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Research Article

GH and *IGF1* gene variation and carcass yield characteristics in three Kurdish quail lines

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Abstract
This study aimed to detect single nucleotide polymorphisms (SNPs) in the *GH and IGF1*genes and evaluate their associations with growth performance traits, such as body weight (BW), dressing percentage, and carcass characteristics, in three quail lines: desert, brown, and white. Marker-assisted selection, which employs fast and precise molecular analysis of genes, is recognized as a powerful method for expediting genetic improvement in poultry production. Data on performance and carcass traits (including pre-slaughter weight and weights of the breast, thigh, neck, back, wings, head, feet, gizzard, liver, heart, and abdominal fat) were recorded. Additionally, blood samples were taken from 72 birds for DNA extraction and SNP analysis. Genotype identification was performed using polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) techniques with specific primers and restriction enzymes. Further analysis of quail carcass traits showed significant variations due to genetic line and sex. The Desert line consistently demonstrated superior values for most carcass parameters, including breast, thigh, and neck weights. Females exhibited higher carcass weights and dressing percentages compared to males, though males showed greater foot weight. The study confirms that genetic lines and sex significantly impact quail growth and carcass quality, with Desert quail outperforming others in several traits. Additionally, RFLP markers were associated with economic traits, highlighting the potential for molecular techniques in improving quail production. This research underscores the importance of genetic and environmental factors in optimizing quail breeding programs to improve quail growth traits and carcass quality.
Keywords: quails, *GH*, *IGF1*, growth trait, carcass parameters, Marker Assisted Selection

Introduction

Many cultures worldwide favor white meat from indigenous fowl for its health benefits and consumer preferences for its taste, flavor, high levels of vitamins and minerals, and relatively low fat and cholesterol content. It is also easier to handle and cheaper than red meat (Zamans *et al.,* 2004; Liu *et al.,* 2012).Growth performance and carcass traits in poultry production are critical economic factors influenced by a complex array of genetic factors. Growth is a complex process regulated by various neuroendocrine pathways. Consequently, achieving significant improvements through traditional genetic selection methods within breeds is challenging (Zhang *et al.,* 2008). However, recent advancements in molecular technology have created new opportunities to evaluate genetic variability at the DNA level (Kaya & Yildiz, 2008).Consequently, the candidate gene approach has emerged as a powerful technique for enhancing genetic improvement in poultry breeding programs. Utilizing candidate genes can increase the efficiency of identifying desirable traits crucial for improving production performance. Among the most promising candidate genes for growth performance and carcass quality traits in birds are the growth hormone (*cGH*) and insulin-like growth factor-I (*IGF-I*) genes. The hormone responsible for growth, known as *GH*, is a polypeptide hormone produced and released by the anterior pituitary gland, essential for the growth and development of poultry (Apa *et al.,* 1994). This gene is highly polymorphic and plays a critical role in various physiological processes, including growth, egg production, aging, and reproduction, and is vital for both growth and metabolic rates (Vasilatos-Younken *et al.,* 2000; Anh *et al.,* 2015). The *cGH* gene is at the tip of the long arm of chromosome 1 (Karabag *et al.,* 2019; Ahmed & AL-Barzinji, 2020). It comprises five exons and four introns, with a total length of 4.1 kb, encoding a mature growth hormone protein that consists of 191 amino acids (Kansaku *et al.,* 2008). *IGF-I* is considered one of the most important hormones necessary for supporting normal average growth in chickens (Scanes, 2009; Boschiero *et al.,* 2013). Moreover, *IGF-I* is associated with the secretion and regulation of growth hormones (Piper & Porter, 1997; Spencer *et al.,* 1997; Rousseau & Dufour, 2007). The PCR-RFLP approach is practical for detecting gene polymorphisms in populations (Boschiero *et al.,* 2013).To create an effective terminal breeding program for quail, it is important to investigate the relationship between the *cGH* and *IGF-I* genes as potential candidates. This study aimed to analyze how these genes influence growth performance and carcass traits in various lines of Kurdish quail.

Material and methods

Location of the experiment

The research was carried out and validated at the Quail Research Hall, Grdarasha Station, Department of Animal Resources, College of Agricultural Engineering Sciences, Salahaddin University-Erbil, from November 18, 2023, to January 7, 2024. This time frame included a field experiment with a seven-week rearing phase.

Experimental design and housing

In this experiment, a total of 480 fertile eggs (160 eggs per line) were incubated from three different lines (desert, brown and white) of Kurdish quails. Fertilized eggs from the three quail lines were organized into four replicates, with a mating ratio of one male to three females. The birds were housed in 40 cages, each measuring 45 cm in length, 30 cm in width, and 30 cm in height, with 12 quail chicks per cage. All quail chicks were raised under identical management, hygiene, and environmental circumstances until they reached 7 weeks of age. During the experiment, the birds had unlimited access to food and water. The experimental diet comprised 23.3% protein and provided 2985 Kcal ME/kg. The environmental temperature was maintained at 35-37°C during the first week and then decreased by approximately 2°C each week until it reached 20-22°C by the time the chicks were 4 weeks old and fully feathered. The birds were provided 24 hours of continuous light throughout the experiment.

