Genetic parameters of test day records in Brazilian Holstein cattle using an autoregressive multiple lactation animal model

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ABSTRACT: Variance components and genetic parameters were estimated for milk (**M**), fat **(F**), protein (**P**) and log-transformed somatic cell count (SCS) of Brazilian Holstein cattle using an autoregressive test day (TD) multiple lactations animal (AR) model. Data consisted of TD records produced by cows calving from 1992 to 2010 in herds under supervised milk recording. Average heritabilities of first three lactations for **M**, **F**, **P** and SCS equal to 0.,28, 0.29, 0.28 and 0.19 respectively, leaded to genetic gains equal to 40.0, 0.98, 1.0 kg/year and -2,16 units/year for cows born from 1987 to 2008 and 34.9, 0.53, 0.69 kg/year and -4,83 units/year for bulls born from 1977 to 2002, respectively. Heritabilities and genetic gains suggest the AR model as a suitable approach to fit TD records to predict breeding values and to realize genetic gains by selection in Holstein cattle in Brazil.
Keywords: Milk components**;** Selection**;** Variance components

Introduction

Most of dairy cattle national genetic evaluation systems have been replacing 305d lactation model by test day (TD) models for breeding value prediction to explore the opportunity for large genetic gain by selection. Analysis of test day records by random regression (RR) models allows the shape of the lactation curve to differ among individual animals by fitting sub-models including random regression coefficients for each animal (Schaeffer, 2004).

In Brazil, genetic evaluations for the Holstein cattle include production (milk, fat and protein) and linear type traits (Costa et al., 2013). Genetic evaluations for the production traits use 305 d adjusted lactation records. There is no genetic evaluation for somatic cell score (SCS) which has been recommended as an indicator trait for reducing clinical mastitis (Miller et al., 2009). Previous studies using first lactation TD records suggested RR models using Legendre polynomials as a feasible option to replace the lactation model to predict breeding values for production traits (Costa et al., 2008) and also for SCS (Costa et al., 2010). An alternative to the RR models is the autoregressive TD approach which assumes that TD yields are the expression of the same set of genes throughout the cow´s productive life (Carvalheira et al., 2002). The aim of this study was to estimate variance components and genetic parameters for test day milk, fat, protein and SCS of Holstein cattle in Brazil, using an AR animal model.

Materials and Methods

Data. Data comprised 3.6 million TD records of Holstein cows provided by the Brazilian Holstein Cattle Breeders Association. The data editing process was performed according to pre-defined criteria for genetic analysis following assumptions of the AR model (Carvalheira et al., 2002). This included deleting test day SCC records that were considered outliers, days in milk (DIM) less than five or greater than 305 days, age, test date or DIM out of sequence in the first three lactations. Another editing criterion considered deleting cows having less than eight SCC records per lactation in order to obtain more robust estimates of variance components. After editing, data sets included TD records of lactations of cows, calving from 1992 to 2010 and their structure varied according the trait analysed. For the pedigree file, all available information was used and it comprised 84,665 animals. Somatic cell count measurements were log transformed to SCS = $\log_2$ (CCS/ 100.000) + 3, the trait analysed in this study. The data sets structures after editing is shown in Table 1.

Table 1. Number of cows and milk, fat, protein and SCS TD records of Brazilian Holstein cows.

Data/Trait	Milk	Fat	Protein	SCS
Initial Rec.[⍰]	2,471,1	2,151,133	1,9660,82	1,760,74
Cows	145,02	140,588	125,339	118,151
Final Rec.[§]	1,269,9	986,288	975,769	961,570
Cows	67,563	52,187	53,225	54,900
1st Lact.[ǂ]				
Records	581,77	450,276	446,980	427,762
Cows	61,940	45,039	28,304	47,712
2nd Lact.				
Records	417,13	326,824	324,242	324,255
Cows	48,836	35,574	22,854	36,345
3rd Lact.				
Records	261,08	209,188	204,547	209,553
Cows	48,846	35,887	22,512	23,411

[⍰] Initial Rec.: Initial Test day Records;
[§] Final Rec.: Final Test day Records;
[ǂ] Lact.: Lactation.

Model. The data for each trait were randomly sampled in six sub sets for the estimation of genetic parameters. Variance component estimations were based on derivative free REML methodology following assumptions of the AR model (Carvalheira et al., 2002). The AR animal model was as follows:

$$y_{ijklmno} = HTD_i + Age_j(H_k) + DIM_m(H_k\ L_l) + a_n + LTE_n + STE_{nl} + e_{ijkmlno},$$

where, **y** is the TD observation, **HTD** is the fixed effect of herd-test-date, **Age(H)** is the fixed effect of the age at calving nested within herd, **DIM(H L)** is the fixed effect of DIM nested within herd and lactation, **a** is the random genetic effect, **LTE** is the random effect of the long-term environmental effects accounting for the autocorrelations generated by the cow across repeated lactations, **STE** is the random effect of short term environmental effects accounting for the cow's autocorrelations between TD within each lactation, and **e** is the random residual effect that is assumed to be normally and independently distributed between lactations. A detailed description of the model expectations and (co)variance structure is in Carvalheira et al. (2002). The convergence criterion was met when the variance of the simplex was less than 10^{-8}.

