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EXPRESSION OF GH GENE POLYMORPHISMS AND THEIR ASSOCIATION WITH GROWTH TRAITS OF LOCAL, EXOTIC BREED AND THEIR RECIPROCAL CROSSBRED CHICKENS USING MOLECULAR MARKERS

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ABSTRACT

This study was aimedto characterize by using two genetic groups of chickens, which were Kurdish indigenous chickens (KK) and commercial Super Harco chickens which bred particularly for dualpurpose (SS),Four combinations were produced by diallel crossing between the two genotypes which are (KK, KS, SK, and SS).. The single nucleotide polymorphisms (SNPs) in the *GH* genes were identified between genotypes. Additionally, assessment oftheir belong to genotypes relationships with growth efficiency (body weight (BW) at hatching and 3,6,9, 12 weeks of age was carried on. The four genotypes were detected by using polymerase chain reaction- restriction fragment length polymorphism (PCR-RFLP) techniques by specific primers and restrictase for *GH* gene.Our data showed that the AA genotype had more values in KK and SK chickens while AB genotype were more in values in KS. The genotype BB was only more in SS (0.56) birds and no values in KK (0.04), KS (0.25) and SK (0.09) birds. The analysis of chi-square test indicated that SK, SS, males and femaleswhich arein (HWE) Hardy-Weinberg equilibrium (p<0.05). The statistical analysis showed that significantcorrelations (p < 0.05) between the *GH* and the following parameters: BW at 3, 6, 9 and 12 weeks of age, it was determined that the hetrozygotes AB genotype values were superior in BW (39.00± 0.37 kg) and (38.50± 0. 70 kg) in KS * Male and KS * Female respectively at hatching. On the other hand, KK * Female with AA genotype had the lowest body weight (31.60e ± 0.50, 219.00e ± 2.45, 456.60g ± 1.64, 752.00e ± 1.70 and 1087.00g ± 1.48) kg at day one, 3,6,9 and 12 weeks of age respectively compared to other genotypes. Based on the findings of this study, we proposed that in pure and crosses lines chicken population selection programs, a candidate gene marker for chicken growth characteristics could be the GH gene.

Key words: **Reciprocal Cross, Growth traits, GH, polymorphism, PCR-RFLP**

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INTRODUCTION

During the past few decades, Researchers have made significantadvanced animal breeding and genetics byevaluating candidate genes as markers of animal production efficiency (Meuwissen, 2007.). In Iraq, the majority of indigenous chicken breeds are described as low in growth rates, and their efficiency of production is poor, which has a significant effect on the growth of the poultry industry. To fully utilize the excellent traits of the indigenous chicken populations and to enhance their production performance, it is essential to search for significant influence genes that control growth and carcass characteristics to assist marker-assisted breeding. Growth could be considered a direct fitness trait that enhances productivity and reduces cost of production (Iraqi, et al. 2013) .Crossbreeding is usually applied in improvement programmes to improve poultry genetically due to increase the number of heterozygous loci which produced in heterosis for production performance which included meat and egg (Amuzu-Aweh, et al. 2015). Because of the alleles combinationresulting fromthe sire and dam, which causes influence on dominance and epistasis, crossbred projeny perform better than the overall of their paternal genotypes in terms of. This phenomenon is known as positive heterosis or hybrid vigour (Fairfull, et al. 1985, Fairfull, et al. 1978). But

