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# IMMUNITY COMPETENCE AND SOME GENETIC ASPECTS RELATED TO PRODUCTIVE TRAITS FOR FIVE DIFFERENT GENETIC GROUPS OF CHICKENS

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**ABSTRACT:** This experiment was carried out to investigate and compare immunity, egg quality and some genetic aspects (Number of alleles, Frequency range and Heterozygosity) of genes responsible for traits under study for five genetic groups of chickens (pure Fayoumi (Fay), Fayoumi naked neck (Fay Nana), Fayoumi frizzle (Fay Ff), Fayoumi naked neck frizzed (Fay NanaFf ) and Brown Hy-Line). The pure Fayoumi and chicken carrying major gene of naked neck (Na) and frizzle (F) genes showed high eggshell strength and thicker eggshell thickness compared to Browne Hy-Line strain. Pure Fayoumi and Fay-NanaFgenetic groups were better in cellular and humoral responses than either Brwon Hy-Line, Fay-Nanaff or Fay-nanaFf genotypes. The pure Fayoumi and Fay-NanaFf genetic group have a higher immunity against bacteria than other genetic groups under study. The lowest numbers of specific alleles were traced in pure Fayoumi (MCW241 associated with AFE, BW, Eg. wt.; ADL273 associated with EN) than Brown Hy-Line strain, Fay-NanaFf, Fay-Nana and Fay-nanaFf genetic groups. No specific alleles were detected in using primers MCW246; HM136609 and HM136610 for Brown Hy-Line strain.

Key Words: immunity, genetic diversity, egg quality

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## INTRODUCTION

Genetic improvement of animal and poultry breeds had been based on phenotypic selection. The past century was characterized by the development of quantitative theory and methodology towards the accurate selection and prediction of genetic response (Walsh, 2000). A great genetic diversity exists in poultry breeds and, therefore, there is a considerable potential to improve economically important traits of poultry. There is a lack of definite markers associated with the relevant traits that could help in selection process. Genotype superiority might be efficiently and quickly identified using molecular markers and, consequently, extra gains could be obtained as well as reduction in cost, time, energy and space (Kaya and Yildiz, 2008).

The Fayoumi breed is characterized by high immunity, good egg quality and high adaptation to our local conditions, but its production traits are low (Yacoub et al., 2010 and Radwan 2015). So, the Fayoumi breed was exposed to extensive selection programs and crossed with foreign strains to produce plurality Egyptian developed strains (Kosba and Abd El-Halim, 2008). On the other hand, introducing the same major and or marker genes (such as Na and F) may had a benefit effect on improving some quantitative traits and also, improve heat tolerance, the relevant literature showed the favorable effects on growth and laying performance (Mérat, 1986 and Fathi et al 2013). The genetic gain for the main traits of economic interest might be maximized if quantitative genetic techniques are known and associated with genetic markers that enable the identification of poultry having higher productive potential. Genome scans for Naked Neck, Normal and Frizzle feathered chicken populations; microsatellite markers have been used as line-specific bands and were mainly attributed to selection. Estimation of rate of coalescence points and tracing ancestral alleles is of significance for small-sized selected and inbred population. The microsatellite markers used were highly informative and may therefore be used with chicken populations in the six geo-political zones or regions of Nigeria (El-Gendy, 2009; Ohwojakpor et al., 2012; Isidahomen and Njidda 2012 and Ajayi et al., 2013).

This study aimed to compare the immunity, egg quality and determining some genetic aspects related to these traits for five different genetic groups of chickens.

## MATERIAL AND METHODS

Naked neck and frizzle genes were introduced into the Fayoumi native breed by crossing a heterozygous naked neck-frizzled male (NanaFf) with Fayoumi females (nanaff).The progeny resulted this mating were compared with the pure Fayoumi breed and also with Brown Hy-Line (commercial layer). These genetic groups were raised on the Poultry Breeding Farm, Ain Shams University during summer season under the same environmental, management and hygienic conditions. At 16 weeks of age, total of ٥٠0 females were randomly assigned to the current experiment. They were housed in individual cages placed in an open-sided house. Feed and drinking water were offered to birds ad libitum. A conventional breeding and management procedures were applied throughout the experimental period which lasted up to 62 weeks of age.

