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Estimation of genetic parameters for some productive traits in New Hampshire chickens using animal model

By

Iraqi, M.M. and Hanafi, M.S.

Faculty of Agriculture, Moshtohor, Zagazig University /Benha Branch, Egypt

Abstract: Data of 4566 New Hampshire chicks (2080 in the first generation and 2486 in the second generation) were produced from 44 sires and 342 dams. Data produced from each generation were separately analysed using uni-trait animal model to estimate genetic parameters of egg weight; body weight at hatch, 4 and 8 weeks; daily gains during the periods from hatch-4 and 4-8 weeks of age and feathering score at 8 weeks traits. Results show that the percentages of additive genetic variance for most studied traits in the first generation were higher (averaged 16%) than in the second generation (averaged 14%). Percentages of common environmental variance in the two generations were very high for egg weight (averaged 72%) and body weight at hatch (averaged 68%) and then markedly decreased thereafter with advancement of chick age (averaged 11% at 8 weeks). Estimates of heritability (h^2) for egg weight and body weight at hatch were low and then increased thereafter up to 4 weeks (0.29). Estimates of genetic correlation r_G between body weight at 4 weeks and/or 8 weeks of age and daily gains were significantly ($P < 0.001$) high and positive in the two generations.

Predicted breeding values (PBV) for birds with records (progeny) were higher than those recorded for birds without records (sires and dams), while the accuracy of PBV for sires were higher compared with estimates obtained for dams and progeny. Responses estimated by direct single-trait selection for most studied traits were higher in the second generation than in the first generation.

Keywords: *(Growth traits, Feathering score, Additive genetic variance, Heritability, Breeding values, Direct genetic response, Animal Model).*

INTRODUCTION

Little information is available in estimation of genetic parameters in broilers of chickens using animal models (Wezyk and Szwaczkowski, 1993, Koerhuis and van der Werf, 1994). Sorensen and Kenedey (1983) reported that applying an animal model with the inclusion of all data (on which selection was based) as well as the full additive relationship matrix lead to an avoidness in most biases in estimates of variance components, that are due to selection. Furthermore, these methods are almost completely ignored in poultry evaluation systems even though strong selection has been carried out on these species for many generations. Moreover, the new parameters (e.g. breeding values, accuracy and common environmental variance) will be considered as basis for genetic evaluations under updated evaluation methodology (i.e. single-trait or multi-trait animal models) that will result in more accurate ranking of birds. This improved ranking will allow broiler breeders to make greater genetic progress for growth traits (Iraqi, 1999 & Iraqi, 2000). Breeders are conformed to the need for making genetic improvement in

species (e.g. poultry), which have been subjected to many generation of selection, and in which multiple objectives must be considered.

Objectives of this study were: (1) estimation of genetic (additive, heritability and genetic correlation) and non-genetic (common environmental variance) effects of some productive traits of New Hampshire chickens during two generations of selection, (2) evaluation of predicted breeding values and their accuracies for sires, dams and their progeny and (3) prediction of direct genetic response from single-trait selection.

MATERIAL AND METHODS

This experiment was carried out at the Department of Poultry Science, Texas A&M University, USA. Recorded data in New Hampshire chickens were utilized to estimate additive and non-additive (e.g. common environment) genetic variances, genetic correlation, predicted breeding values and expected direct genetic responses from single trait selection.

Twenty two sires randomly chosen from the base population were assigned to 22 breeding pens. Each sire was mated to ten randomly chosen dams, with a total of 220, to produce the first generation. The dams were assigned to the sires at random. At sexual maturity the selected birds (22 sires and 220 dams) from the first generation were assigned at random to mating pens to produce second generation chicks. All chicks produced in the first and second generations were equally divided and randomly assigned to two environments of ration (firstly contained 18% protein and secondly contained 24% protein). All chicks produced in the two generations were treated and medicated similarly throughout the experimental period under the same managerial climatic conditions.

