

Genetic Parameters for Growth-Related Traits in Korean Native Chicken

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ABSTRACT Body and carcass weights are always being main focus in poultry industry. The aim of current study was to estimate the heritability, genetic and phenotypic correlations of growth-related traits in Korean native chicken. A total of 596 chickens representing five lines of Korean native chicken (Black, Gray-Brown, Red-Brown, White, and Yellow-Brown) were reared under the standard breeding procedures in the National Institute of Animal Science (NIAS), Korea. Their body weights were observed every two weeks from hatched to 20 weeks of age. In addition, shank length and carcass weight were also measured before and after slaughter, respectively. The ASReml-R program was used to compute genetic parameters. The body weight traits were moderate to high heritability values (ranged 0.29~0.63). The heritabilities of carcass weight ($h^2=0.20$) and shank length ($h^2=0.20$) were categorized as moderate. Moreover, both genetic and phenotypic correlations were ranged from 0.62 to 0.99 and ranged from 0.42 to 0.98, respectively. These findings can be useful information for quantitative genetic studies and breeding plan of Korean native chicken.

(Key words: genetic parameters, growth-related trait, Korean native chicken)

INTRODUCTION

Due to the recent development of both broiler and layer industries are going rapidly, the many breeds of indigenous chicken are endangered or extinct. In Korea, there are some indigenous chicken breeds which are known as Korean native chicken (KNC). As a genetic resource, KNC has been started to be conserved in 1992 by collecting the native chickens from rural areas. In 1994, Korean Society of Poultry Science formally established the conservation project of these animals entitled "Restoration of Korean native chicken". Since then, National Institute of Animal Science (NIAS) intensively took over the breeding system by selecting the birds based on economically important quantitative traits such as growth-related traits. Nowadays, five lines of KNC are established and widely known in Korea. They are separated into five lines on the basis of plumage colors, representing black, gray, red, yellow, and white lines. One of commercial KNC which is launched

to the consumer is Woorimatdag chicken. In spite of slow growth rate, this chicken is preferred by the consumers due to its unique taste and meat quality than commercial broiler even though its price is more expensive (Lee et al., 2011).

However, the lack of uniformity in phenotypic performances of growth-related traits and cannibalism among them, are important issues in development of native chicken breed over the world. Therefore, appropriate breeding strategy is absolutely required to improve the performances of native chicken. The first step for developing meat-type native chicken breed is the selection of growth performance traits, for example body weight, carcass weight, shank length etc. These traits can be used to estimate genetic and phenotypic correlations, and also heritability. Reliable estimations of the genetic parameters are critical to choose the optimal breeding program among various breeding plans and to predict breeding values of candidates for selection (Gjerde and Schaeffer, 1989). In addition, Le Bihan-Duval et al. (1998) reported that high heritabilities

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of body weight and body composition traits have been observed in chicken, and the selection pressure of these traits has largely contributed in improving production traits of meat-type chicken. However, the estimation of genetic parameters for growth related traits has not been done extensively (Sang et al., 2006). The present study was conducted to estimate genetic parameters of growth related-traits in KNC.

MATERIALS AND METHODS

1. Animal and Phenotype

A within line crossing design was applied in this study. Particularly, a total of 88 parents (P) which is consisting 15 sires and 73 dams of five Korean native chicken lines was intercrossed to generate 596 offsprings (F₁). Then, these offspring were divided into five lines based on plum age colors consisting of black (90), gray-brown (110), red-brown (135), white (126), and yellow-brown (135) lines. And the F₁ offspring represented 68 full-sib families. We divided the experimental population into two batches. These birds in each batches were maintained under the standard breeding procedures for 22 weeks in the NIAS, Korea. All samples used in this experiment were reared under the same environment condition and feeding system. The body weight traits were measured every two weeks started from hatch until slaughter age at 22 weeks of age, and carcass weight was also weighed. Then, these data were used to describe the current status of both body and carcass weight traits in Korean native chicken, to figure out growth curves and other further analyses.

2. Statistical Analysis

Initially, the descriptive statistics were obtained from a general linear model (GLM) using Minitab version 14.0 (Minitab ZInc., USA) whether these data can be used for further analysis. The outlier data were detected and removed to improve the quality of the data, and the test for the normality of the distribution of observed traits was also carried out by the Ryan-Joiner method implemented in Minitab version 14.0 (Minitab Inc., USA). Heritability values of each trait were estimated with the following mixed-effects model using ASReml-R program (Gilmour et al., 1995):

$$y = Xb + Zu + e$$

where, y is a vector of the phenotypic values for body weight traits and carcass weight; b is a vector of fixed effects including sex, batch, line; u is a vector of additive polygenic effects; e is a vector of residual environmental effects; X , Z are incidence matrices for b and u respectively. The mean and variance for the residual environmental effect of individuals were assumed to be: $e \sim N(0, I\sigma_e^2)$, where I is the identity matrix and σ_e^2 is the residual variance. The mean and variance for additive polygenic effects can be defined as: $u \sim N(0, A\sigma_a^2)$, where A is the additive genetic relationship matrix computed from the F₁ pedigree in this study and σ_a^2 is the additive polygenic variance.

