Genetic Parameters for Test Day Somatic Cell Count in Brazilian Holstein Cattle

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Introduction

Mastitis is one of the most important diseases in dairy cattle because of large economic losses due to reduced milk production, treatment costs, discard of milk, herd contamination and culling of cows. Mastitis also causes suffering for the animals. Therefore, not only for economic reasons, but also for ethical and animal welfare, strategies to reduce mastitis have received increased attention in dairy cattle breeding (Heringstad *et al*., 2000).

Direct selection for clinical mastitis (CM) is hard to implement because of low heritability (Rupp & Boichard, 2003) and lack of recorded data on incidences (Mrode & Swanson, 2003). Somatic cell count has been recommended as an indicator trait for reducing CM. Heritability of somatic cell score is around 10% and genetic correlation between somatic cell score and clinical mastitis is only moderate (0.7), but ranges from 0.3 to 0.9 (Mrode and Swanson, 1996). Selection for lower somatic cell score is consistent with the goal of maximizing genetic improvement for total economic merit and has been included in breeding objectives of several countries. In most national indices summarized by Miglior *et al*. (2005), log-transformed SCC (i.e., SCS) was the only trait contributing to udder health.

In Brazil, genetic evaluations for the Holstein breed include production and linear type traits (Costa *et al*., 2009). In the last years, SCC from milk samples of individual cows started being measured in large scale in national milk recording services. The aim of this study was to estimate the genetic parameters for test day SCC in the first lactation of Holstein cattle.

Material and methods

Data. Data were extracted from the official milk recording services provided by the Brazilian Holstein Association and were edited to include test day records of first lactation cows with calving dates between 1993 and 2007 and with age at first calving between 18 and 48 months. The editing process considered deleting cows having less than eight SCC records in the first lactation and records with less than 5 or greater then 305 days in milk (DIM).

Data were also edited for contemporary groups (defined by cows in the herd-year-test season - HTS of recording) of less than three records and sires with less than three daughters in at least two herds. Four age at calving classes (20 to 24, 25 to 29, 30 to 34 and 35 to 48 months)

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and four testing seasons (January through March, April through June, July through September and October through December) were combined to produce 16 age-season classes. Somatic cell count measurements were log transformed to somatic cell scores, SCS = $\log_2$ (CCS/ 100.000) + 3, the trait analysed in this study. The data structure after editing is shown in Table 1.

Table 1: Summary statistics of the data analysed in this study.

Herds	732
HTS	8,159
Cows	10,084
Test day records	87,711
Age at First Calving (mo)	30,20 ± 6,72
DIM (days)	153,65 ± 84,19
Milk Yield (kg)	26,53 ± 7,40
CCS	221,07 ± 327,83
SCS	2,94 ± 2,02
Sires	619
Animals in pedigree	20,205

Statistical analyses. A repeatability animal model (RM) and random regression models using Legendre Polynomials of order (degree plus one) three to five (LP3-LP5) were fitted to the data. Variance components were estimated using the average information REML procedure available in the AIREMLF90 program (Misztal, 2007). The convergence criterion was set to 10-9. The RM comprised five fixed effects: herd-year-season of test date, season of calving, breed composition (purebred or grade cows), age at calving as a covariate (linear and quadratic terms) and days in milk also as a covariate (linear term) and random effects of permanent environment of cow, animal and residual error. The random regression equation, assuming homogeneous residual variance (RV) and the same sub model to fit fixed, genetic and permanent environment effects, was:

$$Y_{ijlko} = HTS_i + B_j + \sum_{n=0}^{m-1} \beta_{lm} \Phi_m(t) + \sum_{n=0}^{m-1} \alpha_{km} \Phi_m(t) + \sum_{n=0}^{m-1} \gamma_{km} \Phi_m(t) + \varepsilon_{ijlko}$$

where Y_{ijlko} is the *o*th observation on animal *k* of breed composition *j*, HTS is the herd-year-test season effect *i; β_{lm}* is the *m*th fixed regression coefficient for *l*th age-season, α_{zm} the random genetic and γ_{zm} the random environmental regression coefficients for animal *k*, respectively, *m* the order of the polynomial fit, φ_m (t) the *m*th orthogonal polynomial of DIM **t** (standardized in the range –1 to +1 representing days 5 to 305) and ε_{ijlko} is the temporary environmental effect associated with the specific test day record.

Details of the log likelihood, assumptions and estimation of variance components modeled with orthogonal polynomial regressions have been presented (Meyer, 1998). Fit of different random regression models was compared by examining estimated residual variances, maximum likelihood and Akaike Information Criterion (AIC; Akaike, 2004).

Results and discussion

Values of Log-likelihood functions and AIC increased and RV decreased slightly with increasing the order of LP. RV estimates of LP models were lower than RM model (Table 1).

