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ESTIMATION OF VARIANCE COMPONENTS AND HERITABILITIES FOR GROWTH TRAITS IN THE EGYPTIAN DOKKI-4 CHICKENS USING ANIMAL MODELS

BY

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ABSTRACT

Post-hatching growth traits of 7226 chick of Dokki-4 (as a native breed) were genetically evaluated. Records of individual body weight (**BW**) at hatch and biweekly thereafter up to 16 weeks of age were collected in two generations. Data of daily gain (**DG**) between intervals of hatch-4, 4-8, 8-12 and 12-16 weeks were also used. Variance components and heritability estimates for these growth traits were estimated using **DFREML** procedure of single-trait (**SAM**) and multi-trait (**MAM**) animal models. Percentages of direct additive genetic variance (σ^2_A). for **BW** traits estimated by the **MAM** appeared to be higher than those estimated by the **SAM**. The percentages of σ^2_A for **BW** traits ranged from 6.0 to 19.9% when using the **SAM** and from 9.6 to 17.8% when using the **MAM**. The percentages of common environmental variance (σ^2_c) for **BW** traits obtained by the **MAM** were higher (averaged 22.0%) than those obtained by **SAM** (averaged 17.4%). Little differences were observed in estimation of σ^2_c between the **SAM** and **MAM** for analysis **DG** traits. Generally, estimates of heritability based on direct additive single-trait (h^2_{AS}) and multi-trait (h^2_{AM}) animal models for all growth traits were low or relatively moderate. Estimates of heritability for **BW** traits resulting from **MAM** were somewhat larger (h^2_{AM} ranged from 0.10 to 0.18) than those obtained by **SAM** analysis (h^2_{AS} ranged from 0.06 to 0.20). Most of the genetic correlations (**r$_G$**) among growth traits at different ages were high and averaged 0.52 among **BW** traits and 0.25 among **DG** traits. All estimates of common environmental correlation (**r$_c$**) among **BW** traits and among **DG** traits were positive and with moderate or high magnitudes.

Estimates of environmental (r_E) and phenotypic (r_P) correlations among **BW** traits and among **DG** traits were positive and generally moderate or high.

INTRODUCTION

Little information is available on the estimation of genetic parameters in broilers of chickens using single- and multi-trait animal models. Also, the native breeds like Fayoumi and Baladi are not evaluated genetically by applying single- and multi-trait Animal Models. Besbes *et al.* (1992) and Mrode (1996) reported that applying multi-trait animal model in estimation of variance components and heritabilities is nowadays utilized in many countries all-over the world for various domestic species. Surprisingly, these methods are almost ignored in poultry evaluation systems even though strong selection has been carried out on this species for many generations. Dokki-4 as a native Egyptian breed has superior meat qualities compared to other local breeds such as Fayoumi and White Baladi since this breed is characterized by white skin and shanks. Moreover, its meat has an acceptable taste for the majority of the Egyptian consumers (Abd El-Gawad, 1969).

In an attempt to achieve the maximum economic return for local meat-type chickens in Egypt, the present study was carried out to characterize the Egyptian Dokki-4 chickens in terms of direct additive genetic, common environment, phenotypic variances and heritability estimates for body weight and daily gain traits by applying two animal models.

MATERIAL AND METHODS

Experiment

A native breed named Dokki-4 was used in this study. This work was carried out in the Poultry Research farm at Inshas (Sharkia Governorate) on Dokki-4 chickens. This farm belongs to Animal and Poultry Production Research Institute, Ministry of Agriculture, Egypt. Dokki-4 was developed by crossing between Fayoumi males as a native breed and Barred Plymouth Rock females as a exotic breed together with selection (El-Itriby and Sayed, 1966). The experimental work was carried for two consecutive generations started in 1989. A total number of 7226 chicks of Dokki-4 chickens were used[J1]. Data of individual body weight (**BW**) at hatch and biweekly thereafter up to 16 weeks of age were collected on all individuals of the two generations. Daily gains (**DG**) between intervals of hatch-4, 4-8, 8-12 and 12-16 weeks were also computed. Distribution of the records according to the numbers of progeny per sire and dam in the two generations is presented in Table 1. All chicks of one-day old were wing-banded and reared in a floor brooder, then transferred to the rearing houses. Chicks were fed during the rearing and growing periods on diet containing 20.4% and 16% crude protein, 3.2% and 3.9% crude fiber, 3.7% and 4.3% fat and 3200 and 2997 metabolizable energy kcal/kg, respectively. All birds were treated and medicated similarly throughout the experimental period and they were raised under the same managerial and environmental conditions.

