Body Trait Profiles in Holstein-Friesians Modeled Using Random Regression

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ABSTRACT

Legendre polynomial and cubic spline functions were used in random regression models to model the change in body traits over the course of the first lactation for daughters of 954 sires. Both functions estimated similar genetic variances for d 50 to 250 across lactation for the majority of traits. The heritability of the traits was similar to other studies using univariate models as well as random regression models. There was little difference between the 2 functions in their predictive power for each of the body type traits, as measured by the absolute difference between the predicted and actual type traits and the proportion of the total phenotypic variance explained by the model. Overall, the Legendre polynomial appeared to model these traits slightly better. Plots of the fixed curves and daily sire solutions obtained from the random regression models showed that there were differences in how the traits and sires changed across lactation. The daily sire solutions were then used to predict differences in liveweight of sires' daughters across first lactation and showed that the daughters of some sires grew faster during first lactation than others. The spatial differences in the body traits that are displayed by this study could be an important indicator of the physical and biological changes that cows are undergoing in their first lactation. Information from these sire profiles could be harnessed to indicate production and functional traits later in life.

(**Key words:** type trait, body condition score, random regression)

Abbreviation key: ANG = angularity, BD = body depth, CubS = cubic spline, CW = chest width, LegP = Legendre polynomial, LogL = Log likelihood, RR = random regression, STAT = stature.

INTRODUCTION

Body traits in dairy cattle can be of interest as indicators of growth, maturity, and functionality. For example, linear equations have been developed to use type traits that are usually measured at a single time point to predict liveweight in dairy cows (Koenen and Groen, 1998; Coffey et al., 2003). However, as an animal proceeds through lactation, it is expected that body shape and fatness levels will change due to the lactation curve, growth, and maturity. Using a fixed formula based on type traits recorded at a single point in time to predict liveweight may be suboptimal as it cannot account for these changes in shape across time, differences in an animal's profile, or differences between the profiles for traits. For example, the daughters of one bull may grow in stature at a faster or 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. Examples include milk production, weight information, BCS, and linear type information. Studies have analyzed these data in a number of ways, such as curve fitting (Ali and Schaeffer, 1987; Wilmink, 1987), multivariate analyses (Berry et al., 2003), and random regression (RR) analyses (Olori et al., 1999). Random regression has been used as a method for analyzing 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., DIM). It is usual for a low-order polynomial regression curve (e.g., Legendre polynomial, LegP) to be fitted to the data. Traits that have been shown to vary over a lactation, after modeling with RR using polynomial functions, include milk (e.g., Jaffrezic et al., 2002), liveweight (e.g., Meyer, 1998), BCS (e.g., Jones et al., 1999), and type (e.g., Uribe et al., 2000).

Other functions used in RR to model traits over time include spline functions (e.g., cubic splines; CubS) for

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traits such as lactation yield (White et al., 1999; Druet et al., 2003), weight (Huisman et al., 2002), leptin concentrations (Liefers et al., 2003), and fertility (Roche, 2002). A CubS function fits a smoothing curve across cubic polynomials that have been fitted between adjacent points (knots) such that the smoothing curve and its first and second derivatives are continuous across the range of data (Green and Silverman, 1994).

Previous analyses have shown that single-point linear type measures are correlated to production (Brotherstone et al., 1990; Heuer et al., 1999), health (DeGroot et al., 2002), fertility (Pryce et al., 2001), and longevity (Boettcher et al., 1997; Caraviello et al., 2004). It has also been shown that changes in BCS are antagonistically correlated with fertility, with losses in BCS resulting in increased days open (López-Gatius et al., 2003). Studies have also shown that the magnitude of the correlation between traits and BCS changes across lactation (Berry et al., 2003).

To best understand the relationship of body traits with 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 modeled, the traits can then be combined or used as indicators for traits that vary with time such as maturity and liveweight. For example, Coffey et al. (2003) developed a phenotypic prediction equation for liveweight from linear type records. In this instance, a fixed formula, based on step-wise regression, was used to predict BW from body depth (BD), chest width (CW), stature (STAT), and angularity (ANG) that did not account for stage of lactation but only the age at inspection due to the block calving pattern present in the prediction data set.

The aim of this study was to investigate change in body traits over the course of the first lactation using RR, fitting LegP and CubS functions. Estimated daily sire solutions from the most appropriate model were plotted for illustrative purposes. The daily sire solutions for each of these traits were then used to predict differences in liveweight of sires' daughters across first lactation.

