Egypt. Poult. Sci. Vol. (43) (IV): (647-661)(2023) **(2310-1271)**

Egyptian Poultry Science Journal

http://www.epsj.journals.ekb.eg/

ISSN: 1110-5623 (Print) – 2090-0570 (Online)

PRODUCTIVE TRAITS AND GENETIC DIFFERENCES OF CHICKENS SEGREGATING FOR NAKED NECK AND FRIZZLE GENES AT HIGH AMBIENT TEMPERATURE

A.M. Abdelmoniem1*, M.Y. Mahrous[1], M.M. Fathi[1,4] A. Galal[1] and M. Magdy2,3

1 Poult. Prod.Dep., Fac. of Agri., Ain Shams Uni., 68 Hadayek Shubra, 11241, Cairo, Egypt.

2 Gen.Dep., Fac. of Agric., Ain Shams Uni., 68 Hadayek Shubra, 11241, Cairo, Egypt.

3 Plant Bio. Dep., Fac. of Bio., Murcia Uni.. Campus of Espinardo, 30100, Murcia, Spain.

4 Dep. of Anim. Prod. and Breed.College of Agric. and Veter. Med., Qassim Uni., Al-Qassim 51452, Saudi Arabia

***Corresponding author:** Dr. Abdelmoniem Hanafy, Email: abdelmoniem_hanafy@agr.asu.edu.eg

Received: 15/10/2023 Accepted: 30 /11/2023

ABSTRACT: The present study aimed to conduct genetic diversity of four native chicken genotypes (Naked neck, frizzled, naked neck-frizzled and normally feathered). Diversity was assessed based on morphological measurements and molecular markers. A total of 500 chickens were used in this study. Productive traits of four genotypes were measured. RAPD technique was used to access the genetic diversity using five RAPD molecular markers. Main results referred to that naked neck and naked neck-frizzled genotypes had higher significantly body weight and body weight gain than normal feathering (nana-ff) ones. Naked neck-Frizzled (Nana-Ff) genotype had better carcass characteristics than other genotypes. Nana-Ff and Nana-ff genotypes were significantly higher than other genotypes in egg weight. The percentage of polymorphic bands ranged between 13.33 % and 40 % with a mean of 25.83 %. Genetic diversity ranged between 0.06 and 0.18 with a mean of 0.12. Constantly, the minimum values were scored to the genotype nana-Ff while the maximum values were scored to the genotype Nana-ff. Conclusion indicated that Na- allele is effective in improving meat and egg production traits than frizzle and normal feathering chicken. The Principal Component analysis in this study reflected that a similar results to that of the morphological values to four genetic groups. We provide fundamental evidence to genetic improvement programs by crossing or selection methods based on each productive performance and genetic analysis by modern techniques and software.

Keywords: Genetic Diversity; Naked neck; Frizzle; RAPD; PCA

1. INTRODUCTION

The molecular genetics is considered the main tool of the 21st century for the modern poultry breeding programs. These tools allow for rapid and accurate identification and selection at the gene level of individuals with better performance traits (Fulton, 2008).

With increasing of chicken genomic resources and the rapid developments in genotyping techniques, genotyping assays. Due to the existence of linkage disequilibrium, only a limited number of genetic markers are needed to capture all genetic variation of the genome (Groenen, 2009).

Since most of the layer and broiler breeds or strains have originated and been developed under temperate climate, so they are more prone to tropical climatic stress in Egypt, due to a decrease in feed consumption, feed efficiency accompanied by heavy mortality during summer (Patra *et al.*, 2002).

Huge economic losses in egg production and shell quality resulting from heat stress have occurred in laying hens. Under this unusual condition, the bird resorts to increase panting (Fathi *et al.,* 2022). Fortunately, some mutations, such as naked neck, frizzle, slow-feathering and dwarf confer thermoregulation in hot and humid regions by reducing feather mass or body weight (Desta, 2021).

The naked neck gene (Na) is an autosomal incompletely dominant gene located on the third chromosome. It reduces the feather coverage by about 40% in homozygous chickens and 20-30% in heterozygous chickens compared to their normal plumage counterparts (Lin *et al*., 2006 and Fathi *et al.,* 2013). The Na gene could be considered as a marker gene because the feather appearance of different genotypes can be identified by visual examination upon hatching (Fathi *et al.*, 2022). Galal *et al.* (2019) Found that the Na gene improved heat tolerance by increasing HSP70 gene expression rather than by reducing feather cover in Egyptian local breeds raised under heat stress conditions. The Na gene increases the size of wattle and comb, instigating more body surface to thermoregulation and loss of heat. Reduced feather surface development leaves extra protein for vital physiological functions and produces more eggs and meat (Desta, 2021).

A phenotype of frizzled feather was reported by (Duah *et al.*, 2020) that give the best protection against the severe environment and the specific gene revealing such characteristics expresses in many chicken breeds. The frizzle gene (F) is an incompletely dominant gene, reduces the intensity of feathers, making the birds dissipate the excess body heat more efficiently (Fathi *et al.,* 2022). Dong *et al.* (2018) Demonstrated that a deletion allele in KRT75L4 is responsible for the frizzle feather phenotype. The frizzle gene reduces the feather insulation through curling and reducing the intensity of feathers (Lin *et al*., 2006; Fathi *et al.,* 2013). From the heat tolerance point of view, the frizzle gene behaves as a recessive mutation (Zerjal *et al*., 2013).

The random amplified polymorphic DNA (RAPD) is a simple and easy method to detect polymorphism based on the amplification of random DNA segments with single primers of arbitrary nucleotide sequence (Zhang *et al*., 2002; Mollah *et al.,* 2005 and Dehghanzadeh *et al.,* 2009). The effectiveness of RAPD in detecting polymorphism between chicken populations and establishing genetic relationships among chicken populations was previously reported by (Sharma *et al.,* 2001). The present study was conducted to estimate genetic relatedness using RAPD method to differentiate among (naked neck, frizzle, and naked neck frizzled) compared to normally feathered ones. Additionally, correlation based on Mantel statistical tests was used to figure out the relation of the detected polymorphic bands to the morphological characters measured for all genotypes.

2. MATERIALS AND METHODS

2.1. Mating and management

Heterozygous naked neck (Nanaff) females were artificially inseminated with heterozygous frizzled (nanaFf) males. According to the previous mating, four genotypes were obtained: a total of 500 chicks representing all genotypes and sexes as follow:

1- Naked neck genotype "Nanaff" (125 = "56 male + 69 female").
2- Frizzled genotype "nanaFf" (125 = "59 male + 66 female").
3- Naked neck-frizzled genotype "NanaFf" (100 = "47 male + 53 female").
4- Normally feathered genotype "nanaff" (150 = 70 male + 80 female").

