4 RESULTS AND DISCUSSION

4.1 Means and variations:

Means, phenotypic standard deviations (**SD**) and percentages of variability (**V%**) of body weights (**BW**), daily gains (**DG**) and relative growth rates (**RG**) in Dokki-4 chickens are given in Table 22.

4.1.1 Means:

As expected, means of **BW** and **DG** of Dokki-4 chicks increased with advancing of age. The present estimates were generally fall within the range of those estimates obtained for the same breed by most of the Egyptian studies (Abd El-Gawad, 1969&1970; Sharara, 1974; Ayoub and Magraby, 1976; Abd El-Gawad, 1981; Khalil et al., 1993). Some of reviewed studies on Fayoumi, White Baladi and Dandarawi shown that body weight at hatch, 2, 4, 6, 8 and 12 weeks of age were lower in means than for Dokki-4 chickens of the present study (e.g. Samkari, 1962; Amer et al. 1964; El-Itriby and Sayed, 1966; Abd El-Gawad, 1969; El-Hossari, 1969; El-Maghraby et al., 1969; Ezzeldin, 1970; Abd El-Gawad and El-Itriby, 1971; Sharara, 1974; Ismail, 1980; Kosba and Eid, 1983; Sorour, 1984; Atta, 1985; Amer, 1990). For **RG** in Dokki-4 chickens, rate of gain was high (135.4%) at the early stages (hatch-4 weeks), then decreased generally with the advancement of age which reached 33.6% during the period of 12-16 weeks.

4.1.2 Percentage of variability (V%):

Results given in Table 22 indicate that percentage of variability for each trait of **BW**, **DG** and **RG** tend to increase with the increase of the age. The same trend was observed by Amer et al. (1964), El-Hossari (1969), El-Maghraby et al. (1969), Sharara (1974), Ayoub and Magraby (1976), Farrag (1977) Abd El-Gawad et al. (1979a&b), Sabra (1990) and Khalil et al. (1993). Estimates of V% in present study indicated also that variation of biweekly growth of Dokki-4 chicks was markedly lower during the earlier age interval (hatch-4 weeks) than at the older interval (12-16 weeks). The

Table 22. Means, standard deviations (SD) and percentages of variability (V%) for body weights, daily gains and relative growth rates at different ages in Dokki-4 chickens.

Trait[+]	No.	Mean	SD	V%
Body weight (grams):				
BW0	7226	31.6	3.1	9.7
BW2	6858	75.9	11.9	15.7
BW4	6594	167.9	28.3	16.8
BW6	6421	295.4	55.4	18.7
BW8	6156	428.3	72.7	17.0
BW10	5919	568.5	93.9	16.5
BW12	5645	744.2	130.6	17.6
BW16	4975	1052.8	186.1	17.7
Daily gain (grams):				
DG4	6594	9.8	2.0	20.4
DG8	6156	18.5	4.3	23.0
DG12	5645	22.4	6.5	29.1
DG16	4975	21.7	7.0	32.0
Relative growth rate (%):				
RG4	6594	135.4	10.1	7.5
RG8	6156	86.4	12.1	14.0
RG12	5645	53.2	11.6	21.8
RG16	4975	33.6	8.6	25.5

[+] Traits as defined in Table 20.

estimates of **V%** for **DG** and **RG** during the period of hatch-4 weeks were 20.4 and 7.5% compared to 32.0 and 25.5% during the period of 12-16 weeks, respectively. Lower variability from hatch-4 weeks may be due to the consequence of the expression of the combination of non-genetic maternal environment and the genetic factors (Falconer and Mackay, 1996). While the bird at later ages may be become less sensitive to the non-genetic maternal effects which decreases with advance of age, while the environmental effects increases with advance of age, therefore, **V%** is higher for later ages than for earlier ages (Gupta and Johar, 1975)

Generally, the estimates of V% for growth traits in Dokki-4 chickens are relatively high and they ranged from 7.5 to 32.0% (with an average equal to 18.9%) compared to the other local breeds (e.g. Fayoumi, White Baladi, Alexandria and Mamourah) which have ranged from 8.6 to 27.5% (with an average equal to 16.7%). Consequently improvement of growth rate in Dokki-4 chicks through phenotypic selection is quite possible.

4.2 Non-genetic aspects:

Means and standard errors for the effects of generation and sex on body weights (**BW**), daily gains (**DG**) and relative growth rates (**RG**) are presented in Table 23.

4.2.1 Generation:

Means are presented in Table 23 demonstrated that **BW** of chicks at different ages were significantly heavier in the first generation than those of the second generation at 2, 4 and 16 weeks of age. **BW** of the first and second generations recorded about 76.5 vs 75.1, 173.9 vs 160.4 and 1058.3 vs 1043.8 grams at 2, 4, and 16 weeks of age, respectively. However at 6, 10 and 12 weeks the opposite trend was recorded, i.e. 288.5 vs 304.4, 564.5 vs 573.8 and 740.9 vs 748.9 grams, respectively. Also, means of **DG** and **RG** in the first generation were significantly higher than those obtained in the second generation (except intervals of 4-8 weeks and 8-12 weeks of age). Slight superiority of the first generation relative to the second generation for

Table 23. Means, standard errors (SE) and percentages of progeny numbers (PN%) for body weights, daily gains and relative growth rates in the two generations.

Trait[+]	Generation						Significance
	Generation 1			Generation 2			
	No.	Mean ± SE	PN%	No.	Mean ± SE	PN%	
Body weight (grams):							
BW0	4020	31.6 ± 0.04	55.6	3206	31.6 ± 0.04	44.4	ns
BW2	3877	76.5 ± 0.15	56.5	2981	75.1 ± 0.18	43.5	**
BW4	3683	173.9 ± 0.38	55.9	2910	160.4 ± 0.42	44.1	**
BW6	3621	288.5 ± 0.76	56.4	2800	304.3 ± 0.86	43.6	**
BW8	3490	428.8 ± 0.99	56.7	2666	427.7 ± 1.14	43.3	ns
BW10	3375	564.5 ± 1.30	57.0	2544	573.8 ± 1.50	43.0	**
BW12	3282	740.9 ± 1.81	58.1	2364	748.9 ± 2.13	41.9	**
BW16	3096	1058.3 ± 2.58	62.2	1880	1043.8 ± 3.31	37.8	**
Daily gain (gram):							
DG4	3683	10.2 ± 0.03	55.9	2910	9.2 ± 0.03	44.1	**
DG8	3490	18.2 ± 0.06	56.7	2666	19.0 ± 0.07	43.3	**
DG12	3282	22.2 ± 0.10	58.1	2364	22.7 ± 0.11	41.9	**
DG16	3096	22.3 ± 0.11	62.2	1880	20.8 ± 0.14	37.8	**
Relative growth rate (%):							
RG4	3683	137.4 ± 0.14	55.9	2910	132.9 ± 0.16	44.1	**
RG8	3490	83.8 ± 0.17	56.7	2666	89.6 ± 0.20	43.3	**
RG12	3282	52.8 ± 0.18	58.1	2634	53.7 ± 0.21	41.9	**
RG16	3096	34.3 ± 0.14	62.2	1880	32.4 ± 0.18	37.8	**

[+] Traits as defined in Table 20.

ns= non-significant; **= P<0.01.

Table 23. Means, standard errors (SE) and percentages of progeny numbers (PN%) for body weights, daily gains and relative growth rates in the two sexes.

Trait+	Sex						Signif-icance
	Males			Females			
	No.	Mean ± SE	PN%	No.	Mean ± SE	PN%	
Body weight (grams):							
BW0	1699	32.7 ± 0.05	23.5	5527	31.3 ± 0.03	76.5	**
BW2	1661	80.3 ± 0.24	24.2	5197	74.5 ± 0.13	75.8	**
BW4	1616	179.2 ± 0.57	24.5	4977	164.3 ± 0.32	75.5	**
BW6	1593	323.2 ± 1.15	24.8	4828	286.2 ± 0.66	75.2	**
BW8	1539	469.9 ± 1.50	25.0	4617	414.5 ± 0.86	75.0	**
BW10	1487	628.6 ± 1.96	25.1	4432	548.3 ± 1.14	74.9	**
BW12	1435	843.2 ± 2.73	24.4	4211	710.5 ± 1.59	74.6	**
BW16	1223	1208.2 ± 4.11	24.6	3753	1002.2 ± 2.35	75.4	**
Daily gain (gram):							
DG4	1616	10.5 ± 0.04	24.5	4977	9.5 ± 0.02	75.5	**
DG8	1539	20.7 ± 0.09	25.0	4617	17.8 ± 0.05	75.0	**
DG12	1435	26.5 ± 0.15	25.4	4211	21.0 ± 0.09	74.6	**
DG16	1223	25.3 ± 0.17	24.6	3753	20.5 ± 0.10	75.4	**
Relative growth rate (%):							
RG4	1616	137.1 ± 0.22	24.5	4977	134.8 ± 0.12	75.5	**
RG8	1539	88.8 ± 0.26	25.0	4617	85.5 ± 0.15	75.0	**
RG12	1435	56.2 ± 0.27	25.4	4211	52.2 ± 0.16	74.6	**
RG16	1223	34.5 ± 0.23	24.6	3753	33.3 ± 0.13	75.4	**

+ Traits as defined in Table 20.

**= $P<0.01$.

growth traits may be due to that the numbers of progeny, sires and dams in the first generation were higher than that in the second generation (Hagger, 1991a). This is clear from the percentages of progeny numbers obtained from the two generations since the first generation posed 55.6 to 62.2% of the progeny produced (Table 23). Also, these may be due to different climatic conditions and the performance of birds could possible be genetically different from generation to another. Liu et al. (1994 and Dunnington and Siegel (1996) reported that generation effect on growth traits of chickens was highly significant ($P<0.01$).

4.2.2 Sex:

Males were heavier in weights and gains and higher in their growth rates than females' at all different ages (Table 23). This may be due to metabolic rate, level of growth hormone and feed efficiency for males higher than females. **BW** of males and females were 32.7 vs. 31.3, 179.2 vs. 164.3. 469.9 vs. 414.5, 843.2 vs. 710.5 and 1208.2 vs. 1002.2 grams at hatch, 4, 8,12 and 16 weeks of age, respectively. Since males were faster in their growth rates than females, the **RG** of males versus females were 137.1% vs. 134.8%, 88.8% vs. 85.5%, 56.2% vs. 52.2% and 34.5% vs. 33.3% during the periods hatch-4, 4-8, 8-12 and 12-16 weeks of age, respectively. These results are in full agreement with those findings reported by many investigators (e.g. Gupta and Johar, 1975; Mostageer et al., 1975 Shalash, 1977; Kumar, 1979; Singh and Singh, 1979&1983; Abou El-Ella, 1982; Al Sobyel, 1985; Ramappa et al., 1986; Sabra, 1990, Iraqi, 1991; Le Bihan-Duval et al., 1997). Table 23 show also that the percentages of progeny numbers for females were markedly higher than for males.

4.3 Components of variance:

4.3.1 REML method:

Variance components estimated from the sire model (σ_s^2 & σ_e^2) and variance components estimated from dam model (σ_d^2 & σ_e^2) for body weights (**BW**), daily gains (**DG**) and relative growth rates (**RG**) using **REML** method are given in Table 24.

Table 24. Estimates of sire (σ^2_s), dam (σ^2_d), additive (σ^2_A) and error (σ^2_e) variances for body weights, daily gains and relative growth rates using **REML** method.

