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Research article

Integrating genomics and multi trait model to improve body weight and egg production in yellow-feathered broiler breeders

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Abstract: Body weight and egg production are crucial economic traits in broiler breeding; yet, their negative genetic correlation poses challenges for simultaneous genetic improvement. In this study, we estimated the genetic parameters of these traits in yellow-feathered broiler breeders using a multi-trait model and evaluated the predictive performance of single-step genomic BLUP (ssGBLUP) and pedigree-based BLUP (PBLUP) in both single- and multi-trait analyses. Phenotypic data included cumulative egg production up to 43 weeks and body weight at 8 weeks from 4,712 hens, with pedigrees tracing three generations. Genomic data derived from low-coverage sequencing yielded 315K SNPs. Genetic evaluations were conducted using PBLUP and ssGBLUP models, with prediction accuracy assessed via five-fold cross-validation based on estimated breeding value (EBV) accuracy, rank correlation, and unbiasedness. Heritability estimates were 0.285 for body weight and 0.396 for egg production, while genetic correlation analysis revealed a stable, moderate negative correlation between the traits (approximately -0.30, $P < 0.01$) across pedigree and genomic data. Compared to PBLUP, ssGBLUP significantly enhanced prediction accuracy for egg production by 19.88% (single-trait) and 21.18% (multi-trait), and for body weight by 17.18% and 18.90%, respectively ($P < 0.01$). These results demonstrated that ssGBLUP, particularly when integrated with a multi-trait model, more effectively leverages genomic information and trait correlations, offering a superior strategy for balanced genetic improvement of antagonistic traits in broilers.

Keywords: antagonistic traits; genomic selection; accuracy; negative genetic correlation

1. Introduction

Poultry breeding plays an important role in global food security by providing essential sources of animal protein through meat and egg production. Among the key economic traits in broiler industry, body weight shows a significant positive correlation with slaughter yield, while egg production dictates the supply of hatching eggs; together, these traits shape the efficiency and profitability of broiler operations [1, 2]. However, a persistent scientific challenge is the moderate to strong negative genetic correlation between body weight and egg production. This trade-off, observed across livestock species, is a classic example of antagonistic pleiotropy, where the genetic loci promoting rapid somatic growth exert an inhibitory influence on reproductive physiology [1,3,4]. This antagonism complicates the simultaneous genetic improvement of both traits.

Traditional selection methods, such as pedigree-based BLUP (PBLUP), have been widely used to estimate breeding values, but they often lack the precision needed for complex or antagonistically correlated traits, thereby limiting genetic progress [2,5]. Advances in genomics, including high-density SNP genotyping and whole-genome sequencing, have enabled more accurate genetic evaluations [6–8]. The single-step genomic BLUP (ssGBLUP) model, which integrates pedigree and genomic data [9,10], has demonstrated superior prediction accuracy for growth and egg production traits, especially when trait correlations are considered [2,11]. Multi-trait models further enhance selection efficiency by leveraging genetic correlations, as shown in livestock studies, but their application in broilers remains limited [2,4]. Therefore, there is a need for systematic research comparing ssGBLUP and PBLUP for antagonistic traits in this economically important breed.

We address this gap by evaluating the combined use of genomic information and multi-trait modeling to improve body weight and egg production in broilers. We aim to estimate genetic parameters, compare the predictive performance of ssGBLUP and PBLUP in single- and multi-trait analyses, and quantify the gains in accuracy from genomic integration. Ultimately, our goal is to provide practical strategies, such as optimized selection indices, to achieve balanced genetic improvement of growth and reproductive traits in broiler breeding programs.

2. Materials and methods

2.1. Ethics statement

We utilized historical commercial breeding records with no animal handling, intervention, or experimental procedures; thus, formal ethical review was not required per established standards.

2.2. Population and data

We utilized data on egg production and body weight traits from the 26th generation of caged yellow-feathered broilers, provided by Guangdong Wiz Agricultural Science & Technology Co. Ltd. The population consisted of 5,168 hens from four hatches reared in the same house, with phenotypic records including body weight at 8 weeks of age and cumulative egg production up to 43 weeks of age. During data quality control, individuals with cumulative egg production records deviating by more than three standard deviations from the population mean were removed as outliers [12]. After removing 161, 134, 73, and 88 outlier individuals from hatches 261, 262, 263, and 264, respectively, the final dataset for all subsequent analyses comprised 4,712 hens. All retained individuals had complete records for hatch and cage, as well as pedigrees traceable for three generations. Data processing was performed using R software (v4.4.2) [13]. The descriptive statistics for body weight at 8 weeks of age (BW8) and cumulative egg production up to 43 weeks of age (EN43) are presented in Table 1. The dataset comprised records from four distinct batches, with the number of individuals per batch ranging from 806 to 1,617. The mean values for BW8 were highly consistent across all batches, varying narrowly from 1821.74 g to 1880.00 g. Similarly, the mean for EN43 showed high stability, with values ranging from 93.49 to 95.44 eggs. While the overall average performance was uniform across the batches, the standard deviations, along with the wide ranges between the minimum and maximum values, indicated that considerable individual phenotypic variation existed for both traits within each batch.

