Title	On the Linearity of Heritability and Genetic Correlation for Juvenile Body Weight and Weight Gain in Meat-type Chickens
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Citation	Journal of the Faculty of Agriculture, Hokkaido University, 59(4), 333-345
Issue Date	1980-03
Doc URL	http://hdl.handle.net/2115/12934
Type	bulletin (article)
File Information	59(4)_p333-345.pdf

ON THE LINEARITY OF HERITABILITY AND GENETIC CORRELATION FOR JUVENILE BODY WEIGHT AND WEIGHT GAIN IN MEAT-TYPE CHICKENS

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Received October, 29, 1979

Introduction

Accurate estimates of genetic parameters are essential for the construction of breeding programs. Hitherto, numerous estimates of heritability and genetic correlation and the results of selection experiments have been published for juvenile body weight and weight gain of chickens. In general, the genetic changes which were obtained in the selection experiments are in close agreement with the expected ones based on the estimates of genetic parameters. However, MALONEY *et al.*7) observed an asymmetrical response in a two-way selection for 12 week body weight. Conventional heritability and genetic correlation can be estimated from the variance and covariance components. However, the prediction based on these estimates offers little information on the asymmetry of genetic changes to selection in a different direction or at different intensities. Thus unequal responses may result from asymmetrical heritability and genetic correlation. ABPLANALP1) and later YAMADA14) gave a method for measuring asymmetry of genetic parameters by partioning the total selection differential into genetic and non-genetic selection components. Recently, HILL6) reviewed these methods of heritability estimation and simplified the formula. He also found that the method was slightly biased in small samples.

The objectives of this paper are to obtain linear estimates of heritability and genetic correlation and to evaluate possible asymmetry of selection response, for juvenile body weight and weight gain of chickens.

Materials

The data used in this study were from selected lines of chickens which had been selected for body weight at 9 weeks of age12). The number of

TABLE 1. Size of sample

Flock (generation number)	Year	Number of sire families	Number of dam families	Number of male chicks	Number of female chicks
0	1965	44	268	304	1,230
1	1966	24	96	116	544
2	1967	23	69	125	404
3	1968	16	70	118	514
4	1969	20	60	121	344
Total		127	563	784	3,036

birds, and the number of sire and dam families in each flock (generation) are listed in Table 1. All records of dam family with full-sib less than three chicks were excluded from the analysis for females.

The traits analyzed were body weight at 6 and 9 weeks of age, and weight gain from 6 to 9 weeks of age.

Statistical Methods

Test of Normality: The coefficient of skewness ($\sqrt{b_1}$) and kurtosis (b_2) were calculated to test the normality of frequency distribution for each trait (according to SNEDECOR and COCHRAN[13]).

Estimation of Heritability and Genetic Correlation: The population in each flock constitutes a nested model when each sire was mated to a number of dams and each dam produced a number of chicks. Because of the limitted size of male full-sib, male population was classified into the sire family alone.

Linear estimates of heritability and genetic correlation were calculated according to the procedure set forth by YAMADA[14]. Estimation of genetic correlation was made according to equation (16) of YAMADA[14] which was given by ABPLANALP[1], so that it is possible to measure asymmetry of the correlated response in double selection for each of the two traits. Four combinations of selection direction and intensity which were applied to calculate linear estimates, were as follows; the highest (top) were 25 per cent and 50 per cent, and the lowest (bottom) were 25 per cent and 50 per cent.

Heritability and genetic correlation were also estimated from the variance and covariance components by conventional methods, and compared with the corresponding linear estimates.

All analyses were made within the flock, and then overall averages of heritability and genetic correlation were calculated as the unweighted mean of the flock estimates.

Prediction of Genetic Changes: Expected genetic changes to selection when the genetic parameters are not always the same values between male and female, can be computed according to YAMADA and SCHEINBERG[15]. From equation (14) and (15) in their paper, the expected genetic changes in trait, m, of male progeny and in trait, f, of female progeny, when selection is done simultaneously for trait, M, in male parents and trait, F, in female parents, are expressed as follows;

$$\begin{aligned}\Delta G_{m(M,F)} &= \frac{1}{2}(i_M h_M r_{G_m G_M} + i_F h_F r_{G_m G_F})\, h_m \sigma_{P_m} \\ \Delta G_{f(M,F)} &= \frac{1}{2}(i_M h_M r_{G_f G_M} + i_F h_F r_{G_f G_F})\, h_f \sigma_{P_f}\end{aligned} \qquad (1)$$

