PAPER

Genetic association between herd survival and linear type traits in Holstein cows under tropical conditions

Elisandra L. Kern,[1] Jaime A. Cobuci,[1]
Cláudio N. Costa,[2]
Concepta M. McManus,[3,4]
Gabriel S. Campos,[5] Tatiana P. Almeida,[1]
Rafael V. Campos[6]

[1]Departamento de Zootecnia,
Universidade Federal do Rio Grande do
Sul, Porto Alegre, Brazil
[2]Empresa Brasileira de Pesquisa
Agropecuária Gado de Leite, Juiz de
Fora, Brazil
[3]Campus Darcy Ribeiro, Universidade de
Brasília, Brazil
[4]Instituto Nacional de Ciência e
Tecnologia-Informação Genético-
Sanitária da Pecuária Brasileira, Belo
Horizonte, Brazil
[5]Departamento de Zootecnia,
Universidade Federal de Pelotas, Brazil
[6]Centro de Ciências Agrárias,
Universidade Federal de Santa Catarina,
Florianópolis, Brazil

Abstract

The objective of this study was to estimate genetic parameters for survival measures from birth to 60 and 72 months of age, as well as survival up to 48 and 54 months after first calving. The genetic association of these measures with 20 linear type traits and final score in Holstein cows, born between years 1990 to 2004, was also evaluated. The components of (co)variance were estimated by Bayesian methods, using the programme THRGIBBS1F 90 in bivariate analyses, considering animal threshold model for measures of survival, and animal linear model for linear type traits. The mean posterior heritability for the measures of survival ranged from 0.09 to 0.15, and for those of the linear type traits ranged from 0.07 to 0.36. The posterior genetic correlation between linear type traits and measures of survival varied from -0.37 to 0.50, respectively. Indirect genetic selection for udder depth, rear teat placement, udder texture, bone quality, fore udder attachment, body depth and chest width may lead to correlated gains in longevity in Holstein cows under tropical conditions.

Introduction

Longevity is a highly desirable trait with economic importance in the dairy industry because of its direct relationship with herd profitability (Sewalem *et al*., 2010). Cows that have a long herd life result in increased opportunities for voluntary disposal based on production and the reduction of involuntary culling due to reproductive problems, health or locomotion (Berry *et al*., 2005), thus creating higher selection intensity (Lagrotta *et al*., 2010). Stability or survival in the herd was defined by Hudson and Van Vleck (1981) as the probability of cows remaining in the herd until a certain age. This measure of longevity can be recorded as categorical, assigning a score of 0 for cows that did not remain in the herd and 1 for those that remained for a pre-determined period. The analysis with linear models may, therefore, not be the most appropriate, due to the violation of *a priori* assumptions (Gianola, 1982). In this case threshold models are indicated (Sousa *et al*., 2000). When obtained at an early age, measures of survival may contribute to a reduction in generation intervals (Galeazzi *et al*., 2010) compared with longevity measures obtained after culling or death of the animal. However, in this case, only partial information of the cow's life is known (Potočnik *et al*., 2011). Another alternative is indirect selection for longevity, with the aid of linear type traits, due to the existence of moderate genetic correlations among some type traits and longevity (Cruickshank *et al.,* 2002; Zavadilová *et al.,* 2009). Moreover, type traits can be obtained in the first lactation, are easy to measure and have a higher heritability than longevity (Daliri *et al.,* 2008). Few studies have been conducted in Brazil to evaluate survival to a certain age in Holstein cows with the exception of Teixeira *et al*. (2003) using a linear model and Irano *et al*. (2013) using a threshold model. No study was found that considered the genetic correlation between survival under the threshold model with linear type traits.

To complement the choice of appropriate selection measures for longevity, the present study was undertaken to estimate genetic parameters for measures of survival from birth to 60 and 72 months of age, survival up to 48 and 54 months after the first calving, as well as to evaluate the genetic association of these measures with 21 linear type traits that could permit their use in genetic evaluations.

Materials and methods

The data used were collected by the technicians of the Service for Linear Classification, Milk Control and Genealogy of the Brazilian Association of Holstein Breeders (ABCBRH) and its state affiliates, using information from cows born between 1990 and 2004 and classified for linear type between 1995 and 2010. The linear type classification system used by the ABCBRH included 20 type traits based on direct measurements or visual scores of morphology expressed on a scale of one to nine points. These traits were divided in seven sections as in the Canadian model: i) conformation [stature (ST), top line (TL), chest width (CW), body depth (BD), loin strength (LS)]; ii) rump [rump angle (RA), rump width (RW)]; iii) feet and legs [foot angle (FA), bone quality (BQ), side view of rear legs (SV)]; iv) anterior udder [fore udder attachment (FU), fore teat placement (FT), udder teat length (UTL)]; v) posterior udder [rear udder height (RUH), rear udder width (RUW), rear teat placement (RT)]; vi) mammary system [udder depth (UD), udder texture (UT), udder cleft (UC)]; and vii) dairy form [angularity (AN)], as well as final score (FS). Dairy form accounted for 12%, conforma-

tion for 18%, feet and legs for 20%, mammary system for 8%, rump for 10%, front udder for 14%, and rear udder for 18% (Campos, 2012). Measures of longevity related to survival from birth to 60 (Long1_60) and 72 (Long1_72) months of age, as well as survival to 48 (Long2_48) and 54 (Long2_54) months after first calving were determined using production and reproduction records. The survival measures were defined assuming success (1) for cows that remained in the herd and failure (0) for those who were no longer in the herd at the stipulated dates. To improve the consistency of the database for the linear type traits, data were excluded of cows without pedigree, those with a final score less than 60 points, and cows with more than one classification. Ten stages of lactation at classification were formed (one per month of lactation). Also, cows classified after the third lactation, and age at calving outside the range of 20 to 87 months of age were excluded. Contemporary groups (herd-year and classification season) that did not contain at least three animals and bulls with less than two daughters in two different herds were eliminated. The classification seasons were: one (January to March); two (April to June); three (July to September) and four (October to December), both for linear type traits.

