

Body Trait Profiles During First Lactation

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Introduction

Body traits in dairy cattle can be of interest as indicators of growth, maturity and functionality. As an animal proceeds through her lactation it is expected that body shape and fatness levels will change. For example, the daughters of one bull may grow in stature at a faster/slower rate than the population or one trait may change in a linear manner while another trait changes in a non-linear manner.

Many dairy cattle traits have repeated measurements across time with varying correlations between records for an animal. Random regression has been used as a method for analysing repeated data on individuals over time, from lactation records to growth (Schaeffer, 2004). Random regression can be thought of as a covariance function providing multidimensional covariance matrices across a continuous scale (e.g., days in milk).

To best understand the relationship between body traits and liveweight, mature body weight and functional traits it is important to find the most appropriate model of analysis for each trait, especially if there is a difference between sires and traits in how they change over time. Once modelled, the traits can then be combined and/or used as indicators for traits that vary with time such as maturity and liveweight.

The aim of this study was to investigate change in body traits over the course of the first lactation using RR, fitting Legendre polynomial (LegP) and cubic spline (CubS) functions.

Materials and Methods

The body traits chosen were condition score (BCS), STAT, ANG, BD and (CW) adjusted for recorder. Records for first lactation Holstein-Friesian animals with linear type records and at least three milk tests were taken from 1997 until the end of 2003. Bulls had at

least 5 daughters and up to the first 300 type classified daughters were selected in an effort to remove selection bias from the data but retain an appropriately sized dataset for analysis. Type records were included in the dataset if the days in milk (dim) of the cow were between 10 and 290. A full pedigree was fitted for each sire in the following analyses.

Genetic and environmental variance components were estimated with RR sire models fitted with LegP and CubS functions. The order for the fixed LegP for each trait was studied by varying the order of fit of the curve and examining the significance of the curve parameter solutions. The order for the random LegP for each trait was tested for significance using LogL ratio testing. The RR model fitted with a LegP was:

$$Y_{ijk} = \mu + hys_i + month_j + \beta_1 X_{age} + \beta_2 (X_{age})^2 + \sum_{m=0}^{n-1} \gamma_m P_m(dim) + \sum_{m=0}^{n-1} \alpha_{km} P_m(dim) + e_{ijk}$$

where: Y_{ijk} = type trait record (BCS, BD, CW, STAT, ANG); hys_i = fixed effect of i^{th} herd-by-year-by-season; $month_j$ = fixed effect of the j^{th} month of calving; β_1 and β_2 = linear and quadratic regression coefficients of dependent variable (Y) on age effect; X_{age} = continuous variable representing age of animal (in months) at calving; γ_m = fixed regression coefficients; α_{km} = random regression coefficients for sire k ; m = order of the polynomial; $P_m(dim) = m^{th}$ LegP evaluated at dim

RR models using CubS functions, as defined by White et al. (1999), were fitted with nine knot points that coincided with the residual error classes boundaries with the following model.

$$Y_{ijk} = \mu + hys_i + month_j + \beta_1 X_{age} + \beta_2 (X_{age})^2 + b_0 + b_1 X_{dim} + b_{k0} + b_{k1} X_{dim} + \sum_{l=2}^{q-1} b_l z_l X_{dim} + \sum_{l=2}^{q-1} b_{kl} z_l X_{dim} + e_{ijk}$$

where model is previously defined and b_0 and $b_1 X_{dim}$ = overall linear regression; b_{k0} and $b_{k1} X_{dim}$ = deviation from the overall regression (slope and intercept) for sire k ; $b_l z_l X_{DIM}$ and $b_{kl} z_l X_{DIM}$ = mean spline deviation and deviation from the mean spline for sire k at knot l (where q is the total number of knots).

Models were compared based on log likelihoods (LogL), residual variance estimates and the difference between actual and predicted values for each of the traits analysed and the total phenotypic variance of the trait explained by each model. Individual daily sire solutions for all traits, as estimated by the RR model with the most appropriate function, were calculated. The daily solutions showed how the daughters of a sire deviated from the fixed overall trend curve.

