

## GENETICS OF BODY CONDITION SCORE IN NEW ZEALAND DAIRY CATTLE

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### INTRODUCTION

Body condition score (BCS) is a non-invasive visual estimate of the amount of subcutaneous fat deposition in dairy cows and is assessed independently of body weight and stature. Its main use is in managing the nutritional status of cows at calving, mating and drying off. BCS is considered as a useful tool in predicting the productive and reproductive performance of dairy cows (Wildman *et al.*, 1982).

The objectives of this study were:

1. Estimate genetic parameters for BCS and the genetic relationships between BCS and other traits of interest in New Zealand dairy cattle population, and
2. Investigate the use of random regression models to estimate genetic parameters in the first lactation

### MATERIALS AND METHODS

**Data.** Data on BCS were collected on cows which were either in herds that participated in Livestock Improvement's and Ambreed's sire proving schemes (SPS) or herds that participated in linear type classification in the 2000 season. Two BCS measurements were collected from cows in the SPS herds, the first at the time of live weight recording and the second at the time of linear type classification. In the non-SPS herds one BCS measurement was collected from cows at the time of linear type classification. Body condition score was visually assessed on a 1 to 9 scale. The data set contained records on 45,120 first lactation cows of which 23,837 cows had two BCS measures. Additional data on 270-day milk yield traits, live weight, stature and cow fertility, breed and pedigree information were extracted from the Livestock Improvement national database. The cow fertility trait was measured as percent mated in the first 21 days of mating after the planned start of mating. Breed proportions of the cow, dam and sire were available in 16ths which allowed both the calculation of breed, and heterosis effects (Koch *et al.*, 1985).

**Statistical analysis.** A multivariate analysis was undertaken with a single observation per cow for each trait. Where cows had two measurements recorded the first BCS measurement was used in the analysis. Heritabilities, genetic and phenotypic correlations, and fixed effects were estimated by restricted maximum likelihood (REML) with a multivariate linear sire model including a sire-maternal grandsire relationship matrix using the average information algorithm of Johnson and Thompson (1995). There were 1790 sires in the pedigree. The model for each trait included fixed effects for herd, covariates for percent NZ Holstein Friesian (NZHF), overseas HF (OSHF), Jersey breed (JR), percent NZHF-JR, percent NZ HF-OSHF and percent overseas HF-JR heterosis and random effects for sire. The model for liveweight, stature and BCS included linear and quadratic fixed effects for stage of lactation at the time of measurement and all models included linear and quadratic fixed effects for age at calving. The

model for BCS included a fixed effect for type of measurement which indicated either a linear type classification or live weight recording event.

Analyses of BCS were undertaken using all the BCS records on individual cows. The same fixed effects were the same as used for the multivariate analysis. The components of variance for sire and cow permanent environment (PE) were modelled as a continuous function of time using Legendre polynomials. A link function approach was used to account for model heterogeneity of error variance over time (Jaffrezic *et al.*, 2000). The sire and cow PE variances and the fixed effects were estimated by REML with a linear sire model including a sire-maternal grandsire relationship matrix using ASREML software Gilmour (2001).

## RESULTS AND DISCUSSION

The mean BCS for the 43,212 cows scored at the time of linear type classification was 4.1 with a standard deviation 0.59 and the mid 50% of observations being contained in the range 3.5 – 4.5. The mean BCS for the 23,387 cows scored at the time of weighing was 4.22 with a standard deviation 0.59 and the mid 50% of observations being contained in the range 4.0 – 4.5. The cows scored at the time of weighing were on average 12 days further in to their lactation than those scored at the time of linear type classification. The range in stage of lactation when cows were condition scored was from day 3 to day 200 of lactation for both data collection times. The simple correlation between BCS measured at the time of linear type classification and at the time of weighing on the same cows was 0.41.

**Multivariate analysis** The heritability of BCS was 0.22 with a standard error of 0.02. This result is comparable with previous estimates (Jones *et al.*, 1999, Pryce *et al.*, 2001 and Veerkamp 2001). Body condition score had a genetic coefficient of variation (CV) of 20.1 which was greater than the values for the milk production traits and live weight. Significant ( $p < 0.01$ ) heterosis estimates for NZHF–JR and OSHF–JR were obtained both having with values of 0.07 for the first cross cow. The breed estimates were –0.58, –0.49 and –0.19 for JR, OSHF and NZHF, respectively. The NZHF breed estimate was significantly different ( $p < 0.01$ ) from both JR and OSHF.