Table 1. Summary of statistics for body weight at 8 weeks of age (BW8) and cumulative egg production up to 43 weeks of age (EN43).

		BW8				**EN43**			
Batch	**Count**	**Max**	**Min**	**Mean**	**SD**	**Max**	**Min**	**Mean**	**SD**
261	1617	2240	1641	1879.49	84.98	128	57	93.61	12.22
262	1398	2265	1746	1880.00	84.24	131	54	93.61	13.67
263	806	2259	1703	1821.74	87.85	130	51	95.44	14.91
264	891	2248	1750	1878.53	89.18	131	52	93.49	14.66

2.3. Genomic data

All individuals from the 26th generation were genotyped using low-coverage whole-genome resequencing, and genotype imputation was performed with Beagle [14], yielding 465K SNPs after imputation. To enhance computational efficiency and reduce redundancy due to linkage disequilibrium among densely imputed markers, we uniformly sampled 315K SNPs from the imputed dataset for downstream analyses. The quality control criteria were as follows: SNP markers were removed if they had genotype-missing rates > 0.10, minor allele frequencies (MAF) < 0.05, or a Hardy-Weinberg equilibrium (HWE) p-value $\leq 10^{-5}$ (based on a Chi-squared test). Samples with a call rate lower than 90% were also removed. After quality control, a final set of 4,712 genotyped individuals and 314,649 high-quality SNPs were retained for subsequent analyses. Quality control of the genomic data was performed using PLINK (v1.07) [15].

2.4. Genetic Evaluation

We utilized the complete dataset for all evaluations. Estimated breeding values (EBV) were obtained using both single-trait and multi-trait models, in combination with the pedigree-based BLUP (PBLUP) [16] and single-step genomic BLUP (ssGBLUP) [9,10] methods. To assess the prediction accuracy of these EBV, a five-fold cross-validation was employed. The phenotype individuals were randomly divided into five subsets of approximately equal size. In each fold, one subset was designated the validation set (with its phenotypes masked), while the remaining four subsets constituted the training set for model fitting. This process was repeated five times, ensuring that each subset served as the validation set once [17].

Two genetic evaluation models, PBLUP and ssGBLUP, were implemented. For body weight, the model included only the batch effect as a fixed effect. For egg production, both single- and multi-trait models incorporated hatch and cage as fixed effects, as these factors were identified as significant. All models were fitted using the DMU software package (v5.2) [18] to estimate genetic parameters and solve the model equations via the average information restricted maximum likelihood (AI-REML) algorithm [19]. Both single-trait and multi-trait models were implemented using PBLUP and ssGBLUP approaches.

Single-trait model:

The model for each individual trait was defined as:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e} \tag{1}$$

where $\mathbf{y}$ is the vector of phenotypic observations for body weight or egg production; $\mathbf{b}$ is the vector of fixed effects including batch or cage; $\mathbf{u}$ is the vector of random additive genetic effects; $\mathbf{e}$ is the vector of random residuals; and $\mathbf{X}$ and $\mathbf{Z}$ are incidence matrices for the fixed and random effects, respectively.

Multi-trait model:

The multi-trait model, which simultaneously analyzes all T traits, was specified as:

$$\begin{bmatrix}\mathbf{y}_1\\ \mathbf{y}_2\\ \vdots\\ \mathbf{y}_T\end{bmatrix} = \begin{bmatrix}\mathbf{X}_1 & 0 & \cdots & 0\\ 0 & \mathbf{X}_2 & \cdots & 0\\ \vdots & \vdots & \ddots & \vdots\\ 0 & 0 & \cdots & \mathbf{X}_T\end{bmatrix}\begin{bmatrix}\mathbf{b}_1\\ \mathbf{b}_2\\ \vdots\\ \mathbf{b}_T\end{bmatrix} + \begin{bmatrix}\mathbf{Z}_1 & 0 & \cdots & 0\\ 0 & \mathbf{Z}_2 & \cdots & 0\\ \vdots & \vdots & \ddots & \vdots\\ 0 & 0 & \cdots & \mathbf{Z}_T\end{bmatrix}\begin{bmatrix}\mathbf{u}_1\\ \mathbf{u}_2\\ \vdots\\ \mathbf{u}_T\end{bmatrix} + \begin{bmatrix}\mathbf{e}_1\\ \mathbf{e}_2\\ \vdots\\ \mathbf{e}_T\end{bmatrix}$$

where $\mathbf{y}_T$ is vector of phenotypic observations for the T-th trait [20]. In this study, T=2, which comprising two traits: Body weight and egg production. The fixed effects are consistent with those in the single-trait model.

