (EBV) for BCS between different methods. In addition, the effect of BCS as a covariate in genetic parameter estimation of milk yield will also be investigated.

Materials and Methods

Data: Data on BCS and milk production traits from cows in the first 4 lactations and in the 5th lactation and above were used for this study. BCS was routinely recorded from year 2001 by Holstein Association of Switzerland on 1 to 5 scale with an increment of 0.25 (1=very thin; 5=very fat) and linear type traits are recorded on 1 to 9 scale (for many years). Milk production traits were obtained for cows with a BCS record. For bivariate analysis, two more (previous) years of data on production starting arbitrarily from year 1999, were included in the analysis. This ensured that if the cow had BCS observations only in later lactations, its early lactation record on milk production were also included in the dataset. For the comparison of univariate BCS versus bivariate BCS analyses, data set was edited as follows: each sire had to have at least 50 daughters to ensure that only sires with reasonable accuracy of EBVs and/or recently proven bulls are included in the data set. Each herd in each year of classification/calving had to have at least five records. This editing resulted in a final dataset

Table 1: Description of data sets used for genetic parameter estimation by single and multi-trait animal models

Description (numbers)	Number
Records	38.930
Animals in pedigree	98.197
Herds	1830
Sires in data	243
Herd-year of classification	4077
Herd-year of calving	5543
Lactations	5
Stage of lactation	9
Month of calving/classification	12

of 38 930 records on 29 637 cows, daughters of 243 sires in 1830 herds. The data characteristics are summarized in Table 1. All records had production data and 17 042 records had BCS data. In the entire dataset of 38 930 cow records, there were 22 540, 9096, 4957, 1638 and 699 observations in the 1st, 2nd, 3rd, 4th and 5th lactations, respectively. Out of 17 042 BCS records, there were 9608, 4027, 2276, 782 and 349 observations in the 1st, 2nd, 3rd, 4th and 5th lactations, respectively.

An animal model with additive genetic relationship was used. Pedigrees were traced as far back as possible which included 98 197 animals.

Bivariate Model for Bcs and Milk Yield: The statistical model for bivariate animal model genetic evaluations of BCS and milk yield is:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & W_2 \end{bmatrix} \qquad (1)$$

where, y_1 and y_2 were a vector of records of BCS and of 305-day milk yield records (in kg), respectively, x_1 and x_2 were design matrices relating fixed effects in b_1 and b_2 to y_1 and y_2 respectively. The fixed effects for BCS (b) were different from those for milk yield (b) but were fitted in a single bi-variate analysis with:

b'_1 = [µ HYV MV L SL LxAv Hp]   and
b'_2 = [µ HYC MC L LxAv Hp].

Terms in b_1 are: µ = the overall mean; HYV = herd-year of visit by classifier; MV = calendar month of visit for condition scoring; L= lactation number; SL= stage of lactation (in months) at the time of classification; LxAv = age (in days) at visit as covariate nested within lactations; and Hp = percentage of Holstein genes as covariate. Terms in b_2 are: µ = the overall mean; HYC= herd-year of calving; MC = month of calving; L= lactation number and LxAc = age (in days) at calving as covariate nested within lactations and Hp = percentage of Holstein genes as covariate. Random effects were the same for BCS and milk yield. The vector of random animal effects was in a_1 and a_2 where the design matrices, Z_1 and Z_2 relate records to these animal effects. The vector of random permanent environmental and non-additive genetic effects of cows was in P_1 and P_2 where the design matrices, W_1 and W_2 relate records to these cow effects. The vector of random residuals were, e_1 and e_2 for y_1 and y_2, respectively. The expectation (E) and Variances (V) of model terms were as follows

$$E\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} \quad \text{and} \quad V\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = V\begin{bmatrix} a_1 & a_2 & p_1 & p_2 & e_1 & e_2 \end{bmatrix}'$$