Regarding the consistency of longevity measures, cows without the date of birth and calving, contemporary groups without variation, that is, with identical score information (only score 0 or 1) as proposed by Harville and Mee (1984), were excluded. Contemporary groups for longevity were composed of herd, year and season of calving, with at least three records per group. The classes of milk production in the first lactation (MP1) in kg were: i) MP1<6.500; ii) 6.500≤MP1<7.750; iii) 7.750≤MP1<9.000; and iv) MP1≥9.000. Age at first calving (AFC1), in months, was also subdivided into classes: i) AFC1≤24; ii) 24<AFC1≤26; iii) 26<AFC1≤29; and iv) AFC1>29. After the consistency of linear type traits and measures of longevity was checked, four files were formed for the bivariate analysis between linear type traits with each measure of longevity (Table 1).

The bivariate models used for estimation of (co)variance among linear type traits and longevity included the fixed effects of contemporary group, classification seasons, classifier, stage of lactation and age of cow at classification (covariate with linear and quadratic terms) for linear type traits and fixed contemporary group effects, classes of milk production in first lactation and age at first calving for longevity measures. The animal and residual random effects were common to both models.

The statistical model used to estimate (co)variance among linear type traits and longevity can be described by:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} x_1 & 0 \\ 0 & x_2 \end{bmatrix} \cdot \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} z_1 & 0 \\ 0 & z_2 \end{bmatrix} \cdot \begin{bmatrix} u_1 \\ u_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

where, y_i is the vector of observations of the ith linear characteristic of type (i=1) and measures of longevity (i=2), β_i is the vector of fixed effects for the ith character, u_i is the vector for animal random effect for the ith character, e_i is the vector of residual effects of the ith character, X_i and Z_i are incidence matrices relating the observations for the ith character in the fixed and random effects of animal, respectively. The assumptions for the random additive genetic effects and residual threshold model were:

$$a|G \sim N[0, G], \text{ given } G=A\sigma_a^2$$
$$e|R \sim N[0, R], \text{ given } R=I\sigma_e^2$$
$$G|u_a, S_a \sim IW(\upsilon_a S_a, \upsilon_a)$$
$$R|u_e, S_e \sim IW(\upsilon_e S_e, \upsilon_e)$$

where G, R, A, I are respectively, the matrices of variances of additive genetic effects, residual, kinship coefficient and identity; σ_a^2 is the additive genetic variance; σ_e^2 is the residual variance; IW is the inverted Wishart distribution; u_a and S_a; u_e and S_e are *a priori* values and degrees of freedom for direct additive and residual genetic variances, respectively.

Measures of survival are threshold traits that have a subjacent continuous distribution. The threshold model relates the response observed on a categorical scale with an underlying normal continuous scale. Assuming that the underlying scale (U) has a normal distribution:

$$U|\theta \sim N(W, I\sigma_e^2)$$

where =(b',a') is the vector of parameter location with b (defined from a frequentist point of view, as fixed effects); a (random additive effect); W is a known incidence matrix; I is an identity matrix, and σ_e^2 is the residual variance.

In the Bayesian perspective, it was assumed that the prior distributions for the residual and direct additive genetic effects follow multivariate normal distributions:

$$p(a|\sigma_a^2) \sim N(0, A\sigma_a^2)$$

$$p(e|\sigma_e^2) \sim N(0, I\sigma_e^2)$$

where A is the relationship matrix; σ_a^2 is the additive genetic variance, and I is an identity matrix. For σ_e^2 a residual variance equal to 1 (Gianola and Foulley, 1983) was assumed.

The linkage between the two scales (categorical and continuous) can be unequivocally established, with the contribution of the probability of an observation in the first category, being proportional to:

$$P(Y_v=0|t, 0) = P(U_v \leq t|t, 0) = \Phi[(t-w'_v \theta]$$

where, y_v is the response variable to V^{th} observation, taking values 0 or 1 if the observation belongs to the first or second category, respectively, t is the threshold value; U_v is the value of underlying variable to the aforementioned observation, Φ is the cumulative distribution function of a normal standard variable, and w'_v is a column vector of incidence that unites θ to V^{th} observation.

The (co)variance components were estimated by Bayesian inference using the THRGIBBS1F90 programme (Misztal *et al.*, 2002), considering a threshold model for survival measures and a linear model for all linear type traits. The THRGIBBS1F90 programme generates Markov chains for the model parameters, by Gibbs sampling. To estimate the posterior distributions of (co)variance for the analyses of survival measures with each linear type trait, a single chain of 1,000,000 cycles

Table 1. Number of cows, bulls, cow dams, herds and contemporary groups in each bivariate analysis between linear type traits with different survival measures.

	Long1_60	Long1_72	Long2_48	Long2_54
Cows	20,900	17,628	15,760	13,748
Bulls	1015	922	864	809
Cow dams	17,093	14,564	13,118	13,748
Herds	365	335	311	293
Contemporary groups	1576	1376	1297	1200

Long1_60, survival from birth to 60 months of age; Long1_72, survival from birth to 72 months of age; Long2_48, survival from calving to 48 months of age; Long2_54, survival from calving to 54 months of age.

was used, but with different sizes of burn-in and sample period, depending on the trait analysed, due to the non-convergence of some of these bivariate analyses.