In the above equations, $i_M(i_F)$ is the selection intensity of trait, $M(F)$ in male (female) parents, $h^2_M(h^2_F)$ is the heritability of a trait, $M(F)$ in male (female) parents, and $h^2_m(h^2_f)$ is the heritability of a trait, $m(f)$, in male (female) progeny. And r with subscripts are the genetic correlation coefficient between the corresponding traits (m, f, M and F), and $\sigma_{P_m}(\sigma_{P_f})$ is the phenotypic standard deviation of traits, $m(f)$ in male (female) progeny. In the same equation, the genetic correlation between male and female genotypes to express the same trait, is assumed to be unity. If $i_M = i_F = 1$, the expected genetic changes which are expressed in terms of standard devitation unit for each trait, are simplified as follows;

$$\begin{aligned}\Delta G'_{m(M,F)} &= \frac{1}{2}(h_M r_{G_m G_M} + h_F r_{G_m G_F})\, h_m \\ \Delta G'_{f(M,F)} &= \frac{1}{2}(h_M r_{G_f G_M} + h_F r_{G_f G_F})\, h_f\end{aligned} \qquad (2)$$

Examination of possible asymmetrical response to selection was conducted according to this equation (2).

Result

Flock Means and Patterns of Frequency Distribution: Flock (generation) means of body weight and weight gain are presented in Table 2, by sex. The figures show the variation in means of each trait among flocks, which was due to the effect of selection for body weight at 9 weeks of age and the yearly fluctuating environmenal effects[11,12].

Table 3 represents the coefficient of skewness ($\sqrt{b_1}$) and kurtosis (b_2) obtained for each flock. This shows that the frequency distributions are not always normal for three traits, since the value of $\sqrt{b_1}$ tended to be posi-

TABLE 2. Flock means of body weight and weight gain by sex (g)

Flock (generation)	6 week body weight		9 week body weight		Weight gain	
	Male	Female	Male	Female	Male	Female
0	507	433	945	780	438	345
1	620	491	1,085	796	465	306
2	595	504	1,048	921	454	417
3	721	607	1,326	1,060	605	453
4	609	520	1,083	932	474	412

TABLE 3. The coefficients of skewness $(\sqrt{b_1})$ and kurtosis (b_2)

Flock (generation)	6 week body weight		9 week body weight		Weight Gain	
	Skewness $(\sqrt{b_1})$	Kurtosis (b_2)	Skewness $(\sqrt{b_1})$	Kurtosis (b_2)	Skewness $(\sqrt{b_1})$	Kurtosis (b_2)
	Male					
0	0.02	2.86	0.06	2.68	0.12	3.65
1	0.77**	5.54**	0.19	3.60	0.04	2.63
2	0.10	3.43	0.20	3.16	0.34	4.19**
3	0.23	3.55	0.55**	4.81**	0.66**	5.19**
4	0.03	3.67	0.12	3.78**	0.08	3.95*
	Female					
0	0.00	3.33**	0.00	3.70**	0.01	7.01**
1	0.04	3.57**	0.07	3.13	0.35**	4.15**
2	0.03	3.15	0.02	3.66**	3.30**	5.04**
3	0.00	3.60**	0.00	3.45*	0.13	4.28**
4	0.06	3.73**	0.05	3.51*	1.49**	7.19**

** $P<0.01$, * $P<0.05$.

tive and a number of b_2 values were significantly greater than 3.00 especially for females. Weight gain shows a significant skew in more flocks than in body weights at two ages.

Heritability Estimates: Heritability estimates calculated from variance component and selection components are given in Table 4 with corresponding estimates averaged over flocks. Average heritability estimates from variance component were 0.60, 0.51 and 0.32 respectively for 6 week body weight, 9 week body weight and weight gain of male chicks. Corresponding estimates of female chicks were 0.40, 0.33 and 0.21. KINNEY and SCHOFFNER[8]

TABLE 4. Heritability estimates based on variance components and selection components