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heterosis from epistatic impacts might be unpredictable due to the numerous unknown interactions among loci (Iraqi, et al. 2005). The modern DNA-technologies have been actively introduced into poultry selection, which gave rise to marker-assisted (MAS) and genome selection (Wolc, et al. 2016). Modern DNA technologies and conventional selection methods combined to produce highly productive commercial lines and breeds of poultry. (Sodhi, et al. 2013). The growth hormone (*cGH*) gene of chicken is regarded as one of the major important candidate genes that impact the production traits due toits necessity in growth, body composition, appetite control, ageing, with reproduction and metabolism (Nie, et al. 2005) .It also plays a major role in the natural and also to obtain immune systems by controlling the excretion of thymulin, the growth of the thymus, the growth of lymphoid cells, the activity of phagocytic cells, and hemopoiesis (Gala, 1991.). In avian, the cGH gene is situated on chromosome number 19 Ip*et al.,* (2001) which is made of 4 introns and 5 exons with an average length of 4.1 kb (Kansaku, et al. 2008). The products of *cGH* gene are made of 191 amino acid mature growth hormone protein and 25 amino acid signal peptides (Tanaka, et al. 1992). Growth hormone is a polypeptide generated and released from the anterior lobe of the pituitary gland. This hormone has an impact on traits like immunity, egg production, growth, and physical condition, therefore, the GH gene isregarded an essential gene for poultry production (Nie, et al. 2005). GH functions by activating processes like growth and fat metabolism with the suitable receptors on the target cells' cell walls (Garrett, et al. 2008). RFLP was attributed in the introns of *cGH* gene of layer chickens in White Leghorn breedand it has been believed that the alleles defined were related to egg production traits, resistance to Marek's disease and avian leukosis (Yan, et al. 2003). Additionally, PCR-RFLP was evaluated in several populations of native Chinese chickens, and it was hypothesized that an allele found in intron 1 may be related to laying hens productivity (Ip, et al. 2001). PCR-RFLP analysis of *cGH* in Kadaknath chicken may play a role of A allele at *cGH*1 locus for increasing productivity of egg (Thakur, et al. 2009). A positive correlation was revealed between *GH* and meat quality in Anka and Rugao hens (Sheng-Long, et al. 2008). Moreover researches on the intron 1 of *GH* indicated that this gene has influence on some body composition traits in Arian broiler chickens (Ghelghachi, et al. 2013). The aim of this current study was to evaluate the cGH gene polymorphism in Kurdish local chickens and commercial with their reciprocal chickens by using PCR-RFLP technique.

MATERIALS AND METHODS

Location of the experiment

The experiment was carried outin the private field KaniGraw- Erbil city and Molecular Laboratory in Animal Resources department, Agriculture Engineering Science College, Salahaddin University-Erbil.

Experimental design and housing

The experimental chickens that were used for the study are the Kurdish local (KK) and Super Harco commercial chickens (SS). The indigenous chickens were obtained from several villages surrounding Erbil City, while the commercial breed was taken from the same field and was imported from Hungary. They were weighed from hatching up to 12 weeks of age. The commercial was mainly bred as a dualpurpose bird. The chicks seemed to be healthy and had received their recommended vaccinations to prevent the most common diseases.As instructed by Super-Harco, the feeding system and lighting program were used.six hens were randomly chose in each genetic group and mated with one rooster. 520

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fertile eggs were collected from two genotypes their crosses which categorized according to their breeds and crossbreds. .After hatching, the chicks were separated into four genetic groups according to the breeds and crossbreeds.which obtainedK x K, K x S, S x K, and S x S. The hatched chicks were wing banded until six weeks old after leg banded. At one day, and 3, 6, 12 weeks of age, the chicks were weighed by using a sensitive electronic balance with a sensitivity of 1 gm

DNA extraction

270 chickens' blood samples were collected from the wing vein and transferred to tubes containing 3ml of anti-coagulant Tris-ethylene di amine tetra acetic acid (EDTA and then preserved at −20◦C. Genomic DNA was extracted using a blood DNA extraction kit, the genome's DNA was extracted from the blood (GeNet Bio, korea). By using a Nanodrop (1000 UK) spectrophotometer and gel electrophoresis, the quality and quantity of the DNA were evaluated.

RFLP-PCR amplification and genotyping

The final PCR mixture volume was 25 µL, and it was made up of 10 µL of Green Master Mix (200 M dNTPs, 25 units/mL Taq polymerase, and 1.5 mM MgCl2), 1 µL for each forward and reverse primer, 1 µL of extracted DNA, and 12µL of DNAse-free water. Thermocycling for the GH gene involved an initial denaturation stage at 95 °C for 5 min, followed by 35 cycles of primer annealing at 56 °C for 45 s, extension at 72 °C for 1 min, and final extension at 72 °C for 5 min. The restriction enzyme was used to digest 10 µL of PCR productaccording to Sasazaki *et al.*,(2006) with some minor modifications and also according to the instructions of the manufacturer (Thermo Scientific) Table 1. Obtaind product was examined by gel electrophoresis using 2.5% of agarose that was stained with 3 µL of safe dye (Cat. No. B-2010, GeNet Bio, Korea). The agarose gel was run at a constant voltage of 100 V/cm for 45 min. The bands were subsequently visualized by UV transilluminator and the gel photographed (Proxima 2500 Isogene Life science, Netherland).