Additionally, correlations (r_{xy}) were estimated by:

$$r_{xy} = \frac{Cov(x, y)}{\sqrt{var(x) var(y)}}$$

where, r_{xy} is the estimate of the genetic and phenotypic correlation; $Cov(x, y)$ is the genetic and phenotypic covariance between a pair of traits x and y , and $var(x)$ and $var(y)$ are estimated genetic or phenotypic variances of traits x and y , respectively, using Minitab (Minitab, USA) for phenotypic correlation and ASReml-R for genetic correlation.

RESULTS AND DISCUSSION

1. Descriptive Analysis

An analyses of descriptive statistics for body and carcass weight traits tested in this study was presented in Table 1. The evaluation of normality was also performed to check whether the data can be used for further analyses. The method assesses normality by calculating the correlation between the observed data and expected data computed from the data with a normality assumption. Normality was accepted if the correlation coefficient is close to 1 (Shapiro and Wilk, 1965). The results showed that all traits observed followed normal distribution. The coefficient of correlation was ranged from 0.98 to 0.99 in all traits, and this value was higher when the test of normality distinguished by sex. These normality evaluation

Table 1. Descriptive statistics of growth-related traits in Korean native chicken

Trait	Mean	SD	Minimum	Maximum
BW2 (g)	143.89	24.71	78.00	208.00
BW4 (g)	265.92	70.47	100.00	455.00
BW6 (g)	426.84	130.96	155.00	715.00
BW8 (g)	607.66	195.47	150.00	1,030.00
BW10 (g)	768.27	222.64	250.00	1,305.00
BW12 (g)	992.90	278.1	365.00	1,670.00
BW14 (g)	1,181.00	297.6	450.00	1,920.00
BW16 (g)	1,383.10	337.2	470.00	2,155.00
BW18 (g)	1,587.70	347.1	555.00	2,430.00
BW20 (g)	1,780.90	372.1	625.00	2,675.00
CW (g)	999.32	240.06	340.00	1,688.00
SL (mm)	77.81	9.19	52.09	101.92

Abbreviation: BW2 is body weight at 2 weeks; BW4 is body weight at 4 weeks; BW6 is body weight at 6 weeks; BW8 is body weight at 8 weeks; BW10 is body weight at 10 weeks; BW12 is body weight at 12 weeks; BW14 is body weight at 14 weeks; BW16 is body weight at 16 weeks; BW18 is body weight at 18 weeks; BW20 is body weight at 20 weeks; SW is slaughter weight; CW is carcass weight; and SL is shank length.

emphasized that the data collected in present study was fairly representative of the Korean native chicken population and can be utilized for the breeding and genetic experiments.

2. Estimation of Genetic Parameters for Growth-related Traits

Heritability is the proportion of variance in a particular trait, in a particular population, that is due to genetic factors, as opposed to environmental influences (Falconer and Mackay, 1996). The heritability estimates for body weights, carcass weight, and shank length in Korean native chicken are presented in Table 2. Preston and Willis (1974) reported that heritability was regarded as small (low) if the value of heritability was varied from 0 to 0.2; moderate heritability was 0.2 to 0.4; and if the value was more than 0.4 classified as high heritability. The heritabilities of body weight traits were estimated as moderate to high in Korean native chicken. The heritability estimates (h^2) for body weight traits were ranged

Table 2. Heritability of growth-related traits

No.	Traits	Heritability (h^2)
1.	Body weight at 2 weeks	0.63
2.	Body weight at 4 weeks	0.56
3.	Body weight at 6 weeks	0.44
4.	Body weight at 8 weeks	0.45
5.	Body weight at 10 weeks	0.32
6.	Body weight at 12 weeks	0.39
7.	Body weight at 14 weeks	0.39
8.	Body weight at 16 weeks	0.31
9.	Body weight at 18 weeks	0.29
10.	Body weight at 22 weeks	0.29
11.	Carcass weight	0.20
12.	Shank length	0.20

from 0.29 to 0.63. The h^2 for carcass weight was 0.20 (moderate), and the h^2 for shank length was also 0.20 (moderate). The high heritability values of body weight traits, and moderate heritability values of carcass weight and shank length have been found in five lines of Korean native chicken population. These findings were quit similar with some other native chicken breeds that reported the heritability values of body weights ranged from 0.24 to 0.47 in Mazandaran native chicken, varied form 0.23 to 0.55 in Iranian native fowls, ranged from 0.15 to 0.40 in Horro chicken of Ethiopia, and around 0.3 to 0.5 in slow-growing lines chicken in France (Chabault et al., 2012; Dana et al., 2011; Ghazikhani Shad et al., 2007; Niknafs et al., 2012).

