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GENETIC EVALUATION FOR GROWTH TRAITS OF DOKKI-4 CHICKENS USING ANIMAL MODELS

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Abstract

Post-hatching growth traits of 7226 chick of Dokki-4 chickens were genetically evaluated. Data of individual body weight **(BW)** at hatch and biweekly thereafter up to 16 weeks of age were collected in two generations. Daily gains **(DG)** between intervals of hatch-4, 4-8, 8-12 and 12-16 weeks were also studied. Variance components, heritabilities and breeding values for these growth traits were predicted using single-trait **(SAM)** and multi-trait **(MAM)** animal models.

Percentages of direct additive genetic variance $(\sigma^2_A$) for **BW** traits estimated by the MAM appeared to be higher than those estimated by the **SAM**. The percentages of common environmental variance (σ^2_c) for BW traits obtained by the **MAM** were higher than those obtained by **SAM**. Generally, estimates of heritability resulting from **MAM** were (h^2_{AM}) somewhat larger than those obtained by **SAM** analysis (h^2_{AS}).The estimates of h^2_{AM} ranged from 0.10 to 0.18 for **BW** traits, while, they ranged from 0.06 to 0.20 for (h^2_{AS}).

The ranges in breeding values obtained by both models for birds with records **(PBV)** and their sires **(SBV)** and dams **(DBV)** without records for growth traits were generally moderate. For both models of evaluation, the ranges in estimates of **SBV** and **DBV** obtained for birds without records were moderate and lower than those recorded for birds with records. The direct additive responses of selection **(SRA)** predicted by both models were nearly similar in most cases. The additive selection responses recorded by the dams of birds were lower than those recorded by the sires of birds without records. Across the whole period of growth, the ranges in **SBV** for sires without records estimated by MAM vs **SAM** averaged 73.9 vs 65.0 grams and 4.11 vs 4.01 grams for **BW** and **DG** traits, respectively, while the corresponding ranges in **DBV** for dams without records averaged 43.16 vs 31.6 grams and 1.75 vs 1.65 grams. The accuracy in predictors (i.e. **PBV**, **SBV** and **DBV**) obtained by **MAM** were nearly similar to those predictors obtained by **SAM** for most growth traits in Dokki-4 chickens. Correlations among ranks of genetic predictors (i.e. **PBV**, **SBV** and **DBV**) estimated by **SAM** vs **MAM** for most growth traits were high and significant (P<0.01). Most correlations among ranks of **PBV**, **SBV** and **DBV** estimated by **SAM** and/or **MAM** were high and significant (P<0.01) for body weight at 8-week of age as well as at subsequent ages.

INTRODUCTION

Little information is available for estimation of genetic parameters and/or evaluation of growth performance of broiler populations (progeny and their sires and dams) in chickens using animal models (Koerhuis and Mckay, 1996 and Szwaczkowski, 1999). Evaluation of individuals using animal models are nowadays utilized in many countries all-over the world for various domestic species, although, surprisingly, this method was almost ignored in poultry evaluation systems even though strong selection had been carried out on this species for many generations. In Egypt, the native breeds like Fayoumi, Baladi and Dokki-4 were not evaluated genetically by applying single- or multi-trait animal models.

In an attempt to evaluate meat-type Egyptian strains of chicken, the objectives of the present study were: (1) to estimate direct additive genetic, common environment, phenotypic variances and heritabilities for body weights and daily gains of Dokki-4 broilers using single- and multi-trait animal models, (2) to predict the breeding values for growth traits of these broilers (progeny with records) and their sires and dams (birds without records) applying these two animal models, and (3) to estimate the accuracy and rates of change in accuracy in these estimates predicted by single and multiple trait animal models.

MATERIALS AND METHODS

Experiment and data collected

This work was carried out at Inshas Poultry Research Farm, Animal Production Research Institute, Ministry of Agriculture, Egypt. The native Dokki-4 breed was used in this study. A total of 7226 chicks of Dokki-4 chickens were produced in two generations. Two hatches were taken in each generation. The numbers of progeny produced in each generation were distributed as shown in Table 1 according to the number of progeny per sire and dam. Data of individual body weight (BW) at hatch and biweekly thereafter up to 16 weeks of age were collected from all individuals of the first and second generation. Daily gains (DG) between four intervals of hatch-4, 4-8, 8-12 and 12-16 weeks of age were also computed. Means, phenotypic standard deviations (SD) and coefficients of variability (V%) characterizing BW and DG in Dokki-4 chickens are given in Table 2.

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 groups	No. of sires	Total No. progeny	% of progeny	Dam groups	No. of dams	Total No. progeny	% of progeny
First generation:				**First generation:**			
Sires with <95 progeny	2	184	5	Dams with >4 to <10 progeny	73	545	13
Sires with ≥ 95 to <110 progeny	7	734	18	Dams with ≥ 10 to <20 progeny	243	3326	83
Sires with ≥110 progeny	25	3102	77	Dams with ≥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 <95 progeny	15	1201	38	Dams with >4 to <10 progeny	141	1047	33
Sires with ≥ 95 to <110 progeny	15	1650	51	Dams with ≥ 10 to <20 progeny	185	2140	67
Sires with ≥110 progeny	3	355	11	Dams with ≥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	

All one-day old chicks were wing-banded and reared in floor brooder, then transferred to the rearing houses. Chicks were fed during 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 climatic conditions.