The chicks were wing-banded and brooded in electrical brooding batteries up to 3 weeks of age. Then, they were transferred to a floor-pens from 3 to 8 week of age and finally transported for sex separation in individual cages. All birds were reared under similar environmental, managerial, and hygienic conditions. Feed and water were supplied *ad libitum*. They were fed a commercial diet containing 21% CP and 2900 kcal ME/kg diet. Average high and low ambient temperatures recorded during the experimental period were 32.5 and 28.7°C, respectively.

2.2. The Productive Studied traits

Live body weights were determined individually at 16 weeks of age for males. Also, feed consumption and feed conversion ratio were calculated for chickens representing all genotype males and from 8 to 12 weeks of age. Each bird was weekly weighted, and the relative growth was calculated. Feed consumption was measured weekly and for the whole experiment.

Feed Consumption (FC)
= Feed consumed for one week

Weight Gain (Δwt)
= Weight gain (g) within one week

$$\text{Feed Conversion Ratio} = \frac{\text{FC}}{\Delta\text{wt}}$$

At 16 weeks of age, forty males (10 from each genotype) were slaughtered for carcass assessment. Birds were individually weighed before being slaughtered. They were slaughtered by severing the carotid artery and jugular vein. The birds were eviscerated by removing the viscera. The giblets (liver, heart and gizzard "after cut and cleaned) were weighed in grams. Abdominal fat was removed and weighed. The dressing and breast muscles were weighed in grams. There were expressed as a proportion of the live body weight. And then calculate edible and inedible parts percentages to live body weight pre-slaughtering.

Egg number and egg weight for each hen within a genotype was individually recorded daily during the laying period up to 90 day from the first egg laid. Egg mass in grams was calculated by multiplication egg number by egg weight for each hen within each genotype.

2.3. DNA extraction and purification

Blood was collected in EDTA solution, 0.5M (pH 8.0) from 3 samples *per* genotype. Genomic DNA was isolated and purified from blood using spin column technology of AXYGEN kit (Axygen Scientific, USA, Cat# AP-MN-BL-GDNA-50). DNA quality was checked using 1% (w/v) agarose gel electrophoresis, visualized by pre-added Ethidium bromide dye under UV light, and quantified using a spectrophotometer device (Eppendorf® spectrophotometer x100).

2.4. Polymerase Chain Reaction (PCR)

PCR was performed in 25 µl volumes containing 4 µl of PCR Master mix 5x (CinnaGen/ Iran), 2 µl of primer (10 pmol/ µl), 1 µl genomic DNA (50 ng/ µl) and 13 µl sterile deionized water were added. Amplification was performed in a thermocycler (Long Gene - MG96G / china) following standard temperature profiles: initial denaturation 95°C for 4 min, 35 cycles (denaturation 95°C 1 min, annealing temp 36°C/ 1 min, extension 72°C/ 1 min) and final extension 72°C/ 3 min. PCR products (5 µl) were separated by 1.5 % (1.5

g / 100 ml) agarose gel electrophoresis run at 5V/cm for 15 min. Additionally, one lane was loaded with 2.5µl of GeneRuler™ 100bp DNA Ladder Plus (Fermentas, SM1153). Gels were visualized by a pre-added 1x Ethidium bromide dye under UV light and photographed by a Gel documentation system. Alternatively, in some cases, 10% native Polyacrylamide gel electrophoresis (PAGE) was used to separate the RAPD amplicons, run in 1x Tris-Boric-EDTA buffer (TBE) at 10V/cm for 20 min, along with the previously mentioned DNA ladder.

2.5. Data analysis

2.5.1. Statistical analysis

Data were subjected to a one-way analysis of variance with genetic group effect, using the General Linear Models (GLM) Procedure of SAS User's Guide 9.0, 2002. When significant differences among means were found, means were separated using Duncan's multiple range tests. Gene effect was calculated according to **Galal (2008)** as follows:

$$\text{Gene effect} = \frac{(\text{NanaFf or Nanaff or nanaFf} - \text{nanaff})}{\text{nanaff}} \times 100$$

The modal generated was fitted for the effect of genotype:

$$Yij = \mu + Gi + eij$$

Where Y is the dependent variable, µ is the grand mean, G_i is the fixed effect of the Genotype (i= 1, 2, 3 and 4) and e_{ij} is random error.

2.5.2. Morphological analysis

All measured traits were normalized using z-score transformation (eq. 1) and analyzed based on their variances in order to describe the traits similarity in 2D graphical plot in what is known as principal component analysis (PCA) using PCO3 program (Anderson, 2003). Grouped traits were used as a set to generate a homogenized Euclidean distance matrix (eq. 2).

Equation 1: Z-score transformation standard equation is:

$$Z(x) = \frac{(x\ value - Mean)}{Standard\ Deviation}$$

Equation 2: Euclidean distance [19] between two points (p) and (q) in (n) number of points is:

$$d\ (p,q) = d\ (q,p)\ = \sqrt{\sum_{i=1}^{n} (qi - pi)^2}$$

2.5.3. Genetic analysis

Successful gels were transformed manually to binary form (1 for band presence, and 0 for band absence). A binary data sheet of all combined primers was used to proceed with the genetic variability analysis. Samples were grouped according to their genotype into four groups, each consisting of three equal samples. MULTILOCUS V1.3 (Agapow and Burt, 2001) was used to assess the adequacy of the number of amplified bands to measure genetic variability. Genetic variability was demonstrated by measuring the following indices: Number of Different Alleles (Na), Number of Effective Alleles (Ne), where Ne = 1 / (p^2 + q^2), Shannon's Information Index (I), where I = -1 x (p x Ln (p) + q x Ln (q)) and Genetic diversity (h), where h = 1 - (p^2 + q^2); all indices were calculated using GENEALEX V6.5 software (Peakall and Smouse, 2012). The genetic distance matrix was generated using PCO3 program, first between the 12 samples and the other between the four genotype groups. Since the samples lack population structure, a non-spatial descriptive method using principal coordinate analysis (PCoA) was used instead of phylogenetic analysis, such method was estimated using GENEALEX V6.5 software.

