

Research Article

Genetic Parameter Estimates of Purebreds and Crossbreds for 35-day Body Weight in Broilers Using Terminal Crossbred Model

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Abstract

Records on 35-day body weight from two purebred broiler lines A (n=15,010), B (n=14,111), and their crosses C (n=7600) were used to estimate genetic parameters using within-line and terminal-cross models. The models that were fitted included the fixed environmental effect (such as contemporary group and sex, day of hatching), random additive and random parental dominance effects. The model for purebreds included only one additive effect, whereas the model for crossbreds included two additive effects (additive effect for sire in A on his C offspring and additive effect for dam in B on her C offspring). Heritability estimates for 35-day body weight were 0.24, 0.226 and 0.24 with within-line models for lines A, B, and C, respectively, and 0.25, 0.23, and 0.25 with the crossbred model, respectively. The ratio estimates of dominance to phenotypic variance were 0.19, 0.32, and 0.11 with within-line models for lines A, B, and C, respectively, and 0.18, 0.33, and 0.11 with the crossbred model, respectively. The genetic correlations between purebreds and crossbreds for 35-day body weight were 0.65 (A-C) and 0.56 (B-C). Mean reliabilities of predicted purebred breeding values were 0.52 and 0.41 with within-line models for lines A and B, respectively, and 0.58 and 0.46 with the terminal-cross model, respectively. Mean reliabilities of predicted crossbred breeding values were 0.64 and 0.42 with within-line models for lines A and B, respectively, and 0.69 and 0.44 with the terminal-cross model, respectively. Mean reliabilities of predicted breeding values using the crossbred model were increased in comparison with within-line model.

Keywords

Terminal Crossbred Model, Broiler, Genetic Correlation, Reliability

1. Introduction

The goal of commercial poultry breeding programme is to improve crossbred performance. In order to meet this goal, it is required not only to increase the additive effects of purebreds themselves but also to improve the additive effects of

animals in purebreds on their crossbred offsprings. In this regards, many researches showed that the genetic correlation between purebreds and crossbreds is less than 1 [1, 7, 10, 15].

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Received: 26 May 2025; **Accepted:** 20 June 2025; **Published:** 28 July 2025



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For poultry egg production trait, it has been showed that the genetic correlation between purebreds and crossbreds is a function of dominance effects and the difference in gene frequency between parental populations, and its value is decreased with increasing these two factors [14, 16, 17].

Wei et al [15] estimated genetic parameters from multi-variate model, in which the records from purebreds and crossbreds were treated as separate traits for egg production traits in poultry, and analyzed the interrelation of dominance variance and genetic correlation between purebreds and crossbreds.

Lo et al. [5, 6] proposed the terminal-cross model for joint evaluation of purebreds and crossbreds, which is much simpler in comparison to the model for all types of crossbreds. In this model, there is one additive effect for each pure line and two additive effects for each terminal cross.

Lutaaya et al. [8] estimated genetic parameters from joint evaluation model of purebreds and crossbreds taking dominance effects into consideration, and found that accuracy of this method would be high if the number of crossbreds are greater than that of purebreds.

Recently Duenk et al. [1] calculated the genetic correlations between purebreds and crossbreds performance for body weight in broiler by using the pedigree and genome correlation, respectively, and found that the analysis by genome correlation was better than former. Koerhuis and Thompson [4] evaluated the maternal effect for juvenile body weight in broiler chickens. Especialy, Mulder et al. [12] and Maniatis et al. [9] estimated genetic variance parameters for 35-day body weight.

Motivated by the above cited research, in this paper we are interested in genetic parameter estimates of purebreds and crossbreds for 35-day body weight in broilers using terminal crossbred model. More precisely, the objective of this study is twofold. First, we estimate genetic variance parameters of purebreds and crossbreds for 35-day body weight in broiler by using the terminal crossbred model. This corresponds to the first genetic evaluation by BLUP in Democratic People's Republic of Korea. Second, we compare the reliabilities of predicted breeding values from within-line and terminal cross models under the condition that the records for crossbreds are smaller than those for purebreds.

2. Materials and Methods

2.1. Data

Data for this study were obtained from the Poultry Academy of Sciences, Democratic People's Republic of Korea, and spanned a period of 6yr (From 2018 to 2023). All two lines are Arbor Acres (AA).

Lines A and B are the pure lines used as two-way sire lines for four way crossbreds and line C consists of the crossbreds from lines A and B. Line A is used predominantly as a sire line and line B as a maternal line. After getting rid of the

animals with unclear pedigrees and the records greater than three phenotypic SD from the overall means for 35-day body weight, we used the data with 36 721 records.

Table 1 gives the distribution of records by line and sex.

Table 1. Distribution of records by line and sex.