Trait[+]	Sire model							Dam model						
	σ^2_s	V%[*]	σ^2_e	V%[*]	Additive variance		Total σ^2_P	σ^2_d	V%[*]	σ^2_e	V%[*]	Additive variance		Total σ^2_P
					$\sigma^2_A=4(\sigma^2_s)$	V%						$\sigma^2_A=4(\sigma^2_d)$	V%	
Body weight (grams):														
Bw0	0.50	5.1	9.30	94.9	2.0	20.4	9.8	1.35	13.8	8.42	86.2	5.4	55.1	9.77
BW2	5.35	4.0	128.6	96.0	21.4	16.0	133.95	13.93	10.4	119.8	89.6	55.72	41.7	133.73
BW4	29.24	4.1	675.5	95.9	116.96	16.6	704.74	55.63	7.9	648.4	92.1	222.52	31.6	704.03
BW6	80.01	2.9	2688.3	97.1	320.04	11.6	2768.31	166.88	6.0	2599.0	94.0	667.52	24.1	2765.88
BW8	150.43	3.2	4549.7	96.8	601.72	12.8	4700.13	293.61	6.3	4401.3	93.7	1174.44	25.0	4694.91
BW10	221.27	2.9	7394.2	97.1	885.08	11.6	7615.47	581.89	7.7	7021.2	92.3	2327.5	30.6	7603.09
BW12	290.48	2.1	13315.1	97.9	1161.92	8.5	13605.58	1173.5	8.6	12405.3	91.4	4694.0	34.6	13578.8
BW16	837.59	3.3	24715.3	96.7	3350.36	13.1	25552.89	2085.5	8.2	23411.2	91.8	8342.0	32.7	25496.7
Daily gain (grams):														
DG4	0.139	3.9	3.40	96.1	0.556	15.7	3.539	0.26	7.2	3.28	92.8	1.04	29.4	3.54
DG8	0.419	2.5	16.11	97.5	1.676	10.1	16.529	0.84	5.1	15.68	94.9	3.36	20.3	16.52
DG12	0.687	1.9	35.21	98.1	2.748	7.7	35.897	2.34	6.5	33.51	93.5	9.36	26.1	35.85
DG16	1.121	2.7	40.09	97.3	4.484	10.9	41.211	1.57	3.8	39.73	96.2	6.28	15.2	41.3
Relative growth rate (%):														
RG4	3.597	3.8	92.24	96.2	14.388	15.0	95.837	5.59	5.8	90.16	94.2	22.36	23.4	95.75
RG8	3.669	2.7	132.87	97.3	14.676	10.7	136.539	7.45	5.5	129.03	94.5	29.8	21.8	136.48
RG12	3.014	2.3	125.90	97.7	12.056	9.4	128.914	4.96	3.9	123.91	96.2	19.84	15.4	128.87
RG16	1.542	2.2	68.85	97.8	6.168	8.8	70.392	1.91	2.7	68.49	97.3	7.64	10.9	70.4

[+] Traits as defined in Table 20.

[*] Percentages of σ^2_s or σ^2_d or σ^2_e relative to σ^2_P.

4.3.1.1 REML estimators from the sire model:

The estimates presented in Table 24 show that percentages of variance due to sire effect are variable for all studied traits. They ranged from 2.1 to 5.1% (averaged 3.4%), 1.9 to 3.9% (averaged 2.8%) and 2.2 to 3.8% (averaged 2.8%) for **BW**, **DG** and **RG**, respectively. These percentages of sire component for Dokki-4 chickens were higher than those previously reported by many Egyptian investigators (Ezzeldin, 1970, Ayoub and Magraby, 1976; El-Maghraby and Bakir, 1977; Shalash, 1977, Iraqi, 1991) for some Egyptian breeds of chickens. In addition to that, the sire effects on all growth traits were larger in earlier ages than those later ages (Table 24). Ayoub (1965), El-Maghraby and Bakir (1977) and Farrag (1977) obtained the same trend with Dandarawi, Dokki-4 and Rhode Island Red chickens. On the other hand, some Egyptian investigators (Ayoub, 1965; El-Maghraby and Bakir, 1977; Farrag, 1977; Sorour, 1984) derived higher corresponding estimates from the sire component in Dokki-4, Dandarawi and White Baladi than represented in this study.

4.3.1.2 REML estimators from the dam model:

Results in Table 24 show that percentages of dam variance component were high at all ages comparable to the sire component. They ranged from 6.0 to 13.8% with an average equal to 8.6%. This may be due to maternal effects and possibly due to dominance and other additive and non-additive gene interactions. In addition to that, the dam effects were large in the early ages than those of the later ages. This is because the effect of egg size (as a character of the dam) on the chick's weight decreased quickly with the advancement of age (Jaap et al., 1962; Saeki et al., 1969a; Khalil, 1993; Aggrey and Cheng, 1994). The trend for **DG** and **RG** traits were similar to that obtained for **BW** traits. They ranged from 3.8 to 7.2% for **DG** and from 2.7 to 5.9% for **RG**. From the previous results, it is clear that dam effect could be considered as the most important factor affecting growth traits at hatching and during post hatching periods. This is true, since maternal and non-additive genetic effects are still present up to later ages. Schuele et al. (1996) stated that maternal and non-additive gene effects were important for body weights in Japanese Quail. Thus, sex-linked and maternal effects on body weights should be taken with reservation. One may recommend that broiler procedures should marketing their flocks at the age in which maternal as well as non-additive genetic effects are becoming small or insignificant. Percentages of variance due to dam effects in the present study (based on **REML** method) were lower than those reported by El-Maghraby and Bakir (1977), Farrag (1977), Iraqi (1991) (based on **Henderson**'s method) for the same breed. This is because different genetic models were used in estimation (Schaeffer, 1993).

In general, results given in Table 24 reveal that the dam at all ages studied had greater effect on the chicks' growth traits (6.8%) than of the sire (3.1%). Similarly, Ayoub (1965), Ezzeldin (1977), El-Maghraby and Bakir (1977), Farrag (1977), Shalash (1977), Sorour (1984) and Khalil et al. (1993) who were working on different breeds of chickens reported that the dam components of variance were higher than those of the sire component at all ages studied. In the literature, statistically, the upward bias in the dam component of variance for most reviewed estimates may be a result of the existence of interaction between dams and other fixed effects included in the same model of analysis (Toelle et al., 1990) which results in an inflation in the dam component and thereby downward bias in the sire component.

For comparison of **ANOVA** estimators in the literature and **REML** estimators in this study, estimates of variance components resulted by the **REML** method (**Iterative** method) are more accurate and preferable relative to **ANOVA** method (**Henderson's** method) because: (1) It is unbiased by selection since they have built in optimality properties (Searle, 1989; Hofer, 1998), (2) It does not taken any special demands on the design and hence it is an ideal method for unbalanced designs that arise in quantitative genetics (Toelle et al., 1991; Besbes et al., 1992; Knott et al., 1995), and (3) Sire- or dam-variance components are not affected by the fixed effects included in the model (Beaument, 1991; Smith and Savage, 1992; Ferraz and Johnson, 1993; Dieters et al., 1995; Johanson and Thomson, 1995; Hofer, 1998). However, **ANOVA** method has three significant practical limitations. First, **ANOVA** estimates of variance components require that sample sizes be reasonably well balanced, with the number of observations for each set of conditions being nearly equal. Second, observations collected from field often yield records with variety of relatives, such as offspring, parents, sibs, etc., that cannot be analysed jointly with **ANOVA**, i.e. covariance among effects of genetically related animals, cannot be accounted for. Third, covariances between any two traits can only be estimated from the animals on which both traits are measured. This yields biased estimates in cases where only animals that were selected on the first trait have a chance of expressing the second trait (Sorensen and Kennedy, 1984; Hofer, 1998). For the above reasons more precise estimates were obtained from the **REML** since it considered the relationship among animals (A^{-1}). This leads to an increase in the sire variance and a decrease in the error variance, i.e. analysis under sire mixed model equations (**MME**) which account for the relationships among sires (**REML**) should therefore give more precision in the genetic variance components.

4.3.2 DFREML estimators from single-trait and multi-traits animal models:

Estimates of direct additive genetic (σ^2_A), common environment (σ^2_c) and predicted error (σ^2_e) variance components estimated by **DFREML** method using single-trait and multi-traits animal models (**AM**) are presented in Tables 25 and 26. The direct genetic variance in this study was estimated the individual (progeny) itself.

4.3.2.1 Direct additive genetic variance:

The additive genetic variance is the chief cause of resemblance between relatives and therefore it is the chief determinant of the observable genetic properties of the population for selection. Moreover, it is the only component that can be readily estimated from the observations made on the population in practice, therefore, the important partition is additive genetic variance versus all the rest, the rest being the non-additive genetic and environmental variance (Falconer and Mackay, 1996). Also, Senou and Dempfle (1989) pointed out the factors affecting additive genetic variance

Table 25. 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 single-trait Animal Model.

Trait+	**Variance component of single-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
Relative growth rate (%):							
RG4	11.42	11.9	9.45	9.8	75.20	78.3	96.07
RG8	9.72	7.1	21.88	16.0	105.32	76.9	136.92
RG12	8.26	6.3	16.17	12.3	106.98	81.4	131.41
RG16	5.36	7.4	3.89	5.4	63.11	87.2	72.35

+ Traits as defined in Table 20.

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

Table 26. 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-traits animal model.

Trait[+]	**Variance component of multi-traits**						
	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
DG116	3.20	7.3	3.21	7.3	37.26	85.3	43.67
Relative growth rate (%):							
RG4	13.48	13.9	7.91	8.1	75.63	78.1	97.02
RG8	10.63	7.6	22.69	16.3	106.07	76.1	139.39
RG12	8.37	6.1	16.62	12.2	111.75	81.7	136.74
RG16	5.65	7.6	4.26	5.7	64.27	86.6	74.17

[+] Traits as defined in Table 20.

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

to be: (1) Selection which induced linkage dis-equilibrum, (2) The change of allele frequencies, and (3) The effective population size.

Estimates given in Table 25 show that percentages of direct additive genetic variance (σ^2_A) for all studied growth traits using single-trait **AM** were moderate at the early ages (hatch-4 weeks) and low thereafter up to 16 weeks of age. The percentages of σ^2_A relative to total phenotypic variance 11.9 to 19.9% for growth traits at early ages and from 6.0 to 9.3% for traits measured at later ages (Table 25). These percentages are lower than those obtained by Danbaro et al. (1995a), Koerhuis and McKay (1996) and Kuhlers and McDaniel (1996) for different breeds of chickens. This may be due to presence of inbreeding among sires and dams in the base population, which it reached to 15.3% (as calculated using **MTDFREML** program of Boldman et al., 1995), and/or due to data structure used. In this situation, Tosh and Wilton (1994) pointed out several variables that describe the data structure with respect to sire and they defined these as: (1) The variables number of progeny, (2) The effective number of progeny, (3) The number of contemporary groups in which the sire has progeny, and (4) the relationship coefficient matrix (**A**).

For comparison of additive genetic variance resulting from sire model ($\sigma^2_A = 4\sigma^2_s$) and single-trait **AM** (σ^2_A), the percentages of σ^2_A for all growth traits obtained by single-trait **AM** are lower (ranged from 5.0 to 19.9%) (Table 25) than those obtained by sire model (sire variance components) (ranged from 7.7 to 20.4%) (Table 24). This is because the percentages of σ^2_A resulted from sire model were computed as four times of the covariance between paternal half sibs (σ^2_s) relative to the total phenotypic variance (Meyer, 1989). Therefore, if we have any bias in estimates of additive genetic variance due to sire components (that may be occurred resulting from ignored the common environmental effect in the sire model) and consequently percentages of σ^2_A getting large, because this bias will being four times in the additive genetic variance. Also, the single-trait **AM** is considered the relationship coefficient matrix in the analysis that could be another cause. However, using relationships among animals leads to an increase in σ^2_A and reduction predicted error variance (**PEV**) (Quass et al., 1984; Toelle et al., 1991, Schaeffer, 1993). Thus, one could recommend the poultry breeders in Egypt to use **AM** 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 animals.

