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POLYMORPHISMS OF PIT 1 GENE IN BROILER ROSS 308 HYBRID AND ITS ASSOCIATION ON SOME PRODUCTIVE PERFORMANCES AND BODY SCALES

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Abstract

Pituitary-specific trans**cri**ption factor (PIT 1) expressed in anterior part of pituitary gland regulates muscle growth, growth hormone GH, prolactin PRL and third stimulating hormone β submit (*TSH-β*) genes and regarded as key of candidate gene for productive traits in chicken. This study aims to detect the polymorphisms of PIT1 gene in ROSS308 hybrid broiler. PCR –RFLP and Taq restriction enzyme used to study association of polymorphisms of PIT1 gene with chicken performances and productive traits on weekly body weight and scales with weight gain and live body weight at 35 day, carcasses cuts relative weight, in addition to effect on both sexes were measured too. Result indicate significant effect for both genotype of PIT1 gene on many traits and sexes in population study, that make it easy to be used in selection programs at early chick hatch days to insure the perfect genotype at market weight with lowest cost and highest benefits and many profits.

***Keywords*:** PIT-1gene, Ross308, Polymorphisms, PCR-RFLP, weekly body measurements.

Introduction

Ross 308 is the commercial world's number one broiler breed offers benefits for breeders to use genetic parameters beside productive performance to achieve good body composition and consistent performance with short rearing period. Barton 1994 maintained using classic breeding and genetic selection programs can increase productive traits like body weight, growth rate and feed efficiency, but as a consequence with intensive breeding, many problems related to health arise like obesity, leg problems, immuno suppression and sudden death syndrome (Kadiec *et al*., 2011). Body composition as quantitative traits affected by many genes, and to improve poultry performance depending on genomic selection to evaluate DNA polymorphisms (Burt, 2002 and Tanaka *et al*., 1995). There are enormous amount of genomic information resources available recently for chicken genome (Burt, 2005), by using Polymerase Chain Reaction (PCR) technique and with the advantage of improving molecular biology, genetic markers, single nucleotide polymorphisms (SNP) and sequencing entire genome in order to be used with selection programs between and within commercial breeds to create highly economic traits (Emara & Kim, 2003). Many polygene controlled growth and other important treats in chicken as somatotropic axis genes that consists of the essential components as growth hormone (GH), prolactin (PRL) and insulin-like growth factors (IGF-1,11) act as carrier of proteins and receptors for (GH), INS, leptin and thyroid stimulating hormones β (TSH-β) (Zhao *et al*., 2004). To regulate these hormones, differentiation of anterior pituitary gland plays crucial roles by one of candidate gene, the pituitary–specific transcription factor (PIT1) gene (Cohen *et al*., 1996). Many reports mentioned that PIT1 involved in regulating development of pituitary gland (Li *et al*., 1990), proliferation of pituitary cell (Castrillo *et al*., 1991), synthesis of GH depended on this gene (Harvey 2000). The Pit1 gene is classified as auto-regulated in expression (Sornson *et al*., 1996) and its mRNA is present in any cell types of pituitary, while in 1990 Simmons *et al.* reported that pit1 protein mainly expressed in lactotrophs, somatotrophis and in thyrotrophs which secures PRL., GH and the TSH-β. The PIT-1 mentioned in different species as mammalian in human, cattle, pig, mice, turkey and chicken (Yu *et al*., 1995; Chen, *et al*., 1997; Kurima *et al*., 1998). There are three isoforms of PIT1, PIT1β^{*} and PIT1$_{\emptyset}^{*}$ with 335, 363 and 327 amino acids respectively induced by alternative splicing (Morris *et al*., 1992). In chicken Pit-1 gene located on chromosome1, consists of 7 exon with 2,400-bp discrete region and twenty three SNPs, (Van *et al*., 2000). Genetic effect of these SNPS on production performance or immune competence is unclear (Nie *et al*., 2005), Nie *et al*., 2008 regarded PIT 1 gene as a key for candidate gene for productive traits in chicken. That is why the main goal for this study aims to detect (SNP) of PIT1 gene with PCR-RFLP to evaluate the association between genotype of PIT1 gene SNPs with body scales, growth, relative weight for cuts and body composition traits in order to be used in early selection programs too.