Table 1. Distribution of the records according to the number of progeny per sire and dam in the two generations

Distribution of sires				Distribution of dams			
Sire group	No. of sires	Total No. progeny	% of progeny	**Dam group**	No. of dams	Total No. progeny	% of progeny
First generation:				**First generation:**			
Sires with				Dams with			
<95 progeny	2	184	5	>4 to <10 progeny	73	545	13
$\geq$ 95 to <110 progeny	7	734	18	$\geq$10 to < 20 progeny	243	3326	83
>110 progeny	25	3102	77	>20 progeny	9	149	4
Total of the first generation	34	4020	100	**Total of the first generation**	325	4020	100
Second generation:				**Second generation:**			
Sires with				Dams with			
<95 progeny	15	1201	38	>4 to <10 progeny	141	1047	33
$\geq$ 95 to <110 progeny	15	1650	51	$\geq$10 to < 20 progeny	185	2140	67
>110 progeny	3	355	11	>20 progeny	1	19	0
Total of the second generation	33	3206	100	Total of the second generation	327	3206	100
Total of the two generations	67	7226		Total of the two generations	652	7226	

Single- and Multi-Trait Animal Models

Single- and multi-traits animal models were used in analysing data of growth traits using **MTDFREML** procedure. Starting values of variance components to be used in animal models' analyses were estimated using **REML** procedure of **SAS' procedure** Guide (SAS, 1996).

The single-trait Animal Model in matrix notation used was:

$$\mathbf{y = Xb + Z_a u_a + Z_c u_c + e}$$

Where y = vector of observed body weight or weight gain of birds, b = vector of fixed effects of generation and sex, u_a = vector of random effect of animal (chick); u_c = random common environment of dam family; Z_a and Z_c are the incidence matrices relating records to the additive genetic effects and random common environmental effects of dam, respectively. Both X and Z are termed incidence matrices.

The variances of random effects of animal (chick), common environment and error were:

$$V\begin{bmatrix} y \\ u_a \\ u_c \\ e \end{bmatrix} = \begin{bmatrix} v & Z_aG_a' & Z_cG_c' & R \\ G_aZ_a' & G_a & 0 & 0 \\ G_cZ_c' & 0 & G_c & 0 \\ R & 0 & 0 & R \end{bmatrix}$$

Where $v = Z_a G_a Z_a' + Z_c G_c Z_c' + R$, $G_a = A\sigma^2_a$; σ^2_a= additive genetic variance of the animal (chick), $G_c = I_c\sigma^2_c$; σ^2_c= common environmental variance and $R = I_n\sigma^2_e$; σ^2_e= error variance, **A** is the numerator relationship matrix for animals (chicks), I_c is an identity matrix corresponding to levels of common environmental effects and I_n is an identity matrix corresponding to n observations.

The model for a multivariate analysis resembles a stack of the single-trait animal model for each trait. In the present study, the mixed model equations (**MME**) will be too large when we have more than two traits (e.g. 5 traits for body weights and 4 traits for daily gains). Variance and covariance components of the animal model for body weight (**BW**) and daily gain (**DG**) at different ages were estimated using multi-traits derivative-free algorithm restricted maximum likelihood (**MTDFREML**). Variances and co-variances for single- and multi-trait animal models were calculated using the **MTDFREML** program (Boldman *et al.*, 1995). Convergence rate was assumed when the variance of the log-likelihood values in the simplex reached $<10^{-6}$. Inbreeding coefficients for progeny, sires and dams were calculated using **MTDFREML** program of Boldman *et al.* (1995). Pedigree information was used as far as it exited. Consequently, the number of inbred chicks was 210 with an average inbreeding coefficient of 0.153.

Estimation Of Heritability and Correlations

Heritabilities for growth traits were computed from variance components as:

$$h^2_A = \frac{\sigma^2_a}{\sigma^2_a + \sigma^2_c + \sigma^2_e}$$

Where σ^2_a, σ^2_c and σ^2_e are variances due to the effects of direct additive genetic, common environment and random error, respectively.

