Changes in genetic parameters for traits under genomic selection in poultry

J. Richter[1*], J. Hidalgo[1], V. Breen[2], R. Hawken[2], I. Misztal[1], and D. Lourenco[1]

[1] Department of Animal and Dairy Science, University of Georgia, Athens, GA 30602, USA;
[2] Cobb-Vantress, Inc., Siloam Springs, AR 72761, USA; *jennifer.richter25@uga.edu

Abstract

We investigated changes over time in heritability of a feed efficiency trait (FE), a carcass yield trait (CY), a growth trait (GT), and a leg disorder trait (DIS) in a broiler population. The data contained 200,093 (FE), 42,895 (CY), 203,060 (GT), and 63,349 (DIS), phenotypic records obtained over 55 mating groups then divided into 13 intervals. Pedigrees included 1,250,404 animals, of which 154,318 were genotyped. Genetic parameters were estimated with single-trait models for each interval with (GEN) and without genomic information (PED) using the BLUPF90 programs. Single-step was used in the former. Heritabilities changed from 0.38 to 0.23 (0.38 to 0.26) for GEN (PED) across performance traits and from 0.55 to 0.25 (0.55 to 0.28) for the disorder trait. Heritability estimates by PED were often higher than those from GEN, indicating bias. Genetic parameters should be updated regularly for unbiased estimation of breeding values and selection response.

Introduction

Accurate genetic parameters are crucial for unbiased estimation of breeding values and selection response in breeding programs. Genetic parameters are expected to change under selection, and the magnitude of the changes depends on the intensity of selection and the initial allele frequency (Walsh and Lynch, 2018). The additive genetic variance, and therefore, the heritability, can be reduced under selection due to the increased coancestry among animals (Walsh and Lynch, 2018). Another cause of reduction is the Bulmer effect, which creates negative linkage disequilibrium (i.e., negative covariance between pairs of loci) under directional or stabilizing selection (Bulmer, 1971). Due to strong selection, genetic parameters may change, leading to inaccurate predictions of genetic gain when using the old parameters. Thus, it is important to update the genetic parameters regularly.

Estimating genetic parameters over time is computationally costly with extensive data and under genomic selection because the genomic relationship matrix (**G**) is dense. According to Hidalgo et al. (2020), time intervals are useful to estimate genetic parameters over time so that only a fraction of the data is utilized in each analysis. Intervals need to be large enough and with sufficient data to avoid biases due to the averaged changes (Misztal et al., 2021). The objective of this study was to estimate changes in heritability over time for growth, efficiency, and leg disorder traits in a broiler population under genomic selection using time intervals including or not genomic information.

Materials & Methods

Data. The dataset used in this study was provided by Cobb-Vantress Inc. (Siloam Springs, AR). The whole dataset contained 200,093 phenotypes for FE, 42,895 for CY, 203,060 for GT, and 63,349 for DIS. The pedigree included 1,250,404 purebred broilers hatched over 7 years, resulting from 55 mating groups (MG). A total of 154,318 birds were genotyped with a 60K SNP panel. We defined 13 time intervals, the first interval comprised seven MG, and the remaining 12 of these intervals comprised eight MG. Each subsequent interval had four MG

of overlapping data. For example, the first interval included data from MG one through seven, the second interval included data from MG four through eleven; therefore, the MG four to seven overlapped in intervals one and two. Only the most recent time intervals in the dataset contained genotypes (i.e., from MG 24 to 55). Intervals including genotypes had, on average, 38,000 genotyped animals except for the first interval only having ~16,000 genotyped animals.