In the PBLUP and ssGBLUP models, the distributional assumptions for the additive genetic effects ($\mathbf{u}$) are shown in Equations (2) and (3)

$$\begin{bmatrix} u \\ e \end{bmatrix} \sim N\left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \mathbf{A}\sigma_u^2 & 0 \\ 0 & \mathbf{I}\sigma_e^2 \end{bmatrix}\right) \tag{2}$$

$$\begin{bmatrix} u \\ e \end{bmatrix} \sim N\left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \mathbf{H}\sigma_u^2 & 0 \\ 0 & \mathbf{I}\sigma_e^2 \end{bmatrix}\right) \tag{3}$$

where **A** is the pedigree relationship matrix and **I** is an identity matrix. The $\mathbf{H}$ matrix seamlessly integrates the pedigree relationship matrix (**A**) with the genomic relationship matrix (**G**). The elements of **A** are constructed from pedigree as follows:

The diagonal elements are computed as $A_{ii} = 1 + F_i$, where F_i is the inbreeding coefficient of individual i, calculated as $F_i = \frac{1}{2}A_{sd}$. The off-diagonal elements are computed as $A_{ij} = \frac{1}{2}(A_{i,s_j} + A_{i,d_j})$, where s_j and d_j are the parents of individual j.

In the mixed model equations, its inverse ($\mathbf{H}^{-1}$) is used, which is constructed as follows:

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{pmatrix} 0 & 0 \\ 0 & \mathbf{G}_w^{-1} - \mathbf{A}_{22}^{-1} \end{pmatrix} \tag{4}$$

where $\mathbf{A}^{-1}$ is the inverse of the pedigree relationship matrix for all animals (both genotyped and non-genotyped), and $\mathbf{G}_w^{-1}$ is the inverse of the tuned or weighted genomic relationship matrix for genotyped animals. The genomic relationship matrix ($\mathbf{G}$) is typically tuned using a weighted approach, such as $\mathbf{G}_w = (1-\alpha)\mathbf{G} + \alpha\mathbf{A}_{22}$with α = 0.05 [21] to ensure compatibility with the pedigree-based relationship matrix ($\mathbf{A}$) and to account for potential scale differences or missing pedigree information. This tuning strategy is grounded in a dual rationale: It assigns predominant weight (95%) to genomic information, leveraging its ability to capture true genetic variation more accurately, while incorporating a minor proportion (5%) of pedigree-derived information ($\mathbf{A}_{22}$) as a regularization term. The latter serves to mitigate random errors in $\mathbf{G}$, arising from genotype imputation inaccuracies or allele frequency estimation biases, thereby enhancing numerical stability and ensuring reliable inversion of the combined relationship matrix (**H**). $\mathbf{A}_{22}^{-1}$ is the inverse of the pedigree relationship matrix for the genotyped animals only. The block matrix adds the genomic information component only to the subset of genotyped individuals.

2.5. Model Evaluation

To evaluate the impact of different models and genetic evaluation methods on the accuracy and unbiasedness of breeding value prediction, we conducted the analysis in two steps. First, prediction accuracy was assessed by calculating Pearson and Spearman correlation coefficients between the predicted EBV obtained from the cross-validation and the corrected phenotypes from the full dataset (defined as the sum of EBV and their corresponding residuals). Second, a linear regression of the EBV from the full dataset onto the predicted EBV from the cross-validation was performed. The regression coefficient was used as an indicator of unbiasedness to measure systematic bias in the predictions [22].

3. Results

3.1. Effects of different models and evaluation methods on the prediction accuracy

In this study, the prediction accuracy of different models was evaluated by calculating the correlation coefficients between the predicted EBV, obtained from single-trait and multi-trait models using either PBLUP or ssGBLUP, and the corrected phenotypes from the full dataset.

The results (Table 2) showed that for the prediction of both body weight and egg production, there was no significant difference in accuracy between the single-trait and multi-trait models when using the pedigree-based PBLUP method ($P > 0.05$). This indicates that PBLUP failed to effectively leverage the genetic information in the multi-trait model to improve predictive performance. However, after incorporating genomic information, the ssGBLUP method enhanced the predictive ability of the multi-trait model relative to its single-trait counterpart. For body weight, the improvements in prediction accuracy and rank correlation were 1.47% and 1.56%, respectively. For egg production, the multi-trait ssGBLUP model improved prediction accuracy by 0.78% and rank correlation by 1.01%.

Table 2. Comparison of prediction accuracies for different models and evaluation methods.