2.5.4. Correlation tests

A simple Mantel test (to measure the association between two matrices) was performed by plotting the "matrix" and "log matrix" of the genetic distance matrix against the "matrix" and "log matrix" of each of the morphological data sets and singletons. Logarithmic data were used as an alternative to normal data to find which was the most appropriate to represent a better correlation using the Mantel test **(Bohonak, 2002)**

3. RESULTS AND DISCUSSION

3.1. Morphological traits

3.1.1. Growth traits

3.1.1.1. Body Weight (BW) and Body Weight Gain (BWG)

Data presented in table 1 and figure (1) revealed that BW of NanaFf and Nanaff genotypes were significantly ($P \leq 0.05$) higher than other genotypes at 16 weeks of age with gene effect increasing by **(**8.66% and 7.04%**)** compared to the normal feathered genotype, respectively. The BWG value was observed to be significant ($P \leq 0.05$) among different genotypes, in which the presence of Na- allele increased BWG by about 30.76%, and Na-F- alleles increased BWG by about 11.88% compared to nanaff genotype during the age between (8 to 12) weeks. Increasing in growth rate by naked neck genotype under hot temperatures may be cause of the relative high concentration of T3 hormone (Decuypere *et al.,* 1993).

The results agree with those of Njenga (2005) who compared the growth of naked neck, frizzle, dwarf, and normal feathered birds from one day old to the fifth week and found significantly higher body weight in naked neck birds than all the other chicken genotypes. Similarly, Adomako *et al.* (2014) observed that body weight and weight gain of naked neck birds were significantly higher as compared to their normal feathered counterparts. In contrast to these findings, Duah *et al.* (2020) observed no significant differences between the means of the live weights of the chicken with the three genotypes. Several studies have indicated that possession of the naked neck gene conferred heavier body weights on naked neck chicks due to better feed utilization efficiency (Gunn, 2008; Sharifi *et al,* 2010). This has been attributed to improved ability for dissipation of heat and diversion of protein from feather production to development of muscle tissues in the naked neck strains (Patra *et al*., 2002).

3.1.1.2. Feed Consumption (FC) and Feed Conversion Ratio (FCR)

The naked neck genotype showed the highest significant value in FC during the age between (8 to 12) weeks to record gene effect 22.36% increased than nanaff genotype, while NanaFf recorded the lowest significant value by gene effect 5.63% than nanaff genotype as shown in figure (1). In contrast to these findings, Adomako *et al.* (2014) observed non-significant differences in average weekly feed intake among naked neck and normal feathering chicken genotypes. However, in a study of Alam *et al.* (2021), they found significant variations in feed intake among naked neck, RIR, and their crossbreeds. Increase in body temperature for individuals kept in hotter environment was higher in normally feathered birds than in naked neck ones, due to feathering reduction. Consequently, naked neck birds exhibited higher feed intake and meat yield than normally feathered ones (Deeb and Cahaner, 1994).

Concerning FCR, table 1 showed that Nanaff and NanaFf genotypes recorded more efficient values (3.70 and 3.73) respectively than normally feathered genotypes (3.95) between (8-12) weeks of age. The naked neck chicken showed the best growth performance of other genotypes may be having a good heat tolerance under high ambient temperatures ranging between 32.5 to 28.7°C; over normal feathered genotypes. Our results are supported by Ajayi (2010), who reported that the frizzled and Naked-Neck chickens conferred better FCR than the normal feathered chicken. Adomako *et al.* (2014) Found that the naked neck birds had significantly lower FCR values compared to their normal feathered counterparts, indicating that FCR values may vary among varieties (Alam *et al*., 2021), genetic groups (Das *et al*., 2014) and breeds (Khantaprab and Tarachai, 1998) of poultry. The normal feather chicks were heavier (8.92%) at one day old, and those from the naked neck had better FCR which translated to 8.55% heavier weight at 12 weeks of age (Oleforuh-Okoleh *et al.,* 2021).

3.1.1.3. Carcass characteristics

Data presented in figures (2-4) revealed that the dressing percentage of NanaFf, Nanaff and nanaFf genotypes at 16 weeks of age showed a significant increase over normally feathered ones by gene effect values (5.27%, 4.75%, and 3.73%), respectively. The double segregation genotype and naked neck genotype recorded a significant increase in total breast muscle percentage by gene effect (20.08% and 11.29%) than nanaff genotype, respectively. The presence of Na-F- alleles decreased the abdominal fat percentage by about (54.94%) and Na- allele decreased the same trait by about (11.29%) more than the nanaff genotype. The total value of giblets and their organs individually were recorded as non-significantly different among four genetic groups. With respect to the edible parts, (naked neck-frizzled, naked neck, and frizzled genotypes) showed a significant increase in nanaff genotype as follows (5.32%, 4.69%, and 3.85%), consequently. Increasing in dressing of naked neck genotype than normal siblings been attributed to higher body weight and less losses due to feathering in naked neck birds, and higher meat yield due to the presence of the Na gene (Fathi *et al.*, 2008).

Adedeji *et al.* (2006) recorded a significantly higher body weight among naked neck birds at 15 wk of age compared with normal feathered ones. Galal *et al.* (2007) recorded no significant difference between the heterozygous naked neck and normal feathered birds. The heart weight of NanaFf chicken recorded was not significantly heavier than those of both the Nanaff and nanaff chicken. Duah *et al.* (2020) showed that there were no significant differences between the means of the dressed weights of the chicken between the Nanaff, NanaFf, and nanaff genotypes. The Nanaff genotype was not significantly higher in gizzard weight (47.7 g) compared with the nanaff (42.1 g) and NanaFf (45.7 g) genotype. Frizzled-naked neck chicken had drumstick weight (400.9 g) that was not significantly different from the weights recorded by the other genotypes. Thigh weights of the naked neck (194.7 g) and frizzled-naked neck chicken (192.9 g) were also not significantly higher than those of normal feathered chicken (192.1 g). The breast weights for the 3 genotypes were 248.0, 246.5, and 245.5 g, respectively, for normal feathered, naked neck, and frizzled-naked neck chicken, and there were no significant differences among the 3 genotypes. The breast muscle weight had not significantly higher than that of the normal feathered chicken.

3.1.2. Egg production traits

3.1.2.1. Egg Weight (EW), Egg number (EN) and Egg Mass (EM)

Data presented in table (2) and figure (5) showed that EW of NanaFf and Nanaff genotypes were significantly ($P \leq 0.05$) higher than other genotypes with gene effect to be (11.05% and 9.75%) compared to the normal feathered genotype, respectively. The chicken group carrying Na- allele achieved the efficient gene effect in EN and EM compared to the normally feathered genotype with (13.01% and 24.02%) respectively. Oleforuh-Okoleh *et al.* (2021) found that the normal feather strain laid 11 eggs more ($p<0.01$) than the naked neck, both had similar average egg weight at 280 days of age, and they found that there were significant ($P<0.05$) strain variations in egg weight across the different monthly period of lay except at 37-40 weeks of age.