In multi-traits animal models **(AM)**, of variance components, the percentages of additive genetic variance (σ_A^2) ranged from 9.6 to 17.8%, 4.9 to 10.1% and 6.1 to 13.9% for **BW, DG** and **RG**, respectively (Table 26). Results of Koerhius and Mckay (1996) in juvenile broiler based on bivariate **AM** were higher (28.6% for 6 weeks) than those estimates presented in present study (16.0% for 6 weeks). On the other hand, results in the present study are in agreement with findings of Danbaro et al. (1995a) for White Plymouth Rock chickens.

For comparisons of single-trait and multi-traits **AM** in estimation of direct additive genetic variance, results represented in Tables 25&26 indicated that percentages of σ_A^2 for **BW** and **RG** traits estimated by multi-traits **AM** appeared to be higher than those resulting from single-trait **AM**. The estimates ranged from 9.6 to 17.8% (averaged 13.9%) based on multi-traits AM, while they ranged from 6.0 to 19.9% (averaged 11.2%) based on single-trait **AM** for **BW**. Based on multi-traits AM, the percentages of σ_A^2 were increased by 2.1%, 1.6%, 5.0% and 6.9% than the corresponding percentages obtained by single-trait **AM** for **BW** at 4, 8, 12 and 16 weeks of age, respectively. Similarly, they increased by 2.0%, 0.5% and 0.2% for **RG** at age intervals of hatch-4, 4-8 and 12-16 weeks, respectively. Koerhuis and McKay (1996) came to same conclusion for 6-weeks body weight. Higher additive genetic variance (σ_A^2) obtained by multi-traits **AM** relative to single-trait **AM** may be due to that extra information on correlated traits were existed (i.e. covariances among traits were considered) as well as due to bias selection was smaller (Koerhuis and van der Werf, 1994; Mrode, 1996).

Using of multi-traits **AM** 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 single-trait **AM** for **BW** at 4, 8, 12 and 16 weeks, respectively. Little differences in **PEV** (σ_e^2) were between single-trait and multi-traits **AM** for **DG** and **RG** (Tables 25&26).

4.3.2.2 Common environmental variance:

The inclusion of common environmental effects in an **AM** allows obtaining the true estimates of additive genetic variance. In this respect, Southwood et al. (1989) reported (based on simulation) that when the variances were estimated under the correct model for the data set, estimates of variances agreed with true values. Even in an **AM**, if maternal effects are present but not accounted correctly, estimated additive direct variance (σ_A^2) will also include all or part of the maternal variance. Using single-trait **AM**, results given in Table 25 show that percentages of common environmental variance (σ_c^2) were large at hatching age (25.3%), declined thereafter gradually at the chick grew older (14.2% at 16 weeks). The percentages of σ_c^2 ranged from 11.8 to 25.3% for **BW**, 7.3 to 20.4% for **DG** and 5.4 to 16.0% for **RG**. Aggery and Cheng (1994) observed the same trend for growth traits in Japanese Quail. Also, percentages in present study are all within the range (9.6 to 38.4%) which reported by Danbaro, et al. (1995a) for White Plymouth Rock chickens.

However, common environmental effect affected the growth of the progeny is to some extent the sequence of the genetic variation of some characters of the dam (mothering ability or maternal effect) (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 independently of the dams, the post-hatch maternal influence on the chick growth was not important. Therefore, the common environmental effect that may possibly affect chick growth are pre-ovipositional maternal components, which are mainly oviductal 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 gene action, and any sire-dam interaction that may present, since this component largely represented covariances between full sibs' families (the majority of dams were nested within sire). In addition to that, another source of common environmental variance raised between families may be due to factors such as nutrition and/or climatic conditions. All sorts of relatives are subjected to environmental sources of resemblance (Aggrey and Cheng, 1994; Mrode, 1996)

Using multi-traits **AM,** the estimates of σ_c^2 obtained for **BW** (Table 26) indicate that no clearly trend was observed for growth traits across different ages. The percentages of σ_c^2 were somewhat higher (13.0 to 27.6%) than those resulted by single-trait **AM** for **BW** (11.8 to 25.3%). Results in the present study are in agreement with findings of Koerhuis and McKay (1996) for juvenile broilers. In the present study, percentages of σ_c^2 using multi-traits **AM** were moderate and ranged from 7.3 to 20.4% for **DG** and 5.7 to 16.3% for **RG**. On the other hand, differences in estimation of σ_c^2 between single-trait and multi-traits **AM** for both **DG** and **RG** were low (Tables 25&26) and consequently either of the two models could be used in estimation of variance components of common environment.

4.4 Heritability:

The knowledge of size of the Heritability in chickens' growth traits is of great importance in the decision of which selection methods should be used and its properties as a measurement of the accuracy of the phenotypic value as a guide to the breeding value (Falconer and Mackay, 1996).

Heritabilities were estimated from the four genetic models. The first two models (sire model or dam model) based on variance components estimated from the **REML** methods, which the other two models (single-trait animal model or multi-traits animal model) based on **DFREML** in estimation of variance components. Heritabilities estimated by the sire model (h_s^2), dam model (h_d^2) and animal model (h_A^2) for body weights (**BW**), daily gains (**DG**) and relative growth rates (**RG**) in Dokki-4 chickens are given in Table 27.

4.4.1 Heritabilities estimated from the sire model:

Estimates of h_s^2 for growth traits obtained in this study were low or relatively moderate, i.e. important of growth traits could not be fair enough through selection of sires based on performance of their progenies. The estimates ranged from 0.09 to 0.20 for **BW**, form 0.08 to 0.16 for **DG** and from 0.09 to 0.15 for **RG** traits. This might be due to the large maternal effects and variation in egg sizes of the sires' and dams' daughters (hens) which could have masked any additive genetic variance, i.e. increasing the non-additive genetic effects. Also, the existence of inbreeding (15.3%, as calculated using **MTDFREML** program of Boldman et al., 1995) among sires and dams in the present base population could be an another cause to decrease heritabilities from the sire component.

Estimates of h_s^2 for **BW** traits were moderate at early ages of growth up to 4 weeks (averaged 0.18), while they were low at the age of 12 weeks and increased slightly thereafter (Table 27). In this situation, some investigators (e.g. Gupta and Johar, 1975; Sabri 1979; Stino et al., 1981; Tripathey et al., 1984) reported that h_s^2 for body weights were the highest for weight at hatch, declined to the lowest values at 4 and/or 6 weeks of age and increased again at 8 weeks or older. In the reverse, the reviewed estimates of h_s^2 for chicks' **BW** at different ages (Amer, 1965; Ezzeldin, 1970; Farrag, 1977; Ismail, 1980; Kumar and Acharya, 1980; Kosba and Eid, 1983) were generally high at older ages where they averaged 0.34 at 8 weeks. While they were moderate at younger ages (0.22 at hatch). However, estimates of h_s^2 are fluctuated from study to another (Ezzeldin, 1970,; Khalil et al., 1993; Aggrey and Cheng, 1994) and cannot be explained on strong bases of genetics and statistics stand points. Similar to what found for **BW**, estimates of h_s^2 for **DG** and **RG** traits were large at early age intervals than at the other ones. They were 0.16 and 0.15 at the age interval of hatch-4 weeks, then declined gradually to 0.11 and 0.09 at interval of 12-16

Table 27. Heritabilities (h^2) and standard errors (SE) estimated from the sire model, dam model, single-trait animal model and multi-traits animal model for body weights, daily gains and relative growth rates in Dokki-4 chickens.

Trait[+]	**Sire model**[*]	**Dam model**[*]	**single-trait animal model**[•]	**multi-traits animal model**[*]
	h^2_s±SE	**h^2_d±SE**	**h^2_{AS}**	**h^2_{AM}**
Body weight:				
BW0	0.20±0.043	0.55±0.049	0.20	0.18
BW2	0.16±0.034	0.42±0.042	0.12	
BW4	0.17±0.036	0.32±0.038	0.14	0.16
BW6	0.12±0.027	0.24±0.035	0.07	
BW8	0.13±0.030	0.25±0.036	0.08	0.10
BW10	0.12±0.028	0.31±0.040	0.09	
BW12	0.09±0.023	0.35±0.043	0.06	0.11
BW16	0.13±0.032	0.33±0.044	0.08	0.15
Daily gains:				
DG4	0.16±0.028	0.29±0.040	0.13	0.10
DG8	0.10±0.025	0.20±0.034	0.06	0.06
DG12	0.08±0.021	0.26±0.038	0.05	0.05
DG16	0.11±0.030	0.15±0.036	0.08	0.07
Relative growth rates:				
RG4	0.15±0.033	0.23±0.034	0.12	0.14
RG8	0.11±0.026	0.22±0.035	0.07	0.08
RG12	0.09±0.024	0.15±0.033	0.06	0.06
RG16	0.09±0.024	0.11±0.034	0.07	0.08

[+] Traits as defined in Table 20.

[•] Sire model= fixed effects + sire + error; Dam model= fixed effects + dam + error; single-trait animal model= fixed effects + direct additive genetic effect + common environment + error and multi-trait animal model= fixed effects + direct additive genetic effect + common environment + error.

weeks of age for traits of **DG** and **RG**, respectively. El-Hossari (1970b) and Iraqi (1991) observed the same trend with Fayoumi, Dokki-4 and New Hampshire chickens.

For comparing h_s^2 of growth traits in the present study (based on **REML** method) with those of the reviewed studies (based on **Henderson**' method), estimates of h_s^2 resulting from **REML** method were larger than those obtained by **Henderson**' method (El-Maghraby and Bakir, 1977; Iraqi, 1991) for Dokki-4 chickens. This might be due to that h_s^2 estimated from **REML** were unbiased by selection (Besbes et al., 1992; Ferraz and Johanson, 1993; Gebhardt-Henrich and Marks, 1993; Dieters et al., 1995; Johnson and Thompson, 1995). Also, the low estimates of h_s^2 based on **Henderson**'s method reported in the reviewed studies for growth traits in Dokki-4 chickens could be attributed to that the number of progeny per sire group was small. Sampling effect and non-randomness in the distribution of dams within sire groups could be added as other causes in this respect. On the other hand, estimates of h_s^2 for **BW** traits in different local breeds reported by the old studies (Amer, 1965; Ayoub, 1965; Farrag, 1977; Abd El-Gawad, 1970; Ismail, 1980) were larger than those obtained in present study. This may be due to non-adjustment for the important non-genetic effects (such as generation and month of hatch) that proved to be a highly significant source of variation in their studies. Bias estimates of h_s^2 (based on **Henderson**'s methods) may be mainly due to maternal and dominance effects (Ayoub and Magraby, 1976; El-Maghraby and Bakir, 1977; Gill and Varma, 1983; Kumar et al., 1988; Abd Ellatif, 1989). This biased in h_s^2 obtained in literature based on **Henderson** method may be due to ignoring the effects of selection. In this respect, Gianola et al. (1986) and Spilike and Mielenz (1992) reported that even for moderate selection intensities, variance-covariance estimated by **ANOVA** type procedure are likely to be severally biased by selection, while estimates obtained by **REML** and **DFREML** methods are preferable because: (1) They had the ability to account for selection bias, (2) They give variance components estimators which are unaffected by the fixed effects and characterized by many valuable features, such as non-negativity and unbiasedness, (3) They are applied to an animal model, with the inclusion of full additive relationship matrix, and (4) They are preferable computationally in the multivariate analysis (Sorensen and Kennedy, 1983; Meyer and Thompson, 1984; Meyer, 1989; Searle, 1989; Johnson and Thompson, 1995; Van Tassel et al., 1995; Hofer, 1998).