The variance-covariance structures for the animal genetic effects were:

$$V\begin{bmatrix} a_1 \\ a_2 \end{bmatrix} = G = \begin{bmatrix} s^2_{a_1} & s^2_{a_{12}} \\ s^2_{a_{21}} & s^2_{a_2} \end{bmatrix} \ddot{A} A \; ; \; V\begin{bmatrix} p_1 \\ p_2 \end{bmatrix} = P = \begin{bmatrix} s^2_{pe_1} & s^2_{pe_{12}} \\ s^2_{pe_{21}} & s^2_{pe_2} \end{bmatrix} \ddot{A} I$$

$$V\begin{bmatrix} e_1 \\ e_2 \end{bmatrix} = R = \begin{bmatrix} s^2_{e_1} & s^2_{e_{12}} \\ s^2_{e_{21}} & s^2_{e_2} \end{bmatrix} \ddot{A} I$$

It should be noted that BCS data is missing on some animals; therefore the residual and permanent environmental elements corresponding to rows and columns of animals that have missing BCS observations in R and P were set to zero. Handling of missing observations for one or more traits in multi-trait animal model equations are described by Henderson (1984).

Univariate Model for BCS and Milk Yield: Two types of univariate models were used for BCS 305-day and milk yield. Simple univariate (UV) model for BCS (or milk yield) fitted the same effects as given under bivariate models for BCS (or milk yield) in equation [1]. The other univariate model fitted a covariate in addition to those already in UV model (UVC); the covariate fitted for BCS was 305-day milk yield (in kg) and for milk yield was BCS.

Starting values for variance components for bi-variate BCS analyses were obtained from univariate analyses on BCS and milk yield. BLUP of Breeding Values (EBVs) for BCS from univariate models (UV and UVC) and bivariate (BV) analysis with milk yield were obtained from the same (uni-or bi-variate) variance component analyses.

Variance-Covariance parameters, fixed effects and breeding values were estimated using the software package, ASREML (Gilmour *et al.* 2001). In ASREML, it was possible to get standard errors for all estimated parameters or its ratios as well as the accuracy of EBVs. The accuracy of BCS EBVs (r_{BCS}) was:

$$r_{BCS} = \sqrt{1 - SEP^2 / \hat{S}_a^2}$$
(2)

where SEP is a standard error of prediction for EBVs reported in *.sln file from ASREML (SEP^2 gives the prediction error variance for EBVs) and $\hat{S}_a$ is an estimated additive genetic variance for BCS under univariate or bivariate models.

Results and Discussion

Descriptive Statistics and Non-genetic Effects: The overall mean and standard deviation (SD) of BCS was 2.75 and 0.37, respectively, which is similar to those published for Holsteins by Veerkamp *et al.* (2001) and Kadarmideen and Wegmann (2003). The lactation-wise means (and SD) of BCS were 2.73 (0.35), 2.65(0.35), 2.69(0.37), 2.70(0.38) and 2.73(0.39) for lactations 1,2,3,4 and 5, respectively. The overall mean and SD of 305-day milk yield was 7405 kg and 1679 kg, respectively. The lactation-wise means (and SD) of 305-day milk yield (in kg) were 6781, 7981, 8562, 8743 and 8677 for lactations 1,2,3,4 and 5, respectively. These phenotypic descriptive statistics for multi-lactation cows for BCS and milk yield correspond to those of Kadarmideen (2004) who estimated genetic correlations between BCS, milk, health and other functional traits, using multi-lactations data set.

In Table 2, actual estimated effects of parity on BCS from the univariate analyses (UV and UVC) are shown. Here effect of parity 1 on BCS is set to zero (therefore equal to the overall mean value of 2.75) while effects of other parities are expressed as deviations from this mean. Results show that cows lose a score of 0.27 in the 2nd lactation (compared to the mean), stay around the mean value in 3rd lactation and then gain fat progressively in the 4th lactation and beyond.