Model and Analysis. Single-trait linear models were used for the efficiency, yield, and growth traits (FE, CY, GT). These linear models included fixed effects of contemporary group (CG) and sex while having a random animal effect. Variance components for the linear models were estimated using the average information restricted maximum likelihood algorithm implemented in the AIREMLF90 software (Misztal et al., 2014). A single trait threshold model was used for the leg disorder trait (DIS). This threshold model included a fixed effect of sex with a random effect of CG and a random animal effect. Variance components for the threshold model were estimated using a Bayesian approach via the Gibbs sampling algorithm as implemented in the THRGIBBS1F90 software (Misztal et al., 2014). A single Gibbs chain of a total length of 100,000 rounds was initially generated. After discarding the initial 10,000 samples as burn-in, 1 in every 10 samples were stored to compute means and standard deviations of the posterior distributions. The means were used as estimates of the variance components, and their posterior standard deviations were considered a measurement of their estimation errors. The analyses to estimate variance components for all traits were performed, including (GEN) or not the genomic information (PED) for each interval.

The full form of the linear models was:

$$\mathbf{y} = \mathbf{Xb}+\mathbf{Za}+\mathbf{e}, \quad (1)$$

where $\mathbf{y}$ is a vector of phenotypes; $\mathbf{b}$ and $\mathbf{a}$ are vectors of fixed and random animal effects, respectively; $\mathbf{X}$ and $\mathbf{Z}$ are incidence matrices for $\mathbf{b}$ and $\mathbf{a}$ respectively; and $\mathbf{e}$ is a vector of random residuals.

For the categorical trait (DIS), the threshold model assumed an underlying distribution L. The model was:

$$\mathbf{L} = \mathbf{X_l b_l} + \mathbf{Z_l a_l} + \mathbf{W_l c_l} + \mathbf{e_l}, \quad (2)$$

where $\mathbf{L}$ is a vector of underlying distribution of phenotype y; $\mathbf{b_l}$ is a vector of systematic effects; $\mathbf{a_l}$ is a vector of random animal effects; $\mathbf{c_l}$ is a vector of random CG effects; $\mathbf{X_l}$, $\mathbf{Z_l}$, and $\mathbf{W_l}$ are incidence matrices for $\mathbf{b_l}$, $\mathbf{a_l}$, and $\mathbf{c_l}$, respectively; and $\mathbf{e_l}$ is a vector of random residuals for this threshold model. During the estimation process, the residual variance for DIS was fixed to 1 so that the model is identifiable.

Results

The posterior means and standard deviations for heritabilities estimated by GEN and PED are shown in Figure 1 for broiler performance and leg disorder traits; heritabilities for DIS are presented in the liability scale. Changes in heritability estimated by GEN (PED) from the first to the last interval, that is from 1-7 to 47-54 MG were from 0.31 to 0.19 (0.31 to 0.20) for FE, 0.60 to 0.38 (0.60 to 0.45) for CY, 0.25 to 0.11 (0.25 to 0.13) for GT, and 0.55 to 0.25 (0.55 to 0.28) for DIS.