Materials and Methods

This study was conducted at the poultry farms of animal production Department, College of Agriculture\ University of Baghdad. A total of 100 one day old chick Ross 303 placed in a deep litter with crushed straw in a closed system for five weeks, marked individually with wing ringed markers. Food and water were available free along the experimental period. Birds were vaccinated against New Castel and Gumboro diseases. The experimental diets formulated forisocaloric and isonitrogenic according to NRC (1994), starter diet was 22, 67% crude protein and 2936.3 (Kcal/Kg), while the grower diet was 19% crude protein and 3156 (Kcal/Kg). One day old body weight (OdBW), one day old body length (OdBL), one day old breast circle (OdBC), One day old keel length (OdKL), One day old Thy circle (OdTC) and One day old Shank length (OdSL) were recorded. And Weekly morphological measurements took place too, including Weekly Body Weight (WBW), Weekly Body Length (WBL), Weekly Breast Circle (WBC), Weekly Keel Length (WKL), Weekly Thy Circle (WTC) and (WSL) for Weekly Shank Length. At the end of experiment (5^{th} week) chickens were slaughtered and carcasses eviscerate and dissected. Carcass Weight (CW) recorded, cuts Relative Weights for Breast (BRW), Thy (TRW), Wings (WRW), Back (BRW), Neck (NRW), Heart (HRW), Liver (LRW) and Abdominal Fat Relative Weight (AFRW), including sexes.

At 4^{th} week, blood samples for all birds were collected individually in EDTA-treated tubes. Genomic DNA was isolated from whole blood according to the protocol of Wizard Genomic DNA purification Kit, promega. The accession number for intron 5 with variation of base C / T for PIT 1 gene in chicken as released by NCBI was R_s 13905611, and The polymerase chain reaction assay condition was carried out in a total volume of 25 µL mixture containing 2 ng/µl of chicken genomic DNA, 12.5 of Master Mix, 1µM for each of forward and reverse primer, 8.5 as nuclease free water. The PCR program of PIT 1 gene was with specific Primer design as follow, PIT1-int5-F (5′-CACCTCAACACTCTCATAGTAAA-3′) and the int5-R (5′-GAGTAGAGGAGGCAGGAAA-3′). PCR was run in a Master cycler gradient with the following procedure: The initial Denaturation 5 m, 95 ºC for 1 cycle, Denaturation was at 95 ºC, 30s and for Annealing at 60 ºC for 30s, Extension was 72 ºC for 45s and all these steps were with 30 cycle and the final extension was of 7min at 72 ºC then, holding with 10 ºC for 10 min for one cycle. For DNA loading, 2 µL of loading dye were added to each 5 µL of DNA samples and 10 µL of PCR product. Electrical power was turned on at 100 $_V$ for1 hour and 1 µL of Ethidium Bromide was added to the agarose gel and visualized by using Gel imaging system. Single nucleotide polymorphism for PIT1 gene and allele, genotype frequencies and Hardy-Weinberg equilibrium were estimated by using SAS (2006).

Result and Discussion

Quantus Florometer used to detect the concentration of extracted DNA to detect the goodness of samples for downstream applications, figure1.

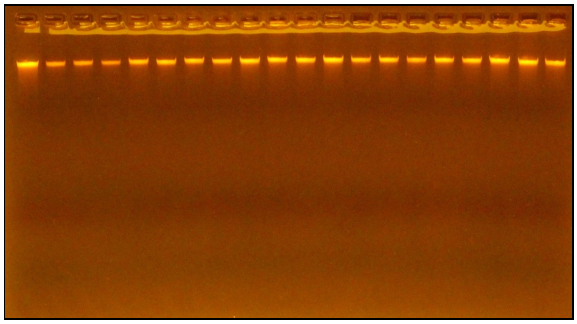

Fig. 1 : Samples of DNA extracted of Ross308 blood.