The following traits were studied:

**PRODUCTIVE PERFORMANCE AND EGG QUALITY TRAITS**

Productive performance traits included body weight at sexual maturity. Age of sexual maturity was a detriment

from hatching day for the first egg by day and egg production was recorded for the first six months of production cycle.

To assess egg quality parameters, 90 eggs for each genotype were randomly collected at 47 weeks of age. The shell breaking strength (kg/cm2) was determined according to Fathi and El-Sahar (1996). The height of albumen measured using a micrometer mounted on a stand with a platform on which the liquid content was placed. Each egg yolk was separated from the albumen using a plastic egg separator, rolled on a tissue paper towel to remove any adhering albumen and weighed. Albumen yield was determined by subtraction of the yolk and shell with shell membranes intact from the whole egg weight. The percentage of egg components (yolk, albumen and shell) were calculated as the ratio of the egg component to egg weight multiplied by 100. Haugh units were calculated according to Stadelman et al. (1988). The thickness (mm) of the shell with intact membranes was measured at three different points in the middle part of the egg using a dial gauge micrometer.

## IMMUNOCOMPETENCE MEASUREMENTS.

Induced response of mitogen in vivo was evaluated by injection of Phytohemagglutinin-P (PHA-P) into the toe-web between the second and the third digits of hens. Ten hens from each genetic group, at 47 weeks of age were used. Each hen was intradermally injected into the toe-web of the left foot with 100µg Phytohemagglutinin-P (Sigma chemical co., st Louis, Mo 63178) in 0.1 ml of sterile saline measured with a constant tension caliper before injection and at 24, 48 and 72 h after PHA-P injection. The toe-web swelling was calculated as the difference between the thickness of the toe-web before and after injection.

## GENOMIC DNA ISOLATION

Thirty blood samples were randomly collected from each genotype into vacuum tubes containing EDTA and stored at -20°C. Genomic DNA was isolated from blood samples using AXYGEN kit (Axyprep TM) from Axygen Scientific, inc. USA Cat. No. AP-MN-BL-GDNA-50. DNA concentration was determined using spectrophotometer and the final concentration was adjusted up to 50 ng/µl for PCR analysis.

## MICROSATELLITE MARKERS

The regions flanking the microsatellite (SSR) are generally conserved among genetic groups of the same species (species – specific). PCR primers complementary to the flanking regions were used to amplify the SSR-containing DNA fragments. A total of nine SSR primers informative microsatellite markers were selected from the Roslin Institute database (http://www.thearkdb.org.) according to the association of QTL loci with the studied egg traits. Microsatellite markers were chosen, locus and chromosomal locations are shown in Table (1).

## PCR CONDITIONS

PCR was performed in 20 µl volumes containing 4 µl of PCR Master mix 5x (Bio Basic inc. Canada), 2 µl of each forward and reverse primer (10 pmol/ µl), 1 µl genomic DNA (50 ng/ µl) and 11 µl sterile deionized water were added. Amplification was performed in a thermo cycler (LongGene - MG96G / china). Microsatellite-PCR products were resolved by electrophoresis on 3% agarose gel containing ethidium bromide for 90 min. at

60 volt, visualized via UV illuminator and then photographed. The molecular size of the amplified fragments separated on gels was measured by analyzing gel images with Gel Analyzer software package version 2007a (freeware) with 100 bp DNA ladder (Larova GmbH- Germany) as a DNA size marker.

## MICROSATELLITE DATA ANALYSIS

Only, clear unambiguous and reproducible bands were considered for scoring each band was considered a single locus. Data were scored as 1 for the presence and 0 in the absence of a DNA band. Effective alleles per locus (Aep) were calculated according to Weir et al. (1989). The matrix was then analyzed using the PAST, ver. 1.90 (Hammer et al., 2001). The data matrices were used to calculate genetic similarity based on Jaccard's similarity coefficients (Hammer et al., 2001). All scored microsatellite data were firstly corrected to estimate each allele size according to its number of repeats for each marker GelAnalyzer software package was adopted for this purpose. Then, a spreadsheet program (Microsoft Excel) was used to arrange the included data for each breed regarding each locus. All possible extracted population figures were carried out employing a GENPOP software package after data conversion using CON. Statistical analysis Data of the egg quality component were statistically analyzed using one-way analysis of variance with genotypes, using the General Linear Models (GLM) procedure of SAS User's Guide, Ver.8.2, 2001. Duncan's for multiple comparisons note for mean separation when separation was relevant. This statistical models were as follows; $Y_{ij}= \mu + G_i + e_{ij}$ Where: Yij = the J $^{th}$ observation in the i $^{th}$ genotype; $\mu$ = the overall mean; $G_i$ = the fixed effect of the i $^{th}$ genotype; $e_{ij}$ = the error.

