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ESTIMATION OF BREEDING VALUES AND THEIR ACCURACIES USING MULTIVARIATES ANIMAL MODEL ANALYSIS FOR GROWTH TRAITS IN THREE LOCAL STRAINS OF CHICKENS

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ABSTRACT: *Breeding values and their accuracies were estimated using multi-traits Animal Model for birds with and without records of three local strains of chickens. A total number of 916, 1137 and 1030 chicks from Golden Montazah (GM), Silver Montazah (SM) and Matrouh (MA) strains, respectively, were used. Data of individual body weight at hatch (BW0), 4(BW4), 8 (BW8) and 12 (BW12) weeks of age were collected from a breeding experiment of one generation. Daily gain (DG) traits between intervals of hatch-4 (DG4), 4-8 (DG8) and 8-12 (DG12) weeks were also used. Results show that estimates of heritability (* h_a^2 *) in GM and SM strains for BW at hatch were higher than that at 12 weeks. The estimates are 0.45 and 0.22 for BW0 and 0.21 and 0.18 for BW12 in GM and SM strains, respectively. For birds with records, the ranges in estimates of predicted breeding value (***PBV***) in GM, SM and MA strains were 4.6, 4.7 and 4.0 grams for BW0, 31.5, 18.7 and 52.9 grams for BW4, 37.9, 111.2 and 68.2 grams for BW8 and 121.8, 178.2 and 288.8 grams for BW12, respectively. The respective ranges in estimates of* ***PBV*** *for DG traits were 1.15, 0.58 and 1.82 grams for DG4, 2.99, 4.05 and 3.31 grams for DG8 and 9.54, 4.23 and 8.73 grams for DG12. For sires and dams without records in GM, SM and MA strains, the minimum and maximum estimates of breeding values predicted for sires (***PBVS***) and dams (***PBVD)*** *of birds and their ranges for BW and DG traits had the same trend obtained for birds with records. MA strain recorded the highest ranges of* ***PBV****,* ***PBVS*** *and* ***PBVD*** *for most growth traits compared to those recorded by GM and SM strains. Accuracies of minimum and maximum estimates of sires breeding values for*

BW and DG traits predicted for MA strain were the highest followed by SM and GM strains. Also, accuracies of predicted breeding values for dams of birds recorded by MA and SM strains were higher than those recorded by GM strain. The averages of accuracies in estimates of predicted breeding values for sires of birds in the three strains were nearly the same.

INTRODUCTION

Growth performance in poultry should be selected on the basis of their estimated breeding values rather than on phenotypic performance. The accuracy of estimation of the breeding value of the chicks becomes more precise together with an extending for the information not only available on their own performance test but also on both the full and half sibs as well as of the ancestors. The Animal Model is nowadays applied in some species of poultry, but it has not been widely used. Derivative-Free Restricted Maximum Likelihood Algorithm (**DFREML**) allows unified approach for genetic evaluation and estimation of variance components for chickens (Mielenz et al., 1994). Recently, multivariate predictions of the genetic merit of the individual (e.g. **MTDFREML, MTGSAM, PEST**, …etc.) requires specification of the covariance structure among the traits considered for true or conceptual base generation (this is neglected with a single-trait analysis). In Egypt, Iraqi (1999) carried out an attempt based on comparison between single- and multi-traits Animal Models for growth traits in Dokki-4 chickens. He concluded that applying multi-traits Animal Model in evaluation allows estimation of additive genetic variance without bias, consequently the predictors are BLUP associated with lower predicted error variance (PEV) and an increase in selection efficiency. An early attempt was done by Abdellatif and Abdou (1977) to estimate breeding values of Fayoumi cocks using different methods (Hungarian Standard, Lauprecht and Siler-Vachal) of progeny testing. For other local strains like Silver and Golden Montazah, Matrouh, Bandara, Alexandria, …etc, no attempts have been made to predict the breeding values of the birds using new methodology such as single or multi-traits Animal Models. Therefore, this study was aimed: (1) to estimate the additive genetic variance and heretability for growth traits of three local strains (e.g. Silver Montazah, Golden Montazah and Matrouh chickens), (2) to predict the breeding values for sires, dams and their progenies and (3) to estimate the accuracy and standard errors of the predicted estimates.

MATERIAL AND METHODS

This experiment was carried out at Inshas Poultry Breeding Research Station, Animal Production Research Institute, Ministry of Agriculture, Egypt. Three pedigreed local strains of poultry named Golden Montazah (GM), Silver Montazah (SM) and Matrouh (MA) were used. The SM strain was developed from the crossing of Rhode Island Red males (exotic breed) and Dokki-4 females (native breed) for three consecutive generations together with selection, then intense matings and selection for several generations were practiced (Mahmoud et al., 1974b). One GM strain was developed from the crossing of Rhode Island Red males and Dokki-4 females for five consecutive generations together with selection, then intense matings and selection for several generations were practiced (Mahmoud et al., 1974c). The MA strain was developed from the crossing of White Leghorn males and Dokki-4 females for three consecutive generations together with selection, then intense matings and selection for several generations were practiced (Mahmoud et al., 1974a).