MATERIALS AND METHODS

The body traits chosen were BCS, STAT, ANG, BD, and CW. These traits are recorded by Holstein UK as part of the national type classification scheme and were adjusted for field officer by scaling records so that individual officer standard deviations were equal to the mean standard deviation of all officers (Brotherstone, 1994). Records for first-lactation Holstein-Friesian animals with linear type records and at least

3 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 data set for analysis. Type records were included in the data set if the DIM of the cow were between 10 and 290. Prior investigations showed that records before and after this time were scarce and subject to database errors. A full pedigree for each sire was selected from the Holstein UK database and fitted in each of the following analyses.

A prior analysis examined the influence of adding additional residual error classes (1 to 15) to account for the variation in the recording of type traits across lactation. The borders for the residual error classes were based on work of Coffey et al. (2002). The optimal number of error classes for this data was 9, based on a log likelihood (**LogL**) ratio test.

Genetic and environmental variance components were estimated with RR sire models fitted with LegP and CubS functions using ASREML (Gilmour et al., 2002). The order for the fixed LegP for each trait was studied by varying the order of fit of the curve and examining the significance (*t*-test) 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 (3 seasons per year) of type classification visit; $month_j$ = 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; dim = DIM at type classification; γ_m = fixed regression coefficients; α_{km} = random regression coefficients for sire *k*; e_{ijk} = residual random error term; *m* = order of the polynomial; and $P_m(dim)$ = *m*th LegP evaluated at *dim*.

Random regression models using CubS functions, as defined by White et al. (1999), were fitted with 9 knot points that coincided with the residual error class boundaries described in Table 1 with the following model:

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

Table 1. Heritability estimates at the midpoint of each of the 9 residual error classes for each of the 5 traits analyzed with a Legendre polynomial (LegP) and cubic spline (CubS) function, and the number of records in each residual class; heritability estimates from the multivariate linear (Lin) analysis at 3 time points; and residual variance for BCS (BCS σ_e^2) across lactation for both functions.

Days	No. of records	Function	Trait ¹					BCS σ_e^2
			BCS	BD	CW	STAT	ANG	
10 to 29	1454	LegP	0.37	0.51	0.34	0.67	0.93	1.41
		CubS	0.66	0.33	0.28	0.56	0.46	1.73
		Lin 10 to 25	0.59	0.57	0.72	0.35	0.81	
30 to 59	3594	LegP	0.26	0.44	0.25	0.56	0.59	1.59
		CubS	0.46	0.33	0.26	0.43	0.39	1.78
60 to 89	4135	LegP	0.45	0.32	0.18	0.42	0.42	1.50
		CubS	0.38	0.32	0.24	0.41	0.36	1.92
90 to 119	4045	LegP	0.51	0.31	0.14	0.33	0.36	1.53
		CubS	0.41	0.32	0.25	0.39	0.37	1.93
120 to 149	3971	LegP	0.44	0.26	0.14	0.27	0.33	1.49
		CubS	0.42	0.33	0.27	0.37	0.39	1.99
		Lin 130 to 150	0.19	0.51	0.38	0.36	0.22	
150 to 179	3411	LegP	0.36	0.26	0.18	0.27	0.28	1.35
		CubS	0.43	0.32	0.29	0.37	0.40	1.99
180 to 209	2947	LegP	0.29	0.26	0.26	0.30	0.22	1.41
		CubS	0.39	0.30	0.28	0.36	0.41	2.07
210 to 239	2343	LegP	0.21	0.29	0.35	0.39	0.21	1.40
		CubS	0.37	0.30	0.30	0.36	0.43	2.11
240 to 290	2298	LegP	0.19	0.33	0.55	0.57	0.41	1.50
		CubS	0.44	0.29	0.30	0.36	0.49	1.99
		Lin 255 to 290	0.63	0.62	0.63	0.28	0.70	

¹Traits: BD = body depth, CW = chest width, STAT = stature, and ANG = angularity.

where model is previously defined, and b_0 and $b_1 X_{dim}$ = overall linear regression fitting a slope and intercept for the overall smoothing spline; b_{k0} and $b_{k1} X_{dim}$ = random deviations from overall regression (slope and intercept) for sire k ; and $b_1 z_1 X_{DIM}$ and $b_{kl} z_1 X_{DIM}$ = 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, residual variance estimates, and the difference between actual and predicted values for each of the traits analyzed. The total phenotypic variance of the trait explained by each model, calculated from the square of the correlation between actual and predicted type trait values, was also calculated in an effort to determine the best function to use within a RR model. The Akaike information criterion and Schwarz Bayesian information criterion are also reported although direct comparison between these values for the CubS and LegP function is not valid as the models have different fixed effects.