## RESULT AND DISCUSSION

### Productive performance and egg quality traits

Productive performance and egg quality traits of different genotypes are illustrated in table 2. Brown Hy-Line strain were significant heavier body weight, earlier age sexual maturity and high percentage of egg production compared to Fayoumi breed, Fay-NanaFf, Fay-Nanaff and Fay-nanaFf genotypes. On the other hand, the Fayoumi chicken carried naked neck (Na) or naked frizzle (F) genes, gene have an advantage effect in improvising productive performance traits (age sexual maturity, body weight at sexual maturity and egg production than Fayoumi breeds (normal feather). The naked neck gene had an advantage in laying performance under either hot or moderate ambient temperatures (Galal 20،0; Singh et al., 2001 and Fathi et al., 2013).

Egg quality determent at 47 weeks of age for genetic groups could be noticed that the egg weight, shell weight, yolk weight, albumen weight and percentage were significantly heaver for Brown Hy-Line eggs than other genotypes under this study. These results reflected correlation between egg weight or/size and albumin and yolk percentage according to Hermiz et al. (2012). Egyptian native chicken carried major gene naked neck and frizzle genes have significantly modify effect on egg weight and size, which is in agreement with Rajkumar et al., 2009 who found that the necked neck gene had a marginal positive effect on egg weight either in single or in double condition. Moreover, Brown Hy-Line strain was significantly decreased in the breaking strength; shell thickness traits as compared to Fayoumi breed, Fay-

NanaFf , Fay-Nanaff and Fay-nanaFf genotypes. The last results reflected that the Egyptian native breeds (Fayoumi breed) and major genes (Na and F) may be carried gene, which play a benefit high shell strength than commercial strain (Brown hy-line strain). The Fayoumi eggs had characterized by a high resistance broken and good mechanical properties than brown Hy-Line eggs Galal et al. (2012). Sharifi and Simianer (2007) and Mahrous (2008) recorded that the major gene Na and F gene leads to a significant improvement, eggshell breaking strength and shell thickness. Immunity

Fig.1. showed that PHA-P mediated swelling response in the toe webs as affected different genotypes (Brown Hy-Line, Fayoumi pure ,Fay NaFf, Fay Nanaff and Fay nanaFf). Thickness of webs were measured at different times (0,24,48 and 72 hours) after injected PHA-P; the webs increase thicker after injected about 0.11, 0.07, 0.08, 0.09 and 0.09mm after 24 hour injection from Brwon Hy-Line, Fayoumi, Fay- NanaFf, Fay- Nanaff, andFay- nanaFf genotypes respectively. But the webs decreased thicker thickness after 48and 72 hours from injection about (0.02;0.06) Brwon Hy-Line, (0.02; 0.02) Fayoumi, (0.02; 0.03) Fay-NanaFf, (0.03; 0.04) Fay-Nanaff and (0.02; 0.05) Fay- nanaFf genotypes respectively. Fig.1. exhibits rabid increases thickness webs after 24 hour injection from Brown Hyline than other genotypes; also, change drop curves thickness webs after 0, 24, 48 and 72 hours injected were more droped curves in Fay-nanaFf and Fay- Nanaff genotypes compared to Fayoumi pure and Fay-NanaFf genotypes ones. These results reflect that Fayoumi and Fay NanaFf genotypes were better cellular and humoral responses than either Brwon Hy-Line, Fay-Nanaff or Fay- nanaFf genotypes. Alvarez et al. (2002) found that the Nana genotype had better cellular and humoral responses than either nana or NaNa genotypes. Also, the last results reflect that, the Fayoumi and Fay- NanaFf genotypes had higher immunity against bacterium than other genotypes under this study. Kougt et al. (1995) reached that the cell-mediated immunity plays an important role in controlling and clearing intracellular bacterium.