Results and Discussion

After editing, the dataset consisted of 28,198 daughter records of 954 sires in 2180 herd-year-season of inspection classes. Results are presented from the LegP model with the best order of fit for each type trait, which was a linear random polynomial for BD, CW and STAT, a quadratic polynomial for ANG a cubic polynomial for BCS.

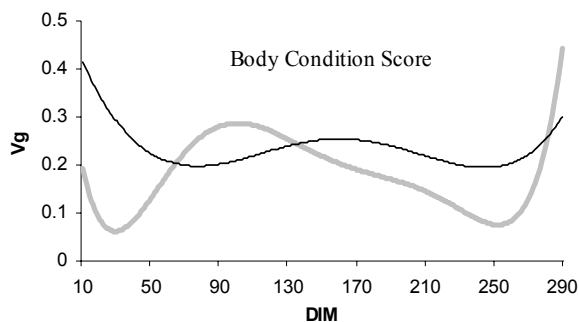


Figure 1. Genetic variance (V_g) across the 1st lactation for BCS using RR model using a LegP function (—) and a CubS function (---).

The genetic variance for all traits when modelled using a LegP function changed more dramatically across lactation than when modelled with a CubS function as illustrated in Figure 1 for BCS. The genetic variance at the start and end of lactation increased when the LegP function was used. However, the estimate of genetic variance for the middle section of lactation (approximately d 50-250) was similar

regardless of function used in the RR model. The genetic variances from multivariate sire analyses, where three time points (early, mid and late lactation) for each type trait were analysed, were similar to the results from the LegP function (results not shown) except for STAT. For STAT, the multivariate estimates tracked the genetic variance estimates from the model with the CubS function. The genetic variance of BCS was highest at either end of the lactation, a result observed in other studies that modelled BCS with RR models using polynomial functions (Berry *et al.*, 2003; Coffey *et al.*, 2003).

Previous studies have suggested that there is an increase in the genetic variance at either end of the lactation for traits modelled with polynomial functions if data points are few (Pool *et al.*, 2000; Berry *et al.*, 2003). However this study truncated early and late lactation records in an effort to improve the modelling of these traits. This study also modelled BCS with a CubS function and saw similar increases at the start and end of lactation, although the increases were not as dramatic as seen in this and other studies that modelled BCS with a LegP function. This suggests that the genetic variance of BCS is truly lower in mid-lactation.

The heritability estimates for from the CubS and LegP function across the majority of lactation agreed closely with previous multivariate studies (Koenen and Groen, 1998; Pryce *et al.*, 2000; Berry *et al.*, 2003).

The residual variance estimated from the RR models was similar for the majority of traits regardless of the function used, although the LegP function tended to give numerically smaller residual variance estimates (not significant). However, the estimated residual variance for BCS was smaller when the LegP function was used ($P < 0.001$), suggesting that the LegP function is a more appropriate function to use in the RR model for BCS.

The absolute difference between the predicted and actual type traits, which is indicative of the average absolute bias induced by the model, was slightly smaller when the LegP function was used in the RR model. A higher proportion of the phenotypic variance is explained by the LegP function compared to the CubS function. Values ranged from 30% for

ANG to 51% for STAT, which equates to a correlation between actual and predicted values of 0.55 and 0.71 respectively. The combination of the above results suggested that the RR model with the LegP function modelled body traits slightly better than the CubS function. The results from here will describe the estimates obtained from the LegP function.

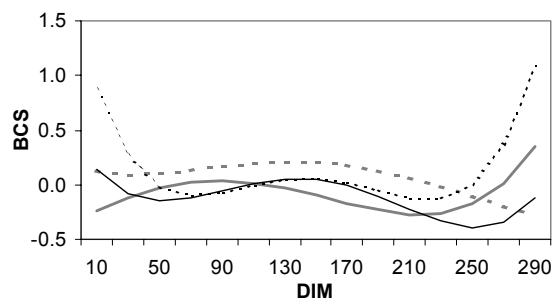


Figure 2. Difference from the fixed population curve for BCS for four sires (sire A —; sire B --; sire C —; sire D ---).