Increased egg number by the normal feather throughout the five months improved their monthly HenDay egg production ($P<0.05$) above those of the naked neck. Nweke-Okorocha *et al.* (2022) found that the naked necks had a higher value for egg weight (44.85) followed by a normal feathered (43.05) and lastly frizzled with least squares means value (40.15). The naked neck had the highest value (929.89) for egg mass followed by the normal feathered (858.95).

Principal Component Analysis (PCA)

PCA analysis based on the variance between the traits showed 2 sets and 2 singles (Fig. 6). The differences between traits were

explained by two axes, in which axis one explains 99.7% of the differences while axis 2 explains only 0.19%. Most of the traits were grouped between quadrate I and IV, while feed efficiency traits except for FCR, dominated quadrate III. Finally, traits of body weight and dressing were found isolated from the other similar traits in quadrate II, forming a singleton trait that is to be tested alone for correlation to the amplified molecular bands.

3.2. Genotyping by RAPD fingerprinting

Five RAPD molecular markers scored 30 amplified bands for the 12 individuals. In which the amplified bands were proved to be sufficient to measure efficiently the genetic diversity through multi-locus analysis, where the maximum genetic diversity of 1.00 was reached by the current amplified bands. The percentage of polymorphic bands ranged between 13.33% and 40% with a mean of 25.83%. The number of alleles ranged between 0.83 and 1.17 with a mean of 0.96. The number of effective alleles ranged between 1.11 and 1.32 with a mean of 1.21. Shannon's information index ranged between 0.08 and 0.25 with a mean of 0.16. Genetic diversity ranged between 0.06 and 0.18 with a mean of 0.12. Constantly the minimum values were scored to the genotype nanaFf while the maximum values were scored to the genotype Nanaff. In commercial chicken genotypes, genetic diversity is commonly low, thus the selection of RAPD markers was ideal to ensure a level of efficiency enough for estimating variability and diversity levels as well as constructing phylogenic relationship trees among different chicken breeds. However, it could not rely on RAPD markers when used for distinguishing breeds by identifying specific bands, hence, the amplified bands are not universal for each breed and primer (Helal and Ahmed 2018).

Principal coordinate analysis based on principal component analysis of the molecular data of the 12 individuals grouped in four genotypes reflected similar results to that of the morphological values (Fig. 7).

In which genotypes nanaFf genetically are more like genotype nanaff. For NanaFf individuals, they form a group away from the other genotype. Genotype Nanaff mostly forms a separate group; however, one individual is more like nanaFf and nanaff group. Consequently, it would explain the high genetic variability parameters in which this genotype scored (Table 3).

3.3. Mantel test and correlation analysis

Mantel test between the previously determined set and singletons with the genetic distance matrix based on the four genotypes group, scored the highest significant correlation value (r-value -0.774 with p-value 0.03) for the body weight trait. While the other tested traits were insignificantly correlated or scored zero values, which means that the actual molecular differences are due to the body weight differences between the tested individuals rather than any other trait. This confirmationthe fact revealed that the genetic component of the naked neck genotypes is negatively correlated with body weight. The negative sign has no biological meaning; as such correlation is an empirical estimate for the differences between the four genotypes at growth rates to the differences between the fingerprinting patterns. Mantel test (Mantel, 1967) allows linear or monotonic comparisons between the elements of two distance matrices. The Mantel test detects the correlation between the variations measured by the molecular markers to the different morphological traits measured for each genotype. It has been used to determine whether local populations that are geographically close are either genetically or phylogenetically similar (Legendre or Fortin, 2010).

4. CONCLUSIONS

In conclusion, we demonstrated that Na-allele is effective in improving body weight, dressing % at slaughtering age and egg production traits in laying hens. We also evidenced that PCA analysis data reflected

similar results to that of the morphological values to four genetic groups. In which genotypes nanaFf genetically are more similar to genotype nanaff. For NanaFf individuals, they form a group away from the other genotype. Genotype Nanaff mostly forms a separate group revealed that the genetic component of the naked neck genotypes is negatively correlated with body weight. Our work provides fundamental evidence for breeders and researchers to genetic improving programs depend on each productive and genetic analysis.

Authors' contributions

M.Y. Mahrous, M. Magdy & A.M. Abdelmoniem contributed to experimental design, interpreted the results, prepared figures, analyzed data and wrote the manuscript; M.Y. Mahrous & A.M. Abdelmoniem performed experiments and collected samples; M. Magdy & A.M. Abdelmoniem analyzed the data; M.Y. Mahrous & M. Magdy participated in experimental design and interpreted the results; A. Galal contributed to methodology & Investigation; M.M. Fathi contributed to review & editing. All authors reviewed results and approved the final manuscript.

Ethics Statements

The Experimental Procedures were approved by the Ethical Animal Care and Use Research Ethics Committee of Ain Shams University's Ethics Code "approval No. 5-2023-13".

Abbreviations

Nanaff = Heterozygous Naked neck Genotype
NanaFf=Heterozygous Naked neck-Frizzle Genotype
nanaFf =Heterozygous Frizzle Genotype
nanaff = Normal feathering Genotype
RAPD= Random Amplified Polymorphic DNA
PCA = Principal Component Analysis

Table (1): Means of meat production traits in various genetic groups of chicken males.

Traits	Genotype				SEM	Prob.
	nanaff	**nanaFf**	**Nanaff**	**NanaFf**		
Growth traits:						
Body weight 16 wk. (g.)	1297.86^{b}	1315.42^{b}	1389.19^{ab}	1410.21^{a}	90.12	0.05
Body weight gain (8-12 wk.)	457.82^{c}	498.75^{b}	598.65^{a}	512.22^{ab}	50.12	0.05
Feed consumption (8-12 wk.)	1810.55^{c}	1945.35^{b}	2215.42^{a}	1912.51^{b}	115.22	0.05
Feed conversion ratio (8-12 wk.)	3.95^{b}	3.90^{b}	3.70^{a}	3.73^{a}	0.14	0.05
Carcass characteristics:						
Dressing (%)	65.89^{b}	68.35^{a}	69.02^{a}	69.36^{a}	1.36	0.01
Breast muscle (%)	10.01^{c}	10.23^{ab}	11.14^{b}	12.02^{a}	1.01	0.001
Abdominal fat (%)	0.91^{a}	0.82^{a}	0.48^{b}	0.41^{b}	0.02	0.05
Heart (%)	0.55	0.56	0.56	0.55	0.02	NS
Liver (%)	1.85	1.93	1.89	1.91	0.14	NS
Gizzard (%)	1.81	1.96	1.92	2.01	0.10	NS
Giblets (%)	4.21	4.45	4.37	4.47	0.12	NS
Edible parts (%)	70.10^{c}	72.8^{b}	73.39^{a}	73.83^{a}	1.86	0.05
Inedible parts (%)	29.90^{a}	27.20^{ab}	26.61^{b}	26.17^{b}	2.01	0.05

a, b, and c Means within the same row with different letters are significantly differed, NS = non-significant

Table (2): Means of egg production traits in various genetic groups of chicken females.