## MICROSATELLITES

Polymorphic microsatellites nine primers highly markers were used in the present study as shown in Table .3. which illustrates the number of detected alleles in base pairs, frequencies range for each locus , population as observed as well as genotypes information content. There are several factors affecting the QTL, the number of alleles, locations of genes affecting the quantitative traits, the distribution of the genes effecting and interactions and trait heritability Wardęcka et al., 2003. The QTL for shell weight was found on chromosome 1 around 327-330 cM, and in a near position a linkage was found (around 358-416 cM) for Haugh unit. Characteristic egg production (age first egg, body weight, egg weight and egg number) was found on chromosome z and a gene effect egg shell strength was found a near position a linkage around 104cM. While, the QTL for albumin and yolk weight was found on chromosome 4.

MCW241 associated with age at first egg, body weight and egg weight traits the Brwon Hy-Line strain was increased number alleles than Fayoumi and other genotypes under this study. ADL365 marker associated Haugh unit (albumin quality) traits the average number alleles 3.4. While, ADL273 locus was associated egg number, two numbers of alleles increase for Brwon Hy-Line and one only

increase for NanaFf compared to other genotypes under studded.

Table 4. presents population-Specific allele(s) per locus, frequencies and heterozygosity regarding each locus. The obtained results demonstrate highly heterozygosity among Brown Hy-Line, Fayoumi, Fay-NaFf, Fay-Nanaff and Fay-genetic variability among such genotypes. Roushdy et al., 2012 recorded for any given number of alleles the expected heterozygosity (gene diversity) is highest when all the allele frequencies are equal; and it means that when we will have the highest effective number of alleles. Highly heterozygous individuals not only enhance the probability of QTL detection, but also improve the accuracy of linkage maps and determination of linkage phases (Zhu et al., 2001).The lowest numbers of specific alleles were traced in Fayoumi breeds (MCW241 associated with AFE, BW, Eg. wt.; ADL273 associated with EN )than Brown Hy-Line strain, Fay- NaFf, Fay -Nanaff and Fay- nanaFf genotypes. No specific alleles were detected with primers of MCW246; HM136609 and HM136610 for Brown Hy-Line strain. It seems from the present results that number specific alleles affect QTL traits. Hillel (1997) used the DNA fingerprinting to select distantly related individuals for mating and thus to obtain highly informative offspring.

The great advantage of SSR analysis is the large number of polymorphisms that method reveals. Furthermore, the ability of this method to differentiate individual markers, the technique is very useful for species identification.

nanaFf genotypes. The reference family was characterised by a high level of polymorphism at the examined microsatellite loci and high heterozygosity. The observed variability of average number of alleles seemed to reflect different potentialities of genetic markers to detect

## CONCLUSION

The distinguished eggshell strength and higher favorable immunity of Fayoumi native breed or other genetic groups derived from it (pure Fayoumi (Fay), Fayoumi naked neck (Fay Nana), Fayoumi frizzle (Fay Ff), Fayoumi naked neck frizzed (Fay NanaFf ) and brown Hy-Line) may be due to the possessed specific allele which they carry as revealed by some primers (MCW246; HM136609 and HM136610). These specific alleles have absent and did not possess by Brown Hy-Line strain. As for egg productive traits in this trend was reversed when the Brown Hy-Line strain recorded a favorable superiority over any other genetic groups handled in this study for the same reason mantises previously. These findings may be useful in designing selection programs aimed to improve traits.

Table 1: Microsatellite loci used herein, location on genome and Linked traits.

| No. | Trait | Marker | Location | Reference |
|---|---|---|---|---|
| 1 | AFE | MCW241 | Chromosome Z-72cM | http://www.ncbi.nlm.nih.gov/genome/sts/sts.cgi?uid=2925 |
| 2 | HU | ADL365 | Chromosome1 358-416 cM | http://www.ncbi.nlm.nih.gov/genome/sts/sts.cgi?uid=356. |
| 3 | EN | ADL 273 | Chromosome Z-65cM | Cheng et al., 1995 |
| 4 | YW | MCW114 | Chromosome 4- 82 cM | http://www.ncbi.nlm.nih.gov/genome/sts/sts.cgi?uid=280137. |
| 5 | ESS | MCW 246 | Chromosome Z-104cM | Crooijmans et al., 1996 |
| 6 | EW | MCW200 | Chromosome 1-327-330 cM | http://www.ncbi.nlm.nih.gov/genome/sts/sts.cgi?uid=43937. |
| 7 | AW33 | MCW 170 | Chromosome 4 | Crooijmans et al., 1996 |
| 8 | Immunity | HM136609 | Chromosome 14 | http://www.ncbi.nlm.nih.gov/genome/sts/sts.cgi?uid=83324 |
| 9 | Immunity | HM136610 | Chromosome 14 | Yacoub et al., 2010 |

AFE= age at first egg; HU= Haugh units; EN=Egg number; YW=Yolk weight; ESS= Egg shell strength; EW= egg weight; AW33= Albumin weight at 33 weeks of age.