Table 1. The name, chromosomal location, sequences of specific primer of GH gen

Gene	Sequence (5'-3')	Ta(ºC)	Location	Enzyme	Reference
GH	F: 5'- ATCCCCAGGCAAACATCCTC -3' R: 5'- CCTCGACATCCAGCTCACAT -3'	56	Intron 1	Msp 1	Zhang *et al.*, (43)

*Ta= annealing temperature

Statistical analysis

Performance (field) data

The experiment was designed as diallel cross within the (General Linear Model) method SAS, was used (32). The following model was applied for the fixed effects in this study:

$Yijk = \mu + Li + Sj + LSij + eijk$

Where; Yijk = Body weightobservation of the chickens of ith line (Li, i=1, K x K, i=2, K x S, i=3, S x K and i=4, S x S), within the jth Sex (Sj, j=1, male and j=2, female), of kth interaction between line and sex, µ = The overallmean, Li= Theeffect of line (K x K, K x S, S x K, and S x S), Sj= The effect of sex (male and female), LSij = The interaction ofline with sex Eijkl= Random error.

RFLP Analysis: The relation between genotypes with body weight was evaluated using the GLM procedure of SAS software (2004) to test the four genotypes (K x K, K x S, S x K and S x S) and age. The significant means were separated by Duncan's Multiple Range Tests. The following model was used to test the influence of the GH gene on the birds bodyweight at different ages: $Yijk = \mu + Gi + Hj + eijk$

Where: Yijk= observed on the i^{th} GH marker on the j^{th} genotype, µ= overall means, Gi= effect of the i^{th} GH marker, Hj= effect of the j^{th}

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genotype, Eijk=random residual effect. The gene frequencies for each locus in each sample were calculated using the following equations:

p = (**AA**)+**AB**/ ,**q** = **2**(**BB**)+**AB** /**2N** where p and q = the gene frequency of allele A and B respectively , and N = the total number of birds tested and tested to Hardy-Weinberg ratios using was calculated using GENPOP software version, 3.3 (Raymond, & Rousset, 1995.).

RESULTS AND DISCUSSIO

Phenotypic evaluation: Body weight: The results showed in Table 2 that there was a significant variation (P≤0.01) among genotypes K×K, K×S, S×K, and S×Sin live chicksweight from hatch till 12 weeks of age. Which the cross KS (38.75 ± 0.39, 336.50 ± 14.43, 660.00± 15.96 and 1521.50 ± 22.61) gm weresignificantly higher in growth performance at most all time point studied when compared to the KK, SS and SK genotypes, in contrast, the lightest chicks were for KK lines (534.20 ± 17.85, 837.50 ± 19.64 and 1198.00 ±25.48) gm) for BW6, BW9, and BW12, respectively. Benyi *et al.*, (2015) detected that the live body weight can be significantly affected by different genotype in poultry. The present result revealed that the genotype had an influence on live body weight of the pure breeds and their crosses. There were variations in chick weights as a result of crossing exotic broiler strains with a native chickens. The same results were found by Shem *et al.*, (2012) when they compared six commercial broiler crosses in live body weights o at various ages and they observed that significant variations in live body weight among these crosses at different ages. In contrast, our statistical analysis regarding the effect of sex on live body weight revealed highly significant differences (p ≤ 0.01) between males and females from 3 to 12 weeks of age, with males consistently showing higher body weights than females. However, no significant differences were observed at hatching.

Table 2.Means ±S.E ofbody weightin differentGenotypes

Traits	Body weights(g)				
	Hatch	3 weeks	6 weeks	9 week	12 weeks
Genotypes	**	**	**	**	**
KK	33.75^{c} ± 0.59	257.00^{c} ± 8.83	534.20^{d} ± 17.85	837.50^{c} ± 19.64	1198.00^{d}±25.48
KS	38.75^{a} ± 0.39	336.50^{a} ± 14.43	660.00^{a} ± 15.96	983.00^{a} ± 17.71	1521.50^{a} ± 22.61
SK	32.85^{c} ± 0.38	249.20^{c} ± 15.54	548.10^{c} ± 15.78	845.00^{c} ± 24.59	1259.50^{c} ± 21.74
SS	36.50^{b} ± 0.51	290.80^{b} ± 4.77	632.80^{b} ± 14.63	964.00^{b} ± 17.94	1496.00^{b} ± 19.31
Sex	NS.	** **	**	**	
Male	35.58^{a}± 0.39	330.25^{a} ± 6.54	663.50^{a} ± 8.19	994.25^{a} ± 9.78	1465.75^{a} ± 21.78
Female	35.35^{a}± 0.59	236.50^{b} ± 6.27	524.05^{b} ± 9.17	820.50^{b} ± 12.19	1271.75^{b} ± 23.78
Overall	35.46 ±0.35	283.38 ± 6.93	593.78 ± 9.94	907.38 ± 12.40	1368.75 ± 19.38