Types	BW8[1]				EN43[2]			
	Single-trait model		**Multi-trait model**		**Single-trait model**		**Multi-trait model**	
	PBLUP	**ssGBLUP**	**PBLUP**	**ssGBLUP**	**PBLUP**	**ssGBLUP**	**PBLUP**	**ssGBLUP**
Pearson	0.291 ± 0.006^{ab}	0.341 ± 0.007^{c}	0.291 ± 0.006^{a}	0.346 ± 0.008^{b}	0.322 ± 0.019^{ab}	0.386 ± 0.015^{c}	0.321 ± 0.019^{a}	0.389 ± 0.015^{b}
Spearman	0.269 ± 0.005^{b}	0.321 ± 0.004^{c}	0.269 ± 0.005^{a}	0.326 ± 0.006^{b}	0.334 ± 0.019^{b}	0.396 ± 0.016^{c}	0.335 ± 0.019^{a}	0.400 ± 0.017^{b}

Values in the table are expressed as mean ± SE. [1]BW8 = body weight at 8 weeks of age; [2]EN43 = cumulative egg production up to 43 weeks of age. Values for the same trait (BW8 or EN43) and correlation type (Pearson or Spearman) with different superscript letters at $P < 0.05$.

Furthermore, compared to using only pedigree information, the introduction of genomic data significantly improved predictive performance. For the body weight trait, the prediction accuracy and rank correlation of the single-trait model increased by 17.18% and 19.33%, respectively. The improvement in the multi-trait model was even more significant ($P < 0.01$), with gains reaching 18.90% and 21.19%, respectively. For the egg production trait, the prediction accuracy and rank correlation of the single-trait model improved by 19.88% and 18.56%, respectively, while the multi-trait model achieved improvements of 21.18% and 19.40%, respectively.

3.2. Effects of Different Models and Evaluation Methods on the Unbiasedness of EBV

In this study, unbiasedness was evaluated by the regression coefficient from the regression of EBVs from the full dataset onto the predicted EBVs from cross-validation. A regression coefficient closer to 1 indicates that the model's predictions are less biased [23]. The results (Figure 1) show that all models and evaluation methods had a minimal impact on unbiasedness, with no significant overestimation or underestimation observed. There were no significant differences in unbiasedness among the models or methods, indicating that all tested approaches can provide unbiased predictions.

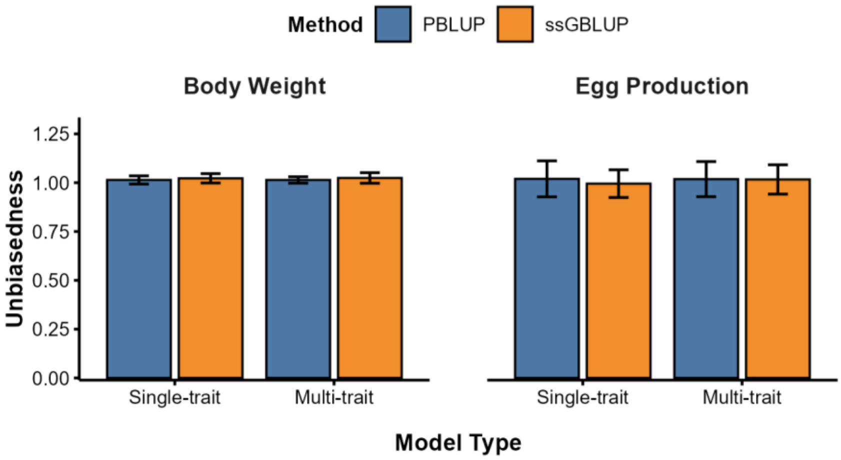

Figure 1. Comparison of unbiasedness for different models and evaluation methods.

3.3.Effects of different models and evaluation methods on genetic parameter estimates

In terms of genetic parameter estimation, we compared the performance of the PBLUP and ssGBLUP methods in both single-trait and multi-trait models using the full dataset (Table 3). For the body weight trait, ssGBLUP yielded higher heritability estimates (single-trait: 0.324; multi-trait: 0.325) and higher additive genetic variance estimates (single-trait: 2,460.084; multi-trait: 2,472.512), which were considerably higher than those from PBLUP. For the egg production trait, the heritability estimate from the single-trait PBLUP model was 0.399, compared to 0.370 from the ssGBLUP model. A similar trend was observed in the multi-trait models (PBLUP: 0.396; ssGBLUP: 0.372). In terms of variance components, ssGBLUP consistently yielded lower additive genetic variance and higher residual variance estimates in both models.

Table 3. Effects of different models and evaluation methods on genetic parameter estimates.