**Table (2):** Productive performance and egg quality traits of different genotypes.

| Trait | Genetic groups | | | | | SEM | Prob. |
|---|---|---|---|---|---|---|---|
| | Brown Hy-Line | Fayoumi | Fay-NanaFf | Fay-Nanaff | Fay-nanaFf | | |
| Body weight at sexual maturity,gm | 1618.32$^{a}$ | 1320.79$^{c}$ | 1412.11$^{b}$ | 1438.32$^{b}$ | 1409.89$^{b}$ | 60.32 | ** |
| Age at sexual maturity | 139.11$^{e}$ | 156.19$^{a}$ | 144.12$^{d}$ | 147.32$^{c}$ | 149.16$^{b}$ | 5.01 | ** |
| Egg production,% | 90.32$^{a}$ | 68.32$^{d}$ | 76.43$^{b}$ | 75.76$^{b}$ | 71.31$^{c}$ | 0.65 | ** |
| Egg weight at 45 week ,g | 65.50$^{a}$ | 45.00$^{d}$ | 52.54$^{c}$ | 55.46$^{b}$ | 54.27$^{b}$ | 0.45 | ** |
| Breaking strength (kg/cm$^{3}$) | 3.99$^{c}$ | 5.67$^{a}$ | 5.04$^{b}$ | 5.59$^{a}$ | 5.06$^{b}$ | 0.36 | ** |
| Shell thickness | 0.36$^{b}$ | 0.401$^{a}$ | 0.394$^{a}$ | 0.392$^{a}$ | 0.403$^{a}$ | 0.008 | * |
| Shell weight, g | 6.06$^{a}$ | 5.82$^{a}$ | 5.01$^{c}$ | 5.32$^{b}$ | 5.29$^{b}$ | 0.14 | * |
| Shell weight % | 9.25$^{b}$ | 12.93$^{a}$ | 9.56$^{b}$ | 9.57$^{b}$ | 9.76$^{b}$ | 0.21 | ** |
| Haugh Unit | 82 | 85 | 83.09 | 84.68 | 84.62 | 1.72 | NS |
| Yolk Weight, g | 18.94$^{a}$ | 13.28$^{c}$ | 15.21$^{b}$ | 15.68$^{b}$ | 15.26$^{b}$ | 0.32 | * |
| Yolk % | 28.92 | 29.52 | 29.04 | 28.29 | 28.22 | 0.54 | NS |
| Albumen Weight, g | 40.50$^{a}$ | 25.90$^{c}$ | 32.32$^{b}$ | 34.46$^{b}$ | 33.72$^{b}$ | 0.98 | * |
| Albumen % | 61.83$^{a}$ | 57.23$^{b}$ | 61.50$^{a}$ | 62.05$^{a}$ | 62.02$^{a}$ | 0.57 | * |

a,b,c,d,e values in the same row for each parameters with different superscripts are significantly different ($P<0.05$).

**Table( 3):** Number of detect alleles in base pair and frequencies range for each locus and population as observed in the present study and genotypes information content.