The existence of high relationship coefficients between dams and sires in the parent population of poultry will lead to a downward bias in the estimates of heritability from the sire model (Mayer et al., 1987). In this respect, van der Werf (1992) reported that sire-dam model will give an underestimating heritability because it ignores the animal relationships other than parents-progeny. Mayer et al. (1987) reported that genetic relationship among dams within and between dam groups must be considered. Thus these results lead to conclude that no much attention would be paid to the sire-dam models in estimation of heritability.

4.4.2 Heritabilities estimated from the dam model:

Heritability estimated from the dam model (h_d^2) for growth traits were mostly moderate (Table 27), i.e. important of growth traits could be possible by selection of dams based on performance of their progeny. The estimates of h_d^2 ranged from 0.24 to 0.55 for **BW**, from 0.15 to 0.29 for **DG** and from 0.11 to 0.23 for **RG** traits. These estimates are agreed with results of Abd El-Gawad (1970), Awad (1978) and Sabri (1979) with Dokki-4, Fayoumi and White Baladi chickens. On other the hand, estimates of h_d^2 for growth traits were seem to be lower than those reported by El-Hossari (1970b), Farrag (1977), Al-Mufti (1978), Ismail (1980) and Iraqi (1991) (which estimated by **Henderson**'s methods) in Fayoumi, Dokki-4 and White Baladi chickens basing on **Henderson** method in estimation of variance components.

The estimates of h_d^2 for growth traits were large comparable to h_s^2 (Table 27). From the previous results, it is appear that the estimates of h_d^2 from the dam component are larger than those estimated from the sire component. This may be due to that growth traits in Dokki-4 chickens were subjected to a large non-genetic maternal influence. It is also clear that maternal effects are of considerable importance in determining phenotypic differences in the growth traits at different ages that bring predominance of the h_d^2 estimate over the estimate of h_s^2 (Willham, 1972&1980). Similar to the present study, most estimates of h_d^2 obtained by the Egyptian investigators (El-Hossari, 1970b; Ezzeldin, 1970; Ismail, 1980; Iraqi, 1991 with Dokki-4 and Fayoumi chickens) and by the other non-Egyptian ones (Smith and Jaap, 1957; Hale, 1961; Saeki, et al., 1969a; Orzco, 1971; Kumar and Acharya , 1980; Verma et al., 1983 with White Leghorn, Desi, and White Wyndotte chickens) appear to be much higher than the corresponding estimates of h_s^2 reported in the same literature, i.e. contribution of maternal effects and dominance in dam variance of growth traits was large. Growth characteristics from hatching time and up to the age of 16 weeks could still give evidence of this maternal effect, probably due to correlation of growth of the chick with its egg quality. However, the dam component of variance included all of the maternal additive genetic variance, the covariance between direct and maternal additive effect, common environmental variance (variation between full-sib families) and both maternal dominance and maternal environmental variances. These were not included in the sire component of variance and four times their contributions would lead to differences between paternal and maternal estimates of heritability. A suggestion of possible maternal effects up 16 weeks on growth traits of chickens at different ages would agree with other reports (Hale, 1961; Saeki et al., 1969a; El-Hossari, 1970a; Orzco, 1971; Ismail, 1980; Kumar and Acharya, 1980; Verma et al., 1983; Iraqi, 1991).

4.4.3 Heritabilities estimated from single-trait and multi-traits animal models:

Estimates of heritabilities using single-trait (h_{AS}^2) and multi-traits (h_{AM}^2) animal models (AM) for body weights (BW), daily gains (DG) and relative growth rates (RG) in Dokki-4 chickens are given in Table 27. These estimates indicate that h_{AS}^2 for BW 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) for. The same trend was observed for most traits of DG and RG. These results of progeny themselves indicate that selection may be effective for improvement the performance of Dokki-4 chickens at early age of 4 weeks. These estimates are lower than those with reported by Aggrey and Cheng (1994) with Japanese Quail at 3 weeks of age and Danbaro et al. (1995a) with White Plymouth Rock chickens at 7 weeks of age. Chambers (1990) reported that heritabilities based on additive genetic effects were about 0.40 for growth traits in chickens. Recently, Le Bihan-Daral et al. (1997) reported that estimates of heritabilities were 0.24 and 0.22 for 3- and 6-weeks body weights using **DFREML** with an **AM**, respectively.

Published estimates for heritability of growth traits in chickens estimated by **AM** are few (Aggrey and Cheng, 1994; Danbaro et al., 1995a; Kuhlers and Mcdaniel, 1996; Le Bihan-Duval et al., 1998). For comparison of heritabilities resulting from sire model (h_s^2) and from single-trait **AM** (h_{AS}^2), the estimates of h_{AS}^2 for all growth traits were lower than those obtained by sire model (h_s^2). This may be attributed to inclusion of common environmental effect in the **AM** and consequently a correction for this effect was considered in the **AM** while it was not considered in the sire model. Estimates of heritability based on single-trait **AM** (h_{AS}^2) were lower than those obtained by sire model (h_s^2). This is because the estimates of h_{AS}^2 is estimated as the direct additive genetic variance relative to the total phenotypic variance, while, estimates of h_s^2 were computed as four times of the covariance between paternal half sibs (σ_s^2) relative to the total phenotypic variance (Meyer, 1989). Therefore, if we have any bias in estimates of additive genetic variance due to sire components (that may be occurred resulting from ignored the common environmental effect in the sire model) and consequently estimates of h_s^2 getting large, because this bias will being four times in the heritability. On the other hand, Fairfull and Gowe (1990), Toelle et al. (1991) and Aggrey and Cheng (1994) found that additive **AM** analysis, yielded higher heritability estimates than those obtained by **Henderson**'s methods.

From the previous notations, one may recommend that using multi-trait **AM** analysis is effective to obtain more accurate estimates of additive genetic variance as well as heritability associated with minimum with predicted error variance (**PEV**).

For **DG** and **RG** traits, no clear differences were observed between estimates of h^2_{AS} and h^2_{AM} (Table 27). Based on **AM** analysis for comparison, 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 Kuhlers and McKay (1996) and Le Bihan-Duval et al. (1998) with juvenile and broiler chickens. According to Danbaro et al., 1995a, the decreasing in estimates of h^2_{AS} and h^2_{AM} in 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 using **MTDFREML** program of Boldman et al., 1995) between parents in the base population, and (3) selection 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.

In general, the variability of heritability estimates in the present and reviewed studied may be due to differences in: (1) The genetic constitution of the breeds, (2) Selection, if practised, (3) The available number of observations used, (4) The structure and distribution of the data set, (5) The models applied for each set of data to correct for the non-genetic factors, (6) The level of inbreeding and coefficient of relationship in the parent population (related progenies, dams- or sires-related or sires related to dams), and (7) The method of analysis and estimation.

4.5 Correlations among growth traits:

Multivariate animal model (**AM**) analyses of variance and covariance were performed on the data of Dokki-4 chickens of the present study in order to derive estimates of additive genetic, common environmental, environmental and phenotypic correlations among growth traits at different ages. Because, the estimates of correlations among growth traits in present study were very lower than expected, the two-traits analysis was used to obtain the optimum estimates of correlation among two traits (Boldman et al., 1995). In general, the negative or very low estimates of $\mathbf{r_G}$, $\mathbf{r_c}$,

r_E and r_P based on multi-trait analysis among some **RG** traits were unexpected (Table 28). Sampling errors may be the cause of these unexpected estimates. Similarly, Ezzeldin (1970), El-Hossari (1971) and Khalil et al. (1993) reported that estimates of r_G among some traits of **BW** and **RG** of Fayoumi chicks were negative and generally low. The same authors stated that birds that showed faster **RG** at later age intervals were higher in weight at earlier ages and consequently negative estimates of correlation were obtained. According to what mentioned for correlations among **RG** traits, these estimates are not discussed here.

Estimates of direct additive genetic (r_G), common environmental (r_C), environmental (r_E) and phenotypic (r_P) correlations are given in Table 28. The estimates of r_G, r_C, r_E and r_P amongst most growth traits 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 the later ages of growth from the early age. No reports are available in estimation of r_G, r_C, r_E and r_P for growth traits of chickens using multi-traits **AM**.

4.5.1 Genetic correlation (r_G):

Estimates of r_G shown in Table 28 indicate that these estimates tended to increase in value as the intervals (from 4 to 16 weeks) between the two ages got larger; i.e. the genetic factors of subsequent weights are closely genetically related. In the reverse, some investigators (e.g. Ahlawat et al., 1980; Kumar and Acharya, 1980; Gill and Varma, 1983; Tripathy et al., 1984; Khalil et al., 1993; Khan et al., 1994; Danbaro et al., 1995a) reported that estimates of r_G were tended to decrease in value as the intervals between the two ages got larger. Differences in present estimates of r_G and those of the reviewed studies might be probably to that: (1) the adjustment for the common environmental effect when applying animal model to the data, (2) the existence of the common environmental effect which could have masked a part of these difference attributed to the additive gene effects, i.e. increasing non-additive genetic effects. Thus, additive genetic covariance becomes relatively smaller.

Table 28. Additive genetic (r_G), common environmental (r_C), environmental (r_E), and phenotypic (r_P) correlations among body weights, daily gains, and relative growth rates estimated from multi-traits animal model.

Traits correlated$^+$	r_G	r_C	r_E	r_P
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
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
Relative growth rates***:**				
RG4 & RG8	-0.45	-0.14	-0.42	-0.38
& RG12	0.01	-0.33	-0.12	-0.14
& RG16	0.12	0.19	-0.10	-0.06
RG8 & RG12	-0.48	-0.46	-0.28	-0.32
& RG16	-0.96	-0.10	-0.02	-0.06
RG12 & RG16	0.48	-0.82	-0.06	-0.04

$^+$ Traits as defined in Table 20.

* Using two traits of the term in calculation.

Estimates of r_G in present study showed that most of these associations were positive and similar in sign to the corresponding estimates of r_P (Table 28). The estimates ranged from 0.17 to 0.84 among **BW**, and -0.35 to 0.65 among **DG** traits. These estimates fall within the range of r_G in the Egyptian studies (Ezzeldin, 1970; Abd El-Gawad and El-Ibiary, 1972) for Fayoumi chickens. Bhushan and Singh (1995) reported that some estimates of r_G between **BW** traits of broiler chicks were positive and generally low.

Estimates of r_G among **BW** and **DG** traits at early age intervals (i.e. up to 8 weeks of age) were generally higher than those estimates of r_C, r_E and r_P (Table 28). This may be due to that genes which influence growth traits are more persistent in their effects than the environmental factors which they are temporary in nature (Kumar and Acharya, 1980; Khalil et al., 1993). Similar trend was reported by some investigators who working on different breeds of chickens (e.g. El-Hossari, 1971; Kumar, 1979; Kumar and Acharya, 1980; Stino et al., 1983). Therefore, it could be safely concluded, on the basis of estimates of r_G (in the present and the other reviewed studies), that growth traits of chickens at earlier ages (4 weeks) could be used for selection at later ages, i.e. correlated improvement in growth traits at later ages (through indirect selection) may be quite possible. The high estimates of r_G reported here (Table 28) are pertinent in constructing efficient selection indices for improvement of growth traits in Dokki4 chickens.

The estimates of r_G among growth traits at different ages were mostly moderate or high and averaged 0.52 **BW** 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 r_G given in Table 28 indicate that measures before the age of 16 weeks could be good indications of the genetic value for growth traits at that age. For local breeds (e.g. Dokki-4, Fayoumi and Baladi White), estimates of r_G among different growth traits reported by some Egyptian investigators (El-Hossari, 1971; Abd El-Gawad and El-Ibiary, 1972; Sorour, 1984; Khalil et al., 1993) fall within the range of these estimates obtained in the this study. In addition, estimates of r_G obtained here were higher than those reported for some exotic breeds (Ahlawat et al., 1980; 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 gaves an encouragement for the chicken breeders in Egypt to improve growth traits of their Dokki-4 chicks through indirect selection.