Results and Discussion

Genetic parameters. Averages of covariance components, autocorrelations and genetic parameters from the six subsets analysed for the first three lactations of daily milk, fat, protein and SCS are shown in Table 2. It was observed heterogeneity on the error variance among lactations which increased with the order of lactation. In contrast, heritability has decreased. The heritability estimates for milk, fat, protein yields (Table 2) decreased from the first to the third lactation ranging from 0.378 (fat) to 0.225 (milk). These estimates are larger than those reported by Costa et al., (2013) using 305d lactation models and those obtained by using Legendre polynomials in random regression (RR) models using first lactation records of Holstein cows (Costa et al., 2008; Biassus et al., 2011). Average of heritability estimates of SCS was 0.195, which is larger than those estimated for SCS in first lactation records adjusted by RR models (Costa et al., 2010). In that study, average of heritability estimates for SCS over DIM for Legendre Polynomials of order three to five was < 0.10. TD records were highly correlated within each lactation, ranging from 0.77 for fat to 0.84 for SCS, both in lactation one.

Table 2. (Co)variance components, autocorrelations and genetic parameters for TD milk, fat, protein and SCS of Brazilian Holstein cows estimated by an AR model.

Par. ¶/Trait	Milk	Fat	Protein	SCS
Genetic v.[#]	9.579	.013	.008	.604
Error v./L1[ϕ]	3.326	.009	.004	.954
Error v./L2[Ψ]	4.892	.016	.006	.917
Error v./L3[φ]	5.545	.019	.006	.895
LTE[γ] v.	<.001	<.001	<.001	<.001
LTE a.[l]	<.001	<.001	<.001	<.001
STE[δ] v./L1	14.128	.013	.011	1.492
STE a./L1	.820	.770	.800	.840
STE v./L2	23.081	.022	.018	1.534
STE a./L2	.830	.800	.810	.810
STE v./L3	27.798	.028	.022	1.693
STE a./L3	.830	.810	.810	.821
Phe[Δ].v./L1	27.033	.035	.024	3.050
Phe.v./L2	37.552	.058	.033	3.055
Phe.v./L3	42.923	.062	.037	3.191
Herita[ð]./L1	.355±.035	.378±.026	.352±.028	.198±.009
Herita./L2	.257±.030	.259±.020	.259±.030	.198±.010
Herita./L3	.225±.028	.229±.019	.228±.029	.190±.011

¶ Par.: parameter
#v.: variance. Variances are in units
ϕL1 = 1st Lactation
ΨL2 = 2nd Lactation
φL3 = 3rd Lactation
la.: autocorrelation
γLTE: Long term environmental effects
δSTE: Short term environmental effects
ΔPhe. = phenotypic
ðHerita. = heritability

Genetic gains. Medium heritability estimates obtained in this study (Table 2) indicate opportunities for genetic gains by selection. Genetic trends were estimated by regressing annual average of estimated breeding values (EBVs) of milk (**M**), fat (**F**) and protein (**P**) yields on birth year, calculated for the dam's (cows with records) and bull´s paths. All means were deviated from the EBV average of cows born in 2005. Genetic gains (kg/year) were 40.0, 0.98 and 1.0 for cows born from 1987 to 2008 and 34.9, 0.53 and 0.69 for bulls born from 1977 to 2002, respectively for **M**, **F** and **P** yields. These values are larger than estimates obtained from first 305d lactation records.

Figure 1 depicts the mean EBV by year of birth for SCS. These curves show trends in realized genetic progress equal to -2.16 and -4.83 score units/year for cows and bulls respectively.

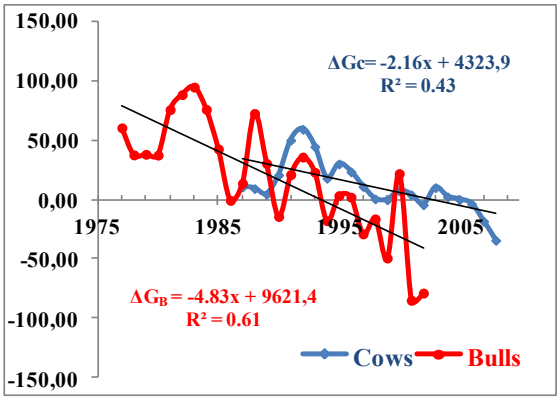

Figure 1. Annual genetic progress (AG) for SCS of Holstein cattle in Brazil (base year = 2005).

Overall, the magnitude of genetic parameters and genetic gains obtained in this study are in agreement with Miller et al. (2000) that indicated that selection for SCS may be effective and produce improvements in decreasing lactation SCS and frequency of culling for mastitis.

Conclusion

Heritability and genetic gains obtained in this study suggest the AR multiple lactation animal model as a suitable approach to fit TD records to predict breeding values and opportunities for larger genetic gains by selection in Holstein cattle in Brazil.

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