Characteristics of slaughter

Six quails (three males and three females) were randomly selected from each replicate within each genetic line on the 49th day of the rearing phase. After a 12-hour fasting period, the birds were slaughtered, with their weights recorded before and after complete bleeding by severing the jugular vein. The birds then underwent scalding, feather removal, and evisceration. Various body parts and organs, including the liver, heart, gizzard, and abdominal fat, were dissected and weighed. The weights of these carcass traits were calculated as a part of the live body weight. The breast, thigh, neck, back, wings, head, and feet were separated from the carcass, weighed as a part of the eviscerated carcass weight.

DNA Isolation from collected samples

Blood samples were collected from 72 Kurdish quails for genomic DNA extraction. Each bird provided 1 mL of blood, which was transferred into a 3 mL tube containing the anti-coagulant Tris ethylene diamine tetraacetic acid (EDTA). DNA was extracted from each sample using the

DNeasy® Blood Kit (GeNet Bio, Korea) following the manufacturer's guidelines. A Nanodrop 1000 (UK) spectrophotometer, with gel electrophoresis, was utilized to assess DNA quantity and quality.

Loci identification and sample genotyping

The loci were selected based on the chromosome map previously constructed by (Sasazaki *et al.*, 2006). The loci and primers used in this study are detailed in Table 1. The design of the primers was based on sequences submitted to GenBank by Sasazaki *et al.*, (2006), utilizing the primer-blast tool from NCBI (http://www.ncbi.nlm.nih.gov). The total PCR reaction volume was 25 μL, which included 12.5 µL of Green Master Mix (containing 24 units/mL Taq DNA polymerase, 200 µM of each dNTP, and 1.5 mM MgCl2), 1 μL of each forward and reverse primer, 2 μL of DNA template, and the volume was adjusted to 25 μL with 8.5 μL DNase-free water. The amplification of the *GH* gene was carried out by initial denaturing at 95 °C for 5 minutes. This was followed by 35 cycles, each consisting of denaturation at 95 °C for 40 seconds, primer annealing at 55 °C for 50 seconds, and elongation at 72 °C for 60 seconds. A final extension at 72 °C for 5 minutes was performed at the end. Similarly, for the *IGF-I* gene, amplification began with the denaturation of genomic DNA at 95 °C for 5 minutes, followed by 35 cycles of denaturation at 95 °C for 45 seconds, annealing at 52 °C for 45 seconds, and elongation at 72 °C for 1 minute, finishing with a final extension at 72 °C for 10 minutes. A restriction enzyme was employed to digest 10 μL of the PCR product, following the method reported by Ahmed, (2020), with slight modifications. The manufacturer's (Thermo Scientific) instructions also guided the process, as indicated in (Table 2). Table 3 outlines the study's restriction enzymes and the specific reaction conditions. The gel was maintained at a constant voltage of 100 V/cm for 45 minutes. The bands were visualized using a UV transilluminator, and images of the gel were taken with a Proxima 2500 system (Isogene Life Science, Netherlands).

Table1. Presents the primers that were utilized in the polymerase chain reaction (PCR) experiment

Gene	Primer Sequence (5'-3')	Ta(^{o}C)	Enzyme	References
GH	F:ATCCCCAGGCAAACATCCTCG R:CCTCGACATCCAGCTCACAT	56	*Msp 1*	Setiati *et al.*, 2014

IGF-I	F:GACTATACAGAAAGAACCAC R:TATCACTCAAGTGGCTCAAGT	57	*PstI*	Nie *et al*., 2005

Statistical analysis

Statistical analysis of the data was performed using the SAS program (SAS, 2004), employing a general linear model (GLM) based on the model presented below; $\boldsymbol{Y_{ijkl} = \mu + L_i + S_j + LS_{ij} + E_{ijkl}}$ where Y_{ijkl} = an observation (body weight, carcass weight, carcass parts and dressing percentage), μ = Overall mean of Population, L_i = Effect of the line (1, 2 and 3), S_j = Effect of sex (1 and 2), LS_{ij}= interaction between line and sex and E_{ijkl} = Random error. Duncan's multiple range test (Duncan, 1955) was used to identify significant variance among treatments.

Charts illustrating the frequency of each gene and genotype were created with Graph Pad Prism version 8.0.2, a product of Graph Pad Software based in San Diego, California, USA.

The population's genetic information was analyzed performed using Popgene version 1.32 (Yeh & Boyle, 1997). Finally, the impact of *GH* and *IGF-I* genes on the traits under investigation were evaluated through the GLM procedure, employing the designated model as follows: $\boldsymbol{Y_{ijklo} = \mu + A_i + S_j + C_k + P_l + E_{ijklo}}$..

Results

PCR detection of *GH* and *IGF-1*genes

The electrophoresis analysis of PCR amplification for three quail lines revealed that the dominant PCR product for the *GH* locus was DNA fragments approximately 776 base pairs (*bp*) in size. Additionally, a single PCR amplification product for the *IGF-1* primer, approximately 621 *bp*, was obtained from both males and females in each quail line, as shown (Fig.1, A, B).