The low unbiased estimates of $\mathbf{r_G}$ resulting from multivariate analysis, while they are upward biased in the reviewed studies, may be arise from two circumstances. Firstly, it can be due to the correction of the data for all possible non-genetic effects such as common environmental effects, i.e. egg size (as a character of the dam), differed 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 using the data chicks surviving to the latest weight at later age was disappeared). Existence of inbreeding (15.3%, i.e. as calculated using **MTDFREML** program of Boldman et al., 1995) between parents (sire and dams) in the base population might be added another cause in reduction of additive genetic variance and covariance among traits.

Evidently, estimates of $\mathbf{r_G}$ obtained here from **DFREML** estimators of (co)variance components were higher and less extreme than the corresponding estimates of genetic correlation based on **Henderson**'s methods in the reviewed studies. This might be due to:

(1) The variance and covariance components obtained by multi-traits **AM** were unbiased by selection (Quass et al., 1984; Toelle et al., 1991; Schaeffer, 1993; Hofer, 1998).

(2) Analysis of growth traits using multi-traits **AM** which includes the relationships among individuals will give more accurate genetic correlations, i.e. an increase in genetic covariance and a decrease in error variance.

(3) Multivariate analysis allows separating the common environment non-genetic effects (caused by non-additive maternal and non-genetic maternal effects) from uncontrolled environmental effects.

(4) Sampling variances based on **AM** 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).

4.5.2 Common environmental correlation (r_C):

No reports are available for estimates of common environmental (r_C) correlation in chickens. Therefore, estimates of 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 (Table 28). The estimates averaged 0.56 among **BW** and 0.27 among **DG** traits (Table 28). Estimates of r_C were mostly higher than estimates of r_E and 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 after hatch in Dokki-4 chickens. Thus, one might recommend that common environmental effects should be considered in multi-traits **AM** of estimation of variance and covariance components to get unbiased estimates of genetic, phenotypic and environmental correlation. In this respect, Wie and van der Werf (1992) reported that if maternal and common environmental effects seemed to be important, a mixed model using data for more than one generation could possibly correct for such effect.

4.5.3 Environmental correlation (r_E):

The r_E estimated by multi-traits **AM** among growth traits of Dokki-4 chickens showed that the relationships among **BW** and among **DG** traits were positive and generally moderate or high (Table 28). The estimates averaged 0.42, among **BW** and 0.15 among **DG** traits. Based on **Henderson**'s methods, similar findings were reported by other investigators (El-Hossari, 1971; Abd El-Gawad and El-Ibiary, 1972; Lien, 1973b; Stino et al., 1983; Sorour, 1984; 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.

In some cases, estimates of $\mathbf{r_G}$ and $\mathbf{r_E}$ are different in magnitude, or even in sign, while in other cases the two correlations are of the same sign and not very different in magnitude, and this is the more usual situation in the present study. A large difference, and particularly a difference in sign, shows that genetic and environmental sources of variation affect the characters through different physiological mechanism (Falconer, 1989; Falconer and Mackay, 1996).

4.5.4 Phenotypic correlation ($\mathbf{r_P}$):

All estimates of $\mathbf{r_P}$ among **BW** and among **DG** traits at different ages were positive and mostly of moderate or high magnitude (Table 28). The estimates tended to decrease relatively in value as the intervals between the two ages got larger. The estimates averaged 0.45 among **BW** and 0.17 among **DG** traits. In agreement with the present results, most of the estimates in the literature (Saeki et al., 1969a; El-Hossari, 1971; Abd El-Gawad and El-Ibiary, 1972; Lien, 1973b; Al-Mufti, 1978; Singh and Singh, 1979; Kumar and Acharya, 1980; Gill and Varma, 1983; Stino et al., 1983; Asuquo and Nwosu, 1987) showed that the $\mathbf{r_P}$ among growth traits of chicken at different ages were positive and generally high. However, such high and positive estimates (in the present and reviewed studies) between two growth traits does not necessarily indicate that selecting one of these traits will lead to an improvement in the other correlated one, because $\mathbf{r_P}$ is not always a reliable estimate of the genetic relationship existing between two growth traits. Sometimes, the environmental effects upon the two growth traits could be strong and positively correlated and consequently a positive $\mathbf{r_P}$ could be obtained. Therefore, it is clear that the $\mathbf{r_P}$ is not a quiet satisfactory indicator to the expected correlated genetic response of growth traits under selection; the $\mathbf{r_G}$ is the one to be used for such prediction.

Estimates of $\mathbf{r_P}$ among growth traits at earlier age intervals with subsequent ages (i.e. up to 16 week of age) indicate that those genetic factors affecting growth traits at early ages are more closely related to those affecting growth traits at later ages. 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.

4.6 Evaluation of Birds

4.6.1 Computational aspects:

For single-trait and multi-traits animal models, the structure of the number of equations and iterations, number of non-zero elements, number of likelihood evaluated, **CPU**-time consumed and storage required in memory of the computer (**MB**) attained in the evaluation of growth traits in Dokki-4 chickens are presented in Tables 29&30.

For single-trait **AM**, the average number of equations and iterations recorded were 9286 and 44, 9278 and 36, and 9278 and 56 for **BW**, **DG** and **RG**, respectively. These results indicate that Dokki-4 chicks recorded higher number of equations and iterations for **BW** traits compared with both **DG** and **RG** traits with the exception of the number of iterations for **RG**. While, the average of non-zero elements per equation and number of likelihood evaluated were 9.50 and 78.9, 9.2 and 67.3, and 9.2 and 100.3 for **BW**, **DG** and **RG** traits, respectively. These results indicate that number of equations and iterations decreased with advance of age.

In general, number of iterations required to reach convergence could be affected by the number of animals (number of equations), the number of random factors in the model and even specific to particular traits (Ducrocq et al. 1989; Gerstmayer et al. 1989; Schaeffer 1993; Groeneveld and Brade 1996). Wiggans and Misztal (1987) and Ducrocq et al. (1989) reported that number of rounds of iterations required to reach adequate convergence criteria might not be before 100 or more iteration.

The **CPU**-time consumed (Minutes) for likelihood evaluation and estimation of breeding values ranged from 0:35 to 0:58 and 2:14 to 2:24 for **BW** traits, from 0:34 to 0:45 and 2:10 to 2:18 for **DG** traits and from 0:28 to 1:44 and 2:14 to 2:20 for **RG** traits, respectively. The memory storage required (**MB**) for solving the iterative

Table 29. Numbers of equations, iterations, non-zero elements used, log likelihood evaluated and CPU-time consumed (Sec.) in analysis of different traits using single-trait animal model.

Method and trait^{+}	No. of equations			No. of iterations	No. of non-zero elements	Average No. of non-zero elements per equation	No. of likelihood evaluated	CPU-time consumed (Sec.)			Maximum storage required (MB)
	Fixed part	Random part	Total					for likelihood evaluated	for estimation of breeding values	Total hr:min:Sec	
Single-trait animal model:											
Body weights:											
BW0	4	9293	9297	54	94581	10.17	92	0:58	2:22	0:03:20	0.925
BW2	4	9292	9296	42	92286	9.93	75	0:47	2:21	0:03:08	0.916
BW4	4	9291	9295	28	90609	9.75	56	0:35	2:22	0:02:57	0.909
BW6	4	9291	9295	35	89529	9.63	64	0:40	2:18	0:02:58	0.905
BW8	4	9286	9290	55	87816	9.45	101	0:58	2:16	0:03:14	0.897
BW10	4	9282	9286	55	86268	9.29	98	0:55	2:18	0:03:13	0.889
BW12	4	9275	9279	41	84489	9.11	78	0:44	2:14	0:02:58	0.880
BW16	4	9244	9248	38	79896	8.64	67	0:36	2:24	0:03:00	0.852
Average	4	9282	9286	44	88184	9.5	79	0:47	2:19	0:02:91	0:897
Daily gains:											
DG4	4	9291	9295	36	90615	9.75	68	0:42	2:18	0:03:00	0.909
DG8	4	9286	9290	42	87816	9.45	75	0:45	2:16	0:03:01	0.897
DG12	4	9275	9279	34	84481	9.10	64	0:37	2:15	0:02:52	0.880
DG16	4	9244	9248	32	79888	8.64	62	0:34	2:10	0:02:44	0.852
Average	4	9274	9278	36	85700	9.24	67	0.40	2:15	0:02:74	0.885
Relative growth rates:											
RG4	4	9291	9295	25	90615	9.75	48	0:32	2:20	0:02:52	0.909
RG8	4	9286	9290	22	87816	9.45	44	0:28	2:19	0:02:47	0.897
RG12	4	9275	9279	49	84481	9.10	84	0:48	2:16	0:03:04	0.880
RG16	4	9244	9248	128	79888	8.64	225	1:44	2:14	0:03:58	0.852
Average	4	9274	9278	56	85700	9.24	100	0:63	2:17	0:02:90	0.885

$^{+}$ Traits as defined in Table 20.

Table 30. Numbers of equations, iterations, non-zero elements used, log likelihood evaluated and CPU-time consumed (Sec.) in analysis of different traits using multi-traits animal model.

Method and trait+	No. of equations			No. of iterations	No. of non-zero elements	Average No. of non-zero elements per equation	No. of likelihood evaluated	CPU-time consumed (Sec.)			Maximum storage required (MB)
	Fixed part	Random part	Total					for likelihood evaluated	for estimation of breeding values	Total hr:min:Sec	
Multi-traits animal model:											
BW (five traits)	20	46465	46485	602	2116601	45.53	799	1:05:55	3:22:34	4:28:29	17.035
DG (four traits)	16	37164	37180	500	1336164	35.94	652	0:46:36	1:50:27	2:37:03	10.903
RG (four traits)	16	37164	37180	500	1336164	35.94	653	0:45:31	1:45:08	2:30:39	10.903

+ Traits as defined in Table 20.

equations using single-trait **AM** ranged from 0.852 to 0.925 for **BW** traits, from 0.852 to 0.909 for **DG** and **RG** traits. These results indicate that **CPU**-time consumed and storage required were increased as the number of equations (number of animals) and the number of non-zero elements got larger (Groeneveld and Brade, 1996). These items were larger for **BW** traits relative to **DG** and **RG** traits.

For multi-traits **AM**, the number of equations and iterations to reach convergence attained, average of non-zero elements, number of likelihood evaluated, **CPU**-time consumed and storage required in memory of the computer (Tables 29&30) were generally larger for **BW** traits (five traits at a time) compared with **DG** and **RG** traits (four traits at a time). Also, these results were higher compared with corresponding results obtained by single-trait **AM**. These results were expected since the number of equations (i.e. number of animals) and number of traits got larger (Groeneveld and Brade, 1996). In general, Gerstmeyer et al. (1989) reported that the limiting factors which could restrict the number of animals and consequently could be included in the analysis:

(1) The complex model required more likelihood to be evaluated for each iteration that are needed in an univariate problem.

(2) The algorithm worked only on the non-zero elements of the matrix, thus utilizing its sparseness.

(3) The algorithm becomes very demanding of computing time and memory space, when the number of animals (number of equations) increased.

(4) The advantages arising from avoiding inversion completely were offset be the extreme expansion of the system of equations.

For comparison of the two analyses used (single-trait and multi-traits animal models), the **CPU**-time consumed and size of the memory storage required were very large in case of multi-traits analysis compared to single-trait analysis. Gerstmeyer et al. (1989) and Groeneveld and Brade (1996) stated that the costs of analysis are dependent on (1) the properties of computer used in analysis, (2) the number of equations to be solved, and (3) the number of traits included in the model. These factors should be carefully considered in application of **AM** analysis, because these could influence the costs of the breeding programs and consequently the economic returns of these programs.