The genetic and phenotypic correlations between BCS and milk production, live weight, stature and cow fertility are given in Table 1. The genetic correlations between the milk production traits and BCS were not significantly different from zero ( $p < 0.05$ ). Low, slightly negative genetic correlations between BCS and milk production traits have also been reported by Veerkamp and Brotherstone (1997) and Pryce *et al.*, (2001). Body condition score had a moderate positive genetic correlation with live weight and slight positive correlation with stature. The genetic correlation with live weight is slightly lower than the value of 0.67 reported by Veerkamp and Brotherstone (1997). Body condition score was highly positively genetically correlated with cow fertility indicating cows with a higher BCS breeding value on average are genetically better for fertility. A similar relationship was reported by Pryce *et al.*, 2001 for calving interval and BCS.

**Table 1. Genetic and phenotypic correlations between body condition score and milk production, live weight, stature and cow fertility**

	Genetic Correlation	SE <sup>2</sup>	Phenotypic Correlation
270 day fat yield	0.02	0.06	0.02
270 day protein yield	-0.02	0.06	0.03
270 day milk volume yield	-0.10	0.06	-0.03
Live weight	0.50	0.04	0.36
Stature	0.13	0.06	0.15
Cow Fertility <sup>1</sup>	0.71	0.10	0.11

<sup>1</sup>Trait is the percent mated in the first 21 days of mating

<sup>2</sup>SE = Standard Error of the genetic correlation

**Longitudinal analysis.** Ten random regression models were fitted to the data. The random regression order for the sire variance was varied from 1 to 4. The order for the cow permanent environment was varied from 1 to order of the sire variance. Table 2 gives a summary of the four models which provide the best fit to the data based on Bayes information criterion (BIC) at each order of sire variance. The model with best fit for each order of sire variance was the model where the cow permanent environment had the same order as the sire variance. The model selection would have been the same if either Akaike information criterion or the model likelihood had been used rather than BIC.

**Table 2. Summary of the random regression models which provide the best fit to the data based on Bayes information criterion at each order of sire variance**

Model Order	-2*LogLikelihood	DF <sup>1</sup>	AIC <sup>2</sup>	BIC <sup>3</sup>
Sire 1, Permanent 1, Error 1	-25206	65501	-23206	-14001
Sire 2, Permanent 2, Error 3	-26241		-24229	-15070
Sire 3, Permanent 3, Error 3	-26440		-24416	-15202
Sire 4, Permanent 4, Error 3	-26722		-24680	-15384

<sup>1</sup>Degrees of freedom

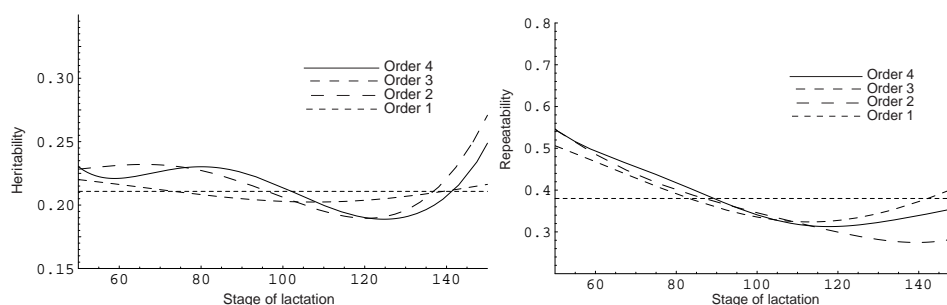
<sup>2</sup>Akaike information criterion

<sup>3</sup>Bayes information criterion

Figure 1 illustrates the heritability estimates by stage of lactation for the four models in Table 2. The lowest heritability estimates occur approximately at day 120 of lactation for the higher order random regression models, whereas, the lowest repeatability estimates occur at day 110 of lactation.

The magnitude of heritability and genetic CV of BCS indicate that selection for BCS would be effective. Selection for BCS is unlikely to change the genetic potential for milk production. The low correlation between milk production and BCS in New Zealand could be due to little or no selection pressure being placed on dairyness or angularity. However, selection for increased BCS would result in improved cow fertility. It is likely that improved BCS results in reduced

negative energy balance around the time of mating and early pregnancy resulting in improved fertility.



**Figure 1. Heritability and repeatability estimates for condition score from 4 random regression models**

The longitudinal data analysis of BCS in the first lactation showed that higher order random regression models provided a better fit to the data than a repeatability model. Random regression models would be preferred for national evaluation where multiple measurements on individual animals are available. The estimates of heritability and repeatability were not constant across time. The Legendre polynomials used in the random regression models are essentially unconstrained at the tails which resulted in dramatic changes in the variance estimates when there was a paucity of data; in particular prior to 40 days and after 150 days of lactation in this analysis. Further research will be undertaken using random regression with cubic splines to improve the variance estimation over time.

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