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Additive genetic and heterosis effects for milk fever in a population of Jersey, Holstein × Jersey, and Holstein cattle under grazing conditions

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ABSTRACT

The aim of this study was to estimate additive genetic and heterosis effects for milk fever (MF) in Costa Rican dairy cattle. A farm-based management information software was used to collect 223,783 parity records between years 1989 and 2016, from 64,008 cows, 2 breeds (Jersey, Holstein × Jersey crosses, and Holstein), and 134 herds. The pedigree file comprised 73,653 animals distributed across 10 generations. A total of 4,355 (1.95%) clinical cases of MF were reported within this population, affecting 3,469 (5.42%) cows. Data were analyzed using 2 animal models, both accounting for repeatability and assuming different distributions for MF event: normal (linear model) or binomial (threshold model). The models included parity as fixed effect, breed and heterosis as fixed regressions, and herd-year-season, additive genetic, and permanent environment as random effects. The models were fit using a generalized linear mixed model approach, as implemented in ASReml 4.0 software. We noted significant regression on the percentage of Holstein breed, depicting a −0.0086% [standard error (SE) = 0.0012] decrease in MF incidence for each 1-unit increase in percentage of Holstein breed. A favorable heterosis of 5.9% for MF was found, although this was not statistically significant. Heritability and repeatability were, respectively, 0.03 (SE = 0.002) and 0.05 (SE = 0.002) for the linear model, and 0.07 (SE = 0.007) and 0.07 (SE = 0.007) for the threshold model. The correlation between BLUP (all animals in pedigree) for linear and threshold models, was 0.89. The average accuracy of the estimated BLUP for all animals were 0.44 (standard deviation = 0.13) for the linear model and 0.29 (standard deviation = 0.14) for the threshold model. Heritability and repeatability for MF within this population was low, though significant.

Key words: milk fever, heritability, repeatability, heterosis

INTRODUCTION

Clinical hypocalcemia in dairy cattle, also known as milk fever (**MF**; Horst et al., 1997), is a metabolic disease characterized by clinical symptoms due to reduction of blood calcium concentration during peripartum, which affects high-yielding multiparous cows (NRC, 2001). A low proportion of females (2–7%) suffer MF (Roche, 2003; Goff, 2008); however, affected cows reduce productive and reproductive performance, causing economic losses (Guard, 1996; Kossaibati and Esslemont, 1996). Ethical issues regarding MF, from an animal welfare approach, also exist.

Previous studies have shown greater susceptibility to MF in the Jersey breed compared with the Holstein breed, whereas Holstein × Jersey crossbred cows have shown intermediate risk of suffering the disease. A meta-analysis by Lean et al. (2006) showed that Jersey cows had 2.37 times the risk of having MF compared with the Holstein breed. Likewise, Roche and Berry (2006) found, in grazing systems, that Jersey cows and Holstein × Jersey crossbred cows had 4.96 and 2.44 times the chance of suffer MF, respectively, compared with Holstein cows. More recently, Saborío-Montero et al. (2017), in a grazing population, reported that Jersey cows, Holstein × Jersey crossbred cows, and Holstein cows had 3.04, 2.53, and 1.61 times the chance of occurrence of MF compared with Brown Swiss breed cows. Whether these differences are due to genetic factors or differential management between breeds is not clear from previous studies. Potential heterosis effects for MF, on the other hand, have not been reported in the literature.

Estimates of genetic parameters for MF vary depending on the genetic model (animal vs. sire models) and the distribution assumed (linear vs. threshold), the number of traits in the model (univariate vs. multivariate), or parity number (first calving vs. multiparous cows), among others factors. Uribe et al. (1995) esti-

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mated a heritability of 0.09 for MF using a threshold sire model. Heringstad et al. (2005), using a similar model, determined heritabilities of 0.09, 0.11, and 0.13 for first-, second-, and third-calving cows, respectively. Another study by Kadarmideen et al. (2000) obtained heritabilities of 0.012 and 0.065 and repeatabilities of 0.039 and 0.065 from multitrait linear and threshold animal models, respectively. For first-parity cows, Van Dorp et al. (1998) obtained heritability of 0.04 using a univariate linear animal model, whereas Tveit et al. (1991) obtained an estimate of 0.11 from a multitrait linear animal model. For multiparous cows, Koeck et al. (2015) found an estimate of 0.01 using a univariate linear sire model. Larger heritabilities for MF have been reported, in the order of 0.30 (Lin et al., 1989) and 0.40 (Lyons et al., 1991), both using a linear sire model, or 0.35 (Abdel-Azim et al., 2005) from a threshold sire model, the latter with standard error of 0.18. In general, higher estimates of heritability for MF are observed when sire models are used compared with animal models.