Line	Total (number)	Male (number)	Female (number)
A	15 010	7568	7442
B	14 111	6836	7275
C	7600	3845	3755

Table 2 shows the mean and standard deviations of 35-day body weight for all lines.

Table 2. Mean and standard deviations of 35-day body weight for all lines.

Line	Mean (g)	Deviation
A	1885	243
B	1820	257
C	1928.5	232

The purebred lines A, B and the crossbred line C were raised in individual cages under a well-controlled environment. Each sire was mated to approximately 5 to 6 dams in purebred lines and 5 to 8 dams in crossbreds.

2.2. Within-line Analysis

Within-line single-trait analyses were carried out using the following model:

$$y = Xb + Zu + Wd + e, \quad (1)$$

where y is a vector of observations; b is a vector of fixed effects; u is a vector of additive effects; d is a vector of parental dominance effects ([3]); e is a vector of residual effects; and X , Z and W are incidence matrices. The vector of fixed effects included contemporary group, sex (male or female) and day of hatching. Variances are:

$$\text{var}(u) = A\sigma_u^2, \text{var}(d) = D\sigma_d^2, \text{var}(e) = A\sigma_e^2$$

where A is additive relationship matrix, D is parental-dominance relationship matrix among individuals, and σ_u^2 , σ_d^2 and σ_e^2 are additive, parental-dominance, and residual variances, respectively.

2.3. Crossbred (Terminal-cross) Model

Combined purebred and crossbred analyses were performed using the following model ([6]):

$$\begin{pmatrix} y_A \\ y_B \\ y_C \end{pmatrix} = \begin{pmatrix} X_A & 0 & 0 \\ 0 & X_B & 0 \\ 0 & 0 & X_C \end{pmatrix} \begin{pmatrix} b_A \\ b_B \\ b_C \end{pmatrix} + \begin{pmatrix} Z_A & 0 & 0 & 0 \\ 0 & 0 & Z_B & 0 \\ 0 & Z_{AC} & 0 & Z_{BC} \end{pmatrix} \begin{pmatrix} u_{AA} \\ u_{AC} \\ u_{BB} \\ u_{BC} \end{pmatrix} \\ + \begin{pmatrix} W_A & 0 & 0 \\ 0 & W_B & 0 \\ 0 & 0 & W_C \end{pmatrix} \begin{pmatrix} d_A \\ d_B \\ d_C \end{pmatrix} + \begin{pmatrix} e_A \\ e_B \\ e_C \end{pmatrix}, \quad (2)$$

where y_A and y_B are vectors of observations for purebred lines A and B, respectively; y_C is a vector of observations for crossbreds (line C); b_A, b_B and b_C are vectors of unknown fixed effects; u_{AA} and u_{BB} are vectors of additive effects of animals in lines A and B, respectively; u_{AC} and u_{BC} are vectors of additive effects of animals in line C originating from lines A and B, respectively; d_A, d_B and d_C are vectors of parental dominance effects; e_A, e_B and e_C are vectors of residual effects; X, Z and W are incidence matrices relating records to corresponding effects.

The vector of fixed effects included contemporary group, sex and day of hatching.

The variances are as follows.

$$\text{var} \begin{pmatrix} u_{AA} \\ u_{AC} \\ u_{BB} \\ e \end{pmatrix} = \begin{pmatrix} g_{AA}A_A & g_{AC}A_A & 0 & 0 & 0 \\ g_{AC}A_A & g_{CC}A_A & 0 & 0 & 0 \\ 0 & 0 & g_{BB}A_B & g_{BC}A_B & 0 \\ 0 & 0 & g_{BC}A_B & g_{CC}A_B & 0 \\ 0 & 0 & 0 & 0 & R \end{pmatrix},$$

$$\text{var} \begin{pmatrix} d_A \\ d_B \\ d_C \end{pmatrix} = \begin{pmatrix} D_A V_A^2 & 0 & 0 \\ 0 & D_B V_B^2 & 0 \\ 0 & 0 & F_C V_A^2 \end{pmatrix},$$

where A_A and A_B are additive relationship matrices for lines A and B, respectively; g_{AA} and g_{BB} are additive genetic variances for lines A and B, respectively; g_{CC} and g_{CC} are additive genetic variances for the alleles of line A and line B in crossbreds (line C), respectively; g_{AC} and g_{BC} are genetic covariances between the purebred parents in line i ($i = A, B$) and their crossbred (line C) progeny; $R = \text{diag}(\sigma_{eA}^2, \sigma_{eB}^2, \sigma_{eC}^2)$, where $\sigma_{eA}^2, \sigma_{eB}^2, \sigma_{eC}^2$ are the residual variances for lines A, B, and C; D_A and D_B are the parental dominance relationship matrices for individuals in lines A and B, respectively; F_C are relationship matrix for full-sib family effects in C; V_A^A, V_B^B and V_C^C are one-fourth of the dominance variances for individuals in lines A, B, and C, respectively.