Age at condition scoring was fitted within lactations as a covariate and estimated effects are also given in Table 2. For all lactations, BCS increased by ~0.01 unit for every day increase in age, except for parity 5. Regression coefficient of BCS on Holstein percentage was -0.008 which indicates that every percent increase in Holstein genes is related to decrease of about 0.01 BCS units. This may be due to the effect of Holstein breed as 'high yielding' cows and the antagonistic correlations between milk yield and BCS. The result for the first lactation for age and Holstein percentage is similar to that of Kadarmideen and Wegmann (2003).

For the univariate analysis of BCS with milk yield as a covariate, the estimated regression coefficient was -0.15 BCS units per kg increase in milk yield (Table 2). Conversely, for the univariate analysis of milk yield with BCS as a covariate, the estimated regression coefficient was -0.25 kg milk per 0.25 unit increase in BCS (Table 2). Both estimated regression coefficients show antagonistic relationship between milk yield and BCS: higher the milk yield level of cows, lower will be the body condition score of those cows (or vice versa). Earlier studies (Veerkamp *et al.* 2001, Berry *et al.* 2002, Kadarmideen and Wegmann 2003 and Kadarmideen 2004) have found not only this direction of relationship at a phenotypic level but also at the genetic level.

Genetic and Phenotypic Parameters: Estimates of heritabilities (h^2) and permanent environmental variances ($ó_{pe}^2$) for BCS and milk yield are given in Table 3 from three types of genetic analyses *a.* univariate analysis of BCS or milk yield, *b.* univariate analysis of BCS with milk yield as a covariate or univariate analysis of milk yield with BCS as a covariate and *c.* bivariate analysis of BCS and milk yield. All estimated correlations for BCS and milk yield (genetic: r_g, permanent environmental: r_{pe} and phenotypic: r_p) together with their standard errors were from bivariate analysis and are also given in Table 3 (except residual correlation which was 0.03).

Table 2: Estimated effects of parity, age at condition scoring, Holstein percentage and milk yield on the body condition score (BCS) of multi-lactation cows

Parity Number	Parity	Age	Holstein percentage	milk yield[1]	BCS[2]
1	2.75	0.0101**	-0.0078**	-0.1495**	-0.2532**
		(0.0012)	(0.0010)	(0.0101)	(0.1810)
2	-0.27**	0.0071**			
	(0.16)	(0.0001)			
	0.03 ns	0.0052			
3	(0.22)	(0.0001)			
4	0.37 ns	0.0003			
	(0.37)	(0.0002)			
5	1.17**	-0.0008			
	(0.43)	(0.0002)			

**significant at p<0.01, ns non significant at p<0.01, [1]From univariate analysis of BCS with Milk Yield as a covariate
[2]From univariate analysis of Milk Yield with BCS as a covariate

Table 3: Heritabilities (h^2), permanent environmental variance ($ó_{pe}^2$) and genetic (r)$_g$ permanent environmental (r) and phenotypic correlations (r_p) for BCS and milk yield, from univariate analyses with and without milk yield and bivariate analysis with milk yield

Trait	Univariate Correlations			Univariate with Milk and BCS as covariate[1]			Bivariate with Milk		
	h^2(s.e.)	$ó_{pe}^2$ (s.e.)	h^2(s.e.)	$ó_{pe}^2$ (s.e.)	h^2(s.e.)	$ó_{pe}^2$ (s.e.)	r_g (s.e)	r_{pe}(s.e)	r_p(s.e)
BCS	0.23	0.31	0.21	0.29	0.26	0.31	-0.50	-0.36	-0.15
	(0.04)	(0.03)	(0.04)	(0.03)	(0.01)	(0.02)	(0.03)	(0.03)	(0.01)
Milk	0.27	0.45	0.23[1]	0.50[1]	0.29	0.45			
	(0.03)	(0.01)	(0.03)	(0.02)	(0.02)	(0.03)			

