

Estimation of heritability and repeatability for milk fever in Costa Rican dairy cattle*A. Saborío-Montero¹, B. Vargas-Leitón², J.J. Romero-Zúñiga² and J. Camacho²**¹University of Costa Rica, Animal Science Department and Animal Nutrition Research Center, San José, 11501 San Pedro, Montes de Oca, Costa Rica, ²National University of Costa Rica, Population Medicine Research Program, Veterinary Medicine School, Heredia, 40701, Lagunilla, Costa Rica; alesabor@gmail.com*

The aim of this study was to estimate genetic parameters and perform genetic evaluation for milk fever in Costa Rican dairy cattle. A farm-based management information system (VAMPP) was used to collect 211 956 lactation records, from 61,611 cows, 2 breeds (Holstein and Jersey) and 125 herds. The pedigree file comprised 70,834 animals born between years 1989 and 2013 and distributed across 16 generations. Data was analyzed using an animal model with repeatability. The model included breed, herd, parity, month/year of calving as fixed effects, and cow additive genetic, permanent environmental and herd×sire interaction as random effects. The model was fit using a Generalized Linear Mixed Models (GLMM) approach, as implemented in ASReml 4.0™ software, assuming two different distributions for milk fever events: Normal (linear model) and Binomial (threshold model). A total of 4,097 (1.93%) clinical cases of milk fever were reported within this population. For the linear model, heritability and repeatability were, respectively, 0.01 (SE=0.002) and 0.03 (SE=0.002). For the threshold model, the variance component for permanent environmental effect was fixed to zero by the optimization algorithm, which resulted in an equal value of 0.11 (SE=0.012) for heritability and repeatability. The correlation between BLUPs of both models was 0.90. The accuracy of the estimated BLUPs were 0.33 (SD=0.12) for the linear model and 0.25 (SD=0.14) for the threshold model. Heritability for milk fever within this population is low, though significant. Estimates of variance components for random effects were more stable with the linear compared to the threshold model.