

GENETIC EVALUATION OF JUVENILE TRAITS TO ESTIMATE BREEDING VALUES IN SYNTHETIC COLORED BROILER MALE LINE (PB-1) BY FULL-SIB ANALYSIS

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ABSTRACT

The coloured synthetic broiler male line (PB-1) was under long-term intensive selection and was subjected to genetic parameters evaluation for the juvenile traits in the colored synthetic broiler male line (PB-1) during the S-29 generation. The heritability estimates of sire+dam component during the day-old, second, fourth, fifth and sixth week were 1.17 ± 0.15 , 0.53 ± 0.09 , 0.34 ± 0.08 , 0.34 ± 0.08 , and 0.38 ± 0.08 , respectively. The h^2 estimates for all components viz., sire, dam, sire+dam components for day-old body weight were higher than the subsequent body weight and the magnitude of the estimates decreases as the age advances. The conformational traits viz., shank length and keel length during the fifth weeks of age has moderate heritability and the sire+dam estimates were 0.27 ± 0.07 and 0.16 ± 0.06 , respectively. The conformational traits in the present study have higher heritability estimates for the dam components than the sire components indicating the presence of maternal influence during the juvenile stage. The genetic correlation of day-old body weights with other juvenile body weights and conformational traits were positive and moderate in magnitude for every component of variance except for the shank length which was positive and low in magnitude. The conformational traits had shown moderate to high genetic correlation with the juvenile body weights except for shank length with day-old body weight. The phenotypic association between the conformational traits viz., shank length and keel length were 0.680 which was positive and high in magnitude.

Keywords: Coloured broiler, Juvenile traits, Full-sib analysis, Genetic parameters

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The Indian poultry industry has turned a long way from a backyard enterprise to an organized commercial industry and it has emerged as a big hope, which provide employment and thereby livelihood security, in-addition to meeting the protein requirements of the nation. Indigenous chickens are also increasingly becoming important in niche markets, given their organic way of being raised and the acceptability of the birds with multi-colour feather pattern is better in rural areas due to aesthetic aspect, native look, cultural and religious reasons. The characteristics of a bird's growth and reproduction reveal its genetic make-up and degree of environmental adaptation. Genetic analysis of traits economically important in poultry has been used extensively in monitoring the genetic variability of each line, where the estimates of the genetic parameters are indispensable in establishing the selection programs. PB-1, coloured synthetic broiler male line was under long-term intensive selection which was used in the production of commercial hybrids, Krishibro which is an attractive multi-coloured and hardy meat type chicken. The present study has been conducted to evaluate the genetic parameters for the juvenile traits in the coloured synthetic broiler male line (PB-1) during the S-29 generation.

MATERIALS AND METHODS

The current study was conducted at Directorate of Poultry Research, Hyderabad, Telangana. The work was approved by the Institutional Animal Ethics Committee

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(IAEC/PDP/B-01). The pedigreed population under present study descended from 40 sires and 200 dams which were raised under uniform farm conditions. Two hatches of chicks were employed during the period of study. All the chicks were wing banded on day one and randomly distributed in separate pens. The experimental birds were intermingled by sex. The birds were housed in intensive system of management under deep litter with adequate floor space, feeding and waterer space according to their body weight and age. The chicks were brooded up to three weeks with a brooding space of 0.5 sq. ft./chick with the brooding temperature of maintained at 33°C.

Data collection: Fasting live weight of mixed sexes was recorded at day-old followed by bi-weekly intervals up to six weeks of age, in-addition during fifth weeks of age using a digital electronic balance nearest to 1.0 g accuracy and were presented in grams. Body linear measurements such as shank length (SL5) and keel length (KL5) were measured at the age of five weeks of age with electronic digital Vernier calipers (calibrated in mm) with an accuracy of 0.01 mm. The distance between the anterior end of keel bone and the point of keel was measured as keel length as described by Semakula *et al.* (2011). Shank length was measured as the length of the tarso-meta-tarsus from the hock joint to the meta-tarsal pad (toe) of the bird, which was an important attribute for any backyard poultry variety.

Full-sib analysis (ANOVA): The data adjusted for the hatch effects was used for the estimation of heritability.