Types	**BW8**[1]				**EN43**[2]			
	Single-trait model		**Multi-trait model**		**Single-trait model**		**Multi-trait model**	
	PBLUP	**ssGBLUP**	**PBLUP**	**ssGBLUP**	**PBLUP**	**ssGBLUP**	**PBLUP**	**ssGBLUP**
V_A	2132.601	2460.084	2118.877	2472.512	76.381	70.926	75.711	71.289
V_E	5309.136	5143.215	5319.154	5138.121	115.205	120.584	115.647	120.437
V_P	7441.737	7603.299	7438.031	7610.633	191.587	191.510	191.358	191.725
h^2	0.287	0.324	0.285	0.325	0.399	0.370	0.396	0.372

[1]BW8 = body weight at 8 weeks of age; [2]EN43 = cumulative egg production up to 43 weeks of age; $\boldsymbol{V_A}$ = Additive variance. $\boldsymbol{V_E}$ = Residual variance. $\boldsymbol{V_P}$ = Phenotypic variance. $\boldsymbol{h^2}$ = Heritability. All the above parameters were estimated based on the full dataset.

Furthermore, analysis of the genetic correlations in the population showed that estimates from the full dataset indicated a significant negative phenotypic correlation ($r = -0.145$, $P < 0.01$) and a moderate negative genetic correlation (pedigree-based: $r_p = -0.313$; genomic + pedigree: $r_g = -0.374$; $P < 0.01$) between body weight and egg production. This confirms, on a genetic basis, the antagonistic relationship between the two traits and provides a theoretical rationale for the application of multi-trait models.

4. Discussion

A key finding of this study is that the predictive superiority of the multi-trait model is contingent upon the integration of genomic information. While the multi-trait model showed no advantage over the single-trait model under traditional PBLUP, indicating that pedigree-based genetic correlations are insufficient for effectively leveraging trait covariance, its benefit became substantial with ssGBLUP. This difference stems from the resolution of the relationship matrices. The pedigree-based matrix in PBLUP only provides the expected proportion of shared genomes, obscuring the complex genetic architecture [16]. In contrast, the genomic relationship matrix in ssGBLUP captures the realized genetic similarity due to Mendelian sampling and linkage disequilibrium [9,10]. This high-resolution data enables ssGBLUP to dissect the genetic architecture, distinguishing loci with specific effects on body weight, egg production, or antagonistic pleiotropic effects on both. Consequently, the multi-trait ssGBLUP model successfully utilizes genetic covariance between traits, leading to a significant leap in prediction accuracy.

Multi-trait models achieve balanced genetic progress in poultry breeding through utilizing inter-trait genetic correlations. For example, studies in Thai native chickens have shown that combining multi-trait animal models with selection indices significantly improves the accuracy of genetic evaluation for traits such as body weight and egg production, and enables simultaneous genetic gains in both traits. It is recommended to use body weight, breast circumference, and egg production as joint selection criteria to maximize breeding benefits [1]. In Chinese indigenous breeds like Qingyuan partridge chickens, multi-trait models enable more accurate estimation of genetic correlations among traits, especially when antagonistic relationships exist, helping to develop breeding strategies that consider multiple traits and avoid negative genetic responses from single-trait selection [24]. Furthermore, multi-trait genomic selection models can borrow information from correlated traits to improve the prediction accuracy of low-heritability traits, especially when some traits are difficult to measure directly, thus optimizing overall selection efficiency [25]. Both simulation and real poultry data show that multi-trait models provide the greatest improvement for high-heritability traits and large reference populations, but even under low-heritability or small population conditions, they still offer a scientific basis for improving complex traits [1,24,25].

Antagonism between growth and reproductive traits in poultry is indeed multifaceted, involving genetic, physiological, and metabolic mechanisms [26–28]. In this study, we focus on the genetic aspect, as evidenced by our findings of a negative phenotypic correlation ($r = -0.145$) and moderate negative genetic correlations (pedigree-based: $r_p = -0.313$; genomic + pedigree: $r_g = -0.374$) between body weight and egg production in yellow-feathered broiler breeders. The ssGBLUP model, by integrating genomic and pedigree information, captures realized genetic relationships and enables the dissection of genetic architecture, including loci with antagonistic pleiotropic effects [8,27–30]. This approach significantly improves prediction accuracy for complex traits and supports the development of more effective multi-trait breeding strategies [8,27,30–32]. While we emphasize genetic effects, we acknowledge the importance of physiological and metabolic influences, which will be addressed in future research. Based on these results, we recommend that practical poultry breeding programs combine multi-trait ssGBLUP models with economic weights to develop customized selection indices, thereby achieving coordinated improvement of economic traits such as body weight and egg production.