^{a,b,c} Different letters within a column for genotypes show significant differences (** P ≤ 0.01), NS - not significant, KK =Kurdish × Kurdish, KS= Kurdish male × Super Harco female, SK = Super Harco male × Kurdish female, SS=Super Harco × Super Harco.

Molecular characterization of chickens

Detection of the gene fragments: Electrophoresis analysis of PCR amplifications of various Genotypes revealed DNA fragments with a size of approximately 776 base pairs (bp) were obtained in each Genotype as dominant PCR product for GH locus according to (Ip, et al. 2001) (Figure 1).

Allelic and genotypic frequencies in pure and crosses lines chicken: The GH/MspI PCR-RFLP analysis of 270 DNA samples from pure and crossed chicken lines showed that the two alleles of A and Bwith the three different genotype profiles were present in intron 1 (Figure 2). These findings are consistent with earlier studies that detected polymorphisms in a 776 bp fragment of the

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GH gene in quails through the PCR-RFLP technique using the MspI enzyme, identifying two alleles (A and B) and three genotypes (AA, BB, and AB) (3, 4, 1). In contrast, Hamad and Al-Barzinji (2023) reported a more diverse RFLP pattern at the GH locus, identifying five distinct alleles (E, B, D, C, and A) and six genotypes (DD, BD, CC, CD, CE, and AA). The two bands (539+237 bp) for the AA genotype, three bands (539+ 414+237bp) for AB genotype, and two bands (414+237 bp) for AA genotype were identified as shown in (Table 3). Allele frequencies of *GH* gene were measured after genotyping the populations of four Chicken lines, as listed in Table 4. The allele A is predominantly higher than allele B, in KK, and SK chicken populations. Whereas, for SS line chicken and males the allele A was the most dominant alleles with a frequency of 0.75 and 0.63 respectively, while, in female allele A and B had the same frequency 0.5. Higher frequency of A allele (0.9028) than B allele (0.0972) was also mentioned by Muin and Lumatauw (2014) in Indonesian local chicken.Yan*et al.*,(2012) also noted there was high frequency of A allele (0.8655) than B allele (0.1335) in a population of hybrid chickens (Broilers Star X Silky). Additionally, a previous study found (Thakur, et al. 2009) higher allele frequency of A allele (0.7075) than B allele (0.2925) in Kadaknath. However, Kulibaba (2015) found that in Vietnamese native chicken breeds, B allele frequency was higher (0.964) than A allele frequency (0.036).

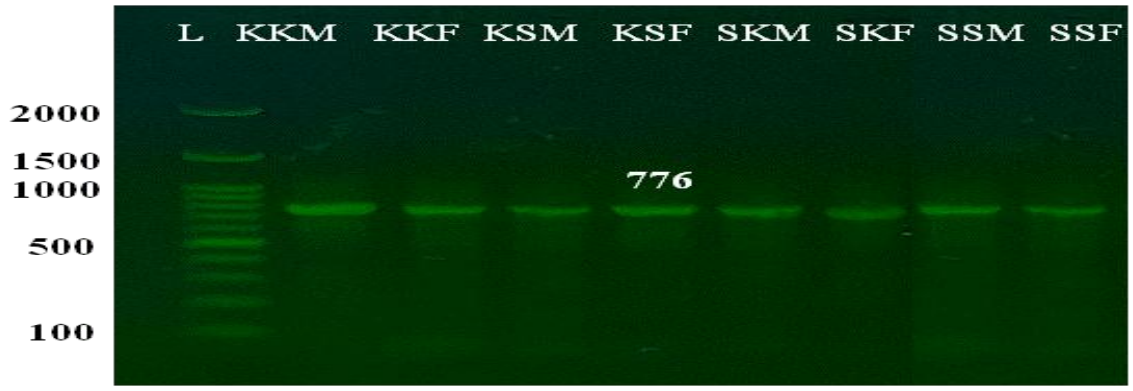

Figure1. Polymerase chain reaction based restriction fragment length polymorphism profiles of GH genes samples in four genotypes of chickens. L: DNA marker, KKM: Kurdish♂s local male, KKF: Kurdish♀s local female, KSM: (K×S) crossbred's male, KSF: (K×S) crossbred's female, SKM: (S×K) crossbred's male, SKF: (S×K) crossbred's female, SSM: Super Harco♂s male, SSF: Super Harco♀s female.

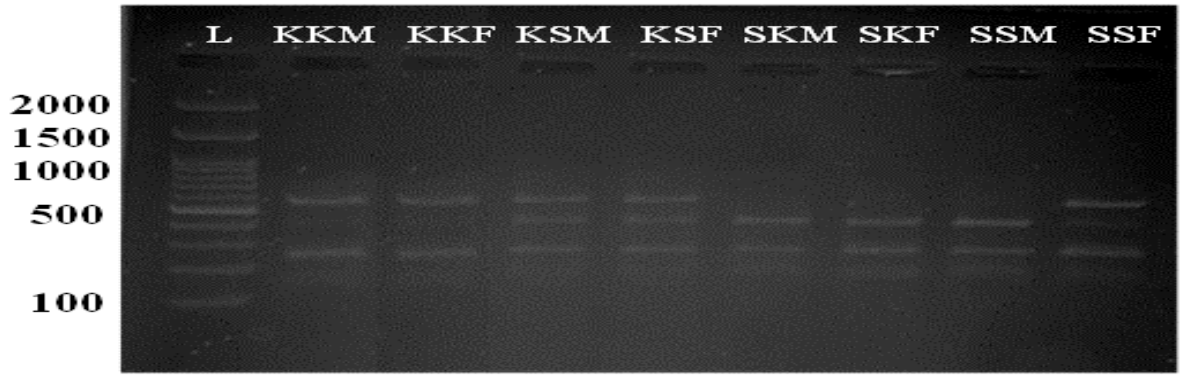

Figure2. Polymerase chain reaction based restriction fragment length polymorphism profiles of GH genes with Msp 1digestion in four genotypes of chickens. L: DNA marker, KKM: Kurdish♂s local male, KKF: Kurdish♀s local female, KSM: (K×S) crossbred's male, KSF: (K×S) crossbred's female, SKM: (S×K) crossbred's male, SKF: (S×K) crossbred's female, SSM: Super Harco♂s male, SSF: Super Harco♀s female.

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Table 3 . B**and number and Fragments size (*Bp*) for *GH* Genes in differentGenotypes**

Population/group	GH		
	Genotype and No. of band		band Size bp
KK * Male	AA	2	539+237
KK * Female	AA	2	539+237
KS * Male	AB	3	539+ 414+237
KS * Female	AB	3	539+ 414+237
SK * Male	BB	2	414+237
SK * Female	BB	2	414+237
SS * Male	BB	2	414+237
SS * Female	AB	3	539+ 414+237

The genotype frequencies and Hardy-Weinberg equilibrium (HWE) of *GH* in chickens' populations are presented in Table 4. The AA genotype had more values in KK and SK chickens while AB genotype were more in values in KS. The genotype BB was only more in SS (0.56) birds and no values in KK (0.04), KS (0.25) and SK (0.09) birds. In a similar study on two local breeds of chicken Vinh *et al.,* (2021) who identified the three genotypes of AA, AB and BB in *GH* gene and detected that the frequencies of genotype AA (*GH*), was low in both local breeds Nurcahya *et al.*,(2021) who studied *GH* genes in, Local Chickens Resulting from three breed crosses were polymorphic and in the Hardy-Weinberg equilibrium state and the genotypes BB (homozygote) value was predominant in this population. Correspondingly, the genotypes AA (homozygote individual) had no values in SS (0.06) and KS (0.25) chickens. This study found that the frequency of genotype AB (heterozygote individual) was the highest in male (0.47), and female (0.50) followed by AA and BB genotypes. The results show that the DNA banding patterns of *GH* was not respectively inthese studiein consistent with what was previously reported by Tanaka *et al.*, (1992), Ip*et al.*, (2001) and Kazemi *et al.*, (2018) these studies showed DNA fragments of 776 base pairs (*bp*) with the polymorphisminintron1of *GH* locus by usingrestriction reaction with *MspI* restriction enzyme. The results revealed three kinds of alleles of A, B and C as well as six distinct haplotype profiles (AA, BB, CC, AB, AC and BC).