Sex was not included as the fixed effects as the sexual dimorphism was observed from the fifth week onwards. The analysis of variance was done for various traits which includes body weights and conformational traits and the heritability estimates of sire, dam and sire+dam was obtained for respective traits. Heritability estimates for different parameters in PB-1 was made by variance component analysis (King and Henderson, 1954). The genetic and phenotypic correlations between different traits were estimated using variance and co-variance component analysis (Becker, 1975). The results obtained includes the phenotypic correlation, genetic correlation (sire, dam and sire+dam component) and the environmental correlation.

RESULTS AND DISCUSSION

Heritability (Full sib analysis, ANOVA): Heritability estimates of different body weights and conformational traits obtained using full-sib analysis were depicted in Table 1. The h^2 estimates for all components *viz.*, sire, dam, sire+dam components for day-old body weight were higher than the subsequent body weight and the magnitude of the estimates decreases as the age advances. The juvenile body weights shown high heritability estimates for dam components at different weeks of age and the estimates were higher for the day-old body weight when compared to the body weights at later stages of growth analogous with Padhi *et al.* (2015a). The heritability of sire component was high for day-old body weight and ranged from low to moderate values in subsequent weeks during the juvenile stage. Moderate to high estimate of the sire component was an indication that additive gene effects probably be higher than the non-additive component, whereas, low estimates observed might be due to non-additive genetic effects such as dominance and epistasis (Adeleke *et al.*, 2011) with less genetic variability relative to the phenotypic variability (Singh *et al.*, 2018).

The shank length for fifth weeks of age has moderate heritability estimates (0.27±0.07) in analogous with the reports by Padhi *et al.* (2012), whereas, the estimates were also moderate for keel length (0.16±0.06) in agreement with reports by Padhi *et al.* (2015b) and contrary to the reports by Adeyinka *et al.* (2006) in which they reported low estimates. The conformational traits in the present study have higher heritability estimates for the dam components than the sire components indicating the presence of maternal influence during the juvenile stage in line with the reports of Padhi *et al.* (2012).

The sire components estimate of the conformational traits were low in magnitude indicating the influence of non-additive genetic effect *viz.*, dominance, epistasis and environmental effects larger than the additive effects (Adeleke *et al.*, 2011). Further, the differences in heritability estimates also attributed to the method of estimation,

Table 1. Heritability estimates for juvenile traits by full-sib analysis

Traits	h^2_s	h^2_D	h^2_{S+D}
BW0	0.50±0.22	>1	>1
BW2	0.16±0.11	0.91±0.20	0.53±0.09
BW4	0.24±0.11	0.43±0.15	0.34±0.08
BW5	0.17±0.10	0.51±0.16	0.34±0.08
BW6	0.06±0.08	0.71±0.18	0.38±0.08
KL5	0.11±0.08	0.21±0.13	0.16±0.06
SL5	0.11±0.08	0.42±0.15	0.27±0.07

(BW0: Day old body weight, BW2: 2nd week body weight, BW4: 4th week body weight, BW5: 5th week body weight, BW6: 6th week body weight, SL5: 5th week shank length, KL5: 5th week Keel length)

Table 2. Genetic correlation between different juvenile traits by full-sib analysis

Traits	r_g (Sire)	r_g (Dam)	r_g (Sire+Dam)
BW0*BW2	0.51±0.34	0.45±0.11	0.46±0.13
BW0*BW4	0.40±0.29	0.36±0.16	0.37±0.18
BW0*BW5	0.51±0.32	0.33±0.15	0.37±0.18
BW0*BW6	0.59±0.59	0.29±0.13	0.32±0.17
BW0*SL5	0.17±0.42	0.43±0.16	0.38±0.16
BW0*KL5	0.45±0.35	0.59±0.23	0.55±0.20
BW2*BW4	1.06±0.15	0.75±0.10	0.80±0.27
BW2*BW5	1.06±0.18	0.71±0.10	0.77±0.24
BW2*BW6	>1	0.61±0.11	0.72±0.22
BW2*SL5	0.89±0.24	0.75±0.11	0.77±0.09
BW2*KL5	0.82±0.26	0.89±0.19	0.85±0.16
BW4*BW5	1.07±0.08	0.95±0.07	0.98±0.09
BW4*BW6	>1	0.84±0.10	0.88±0.08
BW4*SL5	0.97±0.15	0.88±0.10	0.89±0.22
BW4*KL5	1.06±0.15	0.91±0.19	0.97±0.28
BW5*BW6	>1	0.86±0.07	0.88±0.15
BW5*SL5	0.59±0.29	0.80±0.09	0.75±0.17
BW5*KL5	0.86±0.17	0.84±0.15	0.85±0.25
BW6*SL5	0.87±0.38	0.69±0.12	0.70±0.06
BW6*KL5	>1	0.72±0.20	0.75±0.07
KL5*SL5	0.58±0.33	0.94±0.15	0.83±0.09

