6 SUMMARY

The present study was carried out using data of 7226 chick of Dokki-4 chickens (as a native breed) in the Poultry Research farm at Inshas (Sharkia Governorate), Animal and Poultry Production Research Institute, Ministry of Agriculture, Egypt, in two consecutive generations in the period from March 1979 to June 1981. Data of individual body weight (**BW**) at hatch and biweekly thereafter up to 16 weeks of age were collected on all individuals of the first and second generation. Daily gain (**DG**) and relative growth rate (**RG**) between intervals of hatch-4, 4-8, 8-12 and 12-16 weeks were also computed.

Restricted Maximum Likelihood (**REML**) procedure (i.e. sire model and dam model) and Derivative Free Restricted Maximum Likelihood (**DFREML**) procedure (i.e. single-trait and multi-trait animal models) were used for analysis of such data. The results obtained could be summarized as:

1. Means and variation:

Means of **BW** and **DG** of Dokki-4 chicks increased with advancing of age. However, **RG** was high (135.40%) at the early stages (hatch-4 weeks), then decreased generally with the advancement of age which reached 33.57% during the period of 12-16 weeks. Percentages of phenotypic variation (V%) are tended to increase with the chick advanced in age for growth traits. The V% for **DG** and **RG** during the period of hatch-4 weeks was 20.4% and 7.5%, respectively.

2. Non-genetic aspects:

Means of **BW, DG** and **RG** of Dokki-4 chicks at different ages were slightly heavier in the first generation than those of the second generation. Also, males were heavier and higher in their growth than females' at all different ages. Difference between means of the two generations and the two sexes was highly significant (P<0.01) for most growth traits.

3. Variance components:

Variance components due to dam effect (σ_d^2) estimated by dam model are large (6.8%) at all ages comparable to sire effect (σ_s^2) (3.1%) estimated by sire model.

Percentages of direct additive genetic variance (σ_A^2) for **BW** and **RG** traits estimated by multi-trait **AM** appeared to be higher than those estimated by single-trait **AM**. The average percentages of σ_A^2 were 11.2% and 8.2% when using single-trait **AM** vs 13.9% and 8.8% when using multi-traits **AM** for **BW** and **RG** traits, respectively.

Percentages of Common environmental variance (σ_c^2) when using single-trait **AM** for **BW** were large at hatch (25.3%) but declined gradually at the chick grew older (14.2% at 16 weeks). The percentages of σ_c^2 for **BW** traits obtained by multi-trait **AM** were higher (22.0%) than those obtained by single-trait AM (17.4%).

4. Heritability:

Generally, estimates of heritability based on sire components of variance (h_s^2), dam components of variance (h_d^2), direct additive genetic variance when using single-trait (h_{AS}^2) and multi-trait (h_{AM}^2) were highest at younger ages (from hatch to 4 weeks of age) than at later ages (12-16 weeks of age) for all growth traits. The average estimates of h_d^2 were 0.35, 0.23 and 0.18 for **BW**, **DG** and **RG** traits, respectively. While the average estimates of h_s^2 were 0.14, 0.11 and 0.11 for the same order. Estimates of heritability resulting from multi-traits **AM** were somewhat larger (ranged from 0.14 and 0.09) than those obtained by single-trait analysis (ranged from 0.11 and 0.08) for **BW** and **AM** traits, respectively.

5. Correlation among growth traits:

Estimates of Genetic correlation (r_G) among **BW** were tended to increase in value as the intervals between the two ages get larger, and most of these associations among growth traits at different ages were high and indicated that the genetic factors of all growth traits studied were closely additively related. It ranged from 0.17 to 0.84 among **BW**, -0.35 to 0.65 among **DG** and -0.65 to 0.48 among **RG** traits.

All estimates of Common environmental correlation (r_c) among **BW** and among **DG** traits are positive and have moderate of high magnitude, and tended to decrease relatively in value as the intervals between the two ages get larger. The average estimates of r_c among **BW**, **DG** and **RG** were 0.65, 0.27 and -0.28, respectively.

Estimates of Environmental (r_E) and phenotypic (r_P) correlations among **BW** and among **DG** traits were positive and generally moderate or high. The average estimates of r_E among **BW**, **DG** and **RG** were 0.42, 0.15 and -0.16, respectively. While the average estimates of r_P were 0.45, 0.17 and -0.17 among **BW**, **DG** and **RG**, respectively.

6. Evaluation of birds:

Number of iterations required to reach convergence rate, **CPU**-time consumed and storage required could be affected by the number of equations (number of birds), the number of non-zero elements, the number of traits.

Results of Dokki-4 chicks, generally, recorded higher ranges in estimates of predicted breeding value (**PBV**) of birds with records, transmitting ability for sires (**PSTA**) and dams (**PDTA**) for **BW** when using multi-traits **AM** than those single-trait **AM**. The average of ranges in estimates of **PBV** obtained from multi-traits vs single-trait **AM** were 86.58 vs 67.95 grams, 4.17 vs 3.96 grams and 12.66 vs 10.71 % for **BW**, **DG** and **RG** traits, respectively.

The average of ranges in estimates of **PSTA** obtained by multi-traits **AM** vs single-trait **AM** were 36.97 vs 32.54 grams, 2.06 vs 2.11 grams and 5.14 vs 5.17 % for **BW**, **DG** and **RG** traits, respectively. While the average of ranges of **PDTA** when multi-trait **AM** using vs single-trait **AM** were 21.59 vs 15.83 grams, 0.87 vs 0.91 grams and 2.35 vs 1.99 % for **BW**, **DG** and **RG**, respectively.

In general, the accuracy of predictions (i.e. **PBV**, **PSTA** and **PDTA**) obtained by multi-traits **AM** was larger than those estimates obtained by single-trait **AM** for most of growth traits.

7. Rank correlation of predictions:

For data of birds (birds with records), estimates of rank correlation among most ranks of **PBV** estimates estimated by single-trait or multi-traits **AM** for **BW** and **DG** traits were moderate or high. Most estimates of rank correlation were significant ($P<0.01$).

Most estimates of rank correlations among estimates of **PBV**, **PSTA** and **PDTA** estimated by single-trait and/or multi-traits **AM** were high and highly significant ($P<0.01$) for **BW** at 8 weeks and the following ages.