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Genetics of body weights in a control line of Rhode Island Red grower chicken#

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A random-bred control line population of Rhode Island Red (RIR) chicken is being maintained at the Central Avian Research Institute (CARI, Izatnagar) since last few decades. Besides more egg production, optimum growth in body weights is also an important attribute to the farmers for promoting RIR in rural livelihood. It is necessary to have knowledge of factors influencing its growth in body weights, an important factor contributing to the profitability in poultry production (Kausar *et al.* 2016). It is also desirable to have estimates of genetic and phenotypic parameters afresh in each generation for each population, because the estimates vary from one population to another and at different times (Barot *et al.* 2008). Therefore, the present study aimed to investigate genetics of body weights in a control line of RIR grower chicken.

Chicks progeny (543) of 30 sires mated with 73 dams in first hatch and 70 dams in second hatch of RIR control line parental stock maintained at the experimental layer farm of this institute were investigated. The day-old chicks were wing-banded and pedigreed by sire and dam in the hatchery itself. Standard litter brooding, housing and *ad lib.* feeding on the CARI-formulated feed were provided with optimum management along with a standard vaccination schedule being followed at this institute (Das *et al.* 2014ab, Das 2013). The birds were fed on chick mash at the age of 0–8 weeks and grower mash at 9–20 weeks (Das *et al.* 2014a). The chick weight at day-old age and body weights at various weeks of age were measured in grams using digital weigh balance during morning at birds' empty stomach. The data were analyzed by least squares analysis of variance (Harvey 1990) taking sire as random effect, sex and hatch as fixed effects and chick weight as regressor in the linear models. The genetic and phenotypic parameters were estimated using paternal half-sib correlation method (Becker 1975).

The estimated least squares means along with different genetic and non-genetic factors of day-old chick weight and body weights at different ages are presented in Table 1. The present estimates might be compared to the earlier reports in RIR chicken lines/strains (Das *et al.* 2014ab, Das 2013, Anonymous 2011) and White Leghorn strains (Jayalaxmi *et al.* 2010, Chaudhary *et al.* 2009, Paleja *et al.* 2008). The least squares analysis of variance elucidates that male birds demonstrated better estimates of body weights than the females almost throughout the ages with significant sex-differences (Das *et al.* 2016, Das *et al.* 2015a, Das *et al.* 2014ab, Das 2013) indicating counter role of a genetic factor sex to control the growth of body mass. The sires of the chicks progeny had also significant variances for chick weight and body weights at different ages (excepting third week only) indicating that body mass growth is influenced by a factor of sire-inheritance (Debnath *et al.* 2015, Das *et al.* 2015ab, Das 2013). Hatch is considered as a non-genetic factor and the present results indicated highly significant hatch-differences (Das 2013) for chick weight and body weights up to 16th week of age also in corroboration with earlier reports (Debnath *et al.* 2015). The mean sum of squares of variance for regression on day-old chick weight was significant for body weights at first week onwards to 16th week of age indicating significant chick weight effect on the subsequent growth of the birds (Das 2013); results could indicate that body mass growth of the birds could be judged better by its day-old chick weights.

The heritability (h^2) estimates for chick weight and different body weights are presented in Table 2. The h^2 estimates ranged from 0.111±0.156 (BW3) to 0.999±0.235 (CW) with higher magnitudes for the most traits, indicating the possibility of selection based on the flock's own performance to improve these traits would take propagation of short generations for the concerned traits. The present estimates might be compared to the earlier reports in RIR (Das *et al.* 2015ab) and White Leghorn chicken (Qadri *et al.* 2013, Chaudhary *et al.* 2009, Barot *et al.* 2008, Paleja *et al.* 2008).

#Part of first author's Ph.D. thesis

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Table 1. Estimated least squares means along with different genetic and non-genetic factors of chick weight at day-old age and body weights at different ages in a control line of RIR grower chicken

Factor	Least squares means ± standard errors (g)									
	CW	BW1	BW2	BW3	BW4	BW6	BW8	BW12	BW16	BW20
Population means	34.29±0.40 (543)	51.85±0.64 (261)	82.07±0.91 (410)	139.70±1.61 (254)	170.00±1.87 (410)	269.68±3.94 (252)	397.34±6.65 (331)	725.12±12.51 (429)	1060.27±16.19 (410)	1180.29±13.57 (173)
Sex	ns	*	*	***	***	***	***	***	***	-
Male	34.27±0.42^{a} (300)	52.89±0.81^{a} (129)	83.95±1.114^{a} (228)	146.29±2.195^{a} (126)	176.79±2.26 (228)	284.12±5.19^{a} (124)	421.47±7.99^{a} (170)	775.85±14.24^{a} (234)	1172.30±18.56^{a} (228)	-
Female	34.31±0.43^{a} (243)	50.82±0.80^{b} (132)	80.20±1.218^{b} (182)	133.12±2.182^{b} (128)	163.21±2.46 (182)	255.23±5.13^{b} (128)	373.21±8.40^{b} (161)	674.39±14.97^{b} (195)	948.24±19.81^{b} (182)	1180.29±13.57 (173)
Hatch	***	-	***	-	***	-	***	***	***	ns
Hatch-1	33.58±0.42^{b} (282)		88.88±1.13^{a} (223)		177.83±2.30^{a} (223)		439.90±7.16^{a} (238)	820.15±14.34^{a} (232)	1125.93±18.78^{a} (223)	1175.11±16.25^{a} (101)
Hatch-2	34.99±0.43^{a} (261)		75.27±1.22^{b} (187)		162.17±2.46^{b} (187)		354.78±9.91^{b} (93)	630.08±15.03^{b} (197)	994.61±19.84^{b} (187)	1185.47±17.99^{a} (72)
Sire	***	**	*	ns	*	*	*	***	***	*
Regression on CW	-	**	*	***	***	***	***	***	***	ns

CW, day-old chick weight; BW, body weights at different weeks of age; *P≤0.05, **P≤0.01, ***P≤0.001; ns, nonsignificant; Means within a factor and same column having different superscripts differ significantly (P≤0.05); Figures within parenthesis denote number of observations.