A total number of 4566 chicks (2080 and 2486 chicks were produced in the first and second generation, respectively) were produced from 44 sires and 342 dams. Data of individual egg weight (EW), body weight (BW) at hatch (BW0), 4 (BW4) and 8 (BW8) weeks, feathering score at 8 weeks of age (FS8) were recorded. Daily gain (DG) during the periods from hatch-4 (DG4) and 4-8 weeks (DG8) of age were also computed. The data produced from each generation were analyzed using new methodology, i.e. MTDFREML procedure (Boldman et al., 1995).

Model of analysis:

The single-trait animal model using MTDFREML procedure in matrix notation was as follows:

Where $y = nx1$ vector of observed productive traits on bird; $b = px1$ vector of fixed effects

$$y = Xb + Z_a u_a + Z_c u_c + e$$

of environment of ration and sex; $u_a = qx1$ vector of random effect of the bird; $u_c =$ vector of random common environment of dam family; X , Z_a and Z_c are the incidence matrices relating records to fixed effects, the additive genetic effects and random common environmental effect, respectively. $e = nx1$ vector of random residual effects.

The mixed model equations (MME) of the single-trait Animal Model described above were of the form:

$$\begin{bmatrix} X'X & X'Z_a & X'Z_c \\ Z_a'X & Z_a'Z_a + A^{-1}\alpha_a & Z_a'Z_c \\ Z_c'X & Z_c'Z_a & Z_c'Z_c + I_c\alpha_c \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u}_a \\ \hat{u}_c \end{bmatrix} = \begin{bmatrix} X'y \\ Z_a'y \\ Z_c'y \end{bmatrix}$$

Where A^{-1} is the inverse of the numerator relationship matrix (Henderson, 1976), $\alpha_a = \sigma_e^2/\sigma_a^2$ and $\alpha_c = \sigma_e^2/\sigma_c^2$, I_c is identity matrix corresponding to levels of common environmental effects and I_n is an identity matrix corresponding to n observations. Expected direct response is calculated as (Cameron, 1997):

$$\Delta_G = ir_{A,i} \sqrt{\sigma_a^2}$$

Where Δ_G = direct genetic response; i = selection differential of x trait in standard deviation units; $r_{A,i}$ = accuracy of predicted breeding values; σ_a^2 = additive genetic variance.

RESULTS AND DISCUSSION

Variance components:

Estimates of direct additive genetic (σ_a^2), common environmental (σ_c^2) and predicted error (σ_e^2) variance components are presented in Table 1. Results show that the percentages of additive genetic variance for EW and BW0 of New Hampshire were very low compared to weights at 4 and 8 weeks of age. This result may be due to high effects of maternal and other non-additive genetic variation, i.e. common environmental variance, (Mrode, 1996, Cameron, 1997 and Iraqi, 1999). Estimates of additive genetic variance in the present study are in agreement with reports of Ezzeldin (1970) and Shalash (1977) in Rhode Island Red and White Plymouth Rock chickens. The percentage of σ_a^2 for feathering score at 8 weeks was 30% in the first generation and 2% in the second generation.

Percentages of σ_a^2 in the first generation for all traits studied were slightly higher than those in the second generation. The reduction in additive genetic variance could be explained as a result of selection in the progeny of first generation (Cameron, 1997).

Percentages of common environmental variance in the two generations were very high for EW (averaged 72%) and BW0 (averaged 68%) and then markedly decreased thereafter with advancement of age (averaged 11% at 8 weeks) (Table 1). These results indicate that maternal and non-additive genetic effects are very important for EW and BW0 (Khalil, et al 1993). Aggrey and Cheng (1994) with Japanese Quail reported that the variance due to common environmental effects was about 60% at hatch but declined generally as the chicks get older (16% at 4 weeks). Results in the present study are in agreement with results of Danbaro, et al. (1995) in White Plymouth Rock chickens. The σ_c^2 included accounted for maternal permanent environmental variation, non-additive gene action and any sire-dam interaction that may be present (Iraqi, 1999). The percentage of σ_c^2 for FS8 was 10% in the first generation and 5% in the second generation. This reduction could be explained as a result of the homogeneity of birds for this trait due to selection (Cameron, 1997).