| | **Parameters** | **Trait** | **Marker** | **Genotypes** | | | | |
|---|---|---|---|---|---|---|---|---|
| | | | **MCW241** | **Brown Hy-Line** | **Fayoumi** | **Fay- NanaFf** | **Fay-Nanaff** | **Fay- nanaFf** |
| **Primer 1** | No. allele (bp) | AFE, BW, Eg. wt. | | 8 | 6 | 7 | 7 | 6 |
| | | | | Average | (6.8) | | | |
| | Frequencies range | | | 0.044-0.461 | 0.037-0.35 | 0.039-0.39 | 0.029-0.33 | 0.034-0.36 |
| | Alleles:- | | | | | | | |
| | Highest | | | 279 | 310 | 330 | 290 | 279 |
| | Lowest | | | 290,300,340 | 285,295 | 270,288 | 258,278 | 250,260 |
| **Primer 2** | No. allele | HU | ADL365 | 3 | 4 | 3 | 3 | 4 |
| | | | | Average | (3.4) | | | |
| | Frequencies range | | | 0.375-0.647 | 0.126-0.742 | 0.299-0.585 | 0.287-0.498 | 0.224-0.654 |
| | Alleles:- | | | | | | | |
| | Highest | | | 112 | 110 | 120 | 108 | 113 |
| | Lowest | | | 110 | 99 | 110 | 90 | 97 |
| **Primer 3** | No. allele | EN | ADL273 | 5 | 3 | 4 | 3 | 3 |
| | | | | Average | (3.6) | | | |
| | Frequencies range | | | 0.094-0.819 | 0.093-0.511 | 0.091-0.509 | 0.082-0.512 | 0.085-0.496 |
| | Alleles:- | | | | | | | |
| | Highest | | | 180 | 168 | 175 | 165 | 155 |
| | Lowest | | | 40,155 | 54,130 | 15,13,43 | 43 | 143,15 |
| **Primer 4** | No. allele | YW | MCW114 | 5 | 4 | 4 | 3 | 3 |
| | | | | Average | (3.8) | | | |
| | Frequencies range | | | 0.378-0.567 | 0.367-0.645 | 0.347-0.435 | 0.312-0.433 | 0.298-0.402 |
| | Alleles:- | | | | | | | |
| | Highest | | | 132 | 119 | 120 | 125 | 117 |
| | Lowest | | | 120,90 | 90 | 112,86 | 104,87 | 80 |

Cont.Table(3):

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **Primer 5** | No. allele | ESS | MCW246 | 4 | 5 | 4 | 3 | 3 |
| | | | | Average | (3.8) | | | |
| | Frequencies range | | | 0.095-0.504 | 0.079-0.388 | 0.088-0.438 | 0.075-0.365 | 0.069-0.445 |
| | Alleles:- | | | 240 | 190 | 200 | 190 | 170 |
| | Highest | | | 210 | 179 | 190 | 170 | 150 |
| | Lowest | | | | | | | |
| **Primer 6** | No. allele | EW | MCW200 | 7 | 4 | 6 | 5 | 5 |
| | | | | Average | (5.4) | | | |
| | Frequencies range | | | 0.138-0.320 | 0.039-0.271 | 0.028-0.179 | 0.018-0.128 | 0.015-0.126 |
| | Alleles:- | | | | | | | |
| | Highest | | | 123 | 153 | 130 | 120 | 122 |
| | Lowest | | | 110 | 99,120 | 100 | 80 | 90 |
| **Primer 7** | No. allele | AW33 | MCW 170 | 6 | 4 | 5 | 5 | 4 |
| | | | | Average | (4.8) | | | |
| | Frequencies range | | | 0.469-0.689 | 0.289-0.467 | 0.376-0.549 | 0.398-0.598 | 0.298-0.459 |
| | Alleles:- | | | | | | | |
| | Highest | | | 140 | 116 | 137 | 123 | 119 |
| | Lowest | | | 117 | 90,110 | 120,83 | 110,98 | 110,80 |
| **Primer 8** | No. allele | | HM136609 | 2 | 4 | 2 | 2 | 2 |
| | | | | Average | (2.4) | | | |
| | Frequencies range | | | 0.111-0.231 | 0.129-0.324 | 0.126-0.189 | 0.109-0.176 | 0.089-0.123 |
| | Alleles:- | | | | | | | |
| | Highest | | | 140,161 | 138 | 130 | 115 | 125 |
| | Lowest | | | 90,100,112 | 89,109 | 79 | 60,100 | 90 |
| **Primer 9** | No. allele | | HM136610 | 2 | 3 | 2 | 2 | 2 |
| | | | | Average | (2.2) | | | |
| | Frequencies range | | | 0.200-0.309 | 0.143-0.449 | 0.124-0.219 | 0.009-0.184 | 0.089-0.123 |
| | Alleles:- | | | | | | | |
| | Highest | | | 120,90 | 140,100 | 133,129 | 134,117 | 102,83 |
| | Lowest | | | 100,70 | 110 | 119 | 104,100 | 100,86 |

AFE= age at first egg; BW= Body weight; EW= egg weight; HU= Haugh units; EN=Egg number; YW=Yolk weight; ESS= Egg shell strength; AW33= Albumin weight at 33 weeks of age.

