Application of Genomic Information to Longitudinal Traits

A.S. Leaflet R2901

Anna Wolc, Adjunct Assistant Professor;
Jesus Arango, Petek Settar, Janet E. Fulton,
Neil P. O'Sullivan, Poultry Geneticists, Hy-Line International;
Rudolf Preisinger, Poultry Geneticist, Lohmann Tierzucht;
Rohan Fernando, Professor;
Dorian J. Garrick, Professor;
Jack C.M. Dekkers, Professor,
Department of Animal Science

Summary and Implications

Random regression models are commonly used for analysis of longitudinal traits measured across time such as egg production in chickens and milk production in cattle. In this study, we include genomic information for evaluation of longitudinal traits using a random regression reduced animal model with a genomic relationship matrix. Substantial increases in accuracy of estimated breeding values were observed when applying the proposed method to egg production records in chickens.

Introduction

Random regression models allow modeling of changes in variance components over time and thus better account for temporal environmental distortions that may appear in traits that are expressed over a long period of time. Another recent enhancement in breeding value estimation has been the use of high-density marker genotypes to increase accuracy of selection. Because it is very costly to genotype all individuals needed for training, a reduced animal model was applied to utilize phenotypes of non-genotyped progeny of genotyped parents. In this study, we combined all these above-mentioned techniques to evaluate accuracies of estimated breeding values from a pedigree-based or genome-based random regression model applied to egg production data in chickens.

Materials and Methods

Daily egg production up to 46 weeks in lay of 1,122 genotyped hens and their 7,986 daughters from a brown layer line of Hy-Line International was accumulated into bi-weekly records and used to predict performance of 288 hens in the next generation. All animals that had been used as parents in this population were genotyped with 42K SNP marker panel. The model included 5th order Legendre polynomials nested within hatch-week as fixed effects, and random terms for coefficients of quadratic polynomials for genetic and permanent environmental effects. Residual variance was assumed heterogeneous among bi-weekly periods. Analyses were performed using ASReml (Gilmour et al., 2008).

Results and Discussion

Models using pedigree and genomic relationships were compared. Estimates of residual variance were very similar for both models but the model with genomic relationships resulted in a larger estimate of genetic variance. Prediction of total egg number was more accurate with the genomic than with the pedigree-based model (correlation in validation 0.26 vs. 0.16). The genomic model outperformed the pedigree model in most bi-weekly periods. Thus, results of this study show that a random regression reduced animal model can be utilized in breeding programs using genomic information and can result in substantial improvements in the accuracy of selection for longitudinal traits.