Single-trait animal model

Using **MTDFREML** (Boldman *et al*, 1995), the single-trait animal model (SAM) in matrix notation used was:

$$y = Xb + Z_a u_a + Z_p u_p + e$$

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 the bird, u_p= vector of random common environmental effects (representing dam by hatch combination), X, Z_a

and Z_p are the incidence matrices relating records to fixed effects (i.e. sex and genera-tion), the additive genetic effects and random common environmental effects, respec-tively, and e= vector of random residual effects.

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
4-Week weight	**BW4**	6594	167.9	28.3	16.8
8-Week weight	**BW8**	6156	428.3	72.7	17
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	20.4
4-8 Weeks	**DG8**	6156	18.5	4.3	23
8-12 Weeks	**DG12**	5645	22.4	6.5	29.1
12-16 Weeks	**DG16**	4975	21.7	7	32

The mixed model equations **(MME)** of **SAM** described above were of the form:

$$
\begin{bmatrix}
X'X & X'Z_a & X'Z_p \\
Z'_aX & Z'_aZ_a+A^{-1}\alpha_a & Z'_aZ_p \\
Z'_pX & Z'_pZ_a & Z^aZ^a+I_p\alpha_p
\end{bmatrix}
\begin{bmatrix}
\hat{b} \\
\hat{u}_a \\
u_p
\end{bmatrix}
=
\begin{bmatrix}
X'y \\
Z'_ay \\
Z'_py
\end{bmatrix}
$$

where A^{-1} is the inverse of the numerator relationship matrix (Henderson, 1976), $\alpha_a= \sigma^2_e/\sigma^2_A$ and $\alpha_p= \sigma^2_e/\sigma^2_P$, I_P is an identity matrix corresponding to levels of common environmental effects and I_n is an identity matrix corresponding to n observations; $Var(a)= A\sigma^2_A$, $Var(p)= I\sigma^2_P$ and $Var(e)= I\sigma^2_e$. The variances used as starting values in the analyses of single-trait animal model are presented in Table 3. These variances were calculated by SAS Program applying the **REML** procedure (SAS, 1996).

Multi-trait animal model

The multi-trait animal model **(MAM)** resembles a stack of the **SAM** for each trait. The model of multi-trait analysis using **MTDFREML** program (Boldman *et al*, 1995) for two traits could be written as:

$$\begin{bmatrix} y^1 \\ y^2 \end{bmatrix} = \begin{bmatrix} X^1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b^1 \\ b^2 \end{bmatrix} + \begin{bmatrix} Z_{a1} & 0 & Z_{p1} & 0 \\ 0 & Z_{a2} & 0 & Z_{p2} \end{bmatrix} \begin{bmatrix} u_{a1} \\ u_{a2} \\ u_{p1} \\ u_{p2} \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

where: y_i = vector of observations for the ith trait; b_1 = vector of fixed effects (e.g. sex and generation) for the ith trait; u_{ai} = vector of random bird effects for the ith trait; u_{pi} = vector of random common environmental effects for the ith trait; e_i= Vector of random residual effects for the ith trait; and X_i, Z_{ai} and Z_{pi} are incidence matrices relating records of the ith trait to fixed effects, random genetic effect of the bird and random common environmental effects, respectively. The variances and the covariances obtained by SAS program (SAS, 1996) were used as starting values for the estimation of variance and covariance components using multi-trait animal model analysis (Table 3). In the present study, the **MME** in multi-trait animal model are being too large when we have more than two traits. We used five traits for body weights and four traits for daily gain traits.

Table 3. Estimates of direct additive, common environment and error variances (σ2) and covariances (Cov) for different growth traits used in animal models analysis.

Trait[+]	Direct additive		Common		Error	
	σ^2_A	Cov_A	σ^2_c	Cov_c	σ^2_e	
Body weights (garms):						
BW0	1.68		2.4		7.1	
BW0 & BW4		3.2		6.4		12.6
& BW8		7.2		12.5		22.2
& BW12		9.6		31.7		40.7
& BW16		20.8		26.8		51.8
BW4	97.6		88.8		592.3	
BW4 & BW8		160.4		159.8		869.3
& BW12		224.4		290.2		1210
& BW16		396		351.8		1304.2
BW8	464		921.9		3704.6	
BW8 & BW12		378.4		1219.1		4157
& BW16		410.8		1442		4582.6
BW12	686.4		2391.7		11076.6	
BW12 & BW16		1150.8		2764.1		11908.7
BW16	2372.4		3976.2		20944.2	
Daily gains (grams):						
DG4	0.48		0.41		3.02	
DG4 & DG8		0.4		0.4		1.5
& DG12		0.4		0.5		1.8
& DG16		0.8		0.4		0.8
DG8	1.28		3.45		12.94	
DG8 & DG12		0.8		0.7		1.6
& DG16		0.4		1.2		1.8
DG12	1.8		4.74		30.71	
DG12 & DG16		2		1.3		4.6
DG16	4.24		3.45		36.84	

[+] Traits as defined in Table 2

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 existed. Consequently, the number of inbred chicks was 210 with an average inbreeding coefficient of 0.153.