Traits	Genotype				SEM	Prob.
	nanaff	**nanaFf**	**Nanaff**	**NanaFf**		
Egg production traits:						
Egg weight, g	40.73^{b}	41.92^{b}	44.70^{a}	45.23^{a}	1.04	0.05
Egg number	61.82^{c}	63.75^{b}	69.86^{a}	$67.22a^{b}$	3.12	0.05
Egg mass, g	2517.93^{c}	2672.45^{b}	3122.74^{a}	3040.36^{b}	145.22	0.05

a, b and c Means within the same row with different letters significantly differ, NS = non-significant

Table (3): Samples Size (N), Percentage of polymorphic bands (%P), Number of Alleles (Na), Number of Effective Alleles (Ne), Shannon's Information Index (I) and Genetic diversity (h), are shown for the four studied genotypes. The highest values are written in bold.

Genotype	N	%P	Na	Ne	I	h
nanaff	3	20.-00%	0.83± 0.14	1.16± 0.06	0.13± 0.05	0.09± 0.03
Nanaff	**3**	**40.00%**	**1.17± 0.14**	**1.32± 0.07**	**0.25± 0.06**	**0.18± 0.04**
nanaFf	3	13.33%	0.83± 0.12	1.11± 0.05	0.08± 0.04	0.06± 0.03
NanaFf	3	30.00%	1.00± 0.14	1.24± 0.07	0.19± 0.05	0.13± 0.04
Total Mean	12	25.83%	0.96± 0.07	1.21± 0.03	0.16± 0.03	0.12± 0.02

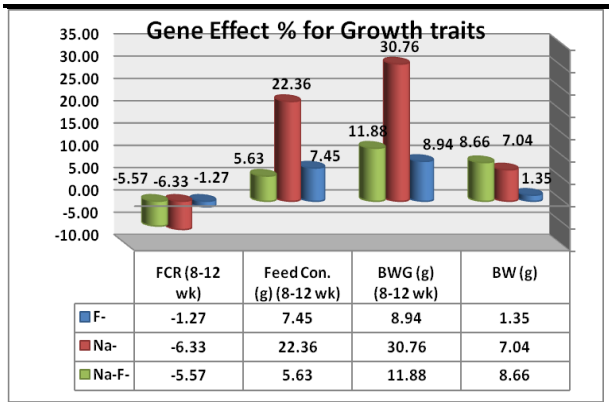

Fig (1) Gene effect of growth performance traits in various genetic groups of chickens

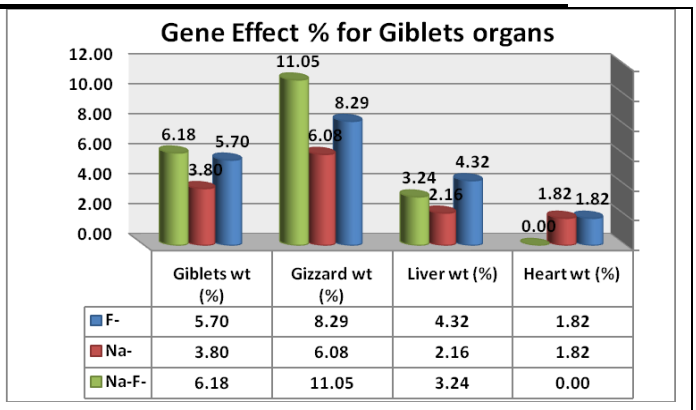

Fig (2) Gene effect of giblet organs in various genetic groups of chickens

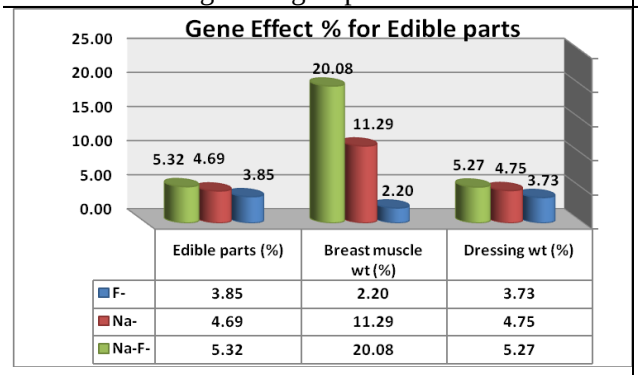

Fig (3) Gene effect of edible carcass traits in various genetic groups of chickens

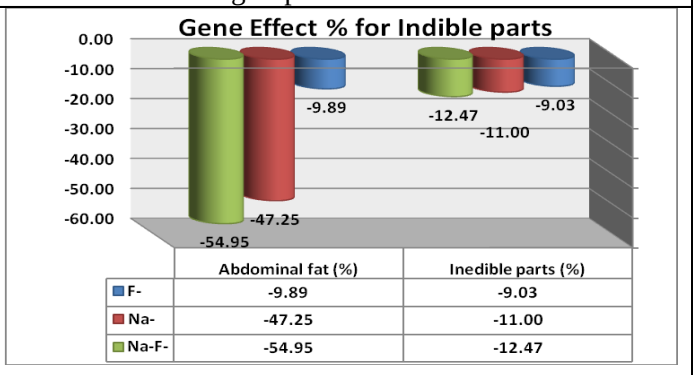

Fig (4) Gene effect of inedible carcass traits in various genetic groups of chickens

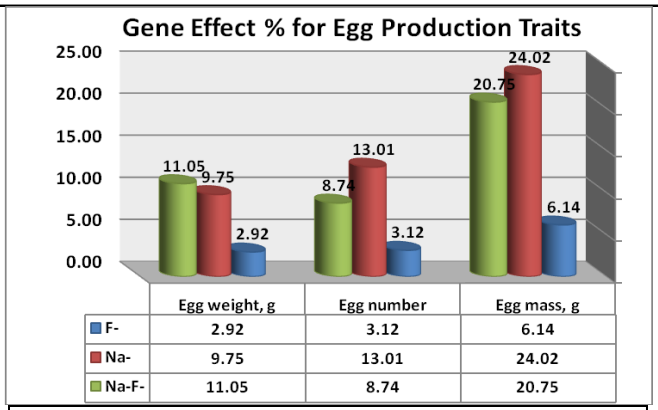

Fig (5) Gene effect of egg production traits in various genetic groups of chickens