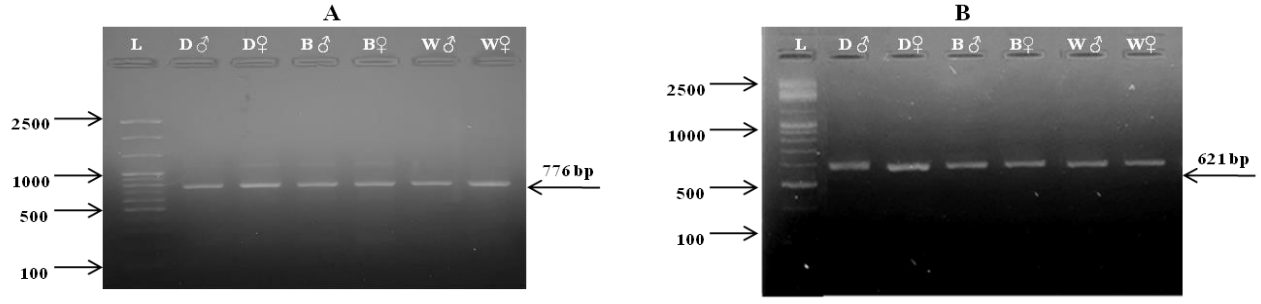

Figure1. Illustrate the PCR-RFLP profiles for A) *GH* and B) *IGF-1* in three lines, L: DNA marker, D♂: desert male, D♀: desert female, B♂: brown male, B♀: brown female, W♂: white male and W♀: white female

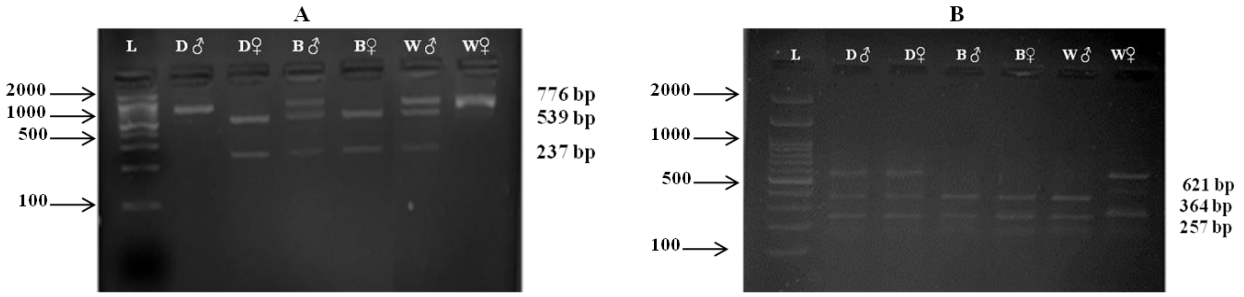

Figure2. Illustrate the digestion of PCR products for A) *GH* and B) *IGF-1* in three lines. L: DNA marker, D♂: desert male, D♀: desert female, B♂: brown male, B♀: brown female, W♂: white male and W♀: white female

Table 2. The *GH* and *IGF-1* gene characteristics, including band numbers and fragment sizes (*bp*) in Kurdish quails

Genetics group	*GH*			*IGF-1*		
	Genotype and No. of band		band Size(bp)	Genotype and No. of band		band Size(bp)
DM	AA	1	776	AB	1	621+365+257
DF	CC	2	539+237	AB	3	621+365+257
BM	AC	3	776+539+237	BB	2	365+257
BF	CC	2	539+237	BB	2	365+257
WM	AC	3	776+539+237	BB	2	365+257
WF	AA	1	776	AA	3	621

The *GH*/ Msp1 PCR-RFLP analysis of 72 DNA samples obtained from males and females belonging to various quail lines desert, brown and white, revealed three genotypes: AA (776*bp*), AC (776+539+237*bp*), and CC(539+237*bp*) as shown in (Fig. 2A). All three genotypes show nearly identical frequencies, with AA and AC each having a frequency of 3.33% (Table 2, Fig. 3A). Correspondingly, the frequency of allele A is much higher (75.00%) than allele C (0.25%) in white line, In contrast, in brown line, genotype C is more prevalent with a frequency of (0.750%), while genotype A has a lower frequency of (0.250%). In the desert line, genotypes A and B are equally distributed, with a frequency of (0.500%) in the investigated quail population, as evident from (Fig. 4A). For *IGF-1*/ Pst I polymorphism, all three genotypes (AA, AB, and BB) were found; however, BB (365+257 bp) homozygotes showed the highest observed genotypic frequency (5.00%) followed by 33.33% and 1.67 % in AB (621+365+257*bp*) and AA (621*bp*), respectively as highlighted in (Fig. 2B) . These findings reveal that both Alleles A and B are equally distributed in desert and white lines, with frequencies of 0.500 for each genotype. However, in brown lines,

genotype A is exclusively present with a frequency of 1.000, while genotype B is illustrated in (Fig. 3B & 4B).