The experimental work was carried out for one generation started in 1997. A total number of 15, 16 and 17 pedigreed cocks and 114, 133 and 134 pedigreed pullets were chosen randomly at sexual maturity from base populations of GM, SM and MA strains, respectively, to be the parents of the first generation. The number of progeny produced from the three strains were 916, 1137 and 1030 chicks, respectively.

Chicks were fed *ad libitum* during the growing period on a commercial ration containing 21% crude protein, 3.9% crude fat and 3.7% crude fibers. All chicks of one-day old were wing-banded and reared in floor brooder, then transferred to the rearing houses. All birds were treated and medicated similarly throughout the experimental period and they were raised under the same managerial and climatic conditions as possible.

Data

Data of body weight (gram) at hatch (BW0), 4 weeks (BW4), 8 weeks (BW8), and 12 weeks (BW12) of age were collected on all individuals of the first generation. Daily gains in weight (DG) between intervals of 0-4 (DG4), 4-8 (DG8) and 8-12 (DG12) weeks were also computed.

Model of analysis

Data of each strain were analysed separately using multi-traits Animal Model (Boldman et al, 1995). The model of multivariate analysis resembles a stack of the single-trait Animal Model for each trait. The model of multivariate analysis for two traits could be written as:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_{a1} & 0 \\ 0 & Z_{a2} \end{bmatrix} \begin{bmatrix} u_{a1} \\ u_{a2} \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

Where y_i = Vector of the ith trait observed on birds; b_i = Vector of fixed effect of sex for the ith trait; u_{ai} = Vector of random bird effects for the ith trait; X_i and Z_{ai} are incidence matrices relating records of the ith trait to fixed effects and the random bird effects, respectively. Writing out the equations for each trait separately in the Multi-traits Animal Model, the mixed model equations (**MME)** become:

$$\begin{bmatrix} X'_1 X_1 & X'_1 X_2 & X'_1 Z_{a1} & X'_1 Z_{a2} \\ X'_2 X_1 & X'_2 X_2 & X'_2 Z_{a1} & X'_2 Z_{a2} \\ Z'_{a1} X_1 & Z'_{a1} X_2 & Z'_{a1} Z_{a1} + A^{-1}\alpha_{a1} & Z'_{a1} Z_{a2} + A^{-1}\alpha_{a12} \\ Z'_{a2} X_1 & Z'_{a2} X_2 & Z'_{a2} Z_{a1} + A^{-1}\alpha_{a21} & Z'_{a2} Z_{a2} + A^{-1}\alpha_{a2} \end{bmatrix} \begin{bmatrix} \hat{b}_1 \\ \hat{b}_2 \\ \hat{u}_{a1} \\ \hat{u}_{a2} \end{bmatrix} = \begin{bmatrix} X'_1 y_1 + X'_1 y_2 \\ X'_2 y_1 + X'_2 y_2 \\ Z'_{a1} y_1 + Z'_{a1} y_2 \\ Z'_{a2} y_1 + Z'_{a2} y_2 \end{bmatrix}$$

Where A^{-1} = inverse of the numerator relationship matrix among birds. In the present study, the **MME** in multi-traits Animal Model are being too large when we have more than two traits (e.g. 4 traits for body weights and 3 traits for daily gains). The multivariate Animal Model is considering the relationship coefficient matrix (A^{-1}) among birds in estimation (Korhonen, 1996). All calculations of BLUP estimates for multi-traits Animal Model were carried out using the MTDFREML program (Boldman et al., 1995) adapted to use the sparse matrix package, SPARSPAK (George and Ng, 1984). Convergence was assumed when the variance of the log-likelihood values in the simplex reached $<10^{-6}$. Occurrence of local maximal was checked by repeatedly restarting the analyses until the log-likelihood did not change beyond the first decimal.

Estimates of variance, covariance and heritability

A multi-traits Animal Model was used to estimate direct additive genetic, error, phenotypic variances and heritability. Variances and covariances obtained by the sire model (REML method using procedure VARCOMP, SAS, 1996) were used as starting values (guessed values) for the estimation of variance and covariance components using multi-traits Animal Model. Heritability was computed according to Boldman et al. (1995) as:

$$h_a^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2}$$

Where σ_a^2 and σ_e^2 are variances due to effects of direct additive genetic and random error, respectively.

Estimation of breeding values

The variances and covariances estimated by multi-traits Animal Model analysis were used for estimation of predicted breeding values (**PBV**), standard errors and their accuracies of predictions ($r_{A\hat{A}}$ **).**

Solutions for equations of birds were computed from the pedigree file, one bird at a time for birds with records and birds without records, i.e. sire and dams. A diagonal element (**d_t**) and an adjusted right-hand side (y^*_t) were accumulated with each pedigree file record for the tth bird. For birds with and without records, the formula (Kennedy, 1989) used to estimate the predicted breeding values (**PBV**) was:

PBV = **[**y^*_t/d_t**]**; where y^*_t/d_t = breeding values of the birds with and without records.