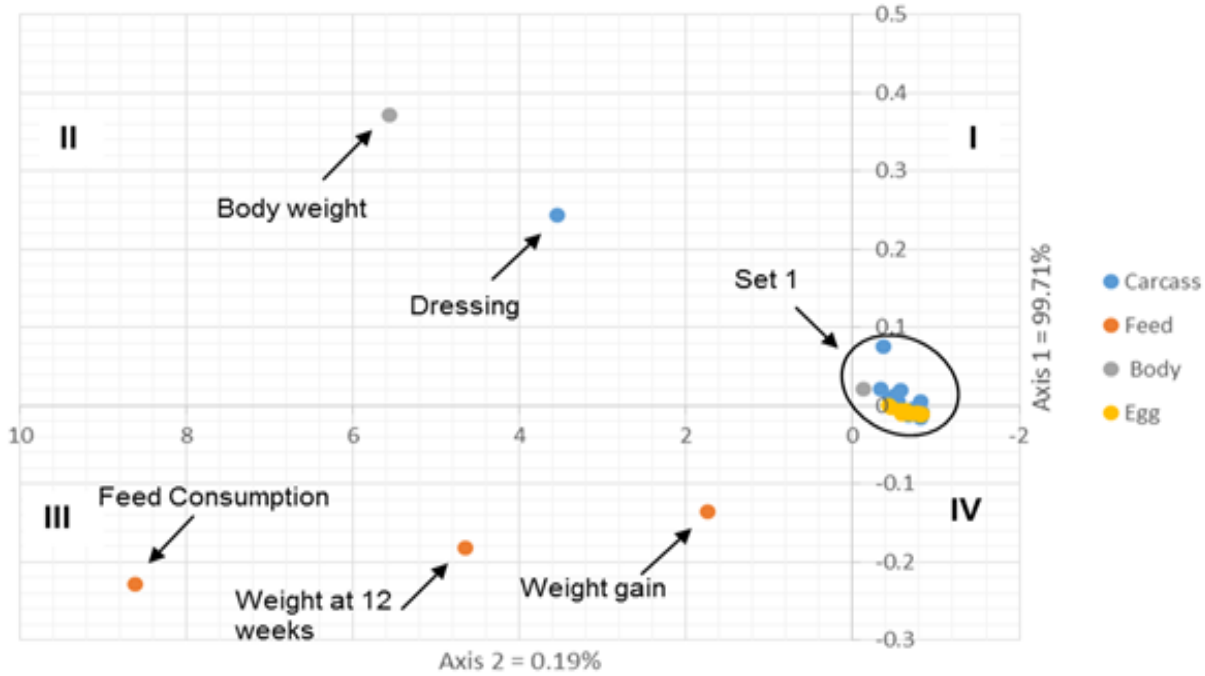

Fig (6): Graphical plot of PCA test of the measured traits of four categories: Carcass yield (Blue), Feed efficiency (Orange), Body weight (Gray) and Egg production (Yellow). The differences between measured traits were explained by two axes (1=99.71% and 2=0.19%)

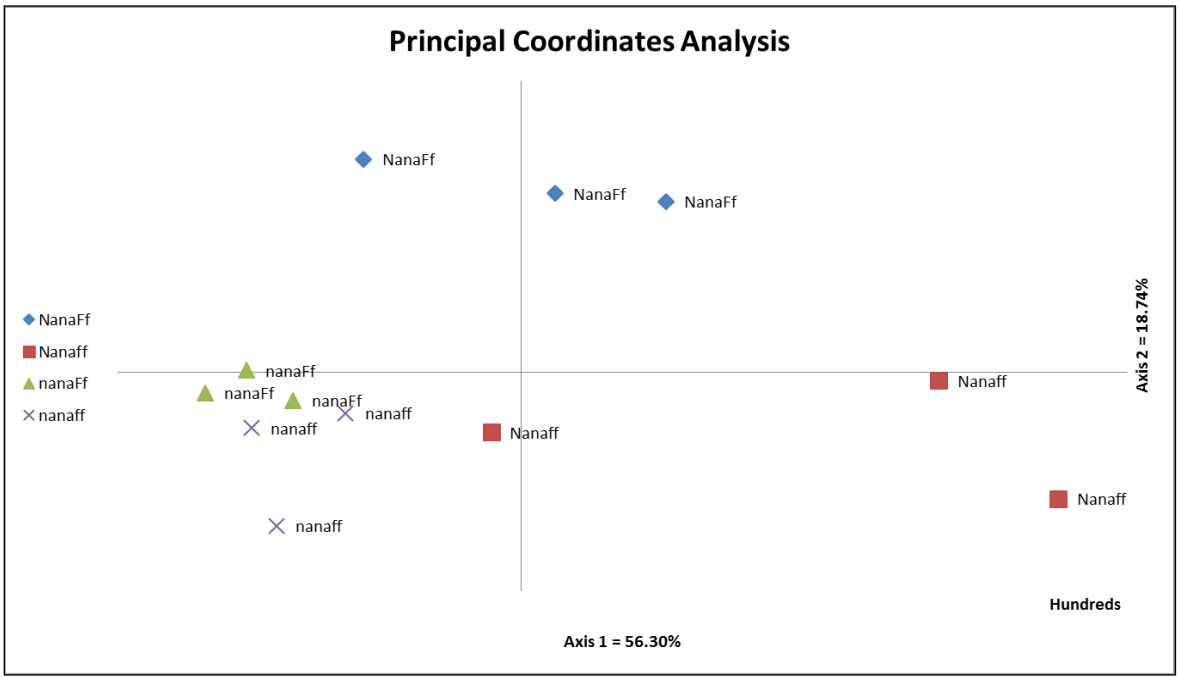

Fig (7): Principal coordinate analysis (PCoA) of the 12 individuals grouped in four genotypes NanaFf (Blue), Nanaff (Red), nanaff (Green) and nanaff (Violet)

REFERENCES

Adedeji, T.A., O.A. Adebambo, S.O. Peters, L.O. Ojedapo and A.O. Ige 2006. Growth performance of crossbred and purebred chickens resulting from different Sire strain in a humid tropical environment. J. Anim. Vet. Adv. 5:674–678.
URL: https://medwelljournals.com/abstract/?doi=javaa.2006.674.678

Adomako, K., O.S. Olympio, J.K. Hagan and J.A. Hamidu 2014. Growth performance of crossbred naked neck and normal feathered laying hens kept in tropical villages. Br. Poult. Sci. 55:701–708. doi: 10.1080/00071668.2014.960805.