Table 1. Estimates of additive (σ_a^2), common environment (σ_c^2), error (σ_e^2) and phenotypic (σ_p^2) variance components for productive traits of New Hampshire chickens in the two generations.

components for productive traits of New Hampshire chickens in the two generations.

Trait	Symbole	Additive		Common environment		Error		σ_F^2
		σ_a^2	%	σ_c^2	%	σ_e^2	%	
First generation:								
Egg weight	EW	0.316	2	14.468	72	5.478	26	20.262
Body weight at hatch	BW0	0.06	1	7.364	72	2.707	27	10.131
Body weight at 4 weeks	BW4	962.46	29	297.065	9	2073.52	62	3333.05
Body weight at 8 weeks	BW8	2036.8	10	1718.98	8	17107.29	82	20863.07
Daily gain from hatch-4 weeks	DG4	5.072	29	1.049	6	11.243	65	17.364
Daily gain from 4-8 weeks	DG8	9.091	14	2.845	4	53.397	82	65.233
Feathering score at 8 weeks	FS8	0.166	30	0.056	10	0.338	60	0.563
Second generation:								
Egg weight	EW	0.133	1	12.12	71	4.723	28	16.975
Body weight at hatch	BW0	0.034	1	6.364	65	3.365	34	9.757
Body weight at 4 weeks	BW4	970.09	28	293.93	8	2223.09	64	3487.1
Body weight at 8 weeks	BW8	2050.50	15	1915.77	14	10108.02	71	14074.29
Daily gain from hatch-4 weeks	DG4	5.08	29	1.203	7	11.236	64	17.521
Daily gain from 4-8 weeks	DG8	8.884	22	3.334	8	28.933	70	41.151
Feathering score at 8 weeks	FS8	0.006	2	0.012	5	0.245	93	0.263

Heritability:

Estimates of heritability (h_o^2) presented in Table 2 show that the h_o^2 for EW and BW0 were low and then increased thereafter up to 4 weeks (0.29) and then decreased at 8 weeks of age. These results are within the range of those estimates reported by Godfray and Goodman (1956) and Singh and Singh (1981), based on sire model, in New Hampshire chickens. On the other hand, estimates of h_o^2 in the first generation were higher than those in the second generation. Koerhuis and McKay (1996) found that h_o^2 was 0.28 at 6 weeks of age (based on uni-variate animal model) in Juvenile female chickens. In addition to that, Danbaro, et al. (1995) reported that h_o^2 for body weight at 7 weeks was 0.20 in Plymouth Rock chickens.

Estimates of h_o^2 for FS8 was 0.30 in the first generation and 0.02 in the second generation. The reduction in h_o^2 of most traits studied in the second generation could be explained as a result of the reduction in additive variance due to selection (Hanafi, 1966 and Cameron, 1997). Generally, with animal model, estimates of h_o^2 are not biased because the relationship coefficient matrix is considered (Meyer and Thompson, 1984; Quaas et al., 1984; Mrode, 1996 and Iraqi, 1999).

Table 2. Estimates of heritability (diagonal) and genetic correlations (off diagonal) between productive traits of New Hampshire chickens in the two generations.