The accuracy of predicted breeding value for each individual was estimated according to Henderson (1975) as:

$$r_{A\hat{A}} = \sqrt{1 + F_j - d_j \alpha_a}$$

Where $r_{A\hat{A}}$ = the accuracy of prediction of the ith bird's breeding value for birds with and without records; F_j= inbreeding coefficient of birds (which equal to zero as calculated using MTDFREML program of Boldman et al., 1995); d_j= the jth diagonal element of inverse of the appropriate block coefficient matrix; and $\alpha = \sigma^2_e/\sigma^2_a$.

Standard error (**SE**) of predicted breeding value for each individual was estimated as follows:

$$s.e._p = d_j \sigma_e^2$$ Where d_j and σ^2_e were defined above.

RESULTS AND DISCUSSION

Means and variations

Means, phenotypic standrd deviations (SD) and percentages of variability of body weights (BW) and daily gains (DG) in GM, SM and MA strains are given in Table 1. Results show that GM and SM strains had higher in growth traits than MA strain. Means in the present study were generally higher than recorded by Mahmoud et al. (1974a&b&c) for the same strains. On the other hand, DG traits in GM and SM strains are high compared to in MA strain. This may be due to the GM and SM strains originated from crossing Rhode Island Red (as dual purpose breed) males with Dokki-4 females, while MA strain originated from crossing White Leghorn (as egg-type breed) males with Dokki-4 females (Mahmoud et al., 1974a&b&c).

Percentages of variability for each trait of BW and DG in the three strains tend to increase with the increase of the age. The same trend was shown by Sabra (1990), Khalil et al. (1993) and Iraqi (1999). Estimates of V% for most of growth traits in MA strain were higher than those in SM and GM trains. The percentage of variability ranged from 8.38 to 29.03%, 6.68 to 24.34% and 8.29 to 23.38% for growth traits in MA, SM and GM strains, respectively.

Variance components and heritabilities

Estimates of additive (σ_a^2), error (σ_e^2), phenotypic (σ_p^2) and heritability (h_a^2) for growth traits in GM, SM and MA strains are presented in Table 2. Results show that most percentages of σ_a^2 for growth traits in MA strain were higher than in SM and GM strains. These results were generally within the range of those estimates obtained by Iraqi et al. (2000) in the comparative study among different methods to estimates variance component for the same strains. Commonly, estimates of σ_a^2 in MA and GM strains in the present study were somewhat high compared to findings' of Iraqi (1999) on Dokki-4 chickens using single- and multi-traits Animal Model. This might be due to these strains were not subjected to any intensive program of selection (Iraqi et al., 2000).

Estimates of heritability (h_a^2) for growth traits in the three strains showed the similar trend of percentages of additive genetic variance (Table 2). Estimates of h_a^2 in GM and SM strains for BW at hatch were higher than at later ages (at 12 weeks). The estimates are 0.45 and 0.22 for BW0 and 0.21 and 0.18 for BW12 in GM and SM strains, respectively. This might be due to the small maternal effects, i.e. decreasing the non-additive genetic variance effects (Danbaro et al., 1995 and Iraqi 1999). Thus, we would recommend the Egyptian poultry breeder to select these strains at early ages without waiting to later ages to save time and efforts. Estimates of h_a^2 in the present study were generally within the range of those estimates obtained for the same strains by Sabra (1990) and Iraqi et al. (2000).

Breeding values estimated for birds with records

The minimum and maximum estimates of predicted breeding value (**PBV)** and their ranges (i.e. the difference between the maximum and minimum value), standard errors (SE) and accuracy of each predictor ($r_{A\hat{A}}$) for growth traits of all birds and the top 50% of progeny birds to be selected in GM, SM and MA strains are presented in Table 3. For the list of all birds, the ranges in estimates of **PBV** in GM, SM and MA strains were 4.6, 4.7 and 4.0 grams for BW0, 31.5, 18.7 and 52.9 grams for BW4, 37.9, 111.2 and 68.2 grams for BW8 and 121.8, 178.2 and 288.8 grams for BW12, respectively. The respective ranges in estimates of **PBV** for DG traits were 1.15, 0.58 and 1.82 grams for DG4, 2.99, 4.05 and 3.31 grams for DG8 and 9.54, 4.23 and 8.73 grams for DG12. Ranges mentioned before indicate that MA strain recorded higher ranges in estimates of **PBV** for BW and DG traits than the GM and SM strains. As stated before, GM and SM strains originated from crossing Rhode Island Red males with Dokki-4 females, while MA strain originated from crossing White Leghorn males with Dokki-4 females (Mahmoud, 1974a&b&c). Consequently, the three strains originated from one dam-breed (Dokki-4) while they differed in sire-breed in terms of Rhode Island Red for both GM and SM and White Leghorn for MA strain. The Rhode Island Red is a dual-purpose breed and the White Leghorn is an egg-type breed and this may explain why genetic variation for growth performance in MA strain could be high compared with SM and GM. The high estimates of **PBV** for growth traits in MA strain indicate that improvement of growth performance of this strain could be achieved through selection relative to the other two strains studied.