[1]Univariate analysis fitting milk yield as a covariate for BCS estimation and BCS as a covariate for milk yield estimation

Univariate Analyses: From simple univariate analysis, the estimated h^2 and $ó_{pe}^2$ for BCS were 0.23 and 0.31, respectively. The estimated h^2 and $ó_{pe}^2$ for milk yield were 0.27 and 0.45, respectively. The s.e. of h was 0.04 for BCS and 0.03 for milk yield. These results are similar to earlier findings by Veerkamp *et al.* (2001), Berry *et al.* (2002), Kadarmideen and Wegmann (2003) and Kadarmideen (2004).

Univariate Analyses with Adjusted Records: he estimated h^2 and $ó_{pe}^2$ for BCS (adjusted for 305-day milk yield) were 0.21 and 0.29, respectively. The estimated h^2 and $ó_{pe}^2$ for milk yield (adjusted for BCS) were 0.23 and 0.50, respectively. The s.e. of h^2 was 0.04 for BCS and 0.03 for milk yield.

Bivariate Analysis of BCS and Milk Yield: he estimated h^2 and $ó_{pe}^2$ for BCS when jointly analysed with milk yield (as a correlated rait) were 0.26 and 0.31, respectively. The estimated h^2 and $ó_{pe}^2$ for milk yield (with BCS as a correlated trait) were 0.29 and 0.45, respectively. The s.e. of h^2 was 0.01 for BCS and 0.02 for milk yield.

From these results, it could be seen that the UVC analysis of BCS records (adjusted for milk yield) resulted in smaller magnitude of estimated h^2 and $ó_{pe}^2$ than those from UV model (unadjusted for milk yield). Similar results were found for milk yield, with or without adjustment for BCS. This result confirm the hypothesis of this study that some of these differences in BCS between cows may have only been due to differences in their milk yield and correction of BCS for milk yield, smaller phenotypic and hence the genetic differences in BCS between cows are expected. Interestingly, when the milk yield is adjusted for BCS and analysed, similar phenomenon happens (i.e., the genetic difference in milk yield between animals become smaller, hence low additive genetic variance or h^2). In all cases, fitting a covariate did not have an effect on precision (s.e.) of estimated genetic parameters. Estimates of h^2 for BCS as well as milk yield from BV analysis were higher (0.26 and 0.29, respectively) than both types of univariate models (UV and UVC) for individual trait. This higher magnitude is as expected, because BCS and milk yield supply information to each other and introduce more genetic variance between animals, than single-trait analyses (with or without 'covariable' option) on each trait. The similar phenomenon has also been shown in the joint genetic evaluation of fertility and milk yield by Kadarmideen *et al.* (2003).

In general, all three sets of heritabilities of BCS were similar to estimates reported by Pryce *et al.* (2001), Berry *et al.* (2002) and Kadarmideen and Wegmann (2003) and Kadarmideen (2004). Further, the magnitude of h^2 estimates was similar to milk yield showing that animals could be selected and bred for good BCS, as this trait is useful as indicator for other functional traits (Kadarmideen and Wegmann 2003, Kadarmideen 2004).

Estimated genetic (r_g) and phenotypic correlations (r_p) between milk yield and BCS were -0.50 and -0.15, respectively (Table 3). The strong antagonistic genetic correlation of -0.50 shows that selection of high genetic merit animals for milk yield will lead to low genetic merit for BCS or genetically thin animals Similar estimates were also reported in literature (Pryce *et al.* 2001 Berry *et al.* 2002 and Kadarmideen 2004). Kadarmideen (2004) showed that animals with (genetic merit for) good BCS would also have desirable characteristics in udder health and fertility. It means that selection for high milk yield would lead to deterioration of not only BCS but also health and fertility. The permanent environmental correlation (-0.36) and phenotypic correlation (-0.15) between BCS and milk yield also were antagonistic, but the magnitude were smaller than the genetic correlation. All correlations were statistically significant at p<0.01.