For the analysis between survival measures with top line, stature, chest width, foot angle, fore udder attachment and teat length a burn-in of 500,000 cycles was used with a sampling frequency of 60 iterations and 8333 samplings. For the analysis of other linear type traits a burn-in 300,000 cycles was used, removing a sample every 80 iterations, leaving 8750 as the final sample. The convergence these analyses was verified by the R® 2.9.0 programme (R Development Core Team, 2009) with the Bayesian Analysis Program Output-BOA package (Smith, 2005), which generates convergence diagnostics according to Geweke (1992) and Heidelberger and Welch (1983). The posterior estimates were obtained with POST-GIBBSF90 (Misztal et al., 2002).

Efficiency for indirect selection in relation to direct selection was obtained as the square root of the heritability of the type trait (for example, udder depth) divided by the square root of the measure of survival (for example, Long2_54), multiplying this result by the genetic correlation between both traits (udder depth and Long2_54).

Results and discussion

The percentage of cows surviving in the herd from birth to 60 or 72 months of age and first birth until 48 and 54 months of age decreased as the length of herd permanence increased, as determined by longevity measures (Figure 1), indicating that, over time, the ability of the cow to delay voluntary and involuntary culling decreases. After 60 months from birth, approximately 50% of the cows were still in production, while at 72 months of age over 60% of the cows were already discarded. Only 34.77 and 28.32% of the cows survived until 48 to 54 months from the first calving, respectively. According to Queiroz et al. (2007), this decrease in survival rate demonstrates the difficulties found by farmers for maintaining cows with good productive and reproductive performance over time.

In herds that have cows that live for a long time, higher rates of voluntary disposal are expected, based on the production levels and the reduction of disposal caused by reproductive, health and locomotion problems (Berry et al., 2005). Thus, allowing the permanence of highly productive cows for a longer period in the herd, as well as reduced replacement of

these animals, may result in an increased selection intensity with animals of higher genetic values (Silva et al., 2003; Lagrotta et al., 2010).

The survival of the animal until a specified time (e.g. at 60 and 72 months of age) is an easily measured alternative, and contrasts with the difficulties related to other commonly used measures of longevity, such as length of productive life and herd life (Vollema and Groen, 1996; Zavadilová el al., 2009). Unlike these measures, survival can be measured at any time during the animal s life. According to Galeazzi et al. (2010), when measured at an earlier age, these traits may contribute to a decrease in the generation interval. However, survival to a certain age provides only partial information on the animal's life, not specifying the date of death or culling, but only if the animal is present or not in the herd (Potočnik et al., 2011).

For the measures of longevity, some researchers suggest that the use of direct selection for longevity is limited, and that indirect selection would be more appropriate (Cruickshank et al., 2002). The use of correlated traits expressed early in the animal's life and with moderate heritability, such as linear type traits, may be a viable alternative for the selection for longevity (Cruickshank et al., 2002; Zavadilová et al., 2009; Zavadilová and Stípková, 2012). Longevity has often been analysed using linear (Zavadilová and Stípková, 2012) and threshold (Ahlman et al., 2011), models as well as survival analysis (Sewalem et al., 2004). The threshold model is more suitable (Sousa et al., 2000) as it pres-

ents a higher ability to detect genetic variability when compared to linear models (Ducrocq et al., 1988; Marcondes et al., 2005).

Posterior means of genetic and residual variances for Long1_60, Long1_72, Long2_48 and Long2_54, obtained using bivariate analysis with type traits, ranged from 0.100 to 0.184 and 1.054 to 1.052, respectively. The low posterior mean of genetic variances, combined with the high posterior mean of residual variances, resulted in low posterior mean heritabilities, with values of 0.09 (Long1_60), 0.12 (Long1_72), 0.15 (Long2_48) and 0.14 (Long2_54). Among these measures, Long2_48 may be responsible for a higher genetic gain for longevity, due to its higher heritability. The mean values of heritability suggest that most of the variation in these measures is the result of non-additive gene effects, and possible gains in longevity may be attained by improving the environment in which the animals are raised. These values are in accordance with those observed by Forabosco et al. (2009) in a study with herds from various countries participating in the international bull evaluation service (Interbull), with values ranging from 0.02 to 0.11, respectively.

In Brazil, survival in the herd using a threshold model in dairy cows has been little studied. Irano et al. (2013) studied this trait in Brazilian Holsteins using a threshold model and found higher heritability for survival to 3rd lactation (0.28). Studies with other breeds in Brazil also reported higher values than those of the present study. Queiroz et al. (2007) reported average value of 0.27 and 0.23 in
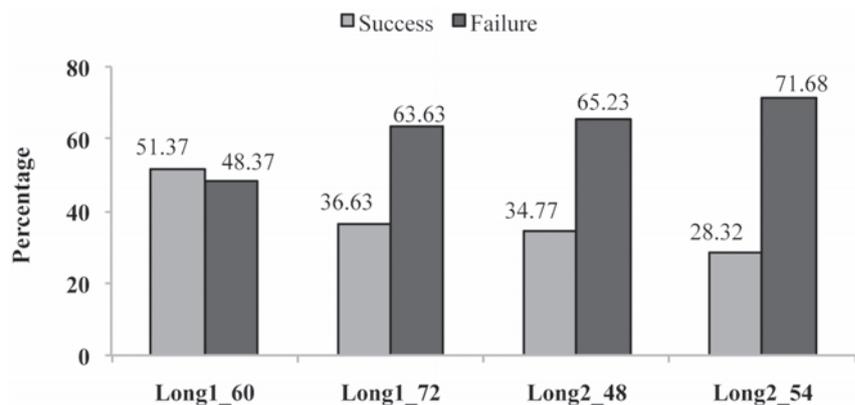
Figure 1. Percentage of success and failure for survival measures Long1_60, Long1_72, Long2_48 and Long2_54.