Table 4 .Allele and Genotype Frequency of *GH* Genes in different lines

Locus	No.	GH					X^2	HWE
Chicken lines		Allelic frequency		Genotype frequency				
		A	B	AA	AB	BB		
KK	50	0.80	0.20	0.64	0.32	0.04	8.66	NS
KS	60	0.50	0.50	0.25	0.50	0.25	6.25	NS
SK	90	0.71	0.29	0.50	0.41	0.09	1.60	*
SS	80	0.25	0.75	0.06	0.38	0.56	5.12	*
male	70	0.37	0.63	0.14	0.47	0.39	1.27	*
female	210	0.50	0.50	0.25	0.50	0.25	0.82	*

* X^2 = chi square test

The probability of random mating in the population was tested by Chi-square ($\chi 2$) test to determine Hardy-Weinberg equilibrium (HWE) of pure and crosses lines chicken. The interpertation of chi-square test indicated that SK, SS, males and females were in (HWE) Hardy-Weinberg equilibrium ($p<0.05$). Similar result was reported in Kampung Sukabumi and Kampung Cawi chicken population showed that this population is in equilibrium ($p<0.05$) (Krisdianto, 2016.). This balance shows that there is no deliberate selection, especially the

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selection made on the *GH* gene. This fixed that the allele frequencies were stable from generation to next generation in this flock and there is no factor driving genetic variation (Allendorf, et al. 2013). Incontrast, both KK and KS chicken populations were not in Hardy-Weinberg equilibrium (Table 4). The Hardy-Weinberg Equilibrium ranges from 0.82 to 8.66.

Genotypes associations with body weight traits in chicken lines

Assessing the correlation between genotypic patterns at the GH gene loci and various phenotypic traits in both pure-bred and cross-bred chicken populations—including body weight measurements taken at day one, as well as at 3, 6, 9, and 12 weeks of age (as detailed in Table 5)—revealed significant associations ($p \leq 0.05$) between the polymorphisms in the GH gene and the body weight traits. This finding suggests that the cGH gene could serve as a promising marker in marker-assisted selection programs. However, further studies exploring the correlation between cGH and growth traits are needed to achieve more precise results (Nguyen, et al. 2015). Regarding the results of association analysis of the studied traits and also the mean comparison analysis between genotypes, it was determined that the hetrozygotes AB genotype values were superior in BW (39.00± 0.37 kg) and (38.50± 0. 70 kg) in KS * Male and KS * Female respectively at hatching. While, superior BW (38.60± 0.19 kg) in SS * Male lines chicken was observed in the genotype BB. This obtained result was in line with the observation of Thomas *et al.,* (2007) and İlhan, (2021) who indicated that heterozygote genotypes for *GH* polymorphism is more valued for characters of sturdiness and adiposity in the breeding plan. Also, the hens with AB genotypes were more competent than AA and BB genotypes at different of ages could also be regarded as the next generation's parents for improving BW traits. Nasirifar *et al.,* (2018) founded that the animals with B allele had higher hatching weights. Studies have also found an association between genotype and live weight. On the other hand, KK * Female with AA genotype had the lowest body weight (31.60e ± 0.50, 219.00e ± 2.45, 456.60g ± 1.64, 752.00e ± 1.70 and 1087.00g ± 1.48) kg at day one, 3,6,9 and 12 weeks of age respectively compared to other genotypes . Conversely, Nie *et al.*,(2005) were discovered that allele A had a positive impact on growth traits.