Table 2: Values of maximazed likelihood function (-2log *L*), Akaike's Information Criterion (AIC) and residual variance estimates for each fitted model.

Model[1]	-2log *L*	AIC	Residual Variance
RM	263520,2087	263526,2087	1.293
LP3	282627,2679	282713,2679	1.078
LP4	289602,8449	289644,8449	1.035
LP5	296754,9443	296816,9443	1.002

[1] RM= Repeatability animal model; LPi= Random regression animal model using a LP of order i = 3, 4 or 5.

Estimates of genetic, permanent environment and phenotypic variances for SCS from RM were 0.15859, 0.76497 and 2.2089, respectively, resulting in heritability and repeatability estimates equal to 0.07 and 0.34. The estimates of heritability for SCS in all three LP decreased from the beggining of the lactation up to 60 DIM and increased thereafter to reach the highest values at the end of lactation (Figure 1). Genetic variances (GV) followed the same pattern of heritability, but the trend of permanent environment (PE) variances (not shown) were different for the LP between DIM 60 to 120 and at the end of lactation. Therefore, the increase in heritability with DIM were due not only the increase in GV but also due to a stabilization of PE, mainly after 120 DIM.

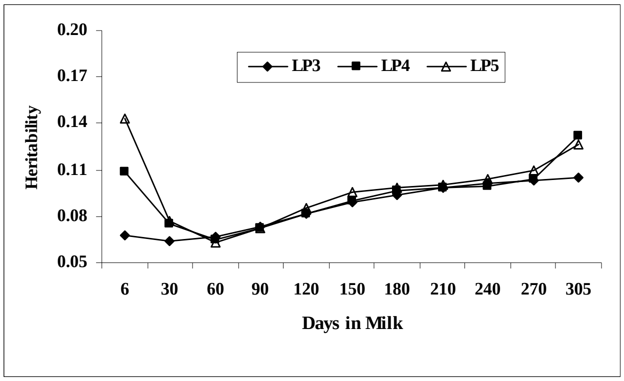

Figure 1: Heritability estimates for SCS in the first lactation of Holstein cows by fitting LP of orders 3 to 5.

Genetic correlation (upper diagonal, Table 3) between adjacent TD were high (>0.94), but decreased as the length between them increased. Phenotypc correlations (lower diagonal, Table 3) were similar in pattern to genetic correlations, but lower than corresponding genetic correlation estimates. These results indicate that RM, which assumes constant correlation among DIM is not appropriate for modelling SCS in first lactation of Brazilian Holstein cows. Overall, trends in genetic parameters estimated by random regression models in this study were similar to those reported by Mrode and Swanson (2003) and Koivula *et al*. (2004). In agreement with these studies and reporting to Miller *et al*. (2000), genetic parameters indicate selection for SCS may be effective and produce improvements in decreasing first-lactation SCS and frequency of culling for mastitis.

Table 3: Genetic correlations (above diagonal), heritabilities (diagonal) and phenotypic correlations (below diagonal) of test day SCS for the first lactation of Holstein cows estimated by LP3.

DIM	6	30	60	90	120	150	180	210	240	270	305
6	**0.07**	0.96	0.80	0.62	0.48	0.38	0.31	0.27	0.26	0.26	0.28
30	0.96	**0.06**	0.94	0.82	0.71	0.62	0.56	0.52	0.49	0.47	0.43
60	0.80	0.94	**0.06**	0.96	0.90	0.85	0.80	0.76	0.72	0.67	0.57
90	0.60	0.80	0.96	**0.07**	0.98	0.95	0.92	0.89	0.84	0.78	0.66
120	0.43	0.66	0.88	0.98	**0.08**	0.99	0.97	0.94	0.91	0.84	0.71
150	0.31	0.55	0.80	0.94	0.99	**0.09**	0.99	0.98	0.94	0.88	0.75
180	0.22	0.47	0.74	0.89	0.96	0.99	**0.09**	0.99	0.97	0.92	0.80
210	0.17	0.41	0.68	0.84	0.93	0.97	0.99	**0.09**	0.99	0.95	0.85
240	0.15	0.37	0.62	0.78	0.86	0.92	0.95	0.98	**0.10**	0.98	0.91
270	0.14	0.33	0.53	0.67	0.75	0.81	0.87	0.92	0.97	**0.10**	0.97
305	0.16	0.27	0.39	0.47	0.53	0.59	0.66	0.74	0.84	0.94	**0.10**

Conclusion

Random regression models best fitted the SCS data, but there was little benefit in fitting a Legendre Polynomial of order greater than three to model animal genetic and permanent environmental effects. Further research is still needed to consider heterogeneity of temporary environment variance before defining the appropriate model to use TD records for breeding value estimation for mastitis resistance of Holstein cows in Brazil.

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