Table 2. Posterior mean and highest posterior density interval of residual variance obtained in bivariate analysis between type traits and survival measures.

Traits	Long1_60		Long1_72		Long2_48		Long2_54	
	Mean	95% HPD	Mean	95% HPD	Mean	95% HPD	Mean	95% HPD
ST	0.88±0.03	0.83-0.94	0.88±0.03	0.82-0.94	0.88±0.03	0.81-0.94	0.90±0.03	0.83-0.96
TL	0.66±0.01	0.64-0.69	0.66±0.01	0.63-0.67	0.67±0.01	0.64- 0.69	0.67±0.03	0.63-0.69
CW	0.99±0.02	0.95-1.02	0.96±0.02	0.91-0.99	0.94±0.02	0.89-0.98	0.95±0.03	0.91-1.00
BD	0.75±0.02	0.71-0.78	0.70±0.02	0.66-0.74	0.70±0.02	0.65-0.73	0.69±0.03	0.65-0.73
LS	1.11±0.02	1.06-1.15	1.05±0.02	1.00-1.10	1.01±0.02	0.96-1.06	0.99±0.03	0.94-1.05
RA	0.64±0.02	0.60-0.67	0.60±0.02	0.56-0.63	0.59±0.02	0.55-0.63	0.61±0.03	0.56-0.64
RW	0.78±0.02	0.73-0.82	0.75±0.02	0.70-0.79	0.75±0.03	0.70-0.80	0.73±0.03	0.68-0.79
FA	1.10±0.02	1.07-1.14	1.10±0.02	1.06-1.13	1.08±0.02	1.04-1.12	1.07±0.03	1.02-1.10
BQ	1.18±0.02	1.13-1.22	1.15±0.03	1.10-1.20	1.13±0.03	1.08-1.18	1.12±0.03	1.05-1.17
SV	0.96±0.02	0.92-1.00	0.95±0.02	0.90-0.98	0.92±0.02	0.88-0.96	0.91±0.03	0.86-0.95
FU	1.60±0.03	1.53-1.66	1.63±0.04	1.56-1.70	1.64±0.04	1.56-1.71	1.64±0.03	1.56-1.71
FT	0.94±0.02	0.89-0.98	0.95±0.02	0.90-0.99	0.93±0.03	0.87-0.98	0.92±0.03	0.86-0.97
UTL	0.74±0.02	0.70-0.77	0.74±0.02	0.70-0.78	0.75±0.02	0.70-0.79	0.75±0.03	0.70-0.79
RUH	1.26±0.02	1.21-1.30	1.23±0.03	1.18-1.28	1.22±0.03	1.16-1.27	1.18±0.03	1.12-1.24
RUW	1.27±0.02	1.22-1.31	1.26±0.02	1.21-1.31	1.26±0.03	1.20-1.31	1.23±0.03	1.17-1.29
RT	0.10±0.02	0.95-1.03	1.00± 0.02	0.95-1.04	0.99±0.02	0.94-1.03	1.00±0.03	0.95-1.04
UD	0.87±0.02	0.83-0.91	0.89±0.02	0.84-0.93	0.87±0.02	0.82-0.91	0.87±0.03	0.82-0.92
UT	0.93±0.02	0.90-0.96	0.92±0.02	0.88-0.94	0.91±0.02	0.87-0.94	0.88±0.03	0.84-0.92
UC	1.56±0.03	1.49-1.62	1.51±0.04	1.43-1.57	1.45±0.04	1.37-1.53	1.45±0.03	1.37-1.53
AN	0.82±0.02	0.79-0.85	0.79±0.02	0.75-0.82	0.77±0.02	0.74-0.81	0.76±0.03	0.71-0.79
FS	4.77±0.10	4.58-4.96	4.73±0.11	4.51-4.93	4.55±0.12	4.31-4.78	4.57±0.03	4.30-4.81

Long1_60, survival from birth to 60 months of age; Long1_72, survival from birth to 72 months of age; Long2_48, survival from calving to 48 months of age; Long2_54, survival from calving to 54 months of age; HPD, posterior density interval; ST, stature; TL, top line; CW, chest width; BD, body depth; LS, loin strength; RA, rump angle; RW, rump width; FA, foot angle; BQ, bone quality; SV, side view of rear legs; FU, fore udder attachment; FT, teat placement; UTL, udder teat length; RUH, rear udder height; RUW, rear udder width; RT, rear teat placement; UD, udder depth; UT, udder texture; UC, udder cleft; AN, angularity; FS, final score.

Table 3. Posterior mean and highest posterior density interval of genetic variance obtained in bivariate analysis between linear type traits and survival measures.

