

# Single-Step Genomic Selection in Turkeys for Health, Welfare, Efficiency and Production Traits

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## Introduction

- Genomic selection has been shown to accelerate the genetic gain in many species by increasing accuracy of prediction and allowing for direct selection of phenotypes that are expensive to measure
- Single-step methodologies have recently been introduced
- Genomic selection has not yet been adopted throughout the entire turkey industry

## Objective

Compare the prediction ability of pedigree-based best linear unbiased prediction (PBLUP) and single-step genomic best linear unbiased prediction (ssGBLUP) models

## Materials and Methods

- Data from one genetic line with extensive pedigree records
- Feed efficiency data (n = 5592) and breast meat yield (n = 9634) collected on toms
- Body weight (n = 170,844) and walking scores (n = 170,844) collected on toms and hens
- Proportion of animals genotyped using a custom 65K SNP array
- The following multi-trait animal model was used:

$$y = Xb + Zu + e$$

- Fixed effects: Sex and hatch week-year; Random effect: Animal
- Three weightings (w; 0.85, 0.90, and 0.95) were used when calculating the genomic relationship matrix
- Adjusted phenotypes were calculated with each model
- Accuracy prediction bias was calculated as:

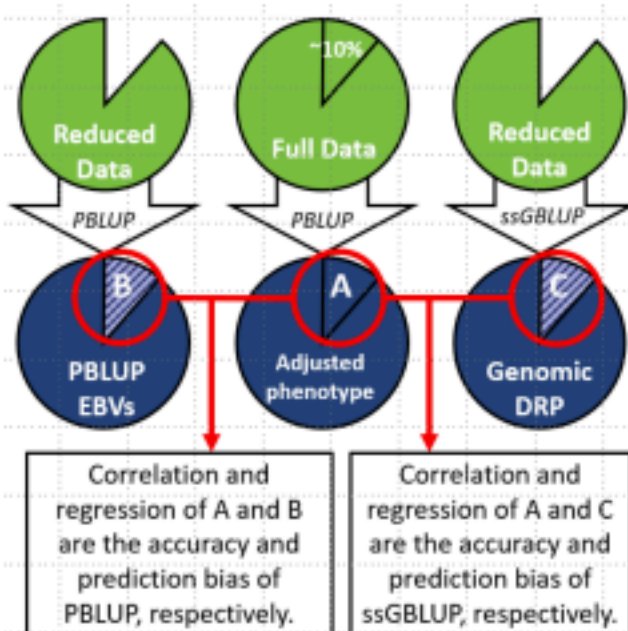


Figure 1: Methodology for calculating the correlation based accuracy and prediction bias of pedigree best linear unbiased prediction (PBLUP) and single-step genomic best linear unbiased prediction (ssGBLUP).

## Results

Table 1: Heritability estimates  $\pm$  standard error for the studied traits based on the pedigree-based best linear unbiased prediction (PBLUP) and the single-step genomic best linear unbiased prediction (ssGBLUP) with three different combinations of blending weights ( $\alpha$  and  $\beta$ ) for genomic (G) and pedigree (A) relationship matrices, respectively.

Model	PBLUP	ssGBLUP_0.95 <sup>1</sup>	ssGBLUP_0.90 <sup>2</sup>	ssGBLUP_0.85 <sup>3</sup>
Feed conversion ratio	0.14 $\pm$ 0.02	0.17 $\pm$ 0.03	0.17 $\pm$ 0.03	0.17 $\pm$ 0.03
Residual feed intake	0.12 $\pm$ 0.02	0.15 $\pm$ 0.02	0.15 $\pm$ 0.02	0.15 $\pm$ 0.02
Body weight	0.35 $\pm$ 0.06	0.41 $\pm$ 0.06	0.41 $\pm$ 0.06	0.40 $\pm$ 0.06
Breast meat yield	0.27 $\pm$ 0.04	0.30 $\pm$ 0.05	0.30 $\pm$ 0.05	0.30 $\pm$ 0.05
Walking score	0.24 $\pm$ 0.04	0.26 $\pm$ 0.04	0.26 $\pm$ 0.04	0.26 $\pm$ 0.05

<sup>1</sup>ssGBLUP\_0.95:  $\alpha = 0.95$  and  $\beta = 0.05$ ; <sup>2</sup>ssGBLUP\_0.90:  $\alpha = 0.90$  and  $\beta = 0.10$ ; <sup>3</sup>ssGBLUP\_0.85:  $\alpha = 0.85$  and  $\beta = 0.15$ .