Trait ⁺⁺	EW	BW0	BW4	BW8	DG4	DG8	FS8
First generation							
EW	0.02	0.59***	0.31***	0.27***	0.25***	0.14***	0.19***
BW0		0.01	0.23***	0.18***	0.17***	0.10***	0.08***
BW4			0.29	0.75***	0.98***	0.42***	0.27***
BW8				0.10	0.73***	0.89***	0.19***
DG4					0.29	0.41***	0.25***
DG8						0.14	0.06**
FS8							0.30
Second generation							
EW	0.01	0.80***	0.13***	0.07***	0.09***	0.06**	-0.06***
BW0		0.01	0.14***	0.10***	0.10***	0.08***	-0.20***
BW4			0.28	0.81***	0.99***	0.47***	-0.16***
BW8				0.15	0.80***	0.88***	-0.25***
DG4					0.29	0.47***	-0.15***
DG8						0.22	-0.16***
FS8							0.02

* Genetic correlation computed as the correlation between predicted breeding values.

⁺⁺ Traits as defined in Table 1.

** = $P < 0.001$; *** = $P < 0.0001$.

Genetic correlation:

Estimates of genetic correlation (r_G) among studies traits are given in Table 2. These results indicated that r_G between EW or BW0 and each of other body weight, daily gain and FS8 traits were generally decrease in value as the differences between the two ages (or intervals) got larger. These results are in agreement with results of some investigators (e.g. Khalil et al., 1993; Khan et al., 1994; Danbaro et al., 1995). Moreover, estimates of r_G among EW or BW0 and other studied traits were significantly low and positive. These results may be due to high effects of common environment on EW and BW0. On other hand, estimates of r_G between BW4 and/or BW8 and daily gains (except between BW4 and DG8 traits) were significantly ($P < 0.001$) high and positive in the two generations. These estimates fall within the range of r_G in some reviewed studies (Bhushan and Singh, 1995; Reddy et al., 1997; Iraqi, 1999) for different breeds.

In general, estimates of r_G between BW4 and/or BW8 and daily gains were somewhat large in the second generation than in the first generation. The estimates of r_G were 0.75 vs 0.81; 0.98 vs 0.99; 0.73 vs 0.80 between BW4 & BW8; BW4 & DG4; BW8 and DG8 in the 1st and 2nd generations, respectively. This may be due to the covariance among that traits were large in the 2nd generation than in the 1st generation, and/or the reduction in additive genetic variance due to selection (Cameron, 1997)(Table 1).

Estimates of r_G between FS8 and all studied traits were significantly low and positive in the 1st generation, while the negative estimates of r_G in the 2nd generation were unexpected. Sampling errors may be the cause of these unexpected estimates. From

the pervious results, we can recommend the poultry breeder to improve growth traits of New Hampshire chicken through direct selection at 4- weeks of age.

Predicted of breeding value:

For birds with records, minimum, maximum and ranges of predicted breeding values (PBV) for birds with records (progeny) in the two generations given in Table 3 show that the ranges in PBV for BW traits and DG traits in the second generation were higher (averaged 104.59 gram for BW traits and 13.46 gram for DG traits) than those in the first generation (averaged 90.08 gram for BW traits and 9.87 gram for DG traits). The reverse trend was observed for FS8 trait. These results could be explained due to response of selecting the best parents in growth from the first generation were selected as to be parents in the second generation (response due to selection) (Mrode, 1996). On the other hand, BW' at 4 weeks of age had larger value of range in PBV than weight at hatch and 8 weeks (Table 3). Thus, we can suggest selecting the New Hampshire chicks at 4 weeks.

The average of accuracy (r_{AA}) across all the minimum and maximum estimates of PBV were large (44% for BW traits and 55% for DG traits) in the second generation than those in the first generation (35% for BW traits and 51% for DG traits). This is because the amount of information in the second generation was large (Mrode, 1996 and Iraqi, 1999). Moreover, accuracy increases as the pedigree relationship and number of records increased (Bourdon, 1997). The reverse trend was observed for FS8 trait (Table 3).