Multivariate analysis was used to calculate genetic (r_G), common environmental (r_c), environmental (r_E) and phenotypic (r_P) correlations among growth traits. The general formula (Boldman *et al.*, 1995) used to calculate the additive genetic (r_g), common environment (r_c), environmental (r_e) and phenotypic (r_p) correlations between growth traits was:

$$r_{xy} = \frac{Cov(x)_{ij}}{\sqrt{(var\ x_{ii})(var\ x_{jj})}}$$

Where $Cov(x)_{ij}$ = the additive genetic (*a*), common environmental (*c*), environmental (*e*) or phenotypic (*p*) covariances between the first and second trait; $varx_{ii}$ and $varx_{jj}$= the additive genetic (*a*), common environmental (*c*), environmental (*e*) or phenotypic (*p*) variances of the first and the second trait, respectively. According to Meyer (1993), the standard errors of heritability and genetic correlations, estimated using the animal models, were not computed.

RESULTS AND DISCUSSION

Means and Variations

Means, phenotypic standard deviations (**SD**) and coefficients of variability (**V%**) characterising body weights (**BW**) and daily gains (**DG**) in Dokki-4 chickens are given in Table 2. Body weight means of Dokki-4 chickens generally fall within the range of those estimates obtained for the same breed by most of the Egyptian studies (Khalil *et al.*, 1993 and others). Some of the reviewed studies on Fayoumi, White Baladi and Dandarawi showed that body weight at hatch, 4, 8 and 12 weeks of age were lower in means than for Dokki-4 chickens of the present study (e.g. Abd El-Gawad and El-Ibiary, 1971; Ismail, 1980; others). Generally, the estimates of V% for growth traits in Dokki-4 chickens, which ranged from 9.7 to 32.0%, are relatively high compared to those of the other local breeds (e.g. Fayoumi, White Baladi, Alexandria and Mamourah), which ranged from 8.6 to 27.5%. Consequently improvement of growth rate in Dokki-4 chicks through phenotypic selection might be quite possible.

Table (2): Means, standard deviations (SD) and percentages of variability (V%) for body weights and daily gains at different ages in Egyptian Dokki-4 chickens.

Trait	Symbol	No.	Mean	SD	V%
Body weight (grams):					
Hatch weight	BW0	7226	31.6	3.1	9.7
2-Week weight	BW2	6858	75.9	11.9	15.7
4-Week weight	BW4	6594	167.9	28.3	16.8
6-Week weight	BW6	6421	295.4	55.4	18.7
8-Week weight	BW8	6156	428.3	72.7	17.0
10-Week weight	BW10	5919	568.5	93.9	16.5
12-Week weight	BW12	5645	744.2	130.6	17.6
16-Week weight	BW16	4975	1052.8	186.1	17.7
Daily gain (grams):					
0-4 Weeks	DG4	6594	9.8	2.0	20.4
4-8 Weeks	DG8	6156	18.5	4.3	23.0
8-12 Weeks	DG12	5645	22.4	6.5	29.1
12-16 Weeks	DG16	4975	21.7	7.0	32.0

Generation Effect

Means and standard errors (SE) for body weights (**BW**) and daily gains (**DG**) in the two generations demonstrated that **BW** of chicks at different ages were significantly ($P<0.01$) heavier in the first generation than that of the second one at 2, 4 and 16 weeks of age. Similarly, Dunnington and Siegel (1996) reported that generation effect on growth traits of chickens was highly significant ($P<0.01$). Means of **DG** in the first generation were significantly ($P<0.01$) higher than those obtained in the second generation (except during the intervals of 4-8 and 8-12 weeks of age). Slight superiority of the first generation relative to the second generation for growth traits may be due to that the numbers of progeny and sires in the first generation were higher than that in the second generation (Table 1). The same interpretation was represented by Hagger (1991).

Estimation Of Variance Components

Estimates of direct additive genetic (σ^2_A), common environmental σ^2_c) and predicted error variance (PEV or σ^2_e) components obtained by **DFREML** method using **SAM** and **MAM** are presented in Tables 3 and 4.

Percentages of direct additive genetic variance (σ^2_A) for all studied growth traits using **SAM** were low or moderate (Table 3). The percentages of σ^2_A relative to total phenotypic variance ranged from 11.9 to 19.9% for growth traits at early ages and from 5.0 to 9.3% for the same traits measured at later ages (Table 3). These percentages are lower than those obtained by Danbaro *et al.* (1995), Koerhuis and Mckay (1996) and Kuhlers and McDaniel (1996) for different breeds of chickens.

In multi-trait animal model (**MAM**), the percentages of additive genetic variance (σ^2_A) ranged from 9.6 to 17.8% and from 4.9 to 10.1% for **BW** and **DG** traits, respectively (Table 4). Results of Koerhius and Mckay (1996) in juvenile broiler based on bivariate animal model were higher than that obtained for 4-week body weight (16.0%) in the present study. On the other hand, results in the present study are in agreement with findings of Danbaro *et al.* (1995) for White Plymouth Rock chickens.