The terminal crossbred model makes it possible to overcome some limitations of the previous models in computa-

tion of genetic correlation (see [7]). But the model has more parameters to be estimated and needs a larger amount of computational work than the before.

2.4. Computations

In this study, the variances were estimated using Bayesian method via Markov Chain Monte Carlo (MCMC) Gibbs sampling using the program *asremlPlus*, where prior distributions for fixed effects and variances were assumed to be flat for each analysis and initial values for location parameters were set to zero ([13]).

Four hundred thousand samples were obtained for each parameter. We carried out the sampling and average of the variance estimations so that their independence and uncorrelation were convinced ([12]). We compared the mean reliabilities to find out whether there are some improvements in breeding value estimations. Reliabilities were obtained using the formula:

$$r_{ij}^2 = 1 - \text{pev}_{ij} / \sigma_j^2$$

where r_{ij}^2 is the reliability for animal i of line j , pev_{ij} is the corresponding prediction error variance, and σ_j^2 is the additive variance for line j (see [2] and [11]).

3. Results and Discussion

As shown in Table 1, line A has about 900 more animals than line B and the data of crossbreds is about half as small as purebred lines. Maintenance of purebred was of the main interest and data of observations for pedigreed crossbreds was not much enough.

The number of observations of male for 35-day body weight was 7568 in line A, 6836 in line B, and 3845 in line C, thus line A was the largest, line B was the second, and line C was the smallest. The number of observations of female was 7442 in line A, 7275 in line B, and 3755 in line C.

Means and standard deviations of 35-day body weight of animals were 1885g and 243g in line A, respectively, 1820g

and 257g in line B, respectively, and 1928.5g and 232g in line C, respectively. Heterosis proportion by phenotype was explicit. Standard deviation was the largest in line B, and similar in lines A and C.

Though the purelines were raised in individual cages, each generation didn't have the same effect due to some environment factors.

3.1. Variance Estimates

Within-line variance estimates for 35-day body weight are presented in Table 3. Additive variances were 8703, 8081, and 10 146 for lines A, B, and C, respectively, one-fourth dominance variances were 1690, 2916, and 1060 for lines A, B, and C, respectively, residual variances were 25 759.79, 24 799.47, 31 233.21, respectively, and phenotypic variances were 36 152.79, 35 796.47, and 42 439.21 for lines A, B, and C, respectively.

Additive variance of line A was bigger than line B. Additive variance of line C was obtained by $2(u_{AC} + u_{BC})$. Variance estimates obtained from the crossbred model are given in Table 4. Additive variances were 9237, 8699, and 10 872 for lines A, B, and C, respectively, one-fourth dominance variances were 1670, 3058, and 1211 for lines A, B, and C, respectively, residual variances were 26 028, 25 365, and 31 015 for lines A, B, and C, respectively, and phenotypic variances were 36 935, 37 122, and 43 398 for lines A, B, and C, respectively.

Additive variance estimate obtained from the crossbred model was higher than one from the within-line models and dominance variance estimate for line A was lower than line B. Residual variance estimates obtained from within-line analyses were lower than those from the crossbred model for lines A, B and C.

One-fourth dominance variances obtained from the with-

in-line model were estimated as 1690, 2916, and 1060 for lines A, B, and C, respectively, and the one obtained from the crossbred model was slightly higher than those obtained using within-line model for lines A and B. Dominance variance estimates for lines A and B were significantly large, especially it was the largest for line B. This will affect the crossbreeding between the two pure lines.

Wei et al. [15] found that the larger the dominance variation and additive variance difference between purebreds and crossbreds are, the lower the genetic correlation is.

The observation in which dominance variances for both pure lines and additive variance difference between purebreds and crossbreds were large suggests that the gene frequency difference between purebreds and crossbreds is large. Especially, the gene frequency difference between line B and crossbreds seems to be bigger than the difference between line A and crossbreds.

This can be an important factor that results in decrease of the genetic correlation between purebreds and crossbreds. With within-line model, estimates of full-sib family variance for crossbreds were smaller than those for purebred, which may be due to the small number of crossbreds compared to pure lines.

Full-sib family variance estimates obtained using the crossbred model was slightly larger than those obtained from the within-line model. This shows that the more the number of records for crossbreds is, the more accurate the variance estimates are. Moreover, the dominance variance estimates obtained from the crossbred model were larger than those using the within-line model. This suggests that both the dominance variance and gene frequency difference in within line may be decrease at the same time if the generation of animals increases and the performances of purebreds and crossbreds are improved at the same time.