For sires without records, ranges in PBV for sires without records were low for BW0 and then increased with the advancement of age in the two generations (Table 4). However, the estimates of ranges in PBV were somewhat larger in the first generation (averaged 54.2 gram for BW traits and 4.88 gram for DG traits) than in the second generation (averaged 53.0 gram for BW traits and 4.7 gram for DG traits) (Table 4). The additive genetic variance between full-sib family was reduced by selection, but the within full-sib family did not change (Cameron, 1997). Estimates of PBV for sire in the present study are in agreement with findings of Iraqi (1999) with Dokki-4 chickens.

The accuracy (r_{AA}) of PBV for sires in the first generation was higher (averaged 45% for BW traits and 65% for DG traits) than those in the second generation (averaged 37% for BW traits and 53% for DG traits). On the other hand, the accuracy of PBV for sires was higher than those for dams without records and progeny. This result may be due to each sire had a large number of progeny (averaged 110) compared to dam which had a smaller number (averaged 12). Estimates of accuracy for sires' PBV in the present study were lower than those reported by Iraqi (1999) with Dokki-4 chickens and Pribyl and Pribylova (1991) with laying hens. Korthonen (1996) reported that the heritability of the trait and the amount of information utilized in evaluation affects the reliability of the predictors.

For dams without records, results of PBV for dams without records for EW, BW, DG and FS8 traits presented in Table 5 show that estimates had the same trend obtained for birds with records. These results are in full agreement with the findings of Iraqi (1999). The ranges of dams' PBV for BW traits were higher in the second generation (averaged 74.14 gram) than those in the first generation (averaged 70.49 gram).

The accuracy (r_{AA}) of minimum and maximum estimates of PBV for dams of birds indicate that the estimates in the second generation were somewhat larger (30% for BW traits and 46% for DG traits) than in the first generation (29% for BW traits and 44% for DG traits). The reverse trend was observed for FS8 trait.

Table 3. Minimum, maximum and ranges of predicted breeding values (PBV) for birds with records (progeny), their standard errors (SE) and accuracy of prediction (r_{AA}) estimated by uni-trait animal model for productive traits in New Hampshire chickens.

Trait [†]	First generation						Second generation							
	Minimum		Maximum		Range in PBV	Minimum		Maximum		Range in PBV				
	PBV	SE	r_{AA}	PBV		SE	r_{AA}	PBV	SE		r_{AA}			
EW	-0.308	0.54	0.07	0.50	0.56	0.26	0.808	-0.303	0.36	0.08	0.167	0.36	0.21	0.470
BW0	-0.107	0.24	0.04	0.082	0.24	0.17	0.189	-0.054	0.18	0.50	0.088	0.18	0.13	0.142
BW4	-70.10	22.7	0.46	84.84	27.6	0.68	154.95	-69.69	22.6	0.45	89.69	27.9	0.69	159.38
BW8	-63.57	39.4	0.28	51.53	43.3	0.49	115.10	-78.43	37.5	0.32	75.82	42.9	0.56	154.25
DG4	-5.18	1.63	0.47	6.09	1.99	0.69	11.27	-5.195	1.61	0.46	8.269	2.01	0.70	13.46
DG8	-4.56	2.50	0.34	3.91	2.83	0.56	8.467	-7.951	2.29	0.39	5.517	2.74	0.64	13.468
FS8	-0.683	0.30	0.46	0.69	0.36	0.69	1.373	-0.073	0.07	0.13	0.064	0.08	0.32	0.137

[†] Traits as defined in Table 1.

Total numbers of progeny with records evaluated were 2080 and 2486 individuals from the first and second generations, respectively.

Table 4. Minimum, maximum and ranges of predicted breeding values (PBV) for sires without records, their standard errors (SE) and accuracy of prediction (r_{AA}) estimated by uni-trait animal model for productive traits in New Hampshire chickens.