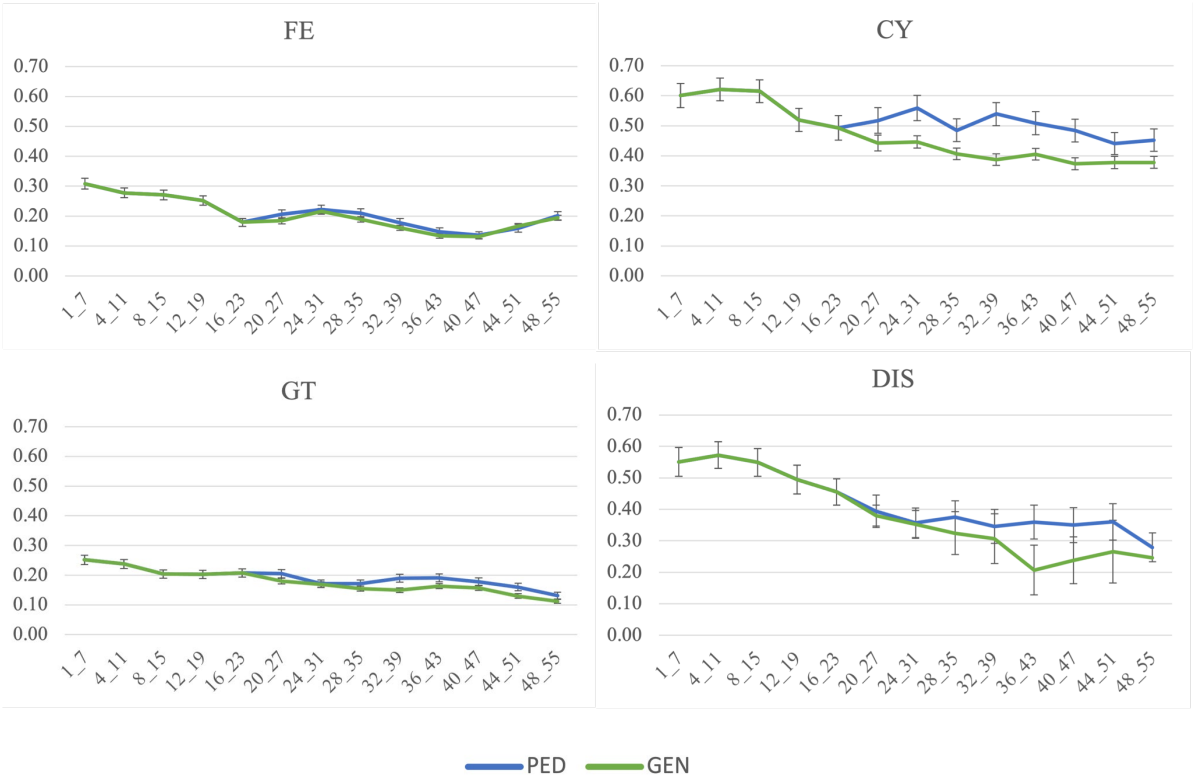

Figure 1. Posterior means and standard errors for estimated heritabilities for FE, CY, GT, and DIS estimated with (GEN) or without genotypes (PED). Heritabilities for all traits decreased over time.

Discussion

Although there was an overall decline, heritabilities seemed to stabilize during the last four intervals for FE, CY, and DIS. The stabilization of heritabilities happens because the recombination between unlinked loci removes linkage disequilibrium, regenerating genetic variance (Bulmer, 1971). Villanueva and Kennedy (1990) proved that a recombination-linkage disequilibrium is achieved after several generations of selection; therefore, the genetic variance and heritability will stabilize, provided that other components of the heritability remain unchanged.

Changes in heritabilities over time were similar with and without the inclusion of genomic information for FE; however, the heritability estimates by PED for CY, GT, and DIS were higher than those from GEN. Our results agreed with those found by Hidalgo et al. (2020). Those authors concluded that heritabilities estimated by GEN and PED were similar for traits under less intensive selection, in contrast, heritabilities differed for traits more intensively selected. Selection reduces heritabilities; therefore, it is important to update genetic parameters regularly to have unbiased estimation of breeding values and selection response. Heritability estimates may be biased if genomic information is ignored. This is a topic under further investigation.

References

Bulmer, M. G. (1976) Genet. Res. 28(2):101-117. https://doi.org/10.1017/S0016672300016797

Hidalgo, J., S. Tsuruta, D. Lourenco, Y. Masuda, Y. Huang et al. (2020) J. Anim. Sci. 99(9):1-10. https://doi.org/10.1093/jas/skab239

Misztal, I., I. Aguilar, D. Lourenco, L. Ma, J. P. Steibel et al. (2021) https://doi.org/10.1093/jas/skab092
Misztal, I., S. Tsuruya, D.A.L. Lourenco, I. Aguilar, A. Legarra et al. (2014b) Manual for BLUPF90 family of programs. Available at http://nce.ads.uga.edu/wiki/lib/exe/fetch.php?media=blupf90_all2.pdf
Villanueva, B. , and B. W. Kennedy (1990) Theor. Appl. Genet. 80: 746-752. DOI:10.1007/BF00224187
Walsh B., and Lynch M. (2018) Evolution and selection of quantitative traits. Oxford University Press, Oxford, UK.