Estimation of heritability

Heritabilities for growth traits were computed from variance component estimates as:

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

where σ^2_A, σ^2_P and σ^2_e are variances due to the effects of direct additive genetic, common environment and random error, respectively.

Estimation of breeding values

Solutions for equations of birds were computed using the package of Boldman *et al.* (1995) to estimate the breeding values of birds with and without records. The accuracy of predicted estimate (r_A) for each bird was computed according to Mrode (1996) as:

$$r_A = \sqrt{1 + F - d_j \alpha_a}$$

where r_A = the accuracy of prediction of the ith bird's breeding value; F= inbreeding coefficient of bird; d_j= the jth diagonal element of inverse of the appropriate block coefficient matrix; and $\alpha_a = \sigma^2_e / \sigma^2_A$. Pooling the estimates of accuracies (r_A) predicted for all individuals, dividing them by the number of individuals gave the average of accuracies (AC) for each trait. Then, the rates of change in accuracy (DA) from using **SAM** and **MAM** were computed as (Van Raden *et al.*, 1990):

$$\Delta_A = \frac{AC_{(M)} - AC_{(S)}}{AC_{(S)}} \times 100$$

where $AC_{(S)}$= average of accuracy resulted from using the **SAM** and $AC_{(M)}$= average of accuracy resulted from using the **MAM**.

Estimation of rank correlation

The Spearman's rank correlation between any two predicted breeding values were computed using SAS procedure (SAS, 1996). By using Spearman's rank correlation, the difference in rank of predictors estimated by the two animal models (SAM and MAM) could be determined. Also, if the rank correlation appeared to be high for a certain pair, the evaluated groups could be selected at the early age (one trait) without waiting for the later age (other traits).

RESULTS AND DISCUSSION

Estimation of variance components

Estimates of direct additive genetic (σ^2_A), common environment(σ^2_c) and error variance (σ^2_e)components estimated by **DFREML** method using single-trait (**SAM**) and multi-traits (**MAM**) animal models are presented in Table 4. Percentages of direct additive genetic variance (σ^2_e)for all growth traits using **SAM** were low or moderate.

Table 4. Estimates of direct additive (σ^2_A), common environment (σ^2_c) and error variance (σ^2_e) variances calculated by single (SAM) and multi-trait animal models (MAM) for growth traits in Dokki-4 chickens.

Trait[+]	Additive		Common		Error	
	σ^2_A	V%[*]	σ^2_c	V%[*]	σ^2_e	V%[*]
Single-trait animal model						
Body weight (grams):						
BW0	1.8	19.9	2.3	25.3	5.1	54.8
BW4	98.5	13.9	83.3	11.8	525.0	74.3
BW8	381.1	8.0	908.3	19.2	3448.1	72.8
BW12	831.9	6.0	2247.5	16.3	10702.1	77.7
BW16	2215.0	8.3	3781.1	14.2	20639.7	77.5
Daily gain (grams):						
DG4	0.46	12.9	0.38	10.8	2.71	76.4
DG8	1.02	6.1	3.41	20.4	12.27	73.6
DG12	1.84	5.0	4.57	12.4	30.48	82.6
DG16	3.49	8.0	3.2	7.3	36.92	84.7
Multi-trait animal model						
Body weight (grams):						
BW0	1.7	17.8	2.5	25.6	5.5	56.6
BW4	97.2	16.0	79.1	13.0	431.6	71.0
BW8	353.5	9.6	1014.0	27.6	2300.9	62.7
BW12	910.1	11.0	2070.3	25.1	5270.4	63.9
BW16	2895.8	15.2	3587.9	18.9	12517.9	65.9
Daily gain (grams):						
DG4	0.36	10.1	0.39	11.1	2.79	78.7
DG8	1.00	6.0	3.41	20.4	12.35	73.7
DG12	1.80	4.9	4.44	12.0	30.77	83.1
DG116	3.20	7.3	3.21	7.3	37.26	85.3

[+] Traits as defined in Table 2

[*] Percentage of σ^2_A or σ^2_P or σ^2_e relative to the total phenotypic variance.

The percentages of relative to the total phenotypic variance not averaged 13.9% for growth traits at early ages and from 6.0 to 8.3% for traits measured at later ages. These percentages were lower than those obtained by Danbaro *et al.* (1995), Koerhuis and Mckay (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 4.9 to 10.1% for **BW** and **DG,** respectively (Table 4). Estimates obtained by Koerhius and Mckay (1996) in juvenile broilers based on bivariate animal models were higher (28.6% for 6 week weight) than estimates obtained in the present study (16.0% for 6-week weight). On the other hand, results in the present study were in agreement with Danbaro *et al.* (1995) for White Plymouth Rock chickens.