For comparison between **SAM** and **MAM** in estimation of direct additive genetic variance, percentages of σ^2_A for **BW** traits estimated by the **MAM** appeared generally to be higher than those resulting from the **SAM** (Tables 3 & 4). The estimates ranged from 9.6 to 17.8% (averaged 13.9%) based on **MAM**, while they ranged from 6.0 to 19.9% (averaged 11.2%) based on **SAM** for **BW** traits. Based on **MAM**, the percentages of σ^2_A were increased by 2.1, 1.6, 5.0 and 6.9% than the corresponding percentages obtained by **SAM** for

BW at 4, 8, 12 and 16 weeks of age, respectively. Koerhuis and Mckay (1996) came to the same conclusion for 6-week body weight. Higher additive genetic variance (σ^2_A) obtained by **MAM** relative to **SAM** may be due to that extra information on correlated traits existed (i.e. covariances among traits were considered).

Table (3): Estimates of direct additive (σ^2_A), common environmental (σ^2_C), predicted error (PEV or σ^2_e) and total phenotypic (σ^2_P) variances calculated by single-trait animal model (SAM).

Trait[+]	Additive		Common environment		Error		Total
	σ^2_A	V%[*]	σ^2_C	V%[*]	PEV	V%[*]	σ^2_P
Body weight (grams):							
BW0	1.8	19.9	2.3	25.3	5.1	54.8	9.2
BW2	16.0	11.9	26.1	19.3	93.1	68.8	135.2
BW4	98.5	13.9	83.3	11.8	525.0	74.3	706.9
BW6	192.8	6.9	499.0	17.9	2093.5	75.2	2785.2
BW8	381.1	8.0	908.3	19.2	3448.1	72.8	4737.5
BW10	711.7	9.3	1203.2	15.7	5737.9	75.0	7652.8
BW12	831.9	6.0	2247.5	16.3	10702.1	77.7	13781.5
BW16	2215.0	8.3	3781.1	14.2	20639.7	77.5	26635.8
Daily gain (grams):							
DG4	0.46	12.9	0.38	10.8	2.71	76.4	3.54
DG8	1.02	6.1	3.41	20.4	12.27	73.6	16.68
DG12	1.84	5.0	4.57	12.4	30.48	82.6	36.89
DG16	3.49	8.0	3.20	7.3	36.92	84.7	43.61

[+] Traits as defined in Table 2.

[*] Percentage of σ^2_A or σ^2_C or σ^2_e relative to σ^2_P.

Table (4): Estimates of direct additive (σ^2_A), common environment (σ^2_C), predicted error (PEV or σ^2_e) and total phenotypic (σ^2_P) variances calculated by multi-trait animal model (MAM).

Trait[+]	Additive		Common environment		Error		Total
	σ^2_A	V%[*]	σ^2_C	V%[*]	PEV	V%[*]	σ^2_P
Body weight (grams):							
BW0	1.7	17.8	2.5	25.6	5.5	56.6	9.6
BW4	97.2	16.0	79.1	13.0	431.6	71.0	607.9
BW8	353.5	9.6	1014.0	27.6	2300.9	62.7	3668.4
BW12	910.1	11.0	2070.3	25.1	5270.4	63.9	8250.8
BW16	2895.8	15.2	3587.9	18.9	12517.9	65.9	19001.7
Daily gain (grams):							
DG4	0.36	10.1	0.39	11.1	2.79	78.7	3.54
DG8	1.00	6.0	3.41	20.4	12.35	73.7	16.76
DG12	1.80	4.9	4.44	12.0	30.77	83.1	37.01
DG16	3.20	7.3	3.21	7.3	37.26	85.3	43.67

[+] Traits as defined in Table 2

[*] Percentage of σ^2_A or σ^2_C or σ^2_e relative to σ^2_P.

Using of **MAM** leads to reduction in the percentages of predicted error variance (**PEV** or σ_e^2) by 3.3, 10.1, 13.8 and 11.6% than those estimates of **PEV** resulted by **SAM** for **BW** at 4, 8, 12 and 16 weeks, respectively. Little differences in **PEV** (σ_e^2) were observed between **SAM** and **MAM** for **DG** traits (Tables 3 & 4). However, using relationships among birds leads a reduction in predicted error variance (**PEV**) (Schaeffer, 1993). Thus, one could recommend the Egyptian poultry breeders to use the animal models in estimation of variance components to obtain accurate estimates of σ_A^2 and minimum **PEV**. Recently, Laloee *et al.* (1996) reported that estimates of **PEV** were decreased for the related animals than for the unrelated ones.