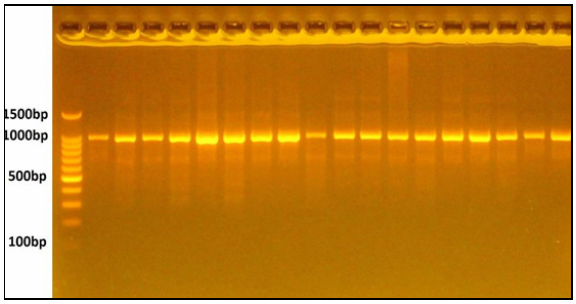

Fig. 2 : The PCR product of PIT1g with 965bp and ladder of 100-1500 bp in Ross308.

PCR-RFLP with Taq restricting enzyme was able to produce two loci and fragments with different band size 965bp, 741bp and 224bp figure 3.

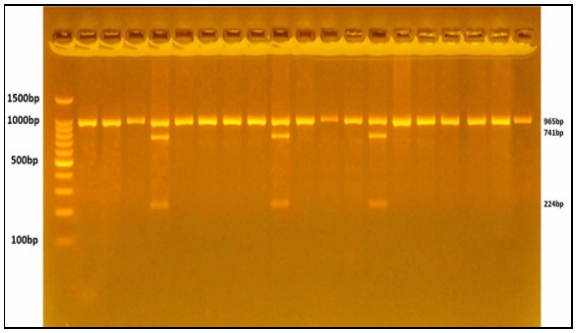

Fig. 3 : PCR-RFLP with Taq digestive enzyme and ladder of 100-1500bp.

The first loci MR1with 965bpwhile the second MR1-MR2 with length of 741bp, 224bp. Result indicates that there are only two genotype forTIP1 gene in Ross308 breed theMR1 which seemed as one bond of identical allele that was the homozygous the Wild, the second was MR1-MR2 the heterozygous while the MR2 was with null band. Table 1shows the genotype frequencies for PIT1gene in Ross308. High frequency P>0.01 between both genotypes with 83%, 17%as a co-dominance for MRI compared with MRI-MR2 genotype respectively.

Table 1 : Genotype frequency for PIT1 gene in broiler Ross 308

% percentage	Number	Genotype
83.00	83	MR1
17.00	17	MR1-MR2
0.00	----------	MR2
100%	100	Total
13.84**	----	X^2

Table 2 : Allele frequency for PIT1g in broiler Ross308 hybrid

Frequency	Allele
0.915	MR1
0.085	MR1

To study association of SNPs for PIT1 gene on productive traits, Table 3 shows the means of One day old body weight and body scales for each genotype, it seems there is no significant difference for OdBW, OdBL, OdBC, OdKL and OdSL, but for one day old thy cercal OdTC there is a significant effect p>0.05 between both genotype with 3.235cm for MR1 MR2 and 3.065cm for MR1. And for the association of PIT1 gene with sexes, there isn't significant different between sexes on all studied productive traits of Ross 308 atone day old body weight or scales. It can be because chicks are all of the same breed and that is why there is no difference between male or female too.

Table 3 : Means for one day old body weights and measurements ±SE. for PIT1g genotype and sexes of Ross3008.

OdSL cm.	OdTC cm.	OdKL cm.	OdBC cm.	OdBL cm.	OdBW g.	Traits
7.108 ±0.067	B 3.065 ±0.031	2.594 ±0.055	8.064 ±0.055	19.49 ±0.101	40.931± 0.091	MR1 No.83
7.164 ±0.163	A 3.235 ±0.106	2.600 ±0.207	8.117 ± 0.207	19.885 ± 0.240	41.021± 0.139	MR1-MR2 No.17
NS	*	NS	NS	NS	NS	Seg.
						Sex
7.040 ±0.090	3.140±0.053	2.582 ±0.072	8.144 ±0.098	19.55 ±0.136	35.810 ±0.310	Mel No.45
7.181 ±0.079	3.056±0.037	2.530 ±0.070	8.018 ±0.095	19.558 ±0.30	34.900±0.190	Female No.55
NS	NS	NS	NS	NS	NS	Seg.

Privations: One day old Body Weight (OdBW g), One day Body Length (OdB cm.), One day Breast Circle (OdBC cm.), One day old Keel Length (OdKL cm.), One day old Thy Circle (OdTC cm.), One day Shank Length (OdSL cm.), * significant P<0.05, not significant NS.

To study body weight and scales for Ross 308 differ in genotype for PIT1 gene at first week, Table 4 shows there were no significant effect between both genotypes for PIT1 gene in Ross308 on traits of W_1BW, W_1BL, W_1BC, W_1KL and W_1TC, but significant effect P>0.05 was on W_1SL traits only with highly means of 8.497 cm for MR1 genotype while was 8.194 cm for MR1-MR2 genotype. And there were also no significant different between sexes for all studded traits also.

Table 4: Means at First week of Body weight and measurement ± SE. for Pit1g genotype and sexes of Ross 308.

W_1SL cm.	W_1TC cm.	W_1KL cm.	W_1BC cm.	W_1BLcm.	W_1BW g.	Traits
8.497 ±0.056	A 4.171 ±0.042	3.434 ± 0.052	9.246 ± 0.086	23.114 ± 0.123	144.311 ±1.553	MR1 No.83
8.194 ±0.118	B 4.258 ±0.099	3.547 ± 0.114	9.235 ± 0.219	23.411 ± 0.172	148.117 ±3.363	MR1-MR2 No.17
*	NS	NS	NS	NS	NS	Seg.
						Sex
8.424 ±0.082	4.242 ±0.061	3.497 ± 0.071	9.344 ±0.118	23.222 ±0.148	144.311±2.160	Male No.45
8.463 ±0.067	4.140 ±0.063	3.418 ±0.063	9.163 ±0.109	23.118 ±0.150	145.490 ±1.874	Female No.55
NS	NS	NS	NS	NS	NS	Seg.

Privation: Week$_1$Body weight (W_1BW_g), Week$_1$ Body length ($W_1BL_{cm.}$), Week$_1$Breast cercal ($W_1BC_{cm.}$), Week$_1$Keel length ($W_1KL_{cm.}$),Week$_1$Thy cercal ($W_1TC_{cm.}$), Week$_1$ Shank length ($W_1SL_{cm.}$), NS not significant.

For the second week body weight and scale Table 5, It seems that there were a significant effect P>0.05 for body length W_2 BL of MR1 genotype at this second week of age compared with MR1-MR2 genotypes that were 30.590 cm for the first one and 29.558 cm for the second one, and beside these there area significant effect P>0.05 for W_2 BC treat between genotype also with means of 18.147 cm for heterogenic MR1-MR2 genotype and 17.698 cm for the wild MR1 one and different significantly between genotype on W_2TC treat with means of 8.601 cm as high on MR1 and 8.252 cm for MR1-MR2. Both sexes are affected significantly P>0.05 at this chick age on treat for body length W_2BL, male was of 30.900 cm while was 30.018 cm for female. There were no relation between all other treats W_2BW, W_2KL cm and W_2SL with PIT1 genotypes, and no relation seems between W_2BW, W_2BC, W_2KL, W_2SC and W_2SL treats as sexes different.

Table 5: Means for Second week of Body weight and measurement ± SE.for Pit1 gene and sexes of Ross 308.

W_2SL cm.	W_2TC cm.	W_2KL cm.	W_2BC cm.	W_2BL cm.	W_2BW g.	Traits
14.410±0.121	A 8.601±0.061	7.477±0.67	B 17.698±0.079	A 30.590 ±0.183	374.680±4.054	MR1 No.83
14.235±0.356	B 8.252±0.186	7.552±0.191	A 18.147±0.200	B 29.558±0.419	372.058±7.851	MR1-MR2 No.17
NS	*	NS	*	*	NS	Seg.
14.426±0.167	8.566±0.098	7.375±0.103	17.688±0.118	30.900±0.223	376.977±5.428	Sex Mel No.45
14.343±0.163	8.521±0.076	7.583±0.079	17.842±0.098	30.018±0.242	372.00±4.846	Female No.55
NS	NS	NS	NS	*	NS	Seg

Privation: Week$_2$Body weight (W_2BW g), Week$_2$ Body length (W_2BL cm), Week$_2$Breast circle (W_2BC cm), Week$_2$ Keel length (W_2KL cm), Week$_2$ Thy cercal (W_2TC cm), Week$_2$ Shank length (W_2SL cm), * Significant P<0.05, NS not significant.

And the relation of genotype for PIT1 gene on broiler hybrid Ross 308 at 3rdweek of age, Table 6 explain that there is not any significant difference between all studied traits W_3BW, W_3BL, W_3BC, W_3KL, W_3TC and W_3SL as genotypes different at this stage of chicken age. And about relation of sexes at this age with treats under study, there are significant effect P>0.05 between each treats of W_3BW, W_3KL andW_3TCwith means of 904.755g, 12.482 cm and 12.226 cm respectively, but was insignificantly with other treats W_3BL, W_3BC and W_3SL as sex differ.

Table 6: Means for third week of Body weight and scales ± SE. for Pit1 gene and sexes of Ross 308.

W_3SL cm.	W_3TC cm.	W_3KL cm.	W_3BC cm.	W_3BL cm.	W_3BW g.	Traits
21.710±0.135	11.906±0.166	12.243±0.118	25.457±0.146	40.568±0.189	863.710±12.661	MR1 No.83
21.470±0.322	12.00±0.121	12.217±0.233	25.470±0.258	40.176±0.530	891.882±25.201	MR1-MR2 No.17
NS	NS	NS	NS	NS	NS	Seg.
21.822±0.186	A 12.266±0.226	A 12.482±0.129	25.422±0.209	40.582±0.278	A 904.755±17.960	Sex Male No.45
21.542±0.167	B 11.672±0.168	B 12.040±0.156	25.480±0.161	40.436±0.237	B 838.831±13.342	Female No.55
NS	*	*	NS	NS	*	Seg.

Privation: Week$_3$Body weight (W_3BW_g), Week$_3$ Body length (W_3BL_{cm}), Week$_3$Breast cercal (W_3BC_{cm}), Week$_3$ Keel length (W_3KL_{cm}), Week$_3$Thy cercal (W_3TC_{cm}), Week$_3$Shank length (W_3SL_{cm}),*Significant P<0.05,NS not significant.

And for the relation of genotypes for PIT1 gene on hybrid Ross308 with body weight and scales at 4th week broiler age table 7 explain that, Breast circle W_4BC it seems with significant P>0.05 effect on MRI genotype with 30.771 cm mean value compared with 29.764 cm for MR1-MR2 genotype respectively, and there is insignificant relation for PIT1 gene with remain treats as genotype differ. Male was effected significantly P>0.05 on Body weight at this chick age W_4BW with mean of 1372.29g compared with 1284.02g for female ,and the mean value for other studied treats W_4BL, W_4BC,W_4KL and at this age seems there is no effect on both sexes.

Table 7 : Means for forth week Body weight and scales ± SE. for Pit1 gene and sexes on Ross 308.

W_4SL cm.	W_4TC cm.	W_4KL cm.	W_4BC cm.	W_4BL cm.	W_4BW g.	Treats
27.781±0.098	15.057±0.077	15.077±0.091	A 30.771±0.146	45.543±0.144	1317.93±16.836	MR1 N0.83
27.882±0.282	15.058±0.200	15.205±0.223	B 29.764±0.407	45.529±0.253	1352.12±27.997	MR1-MR2 N0.17
NS	NS	NS	*	NS	NS	Seg.
27.733±0.143	15.084±0.113	15.171±0.130	30.511±0.259	45.800±0.214	A 1372.29±19.408	Sex Mel N0.45
27.854±0.125	15.030±0.093	15.040±0.109	30.672±0.155	45.781±0.155	B 1284.02±20.27	Female N0.55
NS	NS	NS	NS	NS	*	Seg.

Privation: $Week_4$Body weight (W_4BW g), $Week_4$Body length (W_4BL cm), $Week_4$Breast circle (W_4BC cm), $Week_4$Keel length (W_4KL cm), $Week_4$ Thy circle (W_4TC cm), $Week_4$Shank length (W_4SL cm), * Significant P<0.05, NS not significant.

Table 8about broiler Ross308 at age of 5th week, traits of body weight and scales that has been studied as genotype for PIT1 gene deferent, significant effect P>0.05 for W_5BL with mean of 52.823cm , 51.831cm for MR1-MR2 and MR1 respectively while other treats were not affected during this chick age, and there is a significant effect P>0.05 for male on body weight at this age on W_5BW to reach 2025.9g and 1867.6g for female while there were no significant differences between the rest treats as sexes different.

Table 8: Means for fifth Body weight and scales ± SE. for Pit1 gene and sexes on Ross 308.

$W_5SL_{cm.}$	$W_5TC_{cm.}$	W_5KL	W_5BCL	$W_5BL_{cm.}$	$W_5BW_{g.}$	Treats
29.52±0.26	17.156±0.124	16.704±0.059	36.496±0.235	B 51.831±0.196	1942.17±26.717	MR1 No.83
29.176±0.334	17.388±0.157	16.894±0.118	36.294 ±0.329	A 52.823±0.413	1923.12±56.526	MR1-MR2 No.17
NS	NS	NS	NS	*	NS	Seg.
86.488 ±0.195	29.43 ± 0.134	17.227 ±0.068	36.537 ±0.240	52.111 ± 0.256	A 2025.9 ±38.173	Sex Mel No.45
29.490 ±0.148	17.127 ±0.160	16.661 ±0.078	36.400 ±0.313	51.90 ±0.254	B 1867.0 ±27.37	Female No.55
NS	NS	NS	NS	NS	*	Seg.

Privation: $Week_5$Body weight (W_5BW_g), $Week_5$Body length (W_5BL_{cm}), $Week_5$Breast cercal (W_5BC_{cm}), $Week_5$Keel length (W_5KL_{cm}), $Week_5$Thy cercal (W_5TC_{cm}), $Week_5$Shank length (W_5SL_{cm}), * Significant P<0.05, NS not significant.

To study the relation between genotypes of PIT1 gene on means of weekly weights body gain on both genotypes and sexes for Ross308 Table 9 explain that, there is no significant effect between MR1, MR1-MR2 for PIT1 as weekly body weight gain differ with approximate values per week where it didn't reach the significant level and to study sexes differences relation with weekly body gain it seems that significant P<0.05 effect on 3rd week only for male with 527.778g and 466.836_g for female respectively.

Table 9: Weekly body gain for genotypes of PIT gene different with sexes of broiler Ross.

Seg.	Female	Male	MR1-MR2	MR1	$Weight_g$
NS\NS	87.254 ± 1.289	86.488 ±1.298	89.235 ±2.096	86.433 ±1.011	GAIN I First week
NS\NS	226.509 ±4.691 B	233.668±4.912 A	223.94 ±7.424	230.373 ±3.621	GAIN 2 Second week
*\NS	466.836 ±12.366	527.778 ±16.954	519.823 ±25.579	489.024 ±11.651	GAIN 3 Third week
NS\NS	445.181 ±20.661	467.533 ±18.655	460.235 ±32.577	454.216±15.712	GAIN 4 Fourth week
NS\NS	583.709 ±27.589	653.666 ±33.754	571.00 ±57.959	624.240 ±23.265	GAIN 5 Fifth week

Privation: insignificant NS, significant P<0.05 *.

There isn't significant effect between traits at fifth week for all of live body weight, carcass weight, dressing %, relative weight for cuts (Breast, Neck + Back, Thy, liver, wings, and abdominal fat) in both genotype. Table10

Table 10 : Means of live body weight and dressing percentage and relative weights of cuts as genotypes different for PIT1 gene in Ross 308 hybrid.

Seg.	MR1-MR2	MR1	Treat
NS	2085.00 ± 53.058	2059.38 ± 45.595	LBW g
NS	1546.50 ± 45.607	1500.29± 30.987	CWT g
NS	74,118 ± 0.770	73.105 ± 0.830	DR%
NS	38.694 ± 0.697	37.489 ± 0.369	Breast RW
NS	23.651 ± 0.834	23.82 ± 0.303	Back +Neck RW
NS	26.949 ± 0.632	27.300 ± 0.323	Thy RW
NS	3.360 ± 0.096	3.294 ± 0.111	Liver RW
NS	10.366 ± 0.174	10.758 ± 0.160	Wings RW
NS	1.854 ± 0.102	1.832 ± 0.076	Abdominal fat RW

Privations: Live body weight LBW, Carcass weight CWT, Dressing percent DR%, relative weight RW, Breast RW, Neck + Back RW, Thy RW, Liver RW, Wings RW, Abdominal fat RW, not significant NS.

Table 11: Means of living weight, carcass weight, Dressing % and Relative weight RW+_SE as sexes differ on broiler Ross 308.

Seg.	Female	Male	Traits
*	B 1976.21 ± 49.519	A 2164.09 ± 45.375	LBW g
*	B 1438.67 ± 31.364	A 1592.73 ± 34.671	CWT g
NS	73.175 ± 1.221	73.581 ± 0.277	DR%
NS	37.996 ± 0.399	37.592 ± 0.551	Breast RW
NS	23.756 ± 0.410	23.797 ± 0.470	Back +Neck RW
NS	26.814 ± 0.430	27.638 ± 0.360	Thy RW
NS	3.424 ± 0.087	3.188 ± 0.149	Liver RW
NS	10.679 ± 0.226	10.631 ± 0.112	Wings RW
*	A 1.956 ± 0.088	B 1.661 ± 0.076	Abdominal fat RW

Privations: Live body weight LBW, Carcass weight CWT, Dressing percent DR%, relative weight RW, Breast RW, Neak + Back RW, Thy RW, Liver RW, Wings RW, Abdominal fat RW, *Significant P<0.05, insignificant NS.

At the end of experiment, 35 day male was with significant P<0.05 effect than female on LBW, CWT with means of 2164.09g, 1592.73g and 1976.21g, 1438.67g for female, but female differ significantly on abdominal fat relative weight with means of 1.956than male with 1.661 for the same one treat, Table 11.

Using gene polymorphisms of candidate gene is a powerful tool to investigate economic treats of birds and that is why many studies now a days took place to explain quantitative traits for growth, body scales and measurements too (Li *et al*., 2003; AL-Anbari 2018). Two SNPs found in this study for Pit1 gene in

population of commercial breed Ross 308, genotype frequency for studied gene disagreement with the Hardy-Weinberg equilibrium tested and indicated that genotype frequency for Pit-1 was different significantly ($P<0.01$) in this population, that because this hybrid as commercial broiler type meat chicken was, under intensive breeding selection program. For Pit-1 gene association with studded traits for one day old and weekly body weight scales and measurement there were significant $P<0.05$ for MR1 genotype onW_1SL cm., W_2BL cm, W_2TC cm,, W_4BC cm and W_5BL cm traits and at the same level of significant, MR1-MR2 genotype effect onW_5BLcm and W_2BC cm also, they explain relations of these traits as quantitative trait with gene affected by quantitative trait loci as QTL and clear that MR1 play a crucial role as wild genotype, this results were agreed with Nie *et al*. (2008) and similar to that of Bhattacharya *et al*. (2012) too. Male different significantly $P<0.05$ as period differs on trait of W_2BL cm, W_3BW g,W_3KL cm, W_3TC cm,W_4BW g, W_5BW g, that finding agreed also with Nie *et al*. (2008) and the same as mentioned by Zahra *et al*. (2011). Male also differ with significant $P<0.05$ level on GAIN at third week and for LBW g and CWT g also but Female affected significantly on abdominal fat RW than male. The positive variation association between genotype for PIT1gene with body composition and performance of broiler may become with value in genetic selection programs for hybrid growth trait of broiler chicken

Conclusion

Focusing on development performance of commercial broiler chicken breed with classical breeding methods used, it needs money, spent time, getting results slowly. Quantitative traits affected by unlimited number of genes, nowadays depending on molecular, genetics, PCR technique...Etc in this field make it easy to detect polymorphisms of genes related with growth and body measurements. This study recommend that SNPs of affecting gene on growth of broiler hybrid is a good tool used to improve precocious selection programs to reduce market cost and shorter rearing period.

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Ethical clearance

The project was approved by the local ethical committee (College of Agriculture engineering science/ Baghdad University)

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