Percentages of σ^2_A for **BW** traits estimated by the **MAM** appeared generally to be higher than those resulting from the **SAM** (Table 4). The estimates for **BW** traits 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.** 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 same conclusion for 6-week body weight. Higher additive genetic variance (σ^2_A) obtained by **MAM** relative to **SAM** may be due to extra information from correlated traits (i.e. covariances among traits were considered).

Using **MAM** leads to reduction in the percentages of error variance (σ^2_e) by 3.3%, 10.1%, 13.8% and 11.6% than those estimates from **SAM** for **BW** traits at 4, 8, 12 and 16 weeks, respectively. Little differences in σ^2_e were observed between **SAM** and **MAM** for **DG** traits (Table 4). Schaeffer (1993) stated that using relationships among birds leads to a reduction in error variance. Thus, one could recommend the poultry breeders in Egypt to use animal models in estimation of variance components to obtain accurate estimates of σ^2_A and minimum error variance.

Common environmental variance

Using **SAM**, percentages of common environmental variances (σ^2_e) for growth traits in Dokki-4 chickens (Table 4) were large at hatching age (25.3%), declined thereafter gradually as the chick grew older (14.2% at 16 weeks). The percentages of ranged from 11.8 to 25.3% for **BW** traits, 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 to 38.4% reported by Danbaro *et al.* (1995) for White Plymouth Rock chickens.

Using **MAM**, the estimates of σ^2_c obtained for **BW** traits (Table 4) having indefinite trend were across different ages. The percentages of σ^2_c were somewhat higher (13.0 to 27.6%) than those from **SAM** for **BW** traits (11.8 to 25.3%). These results were in agreement with findings of Koerhuis and Mckay (1996) for juvenile broilers. On the other hand, percentages of σ^2_c using **MAM** for **DG** were moderate and ranged from 7.3 to 20.4%. Differences in estimates of σ^2_p between **SAM** and **MAM** for **DG** traits were generally low (Table 4) and consequently, either of the two models could be used in estimation of variance components of common environment.

Estimates of σ^2_c obtained in the present study showed that growth of the progeny of Dokki-4 chickens could be affected by common environment. This might be to some extent a consequence of the genetic variation of some characters of the dam such as mothering or maternal ability (Mrode, 1996). Common environmental effects on chick growth are divided into two stages, namely, the pre-ovipositional 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 independently of the dams, the post-hatch 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^2_c included in the present study accounted for common environmental variation, non-additive genetic variation, and any sire x dam interaction that may be present, since this component largely represented covariances between full sibs' families (the majority of dams were nested within sire groups). In addition , another source of common environmental variance raised between families may be due to nutritional and/or climatic factors. Also, all sorts of relatives were subjected to environmental sources of resemblance (Aggrey and Cheng, 1994; Mrode, 1996).

Heritabilities

Heritabilities estimated by **SAM** (h^2_{As}) and **MAM**(h^2_{Am}) for body weights (**BW**) and daily gains (**DG**) in Dokki-4 chickens (Table 5) indicated that h^2_{As} for **BW** traits were higher at earlier ages from hatch up to 4 weeks than at later ages from 6 to 16 weeks. The same trend was observed for most traits of **DG**. These results indicated 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 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. How-

Table 5. Heritabilities (h^2) estimated from single-trait (h^2_{AS}) and multi-traits (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
BW4	0.14	0.16
BW8	0.08	0.10
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

ever, estimates published for heritability of growth traits in chickens estimated by the animal model were few (Aggrey and Cheng, 1994; Danbaro et al., 1995; Koerhuis and Mckay, 1996; Le Bihan-Duval *et al.*, 1998; Szwaczkiwski, 1999).

The estimates of h^2_{AS} for all **BW** traits obtained by **SAM** were lower than those h^2_{AM} obtained by **MAM** (Table 5). This may be attributed to the existence of extra information from 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 and with minimum error variance. For **DG** traits, no clear differences were observed between estimates of h^2_{AS} and h^2_{AM} (Table 5). The estimates of h^2_{AS} and h^2_{AM} 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 decrease in estimates observed could be attributed to: (1) The additive genetic variances in the population were low, (2) The existence of inbreeding (15.3% calculated by **MTDFREML** program of Boldman *et al.*, 1995) and relationships between parents in the base population, and (3) Selection may have been carried out prior to the establishment of the base population. Also, data on culled chicks were not available for analysis . The lack of full information on the selection process in the establishment of the base population may have contributed to the reduction of additive variance.

Breeding values predicted for birds with records (PBV)

For all birds with records, minimum and maximum estimates of predicted breeding values in addition to their ranges (**i.e. the** difference between the maximum and minimum value), standard errors **(SE), accuracy of** each predictor (r_A) and direct additive responses from selection are presented in Table 6. The ranges in estimates of **PBV** obtained by both animal models were **moderate**. The estimates of **PBV** and di-

rect additive responses of selection (SR_A) **predicted** for growth traits in Dokki-4 chicks by both animal models were nearly similar at early ages of growth. Growth traits at later ages (12-16 weeks) recorded higher ranges in estimates of **PBV** when using **MAM** than those of **SAM**. Consequently, the additive responses of selection in body weight predicted by **MAM** were higher than those estimated by **SAM**. This may be due to that: (1) prediction error variances **(PEV)** were decreasing in MAM (Quaas *et al.*, 1984), (2) MAM considered the relationships **among traits (i.e.** residual covariances between traits were computed), and (3) traits with lower heritabilities receiving more benefits when analysed with traits of higher heritabilities in multi-traits analysis (Thompson and Meyer, 1986).