Table 2. Estimated heritability (at diagonal), genotypic (above diagonal) and phenotypic (below diagonal) correlations of day-old chick weight and body weights at different ages in a control line of RIR chicken

Trait	CW	BW1	BW2	BW3	BW4	BW6	BW8	BW12	BW16	BW20
CW	0.999±0.235 (543)	0.550±0.231 (261)	0.387±0.322 (513)	0.506±0.446 (254)	0.687±0.220 (479)	0.198±0.438 (252)	0.176±0.393 (331)	0.057±0.264 (429)	0.032±0.284 (410)	0.406±0.320 (179)
BW1	0.246 (261)	0.465±0.215 (261)	0.626±0.372 (246)	0.751±0.430 (246)	-	0.483±0.621 (246)	0.262±0.768 (238)	-	0.362±0.624 (109)	0.274±01.225 (109)
BW2	0.135 (513)	0.339 (246)	0.117±0.091 (513)	1.078±0.137 (246)	0.439±0.473 (479)	0.628±0.544 (246)	0.643±0.467 (331)	0.140±0.386 (429)	0.296±0.403 (410)	2.211±59.951 (179)
BW3	0.346 (254)	0.324 (246)	0.846 (246)	0.111±0.156 (254)	-	0.093±0.930 (246)	0.252±1.153 (238)	-	0.434±0.958 (109)	1.881±4.196 (109)
BW4	0.264 (479)	0.209 (246)	0.240 (479)	0.634 (246)	0.190±0.111 (479)	-	0.684±0.446 (331)	0.457±0.279 (429)	0.602±0.252 (410)	1.047±01.339 (179)
BW6	0.202 (252)	0.107 (246)	0.480 (246)	0.548 (246)	0.346 (246)	0.142±0.163 (252)	1.374±0.948 (109)	-	1.315±1.128 (109)	0.340±1.679 (109)
BW8	0.278 (331)	0.188 (238)	0.305 (331)	0.539 (238)	0.485 (331)	0.693 (109)	0.128±0.128 (331)	0.993±0.116 (306)	0.829±0.268 (109)	1.478±01.730 (109)
BW12	0.221 (429)	0.118 (109)	0.098 (429)	0.193 (109)	0.382 (429)	0.195 (109)	0.814 (306)	0.358±0.152 (429)	1.029±0.039 (410)	1.439±1.079 (179)
BW16	0.237 (410)	0.207 (109)	0.105 (410)	0.385 (109)	0.411 (410)	0.506 (109)	0.736 (306)	0.840 (410)	0.291±0.142 (410)	1.108±0.075 (179)
BW20	0.169 (179)	0.103 (109)	0.205 (179)	0.052 (109)	0.352 (179)	0.020 (109)	0.104 (109)	0.637 (179)	0.865 (179)	0.443±0.266 (179)

CW, day-old chick weight; BW, body weights at different weeks of age; figures within parenthesis denote number of observations.

The lower magnitude of the present h^2 estimates indicated the presence of high environmental variances and its higher magnitude was indicative of greater role of additive genetic variance than the environmental component of variance (Rajkumar *et al.* 2011, Barot *et al.* 2008). The heritability estimates could vary considerably from study to study depending upon breed, strain, line, population sampled, environmental and management conditions, and random as well as systematic errors in the estimation procedures (Mia *et al.* 2013). The numbers of progeny per sire and the entire data set from which these estimates were obtained were relatively small, and could have sampling errors. However, the present h^2 estimates were in the expected range and could suggest for the breeders that the sire selection would be utilized for further genetic improvement in the body weight traits in RIR control line chicken.

The genetic (r_G) and phenotypic (r_P) correlation coefficients estimated from paternal half-sibs for chick weight and different body weigh traits were positive and ranged from low to high in magnitude (Table 2). The ranges of the estimated r_G and r_P in different traits were 0.057 to 0.993 (excluding >1 being beyond the absolute range) and 0.020 to 0.865, respectively, both with moderate to higher magnitudes for the most traits. Previously, similar kinds of genetic and phenotypic correlations were also reported in different chicken genotypes (Qadri *et al*. 2013, Rajkumar *et al.* 2011, Chaudhary *et al*. 2009, Barot *et al.* 2008, Paleja *et al.* 2008). Few estimates in this study were associated with higher standard errors (Qadri *et al.* 2013, Jayalaxmi *et al.* 2010, Barot *et al.* 2008) making them less precise which were due to less number of progeny per sire (Falconer 1989). However, the present performance traits demonstrating a low to high range of genetic and phenotypic correlations could be combined in a construct of standard selection indices and might be adopted in breeding strategy.

SUMMARY

Investigating a control line population of RIR grower chicken to estimate genetic and non-genetic parameters of its body weights, it was summarized that body weight growth is influenced by its sire-inheritance and sex where males being heavier throughout the ages. Significant hatch-differences and chick weight-regression effect were also noticed up to the age of 16th week. The heritability, genetic and phenotypic correlation estimates were mostly with moderate to high magnitudes. Thus the present findings could serve as the pre-requisites for chalking out of breeding strategies for genetic improvement of the chicken genotype.

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