**Table( 4):** Population-Specific allele(s) per locus, heterozygosity (H) regarding each locus, average of heterozygosity (HA) over all loci and average of F-statistics (F-index) over all loci.

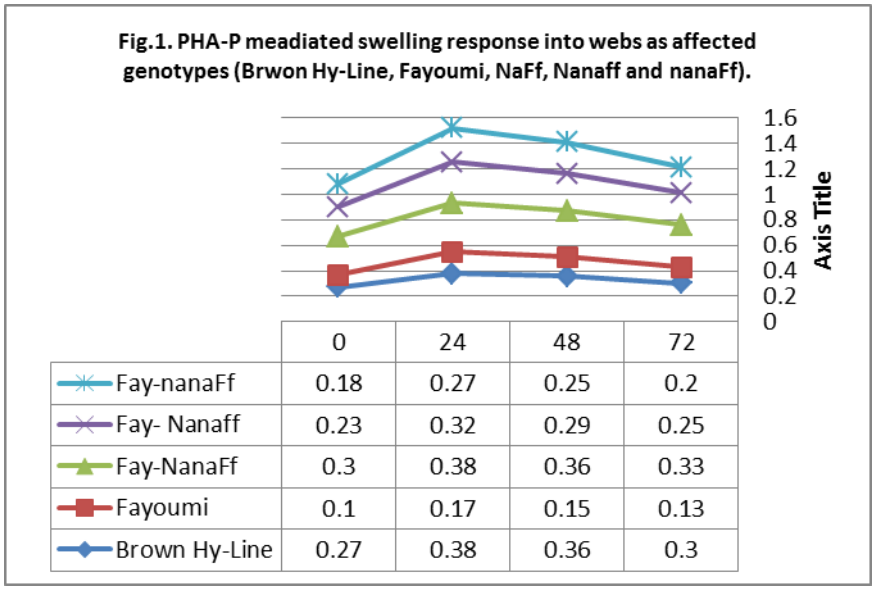
| **Parameters** | **Trait** | **Marker** | **Genotypes** | | | | |
|---|---|---|---|---|---|---|---|
| | | | **Brown Hy-Line** | **Fayoumi** | **Fay- NanaFf** | **Fay-Nanaff** | **Fay-nanaFf** |
| Specific Alleles | AFE, BW, Eg. wt. | MCW241 | 250 | 201 | 250 | 248 | 240 |
| Frequencies | | | 0.184 | 0.0078 | 0.092 | 0.065 | 0.061 |
| Heterozygosity | | | 0.74 | 0.18 | 0.29 | 0.120 | 0.12 |
| | | | Primer 2 | | | | |
| Specific Alleles | HU | ADL365 | 117 | 131 | 125 | 120 | 110 |
| Frequencies | | | 0.151 | 0.161 | 0.132 | 0.111 | 0.101 |
| Heterozygosity | | | 0.44 | 0.46 | 0.40 | 0.31 | 0.26 |
| | | | Primer 3 | | | | |
| Specific Alleles | EN | ADL273 | 180 | 128 | 177 | 160 | 143 |
| Frequencies | | | 0.098 | 0.092 | 0.081 | 0.041 | 0.052 |
| Heterozygosity | | | 0.33 | 0.65 | 0.12 | 0.11 | 0.09 |
| | | | Primer 4 | | | | |