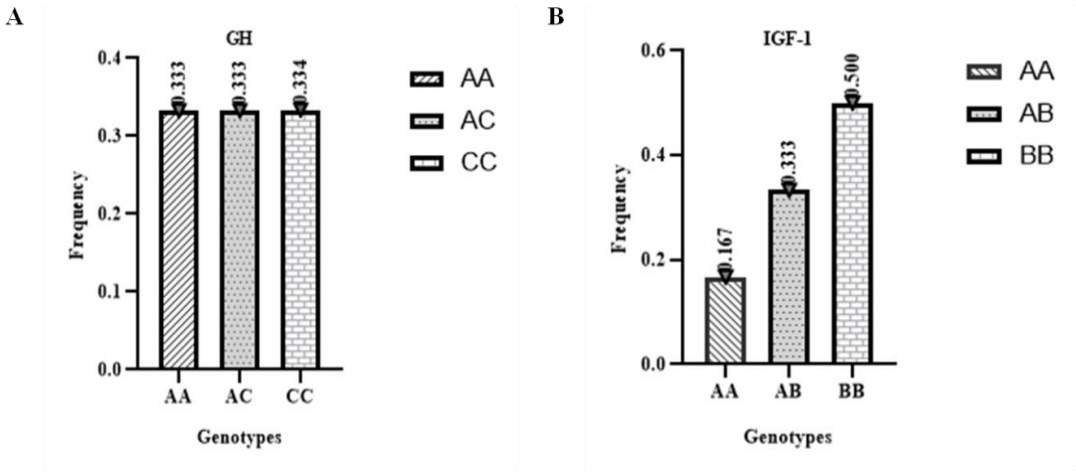

Figure 3. Genotype frequency of *GH* and *IGF-1* gene in quail

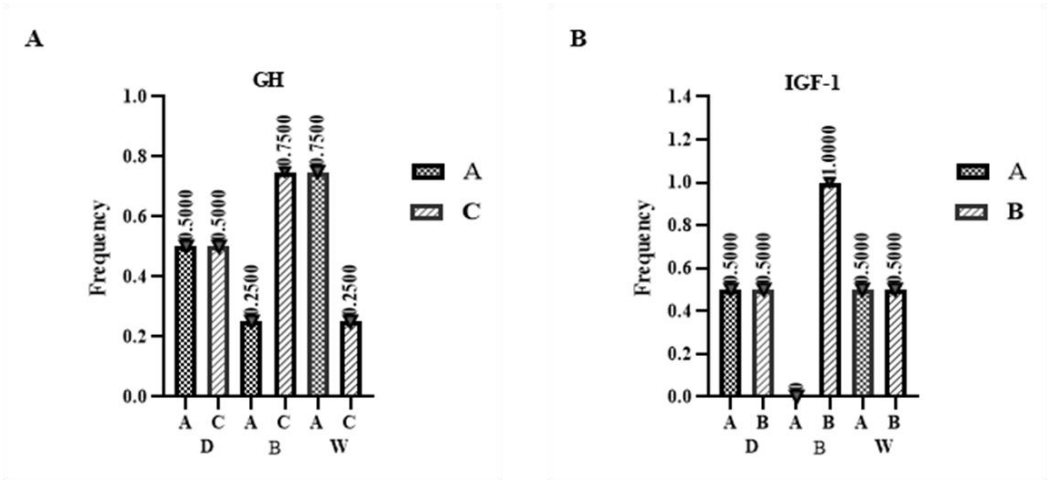

Figure 4. Allele frequency of *GH* and *IGF-1* gene in different lines of local quail

Phenotypic trait evaluation

The data in Table 3 highlights the influence of various lines, sex, and their interaction on the body weight and carcass quality of three Kurdish quail lines. The findings reveal significant effects of both line and sex on body weight, carcass weight, and dressing percentage in Kurdish quail. The desert line exhibited the highest values for body weight (241.00 ± 7.90 g), carcass weight (213.00 ± 6.37 g), and dressing percentage (88.50 ± 0.68%), significantly outperforming the brown and white lines. The brown line showed intermediate values for these traits, while the white line had the lowest values. Sex also had a notable impact, with females showing higher body weight (243.83

± 5.24 g) and carcass weight (207.67 ± 5.05 g) than males, who had lower body weight (211.56 ± 3.32 g) and carcass weight (185.17 ± 3.54 g). However, males had a higher dressing percentage (87.44 ± 0.63%) compared to females (84.97 ± 0.61%). The study also revealed that there are differences in growth patterns between the sexes, with males showing slightly elevated dressing percentages compared to females. Despite these differences, the interaction between line and sex was not statistically significant for any of the traits examined.

