THE EFFECT OF SOME BLOOD LOCI
ON THE PRODUCTIVE TRAITS IN JAPANESE QUAIL

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Abstract

The present study was conducted to detect and determine albu-
min, transferrin and Hi loci and their relation with egg production traits
and body weight of Japanese quail . A total of 305 Japanese quails pro-
duced during twelve hatches from twenty-one sire families were used in
the present study. Individual body weights were recorded at different
ages. Egg production traits were egg number, egg weight and egg com-
ponent weights. The analysis detecting for the three loci was practiced
on the whole blood for Hi gene and in plasma for albumin and transferrin
loci.

Results showed that albumin locus had only two genotypes , the
dominant homozygote (AlAl) has higher egg number (88 eggs), while,
(AlaI) genotype showed seven days earlier in sexual maturity. Transferrin
locus showed that (TfTf) genotype recorded the higher egg number (89
eggs) and earlier sexual maturity with five days. Moreover, Hi locus had
no clear effect on all the characters studied.

INTRODUCTION

Many workers (Ahmed 1982, El-Kaiaty , 1986 and Al-Tikriti, 1988) looked after
the identification of certain genes by simple methods , aiming to find any major rela-
tionship with the main productive traits.

Different genetic parameters for different productive and reproductive traits in
Japanese quail were estimated by several investigators (Roushdy , 1993 and Bahie El-
Deen and El-Sayed , 1999).

In 1968, Peterovsky et al. found polymorphism for an agglutinogen presented on
the red blood cells of hens detected by lectins , that is "Hi" locus which is transmitted
as a single gene with two alleles .

Al-Tikriti (1988) reported that three genotypes (HiHi , Hihi and hihi) were determined for the Hi locus in both Fayoumi and Baladi breeds and their crosses with White Leghorn. The HiHi genotype showed complete agglutination, and hihi genotype showed non-agglutination, while, Hihi showed semi-agglutination; these were controlled by two co-dominant alleles Hi and hi which were responsible for the Hi locus in both pure breeds and their crosses with White Leghorn.

Haley (1965) found in his study on serum albumin polymorphism in quail that three albumin phenotypes Q_1Q_1, Q_1Q_2 and Q_2Q_2 were observed in both sexes.

Mazumder and Mazumder (1990) found that, serum albumin protein in both chicken and quails were polymorphic . They reported that, in chicken only, two types (AA and AB) and in quails two different types (BB and BC) were observed . In quails CC type was not observed .

Pal *et al.* (1994) stated that, no individual variations were identified for serum albumin which showed a single banded phenotype in starch gel electrophoresis in Japanese quail . On the other hand , Lucotte and Kaminski (1975) found individual variations of serum albumin in Japanese quail .

Pal *et al.* (1994) showed that, no individual variations were identified for serum transferrin in starch gel electrophoresis which resolved as two bands phenotypes in Japanese quail . Also, Koska *et al* . (1989) pointed out in their studies, on genetic analysis of protein polymorphism in three strains of Japanese quail, that there were no differences found for transferrin gene frequencies. On the other hand , Lucotte and kaminski (1975) found individual variations of serum transferrin in Japanese quail .

In this study we detected three loci, namely Hi (agglutinogen), Albumin   (Al) and Transferrin (Tf) genes, in the blood of the Japanese quail to determine their effect on some productive traits. The aim of this study was to determine the effect of the combination of the additive effect of each two loci on the character under study. The estimation of the heritability and the other genetic parameters were calculated to compare between the lines of selection.

MATERIALS AND METHODS

The present study was carried out at the Poultry Experimental Center, Animal Production Department, Faculty of Agriculture, Cairo University .

A total of 21 sires and 42 dams of Japanese quail (*Coturnix coturnix japonica*) were used as parents assigning one sire to two dams in single cages, their progeny were transferred into compact system: individual cages from forty-two days till hundred and fifty days of age. The studied characters were individually recorded for each hen .