Traits	Long1_60		Long1_72		Long2_48		Long2_54	
	Mean	95% HPD	Mean	95% HPD	Mean	95% HPD	Mean	95% HPD
ST	0.49±0.03	0.42-0.55	0.47±0.04	0.40-0.55	0.45± 0.04	0.34-0.53	0.42±0.02	0.34-0.50
TL	0.14± 0.01	0.12-0.17	0.13±0.01	0.10-0.16	0.13±0.01	0.10-0.16	0.12±0.02	0.09-0.15
CW	0.20±0.02	0.16-0.24	0.22±0.02	0.18-0.27	0.22±0.02	0.17-0.27	0.21±0.02	0.16-0.26
BD	0.20±0.02	0.16-0.23	0.22±0.02	0.17-0.26	0.22±0.02	0.17-0.26	0.20±0.02	0.15-0.24
LS	0.31±0.03	0.25-0.36	0.27±0.03	0.22-0.33	0.27±0.03	0.22-0.33	0.27±0.02	0.21-0.33
RA	0.26±0.02	0.22-0.30	0.27±0.02	0.23-0.31	0.26±0.02	0.21-0.30	0.23±0.02	0.19-0.28
RW	0.38±0.03	0.33-0.44	0.39±0.03	0.33-0.44	0.37±0.03	0.31-0.43	0.37±0.02	0.31-0.43
FA	0.09± 0.01	0.06-0.12	0.10±0.02	0.07-0.13	0.11±0.02	0.08-0.14	0.12±0.02	0.08-0.15
BQ	0.29±0.03	0.24-0.34	0.27±0.03	0.22-0.33	0.27±0.03	0.21-0.33	0.27±0.02	0.20-0.32
SV	0.18± 0.02	0.14-0.22	0.18±0.02	0.14-0.22	0.19±0.02	0.14-0.23	0.20±0.02	0.15-0.25
FU	0.37± 0.03	0.30-0.43	0.35±0.04	0.27 -0.42	0.34±0.04	0.26-0.42	0.34±0.02	0.25-0.42
FT	0.31± 0.03	0.26-0.36	0.30±0.03	0.24-0.35	0.31±0.03	0.25 -0.37	0.31±0.02	0.25-0.38
UTL	0.31± 0.02	0.26-0.35	0.31±0.03	0.25-0.36	0.30±0.03	0.24-0.35	0.32±0.02	0.26-0.37
RUH	0.24± 0.02	0.19-0.29	0.24±0.03	0.18-0.28	0.25±0.03	0.19-0.30	0.27±0.02	0.20-0.33
RUW	0.24± 0.03	0.19-0.29	0.22±0.03	0.17-0.27	0.21±0.03	0.15-0.26	0.23±0.02	0.16-0.29
RT	0.18± 0.02	0.14-0.22	0.18±0.02	0.14-0.23	0.19±0.02	0.14-0.24	0.18±0.02	0.14-0.23
UD	0.24± 0.02	0.19-0.29	0.23±0.02	0.19-0.28	0.26±0.03	0.20-0.31	0.23±0.02	0.17-0.28
UT	0.09± 0.01	0.06-0.12	0.09±0.01	0.05-0.11	0.08±0.02	0.05-0.11	0.09±0.02	0.05-0.12
UC	0.39± 0.04	0.31-0.46	0.36±0.04	0.29-0.44	0.38±0.04	0.30-0.47	0.35±0.02	0.26-0.43
AN	0.15± 0.01	0.12-0.18	0.14±0.02	0.10-0.18	0.13±0.02	0.09-0.17	0.14±0.02	0.10-0.18
FS	0.91± 0.10	0.70-1.10	0.93±0.12	0.71-1.15	1.01±0.13	0.74-1.25	0.95±0.02	0.67-1.23

Long1_60, survival from birth to 60 months of age; Long1_72, survival from birth to 72 months of age; Long2_48, survival from calving to 48 months of age; Long2_54, survival from calving to 54 months of age; HPD, posterior density interval; ST, stature; TL, top line; CW, chest width; BD, body depth; LS, loin strength; RA, rump angle; RW, rump width; FA, foot angle; BQ, bone quality; SV, side view of rear legs; FU, fore udder attachment; FT, teat placement; UTL, udder teat length; RUH, rear udder height; RUW, rear udder width; RT, rear teat placement; UD, udder depth; UT, udder texture; UC, udder cleft; AN, angularity; FS, final score.

Table 4. Posterior mean and highest posterior density interval of heritabilities obtained in bivariate analysis between linear type traits and survival measures.

Traits	Long1_60		Long1_72		Long2_48		Long2_54	
	Mean	95% HPD	Mean	95% HPD	Mean	95% HPD	Mean	95% HPD
ST	0.36	0.31-0.40	0.35	0.30-0.40	0.34	0.29-0.39	0.32	0.26-0.37
TL	0.18	0.15-0.21	0.17	0.13-0.20	0.16	0.13-0.20	0.16	0.11-0.19
CW	0.17	0.14-0.20	0.19	0.15-0.22	0.19	0.15-0.23	0.18	0.14-0.22
BD	0.21	0.17-0.25	0.24	0.19-0.28	0.24	0.19-0.28	0.22	0.17-0.27
LS	0.22	0.18-0.25	0.21	0.16-0.24	0.21	0.17-0.25	0.22	0.17-0.26
RA	0.30	0.25-0.33	0.31	0.26-0.35	0.30	0.25-0.35	0.28	0.23-0.33
RW	0.33	0.29-0.37	0.34	0.30-0.38	0.33	0.28-0.38	0.34	0.29-0.40
FA	0.07	0.05-0.10	0.08	0.05-0.10	0.09	0.06-0.12	0.10	0.07-0.13
BQ	0.20	0.16-0.23	0.19	0.15-0.22	0.20	0.16-0.23	0.19	0.15-0.24
SV	0.16	0.12-0.19	0.16	0.13-0.20	0.17	0.13-0.21	0.18	0.13-0.22
FU	0.19	0.15-0.22	0.18	0.13-0.21	0.17	0.13-0.21	0.17	0.130-0.21
FT	0.25	0.21-0.28	0.24	0.20-0.28	0.25	0.21-0.29	0.25	0.21-0.30
UTL	0.29	0.25-0.33	0.29	0.24-0.33	0.28	0.24-0.33	0.30	0.25-0.34
RUH	0.16	0.13-0.19	0.16	0.12-0.19	0.17	0.13-0.21	0.19	0.14-0.23
RUW	0.16	0.12-0.19	0.15	0.11-0.18	0.14	0.11-0.18	0.16	0.11-0.19
RT	0.15	0.12-0.19	0.15	0.12-0.19	0.16	0.12-0.20	0.15	0.11-0.19
UD	0.22	0.18-0.25	0.21	0.17-0.25	0.23	0.18-0.27	0.21	0.16-0.25
UT	0.09	0.06-0.12	0.08	0.05-0.11	0.08	0.05-0.11	0.09	0.06-0.13
UC	0.20	0.16-0.23	0.19	0.15-0.23	0.21	0.16-0.25	0.19	0.15-0.24
AN	0.16	0.12-0.19	0.15	0.12-0.19	0.15	0.11-0.18	0.16	0.12-0.20
FS	0.16	0.12-0.20	0.16	0.13-0.20	0.18	0.14-0.22	0.17	0.13-0.22

