

GENETIC PARAMETERS OF BODY AND EGG WEIGHT IN JAPANESE QUAILS (*Coturnix coturnix japonica*) USING PARTIAL DIALLEL ANALYSES

BY

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Abstract: Fifty mating groups of Japanese quails (*Coturnix coturnix japonica*) were used in a partial-diallel method to estimate the genetic parameters of body and egg weight characters. Nine crosses, with two hatches each, were conducted for each group. Studied characters were measured on four chicks (offspring) for each hatch. The 450 crosses as well as the 50 groups were found to be highly significant for the five characters, whereas the two hatches were found to be highly significant for egg, hatching and 6-wk weights, significant for 2-wk weight and not significant for 4-wk weight. The highest significant mean of egg weight, hatching weight, 2-wk body weight, 4-wk body weight and 6-wk body weight were found to be 13.37 gm, 8.96 gm, 71.89gm, 116.78gm and 170.45gm, respectively. The highest significant correlation coefficient estimates were between 2-wk body weight and 4-wk body weight characters (0.83), 4-wk and 6-wk body weights (0.77) and between 2-wk and 6-wk body weights (0.69). The genetic correlation coefficients ranged from 0.005 (between egg weight and 2-wk weight) to 0.19 (between hatching and 4-wk body weights). The mean of the growth rate was found to be $89.32\% \pm 0.01$ and it ranged from 86.38% to 91.0%. The higher significant gca value for egg weight and body weight for each of hatching, 2-wk, 4-wk and 6-wk were 0.73, 0.45, 7.67, 10.28 and 13.33, respectively. The additive variance was found to be negative and diminutive in its magnitude for both egg weight and hatch weight characters. Conversely, the dominance variance estimates were relatively higher and they ranged from 0.14 (hatching weight) to 258.33 (6-wk body weight). Heritability estimates were ranged from 0.29 (egg weight) to 0.65 for 4-wk body weight.

INTRODUCTION

Information pertaining to the different types of gene action, relative magnitude of genetic variance and combining ability estimates are important and vital parameters to mold the genetic makeup of any organism. This

important information could prove an essential strategy to the animal breeders in the screening of better parental combinations for further enhancement (Narayan *et al.*, 1999 and Keeton *et al.*, 2003).

The evaluation of genotypes in crosses is a common practice in animal breeding. The age of genomics forces us to revise basic questions of quantitative genetics in this new era and to examine classic concepts like heritability in a new way. With the development of genomic techniques, it is possible to investigate genetic variation at the gene expression level in terms of classical additive and dominance effects. By viewing the genome wide gene expression as heritable phenotypes, traditional quantitative genetics methods can be used to partition the phenotypic variation. The exploitation of genetically diverse stocks for improving economic traits, such as body weight is one of the approaches in the breeding programs of animals. The combining ability analyses help to identify desirable combiners (Mohammed *et al.*, 2005 and Reis *et al.*, 2005).

Diallel design has been a valuable quantitative genetics tool for plant and animal breeders to select breeding materials that show the greatest promise, and it has also been used by quantitative geneticists to understand the gene action behind quantitative traits. Diallel designs are widely used to estimate genetic variance such as *gca* (general combining ability, or additive genetic effect) of parents and *sca* (specific combining ability, or dominance genetic effect) of crosses (Falconer, 1989 and Kearsley and Pooni, 1996)

The full diallel has disadvantage of labor and resource intensive. As the number of parents increases, the number of crosses sampled increases rapidly, and it becomes impractical to carry out a full diallel for large numbers of parents. In these situations, a partial diallel is carried out which includes only a subset of all possible crosses, and the analysis of the partial diallel can be carried out using an appropriate design matrix. Any crossing design where the same parents are used more than once can be envisioned as a partial diallel cross (PDC). The PDC only includes a fraction of all possible crosses among the available parents. (Fyfe and Gilbert, 1963; Hinkelmann and Kempthorne, 1963; Arya, 1983; Das *et al.*, 1998; Filho and Vencovsky, 1999; Viana *et al.*, 1999, 2000 and 2001; Iraqi *et al.*, 2005 and Reis *et al.*, 2005).

Griffing (1956) proposed three different PDCs. PDC crossing methods vary depending on whether or not the parents or the reciprocal F_1 's are included. Method IV, a PDC, includes only one set of F_1 's, but the parents and the reciprocal F_1 's are not included. The PDC, as proposed by

Kempthorne and Curnow (1961), assumes a random sample of lines (genotypes) from one population (Singh and Hinkelmann, 1998).