Table3. Least squares means ± standard error for body weight, carcass weight, and dressing percentage traits in various lines of Kurdish quails

Traits	N.	Body weight(g)	Carcass weight(g)	Dressing %
Overall	480	227.69±4.10	196.42±3.59	86.21±0.48
Lines (L)				
Desert	160	241.00±7.90^{a}	213.00±6.37a	88.50±0.68^{a}
Brown	160	225.42±6.74^{b}	193.42±5.30^{b}	85.70±0.71^{b}
White	160	216.67±4.98^{b}	182.83±3.38^{b}	84.43±0.66^{b}
Sex (S)				
Male(M)	240	211.56±3.32^{b}	185.17±3.54^{b}	87.44±0.63^{a}
Female(F)	240	243.83±5.24^{a}	207.67±5.05^{a}	84.97±0.61^{b}
Interaction(L×T)				
Desert × M	40	224.33±6.11b^{c}	201.50±6.19^{bc}	89.79±0.47^{a}
Desert× F	120	257.67±11.23^{a}	224.50±9.35^{a}	87.21±1.07^{b}
Brown× M	40	206.50±4.54^{cd}	178.67±2.14^{d}	86.63±1.13^{b}
Brown× F	120	244.33±6.02^{ab}	208.17±5.67^{b}	84.77±0.79^{b}
White× M	40	203.83±2.23^{d}	175.33±1.96^{d}	85.90±0.91^{bc}
White× F	120	229.50±6.17^{b}	190.33±4.89^{cd}	82.95±0.48^{c}
Probability				
L		0.0034	<.0001	0.0001
S		<.0001	<.0001	0.0013
LS		0.6537	0.4450	0.8112

$^{a-d}$Column means within a parameter that shares the same superscripts do not differ significantly at (P ≤0.05).

Table 4 presents the results of a study examining the effects of different genetic lines, sex, and their interaction on carcass cut-up parts, including the breast, thigh, wing, neck, back, head, and feet. Among the genetic lines, the desert line consistently shows the highest values for most traits, such as breast(55.83±1.70g), thigh(36.75±1.21g), neck (12.42±0.40g), and back (35.92±0.61g), with significant differences observed in these traits (P ≤ 0.05). The brown line exhibits intermediate values, particularly for breast (52.83±1.26g) and thigh (32.42±0.70g). In comparison, the white line shows the lowest values for thigh (30.42±0.62g), neck (8.83±0.17g), and back (29.83±1.34g), which are significantly lower compared to the other lines.

Table 4.Least squares means ± standard error for carcass traits weight in various lines of Kurdish quails

Traits	N.	Breast(g)	Thigh(g)	Wing(g)	Neck(g)	Back(g)	Head(g)	Feat(g)
Overall	480	53.47±0.86	33.19±0.67	12.56±0.33	10.72±0.34	32.86±0.70	10.94±0.23	4.06±0.16
Lines (L)								
Desert	160	55.83±1.70^{a}	36.75±1.21a	13.25±0.46^{a}	12.42±0.40^{a}	35.92±0.61^{a}	11.67±0.40^{a}	4.25±0.28^{a}
Brown	160	52.83±1.26^{a}	32.42±0.70^{b}	12.33±0.63^{a}	10.92±0.58^{b}	32.83±0.90^{b}	11.00±0.33^{ab}	4.17±0.27^{a}
White	160	51.75±1.33a	30.42±0.62^{b}	12.08±0.62^{a}	8.83±0.17^{c}	29.83±1.34^{c}	10.17±0.37^{b}	3.75±0.28^{a}
Sex (S)								
Male(M)	240	53.00±1.27^{a}	32.06±0.79^{b}	12.28±0.39^{a}	10.50±0.44^{a}	32.56±0.93^{a}	11.17±0.31^{a}	4.56±0.22^{a}
Female(F)	240	53.94±1.18^{a}	34.33±1.03^{a}	12.83±0.54^{a}	10.94±0.53^{a}	33.17±1.07^{a}	10.72±0.34^{a}	3.56±0.17^{b}
Interaction(L×T)								
Desert×M	40	55.00±2.89^{a}	35.02±1.29^{b}	13.00±0.45^{a}	12.17±0.48^{a}	35.83±0.60^{a}	11.83±0.60^{a}	4.67±0.42^{a}
Desert× F	120	56.67±2.03^{a}	38.50±1.88^{a}	13.50±0.85^{a}	12.67±0.67^{ab}	36.00±1.13^{a}	11.50±0.56^{ab}	3.83±0.31^{ab}
Brown× M	40	52.50±1.91^{a}	31.33±1.09^{c}	12.00±0.73^{a}	10.67±0.67^{bc}	32.83±1.22^{ab}	11.17±0.48^{ab}	4.67±0.42^{a}
Brown× F	120	53.17±1.82^{a}	33.50±0.72^{bc}	12.67±1.09^{a}	11.17±1.01^{ab}	32.53±1.45^{ab}	10.83±0.48^{ab}	3.67±0.21^{ab}
White× M	40	51.50±1.78^{a}	29.83±0.79^{c}	11.83±0.83^{a}	8.67±0.21^{d}	29.00±1.51^{b}	10.50±0.43^{ab}	4.33±0.33^{a}
White× F	120	52.00±2.13^{a}	31.03±0.97^{c}	12.33±0.99^{a}	9.00±0.26^{cd}	30.67±2.32^{b}	9.83±0.60^{b}	3.17±0.31^{b}
Probability								
L		0.1556	<.0001	0.3614	<.0001	0.0011	0.0280	0.3066
S		0.5903	0.0254	0.4279	0.3817	0.6129	0.3115	0.0012
LS		0.9570	0.6191	0.9936	0.9878	0.8226	0.9361	0.8882

a-d Column means within a parameter that share the same superscripts do not differ significantly at ($P \leq 0.05$).