Long1_60, survival from birth to 60 months of age; Long1_72, survival from birth to 72 months of age; Long2_48, survival from calving to 48 months of age; Long2_54, survival from calving to 54 months of age; HPD, posterior density interval; ST, stature; TL, top line; CW, chest width; BD, body depth; LS, loin strength; RA, rump angle; RW, rump width; FA, foot angle; BQ, bone quality; SV, side view of rear legs; FU, fore udder attachment; FT, teat placement; UTL, udder teat length; RUH, rear udder height; RUW, rear udder width; RT, rear teat placement; UD, udder depth; UT, udder texture; UC, udder cleft; AN, angularity; FS, final score.

Table 5. Posterior mean and highest posterior density interval of residual correlations obtained in bivariate analysis between linear type traits and survival measures.

Traits	Long1_60		Long1_72		Long2_48		Long2_54	
	Mean	95% HPD	Mean	95% HPD	Mean	95% HPD	Mean	95% HPD
ST	0.02	-0.03 − 0.06	0.02	-0.03 − 0.06	0.01	-0.04 − 0.07	0.02	-0.04 − 0.07
TL	0.01	-0.02 − 0.04	0.01	-0.02 − 0.05	0.00	-0.04 − 0.04	0.00	-0.05 − 0.04
CW	0.03	-0.01 − 0.06	0.03	-0.01 − 0.07	0.02	-0.02 − 0.06	0.01	-0.04 − 0.05
BD	-0.01	-0.04 − 0.03	-0.01	-0.05 − 0.03	0.00	-0.05 − 0.04	0.01	-0.04 − 0.06
LS	0.02	-0.02 − 0.05	0.00	-0.04 − 0.04	0.02	-0.03 − 0.06	0.00	-0.05 − 0.05
RA	0.02	-0.02 − 0.06	-0.01	-0.05 − 0.04	0.00	-0.05 − 0.05	-0.01	-0.06 − 0.04
RW	0.00	-0.04 − 0.03	-0.02	-0.07 − 0.03	-0.03	-0.08 − 0.02	0.01	-0.05 − 0.06
FA	0.00	-0.03 − 0.02	0.01	-0.02 − 0.04	0.01	-0.02 − 0.05	0.02	-0.02 − 0.06
BQ	-0.02	-0.05 − 0.01	0.00	-0.04 − 0.04	-0.01	-0.05 − 0.03	-0.01	-0.06 − 0.04
SV	-0.02	-0.05 − 0.01	-0.03	-0.07 − 0.01	-0.04	-0.08 − 0.04	-0.01	-0.05 − 0.04
FU	0.03	-0.01 − 0.06	-0.01	-0.04 − 0.03	0.00	-0.04 − 0.04	0.02	-0.03 − 0.06
FT	-0.04	-0.07 − -0.00	-0.02	-0.07 − 0.01	-0.01	-0.06 − 0.03	-0.01	-0.06 − 0.04
UTL	-0.01	-0.04 − 0.03	-0.01	-0.06 − 0.03	0.00	-0.05 − 0.04	-0.01	-0.06 − 0.04
RUH	0.01	-0.03 − 0.05	0.01	-0.03 − 0.04	0.01	-0.03 − 0.05	0.00	-0.05 − 0.05
RUW	0.00	-0.03 − 0.03	0.02	-0.02 − 0.01	0.02	-0.02 − 0.06	0.01	-0.03 − 0.06
RT	-0.05	-0.08 − -0.02	-0.04	-0.08 − -0.01	-0.03	-0.07 − 0.01	-0.04	-0.08 − -0.01
UD	0.04	0.00 − 0.06	0.04	0.00 − 0.08	0.02	-0.03 − 0.06	0.03	-0.02 − 0.08
UT	0.00	-0.03 − 0.03	-0.01	-0.04 − 0.03	-0.01	-0.05 − 0.03	-0.01	-0.05 − 0.03
UC	0.05	0.02 − 0.09	0.05	0.01 − 0.09	0.04	0.00 − 0.09	0.03	0.02 − 0.08
AN	-0.01	-0.04 − 0.02	0.00	-0.04 − -0.04	0.01	-0.03 − -0.05	0.03	-0.01 − -0.08
FS	0.08	0.05 − 0.12	0.07	0.03 − 0.11	0.09	0.04 − 0.13	0.07	0.02 − 0.12

Long1_60, survival from birth to 60 months of age; Long1_72, survival from birth to 72 months of age; Long2_48, survival from calving to 48 months of age; Long2_54, survival from calving to 54 months of age; HPD, posterior density interval; ST, stature; TL, top line; CW, chest width; BD, body depth; LS, loin strength; RA, rump angle; RW, rump width; FA, foot angle; BQ, bone quality; SV, side view of rear legs; FU, fore udder attachment; FT, teat placement; UTL, udder teat length; RUH, rear udder height; RUW, rear udder width; RT, rear teat placement; UD, udder depth; UT, udder texture; UC, udder cleft; AN, angularity; FS, final score. Standard deviation for all traits ranged from 0.01 to 0.02.

