Prediction Accuracy of Pedigree and Genomic Estimated Breeding Values over Generations in Layer Chickens

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Summary and Implications

This study investigated the accuracy of estimated breeding values (EBV) over different training generations in layer chickens using pedigree and marker-based models. On average, the accuracy of EBV based on markers was higher than that based on pedigree. The accuracy of all methods increased with an increase in the number of generations in training data, but slightly dropped or remained even after including training generations far apart from validation.

Introduction

Genomic prediction, which uses markers to estimate breeding values, is widely used in livestock industries. Density of marker information, structure of linkage disequilibrium (LD), genetic relationships between training and validation and other parameters can affect the accuracy of prediction. In contrast, the accuracy of Pedigree-based Best Linear Unbiased Prediction (PBLUP) relies on the additive genetic relationships with individuals with data. Wolc et al. (2011) showed that marker-based EBV were more persistent than pedigree-based EBV. The objective of this study was to evaluate the optimum number of training generations to predict EBV and compare the accuracy of different prediction models in a commercial layer breeding line.

Materials and Methods

Data were from 13,532 birds with records over 7 generations. Each generation had about 300 females genotyped with 23, 356 segregating single nucleotide polymorphisms (SNPs). A total of 6 traits with relatively high heritability (>0.6) were analyzed: weight of the first 3 eggs (eE3), color of the first 3 eggs (eC3), early and late egg weight (eEW, lEW), and early and late egg color (eCO, lCO). Early and late measurements were taken at 26-28 and 42-46 weeks. PBLUP was performed using ASREML (Gilmour et al., 2009). Prediction of genomic EBV was implemented using BayesB (Meuwissen et al., 2001) with own records and/or family means (BayesB-FM) and was performed using the GenSel software (Fernando and Garrick, 2013). All methods accounted for hatch within generation effects. Breeding values in validation sets were estimated based on different numbers of training generations. The prediction accuracy was the correlation between hatch corrected phenotypes divided by the square root of the heritability.

Results and Discussion

Figure 1 shows the prediction accuracy averaged across different validation sets and across the 6 traits. Marker-based methods outperformed pedigree-based method, which indicates that markers capture Quantitative Trait Loci information through LD. By adding information through family means, BayesB-FM had higher accuracy than BayesB using only own records. Accuracy of PBLUP quickly plateaued with increasing number of training generations, as expected. Accuracy of genomic predictions increased more quickly with increasing number of training generations and for more generations but decreased when adding more distant generations. The divergence in gene frequencies in each generation and the interaction between genotype and environment might be the reason that accuracy of marker-based model dropped when including distant generations in the training. For these data, using 4 generations in training was optimal for EBV prediction, although results differed between traits.
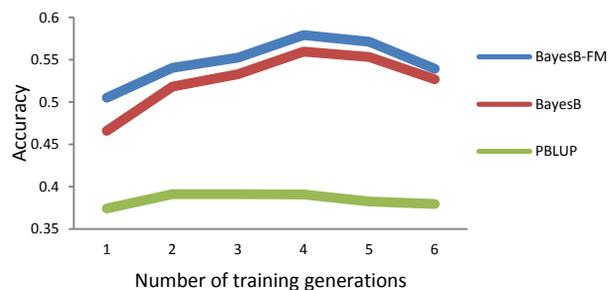
Figure 1. Average accuracy of EBV using the pedigree-based model (PBLUP), BayesB with own records (BayesB), and BayesB with both own records and family means (BayesB-FM).