Common Environmental Variance

Using the **SAM**, percentages of common environmental variances (σ_c^2) for growth traits in Dokki-4 chickens (Table 3) were large at hatching age (25.3%), declined thereafter gradually as the chick grew older (14.2% at 16 weeks). The percentages of σ_c^2 ranged from 11.8 to 25.3% for **BW** traits, from 7.3 to 20.4% for **DG** traits. Aggery and Cheng (1994) reported similar results for growth traits in Japanese Quail. Percentages in the present study are within the range of 9.6-38.4% reported by Danbaro *et al.* (1995) for White Plymouth Rock chickens.

Using the **MAM,** estimates of σ_c^2 obtained for **BW** traits and listed in Table 4 indicate an indefinite trend for σ_c^2 as age of chick advanced. The percentages of σ_c^2 were somewhat higher (13.0-27.6%) than those resulted by the **SAM** for **BW** traits (11.8 -25.3%). These results are in agreement with findings of Koerhuis and Mckay (1996) for juvenile broilers. On the other hand, percentages of σ_c^2 using **MAM** for **DG** were mostly moderate and ranged from 7.3 to 20.4%.

In general, the differences in estimates of σ_c^2 between **SAM** and **MAM** for **DG** were low (Tables 3 & 4) and consequently either of the two models could be used in estimation of variance components of common environment. However, common environment affected the growth of the progeny of Dokki-4 chickens to some extent due to the consequence of the genetic variation of some characters of the dam such as mothering or maternal ability (Mrode, 1996; LE Bihan-Duval *et al.*, 1997). Maternal environmental effects on chick growth are divided into two stages, namely the pre-ovipositional maternal effect and the post-ovipositional effect. The post-ovipositional effect can be divided into pre-hatch (incubation) and post-hatch effects. Because chicks were raised independent of the dams, the post-hatch maternal influence on the chick growth was negligible. Therefore, the common environment that may possibly affect the chick growth was pre-ovipositional maternal components, which are mainly oviduct factors such as egg size, egg weight, shell quality, and yolk composition (Aggrey and Cheng, 1994). The estimates of σ_c^2 included in the present study accounted for maternal permanent environmental variation, non-additive genetic variation, and any sire **x** dam interaction that may present, since this component largely represented covariances between full sibs' families (the majority of dams were nested within sire groups). In addition to that, another source of common environmental variance raised between families may be due to nutritional and/or climatic factors. Also, all sorts of relatives are subjected to environmental sources of resemblance (Aggrey and Cheng, 1994; Mrode, 1996)

Heritability Estimates

Heritabilities estimated by **SAM** (h_{AS}^2) and **MAM** (h_{AM}^2) for body weights (**BW**) and daily gains (**DG**) in Dokki-4 chickens are given in Table 5. These estimates indicate that h_{AS}^2 for **BW** traits were higher at earlier ages from hatch up to 4 weeks (averaged 0.15) than at later ages from 6 to 16 weeks (averaged 0.08). The same trend was observed for most traits of **DG**. These results indicate that selection of progeny themselves may be effective for the improvement of performance of Dokki-4 chickens at early age of 4 weeks. The estimates of the present study were lower than those reported by Aggrey and Cheng (1994) with Japanese Quail at 3 weeks of age and Danbaro *et al.* (1995) with White Plymouth Rock chickens at 7 weeks of age. Recently, LE Bihan-Daval *et al.* (1997) reported that heritabilities were 0.24 and 0.22 for 3- and 6-week body weights using **DFREML** under an animal model, respectively. However, estimates published for heritability of growth traits in chickens estimated by the animal model are few (Aggrey and Cheng, 1994; Danbaro *et al.*, 1995; Kuhlers and McDaniel, 1996; LE Bihan-Duval *et al.*, 1998).