A subset of data was selected and each record was defined as an early (DIM 10 to 25), mid (DIM 130 to 150), or late (DIM 255 to 290) record based on time of type classification. The 3 time points for each type trait were analyzed using a multivariate linear model. Variance and covariance components between each time point for individual traits were estimated by REML using ASREML (Gilmour et al., 2002).

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. Individual daily sire solutions for BCS as estimated from both functions were correlated at specific points across lactation. The formula to predict differences between bulls for daughter liveweight across time was adapted from the liveweight prediction of Coffey et al. (2003), which was derived using data from the Langhill experimental herd. The equation of Coffey et al. (2003) included terms to account for the fixed effect of year of inspection, diet and age of inspection. However, for the purpose of this study, these fixed terms were removed from the equation, as the daily body type trait solutions from the RR models will have adjusted for some of these effects by fitting a herd-year-season effect. We assume that the daughters of a bull were distributed randomly across a range of diets and recorded at a range of ages thus averaging out these effects. The constant term (intercept) from the prediction equation was also removed as this study was interested in examining the differences between sires and traits in how animals changed across lactation rather than predicting solely phenotypic daily liveweight. The individual sire solutions were used to estimate the difference of each sire from the national liveweight curve over time using the following formula (Coffey et al., 2003).

Table 2. Mean, standard deviation (SD), range (minimum and maximum),¹ and order for the fixed and random components for the Legendre polynomial model.

	Mean	SD	Min	Max	Fixed	Random
Age (mo)	27.89	3.598	18	40		
BCS	4.513	1.734	-1.5	10.5	4	3
Body depth	5.703	1.381	0.35	9.7	3	1
Chest width	5.222	1.516	0.13	9.97	0	1
Stature	5.283	1.567	-1.75	9.64	2	1
Angularity	5.657	1.452	-0.9	10.35	3	2

¹Linear score was adjusted for recording officer.

$$\text{Liveweight} = (-7.247 \times \text{ANG}) + (8.505 \times \text{CW}) \\ + (5.548 \times \text{BD}) + (8.529 \times \text{STAT})$$

The validity of assuming a constant liveweight prediction formula across lactation was examined by modeling liveweight as a function of the above type traits, month of lactation, and an interaction between month of lactation and the type traits.

RESULTS

After editing, the data set consisted of 28,198 daughter records for 954 sires in 2180 herd-year-season of inspection classes (Table 1). A description of the traits studied in the analysis is given in Table 2. Table 1 shows that the records were relatively evenly distributed across the 9 residual classes ranging in size from 1454 records (d 1 to 29) to 4135 records (d 60 to 89). Results are presented from the LegP model with the best order of fit for each type trait. The orders of the fixed and random polynomials in these models are in Table 2.

There was little difference between the LegP and the CubS function in predictive power for each of the type traits. The mean absolute difference between the predicted and actual type trait values, 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 (Table 3). The average correlation between individual sire solutions as estimated from the 2 functions was 0.81, with the correlation being higher in midlactation (results not shown). For example, the correlation between breeding values for bulls with 50 or more daughters as estimated from the 2 functions was 0.84, 0.88, and 0.62 on d 40, 120, and 265, respectively.

The proportion of the total phenotypic variance explained by both functions is given in Table 3. A higher proportion of the phenotypic variance is explained by the LegP function compared with the CubS function. Values ranged from 30% for ANG to 51% for STAT, which equates to a correlation between actual and pre-

dicted values of 0.55 and 0.71, respectively. The combination of the above results suggested that the RR model with the LegP function modeled body traits slightly better than did the CubS function. The results hereafter will describe the estimates obtained from the LegP function unless otherwise stated.

Figure 1 shows that the fixed curve (overall trend) for the traits generally increased across lactation. The fixed trend curve for BCS showed a decrease at the start and end of lactation. Conversely, ANG increased at these times. The fixed overall trend for the other traits was generally linear with STAT increasing at a slower rate than BD and CW. It is important to note that the individual sire solutions (random term in the model) are expressed as deviations from these fixed curves.

Figure 2 shows that the genetic variance for all traits when modeled using a LegP function changed more dramatically across lactation than when modeled with a CubS function. The genetic variance at the start and end of lactation increased when the LegP function was used. The CubS function produced a "flatter" profile for the estimate of genetic variance across lactation for all traits except BCS. However, the estimate of genetic variance for the middle section of lactation (approximately d 50 to 250) was similar regardless of the function used in the RR model. Figure 2 shows that the genetic variance of BCS was highest at either end of the lactation, a result observed in other studies that modeled BCS with RR models using polynomial functions (Berry et al., 2003; Coffey et al., 2003; Banos et al., 2004).