In term case of carcass weight, the heritability of carcass weight in KNC was categorized as low to moderate ($h^2=0.20$). This result indicated that carcass weight of Korean native chicken was more affected by environment factors even though genetic factor accounted for took part as 20%. Regarding the heritability of shank length of KNC, moderate heritability ($h^2=0.20$) was found. Previous study reported that heritability of shank length in random mating Broiler population was 0.35 (Gonzalez-Ceron et al., 2015). This different result may be due to different breed using in each experiment.

The genetic and phenotypic correlations between observed traits were ranged from 0.62 to 0.99 and 0.42 to 0.98, res-

pectively. The phenotypic and genetic correlations were gradually decreased between body weight traits whereas phenotypic and genetic correlations between carcass weight and body weight traits were gradually increased. Genetic and phenotypic correlations between shank length and body weight traits were varied from 0.62 to 0.82 and ranged from 0.42 to 0.77, respectively (Table 3). Previous findings reported that genetic correlation between shank length and body weight traits was varied from 0.40 to 0.64 while and phenotypic correlation between shank length and body weight traits was varied from 0.43 to 0.77 in broiler and layer populations (Gonzalez-Ceron et al., 2015; Tierce and Nordskog, 1985).

Since moderate to high heritability and genetic parameters were estimated, selection pressure for growth-related traits will be effective to improve KNC performances, especially for body weight, carcass weight and shank length. From this KNC population, expected genetic gains (ΔG) for body weight at 20 weeks, which is related with market age of KNC (Table 1, 2), were estimated given individual selection scheme (Table 4). Changing selection intensity is one of the major methods to manipulate the ΔG given a certain selection scheme like individual selection. Increased selection intensity can be achieved by reduced proportion of animals for breeding. Given a

Table 4. Expected genetic gain for BW20 estimated based on individual selection scheme

Selection rate	Selection intensity (<i>i</i>)	Phenotype SD (σ_p)	Heritability (h^2)	Expected genetic gain (ΔG)
0.50	0.798	272.1	0.29	86.1
0.10	1.755	372.1	0.29	189.4
0.05	2.063	372.1	0.29	222.6
0.01	2.665	372.1	0.29	287.6

$$\Delta G = i\sigma_p h^2.$$

period of time, changes in the selection intensities from 0.798 to 2.665 resulted in obvious ΔG changes (i.e., 86.1~287.6). However, application of strong selection intensity likely results in increase of inbreeding levels in the population. Therefore, selection intensity level should be chosen after full examinations of impact on both genetic gain and inbreeding.

In conclusion, heritability estimates of body weight traits, carcass weight, and shank length were moderate to high. Genetic and phenotypic correlations were also high between observed traits. These results can be useful as a consideration for selective breeding strategy to improve of growth-related

Table 3. Genetic and phenotypic correlations between growth-related traits

Trait	BW2	BW4	BW6	BW8	BW10	BW12	BW14	BW16	BW18	BW20	CW	SL
BW2	-	0.93	0.93	0.93	0.93	0.91	0.88	0.84	0.78	0.76	0.79	0.64
BW4	0.91	-	0.98	0.97	0.97	0.95	0.89	0.84	0.77	0.77	0.80	0.68
BW6	0.87	0.96	-	0.99	0.98	0.96	0.89	0.83	0.76	0.74	0.76	0.63
BW8	0.85	0.94	0.98	-	0.99	0.97	0.89	0.83	0.73	0.72	0.74	0.62
BW10	0.82	0.90	0.94	0.95	-	0.99	0.94	0.89	0.80	0.80	0.81	0.72
BW12	0.80	0.88	0.92	0.94	0.95	-	0.97	0.92	0.82	0.82	0.84	0.73
BW14	0.75	0.82	0.85	0.87	0.91	0.95	-	0.99	0.95	0.94	0.94	0.78
BW16	0.71	0.77	0.81	0.82	0.87	0.92	0.96	-	0.99	0.97	0.93	0.80
BW18	0.62	0.64	0.67	0.67	0.75	0.81	0.89	0.93	-	0.99	0.98	0.82
BW20	0.60	0.62	0.64	0.65	0.73	0.79	0.87	0.92	0.97	-	0.99	0.82
CW	0.60	0.62	0.64	0.65	0.74	0.79	0.86	0.89	0.93	0.95	-	0.79
SL	0.42	0.43	0.44	0.47	0.55	0.61	0.69	0.72	0.77	0.80	0.80	-

Genetic correlations are above the diagonal and phenotypic correlations are below the diagonal.

traits in Korean native chicken.

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