The accurate estimation of genetic parameters is fundamental to poultry breeding, as it dictates selection response and program sustainability. Estimates of heritability for key economic traits such as body weight and egg production vary considerably across populations, including breeds, such as Taiwan country chickens, Muscovy ducks, turkeys, and yellow-feathered broilers, with body weight heritability ranging from 0.04 to 0.67 and egg production heritability ranging from 0.07 to 0.44 [3,5,27,33], underscoring their genetic potential but also the context-dependency of these parameters [34–39]. Our findings, integrating pedigree and genomic data via multi-trait models, confirm moderate heritability for both traits. Crucially, in this study, ssGBLUP provided a more nuanced variance decomposition than PBLUP. While total phenotypic variance ($\mathbf{V}_P$) remained stable, ssGBLUP increased the additive genetic variance ($\mathbf{V}_A$) for body weight, capturing previously missed genetic variation. Conversely, for egg production, it reduced $\mathbf{V}_A$, likely by accounting for non-genetic confounding effects, yielding a less biased estimate. This refined dissection of $\mathbf{V}_A$ and residual variance ($\mathbf{V}_E$) established a more reliable genetic basis, which is essential for the subsequent success of the multi-trait model. By integrating genomic and pedigree information, ssGBLUP can significantly improve the accuracy of genetic evaluation for traits such as egg production and body weight. Systematic comparisons between ssGBLUP (single-step genomic BLUP) and PBLUP (pedigree BLUP) models across various poultry species and traits have consistently demonstrated this advantage. For example, in Taiwan country chickens, ssGBLUP increased the prediction accuracy for egg production traits by an average of 3.41% compared to PBLUP, making it especially suitable for small populations and breeds with diverse breeding objectives [27]. In other poultry, such as Muscovy ducks and turkeys, the improvement in prediction accuracy for egg production traits using ssGBLUP was more pronounced, with increases ranging from 12.3% to 43.9% under random cross-validation [3,40].

A negative genetic correlation generally exists between body weight and egg production traits in poultry. In this study, analysis of the complete dataset revealed a significant negative phenotypic correlation and a moderate negative genetic correlation between the two traits. This finding aligns with other studies. For instance, Ullengala et al. [41] reported a genetic correlation of -0.31 between body weight at 40 weeks and egg production in dual-purpose chickens. Similarly, Chomchuen et al. [1] found negative genetic correlations ranging from -0.30 to -0.49 in commercial broilers. Other studies for native chicken populations have reported comparable ranges [42–44]. This collective evidence underscores that multi-trait selection must be carefully balanced in practical breeding programs. Additionally, the methods used to estimate genetic parameters, such as multi-trait models, and the type of data (genomic versus pedigree information) can influence the estimated values of heritability and genetic correlations; incorporating genomic information helps improve the accuracy of these estimates and better reflects the true genetic architecture [37]. Therefore, regularly updating genetic parameters and integrating multi-trait analysis with genomic information provide a scientific foundation for the coordinated genetic improvement of body weight and egg production traits in poultry.

Conclusion

By comparing the performance of different models and evaluation methods for predicting egg production and body weight traits in yellow-feathered broilers, we aimed to identify an optimal breeding value prediction strategy that can efficiently integrate genomic information with genetic correlations among multiple traits. The results demonstrate that the multi-trait model based on single-step genomic best linear unbiased prediction (ssGBLUP) significantly outperforms traditional methods. It not only substantially improves the prediction accuracy for body weight and egg production traits but also effectively utilizes the genetic covariance between traits. This provides a theoretical basis and a practical pathway for achieving more precise and efficient genomic breeding in poultry.

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Use of AI tools declaration

The authors declare they have not used Artificial Intelligence (AI) tools in the creation of this article.

Author contributions

T.L. and H.Q. conceived and supervised the study. J.L., S.J., Z.C., J.L. and P.W. conducted experiments and analyzed data. J.L. and T.L. wrote the manuscript. J.L., D.S. and H.Q. revised the content. All authors read and approved the final version.

Conflict of interest

The authors declare no conflict of interest. Tianfei Liu is an editorial board member for *AIMS Animal Science* and was not involved in the editorial review or the decision to publish this article.

References

1. Chomchuen K , Tuntiyasawasdikul V, Chankitisakul V (2022) Genetic evaluation of body weights and egg production traits using a multi-trait animal model and selection index in thai native synthetic chickens (Kaimook e-san2). *Animals (Basel)* 12: 335. https://doi.org/10.3390/ani12030335
2. Yang R, Xu Z, Wang Q (2021) Genome-wide association study and genomic prediction for growth

traits in yellow-plumage chicken using genotyping-by-sequencing. *Genet Sel Evol* 53: 82. https://doi.org/10.1186/s12711-021-00672-9