Generation	6 week body weight					9 week body weight					Weight gain				
	From variance component	From selection component				From variance component	From selection component				From variance component	From selection component			
		Top		Bottom			Top		Bottom			Top		Bottom	
		25%	50%	50%	25%		25%	50%	50%	25%		25%	50%	50%	25%
							Male								
0	0.51	0.82	0.47	0.50	0.65	0.33	0.56	0.40	0.44	0.33	0.81	0.45	0.27	0.27	0.25
1	0.47	1.01[b]	0.86	0.86	0.83	0.64	0.94	0.95	0.94	0.70	0.63	1.04[b]	0.72	0.73	0.42
2	0.64	1.19[b]	0.92	0.87	0.59	0.63	0.73	0.90	0.97	0.66	0.58	0.62	0.61	0.60	0.75
3	0.93	1.37[b]	1.31[b]	1.32[b]	0.98	0.82	1.53[b]	1.04[b]	1.04[b]	0.82	0.21	0.48	0.33	0.28	0.22
4	0.43	0.55	0.60	0.63	0.47	0.14	0.37	0.54	0.54	0.48	−0.15[a]	−0.15[a]	0.27	0.27	−0.09[a]
Average	0.60	0.87	0.77	0.77	0.70	0.51	0.72	0.76	0.78	0.60	0.32	0.51	0.44	0.43	0.33
							Female								
0	0.45	0.69	0.58	0.58	0.46	0.42	0.65	0.56	0.54	0.44	0.27	0.42	0.39	0.44	0.44
1	0.11	0.19	0.21	0.24	0.17	0.12	0.13	0.17	0.20	0.32	0.12	0.02	0.22	0.22	0.34
2	0.52	0.89	0.80	0.80	0.62	0.50	0.71	0.76	0.78	0.71	0.44	0.65	0.68	0.68	0.67
3	0.69	0.90	0.75	0.79	0.57	0.63	0.88	0.79	0.79	0.69	0.24	0.48	0.38	0.38	0.28
4	0.21	0.48	0.33	0.26	3.31	−0.02[a]	0.32	0.10	0.10	−0.02[a]	−0.06[a]	0.09	0.09	0.08	0.04
Average	0.40	0.63	0.53	0.53	0.43	0.33	0.54	0.48	0.48	0.43	0.21	0.33	0.35	0.36	0.35

[a] Treated as 0.0 in obtaining the average. [b] Treated as 1.0 in obtaining the average.

presented unweighted average estimates of heritability reported in literatures for juvenile body weight (4 to 12 weeks of age). The averaged estimates based on sire components of variance were 0.35 and 0.39 for male and females, and there was little difference between sex. The estimates for body weight of females at two ages which were obtained in this study, approximate these reported estimates. However, the estimates of male are somewhat larger than these values. The realized heritability of 9 week body weight which were obtained from the selection experiment used the same source as this study, were 0.22 and 0.36 respectively for male and female. It was shown that effective heritability to selection was smaller in male than in female. The differences between sex obtained in this study, might due to non-random error which was associated with the sample size and the different methods of estimation; they are, half-sib classification for male and full-sib classification for female.

Linear estimates from selection components were consistently larger than the estimates from variance components, for each trait in both sexes. This consistent tendency was clearly shown in separate flock estimates. Comparing the linear estimates of females which were based on the selection of different directions (upward and downward) and at different intensities (25 per cent and 50 per cent selection), the values when selection was done at the top 25 per cent were larger in number of flocks than the estimates in the other direction at different intensities, for body weight at two ages. And the estimates at the bottom 25 per cent were inversely lowest in all traits. However, the difference in estimates at different intensities and direction of selection were relatively small, for weight gain of female chicks. Large fluctuations in linear estimates of separate flocks of male chicks were observed among different intensities and direction of selection, that would be caused by a small size of population. In averaged estimates of male, it was shown that the values at the selection of the top 25 per cent were large and the values at the selection of the bottom 25 per cent were small for two traits of 6 week body weight and weight gain.

Although there were some variations among the heritability estimates by the two methods, the fluctuation of the values were simultaneous with male and female in the same way, except for the flock of generation 1. For instance, in the generation 2 and 3 when high heritability estimates were obtained for male body weight at 6 and 9 weeks of age by both methods, high estimates were also obtained for female chicks, and the estimates of generation 4 were low for 9 week body weight and weight gain in both sexes simultaneously. The fluctuation in estimates among flocks would due

TABLE 5. Estimates of genetic correlation for male chicks, based on variance-covariance component and selection component