Estimated Breeding Values for BCS:

Univariate and Bivariate BLUP EBVs for BCS: The main reason to investigate univariate versus bivariate evaluation of BCS with milk yield was that selection on (genetic merit for) milk yield in early lactations may affect BCS data in later lactations either in terms of presence or absence of BCS data and/or in terms of high frequency of cows with low BCS. High genetic correlation of -0.50 with milk yield further supports our hypothesis that bivariate genetic evaluations for BCS should be preferred in order to account for possible biases and improve accuracy of genetic evaluations. Kadarmideen *et al.* (2003) investigated this approach for fertility evaluations but this is a first study that investigated a bi-variate analysis of body condition score with milk yield, in addition to investigation of impact of milk yield (or BCS) as covariable on estimated genetic parameters for BCS (or milk yield).

An animal model was used to estimate breeding values for all animals but only sire EBVs were considered here since sire selection is more intense and important in dairy cattle. Sires in the dataset, as mentioned earlier, had at least 50 daughter records each. Sire EBVs for BCS along with their standard errors were extracted from the BLUP solutions of bivariate and univariate (UV and UVC) analyses of BCS. Accuracies of EBVs were calculated as per equation [2], using estimated standard errors and genetic variances, from respective analyses. The range of EBVs, SD, kurtosis and skewness values are given in Table 4 and the distributions of EBVs are plotted in Fig. 1, for all 3 methods.

The range and SD of EBVs were higher for bivariate than univariate analyses. Two observations could be made in Fig. 1a). UV EBVs seem to be more peaked at the centre than BV EBVs and, b). distributions of EBVs from 2 univariate methods (UV and UVC) are quite similar. The actual value of kurtosis was lower for bivariate than either univariate analyses (Table 4), with the later having abundance of EBVs with similar values at around the mean (less variability). This indicates that bivariate method could better differentiate sires than univariate methods with respect to their genetic merit.

Table 4: Descriptive statistics for sire estimated breeding values (EBVs) for body condition score (BCS) from univariate evaluations with and without milk yield as covariate (UV and UVC) and bivariate evaluation with milk yield.

	Min	Max	SD	Kurtosis	Skewness
Univariate	-0.53	0.52	0.12	1.39	-0.37
Univariate_cov	-0.51	0.51	0.12	1.68	-0.37
Bivariate	-0.56	0.53	0.16	0.93	-0.46

Table 5: Correlations among BLUP estimated breeding values (EBVs) (above diagonal in bold), accuracies[1] (below diagonal) and sire rankings (above diagonal in parenthesis) for body condition score (BCS) obtained from three methods of genetic evaluations: univariate analyses with and without milk yield as covariate (UV and UVC) and bivariate analysis (BV) of BCS with milk yield

Methods	UV	UVC	BV
UV	-	0.98	(0.96)
		0.96	(0.94)
UVC	1.00	-	0.94
			(0.92)
BV	0.97	0.96	-

[1]Calculated using formula 2 for each sire
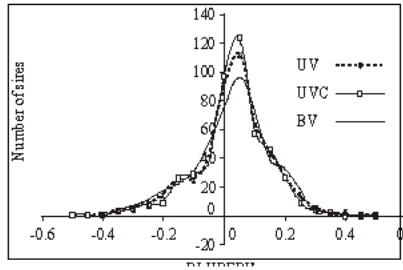
Fig. 1: Distribution of BCS EBVs from univariate analysis with and without milk yield as a covariate and from bivariate analysis with milk yield.
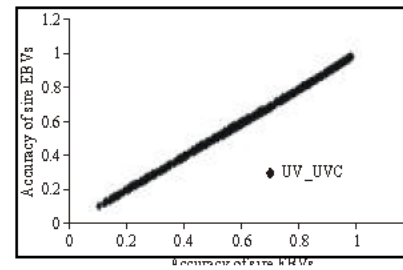