In general, early research has indicated that non-additive genetic variation is not a major contributor to total genetic variation for growth traits. Using diallel crosses, McCartney and Chamberlin (1961) concluded that additive genetic variance was much more important than non-additive genetic variance for body weight (BW) and body conformation measurements (Nestor *et al.*, 2001 and 2004). Analyzing egg and body weight traits together may provide a new procedure to express genetic effects in poultry. Possible relationships between weekly body weight and reproduction might be used to improve both meat and egg production (Saatci *et al.*, 2006 and Fayeye *et al.*, 2006).

The main aim of the diallel analysis is the study of the genetic control of quantitative traits, which is essential for planning and carrying out breeding programs.

MATERIALS AND METHODS

This experiment was carried out at Poultry Research Unit Farm, Poultry Production Dept., Faculty of Agriculture, Kafr El-Sheikh University. The flock of Japanese quails was acquired from closed line which selected short-term for high 4-wks body weight.

Experiment was designed to include 50 mating groups. Each mating group contained three males and three females pedigree using partial diallel method. Each group contained 3 (sires) X 3 (dams) X 4 (progeny) X 2 (hatches) = 72 half-sib progenies. Data were recorded from first generation birds hatched from eggs randomly collected from a breeder stock and were obtained on a total number of 3600 Japanese quail birds. The measurements were conducted on four chicks of the F₁ of each mating for two hatches. The period between each two hatches was 10 days.

All the 60 mating groups of the two hatches were placed in similarly equipped production units with the same management and nutrition regimens (NRC, 1994) regimens at the time of study. Hatched chicks were wing-banded, weighed and raised in floor brooders at a starting temperature of 38°C for the first week of age, then lowered gradually 2.5°C weekly thereafter. At four wks of age all chicks were sexed according to plumage color and pattern and moved to single cages. All chicks were weighted at hatch, 2, 4 and 6 weeks of age and growth rates were calculated.

Birds were fed during 0-2 weeks of age on a starter mash diet containing approximately 26% crude protein and 2980 kcal ME/Kg diet.

Then they were transferred to a grower ration containing 22% crude protein and 3050 kcal metabolic energy (ME)/Kg during the period from 2 to 4 weeks of age. During the last period (4-6 weeks of age), birds were fed on a diet containing approximately 19% crude protein and 2800 kcal ME/Kg diet. Feed and water were offered *ad libitum*

Statistical analysis:

The complete randomized block design was used to test for significant differences between all the mating groups according to Steel and Tori (1980). All the parents were randomly selected. The first analysis was based on individual records, whereas the second analysis of *gca* and *sca* effects was based on replication means. Missing data were attained by using the equation 9.8 of Steel and Tori (1980). The partial-diallel method was applied according to Singh and Chaudhary (1985) as follows:

- 1- The replication (two hatches) mean for every cross was used for testing the significance of genotypic differences.
- 2- A matrix for all the parental genotypes was designed by assigning the number of crosses of each parent to the diagonal elements, the value of 1 was assigned to each cross and all the other elements were equal to zero.
- 3- The inverse of this matrix was calculated (A^{-1}).
- 4- Computation of corrected means of sampled crosses (Q_i), where Q_i = sum of the corrected means for crosses that each parent involved in, the corrected mean of each cross = uncorrected mean – the correction factor (CF), and $CF = 2 \times \text{Grand Mean} / \text{no. of parents } (n) \times \text{no. of crosses } (s)$
- 5- Estimation of *gca* effects by multiplying the inverse matrix times the corrected means : $G = A^{-1} \times Q$.
- 6- Analysis for combining ability, S.S. due to *gca* = $r \sum G_i Q_i$. Table (1) presents the analysis of variance ANOVA used for testing general combining ability (*gca*) and specific combining ability (*sca*) effects.
- 7- Estimation of variance components :

$$a- \sigma_g^2 = (M_g - M_s) / [rs(n-2)/(n-1)]$$

$$b- \sigma_s^2 = (M_s - M_e) / r$$

$$c- \sigma_A^2 = 2 \sigma_g^2$$

$$d- \sigma_D^2 = \sigma_s^2$$

8- Standard errors :

$$a- \text{Average variance } (g_i - g_j) = 2 \left[\frac{na}{n-1} - \frac{1}{2s(n-1)} \right] \left[\sigma_s^2 + \frac{\sigma_e^2}{r} \right]$$

where a is diagonal element of the inverse matrix.