Generation	From variance-covariance component	6 week body weight×9 week body weight							
		From selection component				From selection component			
		9 week body weight c)				6 week body weight c)			
		Top		Bottom		Top		Bottom	
		25%	50%	50%	25%	25%	50%	50%	25%
0	0.93	0.85	0.97	1.00	0.73	0.85	0.78	0.75	1.08[a]
1	0.96	0.84	0.83	0.82	0.79	0.87	0.99	0.98	1.20[a]
2	0.77	0.56	0.92	0.93	1.04[a]	1.04[a]	0.58	0.57	0.72
3	1.08[a]	1.11[a]	1.04[a]	1.03[a]	1.16[a]	0.92	1.09[a]	1.10[a]	1.12[a]
4	1.20[a]	1.13[a]	1.12[a]	1.10[a]	1.01[a]	1.09[a]	0.88	0.95	0.95
Average	0.93	0.85	0.94	0.95	0.90	0.93	0.85	0.85	0.93

Generation	From variance-covariance component	6 week body weight×weight gain							
		From selection component				From selection component			
		Weight gain c)				6 week body weight c)			
		Top		Bottom		Top		Bottom	
		25%	50%	50%	25%	25%	50%	50%	25%
0	0.61	0.88	0.83	0.82	0.16	0.38	0.43	0.41	0.56
1	0.86	0.45	0.86	0.80	1.01[a]	0.51	0.96	0.91	1.39[a]
2	0.03	0.31	0.21	0.10	0.90	0.49	0.06	0.05	0.25
3	1.53[a]	1.24[a]	1.48[a]	1.60[a]	1.12[a]	1.14[a]	1.32[a]	1.44[a]	1.57[a]
4	0.00[b]	0.00[b]	1.31[a]	1.28[a]	0.00[b]	0.00[b]	0.74	0.86	0.00[b]
Average	0.69	0.66	0.78	0.74	0.77	0.60	0.64	0.65	0.73

Generation	From variance-covariance component	9 week body weight×weight gain							
		From selection component				From selection component			
		Weight gain c)				9 week body weight c)			
		Top		Bottom		Top		Bottom	
		25%	50%	50%	25%	25%	50%	50%	25%
0	0.86	1.11[a]	0.97	0.94	0.65	0.83	0.90	0.93	0.87
1	0.97	0.87	0.94	0.92	1.04[a]	0.87	1.15[a]	1.14[a]	1.21[a]
2	0.84	0.86	0.69	0.10	1.22[a]	0.93	0.83	0.92	0.60
3	1.18[a]	0.98	1.23[a]	1.28[a]	0.98	1.22[a]	1.04[a]	1.13[a]	0.99
4	0.00[b]	0.00[b]	1.17[a]	1.17[a]	0.00[b]	0.00[b]	0.85	0.85	0.00[b]
Average	0.92	0.93	0.92	0.79	0.91	0.91	0.92	0.94	0.87

a Treated as 1.00 in obtaining the average. b Estimate between the traits which the heritability are negative is not included in average.

c) Stand for the selected trait.

TABLE 6. Estimates of genetic correlation for female chicks, based on variance-covariance component and selection component

Generation	From variance-covariance component	6 week body weight×9 week body weight							
		From selection component							
		9 week body weight[c)]				6 week body weight[c)]			
		Top		Bottom		Top		Bottom	
		25%	50%	50%	25%	25%	50%	50%	25%
0	0.97	0.95	0.94	0.97	0.99	0.96	0.95	0.95	0.90
1	0.77	0.48	0.69	0.66	1.32[a]	1.36[a]	0.95	1.05[a]	0.65
2	0.83	0.87	0.73	0.74	0.83	0.85	0.82	0.81	0.88
3	0.98	1.01[a]	0.96	0.93	1.01[a]	0.96	0.95	0.92	0.82
4	0.00[b]	0.94	0.53	0.64	0.00[b]	0.68	0.95	0.57	0.00[b]
Average	0.89	0.85	0.77	0.79	0.96	0.89	0.92	0.85	0.81

Generation	From variance-covaraince component	6 week body weight×weight gain							
		From selection component							
		Weight gain[c)]				6 week body weight[c)]			
		Top		Bottom		Top		Bottom	
		25%	50%	50%	25%	25%	50%	50%	25%
0	0.84	0.87	0.73	0.78	0.88	0.83	0.77	0.71	0.56
1	0.30	−1.00	0.46	0.45	0.93	2.73[a]	0.44	0.61	0.35
2	0.33	0.38	0.38	0.38	0.25	0.26	0.32	0.32	0.50
3	0.86	1.14[a]	0.79	0.77	0.79	0.75	0.81	0.70	0.66
4	0.00[b]	0.63	−0.29	−0.43	−0.26	0.08	−0.07	−0.48	−1.36[a]
Average	0.58	0.38	0.41	0.39	0.52	0.58	0.45	0.37	0.21