4.6.2 Breeding values estimated for birds with records:

For birds with available records, breeding value (**PBV**) estimates for body weights (**BW**), daily gains (**DG**) and relative growth rates (**RG**) were predicted by single-trait and multi-traits **AM**. Both models are considered the relationship coefficient matrix (A^{-1}) among birds in estimation (Korhanen, 1996). For all birds and the top 50% (according to Danbaro et al., 1995a; Morris and Pollott, 1997) of birds (progeny), estimates of minimum and maximum **PBV** in addition to their ranges (i. e. the difference between the maximum and minimum value), standard errors (**SE**) and accuracy of each predictor ($r_{A\hat{A}}$) are presented in Table 31. These results indicate that Dokki-4 chicks, generally, recorded higher ranges in estimates of **PBV** for **BW** and **RG** when using multi-trait **AM** than those single-trait **AM**. The average of ranges in estimates of **PBV** obtained from multi-trait 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. Similar to the list of all birds, the top 50% of birds (selected part of progeny) recorded also higher ranges for traits studied when using multi-traits **AM** than those estimated by single-trait **AM**. When considering the top 50% of birds in both models (i.e. single-trait and multi-trait **AM**), the ranges in **PBV** seem to be of a trend nearly similar to the case in which all birds were considered (Table 31). Low estimates of **PBV** obtained by single-trait **AM** for most growth traits compared to multi-trait evaluations may be due to: (1) decreasing of predicted error variance (**PEV**) (Quaas et al., 1984), (2) considering the relationships among traits (i.e. residual covariance between traits was computed for), which it is ignored with single-trait **AM**, (3) bias due to selection was eliminated when using multi-traits analysis, but this bias can be result of a single-trait **AM** (Mrode, 1996) and (4) traits with lower heritabilities give more benefit when analysed with traits of higher heritabilities in a multi-traits

Table 31. Minimum, maximum and ranges of predicted breeding values for birds with records (**PBV**), their standard errors (**SE**) and accuracy of prediction ($r_{A\hat{A}}$) estimated by single-trait and multi-traits animal models for body weights, daily gains and relative growth rates.

Trait⁺	Single-trait animal model								Multi-traits animal model							
	Minimum			Maximum			Range	Top 50%* of birds	Minimum			Maximum			Range	Top 50%* of birds
	PBV	SE	$r_{A\hat{A}}$	PBV	SE	$r_{A\hat{A}}$			PBV	SE	$r_{A\hat{A}}$	PBV	SE	$r_{A\hat{A}}$		
Body weights (gram):																
BW0	-2.24	0.70	0.86	3.10	1.10	0.59	5.34	3.12	-2.14	0.70	0.85	2.92	1.08	0.57	5.06	2.92
BW2	-5.48	3.48	0.49	9.98	3.46	0.50	15.46	9.8								
BW4	-18.14	8.53	0.51	21.46	8.38	0.54	39.60	20.1	-20.90	8.36	0.53	24.64	8.17	0.56	45.54	23.1
BW6	-30.12	9.19	0.75	22.76	12.48	0.44	52.88	20.02								
BW8	-46.66	12.68	0.76	34.34	12.85	0.75	81.00	32.5	-47.28	11.85	0.78	37.44	12.05	0.77	84.70	37.54
BW10	-50.94	16.63	0.78	53.52	16.67	0.78	104.46	50.0								
BW12	-31.82	26.48	0.40	38.32	21.68	0.66	70.16	34.44	-52.38	26.17	0.50	57.96	18.55	0.79	110.34	49.88
BW16	-62.60	42.35	0.44	81.06	41.81	0.46	143.66	74.72	-92.52	44.03	0.57	94.78	43.83	0.58	187.28	87.68
Daily gains (grams):																
DG4	-1.24	0.36	0.85	1.58	0.57	0.53	2.82	1.5	-1.30	0.34	0.83	1.22	0.52	0.50	2.54	1.16
DG8	-1.98	0.70	0.71	2.00	0.71	0.70	3.98	1.94	-2.06	0.69	0.73	1.86	0.69	0.72	3.92	1.8
DG12	-1.50	1.24	0.40	2.10	1.04	0.64	3.60	1.98	-1.66	1.22	0.42	2.06	1.00	0.67	3.74	1.94
DG16	-2.64	1.66	0.45	2.78	1.65	0.46	5.42	2.7	-3.36	1.57	0.48	3.10	1.56	0.49	6.46	2.94
Relative growth rates (%):																
RG4	-10.24	2.91	0.51	5.80	1.83	0.84	16.04	5.54	-15.56	3.02	0.57	6.78	3.01	0.57	22.74	6.32
RG8	-5.24	2.81	0.43	5.74	2.10	0.74	10.98	5.7	-5.48	2.87	0.47	5.94	2.10	0.77	11.42	5.68
RG12	-4.06	1.98	0.73	4.68	1.99	0.72	8.74	4.56	-4.38	2.61	0.73	4.58	1.99	0.73	8.98	4.4
RG16	-4.08	1.58	0.73	3.00	2.06	0.46	7.08	3.06	-4.22	1.56	0.75	3.28	2.08	0.48	7.50	3.14

⁺ Traits as defined in Table 20.

Total number of individuals (progeny) with records evaluated was 7226.

*= 3613 individuals were selected according to Danbaro et al. (1995a) and Morris and Pollott (1997).

analysis (Thompson and Meyer, 1986). In this respect, Barwal et al. (1993) found that the best index included information on all traits.

Accuracy of minimum and maximum **PBV** for birds obtained by multi-traits **AM** were higher than those compared to single-trait **AM**. The average of accuracy across all the minimum and maximum estimates of **PBV** when using multi-trait vs single-trait **AM** was 0.65 vs 0.60 %, 0.61 vs 0.59 %, and 0.64 vs 0.64% for **BW**, **DG** and **RG** traits, respectively (Table 31). In this situation, Quaas et al. (1984) and Mrode (1996) reported that the main advantages of multi-variate **BLUP** is that it increases the accuracy of evaluation.

From the previous results, we conclude that applied multi-traits **AM** allows to estimate an additive genetic variance without bias, consequently the predictors are **BLUP** and results obtained in lower **PEV** and an increase efficiency of selection (Kennedy, 1991). Mrode (1996) reported that selection bias can be the result of a single-trait analysis which does not include the information upon which selection was practised (i.e. generation). He added that a multi-trait evaluation is the optimum methodology to evaluate animals using all traits, because it accounts for the relationship among them. The numbers of birds with positive estimates of **PBV** and their percentages given in Table 32 indicate that low difference between the percentages of birds recorded by single-trait and multi-trait **AM**. The average of percentages for **PBV** with positive signs for single-trait vs multi-trait **AM** were 42.1 vs 41.8%, 43.1 vs 42.5% and 44.1 vs 42.8% for **BW**, **DG** and **RG** traits.

In general, the advantages of using **AM** in poultry breeding are: (1) It eliminates some of fixed effects (e.g. generation sex, etc.), (2) It reduces the estimated error for unbalanced data, (3) It is useful in estimation of **PBV** for progeny, which can shorten the generation interval, (4) It is used in estimation of **PBV** of individuals without records from the relatives' information, (5) It is useful in estimation of sires **(PSTA)** and dams **(PDTA)** transmitting abilities (birds without records) from their progeny records, which can be used for family selection, (6) as genetic and environmental correlation between traits and all relatives' information are considered, it can increase

Table 32. Numbers (and percentages) of birds with positive estimates of predicted breeding values (PBV) recorded by single- and multi-trait animal models (birds with records) for body weights, daily gains and relative growth rates.

Trait⁺	Single-trait animal model		Multi-traits animal model	
	No. of birds	% of birds	No. of birds	% of birds
Body weights:				
BW0	3633	50.3	3618	50.0
BW2	3261	45.1		
BW4	2885	39.9	2884	39.9
BW6	3243	44.9		
BW8	3086	42.7	2960	41.0
BW10	2802	38.8		
BW12	2832	39.2	2635	36.5
BW16	2786	38.6	2992	41.4
Daily gains:				
DG4	2914	40.3	2978	41.2
DG8	3188	44.1	3230	44.7
DG12	2987	41.3	2971	41.1
DG16	3371	46.7	3100	42.9
Relative growth rates:				
RG4	2142	29.6	2860	39.6
RG8	3531	48.9	3106	43.0
RG12	3318	45.9	3140	43.6
RG16	3765	52.1	3254	45.0

⁺ Traits as defined in Table 20.

the accuracy of selection (Pang et al., 1989; Pribyl and Pribylovy, 1991; Danbaro et al., 1995b).

4.6.3 Transmitting abilities estimated for birds without records:

In AM, a simultaneous evaluation of dams and sires in which the genetic merit of all relatives plus the bird's own performance will be obtained, i.e. genetic merit of birds will be attained (Meyer, 1989, Boldman et al., 1995). Often, individuals without records of the present population were evaluated quite accurately through performance of their relative's information using single-trait and multi-traits AM.

4.6.3.1 Transmitting ability estimates for sires of birds:

The results of predicted transmitting ability obtained by multi-trait and single-trait **AM** for sires (**PSTA**) (sires of birds) for **BW**, **DG** and **RG** traits in Dokki-4 chickens were given in Table 33. The minimum and maximum estimates of **PSTA** and their ranges indicate that these estimates had the same trend obtained for birds with records. The average of ranges in estimates of **PSTA** for **BW** obtained by single-trait **AM** vs multi-trait **AM** were 32.54 vs 36.97 grams, 2.11 vs 2.06 grams and 5.17 vs 5.14% for **BW**, **DG** and **RG** traits, respectively. When considering the top 4% of sires of animals in both models of evaluation, the ranges in estimates of **PSTA** are seem to be of the trend similar to the case in which all sires were considered (Table 33). These ranges were small when considering 4% of sires than that when considering of the all sires in the list (Sabra, 1998).

The accuracy of minimum and maximum estimates of transmitting ability for sires indicate that these estimates had the same trend obtained for birds with records. Accuracy of **PSTA** for sires when using multi-trait **AM** were relatively higher than those compared to single-trait **AM**. The averages of accuracy across all the minimum and maximum estimates of **PSTA** when using multi-traits vs single-trait **AM** was 0.82 vs 0.76%, 0.76 vs 0.75% and 0.79 vs 0.77% for **BW**, **DG** and **RG** traits, respectively. This is because covariance structure among traits was considered in multi-trait **AM**. In

Table 33. Minimum, maximum and ranges of predicted transmitting abilities for sires (birds without records) (**PSTA**), their standard errors (SE) and accuracy of prediction ($r_{A\hat{A}}$) estimated by single-trait and multi-traits animal models for body weights, daily gains and relative growth rates.