Accuracies ($r_{A\hat{A}}$) of minimum and maximum estimates of **PBV** recorded for BW and DG traits of birds with records were moderate to high in most cases (Table 3). The estimates of $r_{A\hat{A}}$ for BW traits ranged from 0.46 to 0.65 in GM strain, 0.56 to 0.68 in SM and 0.58 to 0.69 in MA, while the respective figures for DG traits ranged from 0.62 to 0.73, 0.65 to 0.66 and 0.66 to 0.73 (Table 3). However, the accuracies in **PBV** recorded by MA and SM strains were high compared to estimates obtained in GM. This may due to the small number of records used in GM (916 records) vs 1137 records used in SM and 1030 records used in MA. Pribyl and Pribylova (1991) found that reliability of **PBV** was 0.60 for body weight of birds with records at 20-week of age. Based on multi-traits Animal Model, Iraqi (1999) found that averages of accuracies for estimates of **PBV** for BW and DG traits of Dokki-4 birds with records were 0.66 and 0.65, respectively.

The number of birds with positive estimates of **PBV** and their percentages (Table 4) indicate that MA strain recorded high percentages (55%) of birds with positive signs for growth traits compared to those estimates recorded by GM and SM strains. Percentages of birds with positive signs in the present study for all strains were higher than those findings recorded by Iraqi (1999) for Dokki-4 chickens (42%). This indicates that GM, SM and MA strains have high **PBV** with positive signs, and this leads to state that the top 50% of birds to be selected all had positive **PBV**. Thus, selection of birds themselves could be more effective method (individual selection) to improve growth traits of the three strains of chickens under local conditions.

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

The minimum and maximum estimates of breeding values predicted for sires of birds (**PBVS**) and their ranges for BW and DG traits in GM, SM and MA strains (Table 5) indicate that estimates for birds without records had the same trend obtained for birds with records. The ranges in estimates of **PBVS** in GM, SM and MA strains were 3.3, 4.2 and 3.3 grams for BW0, 21.8, 15.4 and 31.6 grams for BW4, 37.6, 82.0 and 62.7 grams for BW8 and 83.5, 176.5 and 239.9 grams for BW12, respectively. The corresponding ranges in estimates of **PBVS** for DG traits were 0.8, 0.2 and 1.2 grams for DG4, 1.8, 2.1 and 2.3 grams for DG8, and 4.5, 2.2 and 6.9 grams for DG12. Ranges given before indicate that MA strain recorded the highest estimates of **PBVS** for all growth traits compared to those recorded by GM and SM strains. In agreement with the present results, Iraqi (1999) found that the predicted sire transmitting abilities for Dokki-4 chickens were 0.09, 0.17, 4.84 and 2.43 grams for BW0, BW4, BW8, BW12, respectively, and 0.35, 0.27 and 0.03 grams for DG4, DG8 and DG12, respectively.

From one age to another, the accuracy ($r_{A\hat{A}}$) of minimum and maximum estimates of **PBVS** for growth traits of sires of birds in the three strains were high and ranged from 0.68 to 0.90 in GM, 0.74 to 0.85 in SM and 0.75 to 0.86 in MA (Table 5). The pattern of change of these estimates had the same trend obtained for birds with records (Table 3). The estimates for GM, SM and MA strains averaged 0.76, 0.81 and 0.80 for BW traits and averaged 0.86, 0.83 and 0.83 for DG traits, respectively. Across all minimum and maximum estimates of **PBVS**, the averages of accuracies in all the three local strains were nearly the same (Table 5). This may be due to the numbers of sires used in the three strains were nearly equal (i.e. 15, 16 and 17 sires were used from GM, SM and MA strains, respectively). Pribyl and Pribylova (1991) found that reliability of **PBVS** was 0.84 for body weights of sires of birds at 20-week of age. Recently, Iraqi (1999) found that averages of accuracy across all the minimum and maximum estimates of **PBVS** were 0.81 and 0.75 for BW and DG traits in Dokki-4 chickens, respectively.

The accuracy in **PBVS** estimated for sires without records (**PBVS**) were higher than those **PBV** estimated for birds with records (Tables 3&5). This may be due to that each sire had an average of 67 progeny records, while birds with records had just only one record in estimation of breeding value. Korhonen (1996) reported that the heritability of the trait and the amount of information utilized in evaluation could affect the reliability of the predictors.

The number of sires with positive estimates of **PBVS** and their percentages for most growth traits (Table 6) indicate that predictors recorded by sires of MA strain, as stated before for **PBVS**, were mostly higher than those recorded by GM and SM strains. Similarly, Iraqi (1999) found that averages of percentages for **PBVS** with positive sign were 48.5% and 50% for BW and DG traits, respectively.