Accuracy (^r_A) of minimum and maximum estimates of **PBV** for birds with records obtained by **MAM** were nearly similar to those obtained by **SAM** (Table 6). Across all the minimum and maximum estimates of **PBV**, the averages of accuracy when using **MAM** vs SAM were 0.65 vs 0.60 for **BW** traits and 0.60 vs 0.59 for **DG** traits (Table 6), i..e. applying both animal models in evaluation of Dokki-4 birds gave the same accuracy.

Breeding values estimated for sires of birds without records (SBV)

Breeding values predicted by **MAM** and SAM for **BW** and **DG** traits in Dokki-4 sires without records (Table 7) indicated that minimum and maximum estimates of **SBV** and their ranges had the same trend observed for **PBV** of birds with records (Table 6). The ranges in estimates of **SBV** obtained by both animal models were moderate and lower than those recorded for birds with records. Also, additive responses of selection (SR_A) for sires without records predicted by both animal models were nearly similar as shown before for birds with records (Tables 6&7).

The accuracy (r_A) of minimum and maximum estimates of **SBV** indicated that these estimates had the same trend obtained for birds with records (Tables 6&7), i.e. accuracy of **SBV** estimated by both animal models were nearly similar in most cases. In confirmation with that, the numbers of sires with positive estimates of **SBV** obtained here for growth traits indicated that differences in percentages of sires with positive estimates predicted by both models of evaluation were somewhat limited. The averages of percentages for estimates of **SBV** with positive signs recorded by SAM vs **MAM** were 49.3 vs 48.8% for **BW** traits. The average accuracies when using MAM vs SAM were 0.82 vs 0.76 for **BW** traits and 0.76 vs 0.75 for **DG** traits. In addition to that, the standard errors of predictors of **SBV** obtained by the two models were nearly simi-

Table 6. Minimum, maximum and ranges of predicted breeding values (PBV) for birds with records, their standard errors (SE), accuracy of prediction (r_A) and direct additive selection responses (SR_A) calculated by single-trait and multi-traits animal models for growth traits in Dokki-4 chickens.

Trait[+]	Minimum PBV	SE	r_A	Maximum PBV	SE	r_A	Range	SR_A
Single-trait animal model								
Body weights (grams):								
BW0	-2.2	0.70	0.86	3.1	1.10	0.59	5.3	0.97
BW4	-18.1	8.53	0.51	21.5	8.38	0.54	39.6	5.21
BW8	-46.7	12.68	0.76	34.3	12.85	0.75	81.0	14.74
BW12	-31.8	26.48	0.40	38.3	21.68	0.66	70.2	15.29
BW16	-62.6	42.35	0.44	81.1	41.81	0.46	143.7	21.18
Daily gains in weight (grams):								
DG4	-1.24	0.36	0.85	1.58	0.57	0.53	2.82	0.468
DG8	-1.98	0.70	0.71	2.00	0.71	0.70	3.98	0.712
DG12	-1.50	1.24	0.40	2.10	1.04	0.64	3.60	0.705
DG16	-2.64	1.66	0.45	2.78	1.65	0.46	5.42	0.85
Multi-trait animal model								
Body weights (grams):								
BW0	-2.1	0.7	0.85	2.9	1.08	0.57	5.1	0.93
BW4	-20.9	8.36	0.53	24.6	8.17	0.56	45.5	5.37
BW8	-47.3	11.85	0.78	37.4	12.05	0.77	84.7	14.57
BW12	-52.4	26.17	0.5	58	18.55	0.79	110.3	19.46
BW16	-92.5	44.03	0.57	94.8	43.83	0.58	187.3	30.94
Daily gains in weight (grams):								
DG4	-1.30	0.34	0.83	1.22	0.52	0.50	2.54	0.399
DG8	-2.06	0.69	0.73	1.86	0.69	0.72	3.92	0.725
DG12	-1.66	1.22	0.42	2.06	1.00	0.67	3.74	0.731
DG16	-3.36	1.57	0.48	3.10	1.56	0.49	6.46	0.868

+ Traits as defined in Table 2.

Number of progeny with records evaluated was 7226 individual.

lar for most growth traits. Pribyl and Pribylova (1991) found that reliability of **PBV** was 0.84, 0.61 and 0.60 with standard error of predictions of 0.086, 0.180 and 0.023 for sires, dams and laying hens at 20-weeks of age, respectively. The accuracies in prediction and selection responses estimated for sires without records (Table 7) were higher than those recorded for birds with records (Table 6). Such higher accuracies in **SBV** might be due to that large numbers of progeny per sire were used (the average number of progeny per sire was 108). At later age (16 weeks), the additive selection responses estimated by the sires without records averaged 60% higher than responses estimated for birds with records.