$$b- \text{S.E. } (g_i - g_j) = \sqrt{\text{average variance}}$$

RESULTS AND DISCUSSION

Ten mating groups were excluded due to different afflicting incidents causing chick mortality before or after hatching. Fifty mating groups were used in the employed partial-diallel method to estimate the genetic parameters of body and egg weight characters. To proceed with the partial-diallel analysis, the whole experimental units should be tested against the presence of significant differences between the crosses. Table (2) presents the ANOVA results for the used five characters.

The 450 crosses as well as the 50 groups were highly significant for the five characters, whereas the two hatches were found to be highly significant in egg weight, hatching and 6-wk body weights, significant in 2-wk and in 4-wk body weights. These results gave the confidence to proceed with the partial-diallel method.

The highest and lowest mean values of the five characters under study as well as growth rates are presented in Table (3).

For the egg weight character, 1.11% of the crosses possessed the highest significant mean of 13.37gm. The lowest mean of 10.86gm was found in three crosses.

According to hatching body weight, only one cross had the highest significant mean value of 8.96 gm. The lowest mean value was estimated to be 7.43 gm which was found in one cross. However, the highest significant mean for 2-wk body weight was found to be 71.89 gm and it was detected in one cross. The lowest mean value of 44.24 gm was found in one cross as well.

At 4-wk of age, only one cross was found to possess the highest significant mean value of body weight (116.78 gm) and the lowest mean value of 80.99 gm was detected in also one cross as well.

For the character of 6-wk body weight, the highest significant mean was found to be 170.45 gm and was detected in one cross. The lowest mean was 119.37 gm and was found also in one cross.

The grand means over all the crosses for egg weight, 2-wk, 4-wk and 6-wk body weights were 12.42 ± 0.0170 , 8.32 ± 0.0092 , 56.73 ± 0.2183 , 101.64 ± 0.2654 and 148.09 ± 0.4141 gm, respectively. These figures are in harmony with those reported by Ipek *et al.* (2004), Krobanek *et al.* (2004), Ozbey and Ozcelik (2004), Avci *et al.* (2005) and Mielenz *et al.* (2006) on Japanese Quail chicks.

Growth rates were estimated as the percentage of the difference between the weight at 6 wks and 2 wks divided by the sum of these two weights which was multiplied by 0.5. The mean of the growth rate was found to be $44.66\% \pm 0.0159$ and it was found to be ranged from 43.19% to 45.5%.

Values of phenotypic and genetic correlation coefficients between the five traits are presented in Table (4). The highest significant phenotypic correlation coefficient estimates were found to be between 2-wk and 4-wk body weight characters (0.83), 4-wk and 6-wk body weights (0.77) and between 2-wk and 6-wk body weights (0.69).

The genetic correlation coefficients were found to be low to medium and ranged from 0.005 (between egg weight and 2-wk body weight) to 0.19 (between hatching weight and 4-wk weight). Mielenze *et al.* (2006) gave similar estimates between egg weight and all the characters of body weight in both females and males.

The low estimated genetic correlation coefficients between egg weight and all body weight characters, which are equal to 0.0, were reported before by Saatci *et al.* (2006) and Mielenz *et al.* (2006). Adeogun and Adeoye (2004), Resende *et al.* (2005) and Mielenze *et al.* (2006) also gave high estimates of correlation coefficients between 4-wk weight and each of 2-wk weight and 6-wk weight. Most of the traits were positively correlated, which indicates that they can be simultaneously improved by selection. These results might be due to the fact that body weight is mainly affected by additive genetic effects which consequently may make its heritability and genetic correlations of growth traits somewhat superior.

Table (5) represents the significant highest and lowest values of *gca* for each sire and Table (6) presents the analysis of variance based on replication means, and the data were consisted of 450 crosses with two

hatches each, and the total number was 900 chicks. Table (6) contains the analysis of *gca* and *sca* effects.