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

The minimum and maximum estimates of **PBVD** and their ranges (Table 7) indicate that these estimates had the same trend obtained for birds with records (Table 3). The ranges in estimates of **PBVD** in GM, SM and MA strains were 2.7, 3.1 and 3.0 grams for BW0, 24.6, 13.0 and 37.9 grams for BW4, 21.2, 82.8 and 56.2 grams for BW8 and 80.3, 142.9 and 168.0 grams for BW12, respectively. The corresponding ranges in estimates of **PBVD** for DG traits were 0.53, 0.48 and 1.21 grams for DG4, 1.33, 2.64 and 3.96 grams for DG8 and 4.45, 3.92 and 4.81 grams for DG12; i.e. MA strain recorded the highest estimates of **PBVD** for most growth traits. Similar to the present results, Iraqi (1999) with Dokki-4 chickens reported that the predicted transmitting abilities for dams were 0.55, 4.32, 9.71 and 12.77 grams for BW0, BW4, BW8 and BW12, respectively, and 0.20, 0.47 and 0.33 grams for DG4, DG8 and DG12, respectively.

Across all minimum and maximum estimates of **PBVD** for growth traits of dams of birds, the accuracies of these estimates in GM, SM and MA strains were moderate to high (Table 7). The estimates of $r_{A\hat{A}}$ in GM, SM and MA strains averaged 0.50, 0.57 and 0.56 for body weight traits and 0.38, 0.57 and 0.63 for gain in weight traits, respectively. These results indicate that accuracy in estimates of **PBVD** for dams of MA and SM strains were higher than those recorded for GM. This may be due to the fact that numbers of dams used in evaluation for MA and SM were the same (i.e. 133 and 134 dams) irrespective to 114 dams used in GM strain (Korhonen, 1996). On the other hand, the accuracy in estimates of **PBVD** recorded by the dams of birds without records were lower than those recorded by the birds themselves (birds with records) and their sires without records (Tables 3&5&7). This may be due to small numbers of progeny per dam utilized (each dam had an average of 8 progeny records).

The numbers of dams and their percentages having positive estimates of **PBVD** (Table 8) indicate that percentages of **PBVD** with positive signs for all growth traits were nearly averaged 50% in the three local strains.

CONCLUSIONS

(1) Estimates of h_a^2 in GM and SM strains for BW traits at hatch were higher than at later ages (at 12 weeks). Therefore, we would recommend the Egyptian poultry breeder to select these strains at early ages without waiting to later ages to save time and efforts.

(2) For birds with and without records, MA strain recorded higher ranges in estimates of PBV, PBVS and PBVD for BW and DG traits than those recorded by GM and SM strains. It could be fairly, therefore, to state that using of MA strain could be an encouraging factor for the poultry breeder to involve this strain in any improvement program to improve growth performance of local chickens in Egypt.

(3) Accuracy of **PBV** increased as the number of records increased. This was evidenced in this study since accuracy in **PBV** for dams (with an average of 8 progeny records) were lower than accuracy in **PBV** for sires (with an average of 67 progeny records).

Table 1. Means and coefficients of variation (V%) for body weight (BW) and daily gains (DG) in Golden Montazah, Silver Montazah and Matrouh strains.

Trait	Symble	Golden Montazah			Silver Montazah			Matrouh		
		No.	M±SD	V%	No.	M±SD	V%	No.	M±SD	V%
Body weights (g):										
BW0	Body weight at hatch	916	33.58±2.78	8.29	1137	33.50±2.91	8.69	1030	33.80±2.82	8.38
BW4 BW0	Body weight at 4 weeks	892	179.06±24.22	13.53	1084	183.60±22.0	11.97	966	171.50±23.47	13.68
BW8	Body weight at 8 weeks	866	490.50±66.39	13.53	1037	464.86±75.63	16.27	926	450.45±68.80	15.27
BW12	Body weight at 12 week	846	893.82±131.99	14.77	983	845.69±147.51	17.44	897	840.63±158.32	18.83
Daily gains (g):										
DG4	Daily gains from hatch-4 weeks	892	5.239±0.876	16.73	1084	5.401±0.796	14.74	966	4.971±0.850	17.10
DG8	Daily gains from 4-8 weeks	866	11.146±1.922	17.25	1037	10.028±2.213	22.07	926	9.979±1.932	19.37
DG12	Daily gains from 8-12 week	846	14.366±3.359	23.38	983	13.555±3.312	24.43	897	13.926±4.043	29.03

Table 2. Estimates of direct additive genetic (σ_a^2), error (σ_e^2), phenotypic (σ_p^2) variances and heritability (h_a^2) for growth traits in in Golden Montazah, Silver Montazah and Matrouh strains.

Trait+	**Golden Montazah**						**Silver Montazah**						**Matrouh**					
	σ_a^2	%	σ_e^2	%	σ_p^2	h_a^2	σ_a^2	%	σ_e^2	%	σ_p^2	h_a^2	σ_a^2	%	σ_e^2	%	σ_p^2	h_a^2
Body weight (BW):																		
BW0	2.880	44.6	3.576	55.4	6.457	0.45	1.569	21.93	5.585	78.07	7.154	0.22	1.010	17.28	4.834	82.72	5.844	0.17
BW4	63.773	19.34	265.82	80.66	329.69	0.19	19.977	6.71	277.944	93.29	297.921	0.07	69.585	18.92	298.269	81.08	367.854	0.19
BW8	360.88	11.50	2776.17	88.5	3137.05	0.12	709.26	21.99	2515.57	78.01	3224.83	0.22	359.72	11.07	2889.75	88.93	3249.471	0.11
BW12	1966.92	20.89	7450.14	79.11	9417.06	0.21	1663.93	18.33	7413.25	81.67	9077.18	0.18	3562.96	29.91	8348.17	70.09	11911.14	0.30
Daily gains (DG):																		
DG4	0.092	19.21	0.387	80.79	0.479	0.19	0.018	1.89	0.935	98.11	0.954	0.02	0.121	21.72	0.436	78.28	0.557	0.22
DG8	0.628	19.50	2.594	80.50	3.221	0.19	0.754	15.02	4.267	84.98	5.021	0.15	0.736	24.48	2.270	75.52	3.006	0.24
DG12	3.713	47.19	4.155	52.81	7.87	0.47	1.224	8.37	13.407	91.63	14.631	0.08	3.234	34.95	6.020	65.05	9.254	0.35