Breeding values estimated for dams of birds without records (DBV)

Breeding values predicted by **MAM** and **SAM** for **BW** and **DG** traits of dams of

Table 7. Minimum, maximum and ranges of predicted breeding values for sires without records (SBV), their standard errors (SE), accuracy of prediction (r_A) and additive selection responses (SR_A) calculated by single-trait and multi-traits animal models for growth traits in Dokki-4 chickens.

Trait[+]	Minimum			Maximum				
	SBV	SE	r_A	SBV	SE	r_A	Range	SR_A
Single-trait animal model								
Body weights (grams):								
BW0	-1.2	0.67	0.87	1.4	0.68	0.86	2.6	1.161
BW4	-15.6	5.77	0.81	14.8	5.08	0.86	30.4	8.287
BW8	-24.6	12.01	0.79	34.4	12.49	0.77	59	15.23
BW12	-39.4	21.42	0.67	33.4	19.5	0.74	72.8	20.33
BW16	-72.4	32.41	0.73	88	29.52	0.78	160.4	35.53
Daily gains in weight (grams):								
DG4	-1.12	0.4	0.81	1.12	0.35	0.85	2.24	0.563
DG8	-1.68	0.72	0.69	1.4	0.71	0.71	3.08	0.707
DG12	-1.7	0.96	0.71	2.26	0.99	0.68	3.96	0.943
DG16	-3.46	1.18	0.77	3.3	1.14	0.79	6.76	1.457
Multi-trait animal model								
Body weights (grams):								
BW0	-1.2	0.67	0.86	1.4	0.69	0.85	2.6	1.115
BW4	-17.4	5.56	0.83	14.6	4.99	0.87	32	8.38
BW8	-25	11.35	0.8	33.6	11.82	0.78	58.6	14.85
BW12	-52.2	20.86	0.72	44.4	18.17	0.8	96.6	22.93
BW16	-86.2	33.01	0.79	93.6	28.62	0.85	179.8	44.13
Daily gains in weight (grams):								
DG4	-1.02	0.37	0.79	0.92	0.33	0.83	1.94	0.486
DG8	-1.44	0.71	0.71	1.82	0.68	0.74	3.26	0.725
DG12	-2.1	0.94	0.71	2.04	0.94	0.71	4.14	0.953
DG16	-3.6	1.09	0.79	3.5	1.05	0.81	7.1	1.431

[+] Traits as defined in Table 2.

Number of sires without records evaluated was 34.

birds (Table 8) indicated that minimum and maximum estimates of **DBV** and their ranges had the same trend observed for **PBV** of birds with records (Table 6) and **SBV** of sires without records (Table 7). The ranges in **DBV** and additive selection responses were low relative to the estimates of PBV and **SBV**. The estimates of **DBV** and additive selection responses recorded by the dams of birds without records were lower than those recorded by the sires of birds without records. In both animal models of evaluation, the estimates of **DBV** and selection responses were nearly in accordance (Table 8).

The accuracy (r_A) of minimum and maximum estimates of **DBV** indicated that these estimates for dams of birds were lower than those obtained for birds with records and their sires without records (Tables 6&7&8). This may be due to that small numbers of progeny per dam were utilised in predicting estimates of **DBV** (the average

number of progeny per dam was 11). Across all minimum and maximum estimates of **DBV**, the averages of accuracies recorded by **MAM** were somewhat higher than those recorded by **SAM**, due to that covariances among traits were considered in evaluation of dams using **MAM**. The averages in accuracies estimated by **MAM** vs **SAM** were 0.29 vs 0.26 and 0.26 vs 0.23 for **BW** and **DG** traits, respectively.

Rates of change in accuracy

For each trait measured on birds with records and birds without records (sires and dams), the rates of change in accuracy ($\Delta_A\%$) for predictors were in favour of **MAM** relative to **SAM** (Table 9). Higher rates in accuracies recorded by **MAM** might be due to that data from correlated traits provided information not contained in data of **SAM** being evaluated (Mrode, 1996).

Rates of change in accuracy of estimates of the **PBV** for birds with records ranged from −2.1 to 27.8% (averaged 10.8%) for BW traits and -3.6 to 6.6% (averaged 2.7%) for **DG** traits (Table 9). Similarly, the rates of change in accuracy of **SBV** ranged from −1.2 to 8.6% (averaged 3.7%) and -2.4 to 3.6% (averaged 1.5%), while, those of **DBV** ranged from −6.5 to 28.6% (averaged 12.5%) and -5.6 to 27.3% (averaged 9.6%) for the previous traits in the same order. These results indicated that advantages in rates of change of predictions for the dams and their small numbers of progenies were higher than those for the sires with large number of progenies (VanRaden et al., 1990). These advantages could be exploited if the true parameter differs from the predictor.