Fig. 2: Pair-wise comparison of accuracy of EBVs of the same sires from univariate analysis without and with milk yield as a covariate (UV and UVC)
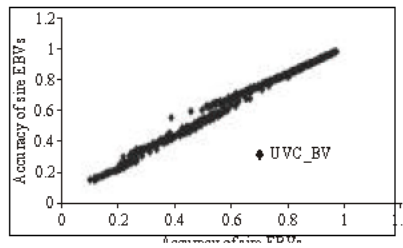

Fig. 4: Pair-wise comparison of accuracy of EBVs of the same sires from univariate analysis (UV) and bivariate analysis with milk yield (BV)
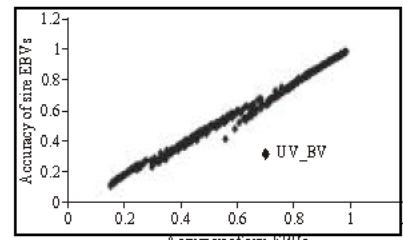

Fig. 3: Pair-wise comparison of accuracy of EBVs of the same sires from univariate analysis with milk yield as a covariate (UVC) and bivariate analysis with milk yield (BV)

Distributions of EBVs for BCS (Fig. 1) were slightly left skewed (long tail to the left) with a value of -0.37 for both univariate analyses and -0.46 for bivariate analysis. This 'not so perfect' symmetric distribution may be due to the fact that BCS observations themselves are not measured on a continuous scale like milk yield but in the increments of 0.25. Regardless of the analysis, the distribution of EBVs tended to be normally distributed, with reasonable number of bulls at both end of the distribution. Along with the h^2 of ~0.26, it shows good potential for selection. Genetic evaluations for BCS would probably begin in the near future, in the light of these new evidences.

Correlations between three genetic evaluations for the same trait, BCS by 3 different methods were computed using the EBVs and accuracy of EBVs as well as sire rankings and are given in Table 5. The two univariate methods for BCS evaluations (with and without milk yield as a covariate) were very similar in terms of genetic evaluations and sire rankings (Table 5) as well as in accuracies. Figure 2. shows a complete super-imposition of pair of accuracies from UV and UVC genetic evaluation models. This is, in spite, of the finding that UV and UVC models differed in estimated genetic variances and heritabilities (Table 3). The univariate analysis of adjusted BCS data (UVC) differed more from bivariate analysis than the univariate analysis of unadjusted BCS data (UV), as seen in low correlations in Table 5. Accuracy of EBVs was not very different between univariate and bivariate methods (Table 5 and Figs. 3 and 4) but correlations still significantly differed from one.

The above results were shown for relatively larger progeny group sizes of sires (minimum 50 per sire). To test whether the current results hold also for smaller progeny group sizes, dataset was re-constructed by including data from all cows that were born to sires with the minimum 10 daughters and the new data were re-analysed (results not shown).

One of the important findings of this investigation was that the correlation between sire EBVs, accuracies and ranks from UV and BV methods, reduced to 0.92, 0.91 and 0.88, respectively. This deviation of UV results from statistically more appropriate and advantageous BV methods (as seen in correlations, significantly different from 1) indicate deficiency of UV analyses, especially when there are many young dairy sires in the data set. Hence, BV method is recommended to account for possible biases and improve accuracy in estimating BCS breeding values. In this study we have considered BCS and milk yield and suggested BV analysis for BCS. But advantages of bivariate analysis will exist also for any type trait that has strong genetic correlation with milk yield, for example, dairy character or udder depth.