Generation	From variance-covariance component	9 week body weight×weight gain							
		From selection component							
		Weight gain[c)]				9 week body weight[c)]			
		Top		Bottom		Top		Bottom	
		25%	50%	50%	25%	25%	50%	50%	25%
0	0.95	0.97	0.90	0.97	1.08[a]	0.97	0.95	0.84	0.75
1	0.84	−0.45	1.02[a]	0.96	1.05[a]	2.71[a]	0.78	0.86	0.68
2	0.80	0.86	0.83	0.82	0.75	0.68	0.92	0.92	0.87
3	0.94	1.16[a]	0.89	0.89	0.83	0.82	1.00	1.01[a]	1.11[a]
4	0.00[b]	0.77	0.34	−0.24	0.00[b]	1.10[a]	0.76	0.74	0.00[b]
Average	0.88	0.63	0.79	0.68	0.90	0.89	0.88	0.87	0.83

a, b, c) see the footnote in TABLE 5.

to the effect associated with variation of average means rather than the random effect.

Estimates of genetic Correlation: Table 5 and 6 list the estimates of genetic correlation among three traits that were calculated from variance components and selection components, for male and female chicks respectively. The coefficient estimates for each flock based on selection components at the top 50 per cent and at the bottom 50 per cent were relatively in good aggreement with estimates from the variance and covariance components, for both sexes, although the male estimates showed more fluctuations than the female estimates. When the top 25 per sent or the bottom 25 per cent were selected, the estimates were more eratic. The results would due to the small number of selected chicks in those selection. Averaged estimates of linear genetic correlation were independent of direction and intensity of selection, and approximated the estimates from variance and covariance components, except for the estimates between 6 week body weight and weight gain of female chicks. The averaged genetic correlation estimates between these traits when selection was done on at the bottom 25 per cent of 6 week body weight (0.21), was smaller than the estimate when weight gain was selected and other estimates, and asymmetry of the genetic correlation was observed. However, this asymmetry might caused by the limited number of selected chicks, because the estimate from the flock of generation 4 was −1.36.

Expected Direct Genetic Changes to Selection: Table 7 represents the expected genetic change to selection for each of three traits, which were predicted by using five sets of average estimates (in Table 4). In this table, the amount of genetic changes were calculated, according to equation (2). The best genetic gain for 6 week body weight could be achieved by

TABLE 7. Expected genetic change when selection was done to different direction and at different intensity. The figures are expressed in terms of standerd deviation unit per one unit of selection intensity

Traits	Predicted by using following estimates;				
	Variance component	Selection component			
		Top		Bottom	
		25%	50%	50%	25%
6 week body weight	0.49	0.75	0.64	−0.65	−0.57
9 week body weight	0.42	0.63	0.61	−0.63	−0.51
Weight gain	0.26	0.42	0.40	−0.40	−0.34

selecting the top 25 per cent and the least change could be achieved by selecting the bottom 25 per cent. For 9 week body weight and weight gain, the least genetic change could be predicted when the selection was done for the bottom 25 per cent, and little difference in change among other three cases of selection were seen. It is shown that strong selection (25 per cent) for decreased juvenile body weight and weight gain might produce a smaller genetic change than a somewhat lesser intense selection (50 per cent) and selection for increased weight. The same results might be predicted from the flock to flock estimates of heritability. Expected genetic change based on the heritability estimates from the variance component, were consistently less than the changes on the selection component for each of the three traits.

Expected Correlated Response to Selection: Expected correlated response when selection was done on its genetically correlated traits, are expressed in terms of standard deviation units according to equation (2). The averaged responses over male and female progenies are listed in Table 8. When the two correlated traits are simultaneously selected in the same direction and in the same intensity in separate flocks, no consistent asymmetry of expected responses are discernible from this table. The correlated response when the selection was done in a different direction or at different intensity, shows the same trend as the response to the direct selection. However, the asymmetry in correlated responses are less than in direct responses. The expected genetic changes which were calculated by using the estimate of genetic parameters from selection components, are consistently larger than the corresponding genetic changes from the variance and covariance components, in a number of cases.