Table 5. Means ±S.E of genotypes for body weight traits at different ages

Population	Genotypes	Hatch	3 weeks	6 weeks	9 week	12 weeks
KK * Male	AA	$35.90^{b} \pm 0.45$	$295.00^{c} \pm 1.49$	$611.80^{c} \pm 2.10$	$923.00^{c} \pm 1.40$	$1309.00^{e} \pm 1.25$
KK * Female	AA	$31.60^{e} \pm 0.50$	$219.00^{e} \pm 2.45$	$456.60^{g} \pm 1.64$	$752.00^{e} \pm 1.70$	$1087.00^{g} \pm 1.48$
KS * Male	AB	$39.00^{a} \pm 0.37$	$399.00^{a} \pm 2.67$	$729.40^{a} \pm 1.13$	$1060.00^{a} \pm 2.40$	$1620.00^{a} \pm 1.05$
KS * Female	AB	$38.50^{a} \pm 0.70$	$274.00^{d} \pm 1.94$	$590.60^{d} \pm 1.96$	$906.00^{cd} \pm 1.25$	$1423.00^{c} \pm 1.23$
SK * Male	BB	$33.50^{cd} \pm 0.52$	$310.40^{b} \pm 0.78$	$616.60^{c} \pm 2.12$	$952.00^{d} \pm 2.49$	$1354.00^{d} \pm 2.20$
SK * Female	BB	$32.20^{de} \pm 0.49$	$182.00^{f} \pm 3.89$	$479.60^{f} \pm 2.02$	$738.00^{e} \pm 2.48$	$1165.00^{f} \pm 2.36$
SS * Male	BB	$38.60^{a} \pm 0.19$	$316.60^{b} \pm 2.25$	$696.20^{b} \pm 3.10$	$1042.00^{a} \pm 2.49$	$1580.00^{b} \pm 2.92$
SS * Female	AB	$34.40^{c} \pm 0.29$	$271.00^{d} \pm 1.94$	$569.40^{e} \pm 1.09$	$886.00^{d} \pm 1.14$	$1412.00^{c} \pm 2.23$

[a,b,c]Different letters within a column for genotypes show significant differences (p≤0.05).

CONCLUSION

The results showed a significant association between the growth hormone GH gene polymorphisms and the body weight of different chicken populations (pure and crossed lines). KS*male, and KS*female hybrids and (SS*male) pure lines of genotypes AB and BB exhibited a better growth performance and had a greater potential to develop than local breeds. In conclusion, *GH* gene polymorphisms can be used in the future as genetic markers for enhancing growth traits

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inbreeding programs for local chicken's breeds, especially in marker-assisted selection (MAS) processes.

CONFLICT OF INTEREST

The authors declare that they have no conflicts of interest.

DECLARATION OF FUND

The authors declare that they have not received a fund.

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التعبير عن تعدد المظاهرلجين *GH* وارتباطها بصفات النموفى دجاج المحلي و دجاج التجاري والتضريب التبادل يبينهما باستخدام تقنية PCR–RFLP

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المستخلص

تهدف الدراسة الى استخدام نوعين من الدجاج وهما الدجاج المحلي الكردي(KK) ودجاج سوبر هاركو التجاري ثنائي الغرض (SS)، في نظام خلط تبادلي لغرض إنتاج أربع مجموعات(SS، SK، KS، KK) للكشف عن تعدد أشكال النوكليوتيدات المفردة (SNPs) في جين GH ، وكذلك ارتباطها بأداء النمو (وزن الجسم (BW) عندعمر0 و 21 و 6 و 9 و 12اسبوعا). تم الكشف عن الأنماط الجينية باستخدام طرق تعدد الأشكال لتفاعل سلسلة البلمرة المتسلسل وتقنية(PCR–RFLP) مع بادئات محددة لجين GH. واوضحت النتائج بانالتركيب الوراثيAA أكثرقيمة في دجاج KK و SK بينما كان التركيب الوراثي AB أكثر القيمة في KS. كان التركيب الوراثي BB أعلى فقط في طيورSSوهو(0.56) وليس لها قيمة في طيورKK(0.04) و(0.25)KS و(0.09)SK. وان نتائج اختبار مربعكايبأن SK، SS ،في الذكور والإناث كانوا في توازن هاردي–واينبرغ (HWE) (p<0.05). إما بالنسبة للتحليل الإحصائي بان هنالك يوجد ارتباطات معنوية (p<0.05) بين GH والصفة وزن الجسمBWعند عمر0 و 3 و 6 و 9 و 12اسبوعا، وبينبأن قيم التركيب الوراثي AB كانت متفوقة في وزن جسم(0.37 ± 39.00) كجم و(70 .0 ±38.50) كجم في KS * ذكر و KS * أنثى على التوالي عند الفقس. من ناحية أخرى ، فانKK * للإناث مع التركيب الوراثي AA أقل وزن للجسمفي جميع الاعمارمقارنة بالتراكيب الوراثية الأخرى. بناءً على نتائج هذه الدراسة ، نستنتجبان يمكننا استخدام جين GHكماشر جينية للصفات نمو في الدجاج عن طريق برامج انتخاب عشائر الدجاج النقي وخليط ، بينما هناك حاجة إلى مزيد من البحث لصفات وزن الجسم.

الكلمات المفتاحية: تضريب التبادلي,الصفات النمو ,GH , تعدد المظاهرPCR–RFLP,