Caracu cattle for Long1_60 and Long1_72, respectively. In Sweden, Ahlman et al. (2011), also using a threshold model in Holstein cows, obtained a low posterior heritability for the ability to remain in the herd to the first (0.05) and second lactation (0.08), and a moderate value to remain until the third lactation (0.20). The posterior mean of residual variance for the linear type traits ranged from 0.59 (rump angle) to 4.77 (final score) (Table 2). These values were higher than the posterior mean genetic variance, which ranged from 0.08 (udder texture) to 1.01 (final score) (Table 3). The highest posterior means of genetic variance were observed for stature, udder cleft, rump width, fore udder attachment, teat placement and teat length. A wide range (0.07 to 0.36) of posterior means for heritability of type traits (Table 4) was observed. With the exception of foot angle, udder texture and udder width, the other linear type traits showed posterior mean heritabilities equal to or greater than 0.15. The highest means were observed for stature (0.36), rump width (0.34), rump angle (0.31) and teat length (0.30). The posterior mean of heritability for linear type traits obtained in conjunction with each measure of

longevity (Long1_60, Long1_72, Long2_48 and Long2_54) showed low variation, which for the most part were 0.01 and 0.02 points, except for stature (0.04) and body depth, rump angle, foot angle and udder cleft that showed variation of 0.03 (Table 4). Low heritabilities for hoof angle (0.10) and udder texture (0.11) were also observed by Campos et al. (2012) in Holstein cows, as well as by Němcová et al. (2011) and Lagrotta et al. (2010) in Holstein and Gir cattle, respectively, for hoof angle (0.09 and 0.12). The posterior residual correlations were low, ranging from -0.05 to 0.09 (Table 5). Values of residual correlations close to nullity suggest that the type traits and survival measures (Long1_60, Long1_72, Long2_48 and Long2_54) are not influenced by the same factors or environmental effects, reinforcing the need to practice selection based on breeding values.

The knowledge of the genetic correlations between traits is essential for directing the selection to be adopted, because when two traits are positively and highly correlated improvement of both can be achieved by selecting for a single trait. The choice of which to select will depend on other important factors

such as cost, ease of measurement and time for obtaining the measure or trait (phenotype). In general, the posterior mean of genetic correlations between linear type traits and survival measures were negative with moderate to low values (Table 6). The highest variation in the estimates of genetic correlation between survival measures with linear type traits were observed with type traits: fore udder attachment, udder cleft, final score and udder depth. The posterior mean of genetic correlations between conformation traits and survival measures were negative and moderate (-0.10 to -0.03), except for the top line with Long1_72, Long2_48 and Long2_54, suggesting that cows with greater stature, chest width, body depth and loin strength show lower survival in the herd (Table 6). Negative correlations of stature, strength and body loin depth with survival to 48, 54 and 84 months of age, corrected and uncorrected for milk production, were also reported by Rogers et al. (1989) in Holstein cows. In general, most measures of longevity reported in the literature show a negative association with conformation traits (Tsuruta et al., 2005; Zavadilová et al., 2009; Samoré et al., 2010).

Table 6. Posterior mean and highest posterior density interval of genetic correlations obtained in bivariate analysis between linear type traits and survival measures.

Traits	Long1_60		Long1_72		Long2_48		Long2_54	
	Mean	95% HPD	Mean	95% HPD	Mean	95% HPD	Mean	95% HPD
ST	-0.22	-0.43 − -0.01	-0.20	-0.40 − 0.01	-0.18	-0.37-0.03	-0.22	-0.44 − 0.07
TL	-0.20	-0.43 − -0.01	-0.10	-0.31 − 0.12	-0.03	-0.24 − 0.17	-0.03	-0.26 − 0.24
CW	-0.36	-0.60 − -0.14	-0.37	-0.57 − -0.17	-0.24	-0.44 − -0.05	-0.21	-0.46 − 0.02
BD	-0.30	-0.54 − -0.08	-0.30	-0.51 − -0.08	-0.31	-0.51 − -0.11	-0.37	-0.60 − -0.12
LS	-0.14	-0.36 − -0.07	-0.21	-0.41 − 0.00	-0.26	-0.46 − -0.06	-0.18	-0.43 − 0.05
RA	-0.05	-0.26 − 0.16	-0.02	-0.22 − 0.18	-0.05	-0.24 − 0.14	-0.02	-0.25 − 0.21
RW	-0.12	-0.31 − 0.08	-0.01	-0.21 − 0.18	-0.01	-0.21 − 0.18	-0.12	-0.34 − 0.09
FA	-0.06	-0.33 − 0.21	-0.10	-0.37 − 0.16	-0.09	-0.33 − 0.16	-0.12	-0.40 − 0.17
BQ	0.21	0.00 − 0.41	0.18	-0.03 − 0.40	0.25	0.05 − 0.45	0.33	0.09 − 0.57
SV	0.15	-0.01 − 0.36	0.05	-0.18 − 0.29	0.16	-0.05 − 0.40	-0.03	-0.26 − 0.23
FU	-0.09	-0.30 − 0.15	0.19	-0.33 − 0.41	0.23	0.01 − 0.45	0.18	-0.08 − 0.43
FT	0.14	-0.07 − 0.32	0.10	-0.10 − 0.31	0.08	-0.12 − 0.26	0.11	-0.11 − 0.34
UTL	0.08	-0.12 − 0.28	0.07	-0.11 − 0.27	0.04	-0.16 − 0.23	0.08	-0.15 − 0.30
RUH	0.13	-0.03 − 0.08	0.14	-0.11 − 0.35	0.05	-0.23 − 0.21	0.16	-0.10 − 0.41
RUW	-0.15	-0.37 − 0.08	-0.11	-0.34 − 0.12	-0.15	-0.37 − 0.07	-0.09	-0.35 − 0.17
RT	0.26	0.03 − 0.48	0.22	-0.03 − 0.45	0.14	-0.10 − 0.36	0.24	-0.01 − 0.50
UD	0.29	0.01 − 0.12	0.41	0.19 − 0.64	0.45	0.23 − 0.64	0.50	0.24 − 0.74
UT	0.08	-0.18 − 0.35	0.24	-0.04 − 0.53	0.20	-0.07 − 0.50	0.27	-0.06 − 0.58
UC	-0.11	-0.33 − 0.12	0.02	-0.21 − 0.23	0.05	-0.15 − 0.28	0.14	-0.13 − 0.40
AN	-0.02	-0.30 − 0.22	-0.06	-0.32 − 0.18	-0.10	-0.35 − 0.12	-0.18	-0.44 − 0.08
FS	-0.06	-0.31 − 0.17	0.14	-0.01 − 0.41	0.09	-0.15 − 0.31	0.18	-0.10 − 0.47