The estimates of h_{AS}^2 for all growth traits obtained by **SAM** were lower than those h_{AM}^2 obtained by **MAM** (Table 5). This may be attributed to the existence of extra information on correlated traits (i.e. covariances among traits were considered) as well as bias due to selection may be smaller (Mrode, 1996). From the previous notations, one may recommend the poultry breeders in Egypt to use **MAM** analysis to obtain accurate estimates of additive genetic variance as well as heritability associated with minimum predicted error variance (**PEV**). For **DG** traits, no clear differences were observed between estimates of h_{AS}^2 and h_{AM}^2 (Table 5). The estimates of h_{AS}^2 and h_{AM}^2 for growth traits in Dokki-4 chickens in this study were generally lower than those reported by Koerhuis and Mckay (1996) and Le Bihan-Duval *et al.* (1998) with juvenile and broiler chickens. According to Danbaro *et al.* (1995), the decreasing in estimates of h_{AS}^2 and h_{AM}^2 in the present study could be attributed to: (1) The additive genetic variances in the population were low, (2) The existence of inbreeding (15.3%, i.e. as calculated by **MTDFREML** program of Boldman *et al.*, 1995) and relationships between parents in the base population, and (3) selection may be carried out prior to the establishment of the base population. Also, data on culled chicks were not available for analysis in this study. The lack of full information on the random selection process in the establishment of the base population may have contributed to the reduction of additive variance.

Correlations Among Growth Traits

Direct additive genetic ($\mathbf{r_G}$), common environmental ($\mathbf{r_C}$), environmental ($\mathbf{r_E}$) and phenotypic ($\mathbf{r_P}$) correlations estimated by **MAM** among most growth traits (Table 6) were favourable for mass selection to increase growth performance of Dokki-4 chicks at different ages, i.e. these high or moderate estimates may be of great importance in predicting the performance of the chick at later ages relative to prediction from early ages. Estimates of $\mathbf{r_G}$ among **BW** and **DG** traits at early age intervals (i.e. up to 8 weeks of age) are generally higher than those estimates of $\mathbf{r_C}$, $\mathbf{r_E}$ and $\mathbf{r_P}$ (Table 6). Reports available on estimation of $\mathbf{r_G}$, $\mathbf{r_C}$, $\mathbf{r_E}$ and $\mathbf{r_P}$ for growth traits of chickens using **MAM** are scarce for comparison with the present results.

Genetic Correlation ($\mathbf{R_G}$)

Estimates of $\mathbf{r_G}$ showed that most of these correlations were positive and similar in sign to the corresponding estimates of $\mathbf{r_P}$ (Table 6). The estimates ranged from 0.17 to 0.84 among **BW** traits and from 0.11 to 0.65 among **DG** traits. Bhushan and Singh (1995) reported that estimates of $\mathbf{r_G}$ between **BW** traits of broiler chicks were positive and generally low.

The estimates of $\mathbf{r_G}$ among growth traits at different ages were mostly moderate or high and averaged 0.52 among **BW** traits and 0.25 among **DG** traits. These estimates indicated that the genetic factors of all growth traits studied were closely additively related. The high estimates of $\mathbf{r_G}$ given in Table 6 indicate that measures before the age of 16 weeks in Dokki-4 chickens could be good indicators for the genetic value of growth traits. For local breeds (e.g. Dokki-4, Fayoumi and Baladi White), estimates of $\mathbf{r_G}$ among different growth traits reported by some Egyptian investigators (Khalil *et al.*, 1993; others) fall within the range of estimates obtained in this study. In addition, estimates of $\mathbf{r_G}$ obtained here were higher than those reported for some exotic breeds (Kumar and Acharya, 1980; Bhushan and Singh, 1995; Reddy *et al.*, 1997). This may be due to that local breeds were not subjected to any intensive programme of selection, while the exotic breeds may be subjected to aggressive selection. This might encourage the chicken breeders in Egypt to improve growth traits of Dokki-4 chicks through indirect selection.

The low unbiased estimates of $\mathbf{r_G}$ resulting from multivariate analysis may arise from two causes. Firstly, it can be due to the correction of the data for all possible non-genetic effects such as common environmental effect, i.e. egg size (as a character of the dam), which differs from one generation to another and this will lead to a reduction in the dam component of variances and covariances. Secondly, bias due to selection was eliminated (i.e. bias resulting from the data of chicks surviving to the latest weight had disappeared). Existence of inbreeding (15.3%, i.e. as calculated using **MTDFREML** program of Boldman *et al.*, 1995) in the parental base population (sire and dam) might be added as another cause in such reduction of additive genetic variance and covariance among traits.

Evidently, estimates of $\mathbf{r_G}$ obtained here from **DFREML** estimators of variance and covariance components were higher and less extreme than the corresponding estimates of genetic correlation in the reviewed studies. This might be due to that: (1) The variance and covariance components obtained by **MAM** were unbiased by selection (Schaeffer, 1993; Hofer, 1998), (2) Analysis of growth traits using **MAM** which includes the relationships among individuals will give more accurate genetic correlations, i.e. an increase in genetic covariance and a decrease in predicted error variance (**PEV**), (3) Multivariate analysis allows separating the common environmental non-genetic effects (caused by non-additive maternal and non-genetic maternal effects) from uncontrolled environmental effects, and (4) Sampling variances based on animal model analysis were approximated since, the matrix of asymptotic lower bound sampling covariances of the parameters estimated is given by the inverse of the information matrix, i.e. the matrix of expected value of second derivatives of the log (Meyer, 1993).