Table 2: Accuracy (Pearson correlation coefficient) of estimated breeding values for the studied traits based on the pedigree-based best linear unbiased prediction (PBLUP) and the single-step genomic best linear unbiased prediction (ssGBLUP) with three different combinations of blending weights (w) for genomic (G) and pedigree (A<sub>22</sub>) relationship matrices.

Model	PBLUP	ssGBLUP_0.95 <sup>1</sup>	ssGBLUP_0.90 <sup>2</sup>	ssGBLUP_0.85 <sup>3</sup>
Feed conversion ratio	0.29	0.38	0.38	0.37
Residual feed intake	0.21	0.26	0.27	0.26
Body weight	0.36	0.40	0.40	0.39
Breast meat yield	0.30	0.37	0.37	0.36
Walking score	0.26	0.30	0.30	0.30

<sup>1</sup>ssGBLUP\_0.95: w = 0.95; <sup>2</sup>ssGBLUP\_0.90: w = 0.90; <sup>3</sup>ssGBLUP\_0.85: w = 0.85.

Table 3: Regression coefficients of estimated breeding values from the full PBLUP model on their corresponding EBV from the reduced PBLUP model and on their corresponding EBV from the reduced ssGBLUP model with three different combinations of blending weights (w) for genomic (G) and pedigree (A<sub>22</sub>) relationship matrices.

Model	PBLUP	ssGBLUP_0.95 <sup>1</sup>	ssGBLUP_0.90 <sup>2</sup>	ssGBLUP_0.85 <sup>3</sup>
Feed conversion ratio	0.95 $\pm$ 0.17	0.95 $\pm$ 0.17	0.95 $\pm$ 0.06	0.95 $\pm$ 0.17
Residual feed intake	0.79 $\pm$ 0.12	0.79 $\pm$ 0.12	0.80 $\pm$ 0.05	0.80 $\pm$ 0.12
Body weight	0.82 $\pm$ 0.03	0.82 $\pm$ 0.03	0.83 $\pm$ 0.06	0.82 $\pm$ 0.03
Breast meat yield	1.41 $\pm$ 0.21	1.38 $\pm$ 0.21	1.38 $\pm$ 0.06	1.38 $\pm$ 0.21
Walking score	0.73 $\pm$ 0.04	0.75 $\pm$ 0.04	0.75 $\pm$ 0.10	0.76 $\pm$ 0.04

<sup>1</sup>ssGBLUP\_0.95: w = 0.95; <sup>2</sup>ssGBLUP\_0.90: w = 0.90; <sup>3</sup>ssGBLUP\_0.85: w = 0.85.

## Results and Discussion

- ssGBLUP showed higher heritability estimates than PBLUP
- Across the studied traits, the ssGBLUP model outperformed PBLUP
  - Accuracies of PBLUP ranged from 0.21 to 0.36 vs 0.26 to 0.40 in ssGBLUP
- Lower heritability traits showed a higher increase in accuracy between PBLUP and ssGBLUP.
- The ssGBLUP\_90 had an increase in accuracy of 31%, 29%, 12%, 23%, and 16% for FCR, RFI, BW, BM, and WS, respectively.
- This agrees with other studies that marker-based EBV have in general higher predictive ability than those estimates using pedigree relationships
- Except for BM, all traits had regression coefficients lower than one (inflation).
- In general, bias estimates were quite similar among models, but varied among trait.

## Conclusions

- Incorporating genomic information was tested in terms of prediction ability and bias using two feed efficiency traits, body weight, breast meat yield, and walking ability in turkeys
- It showed substantially higher accuracy estimates than the pedigree-based approach (PBLUP)
- Slightly different levels of bias were observed across the alternate models, but high across the traits
- Such traits are expensive to measure and genomic selection has strong potential to reduce the cost of turkey breeding programs, as the reliance on phenotypic, pedigree, and progeny information is reduced.

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