The highest significant *gca* value for the egg weight character was found to be 0.7268 and it was assigned for sire no. 2163 of the fifth group. This cross of sire with dam no. 15 scored the highest significant mean value for this trait (13.37gm). The lowest value of *gca* effect for this trait was -0.5670 and it was recorded for sire no. 924 in the ninth group. The cross of this sire with dam no. 27 scored lower mean value of egg weight of 11.2 gm which did not differ significantly from the lowest mean value of 10.86 gm. However, this dam scored well with sire no. 915 and gave a mean value of 12.91 gm.

Sire no. 947 exhibited the highest significant estimate of *gca* effect of 0.4577 (16th group) for hatching body weight character. The cross 947 x 50 gave a highly significant mean value of 8.92 gm for this trait. The lowest estimate of *gca* effects was found to be -0.3731 and it was belonged to sire 963 in the 20th group.

As for the 2-wk body weight character, the higher significant value of *gca* effect was 7.6770, and it was assigned to sire 2173 in the 33rd group. The mean values of the cross of this sire and each of dams 111 and 110 were 66.33 and 64.03 gm, respectively, and they were not significantly different from the highest mean value of 71.89 gm. The lowest estimated value of *gca* effect was -8.2757 and was exhibited by sire 602 in the 7th group.

The highest estimated value of *gca* effects for 4-wk weight character was 10.2853 and it was assigned to sire 2116 in the 45th group. The cross of this sire and dam161 exhibited the highest significant mean value of 116.78 gm for this trait. The lowest estimated value of *gca* effect (-11.0974) was belonged also to sire 602.

For 6-wk body weight character, 13.3369 was the highest estimated value of *gca* effect and it was exhibited also by sire 2116. Sire 2108 recorded the lowest estimated value of *gca* effect.-13.8790

The mean squares of *gca* and *sca* effects, which are presented in Table (6), were found to be highly significant for the five characters under study. The additive variance was found to be negative and very small for both egg weight and hatching weight characters. Conversely, the dominance variance estimates were higher than those of additive estimates and ranged from 0.14 (hatching weight) to 258.33 (6-wk weight).

Heritability estimates ranged from 0.29 (egg weight) to 0.65 for 4-wk body weight. The estimated values of heritability of the body weight of the Japanese quail at different ages were reported, for example, by Resende *et al.* (2005) who gave lower estimates of heritability (0.1) for hatching, 2-wk and 4-wk body weights. However, they gave higher estimates of heritability (0.87) for body weight at 2 and 4 wks. Saatci *et al.* (2006) examined the heritability of body weights during the hatching period and from wk 1 to wk 6, and reported values between 0.18 and 0.25. Mielenz *et al.* (2006) gave an estimate of 0.64 for 6-wk weight heritability, which is very close to our estimate. These studies normally used body weights at different ages and often used different methods to estimate the heritability. The differences in heritability estimates might be attributed to our method of estimation, strains, environmental effects or a sampling error due to small data sets or sample sizes.

Various forms of diallel crosses play an important role in evaluating the breeding potential of genetic material both in animal and plant breeding. The combining ability analyses help to identify desirable combiners that may be utilized to exploit heterosis. The advent of modern statistical computing opens new avenues for analyses. Partial diallel designs are easily handled when the appropriate design matrices are calculated. In fact, virtually any crossing scheme which reuses parents can be viewed as a partial diallel and genetic effects tested in a straightforward manner.

Since only a sample of all possible crosses is selected in a partial diallel, the information available from the partial diallel analysis is expected to be less precise than that from the full diallel. However, Kempthorne and Curnow (1961) pointed out that the partitioning of the degree of freedom between *gca* and *sca* are to the advantage of the *gca*, and results in more precision for *gca* in a partial diallel cross. Bray (1971) found that the expected values of the variance components for *gca*, *sca* are not dependent on the size of the partial diallel except in precision of estimates. The larger partial diallels show less variation. Little confidence can be placed on estimates of heritability from small partial diallels. Bray concluded that the bias in the estimates obtained by partial diallel analysis depended on the character studied and the number of crosses sampled.

Results indicated that the proposed procedure may furnish reliable estimates of means of hybrids for large number of sires and dams. Applying such detailed analyses studies concerning both egg and body weight traits may provide procedures to evaluate specifically Japanese quail and poultry in general.

Table 1. ANOVA for combining ability analysis in partial diallel.