+Traits as defined in Table 1.

Table 3. **Minimum, maximum and ranges of predicted breeding values (PBV) for birds with records, their standard errors (SE) and accuracy of prediction ($r_{A\hat{A}}$) estimated by multi-traits animal model for growth traits in Golden Montazah, Silver Montazah and Matrouh strains*.**

Trait+	**Golden Montazah**							**Silver Montazah**							**Matrouh**						
	Minimum			Maximum			Ran in PB	Minimum			Maximum			Ran in PB	Minimum			Maximum			Rang in PB
	PB	**S**	r_A	**PB**	**S**	r_A		**PB**	**S**	r_A	**PB**	**S**	r_A		**PB**	**S**	r_A	**PB**	**S**	r_A	
Body weights in grams (BW):																					
BW0	-2.	0.	0.	2.	0.	0.	4.	-2.	0.	0.6	2.	0.	0.6	4.7	-2.4	0.8	0.63	1.6	0.8	0.63	4.0
BW4	-15	5.	0.	15.	5.	0.	31.	-11	3.	0.5	7.	3.	0.5	18.	-25.9	6.3	0.66	27.0	6.3	0.65	52.9
BW8	-18	11	0.	19.	11	0.	37.	-53	20.	0.6	57.	20.	0.6	111.	-33.0	15.4	0.58	35.2	15.4	0.58	68.2
BW12	-58	25	0.	63.	25	0.	121	-83	32.	0.6	95.	31.	0.6	178.	-139.5	43.0	0.69	149.3	43.3	0.69	288.8
Daily gains in grams (DG):																					
DG4	-0.	0.	0.	0.5	0.	0.	1.1	-0.	0.1	0.6	0.2	0.1	0.6	0.5	-0.97	0.26	0.66	0.85	0.26	0.66	1.82
DG8	-1.	0.	0.	1.4	0.	0.	2.9	-1.	0.6	0.6	2.6	0.6	0.6	4.0	-1.72	0.61	0.70	1.59	0.61	0.70	3.31
DG12	-5.	1.	0.	4.4	1.	0.	9.5	-1.	0.8	0.6	2.2	0.8	0.6	4.2	-4.10	1.24	0.73	4.63	1.25	0.72	8.73

+Traits as defined in Table 1.

*** Total numbers of progeny with records evaluated were 916, 1137 and 1030 individuals for Golden Montazah, Silver Montazah and Matrouh strains, respectively.**

Table 4. Numbers (and percentages) of birds with records which having positive estimates of breeding values predicted by multi-traits animal model for growth traits in Golden Montazah (GM), Silver Montazah (SM) and Matrouh (MA) strains.

Trait	Birds with positive PBV[+]					
	GM		**SM**		**MA**	
	No	**%**	**No**	**%**	**No**	**%**
Body weights (BW):						
BW0	437	48	546	48	582	57
BW4	514	56	590	52	612	59
BW8	453	49	521	46	507	49
BW12	478	52	564	50	551	53
Average		**51**		**49**		**55**
Daily gains (DG):						
DG4	488	53	576	51	603	59
DG8	459	50	543	48	495	48
DG12	480	52	599	53	550	53
Average		**52**		**51**		**53**

[+] Total numbers of birds evaluated were 916, 1137 and 1030 individuals in GM, SM and MA strains, respectively**.**

Table 5. Minimum, maximum and ranges of predicted breeding values for sires without records (**PBVS**), their standard errors (**SE**) and accuracy of prediction ($r_{A\hat{A}}$) estimated by multi-traits animal model for growth traits in Golden Montazah, Silver Montazah and Matrouh strains[+].