Conclusions

This study performed single-trait genetic evaluations of body condition score (BCS), with and without milk yield as a covariate and a joint two-trait analysis of BCS with milk yield as a correlated trait. The differences between three methods of genetic parameter estimations / evaluations were quantified, in terms of magnitude of estimated heritabilities, distribution and precision of sire's estimated breeding values and ranking of sires. The magnitude of estimated parameters (heritabilities and permanent environmental variances) was smaller when BCS records adjusted for milk yield was analysed than when unadjusted BCS records were analysed. Similar results were found for milk yield, with or without adjustment for BCS. This result prove that some of the differences in milk yield levels of cows when properly taken into account during the BCS analysis, could reduce the genetic variation between animals and hence results in smaller heritabilities and less spread of estimated breeding values. Significant differences exist (especially when sire evaluations were based on small progeny group sizes) between bivariate (multi-trait) genetic evaluation and univariate (single-trait) methods. Bivariate analysis of BCS with milk yield, produced higher heritabilities, wide spread of estimated breeding values and better precision of estimates than both types of univariate analysis, showing that response to selection on BCS is likely to be higher when based on bivariate (multi-trait) evaluations. Based on this result, a bivariate or multi-trait genetic evaluation with milk yield is recommended for BCS.

References

Berry, D.P., F. Buckley, P. Dillion, R.D. Evans, M. Rath and R. F.Veerkamp, 2002. Genetic parameters of body condition score and body weight in dairy cows. J. Dairy Sci., 85: 2030-2039

Gilmour, A. R., B. R. Cullis, S. J. Welham and R. Thompson, 2001. ASREML Reference Manual. New South Wales Agriculture, Orange Agricultural Institute, Orange, NSW, Australia

Henderson, C.R., 1984. Applications of linear models in animal breeding. University of Guelph, Guelph, Canada

Heuer, C., Y.H. Schukken and P. Dobbelaar, 1999. Postpartum body condition score and results from the first test day milk as predictors of disease, fertility, yield and culling in commercial dairy herds. J. Dairy Sci., 82: 295-304

Kadarmideen, H.N., 2004. Genetic Correlations among Body Condition Score, Somatic Cell Count, Production, Reproduction and Conformation Traits in Swiss Holsteins. Anim. Sci., 79:191-201

Kadarmideen, H.N. and J.E. Pryce, 2001. Genetic and economic relationship between somatic cell count and clinical mastitis and their use in selection for mastitis resistance in dairy cattle. Anim. Sci., 73: 19-28

Kadarmideen, H.N. and S. Wegmann, 2003. Genetic Parameters for Body Condition Score and its Relationship with Type and Production Traits in Swiss Holsteins. J. Dairy Sci., 86: 3685-3693

Kadarmideen, H.N., R. Thompson and G. Simm, 2000. Linear and Threshold Model Genetic Parameter Estimates for Disease, Fertility and Production traits in UK dairy cattle. Anim. Sci., 71: 411-419

Kadarmideen, H.N., R. Thompson, M.P. Coffey and M.A. Kossaibati, 2003. Genetic parameters and evaluations from single and multiple- trait analysis of dairy cow fertility and milk production. Livest. Prod. Sci., 81:183-195

Neuenschwander, T., H.N. Kadarmideen, S. Wegmann and Y. de Haas, 2004. Genetics of Parity-dependant Production Change and its Relationship with Health, Reproduction, Longevity and Conformation in Swiss Holsteins, J. Dairy Sci., (In Press)

Pryce, J.E., M.P. Coffey and G. Simm, 2001. The relationship between body condition score and reproductive performance. J. Dairy Sci., 84:1508-1515

Schaeffer, L.R., 1984. Sire and cow evaluation under multiple trait models. J. Dairy. Sci., 67: 1567-1580

Veerkamp, R.F., E.P. C. Koenen and G. De Jong, 2001. Genetic correlations among body condition score, yield and fertility in first-parity cows estimated by random regression models. J. Dairy Sci., 84: 2327-2335

Wildmann, E.E., G.M. Jones, P.E. Wagener, R.L. Boman, H.F. Troutt Jr and T.N. Lesch, 1982. A dairy cow body condition scoring system and its relationship to selected production characteristics. J. Dairy Sci., 65: 495-501