Trait ⁺	First generation						Second generation							
	Minimum			Maximum			Minimum			Maximum				
	PBV	SE	r_{AA}	PBV	SE	r_{AA}	PBV	SE	r_{AA}	PBV	SE	r_{AA}		
EW	-0.161	0.55	0.15	0.146	0.56	0.21	0.31	-0.135	0.35	0.11	0.094	0.36	0.23	0.229
BW0	-0.042	0.24	0.09	0.058	0.24	0.14	0.10	-0.035	0.18	0.07	0.039	0.18	0.14	0.074
BW4	-34.57	20.51	0.60	27.42	24.8	0.75	62.0	-27.32	21.54	0.36	42.66	29.0	0.72	69.97
BW8	-52.75	35.24	0.49	47.79	39.4	0.62	100.5	-38.64	34.7	0.27	50.44	43.6	0.64	89.08
DG4	-2.55	1.47	0.61	2.07	1.78	0.76	4.616	-2.028	1.54	0.37	3.101	2.09	0.73	5.129
DG8	-2.74	2.19	0.55	2.39	2.51	0.69	5.14	-2.395	2.14	0.32	2.019	2.82	0.70	4.414
FS8	-0.677	0.27	0.60	0.623	0.33	0.75	1.30	-0.059	0.07	0.11	0.072	0.08	0.45	0.131

⁺ Traits as defined in Table 1.

Total numbers of sires without records evaluated were 22 from each generation.

Table 5. Minimum, maximum and ranges of predicted breeding values (PBV) for dams without records, their standard errors (SE) and accuracy of prediction (r_{AA}) estimated by uni-trait animal model for productive traits in New Hampshire chickens.

Trait [†]	First generation					Second generation				
	Minimum		Maximum		Range in PBV	Minimum		Maximum		Range in PBV
	PBV	SE	r_{AA}	PBV	SE	PBV	SE	r_{AA}	PBV	SE
EW	-0.135	0.56	0.06	0.281	0.56	0.15	0.416	-0.101	0.36	0.04
BW0	-0.029	0.24	0.04	0.093	0.24	0.09	0.122	-0.032	0.18	0.03
BW4	-56.63	22.59	0.27	49.98	29.8	0.69	106.62	-55.11	22.72	0.27
BW8	-67.59	39.61	0.16	37.14	44.6	0.48	104.72	-53.86	38.79	0.19
DG4	-4.33	1.59	0.27	3.86	2.17	0.71	8.19	-4.166	1.59	0.27
DG8	-4.76	2.45	0.19	3.685	2.96	0.58	8.44	-3.917	2.29	0.23
FS8	-0.513	0.30	0.28	0.614	0.39	0.69	1.127	-0.051	0.07	0.08

[†] Traits as defined in Table 1.

Total numbers of dams without records evaluated were 159 and 183 individuals from the first and second generations, respectively.

Response due to direct selection:

Expected direct response due to single-trait selection given in Table 6 showed that the response from sire, dam and their progeny were higher in the first generation than in the second generation with respect to **EW**, **BW0** and **FS8**. While the response from sire and their progeny in **BW4**, **BW8**, **DG4** and **DG8** were slightly higher in the second generation than the first. These results show that the expected direct response for **EW** and **BW0** did not give sufficient scope for improvement of **BW** traits through direct selection, while its sufficient effect to improvement the growth traits through direct selection for **BW4** and **BW8** of New Hampshire chickens. The direct response of **EW** and **BW0** from dam in the first generation was clear only in **BW4** and **DG4** traits, while the other traits were lower in values than the corresponding values in the second generation. Estimates of direct response obtained in the present study are within the range reported by Shalash (1977) on White Plymouth Rock chickens. On the other hand, the expected direct response for progeny is nearly the average of direct response for sires and dams, because each parent contributes the 50% of genotype to their progeny.

CONCLUSION

1. Percentages of common environmental variance in the New Hampshire chickens were very high for both **EW** and **BW0**. This indicate the maternal and non-additive genetic effects are very important for growth and we can recommend the poultry breeder in Egypt to utilize from this breed by crossing with local breeds.
2. High and positive genetic correlations among predictors lead to conclude that birds could be selected based on breeding values predicted at 4 weeks as to be parents for the next generation to improve the productive traits of New Hampshire, i.e. the cost of breeding program is reduced.
3. Results show that the expected direct response for **EW** and **BW0** did not give sufficient scope for improvement of **BW** traits through direct selection, while its sufficient effect to improvement the growth traits through direct selection for **BW4**.