Trait	**Golden Montazah**							**Silver Montazah**							**Matrouh**						
	Minimum			Maximum			**Range in PBVS**	Minimum			Maximum			**Range in PBVS**	Minimum			Maximum			**Range in PBVS**
	PBVS	**SE**	$r_{A\hat{A}}$	**PBVS**	**SE**	$r_{A\hat{A}}$		**PBVS**	**SE**	$r_{A\hat{A}}$	**PBVS**	**SE**	$r_{A\hat{A}}$		**PBVS**	**SE**	$r_{A\hat{A}}$	**PBVS**	**SE**	$r_{A\hat{A}}$	
Body weights in grams (BW):																					
BW0	-1.7	0.7	0.81	1.9	0.7	0.81	3.6	-2.2	0.7	0.85	2.0	0.7	0.84	4.2	-1.9	0.6	0.80	1.4	0.6	0.82	3.3
BW4	-12.4	4.3	0.79	9.4	4.3	0.79	21.8	-9.7	2.9	0.77	5.7	3.0	0.74	15.4	-19.9	4.8	0.82	11.8	5.0	0.80	31.6
BW8	-18.6	9.6	0.68	19.1	9.3	0.70	37.6	-41.6	14.1	0.85	40.4	15.1	0.82	82.0	-29.1	12.6	0.75	33.5	12.6	0.75	62.7
BW12	-36.8	20.6	0.76	46.7	20.6	0.76	83.5	-113.5	23.2	0.82	63.0	25.2	0.79	176.5	-135.9	34.2	0.82	104.1	32.3	0.85	239.9
Daily gains in grams (DG):																					
DG4	-0.49	0.17	0.84	0.36	0.16	0.84	0.85	-0.11	0.08	0.82	0.12	0.08	0.82	0.23	-0.82	0.19	0.83	0.43	0.20	0.82	1.25
DG8	-1.01	0.42	0.84	0.76	0.44	0.83	1.77	-0.99	0.48	0.83	1.16	0.49	0.83	2.15	-1.33	0.48	0.83	0.95	0.48	0.83	2.28
DG12	-2.19	0.87	0.89	2.33	0.84	0.90	4.52	-1.25	0.61	0.84	0.92	0.61	0.83	2.17	-3.93	1.00	0.83	3.06	0.91	0.86	6.98

[+] Total numbers of birds without records evaluated were 15, 16 and 17 sires for Golden Montazah, Silver Montazah and Matrouh strains, respectively.

Table 6. Numbers (and percentages) of sires without records which having positive estimates of breeding values (PBVS) predicted by multi-traits animal model for growth traits in Golden Montazah (GM), Silver Montazah (SM) and Matrouh (MA) strains.

Trait	Birds with positive **PBVS**[+]					
	GM		**SM**		**MA**	
	No	%	No	%	No	%
Body weights (BW):						
BW0	6	40	7	45	11	65
BW4	8	53	8	50	11	65
BW8	7	47	7	45	8	47
BW12	7	47	6	38	11	65
Average		**47**		**45**		**61**
Daily gains (DG):						
DG4	8	53	7	45	11	65
DG8	8	53	8	50	8	47
DG12	8	53	10	63	9	53
Average		**53**		**53**		**55**

[+] Total numbers of sires evaluated were 15, 16 and 17 in GM, SM and MA strains, respectively.

Table 7. Minimum, maximum and ranges of predicted breeding values for dams without records (**PBVD**), their standard errors (**SE**) and accuracy of prediction ($r_{A\hat{A}}$) estimated by multi-traits animal model for growth traits in Golden Montazah, Silver Montazah and Matrouh strains[+].

Trait	**Golden Montazah**							**Silver Montazah**							**Matrouh**						
	Minimum			Maximum			**Range in PBVD**	Minimum			Maximum			**Range in PBVD**	Minimum			Maximum			**Range in PBVD**
	PBVD	**SE**	$r_{A\hat{A}}$	**PBVD**	**SE**	$r_{A\hat{A}}$		**PBVD**	**SE**	$r_{A\hat{A}}$	**PBVD**	**SE**	$r_{A\hat{A}}$		**PBVD**	**SE**	$r_{A\hat{A}}$	**PBVD**	**SE**	$r_{A\hat{A}}$	
Body weights in grams (BW):																					
BW0	-1.3	0.9	0.60	1.4	0.9	0.56	2.7	-1.7	1.0	0.63	1.4	1.0	0.65	3.1	-1.8	0.8	0.55	1.2	0.8	0.55	3.0
BW4	-13.4	5.9	0.54	11.2	6.0	0.52	24.6	-5.9	3.7	0.55	7.2	3.8	0.51	13.0	-18.7	6.8	0.58	19.2	6.8	0.58	37.9
BW8	-10.1	12.2	0.35	11.2	11.9	0.40	21.2	-42.2	21.4	0.59	40.6	22.3	0.55	82.8	-35.2	16.3	0.51	21.0	16.8	0.46	56.2
BW12	-44.8	27.1	0.52	35.5	27.6	0.50	80.3	-51.3	34.0	0.55	91.6	35.5	0.49	142.9	-86.7	46.0	0.64	81.3	48.7	0.58	168.0
Daily gains in grams (DG):																					
DG4	-0.32	0.28	0.35	0.21	0.28	0.35	0.53	-0.26	0.11	0.55	0.22	0.11	0.58	0.48	-0.67	0.28	0.59	0.54	0.28	0.59	1.21
DG8	-0.53	0.74	0.34	0.80	0.74	0.37	1.34	-1.05	0.71	0.57	1.59	0.70	0.59	2.64	-2.19	0.65	0.65	1.77	0.66	0.64	3.96
DG12	-2.41	1.72	0.45	2.05	1.75	0.42	4.45	-1.82	0.91	0.57	2.10	0.93	0.54	3.92	-2.36	1.33	0.67	2.45	1.42	0.61	4.81

[+] Total numbers of birds without records evaluated were 114, 133 and 134 dams in Golden Montazah, Silver Montazah and Matrouh strains, respectively.