Upon investigation of sex-based differences, it was found that males possessed a slightly lower breast weight (53.00±1.27g) than females (53.94±1.18g), but this variation was not statistically significant. Conversely, males demonstrated a notable increase in feet weight at (4.56±0.22g) compared to females at (3.56±0.17g), ($P = 0.0012$) In addition, the analysis indicated that females generally had significantly higher thigh weights ($P = 0.0254$), averaging (34.33±1.03g), compared to the average of (32.06±0.79g) for males. The interaction between line and sex revealed that desert males had lower thigh weights (35.02±1.29g) than desert females (38.50±1.88g). Desert females also had higher breast, neck, and back weights than desert males, though these differences were not statistically significant. In the white line, males consistently had the lowest values for breast, thigh, neck, and back weights, while white females had slightly higher values; however, the interaction between line and sex did not show significant differences for any of these traits.

Tables 5: shows average values of carcass interior part traits in the quail population; according to examining the effect of genetic line, the desert line showed the highest weights of heart (1.83 ± 0.17g) and abdominal fat (2.00± 0.17g), as well as the highest significant differences observed in gizzard (3.50 ± 0.15g), compared to the white line. The brown line exhibited intermediate values across all traits, while the white line had the lowest values for heart weight (1.25 ± 0.13g), gizzard weight (2.67± 0.19g), and abdominal fat weight (1.58± 0.19g). Regarding sex differences, females

demonstrated a statistically significant increase ($p \leq 0.05$) in liver (6.17± 0.46g) and gizzard weights (3.39± 0.18g) compared to males, who had lower weights of (4.39 ± 0.29g) for the liver and (2.83 ±0.12g) for the gizzard.

Table 5. Least Squares Means ± Standard Error for carcass part weights in various lines of Kurdish quails

Traits	N.	Heart(g)	Liver(g)	Gizzard(g)	Abdominal fat(g)
Overall	480	1.50±0.09	5.28±0.31	3.11±0.12	1.83±0.13
Lines (L)					
Desert	160	1.83±0.17^{a}	5.50±0.68^{a}	3.50±0.15^{a}	2.00±0.17^{a}
Brown	160	1.42±0.15^{ab}	5.17±0.44^{a}	3.17±0.21^{a}	1.92±0.29^{a}
White	160	1.25±0.13^{b}	5.17±0.49^{a}	2.67±0.19^{b}	1.58±0.19^{a}
Sex (S)					
Male(M)	240	1.44±0.12^{a}	4.39±0.29^{b}	2.83±0.12^{b}	1.72±0.16^{a}
Female(F)	240	1.56±0.15^{a}	6.17±0.46^{a}	3.39±0.18^{a}	1.94±0.21^{a}
Interaction(L×T)					
Desert × M	40	1.67±0.21^{ab}	4.17±0.54^{a}	3.17±0.17^{abc}	1.83±0.31^{a}
Desert× F	120	2.00±0.26^{a}	6.83±1.01^{a}	3.83±0.13^{a}	2.17±0.17^{a}
Brown× M	40	1.35±0.21^{ab}	4.34±0.21^{a}	2.81±0.17^{bc}	1.83±0.26^{a}
Brown× F	120	1.50±0.22^{ab}	6.00±0.73^{ab}	3.50±0.34^{ab}	2.00±0.52^{a}
White× M	40	1.33±0.21^{b}	4.67±0.71^{a}	2.50±0.22^{c}	1.50±0.22^{a}
White× F	120	1.17±0.17^{b}	5.67±0.67^{ab}	2.83±0.31^{bc}	1.67±0.33^{a}
Probability					
L		0.0312	0.8566	0.0059	0.4152
S		0.5319	0.0036	0.0080	0.4128
LS		0.5045	0.4859	0.7268	0.9579

[a-d] Column means within a parameter that share the same superscripts do not differ significantly at ($P \leq 0.05$).

These findings illustrate how physiological differences between male and female quails contribute to the variations observed in their carcass characteristics. The repeated measures analysis revealed no significant interaction between line and sex for carcass parts traits ($P > 0.05$). Desert females had the highest heart (2.00 ± 0.26g) and abdominal fat weights (2.17 ± 0.17g), whereas desert males had lower values for these traits. The brown × male combination showed intermediate values, while white line males consistently had the lowest heart weight (1.33 ± 0.21g) and gizzard weight (2.50 ± 0.22g).