1. Productive traits

1.1. Body weight

Individual body weights were recorded at day-old , fourteen, twenty-eight , forty-two, ninety, hundred and twenty and hundred and fifty days of age.

1.2. Egg production data

The data used to study egg production traits were collected from 305 females produced from the pedigreed eggs. After six weeks of age , egg production and sexual maturity were recorded from the individual caged females. Total number of eggs produced during the first hundred days of egg production were recorded individually. On hundred and fifty days of age, one egg per hen was taken to study egg characteristics.

2. Genetic loci associated with egg production

2.1. Detection of (Hi) gene

On hundred and fifty days of age, blood samples of 1 cc volume were collected from the heart of each hen to detect (Hi) gene using specific extract called lectins as described by Scheinberg and Reckel (1961a).

2.2. Detection of Albumin and Transferrin loci

Blood samples were obtained from each hen on hundred and fifty days, collected in heparinized tubes and centrifuged for 10 minutes at 3000 rpm. The clear to yellow plasma was separated . Electrophoretic analysis using SDS-polyacrylamide gel electro-

phoresis according to Laemmli (1970) was practiced for detection. The genotypes of albumin locus were described by Haley (1965) and the albumin migration was faster than the transferrin.

3. Statistical analysis

1. The models used for each observation from each trait studied were as follows:

Model 1: Mixed, for calculating the effect of sire with hatch correction for egg number, sexual maturity, egg weight, egg component weights and body weight and calculating the genetic parameters (h^2, r_g, r_p) :

$$X_{ijk} = \mu + S_i + H_j + e_{ij}$$

Where:

X_{ij} = observation on the ith sire .

μ = overall mean of X_{ij}

S_i = effect of ith sire

H_j = effect of jth hatch

e_{ij} = random error .

Model 2: Fixed, for calculating the effect of each locus :

$$X_{ij} = \mu + L_i + e_{ij}$$

Where:

L_i = effect of ith locus

Model 3: Fixed, for calculating the effect of combination between each tow loci or the combination between the three loci :

$$X_{ij} = \mu + c_i + e_{ij}$$

c_i = the effect of ith combination

Model 4: Random, for calculating the variance due to each locus :

$$X_{ij} = \mu + L_i + e_{ij}$$

L_i = effect of ith locus .

2. Data had been analyzed using Harvey (1990) program.

3. Individual selection was calculated as follows :

$$\Delta g\,(R) = h^2\,(x - \overline{x})$$

where :

$\Delta g\,(R)$ = Genetic improvement (response to selection)

h^2 = heritability of the traits

$(x - \overline{x})$ = selection differential (s)

4. Family selection was calculated as follows :

$$\Delta g\,(R) = h^2{}_F\,(x - \overline{x})$$

$$= h^2\,\frac{1 + (n-1)r_g}{1 + (n-1)r_p}\,(x - \overline{x})$$

$h^2{}_F$ = the heritability of family means

h^2 = heritability of individual values

n = number of individuals in the families

r_g = genetic correlation (with half-sib families = $1/4$)

r_p = correlation of phenotypic values of members of the families

RESULTS AND DISCUSSION

The identification of a locus by electrophoresis technique became one of the goals for the genetic improvement of different characters in animal breeding. Several workers identified many loci and determined their gene effect on many characters .

In this study, three loci had been determined, and the individuals used in this study had been studied according to their available genotypes.

Albumin locus

There were two alleles for albumin locus and accordingly, three genotypes found. Here in this study, two genotypes only were detected in the blood of the individuals un-

der study (Table 1) . The homozygote geneotype for the dominant gene (AlAl) was represented by 126 individuals and 129 for the heterozygote one (Alal). This result is in a good agreement with Gilewski and Kuryl (1986) and Mazumder and Mazumder (1990) who found that serum albumin in quail were polymorphic and had two different genotypes. Haley (1965) and Lucotte and Kaminski (1975) in their study on serum albumin polymorphism in Japanese quail, found that three albumin genotypes were observed. On the other hand , Pal *et al.* (1994) reported that no individual variations were identified for serum albumin in Japanese quail.