TABLE 8. Expected correlated response to selection. The figures are expressed in terms of standard deviation unit per one unit of selection intensity

	Expected correlated response					
Correlated traits;	9 w. body wt.	6 w. body wt.	6 w. body wt.	Weight gain	9 w. body wt.	Weight gain
Selection for;	6 w. body wt.	9 w. body wt.	Weight gain	6 w. body wt.	6 w. body wt.	9 w. body wt.
Variance-covariance component	0.42	0.42	0.23	0.23	0.30	0.30
Top 25%	0.63	0.58	0.33	0.30	0.46	0.41
Top 50%	0.56	0.54	0.28	0.31	0.45	0.42
Bottom 50%	−0.57	−0.56	−0.27	−0.29	−0.45	−0.37
Bottom 25%	−0.47	−0.49	−0.22	−0.28	−0.36	−0.38

Discussion

The frequency distributions are not always normal for three traits of body weight and weight gain, since data consistently showed positive skewness and significant leptokurtosis. It has been widely assumed that production traits in animal and poultry are normally distributed, but this has seldom been examined. CLAYTON[3] reported significant negative skewness and leptokurtosis for egg production in four control strains of egg laying chickens. Negative skewness was considered to more likely due to non-random environmental factors than fixation of recessive genes. In this study, data showed positive skenwess. This implies an excess of individuals at the upper tail of the distribution curve. In an examination of the hatch by the sire interaction effect which was conducted on the same strain as in this study and other two strains, significant interaction effects were observed in juvenile body weight and weight gain[10]. However, all data were corrected for the hatch effect by adding the differences between the mean of the hatch of the control strain. This correction method and its interaction effects may be a possible cause for the positive skewness and may also be a cause of leptokurtosis.

For all three traits of juvenile body weight and weight gain which were studied in this paper, asymmetry of response to different direction of selection was expected from linear estimates of heritability, when selection was done at an intensity of 25 per cent. The pattern of asymmetry were in the same manner as realized for 12 week body weight of chickens by MALONEY *et al*[7].

FALCONER[4] reported that the asymmetrical response to selection for 6 week body weight of mice exsisted, and that the selection for large size was less than the selection for its small size. He concluded that the cause of asymmetry for body size of mice were the directional dominance, inbreeding depression and maternal effect. FALCONER[5] also discussed the possible cause of the asymmetrical response to selection and added other causes as follows; (1) different selection differential, (2) genetic asymmetry (directional dominance and directional gene frequency) and (3) selection for heterozygotes. A significant inbreeding depression was detected for body weight at 6 and 9 weeks of age, in the same strain as used in this study[11]. In the same paper, weight gain tended to decrease as the inbreeding coefficient increased, although the amount was not significant. However, asymmetrical response expected in this study of chickens is the opposite from the pattern of the mice[4]. Therefore, it seems that asymmetry in chickens would not be caused by the inbreeding depression and directional dominance.

In a statistical study of butterfat records of dairy cattle which was made by BREADSLEY *et al*[2], the heritability estimates on the basis of curvilinear regression gave the values decreasing with increased butterfat yield. The possible explanation was that non-additive genetic and gene-environmental action seems to be the more likely factors. NISHIDA and ABE[9] showed that in some cases the skewness of frequency distribution was a cause of curvilinearity in heritability.

In this study, the linear estimates of heritability when selection was done at the top 25 per cent were the largest value among four estimates, and the estimates at the bottom 25 per cent were inversely lowest. This pattern of heritability, corresponds to the upward concave shape of heritability prepared by NISHIDA and ABE[9] (Regression no 2 and 4 in Fig. 2). According to the results examinated by them, asymmetry of linear heritability for juvenile body weight and weight gain in this study were considered to be due likely to skewness of the gene effect toward low values.

Summary

An analysis was conducted to measure the linear estimates of heritability and genetic correlations for body weight at 6 weeks of age and at 9 weeks of age, and weight gain from 6 to 9 weeks of age, by using the records of a selected strain.

Asymmetrical estimates of heritability when selection was done in different direction, were observed for male and female body weight at 6 and 9 weeks of age. These linear estimates from selection components tended to be larger than the estimates from variance components. Results for weight gain of male chicks showed the same trend as in body weight. However, no asymmetrical estimates of linear heritability was observed for weight gain of female chicks, when the selection was conducted in a different direction and at a different intensity.

There is no difference among linear estimates of genetic correlation when selections were made for different traits, in different directions and at different intensity of selection, and these estimates were in good agreement with the corresponding estimates derived from variance and covariance components.

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