Agapow, P.M. and A. Burt 2001. Indices of multilocus linkage disequilibrium. Molecular Ecology Notes 1: 101-102. doi.org/10.1046/j.1471 8278.2000.00014.x

Ajayi, F. O. 2010. Nigerian indigenous chicken: a valuable genetic resource for meat and egg production. Asian J. Poult. Sci. 4:164–172. DOI: 10.3923/ajpsaj.2010.164.172

Alam, M., N. Chand, S. Khan and S. M. Suhail 2021. Growth performance, proximate composition and immune competence of naked neck, Rhode Island Red and their F1 crossbred chickens in a tropical climate. J. Anim. Health Prod. 9:303–311. DOI: doi.org/10.17582/journal.jahp/2021/9.3.303.311

Anderson, M.J. 2003. PCO: A Fortran Computer Program for Principal Coordinate Analysis., Distributed by the Author. University of Auckland, New Zealand.

Bohonak, A.J. 2002. IBD (Isolation by Distance): a program for analyses of isolation by distance. J. Heredity, 93: 153–154. doi.org/10.1093/jhered/93.2.153

Das, A.K., S. Kumar, A. Rahim, L.S. Kokatate and A.K. Mishra 2014. Assessment of body conformation, feed efficiency and morphological characteristics in Rhode Island Redwhite strain chicken. Indian J. Anim. Sci. 84:984–991. researchgate.net/publication/280774042

Decuypere, E., Buyse, J., Mérat, P., Zoons, J. and Vloeberghs, I. 1993. Growth, abdominal fat content, heat production and plasma hormone levels of naked-neck and control broiler chickens. Animal Production, 57: 483-490**.**

Deeb, N. and Cahaner, A. 1994. Genotype-environment interaction and heat tolerance of naked neck broilers. P. 65-68: Proc. of the 5th World Congress on Genetics Applied to Livestock Production. V. 20 Guelph, on, Canada.

Dehghanzadeh, H., S.Z. Mirhoseini, M.N. Romanov and A. Ghorbani 2009. Evaluation of genetic variability and distances among five iranian native chicken populations using RAPD markers. Pak. J. Biol. Sci., 12: 866-871. doi: 10.3923/pjbs.2009.866.871.

Desta, T.T. 2021. The genetic basis and robustness of naked neck mutation in chicken. Trop. Anim. Health Prod., 53, p. 95. doi.org/10.1007/s11250-020-02505-1

Deza, M.M. and E. Deza 2009. Encyclopedia of Distances. Springer, New York. Ed.1, Pg.XIV, 590, ISBN:978-3-642-00234-2, doi.org/10.1007/978-3-642-00234-2

Dong, J., C. He, Z. Wang, Y. Li, S. Li, L. Tao, J. Chen, D. Li, F. Yang, N. Li, Q. Zhang, L. Zhang, G. Wang, F. Akinyemi, H. Meng, and B. Du. 2018. A novel deletion in KRT75L4 mediates the frizzle trait in a Chinese indigenous chicken. Genet. Sel. Evol. 50:68. doi.org/10.1186/s12711-018-0441-7

Duah, K.K., Essuman E.K., Boadu V.G., Olympio O.S., Akwetey W. 2020. Comparative study of indigenous chickens on the basis of their health and performance. Poult Sci. 99:2286–92. doi: 10.1016/j.psj.2019.11.049

Fathi, M.M., A. Galal, S. El-Safty and M. Mahrous 2013. Naked neck and frizzle genes for improving chickens raised under high ambient temperature: I. Growth performance and egg production. Worlds Poult. Sci. J. 69:813–832. DOI: 10.1017/S0043933913000834

Fathi, M.M., Ahmed Galal, Lamiaa M. Radwan, Osama K. Abou-Emera, Ibrahim H. Al-Homidan 2022. Using major genes to mitigate the deleterious effects of heat stress in poultry: an updated review. Poultry Science, Volume 101, Issue 11,102157, ISSN 0032-5791, doi.org/10.1016/j.psj.2022.102157

Fathi, M.M., El-Attar, A.H., Ali, U.M. and Nazmi, A. 2008. Effect of naked neck gene on carcase composition and immunocompetence in chicken. British Poultry Science 49 (2): 103-110.

Fulton, Janet. 2008. Molecular genetics in a modern poultry breeding organization. Worlds Poult. Sc. J. - World Poultry Sci J. 64. 10.1017/S0043933907001778

Galal.A., L.M. Radwan, H.H. Rezik, H. A youb 2019. Expression levels of HSP70 and CPT-1 in three local breeds of chickens reared under normal or heat stress conditions after the introduction of the naked neck gene. J. Therm. Biol., 80, pp. 113-118, doi.org/10.1016/j.jtherbio.2018.12.018

Galal, A. 2008. Immunocompetence and some hematological parameters of naked neck and normally feathered chicken. Journal of Poultry Science. 45:89-95.

Galal, A.A., M.H. Ahmed, U.M. Ali and H.H. Younis. 2007. Influence of Naked Neck gene on laying performance and some haematological parameters of dwarfing hens. Int. J. Poult. Sci. 6:807–813. DOI: 10.3923/ijps.2007.807.813

Groenen, M.A., P. Wahlberg, M. Foglio, H.H. Cheng, H.J. Megens, R.P. Crooijmans, F. Besnier, M. Lathrop, W.M. Muir, G.K. Wong, I. Gut and L. Andersson 2009.A high-density SNP-based linkage map of the chicken genome reveals sequence features correlated with recombination rate. Genome Res 19: 510 - 519. doi: 10.1101/gr.086538.108.

Gunn, H.H. 2008. Effect of frizzling and naked neck gene on growth, haematology, carcass traits and organ weights of the Nigerian local chicken (Doctoral dissertation, Ph. D. Thesis, Department of Animal Breeding and Genetics, University of Agriculture, Abeokuta).

Helal, M. and A.S. Ahmed 2018. Molecular Comparison of Egyptian and Saudi Local Chickens using RAPD Markers. Int J Anim Sci; 2 (5): 1029. ISSN: 2575-7806

Khantaprab, S. and P. Tarachai 1998. Comparison of growth and weights of muscle, viscera, bone and fat in three breeds of meat duck. Pages 329-375 in Research Report 1997-98. Pages 329-375 in Research Report 1997-98. Office Agri Res and Ext, Maejo Univ, Chiang Mai, Thailand.