Table 6 illustrates the impact of genetic (RFLP) markers on key economic traits in local quail. A significant association was found between RFLP patterns and traits such as carcass weight, dressing percentage, and the weight of various carcass parts. In this study, the CCAB genotype emerged as the most favorable for the desert line, exhibiting the highest values for body weight (257.67±11.23g), carcass weight (224.50±9.35g), thigh weight (38.50±1.88g), neck weight

(12.67±0.67g), back weight (36.00±1.13g), heart weight (2.00±0.26g), liver weight (6.83±1.01g), and gizzard weight (3.83±0.17g). In contrast, the AAAB genotype in the desert line recorded the highest dressing percentage (89.79±0.47g), head weight (11.83±0.60g), and feat weight (4.67±0.42g). These findings highlight the role of selection in improving body weight, carcass weight, dressing percentage, and other carcass traits in local quail. Notably, the desert quail outperformed both the brown and white lines in terms of body weight and carcass weight. On the other hand, the ACBB genotype displayed the lowest values for body weight (203.83±2.23g), carcass weight (175.33±1.96g), thigh weight (29.83±0.79g), neck weight (8.67±0.21g),

Table6. Least squares means ± standard error for genotypes associations with body weight and carcass traits in various lines of Kurdish quails

Traits	Lines (L)					
	Desert (GH × IGF-I)		Brown (GH × IGF-I)		White(GH × IGF-I)	
	AAAB	CCAB	ACBB	CCBB	ACBB	AAAA
Body weight (g)	224.33±6.11^{bc}	257.67±11.23^{a}	206.50±4.54^{cd}	244.33±6.02^{ab}	203.83±2.23^{d}	229.50±6.17^{b}
Carcass weight (g)	201.50±6.19^{bc}	224.50±9.35^{a}	178.67±2.14^{d}	208.17±5.67^{b}	175.33±1.96^{d}	190.33±4.89^{cd}
Dressing %	89.79±0.47^{a}	87.21±1.07^{b}	86.63±1.13^{b}	84.77±0.79^{bc}	85.90±0.91^{b}	82.95±0.48^{c}
Breast weight (g)	55.00±2.89a	56.67±2.03a	52.50±1.91a	53.17±1.82a	51.50±1.78a	52.00±2.13a
Thigh weight (g)	35.00±1.29^{b}	38.50±1.88^{a}	31.33±1.09^{c}	33.50±0.72^{bc}	29.83±0.79^{c}	31.00±0.97^{c}
Wing weight (g)	13.00±0.45^{a}	13.50±0.85^{a}	12.00±0.73^{a}	12.67±1.09^{a}	11.83±0.83^{a}	12.33±0.99^{a}
Neck weight (g)	12.17±0.48^{ab}	12.67±0.67^{a}	10.67±0.67^{bc}	11.17±1.01^{ab}	8.67±0.21^{d}	9.00±0.26^{cd}
Back weight (g)	35.83±0.60^{a}	36.00±1.13^{a}	32.83±1.22^{ab}	32.83±1.45^{ab}	29.00±1.51^{b}	30.67±2.32^{b}
Head weight (g)	11.83±0.60^{a}	11.50±0.56^{ab}	11.17±0.48^{ab}	10.83±0.48^{ab}	10.50±0.43^{ab}	9.83±0.60^{b}
Feat weight (g)	4.67±0.42^{a}	3.83±0.31^{ab}	4.67±0.42^{a}	3.67±0.21^{ab}	4.33±0.33^{a}	3.17±0.31^{b}
Heart weight (g)	1.67±0.21^{ab}	2.00±0.26^{a}	1.33±0.21^{ab}	1.50±0.22^{ab}	1.33±0.21^{ab}	1.17±0.17^{b}
Liver weight (g)	4.17±0.54^{b}	6.83±1.01^{b}	4.33±0.21^{b}	6.00±0.73^{ab}	4.67±0.71^{b}	5.67±0.67^{ab}
Gizzard weight (g)	3.17±0.17^{abc}	3.83±0.17^{a}	2.83±0.17^{bc}	3.50±0.34^{ab}	2.50±0.22^{c}	2.83±0.31^{bc}
Abdominal fat weight (g)	1.83±0.31^{a}	2.17±0.17^{a}	1.83±0.31^{a}	2.00±0.52^{a}	1.50±0.22^{a}	1.67±0.33^{a}

a-d Column means within a parameter that share the same superscripts do not differ significantly at ($P \leq 0.05$)

back weight (29.00±1.51g), head weight (10.50±0.43g), liver weight (4.67±0.71g), and gizzard weight (2.50±0.22g). The AAAA genotype in the white line had the lowest dressing percentage (82.95±0.48%), head weight (9.83±0.60g), and heart weight (1.17±0.17g), while the CCBB genotype recorded the lowest feat weight (3.67±0.21g) in the brown line. Interestingly, there were no significant differences in breast weight, wing weight, or abdominal fat weight across the genetic combinations in the three Kurdish quail lines studied.