(BW0: Day old body weight, BW2: 2nd week body weight, BW4: 4th week body weight, BW5: 5th week body weight, BW6: 6th week body weight, SL5: 5th week shank length, KL5: 5th week Keel length)

Table 3. Phenotypic correlation between the juvenile traits

	BW0	BW2	BW4	BW5	BW6	SL5	KL5
BW0	1						
BW2	.208	1					
BW4	.136	.698	1				
BW5	.142	.616	.757	1			
BW6	.116	.541	.639	.741	1		
SL5	.120	.589	.682	.784	.646	1	
KL5	.132	.515	.597	.710	.491	.680	1

(BW0: Day old body weight, BW2: 2nd week body weight, BW4: 4th week body weight, BW5: 5th week body weight, BW6: 6th week body weight, SL5: 5th week shank length, KL5: 5th week Keel length).

breed, environment effects and sampling error due to small data set or sample size (Padhi *et al.*, 2012). Environmental (high temperature and humidity) and poor management conditions are known to increase the residual variance and decrease the heritability estimates (Singh *et al.*, 2018).

Genetic correlation: Genetic correlation between the traits from sire, dam and sire+dam component of variance and co-variance components obtained using full-sib analysis were depicted in table 2. The genetic correlation of day-old body weights with other juvenile body weights and conformational traits were positive and moderate in magnitude for every component of variance except for the shank length which was positive and low in magnitude. The moderate positive genetic correlation was in contrary to Padhi *et al.* (2012), which might be due to the presence of additive genetic variation and the sire component had higher values than the dam component estimates. Similar to the present findings, strong genetic association for body weights with shank length (Haunshi *et al.*, 2012 and Rajkumar *et al.*, 2018) and keel length (Padhi *et al.*, 2015c) were also been reported. Padhi *et al.* (2012) observed the maternal influence on juvenile traits, as the dam component shown higher value than sire component and were true with our present study.

The genetic association between the conformational traits (SL5 and KL5) were high and positive as similar to the studies by Ibe (2013) and Padhi *et al.* (2015b) during the juvenile stages. The strong genetic association between the body weights and conformational traits is an indication of selection for the body weight will indirectly improve the conformational traits as a correlated response. Further, conformational traits such as shank and keel length can also be included in the selection criteria for the genetic improvement of the line, in addition to the fifth week body weight.

Phenotypic correlation: Phenotypic correlation obtained between various juvenile traits was depicted in the Table 3. Association between the body weights during the juvenile stage were moderate to high in magnitude except for day-old body weight. The correlation between the conformational traits *viz.*, shank length and keel length were 0.680 which was positive and high in magnitude.

The precise estimation of correlation coefficients helps the breeder in choosing the traits of significant positive association for simultaneous improvement of the traits. Rajkumar *et al.* (2012) and Mohammadi *et al.* (2018) opined that selection for one trait with positive correlation would improve the performance and the negative correlation reduces the performance in other traits. Hence, the positive association between these juvenile traits paves the way for consideration of them for future selection strategies, with which simultaneous improvement in the economic traits could be achieved.

CONCLUSION

The presence of maternal effects during the juvenile stages for body weights and the conformational traits has

been evident with the current study. The conformational traits have high positive genetic association with the juvenile body weights and hence the conformational traits can also be included in the selection criteria for the genetic improvement of the line.

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