Legendre, P. and M.J. Fortin 2010. Comparison of the Mantel test and alternative approaches for detecting complex multivariate relationships in the spatial analysis of genetic data. Molec Ecol Resour, 10: 831-844. doi.org/10.1111/j.1755-0998.2010.02866.x

Lin, H., C. Jiao, J. Buyse and E. Decuypere 2006. Strategies for preventing heat stress in poultry. Worlds Poult. Sci. J. 62:71–86. doi: 10.1079/WPS20058

Mantel, N. 1967. The detection of disease clustering and a generalized regression approach. Cancer Res, 27: 209-220. PMID: 6018555.

Mollah, M.B.R., M.S. Alam, F.B. Islam and M.A. Ali 2005. Effectiveness of RAPD marker in generating polymorphism in different chicken population. Biotechnology, 4: 73-75. DOI: 10.3923/biotech.2005.73.75

Njenga, S.K. 2005. Productivity and socio-cultural aspects of local poultry phenotypes in coastal Kenya. Doctoral

diss. Royal Veterinary and Agricultural University, Network for Smallholder Poultry Development.

Nweke-Okorocha, Obiageri Genevieve, agaviezor, Brilliant Ogagaoghene, aro, Samuel Olanrewaju and Chineke, Clifford Adinma 2022. Laying Performance and Egg Quality Traits of Naked neck, Noiler, Frizzle and Normal Feathered Chickens in South-South, Nigeria. Quest Journals, J. of Research in Agric. and Animal Science, V.9 (3) pp:23-27. ISSN: 2321-9459

Oleforuh-Okoleh, V.U., O.C. Emeka, E.U. Obianwuna and B.S. Nnam 2021. Strain variations in some reproductive and production traits of purebred normal feather and naked neck FUNAAB Alpha chicken. Nig. J. Anim. Prod., 48(1): 12 - 23. doi.org/10.51791/njap.v48i1.2899

Patra, B.N., R.K.S. Bais, R.B. Prasad and B.P. Singh 2002. Performance of Naked Neck versus Normally Feathered Coloured Broilers for Growth, Carcass Traits and Blood Biochemical Parameters in Tropical Climate. Asian-Aust. J. Anim. Sci. Vol. 15, No. 12: 1776-1783. DOI:10.5713/ajas.2002.1776

Peakall, R. and P.E. Smouse 2012. GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research-an update. Bioinformatics 28(19), 2537-2539. doi: 10.1093/bioinformatics/bts460

SAS Institute 2002. SAS/STAT User's Guide v.9.0 ed.:Statistics. SAS Institute Inc., Cary, NC

Sharifi, A.R., P. Horst and H. Simianer 2010. The effect of naked neck gene and ambient temperature and their interaction on reproductive traits of heavy broiler dams. Poultry Science, 89 :1360–1371.

Sharma, D., K.B.C Appa Rao, R.V. Singh and S.M. Totey 2001. Genetic diversity among chicken breeds estimated through randomly amplified polymorphic DNA. Anim. Biotechnol. Vol; 12: 111-120. doi: 10.1081/ABIO-100108337.

Zerjal, T., D. Gourichon, B. Rivet and A. Bordas 2013. Performance comparison of laying hens segregating for the frizzle gene under thermoneutral and high ambient temperatures. Poult. Sci. 92(6):1474-1485. doi.org/10.3382/ps.2012-02840

Zhang, J.Q., S.M. Geng, Z.J. Sun, X.F. Zhang, Y.L. Gu and L.J. Zhang 2002. Analysis on RAPD markers of two chicken populations. Proc. of 8th National Symposium on Animal Genetic Markers, 8(1):209-212, Yangling, China.

Genetic Diversity; Naked neck; Frizzle; RAPD; PCA

الملخص العربى

الصفات الانتاجية والاختلافات الوراثية في الدجاج الحامل لجينات عري الرقبة وتجعد الريش في درجة الحرارة المحيطة المرتفعة

عبدالمنعم محمد عبدالمنعم حنفي1*، محمود يوسف محروس[1]، معتز محمد فتحي[1,4]، أحمد جلال السيد[1]، محمود مجدي عبدالله[2,3]

[1] قسم إنتاج الدواجن، كلية الزراعة، جامعة عين شمس، القاهرة، مصر

[2] قسم الوراثة، كلية الزراعة، جامعة عين شمس، القاهرة، مصر

[3] قسم بيولوجيا النبات، كلية علم البيولوجي، جامعة ميوركا، إسبانيا

[4] قسم إنتاج وتربية الحيوان، كلية الزراعة والطب البيطري، جامعة القصيم، القصيم، المملكة العربية السعودية

هدف الدراسة هو قياس مدي التنوع الوراثي لعدد أربعة تراكيب وراثية من الدجاج المحلي "عاري الرقبة Nanaff، مجعد الريش nanaFf، عاري الرقبة مجعد الريش NanaFf وطبيعي التريش nanaff" والمربي تحت الظروف البيئية المصرية وذلك اعتماداً على القياسات المورفولوجية والمرقمات الجزيئية. تم تربية إجمالي عدد 500 طائر في تلك الدراسة، وقياس الصفات الإنتاجية للتراكيب الوراثية الأربعة. تم استخدام تقنية RAPD الوراثية لقياس مدى التنوع الوراثي بين التراكيب الأربعة بواسطة عدد أربع مرقمات جزيئية. أظهر الدجاج الحامل للتراكيب الوراثية "عري الرقبة – وعري الرقبة مع تجعد الريش" وزن جسم ووزن جسم مكتسب أعلي معنوياً عن بقية التراكيب. سجل التركيب الحامل لكلا الجينين NanaFf أفضل صفات ذبيحة مقارنة ببقية التراكيب الوراثية. كمل سجل نفس التركيب مع التركيب عاري الرقبة Nanaff زيادة معنوية عن بقية التراكيب في صفة وزن البيض. تراوحت النسبة المئوية للاختلاف الشكلي في التتابعات الوراثية ما بين 13.33% الي 40% بمتوسط بلغ 25.83%. في حين تراوح معدل التنوع الوراثي ما بين 0.06 الي 0.18 بمتوسط بلغ 0.12. عند دراسة مدي التنوع الوراثي بين المجاميع الوراثية سجل الدجاج مجعد الريش القيم الصغرى لدليل شانون، في حين سجل الدجاج عاري الرقبة القيم العظمي. مضمون هذه الدراسة يتلخص في أن تركيب عري الرقبة مؤثر في عمليات تحسين صفات انتاج اللحم والبيض ويليه تركيب تجعد الريش عن الدجاج طبيعي التريش. وأشارت تلك الدراسة الي التقارب في القيم المورفولوجية للمجاميع الوراثية الأربعة للصفات المختلفة.

الكلمات الدالة: التنوع الوراثي، عاري الرقبة، مجعد، RAPD، PCA.