Daily sire solutions were estimated for all traits from the results of the RR model with the LegP function. Four sires were chosen from the 26 sires in the dataset with more than 150 daughters (Figure 2) to illustrate the differences in sire profiles for BCS. There are differences between sires and between traits in the profile of their daughters' type change over lactation. For example, the daughters of some sires grow in stature faster than others and the daughters of some sires lose more body condition across lactation than others.

All sires dropped beneath the fixed trend curve for BCS at some stage in lactation. Interestingly, sire B started and finished lactation a BCS unit above the fixed overall trend where sire D appears to differ only slightly from the overall trend. The sire profiles for ANG (not shown) were less dramatic than BCS but still showed differences in the profiles for the same four sires and visually it was the mirror image of the BCS sire profiles (e.g., sire B started and finished lactation below the fixed overall trend).

The sire deviations from the fixed overall trend curve of the body traits could be used as indicators of body changes in 1st lactation and therefore related to traits such as maturity and liveweight. Sire B was consistently above the fixed overall trend for BD, CW and STAT

suggesting that the daughters of this sire are bigger than the rest of the population and are still growing throughout their first lactation. This could be indicative that the daughters of this bull are still maturing throughout their first lactation.

Figure 3 shows how the daily individual sire solutions of ANG, BD, CW, and STAT were used to predict daughter liveweight using the prediction equation of Coffey et al (2003). The daughters of sire A grow consistently faster than the rest of the population indicating that not only do his daughters start their first lactation heavier than their counterparts (+3 kg heavier) they also finish lactation heavier (+8 kg). However, the daughters of sire B start off lactation heavier (+5 kg) but their growth slows down and at the end of lactation are 2 kg lighter than their counterparts.

Sire C, whose daughters started off heavier than the population but their growth rate slowed down relative to the fixed trend curve, had the highest PTA for kgs of milk, fat and protein for all the sires. Conversely, the daughters of sire A grew faster than the population but this sire had the lowest PTA for the milk production traits. These differences in liveweight and inverse production PTA could be indicative of the daughters of sire A partitioning food towards their own growth while the daughters of sire B may partition food towards milk production. Sire B, whose daughters growth rate increased relative to the population towards the end of lactation, had the best calving interval PTA out of the 4 sires (-0.5 d, Wall et al, 2003), which could indicate that the animal may sacrifice some body weight towards early and peak lactation production but regains it to maximise reproductive function.

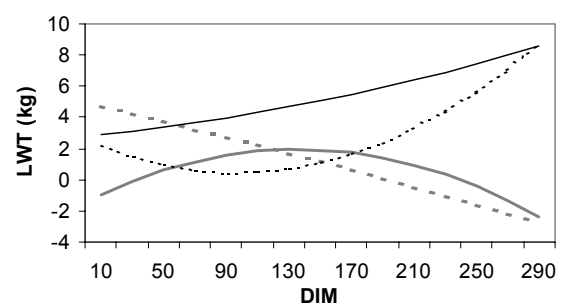


Figure 3. Difference from the fixed population curve for predicted LWT for four sires (sire A —; sire B ---; sire C —; sire D ---).

These results show that there are differences in how cows grow and change shape over their first lactation, some changing very little for these traits while others may increase/decrease over the duration of the lactation. This is a critical time in the biological development of a cow as she prepares for second calving and successive lactations, essential for her survival in the herd. The linear traits BD and CW have been shown to be moderately correlated to weight and size (Koenen and Groen, 1998). Also, animals with deeper bodies have been shown to be more profitable than smaller animals (Pérez-Cabal and Alenda, 2002) even though BD has a negative correlation with herd life indicating that there could be a balance between size, production levels and longevity (Short and Lawlor, 1992). The results of this study could be used to help identify the optimum profile of body shape change over the first lactation that is most highly correlated to traits such as lifespan and profitability.

Random regression models allow us to estimate body changes in first lactation in the national population. These methods could be used to highlight bulls that produce lighter/heavier or slower/faster growing daughters and these types of trends could be indicative of later life performance, both for production and non-production traits.

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