Common Environnemental Correlation ($\mathbf{R_C}$)

The estimates of $\mathbf{r_C}$ among **BW** traits and among all **DG** traits were positive and mostly of moderate or high magnitude, and tended to decrease relatively in value as the intervals between the two ages got larger. No reports are available for estimates of common environmental correlation ($\mathbf{r_C}$) in chickens. The estimates averaged 0.56 among **BW** traits and 0.27 among **DG** traits (Table 6). Estimates of $\mathbf{r_C}$ were mostly higher than estimates of $\mathbf{r_E}$ and $\mathbf{r_P}$. These findings indicate that non-genetic maternal effects of full-sib families on growth traits are of considerable importance up to 16 weeks of age after hatch in Dokki-4 chickens. Thus, one might recommend that common environmental effects should be considered in **MAM** for the estimation of variance and covariance components to get unbiased estimates of genetic, phenotypic and environmental correlation.

Environnemental Correlation ($\mathbf{R_E}$)

The $\mathbf{r_E}$ estimated by **MAM** among growth traits of Dokki-4 chickens showed that the relationships among **BW** traits or among **DG** traits were positive and generally moderate or high (Table 6). The estimates averaged 0.42 among **BW** traits. Similar findings were reported by other investigators (Stino *et al.*, 1983; Khalil *et al.*, 1993). Estimates of r_E reported herein for different growth traits indicated that the magnitude of the coefficients decreased as the chick advanced in age.

Table (5): Heritabilities (h^2) estimated from single-trait (h^2_{AS}) and multi-trait (h^2_{AM}) animal models for body weights and daily gains in Dokki-4 chickens.

Trait[+]	single-trait animal model (h^2_{AS})	Multi-trait animal model (h^2_{AM})
Body weights:		
BW0	0.20	0.18
BW2	0.12	
BW4	0.14	0.16
BW6	0.07	
BW8	0.08	0.10
BW10	0.09	
BW12	0.06	0.11
BW16	0.08	0.15
Daily gains:		
DG4	0.13	0.10
DG8	0.06	0.06
DG12	0.05	0.05
DG16	0.08	0.07

[+] Traits as defined in Table 2.

Table (6): Additive genetic (r_G), common environmental (r_C), environmental (r_E), and phenotypic (r_P) correlations among body weights and among daily gains estimated from multi-trait animal model.

Traits correlated[+]	r_G	r_C	r_E	r_P
Among body weights:				
BW0 & BW4	0.17	0.43	0.22	0.25
& BW8	0.34	0.23	0.14	0.18
& BW12	0.22	0.42	0.16	0.21
& BW16	0.24	0.23	0.13	0.15
BW4 & BW8	0.77	0.62	0.60	0.61
& BW12	0.84	0.57	0.49	0.52
& BW16	0.83	0.56	0.36	0.41
BW8 & BW12	0.68	0.80	0.69	0.70
& BW16	0.35	0.76	0.55	0.58
BW12 & BW16	0.77	0.94	0.82	0.84
Among daily gains:				
DG4 & DG8	0.31	0.35	0.25	0.27
& DG12	0.56	0.20	0.20	0.22
& DG16	0.44	0.30	0.07	0.11
DG8 & DG12	0.11	0.14	0.10	0.10
& DG16	0.35	0.39	0.11	0.13
DG12 & DG16	0.65	0.24	0.18	0.20

[+] Traits as defined in Table 2.

Phenotypic Correlation (R_P)

All estimates of r_P among **BW** traits or among **DG** traits at different ages were positive and mostly of moderate or high magnitude (Table 6). The estimates of DG tended to decrease relatively in value as the intervals between the two ages got larger. The estimates averaged 0.45 among **BW** traits. In agreement with the present results, most of the estimates in the literature (Kumar and Acharya, 1980; Stino *et al.*, 1983) showed that the r_P among growth traits of chicken at different ages were positive and generally high. This result may be due to their part/whole relationship. In practice, the positive and generally moderate or high r_P among growth traits at different ages give the management policy and culling decisions considerable advantage.