Table 3. Within-line estimates of variances for 35-day body weight.

Line	Additive variance	One-fourth Dominance variance	Residual variance	Phenotypic variance
A	8703	1690	25 759.79	36 152.79
B	8081	2916	24 799.47	35 796.47
C	2 (2877+2196)	1060	31 233.21	42 439.21

Table 4. Estimates of variances for 35-day body weight.

Line	Additive variance	One-fourth Dominance variance	Residual variance	Phenotypic variance
A	9237	1670	26 028	36 935
B	8699	3058	25 365	37 122
C	2 (3066+2370)	1211	31 015	43 398

Table 5. Heritabilities and Genetic Correlations.

Line	Within-Line model		Crossbred model		Genetic Correlation
	Heritability	Ratio of dominance Variances	Heritability	Ratio of dominance variances	
A	0.24	0.19	0.25	0.18	0.68
B	0.226	0.32	0.23	0.33	0.62
C	0.24	0.11	0.25	0.11	

3.2. Heritabilities and Genetic Correlations

Heritability estimates obtained from within-line and crossbred models, and estimates of genetic correlations between purebreds and crossbreds are given in Table 5. With within-line model the genetic correlations between purebreds and crossbreds set to 0. Heritability estimates obtained from the crossbred model were slightly higher than those obtained from within-line analyses.

In both models, heritability estimates for line A was the largest, as about 0.24 to 0.25 and heritability estimates for line B was about 0.22 to 0.23, which is similar to those reported in previous literatures [1, 4]. Heritability estimates for C was about 0.24 to 0.25.

Crossbreds seemed to be adapted better themselves for environment effects than purebreds. Nevertheless, the residual variance was about 5000 to 6000 and bigger for crossbreds than purebreds. It may be explained by the environment effects and the small of crossbreds compared to purebreds.

Thus, in joint evaluation of purebreds and crossbreds the reliability for crossbreds tends to decrease, so the purebred evaluation may be more suitable. We think that if the number of crossbreds increases and the environment for purebreds and crossbreds is well controlled, then the crossbred heritability estimates may possibly increases.

Although the genetic correlation for line A (0.68) is higher than for line B (0.62), it isn't as higher as in other literatures [1, 7]. This was already anticipated but had a certain similarity to the result from Wei et al. [15].

Hence, it is expected that the genetic correlation may increase when the main purpose of breeding is being the improvement of crossbred performance.

3.3. Reliability

The estimates of mean reliabilities are given in Tables 6 and 7. Mean reliabilities of predicted purebred breeding values from within-line model was clearly lower than from the crossbred model. For lines A and B, mean reliabilities for the crossbred model were 0.06 and 0.05 higher than those for within-line model, respectively. It may be because we took

into account the evaluations of crossbreds as well as purebreds themselves and the genetic correlation between purebreds and crossbreds.

For the within-line model, mean reliabilities of predicted crossbred breeding values were 0.64 for line A and 0.42 for line B. For the terminal-cross model, they were 0.69 and 0.44, respectively.

One can see that mean reliability for line A is much greater than one for line B. The reason may be because line A was used as sire line and line B was used as dam line.

Table 6. Mean Reliability of predicted purebred breeding values.

Model	Line A	Line B
Within-line	0.52	0.41
Crossbred	0.58	0.46

Table 7. Mean Reliability of predicted crossbred breeding values.

Model	Line A	Line B
Within-line	0.64	0.42
Crossbred	0.69	0.44

4. Conclusion

The use of the crossbred model by means of joint evaluation of purebreds and crossbreds gives us many benefits. Though the amount of data for crossbreds is smaller than one for purebreds, it would be of certain benefit to purebreds used as sire line. It may be of great significance because the affect of sire line is very important in broilers. Thus, when the breeding goals are to improve the proportion of additive effects of animals in crossbred origination from purebred parents and to increase genetic correlation between purebreds and crossbreds, the selection by crossbred model would be more suitable than within-line model.

In the future, we will investigate genetic parameter esti-

mation from genomic data of purebreds and crossbreds for various livestock using terminal crossbred model.

Abbreviations

BLUP Best Linear Unbiased Prediction
SD Standard Deviation

Acknowledgments

The authors would like to express their sincere thanks to the editor and the anonymous referees for their valuable comments concerning the paper.

Author Contributions

Doil Kim: Conceptualization, methodology, writing original draft

Yongho Kim and Namhyok Ryang: Data curation, software, validation

Uyon Paek: Writing original draft

Myonghak Pak: Writing-review-editing

Gyongsik Jon: Data curation, Investigation

Aehua Mun: Formal Analysis, Data curation

Funding

The authors declare that no funds, grants, or other support were received during the preparation of this manuscript.

Conflicts of Interest

The authors declare no conflicts of interest.

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