Correlations among ranks of BLUP estimated by SAM or MAM

Spearman's correlations among ranks of **BLUP** of **SAM** or **MAM** for different growth traits were estimated to simplify the method of analysis and to save time and money especially when using complicated models. The correlations (and their significance) among ranks of **BLUP** estimated by **SAM** vs **MAM** for different growth traits for birds with and without records are shown in Table 10. For birds with and without records, most of the correlations among ranks of **BLUP** (i.e. **PBV**, **SBV** and **DBV**) estimated by **SAM** vs **MAM** were moderate or high (31 estimates out of 48 were found with correlations greater than 0.4). On the other hand, the rank correlations among estimates predicted by **MAM** were higher than those predicted by **SAM.** For birds with records, correlations among ranks of **PBV** estimated by **SAM** vs **MAM** ranged from 0.26 to 0.78 for **BW** traits, and from 0.14 to 0.61 for **DG** traits, while, the estimates of **SBV** and **DBV** ranged from 0.15 to 0.85 for **BW** traits, and from 0.01 to 0.62 for

Table 8. Minimum, maximum and ranges of predicted breeding values for dams without records (DBV), their standard errors (SE), accuracy of prediction (r_A) and additive selection responses (SR_A) calculated by single-trait and multitraits animal models for growth traits in Dokki-4 chickens.

| Trait[+] | Minimum | | | Maximum | | | | |
	DBV	SE	r_A	DBV	SE	r_A	Range	SR_A
Single-trait animal model								
Body weights (grams):								
BW0	-1.4	1.31	0.27	1.4	1.27	0.35	2.8	0.42
BW4	-9	9.95	0.24	9	9.53	0.28	18	2.58
BW8	-10	19.15	0.20	19.4	18.61	0.30	29.4	4.88
BW12	-16.2	28.38	0.18	21	27.93	0.25	37.2	6.2
BW16	-33.8	46.04	0.21	18.5	45.23	0.28	70.8	11.5
Daily gains in weight (grams):								
DG4	-0.54	0.66	0.23	0.62	0.64	0.31	1.16	0.18
DG8	-0.52	0.99	0.17	0.94	0.96	0.27	1.46	0.22
DG12	-0.78	1.34	0.17	0.96	1.32	0.24	1.74	0.28
DG16	-1.04	1.83	0.19	1.22	1.79	0.27	2.26	0.43
Multi-trait animal model								
Body weights (grams):								
BW0	-1.2	1.27	0.25	1.4	1.24	0.33	2.6	0.378
BW4	-11.2	9.53	0.26	10.8	9.40	0.30	22	2.761
BW8	-13	18.57	0.26	22.4	17.87	0.31	35.4	5.358
BW12	-27.4	29.40	0.22	30.8	28.84	0.29	58.2	7.693
BW16	-48.0	51.66	0.28	49.6	50.34	0.35	97.6	16.95
Daily gains in weight (grams):								
DG4	-0.48	0.59	0.22	0.52	0.57	0.29	1.0	0.153
DG8	-0.5	0.96	0.28	1.06	0.96	0.28	1.56	0.28
DG12	-1.0	1.31	0.20	0.86	1.29	0.27	1.86	0.315
DG16	-1.26	1.76	0.17	1.34	1.71	0.30	2.6	0.42

[+] Traits as defined in Table 2.

Number of dams without records evaluated was 325

DG traits for birds without records (Table 10). These estimates were mostly high (P<0.01) and indicated that ranking of **BLUP** estimated by **SAM** were not greatly different from the ranking of **BLUP** estimated by **MAM.** Therefore, evaluation of Dokki-4 birds for growth traits using the SAM would give **BLUP** estimates with the same accuracy when using the **MAM.**

High correlations (P<0.01) among ranks of **PBV, SBV** and **DBV** predicted by **SAM** vs **MAM** for **BW** at 8 weeks and the following ages indicated that selection of birds, or their sires and dams (based on their progenies), could be used to bring genetic improvement in Dokki-4 chickens at 8-week of age or at market weight. Consequent-

Table 9. Rates of change in accuracy ($\Delta_A\%$) from using single-trait (SAM) vs multi-traits (MAM) animal models for birds (progeny) with records, and birds without records (sires and dams) for growth traits in Dokki-4 chickens.

Trait[+]	Birds with records ($\Delta_A\%$)	Birds without records	
		Sires ($\Delta_A\%$)	Dams ($\Delta_A\%$)
Body weights (grams):			
BW0	-2.1	-1.2	-6.5
BW4	3.8	1.8	7.7
BW8	2.6	1.3	14.0
BW12	21.7	7.8	18.6
BW16	27.8	8.6	28.6
Daily gains in weight (grams):			
DG4	-3.6	-2.4	-5.6
DG12	2.8	3.6	27.3
DG12	4.8	2.2	14.6
DG16	6.6	2.6	2.2

[+] Traits as defined in Table 2.

$\Delta A\% = \{[AC_{(M)} - AC_{(S)}]/ AC_{(S)}\} \times 100$ as defined in Material and Methods.

ly, selection of birds at 8 weeks of age without saving all birds to later ages was more effective in selection programs, and thus, the cost of breeding program is reduced. These results were in agreement with those reported by Raheja and Singh (1993).

Table 10. Correlations among ranks of breeding values predicted by single-trait animal model vs multi-trait animal model for growth traits of birds with and without records.