CONCLUSIONS

(1) Estimates of variance components and heritabilities estimated by single-trait and multi-trait animal models for growth traits of Dokki-4 chickens are large in earlier ages than in later ages. Therefore, Dokki-4 chickens could be improved through selection at the younger ages. In addition, results of the present and reviewed studies indicated that Dokki-4 chicken has higher means of body weight (BW) and rate of gains than other local breeds. Also, it has acceptable taste for the majority of the Egyptian consumers (ABD EL-GAWAD, 1969). Accordingly, it is safe to conclude that Dokki-4 chickens may be considered as a meat-type chicken in Egypt. Therefore, utilization of this breed in meat production in Egypt is recommended.

(2) High and positive genetic and phenotypic correlations among growth traits reported here lead to conclude that body weight at earlier age could be used for early selection in Dokki-4 chickens. High and positive common environmental correlations among body weight lead also to conclude that common environmental effects on growth traits should be considered in estimation of variance and covariance components.

(3) Animal models used in the present study accounted for A^{-1} and eliminated the fixed effects (e.g. generation, sex) affecting growth performance of Dokki-4 chicks and therefore they reduced the predicted error variance (PEV) for such unbalanced data.

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تقدير مكونات التباين والمكافآت الوراثية لصفات النمو فى دجاج دقى ـ٤ المصرى باستخدام نماذج الحيوان

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أجريت هذه الدراسة على ٧٢٢٦ كتكوت من دجاج دقى-٤ (كسلالة محلية)، حيث أخذت بيانات وزن الجسم عند عمر الفقس وكل أسبوعين حتى عمر ١٦ أسبوع من العمر ولمدة جيلين متتاليين. كما حسبت مقدار الزيادة اليومية بين الفترات من عمر الفقس-٤ ، ٤-٨ ، ٨-١٢ ، ١٢-١٦ أسبوع.

وكان الهدف هو تقدير مكونات التباين الوراثى المضيف والتباين البيئى العام والمظهرى وكذلك معاملات الارتباط الوراثى المضيف والبيئى العام والبيئى والمظهرى باستخدام نموذج الحيوان الوراثى للصفة الواحدة وللصفات المتعددة.

وأظهرت النتائج مايلى:

١- أظهرت نسب التباين الوراثى المضيف لوزن الجسم والمقدرة بواسطة نموذج الحيوان متعدد الصفات أنها أعلى من تلك المقدرة بواسطة نموذج الحيوان للصفة الواحدة . حيث تراوحت نسب التباين الوراثى المضيف من ٦-١٩,٩% عند استخدام نموذج الحيوان للصفة الواحدة فى حين كانت ٩,٦-١٧,٨% عند استخدام نموذج الحيوان متعدد الصفات وذلك لصفات وزن الجسم.

٢- كانت نسب التباين البيئى العام عند استخدام نموذج الحيوان للصفة الواحدة مرتفعة عند عمر الفقس (٢٥,٣%) ولكنها انخفضت تدريجيا كلما تقدمت الكتاكيت فى العمر (١٤,٢% عند عمر ١٦ أسبوع) ، كما كانت نسب التباين البيئى العام لصفات وزن الجسم الناتجة عن تحليل نموذج الحيوان متعدد الصفات أعلى (بمتوسط ٢٢%) عن تلك الناتجة عند نموذج الصفة الواحدة (بمتوسط ١٧,٤%)

٣- كان هناك اختلافات بسيطة بين نموذج الحيوان للصفة الواحدة ومتعدد الصفات فى تقدير مكونات التباين البيئى العام وذلك لصفات معدل الزيادة اليومية.

٤- بصفة عامة كانت تقديرات المكافئ الوراثى لكل صفات النمو منخفضة أو متوسطة نسبيا. كما كان المكافئ الوراثى الناتج عن نموذج الحيوان متعدد الصفات أعلى قليلا (حيث تراوحت القيم من ٠,٠١-٠,١٨) عن تلك الناتجة عن نموذج الحيوان للصفة الواحدة (تراوح من ٠,٠٦-٠,٢٠) وذلك لصفات وزن الجسم.

٥- كانت معظم الارتباطات الوراثية بين صفات النمو عالية عند الأعمار المختلفة وكان متوسطها ٠,٥٢ بين صفات وزن الجسم ، ٠,٢٥ بين صفات معدل الزيادة اليومية.

٦- كانت كل تقديرات الارتباط البيئى العام والبيئ والمظهرى بين صفات وزن الجسم وبين صفات الزيادة اليومية موجبة ومتوسطة أو مرتفعة.