Generalized mixed linear model for the genetic evaluation of somatic cell count

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Somatic Cell Count (SCC) is an important parameter of milk quality due to its association with a disease of great incidence in dairy herds, mastitis. This way, it is an objective in animal breeding programs the selection of animals less susceptible to this disease in order to reduce production losses and changes on milk composition. Because of the non-normal distribution of SCC, its logarithmic transformation (somatic cell score, SCS) is generally used to allow the adoption of methodologies whose normality of residuals is one of the assumptions. However, with the advancement of computational tools, it is possible to evaluate this trait in its original scale by using the methodology of generalized linear model (GMLM). The aim in this research was to compare the selection of Holstein cows according to the predicted breeding value for SCS using a mixed linear model (LMM) and GMLM for SCC. Monthly collected phenotypes (n = 12,727) of SCC and SCS of 2,010 primiparous cows from four herds were used. Data were collected between 5 and 305 days in milk (DIM) and it was considered only animals with more than 4 measurements during the lactation. Variance components and breeding values for SCS were obtained through a MLM whereas a MGLM was used for SCC, considering the logarithmic function as the link between SCC and the linear predictor. Therefore, a normal distribution and Poisson distribution were assumed for SCS and SCC, respectively. Both models included the fixed effects of contemporary groups, the covariable of the logarithm of DIM at the milk test-day, and the random effects of animal and permanent environment. Spearman correlation was used to compare the cows' ranking according to the breeding value obtained for SCS and SCC. The analyses were ran in the *pedigreemm* R package. The correlation was high, with a value equal to 0.85, indicating that the original and transformed trait represent the same phenomenon. The number of animals in common between the rankings considering the top 10% (n = 201), 20% (n = 402) and 40% individuals (n = 804) were 129, 289 and 654, respectively. The use of the transformed variable had low impact on animal selection compared to the variable in its original scale. Thus, the selection based on SCS would be preferable, due to the greater availability of softwares that use LMM for genetic evaluation and the adoption of this methodology for other traits of economic interest.

Keywords: animal breeding, holstein, primiparous, , selection

Promoção e Realização: Apoio Institucional: Organização: