*Kirkuk University Journal for Agricultural Sciences*
**ISSN:2958-6585**
https://kujas.uokirkuk.edu.iq

***RESEARCH ARTICLE***

https://doi.org. 10.58928/ku24.15413

# Detection of MC4R Gene (c.944 C>T) and its Relationship with productive Performance and Carcass traits in Ross 308.

**Alaa M. Mohammad-Ameen[1]** **Eman H. ALanbari[1]**
*Dept. Anim. Prod., Coll. of Agric. Engin. Sci., University of Baghdad, IRAQ.*
*Corresponding Author: aalaa.faeq2201m@coagri.uobaghdad.edu.iq.

**Received: 01/07/2024** **Revised: 04/08/2024** **Accepted: 02/09/2024** **Published: 01/12/2024**

## ABSTRACT

The objective of this study was to detect the effects of genotypes of MC4R gene in broiler chicken Ross 308. And its relationship with growth and carcass traits. studying the genetic polymorphism of this gene and determining its genotypic to find the relationship between this gene and economic traits in broilers. Weekly measurements were taken (body weight, weight gain, body length, breast circumference, breast depth, leg length, drumstick length and drumstick circumference). Blood samples were collected from 100 bird (21 days old age), and at 42-day carcass measurements were taken for each bird individually, then process of extracting DNA from blood samples was performed and primer for MC4R gene – foreword and revers were used and PCR technic was used to amplified DNA copies in order to determining the locations of quantitative traits and determine the single nucleotide polymorphisms (SNP) sequencing of nitrogenous bases. The results show that Genetic variant within MC4R gene were screened through DNA sequencing methods. Molecular Detection showed a SNP at position (c.944C>T), and detected two alleles and three genotypes (CC,CT,TT). A highly significant differences for CC and TT genotype in body weight at 5th and 6th wk, and in weight gain at 6th wk, and in breast circumference at 3rd wk, and in drumstick weight, and was produced significantly in breast depth trait at initial, 2nd and 6th wk, and in leg length at 6th wk, and in carcass weight, back weight, abdominal fat.

***Keywords*:** MC4R Gene, Ross 308, SNP, Growth traits, carcass traits , mutation.



## INTRODUCTION

Recently, poultry selection plans have relied on quantitative traits, which aim to enhance growth and carcass traits, in response to recent population density challenges [1, 2, 3], and growth is one of the complex traits that is influenced by a large number of genes and pathways [4, 5, 6], as it was found that there are more than 1,500 quantitative trait sites associated with growth traits in poultry [7]. Genetic improvement programs have achieved great progress in past years in order to improve growth traits, Many of these genes are associated with production traits, and some of them are considered candidate genes for this, and by conducting research on mutations in useful genes (candidate genes) and their relationship to economic traits to determine the genetic basis of production traits and to develop SNP molecular genetics tests (nucleic acid tests) [8]. As a method of selection in breeding and genetic improvement projects [9, 10]. many phenotypic polymorphisms were associated with body weight, and candidate genes such as PIT1 gene [11], growth hormone GH [12, 13], INSg [14] and insulin-like growth factor hormone IGF-2 [15].

The melanocortin 4 receptor gene (MC4R) gene is considered as a one of the main candidate genes that effect on productivity traits, especially weight gains [16], as the function of this gene has been linked to the regulation of feeding behavior and energy hemostasis balance in poultry [17]. Mutations in this gene have also been associated with appetite, obesity, and growth in humans, pigs, and rodents [18, 19, 20]. Therefore, In view of these effects, understanding the important roles played by the MC4R gene in regulating energy use and its impact on nutrition and raising economic species is very important in the poultry and animal industry [21].

Due to MC4R gene functions on body weight dynamics and growth parameters, we were inspired by this study to find out the effect of SNPs for this gene in productive and carcass traits in Ross 308 broilers.

**Material and Methods:**

This study was carried out from (27/9/2023-8/11/2023) at the Poultry farm /Department of Animal Production /College of Agricultural Engineering Sciences, University of Baghdad. to study the genetic polymorphism of (MC4R) gene witch is related to the growth characteristics, determine its genotypes, allelic frequency, and acquaintance the relationship of these genotypes with some economic traits and carcass traits, as well as finding the correlation between them in Ross 308 broilers. 100 chicks aged one-day old were reared randomly, numbered individually using metal numbers (installed in the wing) and they were placed in a deep litter in closed system for six weeks, food and water were given according to the production guide

for broilers [22]. The initial and weekly measurements were measured as follows: Body Weight, weight gain, body length, sternum length, Breast depth, Breast circumference, leg length, drumstick length and thigh circumference to find out the relation between these traits and the genotypes for MC4R gene, at the age of 42 day, the birds were slaughtered after measurements were taken for the 6th week, after slaughtering, the carcass weight, breast, drumstick, neck, back, wings, liver, heart, gizzard and abdominal fat were taken. A blood samples (3 ml) was collected into vacuum tubes containing EDTA k3 and stored at (20C°), until used for molecular analysis later. Molecular tests were carried out, starting with DNA extraction (Biolabs nebs monarch kits) and migration to ensure the purity and concentration of the DNA samples using Qubit 4 and it record 17-25 ng/µL, the primers were designed and prepared (from macrogene humanizing genomics – Accession numder AY 545056) for MC4R gene as follows:

F: TCAGAGGAATGCAAAAAGGAC - R: GCTGTATGCTGAATACACAGTA.

The primers were prepared to work according to the supplied company's instructions, in a volume of 300 µl and a concentration of 100 pmol, the stock solution was diluted by adding 10 µl of solution. Stoke into 90 µl of enzyme-free water to obtain the working solution. Amplification of promoter MC4R gene the primer used for the amplification of a fragment of MC4R gene (1150bp). Twenty-five microliters of PCR amplification reaction contained 12.5 µl from One Taq (NEB®) mastermix, 3 µl of DNA sample, 1.5µl of 10 pmol/µl from each primer and 6.5 µl of free-nuclease water. Performing the PCR reaction to amplify the target piece under study as the following, 1 min 94 C̊ for the first cycle, 3 min extension at 72 C̊ finale extension 72 C̊ for last 5 min, the samples are loaded by adding 5 µl of PCR product in wells and electrophoresis 4 microliters of DNA Ladder, the lid is placed and an electric current of 80 volts/1hr. To study the product sequencing to determine the genetic structure of the gene more than 20µl PCR product from each sample have been send to macrogen Korea for sequencing by Sanger method to identify the single nucleotide polymorphism. Analysis of sequence FASTA files have been done by Geneious Prime software and aligned to Ref Seq of (MC4R) gene. Data were analyzed with the statistical analysis system SAS [23] program to study the influence of Characterization according to the significant comparative between the means in the Duncan polynomial test [24]. The genotype distribution was analyzed according to the Hardy Weinberg equilibrium (HWE) rule and using the chi-square test ($\chi 2$). and association analyzes between MC4R-SNP genotypes.

**Results And Discussion:**

Fig. 1. showed the electrophoresis PCR technique for samples DNA ladder have been loaded into the wells of agar gel, and it produce one loci with product size of the MC4R gene (1050 bp).

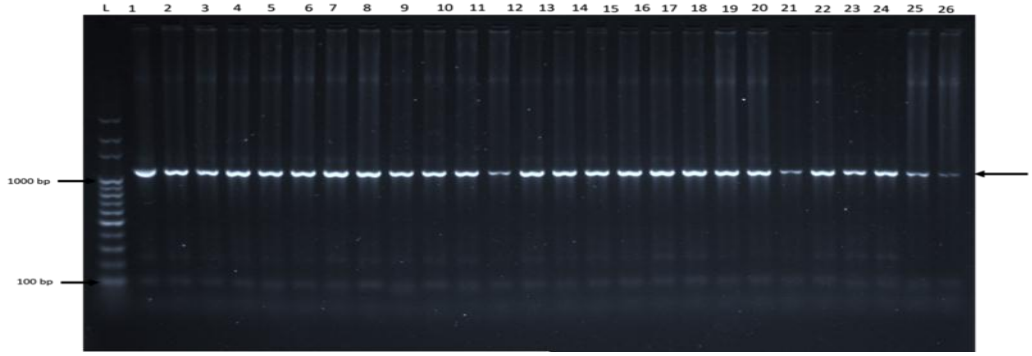


Figure 1. Electrophoresis result of the MC4R gene (size 1050bp), ladder size (2000)pb on the gel at a concentration of 2% the voltage of power supply at 80V for 80 mins.

To Determine the polymorphisms and genotypes for MC4R gene, Figure 2. the nucleotide sequence for analyzing DNA samples by using the Sequence sequencing program. The nitrogenous bases sequence was known, and showed one SNP variation. As for the variation SNP at location (944), result indicates that there were three genotypes, and classified on the basis of them into the homozygous genotype, which represents the wild type CC, followed by individuals carrying the hybrid genotype, CT, and then individuals carrying the mixed genotype, TT, which represents the mutant genotype

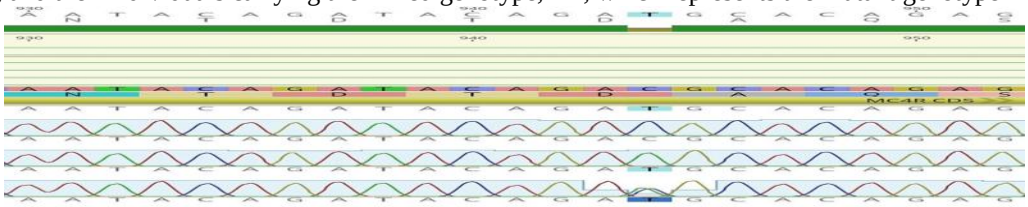

Figure 2. Shows single nucleotide polymorphisms SNP (c.944C>T) for the MC4R gene.

Table.1 shows the genotypes and allele frequencies of MC4R, the percentage of the genotypes record a highly significant ($p \leq 0.01$) in distribution of genotypes CC, CT and TT (18.19, 38.30, 43.61). also there were highly significant ($p \leq 0.01$) in allele frequencies for C and T and they were 0.37 and 0.63, respectively.

Table 1.The number and percentage of MC4R/SNP:C>T genotypes in the blood samples studied

| Genotype | No. of hens | Genotypic percentage | Allele | Allele Frequency |
|---|---|---|---|---|
| CC | 17 | 18.19 | C | 0.37 |
| CT | 36 | 38.30 | T | 0.63 |
| TT | 41 | 43.61 | - | ** |
| Total | 94 | % 100 | - | |
| $\chi^2$ | | 17.404** | | |
| P-value | (P≤0.01) | | | |

** Indicates the presence of significant differences between the genotypes at a significant level (P≤0.01).

The effect of the genotypes of SNP in the MC4R gene on the body weight trait in Ross 308 broilers were pointed in Table 2. there were no significant differences between the genotypes in the initial body weight and the 1st, 2nd,3rd and 4th weeks. In contrast, highly significant differences (p≤0.01) were recorded between the genotypes, as CC and TT Statistically superior than CT in the 5th week with 2152.57, 2111.36 and 1851.13 g. Same with 6th week, which means 3040.33, 2831.74 and 2575.79 g.

It is clear that there is a relationship and association between the genotype for MC4R gene and body weight, and this is consistent with [25] also deal [21] and agree with [16] in their study on analyze the association between genetic diversity of the MC4R gene receptor and productive performance in turkeys. They found a highly significant effect (P≤0.01) between genotypes and live body weight.

Table 2. The relationship of genetic polymorphism of the MC4R gene (SNP) (c.944C>T) on the initial and weekly body weight in hybrid broilers Ross 308.

| Genotypes | Weight gain (g.) | | | | | | |
|---|---|---|---|---|---|---|---|
| | 1 wk | 2 wk | 3 wk | 4 wk | 5 wk | 6 wk | Total |
| CC | 146.81± 4.43 | 289.37± 9.88 | 483.37± 35.63 | 415.62± 46.21 | 698.28± 50.07 | 889.00± 109.21 | 2996.33± 144.22 a |
| CT | 150.11± 3.29 | 273.85± 5.43 | 456.90± 10.10 | 410.71± 17.50 | 557.66± 53.29 | 656.41± 53.67 | 2533.13± 63.99 b |
| TT | 152.19± 4.05 | 271.09± 7.217 | 479.88± 9.69 | 442.64± 18.26 | 607.50± 61.90 | 898.77± 72.21 | 2787.61± 60.47 a |
| p-value | N.S | N.S | N.S | N.S | N.S | N.S | ** |

Values with different letters contents indicate significant differences. ** Indicates the presence of significant differences between the genotypes at a significant level (P≤0.01)

To study the effect of genotypes of SNP for MC4R gene on weekly and total weight gain. There are no significant differences between the genotypes in weekly weight gain. In contrast, highly significant differences were found (p≤0.01) for CC and TT genotype outperformed the genotype CT in total weight gain, with means 2996.33, 2787.61 and 2533.13 g. respectively. Table 3. This result agrees with many researchers who shows the relationship between genotypes in this gene and with weight gain, and this agrees with [26] and [27] in their study on other animals.

| Genotypes | Body weight (g.) | | | | | | |
|---|---|---|---|---|---|---|---|
| | 0 wk | 1 wk | 2 wk | 3 wk | 4 wk | 5 wk | 6 wk |
| CC | 45.50± 1.27 | ± 192.31 4.23 | ± 481.68 12.12 | 979.00± 41.28 | 1397.75± 44.44 | 2152.57± a114.26 | 3040.33± a144.36 |
| CT | ± 43.37 0.73 | 193.48± 3.69 | ± 467.34 7.83 | 923.85± 19.82 | 1312.66± 22.69 | 1851.13± b55.72 | 2575.79± b64.18 |
| TT | 44.22 ± 0.63 | 196.41± 4.38 | 467.51± 9.11 | 963.92 ± 19.10 | 1381.61± 24.71 | 2111.36± a83.29 | 2831.74± a61.01 |
| p-value | N.S | N.S | N.S | N.S | N.S | ** | ** |

Values with different letters contents indicate significant differences. ** Indicates the presence of significant differences between the genotypes at a significant level (P≤0.01).

Table 4. To explain the effect of the CC, CT, and TT genotypes of MC4R gene on weekly and total weight gain. it seems

there is no significant differences between the genotypes in weekly weight gain,
hile a highly significant differences were found (p≤0.01) in the CC and TT genotype who were superiority than CT genotype in the total weight gain.

| Genotypes | Body Length (Cm) | | | | | | |
|---|---|---|---|---|---|---|---|
| | 0 wk | 1 wk | 2 wk | 3 wk | 4 wk | 5 wk | 6 wk |
| CC | 22.37± 0.23 | 27.60± 0.40 | 33.93± 0.35 | 41.00± 1.21 | 46.37± 0.45 | 53.58± 0.45 | 57.71± 1.75 |
| CT | 22.02± 0.16 | 27.11± 0.24 | 34.55± 0.18 | 42.00± 0.40 | 46.05 ± 0.27 | 52.82± 0.50 | 57.34± 0.71 |
| TT | 22.07± 0.16 | 27.58± 0.27 | 33.96± 0.26 | 42.25± 0.37 | 45.56± 0.32 | 52.90 ± 0.348 | 78.62± 19.72 |
| p-value | N.S | N.S | N.S | N.S | N.S | N.S | N.S |

Table 4. The relationship of genetic polymorphism of the MC4R gene (SNP) (c.944C>T) on the initial and weekly body length in the hybrid broilers Ross 308.

N.S means no significant.

About the effect of the MC4R gene on the characteristic of breast circumference in Ross 308 broilers is Table 5. Shows that there were highly significantly (P≤0.01) in the TT and CT genotypes than CC genotype in the 3rd wk., with means 24.66, 24.19 and 22.41 cm., respectively. while there was no significant difference between the genotypes in initial and 1st, 2nd, 4th, 5th and 6th wk. [28] pointed on the positive relationship between carcass characteristics and Breast circumference, and the possibility of using breast circumference as an indirect criterion for carcass characteristics in broilers.

Table 5. The relationship of genetic polymorphism of the MC4R gene (SNP) (c.944C>T) on the initial and weekly breast circumference in the hybrid broilers Ross 308.

Values with different letters contents indicate significant differences. ** Indicates the presence of significant differences between the genotypes at a significant level (P≤0.01).

| Genotypes | breast circumference (cm) | | | | | | |
|---|---|---|---|---|---|---|---|
| | 0 wk | 1 wk | 2 wk | 3 wk | 4 wk | 5 wk | 6 wk |
| CC | 10.31± 0.253 | 14.00± 0.707 | 18.33± 0.232 | 22.41± b 2.026 | ±27.90 0.418 | 34.35± 0.496 | 41.40± 1.029 |
| CT | 10.34± 0.135 | 13.14± 0.296 | 18.28± 0.153 | 24.19± a0.272 | 27.80± 0.241 | 33.75± 0.394 | 39.74± 0.388 |
| TT | 10.28± 0.103 | 13.30± 0.232 | 18.35± 0.179 | 24.66± a0.286 | 28.09± 0.227 | 34.00± 0.387 | 40.46± 0.521 |
| p-value | N.S | N.S | N.S | ** | N.S | N.S | N.S |

Table 6. about the effect of genotypes for SNP of MC4R gene on the trait of breast depth in Ross 308 broilers, there are significant differences (p≤0.05) in the CT than CC genotype in the initial breast depth with means 3.45 and 3.16 cm., for 2nd wk CT genotype was superior than CC genotype with means 8.47 and 8.06 cm., the CC genotype outperformed the CT genotype at the 6th wk with 18.40 and 17.04 cm. respectively. There were no significant differences between the genotypes in the1st, 3rd , 4th and 5th wk.

Table 6. The relationship of genetic polymorphism of the MC4R gene (SNP) (c.944C>T) on the initial and weekly breast depth in the hybrid broilers Ross 308.

Values with different letter contents indicate significant differences. * Indicates the presence of significant differences between the genotypes at a significant level (P≤0.05).

| Genotypes | Leg length (cm) | | | | | | |
|---|---|---|---|---|---|---|---|
| | 0 wk | 1 wk | 2 wk | 3 wk | 4 wk | 5 wk | 6 wk |
| CC | 12.09 ± 0.15 | 13.75± 0.47 | 19.73± 0.28 | 24.33± 0.42 | 27.31± 0.29 | 29.25± 0.47 | 36.00± a1.64 |
| CT | 11.88 ± 0.19 | 13.03± 0.27 | 19.72± 0.20 | 23.68± 0.19 | 26.85± 0.18 | 28.04± 0.34 | 33.64± b0.34 |
| TT | 11.68± 0.15 | 13.36± 0.29 | 19.56± 0.22 | 24.27± 0.22 | 26.87± 0.21 | 29.00± 0.55 | 34.16± b0.40 |
| p-value | N.S | N.S | N.S | N.S | N.S | N.S | * |
| Genotypes | breast depth (cm) | | | | | | |
| | 0 wk | 1 wk | 2 wk | 3 wk | 4 wk | 5 wk | 6 wk |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| CC | 3.16± 0.10b | 6.70± 0.20 | 8.06± b0.18 | 10.64± 0.21 | 11.37± 0.18 | 17.08± 0.52 | 18.40± a0.24 |
| CT | 3.54± 0.10a | 6.28± 0.12 | 8.47± a0.10 | 10.87± 0.17 | 11.47± 0.12 | 16.73± 0.44 | 17.04± b0.17 |
| TT | 3.36± 0.09 ab | 6.45± 0.19 | 8.41± ab0.11 | 10.93± 0.13 | 11.68± 0.12 | 17.52± 0.42 | ±17.73 ab0.33 |
| p-value | * | N.S | * | N.S | N.S | N.S | * |

And For the leg length table 7. explain that there is no significant differences between the genotypes CC, CT, and TT in the average initial and weekly leg length, except the 6th wk, as it was found thatthere were significant difference (P≤0.05) in the CC than CT and TT genotypes in the 6th wk, and this was similar to [29] who found in their study of the phenotypic polymorphism relationship. MC4R gene is associated with body composition traits in chickens.

Table7. The relationship of genetic polymorphism of the MC4R gene (SNP) (c.944C>T) on the initial and weekly leg length in the hybrid broilers Ross 308.

Values with different letters contents indicate significant differences. * Indicates the presence of significant differences between the genotypes at a significant level (P≤0.05).

Table 8. shows that there were no significant differences between the genotypes CC, CT, and TT, for MC4R gene on Drumstick length during all different weeks.

Table8. The relationship of genetic polymorphism of the MC4R gene (SNP) (c.944C>T) on the initial and weekly drumstick length in the hybrid broilers Ross 308.

N.S means no significant.

Also there were no significant differences between the genotypes in the average initial and weekly drumstick circumferences Table 9.

Table 9. The relationship of genetic polymorphism of the MC4R gene (SNP) (c.944C>T) on the initial and weekly drumstick circumference in the hybrid broilers Ross 308.

N.S means no significant.

| Genotypes | Drumstick circumference (cm) | | | | | | |
|---|---|---|---|---|---|---|---|
| | 0 wk | 1 wk | 2 wk | 3 wk | 4 wk | 5 wk | 6 wk |
| CC | 4.187 ± 0.12 | 5.33 ± 0.33 | 8.00 ± 0.16 | 9.66 ± 0.49 | 11.56± 0.34 | 14.37± 0.53 | 16.80± 0.80 |
| CT | 4.17 ± 0.07 | 5.03± 0.14 | 8.04 ± 0.09 | 9.72± 0.13 | 11.44± 0.14 | 13.65± 0.24 | 16.52± 0.25 |
| TT | 4.24 ± 0.08 | 5.35 ± 0.18 | 8.17± 0.13 | 9.90 ± 0.15 | 11.31± 0.14 | 14.31± 0.16 | 16.82± 0.20 |
| p-value | N.S | N.S | N.S | N.S | N.S | N.S | N.S |

Table 10. Due to the effect of the CC, CT, and TT genotypes on the SNP variation of the MC4R gene on carcass traits, there was a significant superiority (p≤0.05) between the genotypes in the average carcass weight as the CC genotype was superior than CT genotype with means 2269.40 and 1970.81 g. for CC and CT respectively, The CC genotype was superior than CT in the back weight trait with means 376.20 and 325.14 g., and abdominal fat trait was also significant for CC genotype compared with CT and TT genotypes, with 35.00, 32.52 and 32.00 g. respectively, there were no significant differences between CC and CT with the TT genotype. High Significant differences were found (p≤0.01) in the drumstick weight for CC genotype than CT genotype with means 628.20 and 524.09 g. for CC and CT. At the same time, it was observed that there were no significant differences between the genotypes in the breast weight, neck, wings, liver, heart, gizzard weights.

This has been confirmed by several studies of the gene's relationship with cleaned carcass weight, thigh weight, and abdominal fat in several breeds of chicken [30, 31]. also [32] indicated that some of polymorphism for MC4R gene may be associated with body weight, feed conversion efficiency and weight gain in the chickens. and these also agrees with [27].

| genotypes | Drumstick length (cm) | | | | | | |
|---|---|---|---|---|---|---|---|
| | 0 wk | 1 wk | 2 wk | 3 wk | 4 wk | 5 wk | 6 wk |
| CC | 6.18 ± 0.359 | 7.64± 0.496 | 10.20± 0.326 | 12.91± 0.416 | 15.31± 0.284 | 15.37± 0.263 | 20.80± 1.11 |
| CT | 5.90 ± 0.198 | 7.08± 0.243 | 10.33 ± 0.178 | 12.25 ± 0.182 | 15.17± 0.194 | 15.21± 0.292 | 19.17± 0.34 |
| TT | 5.90 ± 0.17 | 6.94 ± 0.23 | 10.35± 0.21 | 12.68± 0.21 | 15.73± 0.18 | 16.00 ± 0.38 | 19.30 ± 0.40 |
| p-value | N.S | N.S | N.S | N.S | N.S | N.S | N.S |

Table 10. The relationship of the genetic manifestations of the MC4R gene (SNP) (c.944C>T) on the average of the carcass traits in the hybrid broilers Ross 308.

Values with different letter contents indicate significant differences. ** Indicates the presence of significant differences between the genotypes at a significant level (P≤0.01).

* Indicates the presence of significant differences between the genotypes at a significant level (P≤0.05)

| Traits | Genotypes | | | P-Value |
|---|---|---|---|---|
| | TT | CT | CC | |
| Carcass weight | 2137.61± 53.74ab | 1970.81± 48.28 b | 2269.40± 87.99 a | * |
| breast weight | 883.56± 43.12 | 816.66 ± 22.98 | 929.4 ± 46.89 | N.S |
| Drumstick weight | 573.34 ± 14.17ab | 524.09 ± 14.95 b | 628.20± 25.24 a | ** |
| Back weight | 358.30 ± 9.96 ab | 325.14 ± 8.12 b | 376.20 ± 12.17 a | * |
| Neck weight | 131.65 ± 3.04 | 121.71 ± 3.45 | 129.60 ± 5.98 | N.S |
| Weight of wings | 208.73 ± 6.38 | 190.71 ± 4.71 | 213.80 ± 4.83 | N.S |
| Liver weight | 55.65 ± 2.21 | 50.90 ± 2.11 | 51.80 ± 2.88 | N.S |
| Heart weight | 14.69 ± 0.62 | 12.71 ± 0.58 | 15.00 ± 0.70 | N.S |
| Gizzard weight | 38.47 ± 1.17 | 36.14 ± 0.92 | 37.40 ± 1.53 | N.S |
| abdominal fat weight | 35.00 ± 1.41 | 32.52 ± 1.95 | 32.00 ± 3.34 | * |

**Conclusion:**

A significant association of MC4R (SNP) (c.944C>T) polymorphism and production traits in hybrid broiler Ross 308 was observed. The results shows that MC4R gene for (SNP) (c.944C>T) is useful as a candidate gene for chicken selection for body weight, weight gain, breast depth, leg length, and for carcass weight, Drumstick weight, Back weight and abdominal fat weight. It showed that genotype CC and TT genotype for MC4R gene were useful for selecting excellent individuals as an assisted to breeding program selection to some productive performance and carcass traits in hybrid broiler Ross 308.

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# الكشف عن جين MC4R (c.944 C>T) وعلاقته مع الأداء الانتاجي وصفات الذبيحة في روز 308

**الاء محمد فائق  محمد امين الخالدي  ايمان حسن الانباري**

*قسم الإنتاج الحيواني, كلية العلوم للهندسة الزراعية , جامعة بغداد , العراق.*

الخلاصة

هدفت هذه الدراسة إلى الكشف عن تأثير التراكيب الوراثية لجين ***MC4R***في دجاج اللحم ***Ross 308***، وعلاقته مع صفات النمو وصفات الذبيحة. دراسة التشكل الوراثي للجين وتحديد التراكيب الوراثية لإيجاد العلاقة بين هذا الجين والصفات الاقتصادية في فروج اللحم. وتم أخذ القياسات الأسبوعية (وزن الجسم، الزيادة الوزنية، طول الجسم، محيط الصدر، عمق الصدر، طول الرجل، طول الفخذ و محيط الفخذ). تم جمع عينات الدم من 100 طير (بعمر 21 يوم)، وتم أخذ قياسات الذبيحة في يوم 42 لكل طير على حدة، إجريَ عملية استخلاص الحمض النووي من عينات الدم واستخدم بادئات امامية وخلفية للجين ***MC4R*** واستخدم تقانة تفاعل الكوثرة المتسلسل لتضخيم و نسخ الحمض النووي لغرض تحديد مواقع الصفات الكمية وتحديد أشكال النوكليوتيدات الفردية ***(SNP)***وتسلسل القواعد النيتروجينية، أظهرت النتائج أنه تم فحص التغايرات الجينية داخل جين ***MC4R*** من خلال طرق تسلسل الحمض النووي. أظهرت نتائج الكشف الجزيئي عن تغاير في موقع ***(c.944C>T)***، والكشف عن وجود اليلين وثلاثة تراكيب وراثية ***(CC,CT,TT)***، أظهرت النتائج وجود فروق عالي المعنوية للتراكيب الوراثية ***CC***و ***TT*** في وزن الجسم للاسبوع الخامس والسادس، وفي الزيادة الوزنية للاسبوع السادس، و محيط الصدر للاسبوع الثالث، و وزن الفخذ، وأنتج فروقاً معنوياً في صفة عمق الصدر الابتدائي ولاسبوع الثاني و السادس، و طول الرجل للاسبوع السادس، وزن الذبيحة، و وزن الظهر و دهن البطن.

الكلمات المفتاحية: جين ***MC4R***، روز 308، ***SNP***، صفات النمو، صفات الذبيحة، الطفرة.