The least squares means obtained for the dominant homozygote (AlAl) showed a higher number of eggs (88) and early sexual maturity with seven days than the heterozygote (Alal). Similarly , Ahmed (1982) found significant relationships between albumin locus and each of egg number and sexual maturity in Fayoumi chicken . Also, Al-Tikriti (1988) reported that highly significant effect was obtained for albumin locus on average egg number and sexual maturity in both Fayoumi, Baladi and their crosses with White Leghorn.

Egg weight showed a small difference between the two genotypes of about 0.17 grams in favour of Alal genotype, which proved to be significant at the 5% level. The other components of the egg were not affected by the Al locus.

The analysis of variance for the difference between the two genotypes for body weight proved to be highly significant for the ages fourteen, twenty eight and forty-two days. This could explain the difference between the two genotypes which were about 3, 8 and 12 grams, for the same ages of body weight, respectively (Table 2) . Gilewski and Kuryl (1986) studied the effect of the two plasma albumin genotypes $(Q_1Q_1$ and $Q_1Q_2)$ on body weight at one , three and five weeks of age over two years in a heavy line of Japanese quail . They found that Q_1Q_2 genotype was heavier than the homozygote one with about 22% , 18% and 12.25% , 10.90% for body weight at three and five weeks over two years , respectively.

2. Transferrin locus

Three genotypes had been detected for transferrin locus (Table 3) . The individuals with (TfTf) were 99 and the heterozygotes one (Tftf) were 122 and the homo-

zygote recessive were 84 individuals. The difference between the genotypes for both egg number (100 days) and sexual maturity was highly significant . The differences between the other traits proved to be insignificant .

The genotype (TfTf) showed the highest egg number (89 eggs). Meanwhile, the other two genotypes showed lower egg numbers 78 for (Tftf) and 69 for (tftf)). The difference between the mean egg number (TfTf) and the overall mean was about eleven eggs. The difference between the homozygote dominant genotype and the other two genotypes were −12 eggs for (Tftf) and −21 eggs for the recessive one.

This suggests that the transferrin has a major effect on egg number. The above results indicated that, practicing, the selection for (TfTf) genotype could lead to a genetic gain of 11 eggs from the overall mean and 12 eggs from (Tftf) and 21 eggs from (tftf) . The differences, as a percentage, between (TfTf) and the other three means, (overall mean, (Tftf) mean and (tftf) means) were 14%, 15% and 27%. Those percentages were very high.

Similarly, Lucotte and Kaminski (1975) found individual variations of serum transferrin in Japanese quail, while, Kosaka *et al.* (1989) and Pal *et al.* (1994) reported that no individual variations were identified for serum transferrin in Japanese quail.

In chicken , Al-Tikriti (1988) found that all blood samples proved to be homozygous for transferrin locus (BB type) in Fayoumi, and Baladi breeds and their crosses with White Leghorn .

The body weights at three different ages (fourteen , twenty-eight and forty-two days) showed significant differences between genotypes (Table 4).   Mean body weights of the individuals (TfTf) were higher at these three ages. The differences were in favour of (TfTf) body weight on forty-two days of age, and also the differences were −8, -9 and −16 grams for the overall mean and the other genotypes in their respective order. These differences represent about 4%, 5% and 8% less than the genotype means. The selection for body weight in Japanese quail is very important to the breeder.   Here, selection for (TfTf) genotype will lead to increase the genetic gain for egg number , body weight and egg weight which is in favour of the breeder .

3. Hi gene

Hi locus , inspite of having the genotypes governed by two alleles, there was no significant effect observed for the three genotypes for all the characters studied.

In chicken, El-Kaiaty (1986) and Al-Tikriti (1988)stated that Hi locus had a significant effect on egg number and sexual maturity for Fayoumi breed, and had a highly significant effect on egg number for Baladi breed.

The combinations between two or more loci

1. Albumin and transferrin loci

The effect of combining the two loci on egg number and sexual maturity is presented in Table 5.