3. Begli HE, Wood B, Abdalla E (2019) Genetic parameters for clutch and broodiness traits in turkeys (Meleagris Gallopavo) and their relationship with body weight and egg production. *Poult Sci* 98: 6263–6269. https://doi.org/10.3382/ps/pez446
4. Tarsani E, Kranis A, Maniatis G (2021) Detection of loci exhibiting pleiotropic effects on body weight and egg number in female broilers. *Sci Rep* 11: 7441. https://doi.org/10.1038/s41598-021-86817-8
5. Fang X, Ye H, Zhang S (2023) Investigation of potential genetic factors for growth traits in yellow-feather broilers using weighted single-step genome-wide association study. *Poult Sci* 102: 103034. https://doi.org/10.1016/j.psj.2023.103034
6. Georges M, Charlier C, Hayes B (2019) Harnessing genomic information for livestock improvement. *Nat Rev Genet* 20: 135–156. https://doi.org/10.1038/s41576-018-0082-2
7. Meuwissen T, Hayes B, Goddard M (2016) Genomic selection: A paradigm shift in animal breeding. *Anim Front* 6: 6–14. https://doi.org/10.2527/af.2016-0002
8. Misztal I, Lourenco D, Legarra A (2020) Current status of genomic evaluation. *J Anim Sci* 98: skaa101. https://doi.org/10.1093/jas/skaa101
9. Legarra A, Aguilar I, Misztal I (2009) A relationship matrix including full pedigree and genomic information. *J Dairy Sci* 92: 4656–4663. https://doi.org/10.3168/jds.2009-2061
10. Misztal I, Legarra A, Aguilar I (2009) Computing procedures for genetic evaluation including phenotypic, full pedigree, and genomic information. *J Dairy Sci* 92: 4648–4655. https://doi.org/10.3168/jds.2009-2064
11. Liu B, Liu H, Tu J (2025) An investigation of machine learning methods applied to genomic prediction in yellow-feathered broilers. *Poult Sci* 104: 104489. https://doi.org/10.1016/j.psj.2024.104489
12. Williams YJ, Pryce JE, Grainger C (2011) Variation in residual feed intake in Holstein-Friesian dairy heifers in southern Australia. *J Dairy Sci* 94: 4715–4725. https://doi.org/10.3168/jds.2010-4015
13. R Core Team R, *R: A language and environment for statistical computing*. 2020, Citeseer.
14. Browning BL, Zhou Y, Browning SR (2018) A one-penny imputed genome from next-generation reference panels. *Am J Hum Genet* 103: 338–348. https://doi.org/10.1016/j.ajhg.2018.07.015
15. Purcell S, Neale B, Todd-Brown K (2007) PLINK: A tool set for whole-genome association and population-based linkage analyses. *Am J Hum Genet* 81: 559–575. https://doi.org/10.1086/519795
16. Henderson CR (1973) Sire Evaluation and Genetic Trends. *J Anim Sci* 1973: 10–41. https://doi.org/10.1093/ansci/1973.Symposium.10
17. Villumsen TM, Su G, Guldbrandtsen B (2021) Genomic selection in American mink (Neovison vison) using a single-step genomic best linear unbiased prediction model for size and quality traits graded on live mink. *J Anim Sci* 99: skab003. https://doi.org/10.1093/jas/skab003
18. Jensen PMJ (2008) DMU: A Package for Multivariate Analysis. *University of Copenhagen.*
19. Stranden I, Mantysaari EA, Lidauer MH (2024) A computationally efficient algorithm to leverage average information REML for (co)variance component estimation in the genomic era. *Genet Sel*