Table 6. Expected direct response based on additive genetic variance per generation from single-trait selection for productive traits of New Hampshire chickens.

Trait ⁺	Sire	Dam	Progeny
First generation			
EW	0.101	0.045	0.090
BW0	0.027	0.012	0.024
BW4	20.476	17.473	17.68
BW8	24.37	16.25	18.05
DG4	1.486	1.306	1.306
DG8	1.809	1.387	1.417
FS8	0.269	0.224	0.232
Second generation			
EW	0.061	0.024	0.047
BW0	0.020	0.008	0.015
BW4	20.99	16.975	17.787
BW8	26.63	17.751	20.42
DG4	1.542	1.276	1.321
DG8	1.934	1.490	1.580
FS8	0.030	0.016	0.020

⁺Traits as defined in Table 1.

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تقدير المعايير الوراثية لبعض الصفات الانتاجية في دجاج النيو هامبشير باستخدام نموذج الحيوان

محمود مغربي عراقي

محمد حنفي سيد محمود

قسم الانتاج الحيواني - كلية الزراعة بمشهر - جامعة الزقازيق / فرع بنها - مصر

الملخص العربي

أخذت بيانات ٤٥٦٦ ككتوت من دجاج النيو هامبشير (٢٠٨٠ ككتوت في الجيل الأول ، ٢٤٨٦ ككتوت في الجيل الثاني) ، كانت قد نتجت من ٤٤ أب & ٣٥٦ أم). وقد تم تحليل بيانات كل جيل على حدة باستخدام نموذج الحيوان للصفة الواحدة بهدف تقدير المعايير الوراثية لصفات وزن البيضة ووزن الككتوت عند عمر الفقس ، ٤ ، ٨ أسابيع & صفات الزيادة اليومية في الفترة من عمر الفقس-٤ ، ٤-٨ أسابيع & وصفة درجة التريش عند عمر ٨ أسابيع). وقد أظهرت النتائج مايلي:-

- ١- كانت نسب التباين الوراثي التجمعي لمعظم الصفات المدروسة مرتفعة في الجيل الأول (بمتوسط ١٦%) عن الجيل الثاني (بمتوسط ١٤%).
- ٢- كانت نسب التباين البيئي العام في الجيلين مرتفعة جدا لصفة وزن البيضة (بمتوسط ٧٢%) ووزن الككتوت عند عمر الفقس (بمتوسط ٦٨%) ، ثم انخفضت تدريجيا مع تقدم عمر الككتوت (بمتوسط ١١% عند عمر ٨ أسابيع).
- ٣- كانت قيم المكافئ الوراثي لوزن البيضة ووزن الفقس منخفضة ، ثم ازدادت بعد ذلك الى أن وصلت ٠.٢٩ عند عمر ٤ أسابيع.
- ٤- كانت الارتباطات الوراثية بين وزن الجسم عند عمر ٤ و/أو ٨ أسابيع والزيادة اليومية موجبة وعالية المعنوية (٠.٠٠١) في الجيلين .
- ٥- كانت القيم التربوية المتوقعة للطيور التي لها سجلات (النسل) أعلى من تلك المسجلة للطيور التي ليس لها سجلات (الذكور والأمهات) ، بينما كانت معاملات الدقة للقيم التربوية المتوقعة للذكور أعلى بالمقارنة بالتقديرات المتحصل عليها من الأمهات والنسل.
- ٦- كان التحسين الوراثي المتوقع من الانتخاب المباشر للصفة مرتفع في الجيل الثاني عن الجيل الأول لمعظم الصفات المدروسة.