The heritability of BCS (Table 1) was more consistent across lactation when estimated with the CubS function, ranging from 0.44 in midlactation to 0.66 at the start of lactation, whereas the estimates from the LegP function ranged from 0.19 at the end of lactation to 0.51 in midlactation and 0.37 at the start of lactation. Both the CubS and LegP functions produced moderate heritability estimates for BD (0.26 to 0.55) and CW (0.14 to 0.55) across the majority of lactation. Table 1 shows that both functions produced moderate

Table 3. $-2 \times$ Logarithm of the likelihood function (-2LogL), Akaike information criterion (AIC), Schwarz Bayesian information criterion (BIC) values, mean absolute difference between actual and predicted values (AbDif), and the proportion of the total phenotypic variance of the trait explained by the model (PhenV) for the Legendre polynomial (LegP) and cubic spline (CubS) models for each trait.

		Trait ¹				
		BCS	BD	CW	STAT	ANG
-2LogL^2	LegP	223	159.2	123	222.8	145.4
	CubS	0	0	0	0	0
AIC ²	LegP	233	155.2	119	218.8	147.4
	CubS	0	0	0	0	0
BIC ²	LegP	245.2	150.4	114.2	214.0	149.8
	CubS	0	0	0	0	0
AbDif	LegP	1.027	0.852	0.986	0.864	0.938
	CubS	1.032	0.854	0.989	0.867	0.944
PhenV	LegP	0.421	0.378	0.322	0.505	0.309
	CubS	0.415	0.374	0.318	0.501	0.300

¹Traits: BD = body depth, CW = chest width, STAT = stature, and ANG = angularity.

²Values are expressed as a deviation of the lowest value.

to high heritabilities for STAT (0.27 to 0.68) and a moderate estimate for the heritability of ANG (0.22 to 0.38) for the majority of lactation. However, the heritabilities estimated with the LegP and the multivariate linear models at the start of lactation were higher than previous estimates. The genetic variances from multivariate sire analyses at 3 times (early, mid, and late lactation) were similar to the results from the LegP function except for STAT. For STAT, the multivariate estimates tracked the genetic variance estimates from the model with the CubS function.

The residual variance across lactation was relatively constant for all traits, with no evidence of higher or lower residual variance at any stage of lactation (Table 1). 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 when tested with a *t*-test). How-

ever, 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.

Daily sire solutions were estimated for BCS, BD, CW, STAT, and ANG from the results of the RR model with the LegP function. Four sires were chosen at random from sires with more than 150 daughters in the data set (Figure 3) to illustrate the differences in sire profiles. Figure 3 shows that there are differences between sires and between traits in the profile of their daughters' type 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.

Figure 3 shows that 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 were less dramatic than BCS but still showed differences in the profiles for the same 4 sires and visually were the mirror images of the BCS sire profiles (e.g., sire B started and finished lactation below the fixed overall trend). Body depth and CW showed linear differences with the daughters of 3 of the sires generally rising faster for the 2 traits than the rest of the population, whereas sire D started above the overall trend curve and finished lactation beneath. This suggested that the daughters of sire D do not change body shape during lactation, which could suggest that they do not put on much weight during lactation.

There was no significant change in the prediction formula for liveweight across the lactation; and therefore, the equation as described by Coffey et al. (2003)

Figure 1. Fixed curve from the random regression model using Legendre polynomial function for BCS (■), body depth (●), chest width (○), stature (▲), and angularity (△), across DIM 10 to 290.

Figure 2. Genetic variance (Vg) across the first lactation for BCS, body depth, chest width, stature, and angularity using random regression model using a Legendre polynomial function (thick gray line) and a cubic spline function (thin black line).

was applied to the type trait solutions. Figure 3 shows that some sires grow at a faster rate than the population (sire A), whereas other sires have slower growth (sire D). 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), but 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.

DISCUSSION

The results showed that the selected linear type traits could be modeled across time using RR models. Generally, the LegP function resulted in an increase of the genetic variance at the extremities of the period, whereas CubS tended to have a flatter profile.