Long1_60, survival from birth to 60 months of age; Long1_72, survival from birth to 72 months of age; Long2_48, survival from calving to 48 months of age; Long2_54, survival from calving to 54 months of age; HPD, posterior density interval; ST, stature; TL, top line; CW, chest width; BD, body depth; LS, loin strength; RA, rump angle; RW, rump width; FA, foot angle; BQ, bone quality; SV, side view of rear legs; FU, fore udder attachment; FT, teat placement; UTL, udder teat length; RUH, rear udder height; RUW, rear udder width; RT, rear teat placement; UD, udder depth; UT, udder texture; UC, udder cleft; AN, angularity; FS, final score. Standard deviation for all traits ranged from 0.10 to 0.13.

The rump angle and width showed the same behaviour as the traits in the conformation section, with negative, but close to nullity, posterior genetic correlations. Caravielho *et al.* (2003) reported that cows with high, medium and low scores for rump angle and width, exhibit weak genetic association with survival time until death or disposal. Bone quality in the legs and feet section showed positive favourable posterior genetic correlations with Long6_60 (0.21), Long6_72 (0.18), Long2_48 (0.25) and Long2_54 (0.33), indicating that cows with good bone quality have the genetic potential for survival in the herd until determined ages using the survival measures studied here. In contrast, foot angle showed low and negative posterior genetic associations (-0.06 to -0.12), which, when combined with the low heritability for this trait, suggests that there is little possibility of correlated gains in longevity of cows through selection for foot angle. Low and positive values of genetic correlations were reported by Short and Lawlor (1992) between foot angle and measures of survival up to second calving (0.05), up to 54 (0.05) and 84 months of age (0.06).

Among the traits related to the udder and mammary system sections, the higher posterior genetic correlations were observed between the rear teat placement and udder depth with Long1_60, Long1_72, Long2_48 and Long2_54, respectively, and between udder texture and fore udder attachment with Long1_72, Long2_48 and Long2_54 respectively. The remaining posterior genetic correlations between measures of longevity and linear type traits in these sections and angularity were low, indicating that indirect selection for these traits result in lower response correlated to longevity or survival from birth to 60 and 72 months of age, and survival of calving to 48 and 54 months of age. The positive posterior genetic correlations between traits related to the udder and mammary system sections with Long1_60, Long1_72, Long2_48 and Long2_54 show that cows that were long-lived tended to present a strongly inserted, soft, elastic and shallower udders and teats located in center of the posterior limbs, demonstrating that when the selection for mammary system is practiced, desirable effects on longevity may occur.

Among the type traits, those related to the mammary system may be considered as the most important due to the genetic association with milk production (Rennó *et al.*, 2003; Lagrotta *et al.*, 2010) and longevity (Zavadilová *et al.*, 2009). The low posterior genetic correlations between final score and survival measures indicate that genetic gains for longevity will be insignificant if selection is based exclusively on the final score, although this trait is used as selection criteria by Brazilian farmers (McManus and Saueressig, 1998).

Considering the similarities in heritability for Long1_60 (0.09), Long1_72 (0.12), Long2_48 (0.15) and Long2_54 (0.14) and the shorter time necessary for obtaining Long2_48, this latter can be indicated as the most appropriate measure for selection that can be obtained early in the animal's life. These heritabilities suggest that direct selection of sires for higher survival of their daughters from birth to 60 and 72 months of age, and from calving to 48 and 54 months of age, will probably not be effective for obtaining expressive genetic progress in longevity. Looking at the type trait that showed the highest genetic correlation with longevity (udder depth, 0.50), the efficiency for indirect selection with a value of 0.61, indirect selection is not advantageous when compared to direct selection for Long2_54, but this without taking the generation interval into consideration. Possibly, if this component is included in the calculation of efficiency, the type traits with the highest genetic correlations with longevity may generate higher gains, since longevity requires a long time to measure compared to the type trait, which is generally obtained during the first lactation.

Conclusions

The best measure of longevity is the survival of cows from the calving to 48 months of age. In general, when practicing genetic selection for linear type traits, one cannot expect significant improvements in breeding values for longevity. The udder depth, rear teat placement, udder texture, bone quality, fore udder attachment, body depth and chest width can be used as auxiliary measures in the selection of longer-lived animals in the herd.

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