Source	d.f.	E.M.S.
Hatches	$r-1$	$\sigma_e^2 + r \sigma_s^2 + [rs(n-2)/(n-1)]$
Crosses	$(ns/2) - 1$	
<i>gca</i>	$n - 1$	
<i>sca</i>	$(ns/2) - n$	
Error	$(r-1)[(ns/2) - 1]$	
Total	$(rns/2) - 1$	σ_e^2

Where r=no. of hatches, n=no. of sires, and s=no. of crosses for each sire

Table 2. Mean squares for different factors affecting the five studied characters in Japanese quails.

Source	d.f.	Egg weight	Hatch weight	2-wk weight	4-wk weight	6-wk weight
Hatches	1	1.9136**	0.7783**	203.019*	320.7971*	1963.3932**
Groups	49	1.1217**	0.4843**	184.4837**	283.6686**	613.04128**
Crosses	224	2.3477**	0.6766**	356.3647**	550.5936**	1209.8331**
Error	3325	0.1089	0.0691	50.6506	76.43203	221.4001

* and ** means significant at *P* level of 0.05 and 0.01, respectively.

Table 3. Estimates of highest and lowest mean values with L.S.D. values for the five evaluated traits as well as growth rate of the 450 partial circulant crosses in Japanese quails.

Partial Circulant Cross	Egg weight	Hatch weight	2-wk body weight	4-wk body weight	6-wk body weight	Growth rate
Significant highest mean values						
Cross no.	2163 X15	2130 X13	984 X95	2116 X161	955 X63	936 X45
Trait value	13.37	8.96	71.89	116.78	170.45	91.0
Lowest mean values						
Cross no.	733 X107	2164 X145	934 X42	935 X43	2108 X114	982 X176
Trait value	10.86	7.43	44.24	80.99	119.37	86.38
L.S.D (0.05)	0.6467	0.5152	13.94	17.49	29.16	
L.S.D (0.01)	0.8500	0.6772	18.33	22.99	38.33	

Table 4. Estimates of genetic correlation coefficients (above the diagonal) and phenotypic correlation coefficients (below the diagonal) between the five characters under study.

	Egg weight	Hatch weight	2-wk body weight	4-wk body weight	6-wk body weight
Egg weight		0.01	0.005	0.001	0.09
Hatch weight	0.05**		0.03	0.19*	0.14*
2-wk weight	0.00	0.02		0.16*	0.15*
4-wk weight	0.00	0.03*	0.83**		0.16*
6-wk weight	0.01	0.01	0.69**	0.77**	

Table (5). Significant highest and lowest estimates of *gca* effects for 150 sires of Japanese quails for the five characters under study.

Groups	Sires	Egg weight	Hatching weight	2-Wk weight	4-Wk weight	6-Wk weight
5	2163	0.7268	0.4202	0.3026	1.7102	3.9437
	790	-0.4920	-0.1194	5.9693	7.5644	10.9121
	2130	0.2268	0.1765	-4.8224	-5.3314	-5.9185
7	602	0.1830	-0.0552	-8.2757	-11.0974	-7.8209
	914	-0.4420	0.0031	5.7306	7.7762	9.0456
	916	0.5580	-0.0531	3.1722	4.5616	3.6253
9	915	0.3080	0.0315	3.9701	2.0519	-1.7319
	917	0.0580	0.1523	-2.5465	-2.5939	-1.4715
	924	-0.5670	-0.0123	-1.8174	-1.4898	-2.3881
16	947	0.2580	0.4577	-3.23191	-9.0521	-8.4219
	464	-0.1795	-0.0475	2.022377	3.3737	-1.7643
	938	-0.0545	-0.2975	4.880597	6.4118	8.7850
20	956	-0.5170	-0.0148	-1.9740	-2.8854	-11.3182
	961	0.2330	0.2644	5.5329	1.7724	1.0285
	963	-0.0170	-0.3731	-3.2952	-1.3548	6.5656
33	2173	-0.1170	0.1165	7.6770	2.3446	1.4844
	582	-0.1170	-0.1189	-1.1816	-0.8000	-11.8286
	2107	-0.1170	0.0165	-3.3589	-0.8209	4.6987
34	409	0.0080	0.0215	-1.1177	0.2299	1.2968
	2106	0.2580	-0.0764	-2.1678	-2.8462	1.1485
	2108	-0.1170	-0.1285	-3.5854	-2.9518	-13.8790
45	537	0.7080	-0.0939	-4.6264	-3.7237	-8.0144
	2116	-0.5420	0.1748	6.0876	10.2853	13.3369
	833	-0.1670	0.0081	1.9472	0.5897	1.8770
SE(<i>g-g</i>)		0.6758	0.3617	0.7836	0.7009	0.3372

Table (6). Mean square estimates for five characters under study.