The analysis of variance for both egg number and sexual maturity, within genotype, was highly significant. The best genotypes which gave high egg number and early sexual maturity were AlAlTfTf, AlAlTftf, AlAltftf compared to the other three genotypes (AlalTfTf, AlalTftf, Alaltftf). The average of the first three genotypes was 87.32 eggs, while, the last three genotypes showed an average of 74.72 eggs. Meanwhile, the first three genotypes showed an average age at sexual maturity of 53.97 days compared to 60.09 days of the last three genotypes.

Similar trend was observed for body weight on twenty-eight and forty-two days of age (Table 6). The average body weight on twenty-eight days for the first three genotypes was 125.39 grams compared to 121.38 grams for the other three genotypes. The average of body weight on forty-two days for the first three genotypes was 196.04 grams compared to 190.26 grams for the last three genotypes.

Thus, the first three genotypes could be considered as the most important ones in any selection program (specially the genotype AlAlTfTf) for improving egg number, sexual maturity and body weight in Japanese quail .

2. Hi gene and each of albumin and transferrin loci

As mentioned before, the locus of Hi gene did not show any effect on the productive traits studied. Also, the same trend was found with the combination between

the Hi gene and each of albumin and transferrin loci.

General conclusion

The goal of any breeder is to increase the economical units of his products. Quails can be used as a source of meat and eggs. Genetic engineering enables the breeders , nowadays, to reach their target for increasing meat and eggs within few generations.

In our study, we suggest a comparison between the classical ways of selection "considering that the intensity of selection is equal one for simplicity" and the genetic gain from the genotypic values obtained from each locus or from the additive effect of every two loci or more.

The genetic gain from mass selection, for the higher individual produced eggs up to hundred days was 6.29 eggs (only one individual chosen with a higher production, as an example). Family selection (for the higher family production) showed an expected genetic gain of 2.26 eggs.

Concerning egg number, the variances of each locus for albumin and transferrin proved to be 72.71% and 70.62%, respectively. This shows that the effect of the two loci are major effects on the character of egg number. The same variances for body weight, on forty-two days, proved to be 12.05% and 9.36%, respectively .

On the other hand, the differences between the overall mean of egg number for each of albumin genotypes were +7.77eggs and −7.76 eggs, respectively. Transferrin had three genotypes, the difference between the overall mean and each of those genotypes were +10.63 , -0.73 and −9.89 eggs, respectively. These results showed that, in one generation, we can gain 7.7 eggs for selecting in favour of albumin (AlAl) and 10.63 eggs when selecting in favour of transferrin (TfTf).

In this study, it was possible to detect each of the albumin and the transferrin loci. Thus, it was easy to choose the best individuals which showed high values of productive traits according to their genotypes.

ACKNOWLEDGEMENT

Table 1. Least squares means (±S.E.) of egg number (EN), sexual maturity (SM), egg weight (EW) and egg component weights for Albumin locus.

Item	No.	EN	SM(days)	EW(gm)	SHW(gm)	ALW(gm)	YW(gm)	SHT(mm)
Overall mean	305	80.43±0.39	56.75±0.48	12.40±0.04	1.40±0.01	6.88±0.04	4.05±0.02	0.22±0.001
A/A	126	88.20±0.60[a]	53.03±0.74[b]	12.32±0.07[b]	1.42±0.01[a]	6.83±0.07[a]	4.03±0.04[a]	0.22±0.002[a]
A/al	129	72.67±0.50[b]	60.47±0.62[a]	12.49±0.06[a]	1.39±0.01[a]	6.93±0.05[a]	4..06±0.03[a]	0.23±0.001[a]

a and b : Means within the same column with different superscripts are significantly different (P<0.05).

SHW: Shell weight, ALU: Albumen weight, YW: Yolk weight and SHT: Shell thickness.

Table 2. Least squares means (±SE) of body weight traits at different ages studied for Albumin locus .