Trait[+]	Single-trait animal model								Multi-traits animal model							
	Minimum			Maximum			Range	Top 4%* of sires	Minimum			Maximum			Range	Top 4%* of sires
	PSTA	SE	$r_{A\hat{A}}$	PSTA	SE	$r_{A\hat{A}}$			PSTA	SE	$r_{A\hat{A}}$	PSTA	SE	$r_{A\hat{A}}$		
Body weights (grams):																
BW0	-0.64	0.67	0.87	0.73	0.68	0.86	1.37	0.10	-0.64	0.67	0.86	0.72	0.69	0.85	1.36	0.09
BW2	-2.86	2.34	0.81	5.31	2.24	0.83	8.17	3.38								
BW4	-7.82	5.77	0.81	7.40	5.08	0.86	15.22	0.63	-8.70	5.56	0.83	7.28	4.99	0.87	15.98	0.17
BW6	-6.39	9.20	0.75	14.75	9.10	0.76	19.63	4.35								
BW8	-12.3	12.01	0.79	17.17	12.49	0.77	29.44	5.00	-12.53	11.35	0.80	16.78	11.82	0.78	29.31	4.84
BW10	-14.3	16.20	0.79	15.37	16.28	0.79	29.65	2.76								
BW12	-19.70	21.42	0.67	16.71	19.50	0.74	36.46	0.73	-26.10	20.86	0.72	22.22	18.17	0.80	48.31	2.43
BW16	-36.20	32.41	0.73	44.00	29.52	0.78	80.22	8.84	-43.06	33.01	0.79	46.84	28.62	0.85	89.90	6.61
Daily gains (grams):																
DG4	-0.56	0.40	0.81	0.56	0.35	0.85	1.12	0.10	-0.51	0.37	0.79	0.46	0.33	0.83	0.97	0.35
DG8	-0.84	0.72	0.69	0.70	0.71	0.71	1.55	0.14	-0.72	0.71	0.71	0.91	0.68	0.74	1.63	0.27
DG12	-0.85	0.96	0.71	1.13	0.99	0.68	1.98	0.27	-1.05	0.94	0.71	1.02	0.94	0.71	2.08	0.03
DG16	-1.73	1.18	0.77	1.65	1.14	0.79	3.78	0.28	-1.80	1.09	0.79	1.75	1.05	0.81	3.55	0.59
Relative growth rates (%):																
RG4	-2.50	2.00	0.81	2.72	1.79	0.85	5.22	0.93	-2.74	1.98	0.84	2.37	1.76	0.88	5.11	0.57
RG8	-3.43	2.12	0.73	3.29	2.08	0.74	6.73	1.16	-3.25	2.12	0.76	3.48	2.09	0.77	6.73	1.27
RG12	-2.31	1.98	0.72	2.63	2.00	0.72	4.94	0.25	-2.45	1.98	0.73	2.49	2.00	0.72	4.93	0.07
RG16	-2.10	1.48	0.77	1.68	1.42	0.79	3.77	0.13	-2.17	1.47	0.78	1.60	1.55	0.80	3.77	0.07

[+] Traits as defined in Table 20.

Number of sires without records evaluated was 34.

*=2 sires were selected according to Danbaro et al. (1995a) and Morris and Pollott (1997).

addition to that, the standard errors of predictors of **PSTA** obtained by multi-traits **AM** were lower than those compared with single-trait **AM** for most growth traits. Pribly and Pribylova (1991) found that reliability of **PBV** were 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. On other hand, the accuracy of predictors of sires **(PSTA)** was higher than those recorded for birds with records **(PBV)**. This may be due to a large amount of information were available for each sire (i.e. large numbers of progeny per sire were utilized) (Table 19). In this respect, Korthonen (1996) reported that the heritability of the trait and the amount of information utilized in evaluation affect the reliability of index.

The numbers of sires with positive estimates of **PSTA** and their percentages given in Table 34 indicate that single-trait **AM** estimates were mostly higher in transmitting ability for **BW** than those obtained from multi-trait **AM**. The average of percentages for **PSTA** with positive signs for single-trait vs multi-trait **AM** was 49.3 vs 48.8% for **BW**. However the opposite trend was recorded, i.e. these averages were 48.5 vs 49.3% and 50.0 vs 51.5% for **DG** and **RG** traits, respectively. From the percentages of **PSTA** with positive signs for all growth traits (nearly 50%) obtained by single- or multi- traits **AM**, we expect that the transmitting ability of sires of birds in the present study are normally distributed with **N**≈($A^{-1}S$, **VW**/ $\hat{A}$).

4.6.3.2 Transmitting ability estimates for dams of birds:

The results of predicted transmitting ability obtained by multi-trait and single-trait **AM** for dams **(PDTA)** (dams of birds) for **BW**, **DG** and **RG** traits were given in Table 35. The minimum and maximum estimates of **PDTA** and their ranges indicate that these estimates had the same trend obtained for birds with records. The ranges of **PDTA** for **BW** and **RG** were higher when using multi-trait **AM** than those obtained by single-trait **AM**. The average of ranges of **PDTA** when using single-trait **AM** vs multi-trait **AM** were 15.83 vs 21.59 grams, 0.91 vs 0.87 grams and 1.99 vs 2.35% for **BW**, **DG** and **RG**, respectively. When considering the top 23% of dams of birds in

Table 34. Numbers (and percentages) of sires with positive estimates of predicted transmitting abilities (**PSTA**) recorded by single- and multi-trait animal models (birds without records) for body weights, daily gains and relative growth rates.

Trait$^+$	**Single-trait animal model**		**Multi-traits animal model**	
	No. of sires	**% of sires**	**No. of sires**	**% of sires**
Body weights:				
BW0	17	50.0	17	50.0
BW2	14	41.2		
BW4	16	47.1	15	44.1
BW6	16	47.1		
BW8	18	52.9	18	52.9
BW10	16	47.1		
BW12	11	52.4	16	47.1
BW16	15	44.1	17	50.0
Daily gains:				
DG4	15	44.1	15	44.1
DG8	18	52.9	18	52.9
DG12	17	50.0	18	52.9
DG16	16	47.1	16	47.1
Relative growth rates:				
RG4	15	44.1	15	44.1
RG8	16	47.1	18	52.9
RG12	18	52.9	19	55.9
RG16	19	55.9	18	52.9

$^+$ Traits as defined in Table 20.

Table 35. Minimum, maximum and ranges of predicted transmitting abilities for dams (birds without records) (**PDTA**), their standard errors (**SE**) and accuracy of prediction ($r_{A\hat{A}}$) estimated by single-trait and multi-traits animal models for body weights, daily gains and relative growth rates.

Trait[+]	Single-trait animal model								Multi-traits animal model							
	Minimum			Maximum			Range	Top 23%[*] of dams	Minimum			Maximum			Range	Top 23%[*] of dams
	PDTA	SE	$r_{A\hat{A}}$	PDTA	SE	$r_{A\hat{A}}$			PDTA	SE	$r_{A\hat{A}}$	PDTA	SE	$r_{A\hat{A}}$		
Body weights (grams):																
BW0	-0.69	1.31	0.27	0.73	1.27	0.35	1.42	0.59	-0.65	1.27	0.25	0.68	1.24	0.33	1.33	0.55
BW2	-1.30	3.88	0.24	2.33	3.82	0.30	3.63	2.04								
BW4	-4.51	9.95	0.24	4.49	9.53	0.28	9.00	3.53	-5.58	9.53	0.26	5.45	9.40	0.30	11.03	4.32
BW6	-4.13	13.28	0.29	5.48	13.28	0.29	9.61	4.63								
BW8	-5.03	19.15	0.20	9.74	18.61	0.30	14.76	8.67	-6.47	18.57	0.26	11.18	17.87	0.31	17.65	9.71
BW10	-8.44	26.33	0.16	12.68	25.31	0.32	21.12	10.68								
BW12	-8.10	28.38	0.18	10.46	27.93	0.25	18.56	8.88	-13.67	29.40	0.22	15.43	28.84	0.29	29.10	12.77
BW16	-16.91	46.04	0.21	18.51	45.23	0.28	35.43	15.04	-24.00	51.66	0.28	24.84	50.34	0.35	48.85	19.15
Daily gains (grams):																
DG4	-0.27	0.66	0.23	0.31	0.64	0.31	0.58	0.25	-0.24	0.59	0.22	0.26	0.57	0.29	0.49	0.20
DG8	-0.26	0.99	0.17	0.47	0.96	0.27	0.72	0.41	-0.25	0.96	0.28	0.53	0.96	0.28	0.78	0.47
DG12	-0.39	1.34	0.17	0.48	1.32	0.24	0.87	0.40	-0.50	1.31	0.20	0.43	1.29	0.27	0.93	0.33
DG16	-0.52	1.83	0.19	0.61	1.79	0.27	1.48	0.47	-0.63	1.76	0.17	0.67	1.71	0.30	1.29	0.51
Relative growth rates (%):																
RG4	-1.21	3.31	0.20	1.56	3.22	0.31	2.77	1.26	-1.68	3.47	0.33	1.66	3.36	0.41	3.34	1.29
RG8	-1.02	3.06	0.19	0.99	2.98	0.30	2.01	0.76	-1.40	3.17	0.23	1.14	3.10	0.30	2.55	0.89
RG12	-0.70	2.76	0.28	1.02	2.76	0.28	1.71	0.84	-0.85	2.84	0.19	1.07	2.77	0.29	1.91	0.87
RG16	-0.73	2.21	0.29	0.74	2.23	0.27	1.48	0.59	-0.85	2.32	0.22	0.76	2.27	0.29	1.61	0.59

[+] Traits as defined in Table 20.

Number of dams without records evaluated was 325.

[*]= 75 dams were selected according to Danbaro et al. (1995a) and Morris and Pollott (1997).

both models of evaluation, the ranges in **PDTA** are seen to be of the trend similar to the case in which all dams were considered (Table 35).

The accuracy of minimum and maximum estimates of transmitting ability for dams indicate that these estimates were lower than those obtained for birds (birds with records) and sires (sires of birds). This may be due to a small amount of information available for each dams (i.e. small numbers of progeny per dam were utilized) (Table 19). The average of accuracy across all the minimum and maximum estimates of **PDTA** for dams using multi-trait **AM** were relatively higher than those compared to single-trait **AM**. These averages when using multi-traits vs single-trait **AM** were 0.29 vs 0.26%, 0.26 vs 0.23% and 0.28 vs 0.27% for **BW**, **DG** and **RG** traits, respectively. This is because covariance structure among traits was considered in multi-trait **AM**.

The numbers of dams with positive estimates of **PDTA** and their percentages given in Table 36 indicate that single-trait **AM** estimates were mostly higher in transmitting ability than those obtained from multi-trait **AM**. The average of percentages for **PSTA** with positive signs for single-trait vs multi-trait **AM** was 52.0 vs 50.5%, 52.6 vs 50.9% and 50.2 vs 48.9% for **BW**, **DG** and **RG** traits, respectively. From the percentages of **PDTA** with positive signs for all growth traits (nearly 50%) obtained by single- or multi- traits **AM**, we expect that the transmitting ability of dams of birds in the present study are normally distributed with $\mathbf{N}\approx(A^{-1}D , \mathbf{VW}/\hat{A})$.

4.6.4 Rates of change in accuracy

Comparisons of accuracy for predictor resulting from single-trait and multi-trait **AM** and rates of changes in accuracy occurred for birds with records and birds without records (sires and dams) are presented in Table 37. These results indicate that accuracy of multi-trait evaluations were higher than those obtained by single-trait **AM**, because data from correlated traits provide information not contained in data of the trait being evaluated (Foully et al., 1982; Mrode, 1996).

Rates of changes occurred in accuracy for birds breeding values (**PBV**) ranged from –2.1 to 27.8% (averaged 10.8%), -3.6 to 6.6% (averaged 2.7%) and –15.6 to

Table 36. Numbers (and percentages) of dams with positive estimates of predicted transmitting abilities (**PDTA**) recorded by single- and multi-trait animal models (birds without records) for body weights, daily gains and relative growth rates.

Trait[+]	Single-trait animal model		Multi-traits animal model	
	No. of dams	% of dams	No. of dams	% of dams
Body weights:				
BW0	157	48.3	158	48.6
BW2	179	55.1		
BW4	167	51.4	164	50.5
BW6	171	52.6		
BW8	170	52.3	176	54.2
BW10	172	52.9		
BW12	169	52.0	166	51.1
BW16	166	51.1	156	48.0
Daily gains:				
DG4	166	51.1	165	50.7
DG8	181	55.7	173	53.2
DG12	171	52.6	166	51.1
DG16	166	51.1	158	48.6
Relative growth rates:				
RG4	157	48.3	154	47.4
RG8	172	52.9	170	52.3
RG12	167	51.4	160	49.2
RG16	156	48.0	152	46.8

[+] Traits as defined in Table 20.

Table 37. Averages of accuracies and rates of changes in accuarcy from using single-trait vs multi-traits bird models for birds (progeny) with records, and birds without records (sires and dams) for body weights and daily gains, and relative growth rates.