Rank correlated traits[+]	Single-trait vs multi-trait animal models		
	Birds with records	Birds without records	
		Sires	Dams
Body weights (grams):			
BW0 & BW4	0.34**	0.48**	0.41**
& BW8	0.26**	0.15NS	0.32**
& BW12	0.30**	0.36*	0.31**
& BW16	0.31**	0.59**	0.28**
BW4 & BW8	0.61**	0.49**	0.60**
& BW12	0.67**	0.63**	0.61**
& BW16	0.66**	0.67**	0.57**
BW8 & BW12	0.78**	0.72**	0.85**
& BW16	0.57**	0.34*	0.72**
BW12 & BW16	0.73**	0.75**	0.84**
Daily gains in weight (grams):			
DG4 & DG8	0.48**	0.25NS	0.60**
& DG12	0.53**	0.48**	0.56**
& DG16	0.61**	0.62**	0.61**
DG8 & DG12	0.20**	0.16NS	0.13*
& DG16	0.14**	0.35*	0.01NS
DG12 & DG16	0.54**	0.56**	0.53**

[+] Traits as defined in Table 2.

NS = non-significant, *= P<0.05 and **= P<0.01.

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التقييم الوراثي لصفات النمو في دجاج دقي-٤ باستخدام نماذج الحيوان

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تم التقييم الوراثي لصفات النمو بعد الفقس لعدد ٧٢٢٦ كتكوت من دجاج دقي-٤ حيث أخذت بيانات وزن الجسم عند عمر الفقس و كل أسبوعين حتى عمر ١٦ أسبوعا من العمر لمدة جيلين . كما درس معدل الزيادة اليومية بين الفترات من الفقس-٤ ، ٤-٨ ، ٨-١٢ ، ١٢-١٦ أسبوعا كما تم التنبؤ بمكونات التباين و المكافئ الوراثي و القيم التربوية لصفات النمو باستخدام نموذج الحيوان وحيد الصفة و نموذج الحيوان متعدد الصفة .

أظهرت النتائج ان التباين الوراثي التجمعي لصفات وزن الجسم المقدرة بواسطة نموذج الحيوان متعدد الصفة أعلى من تلك المقدرة بواسطة نموذج الحيوان وحيد الصفة . كما كانت نسبة التباين البيئية العامة لصفات وزن الجسم الناتجة من نموذج الحيوان متعدد الصفة أعلى من تلك الناتجة من نموذج الحيوان وحيد الصفة ,و بصفة عامة كانت قيم المكافئ الوراثي الناتجة من نموذج الحيوان متعدد الصفة أعلى من تلك المقدرة من تحليل نموذج الحيوان وحيد الصفة حيث تراوحت قيم المكافئ الوراثي من ٠.١و – ٠.١٨و مقابل ٠.٦و – ٠.٢٠و .

كانت قيم المدى للقيم التربوية الناتجة من كلا النموذجين للطيور التى لها سجلات و كذلك للأباء (الذكور و الأمهات) التى ليس لها سجلات متوسطة القيمة . كما كانت قيم المدى للذكور و الأمهات (التى ليس لها سجلات) الناتجة من النموذجين منخفضة عن تلك المسجلة للطيور التى لها سجلات . كانت الاستجابة المباشرة للانتخاب المتوقعة من كلا النموذجين تقريبا واحدة فى معظم الحالات . بينما كانت الاستجابة المباشرة المسجلة للأمهات اقل من تلك المسجلة للذكور التى ليس لها سجلات و كانت قيم المدى للقيم التربوية للأباء (التى ليس لها سجلات) المقدرة بواسطة نموذج الحيوان متعدد الصفة مقابل نموذج الحيوان وحيد الصفة بمتوسط ٧٣و٩ مقابل ٠.٦٥ جرام ، ١١و٤ مقابل ٠.١و٤ جرام لصفات وزن الجسم و الزيادة اليومية على التوالي . بينما كانت القيم المناظرة للأمهات (ليس لها سجلات) بمتوسط ١٦و٤٣ مقابل ٦و٣١ جرام ، ٧٥و١ مقابل ٦٥و١ جرام .

كانت قيم معامل الدقة للمتنبئات (القيم التربوية للطيور و الذكور و الأمهات) الناتجة من نموذج الحيوان متعدد الصفة متشابهة تقريبا بتلك المتنبئات المتحصل عليها بواسطة نموذج الحيوان وحيد الصفة لمعظم صفات النمو فى دجاج دقى -٤ . كانت قيم معامل ارتباط الرتب بين المتنبئات المقدرة بواسطة نموذج الحيوان وحيد الصفة مقابل نموذج الحيوان متعدد الصفة مرتفعة لمعظم صفات النمو و معنوية (١٪) . كما كانت معظم الارتباطات بين الرتب للقيم التربوية للأفراد و الذكور و الأمهات المقدرة من نموذج الحيوان وحيد الصفة و/أو متعدد الصفة مرتفعة و معنوية لصفات وزن الجسم عند عمر ٨ أسابيع بالإضافة إلى الأعمار المتتالية .