Sources	d.f.	Egg weight	Hatch weight	2-wk weight	4-wk weight	6-wk weight
Rep	1	0.4900*	0.2344*	53.8171	46.7086	130.0347
Sets	49	0.2920**	0.1178**	47.7**	72.5306**	167.9184**
Crosses	224	0.5882**	0.1766**	89.2689**	139.1903**	312.8707**
GCA	149	0.3117**	0.1015**	48.0866**	67.9461**	159.1122**
SCA	75	1.1373**	0.3259**	171.0845**	280.7288**	618.3376**
Error	674	0.1519	0.0419**	27.4894**	38.2526	101.6721**
σ_g^2		-0.1385	-0.0376	-20.6381	-2.4487	-1.0274
$\sigma_s^2 = \sigma_D^2$		0.4927	0.1419	71.7975	121.2381	258.3328
σ_A^2		-0.2771	-0.0753	-41.2763	-4.8974	-2.0548
h^2		0.29	0.30	0.26	0.65	0.62

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الملخص العربي

المقاييس الوراثية لصفتي وزن الحسم ووزن البيض في السمان الياباني باستخدام تحليل التزاوج الثنائي الجزئي

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استخدمت خمسون مجموعة من السمان الياباني في تحليل التزاوج الثنائي الجزئي لحساب المقاييس الوراثية لصفة وزن الجسم ووزن البيض، أجريت تسعة هجن بكل مجموعة ومكررتين (تفريختين) بكل هجين، وأخذت المقاييس علي أربعة أفرخ لكل مكررة. وجد أن الفروق بين الـ ٤٥٠ هجين عالية المعنوية وكذلك بين الخمسين مجموعة. ووجدت الفروق بين المكررتين عالية المعنوية في صفات وزن البيض والوزن عند كل من الفقس وعند ستة أسابيع، ومعنوية فقط عند صفات الوزن عند أسبوعين وعند أربعة أسابيع، وكانت أعلى لقيم المتوسطات عالية المعنوية لصفات وزن البيض، الوزن عند الفقس، عند أسبوعين، عند أربعة أسابيع وعند ستة أسابيع ١٣,٣٧ جم، ٨,٩٦ جم، ٧١,٨٩ جم، ١١٦,٧٨ جم، ١٧٠,٤٥ جم، علي التوالي. ووجد أن اعلي قيم معنوية لمقاييس التلازم المظهري كانت بين كلا من صفتي الوزن عند أسبوعين وعند أربعة أسابيع (٠,٨٣) وبين الوزن عند أربعة أسابيع وعند ستة أسابيع (٠,٧٧) وبين الوزن عند أسبوعين وعند ستة أسابيع (٠,٦٩). تراوحت قيم التلازم الوراثي بين ٠,٠٠٥ (بين صفتي وزن البيض والوزن عند أسبوعين) و ٠,١٩ (بين الوزن عند الفقس وعند أربعة أسابيع). وجد أن متوسط معدل النمو كان ٨٩,٣٢% ± ٠,٠١٥٩ وتراوحت بين ٨٦,٣٨% إلي ٩١%. وقد وجد أن اعلي قيم عالية المعنوية لتأثيرات القدرة العامة علي الخلط لصفات وزن البيض، الوزن عند كل من الفقس،

عند أسبوعين، عند أربعة أسابيع وعند ستة أسابيع هي ٧,٦٧، ٠,٤٥، ٠,٧٢، ١٠,٢٨ و ١٣,٣٣ علي التوالي . وقد وجد أن التباين المضيف كان سالبا وقيمته منخفضة جدا لصفتي وزن البيض والوزن عند الفقس وعلي العكس كانت قيم تباين السيادة اعلي من تلك الخاصة بالتباين المضيف وتراوحت من ٠,١٤ (الوزن عند الفقس) و ٢٥٨,٣٣ (الوزن عند ستة أسابيع) . وقد تراوحت قيم المكافئ الوراثي من ٠,٢٩ (وزن البيض) إلي ٠,٦٥ (الوزن عند ستة أسابيع).