Table 8. Numbers (and percentages) of dams without records which having positive estimates of breeding values (PBVD) predicted by multi-traits animal model for growth traits in Golden Montazah (GM), Silver Montazah (SM) and Matrouh (MA) strains[+].

Trait	Birds with positive PBVD[+]					
	GM		**SM**		**MA**	
	No	**%**	**No**	**%**	**No**	**%**
Body weights (BW):						
BW0	56	49	67	50	69	51
BW4	52	54	72	54	73	54
BW8	59	52	63	47	65	49
BW12	56	49	57	43	73	54
Average		**51**		**49**		**52**
Daily gains (DG):						
DG4	56	49	71	53	66	49
DG8	59	52	75	56	72	54
DG12	56	49	67	50	72	54
Average		**50**		**53**		**52**

[+] Total numbers of dams evaluated were 114, 133 and 134 in GM, SM and MA strains, respectively**.**

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Chickens, Egyptian local strains, Growth performance, heritability, Breeding values, Multi-traits Animal Model.

الملخص العربى

تقدير القيم التربوية ومعاملات الدقة باستخدام تحليل نموذج الحيوان الوراثى متعدد الصفات - لصفات النمو فى ثلاث سلالات محلية من الدجاج

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تم التنبؤ بالقيم التربوية ومعاملات الدقة باستخدام نموذج الحيوان متعدد الصفات للطيور سواء فى وجود أو عدم وجود سجلات لثلاثة سلالات من الدجاج. استخدم عدد 916 & 1137 & 1030 كتكوت من سلالات المنتزة الذهبى والمنتزة الفضى والمطروح – على التوالى.

سجلت بيانات وزن الجسم لكل كتكوت عند عمر الفقس ، 4 ، 8 ، 12 أسبوع فى تجربة لمدة جيل واحد وتم حساب معدل الزيادة اليومية بين الفترات من عمر الفقس- 4 أسابيع & 4-8 أسابيع & 8-12 أسبوع.

أظهرت النتائج مايلى:

1- كانت قيم المكافئ الوراثى المقدر من التباين الوراثى المضيف لصفة وزن الجسم عند عمر الفقس أعلى عن تلك المقدرة فى الأعمار المتأخرة (12 أسبوع) لكل من سلالة المنتزة الذهبى والمنتزة الفضى. وكانت تلك القيم لصفة وزن الجسم 0.45 ، 0.22 عند عمر الفقس & 0.21 ، 0.18 عند عمر 12 أسبوع لكل من سلالة المنتزة الذهبى والمنتزة الفضى – على التوالى.

2- **في الطيور التي لها سجلات** : كان المدى للقيم التربوية المتنبأ بها لصفة وزن الجسم 4.6 ، 4.7 ، 4.0 جم عند عمر الفقس & 31.5 ، 18.7 ، 52.9 جم عند عمر 4 أسابيع & 37.9 ، 111.2 ، 68.2 جم عند عمر 8 أسابيع & 121.8 ، 178.2 ، 288.8 جم عند عمر 12 أسبوع لسلالات المنتزة الذهبى والمنتزة الفضى والمطروح – على التوالى.

وكانت القيم المناظرة لصفة معدلات الزيادة اليومية للسلالات الثلاثة على التوالى 1.15 ،

0.58 ، 1.82 جم فى الفترة من عمر الفقس– 4 أسابيع & 2.99 ، 4.05 ، 3.31 جم فى الفترة من عمر 4–8 أسابيع & 9.54 ، 4.23 ، 8.83 جم فى الفترة من 8–12 أسبوع.

3- **فى الآباء (الذكور والاناث) التى ليس لها سجلات** : كان الحد الأدنى والحد الأعلى للقيم التربوية المتوقعة والمدى لصفة وزن الجسم ومعدلات الزيادة اليومية تأخذ نفس الاتجاه للطيور (النسل) التى لها سجلات.

4-سجلت سلالة المطروح بصفة عامة أعلى مدى للقيم التربوية فى الطيور التى لها سجلات والآباء (الذكور والاناث) التى ليس لها سجلات لصفات النمو عند مقارنتها بتلك المسجلة لسلالات المنتزة الفضى والذهبى.

5-أظهرت سلالة المطروح أعلى معاملات دقة للحد الأدنى والحد الأعلى للقيم التربوية للآباء (الذكور) لصفات وزن الجسم ومعدلات الزيادة اليومية يليها سلالات المنتزة الفضى والذهبى. كما سجلت أيضا أمهات سلالات المطروح والمنتزة الفضى أعلى معامل دقة للقيم التربوية عن تلك المسجلة للمنتزة الذهبى. وكانت متوسطات معاملات الدقة للقيم التربوية المتوقعة لكل السلالات واحدة تقريبا لكل الآباء الذكور.