Trait[+]	Birds with records			Birds without records					
				Sire			Dam		
	Single-trait	Multi-traits	Δ_A^*%	Single-trait	Multi-traits	Δ_A^*%	Single-trait	Multi-traits	Δ_A^*%
Body weights:									
BW0	0.725	0.710	-2.1	0.865	0.855	-1.2	0.310	0.290	-6.5
BW4	0.525	0.545	3.8	0.835	0.85	1.8	0.26	0.28	7.7
BW8	0.755	0.775	2.6	0.78	0.790	1.3	0.250	0.285	14.0
BW12	0.530	0.645	21.7	0.705	0.76	7.8	0.215	0.255	18.6
BW16	0.450	0.575	27.8	0.755	0.820	8.6	0.245	0.315	28.6
Daily gains:									
DG4	0.690	0.665	-3.6	0.830	0.810	-2.4	0.270	0.255	-5.6
DG12	0.705	0.725	2.8	0.700	0.725	3.6	0.220	0.280	27.3
DG12	0.520	0.545	4.8	0.695	0.710	2.2	0.205	0.235	14.6
DG16	0.455	0.485	6.6	0.780	0.800	2.6	0.230	0.235	2.2
Relative growth rates:									
RG4	0.675	0.570	-15.6	0.830	0.860	3.6	0.255	0.370	45.1
RG12	0.585	0.620	6.0	0.735	0.77	4.8	0.245	0.265	27.3
RG12	0.575	0.580	0.9	0.720	0.73	1.4	0.280	0.240	-14.3
RG16	0.595	0.615	3.4	0.780	0.790	1.3	0.280	0.255	-8.9

[+] Traits as defined in Table 2.

[*] Δ_A = rate of change in accuracy.

6.0% (averaged –1.3%) for **BW**, **DG** and **RG** traits, respectively. Similarly, the rates of changes in accuracy of sires transmitting abilities (**PSTA**) ranged from –1.2 to 8.6% (averaged 3.7%), -2.4 to 3.6% (averaged 1.5%) and 1.3 to 4.8% (averaged 2.8%) for the same order. While the rates of changes in accuracy of dams transmitting abilities (**PDTA**) ranged from –6.5 to 28.6% (averaged 12.5%), -5.6 to 27.3% (averaged 9.6%) and –14.3 to 45.1% (averaged 12.3%) for the same order. These results indicate that advantages of the rate of changes for predictions were largest for both dams and birds and decreased for sires as number of progenies increased (VanRaden et al., 1990). Advantages could be overstated if true parameter differs from estimates (Table 37).

4.6.5 Rank correlation:

Spearman's rank correlations were calculated among estimates ranks of **BLUP** which were estimated by single-trait **AM** for different growth traits to detect which trait can be replaced by the other to simplify the method of analysis and to safe the time and money specially when using complicated ~~models.~~ Also, a rank ~~correlations~~ were estimated among ranks of transmitting ability estimates calculated by the two animal models (single-trait and multi-traits **AM**) were used to decide whether the two models are quite different from each other in evaluation of birds under questions or not.

4.6.5.1 Rank correlations among estimators predicted by single-trait animal models:

Rank correlations (and their significances) among ranks of breeding values of birds with records (**PBV**) and among ranks of transmitting ability of birds without records (sires, **PSTA**, and dams **PDTA**) in single-trait and multi-trait **AM** are given in Table 38.

For data of birds (birds with records), estimates of rank correlation among most ranks of **PBV** estimates estimated by single-trait **AM** for **BW** and **DG** traits were

Table 38. Rank correlations among predictions for growth traits of birds with and without records in single- and multi-traits bird models.

Rank correlated traits^{+}	Single-trait animal model			Multi-traits animal models			Single-trait vs multi-traits animal models		
	Birds with records	Birds without records		Birds with records	Birds without records		Birds with records	Birds without records	
		Sire	Dam		Sire	Dam		Sire	Dam
Body weights:									
BW0 & BW2	0.32**	0.19^{ns}	0.51**						
& BW4	0.31**	0.46**	0.37**	0.35**	0.49**	0.43**	0.34**	0.48**	0.41**
& BW6	0.24**	0.29^{ns}	0.34**						
& BW8	0.23**	0.13^{ns}	0.29**	0.27**	0.18^{ns}	0.37**	0.26**	0.15^{ns}	0.32**
& BW10	0.23**	0.24^{ns}	0.26**						
& BW12	0.28**	0.35*	0.28**	0.29**	0.35*	0.33**	0.30**	0.36*	0.31**
& BW16	0.29**	0.59**	0.25**	0.31**	0.62**	0.35**	0.31**	0.59**	0.28**
BW2 & BW4	0.71**	0.67**	0.60**						
& BW6	0.66**	0.32^{ns}	0.51**						
& BW8	0.47**	0.19^{ns}	0.40**						
& BW10	0.44**	0.20^{ns}	0.37**						
& BW12	0.44**	0.30^{ns}	0.37**						
& BW16	0.37**	0.29^{ns}	0.31**						
BW4 & BW6	0.77**	0.69**	0.71**						
& BW8	0.56**	0.51**	0.59**	0.61**	0.53**	0.64**	0.61**	0.49**	0.60**
& BW10	0.66**	0.52**	0.55**						
BW4 & BW12	0.67**	0.61**	0.53**	0.66**	0.65**	0.68**	0.67**	0.63**	0.61**
& BW16	0.62**	0.64**	0.46**	0.71**	0.73**	0.73**	0.66**	0.67**	0.57**

Table 38. Cont.

Rank correlated traits^{+}	Single-trait animal model			Multi-traits animal models			Single-trait vs multi-traits animal models		
	Birds with records	Birds without records		Birds with records	Birds without records		Birds with records	Birds without records	
		Sire	Dam		Sire	Dam		Sire	Dam
BW6 & BW8	0.86**	0.91**	0.82**						
& BW10	0.79**	0.86**	0.75**						
& BW12	0.69**	0.73**	0.70**						
& BW16	0.52**	0.41*	0.61**						
BW8 & BW10	0.89**	0.89**	0.87**						
& BW12	0.75**	0.67**	0.76**	0.78**	0.77**	0.89**	0.78**	0.72**	0.85**
& BW16	0.52**	0.27^{ns}	0.63**	0.57**	0.40*	0.75**	0.57**	0.34*	0.72**
BW10 & BW12	0.84**	0.81**	0.84**						
& BW16	0.63**	0.46**	0.71**						
BW12 & BW16	0.82**	0.78**	0.87**	0.61**	0.77**	0.85**	0.73**	0.75**	0.84**
<u>Daily gains:</u>									
DG4 & DG8	0.33**	0.11^{ns}	0.26**	0.45**	0.19^{ns}	0.53**	0.48**	0.25^{ns}	0.60**
& DG12	0.38**	0.32^{ns}	0.34**	0.59	0.52**	0.66**	0.53**	0.48**	0.56**
& DG16	0.36**	0.45**	0.14**	0.71**	0.69**	0.77**	0.61**	0.62**	0.61**
DG8 & DG12	0.06**	-0.04^{ns}	0.25**	0.04**	-0.15^{ns}	0.16**	0.02**	-0.16^{ns}	0.13*
& DG16	-0.11**	-0.35*	0.12**	-0.10**	-0.34*	0.08^{ns}	-0.14**	-0.35*	-0.01^{ns}
DG12 & DG16	0.39**	0.49**	0.34**	0.78**	0.75**	0.88**	0.54**	0.56**	0.53**

Table 38. Cont.

Rank correlated traits^{+}	Single-trait animal model			Multi-traits animal models			Single-trait vs multi-traits animal models		
	Birds with records	Birds without records		Birds with records	Birds without records		Birds with records	Birds without records	
		Sire	Dam		Sire	Dam		Sire	Dam
Relative growth rates:									
RG4 & RG8	-0.40**	-0.50**	-0.41**	0.07**	-0.39*	0.33**	-0.18**	-0.43**	-0.04^{ns}
& RG12	-0.01^{ns}	0.08^{ns}	-0.03^{ns}	0.18**	0.09^{ns}	0.37**	0.04**	0.04^{ns}	0.08^{ns}
& RG16	0.08**	0.09^{ns}	-0.12*	0.42**	0.21^{ns}	0.50**	0.29**	0.17^{ns}	0.30**
RG8 & RG12	-0.43**	-0.47**	-0.23**	-0.27**	-0.43**	0.18**	-0.42**	-0.48**	-0.12*
& RG16	-0.44**	-0.68**	-0.11*	-0.35**	-0.75**	-0.03^{ns}	-0.48**	-0.74**	-0.19**
RG12 & RG16	0.22**	0.47**	0.02^{ns}	0.46**	0.63**	0.46**	0.33**	0.55**	0.24**

$^{+}$Traits as defined in Table 20.

^{ns}= non-significant; *= P<0.05 and **= P<0.01.

moderate or high. The estimates ranged from 0.23 to 0.89 (P<0.01) and –0.11 to 0.39 (P<0.01) for **BW** and **DG**, respectively. For data set of sires without records (**PSTA**), estimates of rank correlations ranged from low to high (i.e. 0.13 to 0.91 for **BW**) estimates obtained from data set of sires. Most estimates of rank correlation were significant (P<0.01). For data set of dams without records (**PDTA**), estimates of rank correlations showed a trend similar to that observed to estimates obtained from data set of birds.

4.6.5.2 Rank correlations among estimators predicted by single-trait vs multi-trait animal models:

Rank correlations (and their significances) among ranks of predictors estimated by single-trait and multi-trait **AM** for different growth traits for data set of birds (birds with records), sires and dams (birds without records) are shown in Table 38. For data set of birds (with and without records), most of correlations among ranks of predictors (i.e. **PBV**, **PSTA** and **PDTA**) estimated by single-trait and multi-trait **AM** for **BW**, **DG** and **RG** traits were relatively moderate or high; (29 estimates out of 66 were found with correlations less than 0.4). On the other hand, the rank correlations among predictors were higher for multi-traits than single-trait evaluations. Rank of correlations among ranks of **PBV**, **PSTA** and **PDTA** ranged from 0.23 to 0.89%, 0.13 to 0.91% and 0.26 to 0.87 for **BW** traits when using single-trait evaluation, respectively. While it ranged from 0.27 to 0.78, 0.18 to 0.77 and 0.33 to 0.89 among the same predictors when using multi-trait evaluations (Table 38). These estimates mean that ranking of predictors estimated by single-trait differed from the ranking of predictors estimated by multi-trait **AM**. Therefore, evaluation of birds for growth traits in Dokki-4 chickens using multi-trait **AM** would give **BLUP** estimates with more accuracy than using single-trait **AM**. This was expected since covariances between traits play an important role in the accuracy of the **BLUP** estimates by multi-trait **AM**.

High estimates of rank correlations (and highly significant, P<0.01) between estimates of **PBV**, **PSTA** and **PDTA** estimated by single-trait and multi-traits **AM** for **BW** at 8 and the following ages suggested that breeding birds, sires and dams could be selected at 8-weeks of age to bring genetic improvement and to breed Dokki-4 chickens for higher market weight. Consequently, selection of birds at 8 weeks of age is more effective without saving of all birds to later ages and thus the cost of breeding program is reduced. These results were agreed with reports' of Raheja and Singh (1993). On the other hand, high estimates of rank correlations among predictions of transmitting abilities for all growth traits, when comparisons were done between single-trait and multi-trait **AM,** indicate that low differences were observed between both models of evaluation. From the previous results, we can conclude that the single-trait **AM** is satisfactory model to application in evaluation of poultry breeding programs, because (1) it reduce the time of computation required in an analysis, (2) it reduce the specific requirements of the computer, and (3) it reduce the cost of breeding programs.