The BCS heritability at various points of the lactation were similar to results reported by Berry et al. (2003) who found a early lactation heritability of 0.39 at d 0 (vs. 0.37 at d 19) up to 0.51 at d 151 (vs. 0.51

at d 105 and 0.41 at d 151). The moderate heritability estimates in the majority of the lactation for ANG agreed with the results of the RR analysis of dairy form of Dechow et al. (2004). However, there were discrepancies between the 2 studies for the heritability estimates in early lactation. The moderate heritability estimates for BD and CW and slightly higher estimates for STAT agreed closely with previous multivariate studies (Pryce et al., 2000).

Heritability estimates for the traits tended to be moderate across the lactation but higher at the extreme points of the curve using a LegP function. Previous studies have suggested that there is an increase in the genetic variance at either end of the lactation for traits modeled 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 modeling of these traits. This study also modeled 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 modeled BCS with a LegP function. This suggests that the genetic

Figure 3. Difference from the fixed population curve for BCS, body depth (BD), chest width (CW), stature (STAT), and angularity (ANG) for 4 sires (sire A, solid line; sire B, dotted line; sire C, thick line; sire D, dashed line) and prediction of liveweight (LWT) from the daily solutions for the 4 sires using the equation of Coffey et al., 2003.

variance of BCS is truly lower in midlactation. This was further demonstrated by the favorable correlation between the breeding values for BCS estimated from either function across the lactation, although it did drop off slightly at the end of the lactation.

The profiles of variance and heritability for BCS and ANG were similar across the lactation. This is to be expected because BCS and ANG have been shown to be highly correlated (-0.74 ; Veerkamp and Brotherstone, 1997). The genetic variance at the extremities of the data (early and late lactation) rose when analyzing BCS and ANG with a LegP function. However, when using CubS, the variance of BCS was highest at the start and end of lactation, whereas ANG displayed a relatively flat curve. The data at the early and late stages of lactation are fewer compared with the middle of lactation (1359 and 1123 records in the first and last 30 d of lactation, respectively). There is also a higher variance associated with the BCS records at the start or end of lactation than with ANG. For example, for the first 30 d of lactation, the mean BCS is 4.49 (SD 1.68) whereas ANG has a mean of 5.5 (SD 1.37). The increased phenotypic variance of BCS data in early and later lactation could have a bigger influ-

ence on the polynomial function, and thus could “inflate” the genetic variance curve at these points.

The sire deviations from the fixed overall trend curve of the body traits could be used as indicators of body changes in first 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 larger 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.

These results show that there are differences in the genetic profiles across first lactation for certain type traits, indicating that there are differences between sires in their daughters’ body change in first lactation. It is necessary to account for the differences between sires across time to get the best estimate of a daughter’s performance in these traits at any particular time. An example where the differences between sires should be accounted for is in the prediction of traits such as BW from linear type traits as done by Coffey et al. (2003). These results show that the component traits (BD, CW, STAT, and ANG) in the prediction of

liveweight do vary relative to each other across lactation. The 4 chosen sires are good examples of the differences in liveweight that occur during first lactation.

Although the differences in daughter liveweight change for the chosen 4 sires may appear low, some sires with large (>150) progeny group sizes differed from the fixed trend curve by over 15 kg. Sire C, whose daughters began lactation heavier than the population but their growth rate slowed down relative to the fixed trend curve, had the highest PTA for kilograms of milk, fat, and protein for all the sires. Conversely, the daughters of sire A grew faster than the population but sire A had the lowest PTA for the milk production traits. These differences could be indicative of the daughters of sire A partitioning food toward their own growth, whereas the daughters of sire B may partition food toward milk production. Sire B, whose daughters' growth rate increased relative to the population toward the end of lactation, had the best calving interval PTA of the 4 sires (−0.5 d; Wall et al., 2003), which could indicate that the animal may sacrifice some body weight toward peak lactation production but regain it to maximize reproductive functions.

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 and others increasing or decreasing over the duration of the lactation. This is a critical time in the biological development of a cow as it prepares for second calving and successive lactations, essential for its 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). Moreover, 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 life span 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 or heavier and slower or faster growing daughters; these types of trends could be indicative of later life performance, both for production and nonproduction traits.

CONCLUSIONS

Body traits vary over lactation with differences between sires for the profile of change of their daughters.

Random regression models with both LegP and CubS functions were used to model the change in linear type traits across lactation but the LegP function was marginally more appropriate. Our genetic variance and heritability estimates for the type traits agree, for the most part, with estimates from other studies. There are differences in the profiles of change in linear type traits associated with volume and size (BD, CW, STAT) and BCS across lactation for daughters of sires. These changes could be indicative of animals utilizing body reserves to maintain lactation or differences in the rates of maturity and growth.

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