**Cont. table(4):**

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| Specific Alleles | YW | MCW114 | 144 | 139 | 132 | 128 | 103 |
| Frequencies | | | 0.123 | 0.109 | 0.095 | 0.080 | 0.063 |
| Heterozygosity | | | 0.499 | 0.402 | 0.308 | 0.213 | 0.165 |
| | | | Primer 5 | | | | |
| Specific Alleles | ESS | MCW246 | NII | 112 | 110 | 100 | 86 |
| Frequencies | | | NII | 0.122 | 0.112 | 0.098 | 0.076 |
| Heterozygosity | | | 0.65 | 0.84 | 0.74 | 0.59 | 0.55 |
| | | | Primer 6 | | | | |
| Specific Alleles | EW | MCW200 | 150 | NII | 120 | 110 | 100 |
| Frequencies | | | 0.199 | NII | 0.109 | 0.081 | 0.041 |
| Heterozygosity | | | 0.73 | 0.81 | 0.61 | 0.49 | 0.31 |
| | | | Primer 7 | | | | |
| Specific Alleles | AW33 | MCW 170 | 183 | 152 | 141 | 129 | 105 |
| Frequencies | | | 0.201 | 0.117 | 0.107 | 0.094 | 0.077 |
| Heterozygosity | | | 0.387 | 0.312 | 0.291 | 0.176 | 0.143 |
| | | | Primer 8 | | | | |
| Specific Alleles | | HM136609 | NII | 110 | 90 | 70 | 50 |
| Frequencies | | | NII | 0.098 | 0.081 | 0.060 | 0.037 |
| Heterozygosity | | | 0.199 | 0.213 | 0.121 | 0.123 | 0.076 |
| | | | Primer 9 | | | | |
| Specific Alleles | | HM136610 | NII | 90 | 50 | 60 | 30 |
| Frequencies | | | NII | 0.069 | 0.075 | 0.087 | 0.095 |
| Heterozygosity | | | 0.124 | 0.196 | 0.166 | 0.173 | 0.188 |

AFE= age at first egg; BW= Body weight; E W= egg weight; HU= Haugh units; EN=Egg number; YW=Yolk weight; ESS= Egg shell strength; AW33= Albumin weight at 33 weeks of age.

Fig1. PHA-P meadiated swelling response in toe webs as affected different genotypes (Brown Hy-Line, Fayoumi,Fay- NanaFf, Fay-Nanaff and Fay- nanaFf).




| | 0 | 24 | 48 | 72 |
|---|---|---|---|---|
| Fay-nanaFf | 0.18 | 0.27 | 0.25 | 0.2 |
| Fay- Nanaff | 0.23 | 0.32 | 0.29 | 0.25 |
| Fay-NanaFf | 0.3 | 0.38 | 0.36 | 0.33 |
| Fayoumi | 0.1 | 0.17 | 0.15 | 0.13 |
| Brown Hy-Line | 0.27 | 0.38 | 0.36 | 0.3 |

0, 24, 48 and 72: tow-web swelling measured at 0, 24, 48 and 72 hours post PHA-P injection, respectively.

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## الملخص العربى

## المقدره المناعيه وبعض الجوانب الوراثيه المتصله بالصفات الانتاجيه لخمس مجموعات وراثيه مختلفه من الدجاج

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إجريت هذه التجربه بهدف فحص ومقارنه المناعه وجودة البيض و الجوانب الوراثيه (عدد الاليلات ، مدى التكرار ، التغاير الجنينى) للجينات المسئوله عن الصفات تحت الدراسه فى خمس مجموعات وراثيه للدجاج ( الفيومى ، الفيومى عارى الرقبه ، الفيومى المجعد الريش، الفيومى عارى الرقبه ومجعد الريش ، الهايلين البنى). أظهر دجاج الفيومى النقى و الفيومى حامل الجينى عرى الرقبه والمجعد أرتفاع فى متانة القشره وسمك القشره مقارنه بسلالة الهاى لاين البنى. كما انه الفيومى النقى والفيومى عارى الرقبه وذو الريش المجعد سجل افضل استجابه خلويه عن كلا من التراكيب الوراثيه للهاى لاين البنى و الفيومى عارى الرقبه. الفيومى النقى والفيومى عارى الرقبه ذو الريش المجعد لديه مناعه ضد البكتريا أعلى من المجموعات الوراثيه الاخرى تحت هذه الدراسه. ولقد سجل اقل عدد للاليلات فى سلالة الفيومى النقيه للبريمر MCW241 المرتبط بصفات العمر عند اول بيضه AFE ، وزن الجسمBW ، وزن البيض Eg. wt ; البريمر ADL273 المرتبط بصفة عدد البيض EN عن سلالة الهايلين البنى ،الفيومى عارى الرقبه ذو الريش المجعد- Fay-NanaFf ،الفيومى عارى الرقبه Fay-Nanaff، الفيومى ذو الريش المجعد- Fay- nanaFf . لم يتم اكتشاف الليلات خاصه فى سلالة الهايلين البنى عند استخدام البريمر، MCW246 ،HM136610 ،HM136609 .