Item	No.	BW1(gm)	BW14(gm)	BW28(gm)	BW42(gm)	BW90(gm)	BW120(gm)	BW150(gm)
Overall mean	305	8.00±0.04	45.31±0.53	124.27±0.96	193.53±1.30	238.69±1.34	250.28±1.18	254.06±1.32
A/A	126	7.74±0.07[a]	46.73±0.81[a]	128.43±1.46[a]	199.55±2.00[a]	239.16±2.05[a]	250.05±1.81[a]	252.44±2.03[a]
A/al	129	8.06±0.06[a]	43.89±0.68[b]	120.11±1.23[b]	187.5±1.68[b]	238.22±1.72[b]	250.51±1.52[a]	255.68±1.70[a]

a and b : Means within the same column with different superscripts are significantly different (P<0.05).

Table 3. Least squares means (±S.E.) of egg number (EN), sexual maturity (SM),egg weight (EW) and egg component weights for Transferrin locus .

Item	No.	EN	SM(days)	EW(gm)	SHW(gm)	ALW(gm)	YW(gm)	SHT(mm)
Overall mean	305	78.65±0.37	57.54±0.48	12.43±0.04	1.40±0.01	6.90±0.04	4.05±0.02	0.22±0.001
TfTf	99	89.28±0.64 a	52.25±0.83 c	12.29±0.07 a	1.42±0.02 a	6.87±0.07 a	4.07±0.04 a	0.22±0.002 a
Tftf	122	77.92±0.57 b	58.52±0.74 b	12.44±0.07 a	1.40±0.01 a	6.86±0.07 a	4.01±0.04 a	0.23±0.002 a
tftf	84	68.76±0.69 c	61.84±0.90 a	12.45±0.08 a	1.39±0.02 a	6.97±0.08 a	4.08±0.05 a	0.23±0.003 a

a, b and c : Means within the same column with different superscripts are significantly different (P<0.05).

SHW: Shell weight, ALU: Albumen weight, YW: Yolk weight and SHT: Shell thickness.

Table 4. Least squares means (±S.E.) of body weight traits at different ages studied for Transferrin locus.

Item	No.	BW1(gm)	BW14(gm)	BW28(gm)	BW42(gm)	BW90(gm)	BW120(gm)	BW150(gm)
Overall mean	305	8.01±0.04	45.05±0.53	123.46±0.96	192.12±1.30	238.28±1.33	250.21±1.17	254.38±1.32
TfTf	99	7.90±0.08 a	47.11±0.91 a	128.95±1.66 a	200.14±2.25 a	237.65±2.30 a	248.80±2.04 a	251.57±2.29 a
Tftf	122	8.06±0.07 a	44.35±0.82 b	121.95±1.50 b	191.89±2.03 b	241.13±2.08 a	251.61±1.84 a	255.19±2.06 a
tftf	84	8.06±0.08 a	43.70±0.99 b	119.49±1.80 b	184.33±2.45 b	236.07±2.51 a	250.23±2.21 a	256.39±2.48 a

a, b and c : Means within the same column with different superscripts are significantly different (P<0.05).

Table 5. Least squares means (±SE) of egg number (EN), sexual maturity (SM), egg weight (EW) and egg components weights for the combination between Albumin and Transferrin loci .

Item	No.	EN	SM(days)	EW(gm)	SHW(gm)	ALW(gm)	YW(gm)	SHT(mm)
Overall mean	305	81.02±0.52	57.03±0.80	12.36±0.07	1.41±0.02	6.80±0.70	4.01±0.40	0.23±0.002
AlAlTfTf	88	90.40±0.55 a	51.42±0.86 c	12.28±0.08 a	1.41±0.02 a	6.88±0.08 a	4.06±0.04 a	0.22±0.003 a
AlAlTftf	33	82.15±0.90 b	57.30±1.40 ab	12.47±0.13 a	1.39±0.03 a	6.77±0.13 a	3.98±0.07 a	0.22±0.004 a
AlAltftf	5	89.40±2.32 a	53.20±3.60 bc	12.03±0.33 a	1.46±0.07 a	6.44±0.33 a	3.77±0.19 a	0.24±0.010 a
AlalTfTf	11	80.36±1.56 b	58.91±2.43 ab	12.40±0.22 a	1.40±0.05 a	6.80±0.22 a	4.16±0.13 a	0.22±0.007 a
AlalTftf	89	76.35±0.55 c	58.97±0.85 ab	12.43±0.08 a	1.40±0.02 a	6.89±0.08 a	4.02±0.05 a	0.23±0.002 a
Alaltftf	79	67.46±0.59 d	62.39±0.91 a	12.58±0.08 a	1.38±0.02 a	7.00±0.08 a	4.10±0.05 a	0.22±0.003 a