To the best of our knowledge, the heterosis effect for MF has not been studied yet. The analysis of the heterosis effect for MF is an innovative contribution that we will address in the current paper. Our study aims to determine the relative contributions of additive genetic and heterosis effects on MF in grazing dairy cattle to explore the genetic background of this imbalance. Genetic selection might be a useful tool contributing to an integral approach focused on reduction of MF.

MATERIALS AND METHODS

Study Design

A longitudinal observational study design was used to analyze health data regarding MF from records collected in the Veterinary Automated Management and Production Control Program software (Noordhuizen and Buurman, 1984) between 1989 and 2016. The study population consisted of 64,008 cows, 2 breeds (Holstein, Jersey, and Holstein × Jersey crosses) from 134 herds, with a total of 223,783 recorded parities along 10 generations of cows in pedigree in Costa Rica.

The follow-up period varied widely between herds, from a minimum of 3 yr to a maximum of 28 yr, with an average of 19.4 yr. To eliminate herds that did not register MF events on a regular basis, only those herds that reported at least 5 cases of MF were included in the study. A minimum of 5 cows within herd-year-season was also required. Consistency checks were performed on individual animal data regarding the logical sequence of reproductive events and genealogical records.

Cases of MF reported during the first 12 wk after calving were included in the analysis, although 75% of cases occurred immediately after calving and 90% within the first 3 wk after calving. For this study, we assumed that a reasonably accurate diagnosis of MF was made by herd managers based on symptomology, such as those mentioned by Horst et al. (1997), as well as the time of development of symptoms relative to calving and response of the cow to treatment with intravenous calcium.

Statistical Analysis

Several statistical and genetic models have been used in the analysis of categorical events, such as MF (Gianola, 1980, 1982). The use of nonlinear mixed models based on threshold theory has been suggested a more appropriate alternative to linear models (Gianola, 1982; Gianola and Foulley, 1983; Kadarmideen et al., 2000). Threshold model is based in the postulate that the binomial response variable is indeed a subjacent continuous variable that takes a value of 1 if it exceeds a fixed threshold value and a value of 0 if it does not (Heringstad et al., 2005).

Two statistical models were evaluated, defined as linear-animal model (**LA**) and threshold-animal model (**TA**). Linear and threshold are referred to the dependent variable (MF). For LA a normal distribution with identity link function was assumed, whereas for TA a binomial distribution with a probit link function was used. Equation 1 describes the effects included in both models:

$$y = \mu + P + HYS + \beta_1 \times (\%\ Hol) + \beta_2 \times (\%\ het) + a + p + \varepsilon, \qquad [1]$$

where y = occurrence of milk fever event (recorded as: 0/1 = absent/present); μ = general mean; P = fixed effect of parity (6 classes, from 1 to $\geq$6); HYS = random effect of herd-year-season of calving, with season arranged in 3-mo length periods (9,699 classes); $\beta_1 \times (\%\ Hol)$ = linear regression on the percentage of Holstein breed, as Holstein (**H**) = 100%, Jersey (**J**) = 0%, 3/4H 1/4J = 75%, 1/2H 1/2J = 50%, and 1/4H 3/4J = 25%; $\beta_2 \times (\%\ het)$ = linear regression on the expected percentage of heterosis retained (VanRaden, 1992) according to breed type, as H = 0%, J = 0%, 3/4H 1/4J = 50%, 1/2H 1/2J = 100%, 1/4H 3/4J = 50%; a = random additive genetic effect linked to pedigree (n = 73,653); p = random permanent environment effect (n = 64,008); and ε = Random residual error, $N\left(0, \sigma_e^2\right)$, where σ_e^2 is the residual variance. Herds