Evol 56: 73. https://doi.org/10.1186/s12711-024-00939-x

20. Henderson C, Quaas R (1976) Multiple trait evaluation using relatives' records. *J Anim Sci* 43: 1188–1197. https://doi.org/10.2527/jas1976.4361188x
21. Abdalla EEA, Schenkel FS, Begli EH (2019) Single-step methodology for genomic evaluation in turkeys (Meleagris gallopavo). *Front Genet* 10: 1248. https://doi.org/10.3389/fgene.2019.01248
22. Legarra A, Reverter A (2018) Semi-parametric estimates of population accuracy and bias of predictions of breeding values and future phenotypes using the LR method. *Genet Sel Evol* 50: 53. https://doi.org/10.1186/s12711-018-0426-6
23. Piñeiro G, Perelman S, Guerschman JP (2008) How to evaluate models: Observed vs. predicted or predicted vs. observed? *Ecol Model* 216: 316–322. https://doi.org/10.1016/j.ecolmodel.2008.05.006
24. Kang H, Ren M, Li S (2023) Estimation of genetic parameters for important traits using a multi-trait model in late-feathering Qingyuan partridge hens in China. *J Anim Breed Genet* 140: 158–166. https://doi.org/10.1111/jbg.12739
25. Momen M, Mehrgardi AA, Sheikhy A (2017) A predictive assessment of genetic correlations between traits in chickens using markers. *Genet Sel Evol* 49: 16. https://doi.org/10.1186/s12711-017-0290-9
26. Kumar M, Ratwan P, Dahiya SP (2021) Climate change and heat stress: Impact on production, reproduction and growth performance of poultry and its mitigation using genetic strategies. *J Therm Biol* 97:102867. https://doi.org/10.1016/j.jtherbio.2021.102867
27. Tu TC, Lin CJ, Liu MC (2024) Comparison of genomic prediction accuracy using different models for egg production traits in Taiwan country chicken. *Poult Sci* 103:104063. https://doi.org/10.1016/j.psj.2024.104063
28. Zhang XY, Wu MQ, Wang SZ(2018) Genetic selection on abdominal fat content alters the reproductive performance of broilers. *Animal* 12: 1232–1241. https://doi.org/10.1017/S1751731117002658
29. Ning G, Zhang H, Zhang XQ (2022) Incorporating genomic annotation into single-step genomic prediction with imputed whole-genome sequence data. *J Integr Agric* 21: 1126–1136. https://doi.org/10.1016/S2095-3119(21)63813-3
30. Tu TC, Lin CJ, Liu MC (2025) Genomic prediction and genome-wide association study for growth-related traits in Taiwan country chicken. *Animals* 15: 376. https://doi.org/10.3390/ani15030376
31. Chen CY, Misztal I, Aguilar I (2011) Genome-wide marker-assisted selection combining all pedigree phenotypic information with genotypic data in one step: An example using broiler chickens. *J Anim Sci* 89: 23–28. https://doi.org/10.2527/jas.2010-3071
32. Gao N, Teng J, Pan R (2019) Accuracy of whole genome prediction with single-step GBLUP in a Chinese yellow-feathered chicken population. *Livestock Sci.* 230: 103817. https://doi.org/10.1016/j.livsci.2019.103817
33. Hu YH, Poivey JP, Rouvier R (1999) Heritabilities and genetic correlations of body weights and feather length in growing Muscovy selected in Taiwan. *Br Poult Sci* 40: 605–612. https://doi.org/10.1080/00071669986972
34. Afrin S, Lee YM, Haque MA (2024) Estimation of genetic parameters and breeding value

accuracy for growth and egg production traits in Korean native chicken pure lines. *Livestock Sci* 282: 105436. https://doi.org/10.1016/j.livsci.2024.105436

35. Begli EH, Schaeffer LR, Abdalla E (2021) Genetic analysis of egg production traits in turkeys (Meleagris gallopavo) using a single-step genomic random regression model. *Genet Sel Evol* 53: 61. https://doi.org/10.1186/s12711-021-00655-w
36. Fu M, Wu Y, Shen J (2023) Genome-wide association study of egg production traits in shuanglian chickens using whole genome sequencing. *Genes (Basel)* 14: 2129. https://doi.org/10.3390/genes14122129
37. Kour A, Chatterjee RN, Rajaravindra KS (2025) Bayesian genetic estimation towards optimising selection strategy for higher egg production in white leghorn chickens. *J Anim Breed Genet* 142: 617–629. https://doi.org/10.1111/jbg.12931
38. Ma X, Ying F, Li Z (2024) New insights into the genetic loci related to egg weight and age at first egg traits in broiler breeder. *Poult Sci* 103:103613. https://doi.org/10.1016/j.psj.2024.103613
39. Wang J, Liu J, Lei Q (2024) Elucidation of the genetic determination of body weight and size in Chinese local chicken breeds by large-scale genomic analyses. *BMC Genom* 25: 296. https://doi.org/10.1186/s12864-024-10185-6
40. Hu YH, Poivey JP, Rouvier R (2004) Heritabilities and genetic correlations of laying performance in Muscovy ducks selected in Taiwan. *Br Poult Sci* 45: 180–185. https://doi.org/10.1080/00071660410001715777
41. Ullengala R, Prince LLL, Paswan C (2021) Variance component analysis of growth and production traits in Vanaraja male line chickens using animal model. *Anim Biosci* 34: 471–481. https://doi.org/10.5713/ajas.19.0826
42. Lwelamira J, Kifaro GC, Gwakisa PS (2009) Genetic parameters for body weights, egg traits and antibody response against Newcastle Disease Virus (NDV) vaccine among two Tanzania chicken ecotypes. *Trop Anim Health Prod* 41: 51–59. https://doi.org/10.1007/s11250-008-9153-2
43. Niknafs S, Nejati-Javaremi A, Mehrabani-Yeganeh H (2012) Estimation of genetic parameters for body weight and egg production traits in Mazandaran native chicken. *Trop Anim Health Prod* 44: 1437–1443. https://doi.org/10.1007/s11250-012-0084-6
44. Tongsiri S, Jeyaruban GM, Hermesch S (2019) Genetic parameters and inbreeding effects for production traits of Thai native chickens. *Asian-Australas J Anim Sci* 32: 930–938. https://doi.org/10.5713/ajas.18.0690

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