a , b , c and d : Means within the same column with different superscripts are significantly different (P<0.05).

SHW: Shell weight, ALU: Albumen weight, YW: Yolk weight and SHT: Shell thickness.

Table 6. Least squares means (±S.E.) of body weight traits at different ages studied for the combination between Albumin and Transferrin loci loci .

Item	No.	BW1	BW14	BW28	BW42	BW90	BW120	BW150
Overall mean	305	7.94±0.07	45.33±0.09	123.39±1.64	193.15±2.23	239.38±2.29	250.73±2.02	251.90±2.27
AlAlTfTf	88	7.88±0.08 a	46.91±0.97 a	129.50±1.76 a	200.49±2.38 a	237.26±2.46 a	248.49±2.17 a	252.07±2.43 a
AlAlTftf	33	8.20±0.13 a	46.93±1.58 a	126.88±2.87 a	198.64±3.89 a	244.39±4.01 a	254.30±3.54 a	254.64±3.97 a
AlAltftf	5	7.36±0.34 a	42.21±4.06 a	119.80±7.37 ab	189.00±10.00 ab	238.00±10.3 a	249.40±9.10 a	244.60±10.20 a
AlalTfTf	11	8.12±0.23 a	48.72±2.74 a	124.55±4.97 ab	197.36±6.74 ab	240.73±6.95 a	251.27±6.14 a	247.55±6.88 a
AlalTftf	89	8.01±0.08 a	43.39±0.96 a	120.12±1.75 b	189.38±2.37 b	239.92±2.44 a	250.62±2.16 a	255.39±2.41 a
Alaltftf	79	8.10±0.08 a	43.79±1.02 a	119.47±1.85 b	184.04±2.52 b	235.95±2.59 a	250.28±2.29 a	257.14±2.57 a

a and b : Means within the same column with different superscripts are significantly different (P<0.05).

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تأثير بعض المواقع الوراثيه على الصفات الانتاجيه فى السمان اليابانى

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أجريت هذه الدراسه فى مركز أبحاث الدواجن قسم الإنتاج الحيوانى كلية الزراعه جامعة القاهره. إشتملت الدراسه على عدد ٣٠٥ طائر من السمان اليابانى و التى تم إنتاجها من خلال ١٢ دفعه تفريخ من ٢١ عائله ذكور. وتهدف هذه الدراسه إلى تحديد و تقدير للمواقع الوراثيه الألبيومين ، الترانسفيرين ، Hi ودراسة علاقتها بصفات إنتاج البيض. بالإضافة إلى دراسة وزن الجسم للطيور فى أعمار مختلفة.

ويمكن تلخيص النتائج المتحصل عليها فيما يلى :

١- أمكن تحديد تركيبين وراثيين فقط فى دم الأفراد المدروسه بالنسبه للموقع الوراثى الألبيومين. وكان عدد الأفراد الممثله للتركيب الوراثى AlAl السائد ١٢٦ فرداً ، عدد الأفراد الممثله للتركيب الوراثى Alal الخليط ١٢٩ فرداً.

٢- كان متوسط إنتاج الأفراد ذات التركيب الوراثى السائد ٨٨ بيضه أما التركيب الوراثى الخليط فقد كان متوسط أفراده ٧٢ بيضه. كذلك فإن التركيب الوراثى الخليط Alal وصل لعمر النضج الجنسى ٧ أيام مبكراً عن التركيب الوراثى السائد الأصيل AlAl.

٣- بالنسبه لصفة وزن البيضه فقد كان وزن بيض الأفراد Alal أثقل بمقدار ٠٬١٧ من الجرام و كان هذا الفرق معنوياً ، أما باقى مكونات البيضه فقد كانت الفروق غير معنويه.

٤- أوضح تحليل التباين أن الإختلاف بين التركيبين الوراثيين بالنسبه لصفة وزن الجسم عالى المعنويه للأعمار ١٤ ، ٢٨ ، ٤٢ يوماً.

٥- كانت الإختلافات بالنسبه للموقع الوراثى ترانسفيرين لكل من عدد البيض و العمر عند النضج الجنسى عالى المعنويه ، بينما كانت الإختلافات فى باقى صفات البيضه غير معنويه. أعطت الأفراد ذات التركيب الوراثى TfTf أعلى عدد من البيض (٨٩ بيضه) بينما التركيبين الآخرين أظهروا إنخفاضاً فى عدد البيض وكان ٧٨ لـ TfTf ، ٦٩ لـ tftf. و قد أوضح التركيب الوراثى TfTf فروقاً عاليه سواء بينه و بين المتوسط العام أو بينه و بين التركيبين الآخرين.

٦- كانت الإختلافات معنويه بالنسبه للموقع الوراثى ترانسفيرين لوزن الجسم على أعمار ١٤، ٢٨، ٤٢ يوماً و كان متوسط التركيب الوراثى TfTf أعلى لكل من الأوزان على أعمار ١٤، ٢٨، ٤٢ يوماً.

٧- بالنسبه للموقع الوراثى Hi فبالرغم من أن له أليلان إلا أنه لا يوجد أية فروق واضحه بين الثلاث تراكيب وراثيه لكل الصفات المدروسه .

٨- أوضحت المتوسطات المأخوذه لكل عائله لصفة عدد البيض إختلافات عالية تتراوح بين ٥ إلى ٢١ بيضه للموقع الوراثى الألبيومين . و يمكن لهذه الإختلافات بين التركيبين الوراثيين للألبيومين إعطاء فكره عن المكسب الوراثى الذى يمكن الحصول عليه فى جيل واحد من الإنتخاب .

٩- كان متوسط التركيب الوراثى AlAl أقل من Alal لصفة العمر عند النضج الجنسى . و كانت الإختلافات فى صالح Alal و كانت تتراوح من ٠,٣١ إلى ١٣ يوماً .

١٠- ظهر عدم وجود فروق بين وزن البيض و مكوناته داخل العائلات بالنسبه للموقع الوراثى الألبيومين.

١١- كانت الفروق بين وزن الجسم عند الفقس و ١٤ يوماً بين العائلات منخفضة جداً بالنسبه للموقع الوراثى الألبيومين . أما بدايةً من عمر ٢٨ يوماً فقد كانت الفروق بين التركيبين الوراثيين عاليه ، فعند ٢٨ يوماً كانت الفروق تتراوح بين ٠,٢٢ إلى ١٧ جراماً . أما وزن الجسم عند ٤٢ يوماً فقد كانت الفروق تتراوح بين ٠,١٥ إلى ٣٢ جراماً . و عند ٩٠ يوم كانت الفروق تتراوح بين ٠,٢ إلى ٩٩ جراماً .

١٢- بالنسبه للتوالف بين الموقعين الألبيومين و الترانسفيرين فقد وجد أن التركيب الوراثى AlAlTfTf له أعلى متوسط إنتاج من البيض (٩٠ بيضه) . و كان المتوسط التالى له (٨٩ بيضه) للأفراد التى تحمل التركيب الوراثى AlAltftf . و قد كانت هذه التراكيب الوراثيه لها أيضاً أقل عمر عند النضج الجنسى و كان ٥١ ، ٥٣ يوماً على التوالى و هذا يمثل حوالى ١٠ ٪ أكبر من كل القطيع .