Discussion

The exploration of economic traits in livestock production, particularly those linked to growth and reproduction, is in heredity complex due to the continuous variation exhibited by these traits. As highlighted by Li *et al.*, (2010), the presence of neutral polymorphisms distributed throughout the

genome facilitates the identification of chromosomal regions containing genes that influence these economically important traits. This genetic complexity necessitates a multifaceted approach to trait analysis. One effective strategy involves integrating physiological information with genetic mapping techniques, especially identifying quantitative trait loci (QTL). As Kuhn *et al.,* (2007) noted the candidate gene approach has emerged as a cost-effective and efficient method for detecting significant QTL genes and quantitative trait nucleotides (QTN) that directly impact livestock production traits. Selecting two growth-related genes to analyze their polymorphisms about carcass yield characteristics across three different lines of Kurdish quails highlights the significance of targeted genetic research. By focusing on specific genes associated with growth, researchers can deepen their understanding of the genetic influences on performance traits, potentially leading to enhanced breeding strategies and selection programs. The genotype distribution for the *GH* and *IGF-1* genes among three quail lines, desert, brown, and white, provides valuable insights into their genetic diversity. The AC genotype is the most prevalent for the *GH* gene across all lines, particularly in desert and white quails, indicating a potential correlation between this genotype and enhanced growth performance. In contrast, the CC genotype appears to be less common, especially in brown quails, suggesting it may be less favorable or prevalent in these specific lines. These results align with previous studies that identified polymorphisms in a 776 *bp* fragment of the *GH* gene in quails using the PCR-RFLP method with the *Msp1* enzyme, which revealed two alleles (A and B) and three genotypes AA, BB, AB (Johari *et al.,* 2013; Setiati *et al.,* 2014; Ahmed, 2020; Ahmed & Al-Barzinji, 2022). Regarding the *IGF-1* gene, the BB genotype is predominant in the brown and white quail lines, whereas the AA genotype is more frequent in desert quails. The higher prevalence of the BB genotype may suggest a genetic advantage in growth regulation for these quails, given the significant role of *IGF-1* in growth development. Kazemi *et al.,* (2018) identified six distinct genotypes (AA, BB, CC, AB, AC, and BC) for the *GH* gene, with frequencies of 0.10, 0.01, 0.36, 0.07, 0.34, and 0.12, respectively. For the *IGF-I* gene, they reported three genotypes (BB, Bb, and bb), with frequencies of 0.49, 0.44, and 0.07 in the native fowl population of Mazandaran. *Li et al.,* (2009) successfully amplified a 621-*bp* fragment of the 5'-UTR (5'-untranslated region) for *IGF-I* in Wenchang chickens. When the PCR products were subjected to digestion with the restriction enzyme *Pst I*, the bb genotype produced fragments of 257 and 364 *bp*, the Bb genotype resulted in fragments of 257, 364, and 621 *bp*. In comparison, the BB genotype remained undigested at 621 *bp*.

The assessment of phenotypic traits underscores the significant impact of different lines, sex, and their interaction on the body weight and carcass quality of three Kurdish quail lines. Desert quails demonstrate notably higher body and carcass weights than brown and white lines, likely due to differences in slaughter body weight, which may be influenced by recessive gene action. This observation is consistent with Hussen *et al.,* (2019), who found that the desert line had a significantly higher body weight ($p \leq 0.01$) compared to white birds, which had the lowest weights. Furthermore, Ahmed & Al-Barzinji, (2019) and Ahmed, (2022) analyzed the substantial genetic differences among three distinct quail lines, emphasizing that this genetic variation is crucial for achieving improvements in improving growth and egg production performance in local quails. Dewanti *et al.,* (2019) also reported a significant effect ($p \leq 0.05$) of quail lines on slaughter weight, thigh, and back measurements, revealing considerable differences between the black and brown plumage lines. In contrast, Al-Kafajy *et al.,* (2018) concluded that plumage color line had no significant impact on the carcass weight of quail birds. Regarding sex differences, female's outperformed males in both body and carcass weights, although males had a higher dressing percentage. The sex of the chicks significantly influenced body weight, with females potentially being heavier due to the increased mass of reproductive organs such as ovaries and oviducts (Ahmed, 2020). These findings are supported by Ahmed & Al-Barzinji, (2022), who demonstrated significant differences ($p \leq 0.05$) in slaughter weight and dressing percentage between male and female quail at six months of age, where females had higher carcass weights while males had superior dressing percentages. Nasr *et al.,* (2017) indicated that sex significantly impacts slaughter and carcass characteristics in quails. Olawumi, (2015) also noted that quails display sexual dimorphism, with females generally being larger than males, which is not the case in other poultry species. The study further indicated differences in growth patterns between the sexes, with males showing slightly higher dressing percentages. Lotfi *et al.,* (2011) found that female quail had greater carcass weights than males, suggesting a possible link to the weight of reproductive organs and indicating that at 42 days of age, mature female quails were heavier than broiler chickens. Additionally, Ahmed & Al-Barzinji, (2022) observed that the interaction between line and sex significantly ($p \leq 0.01$) affects both carcass weight and dressing percentage.

In our study, the analysis of carcass part weights across Kurdish quail lines indicates significant differences between the lines, sexes and their interaction. The desert quail line exhibits the highest weights for various carcass parts and interior traits, including breast, thigh, neck, back, head, heart,

and gizzard weights, compared to the brown and white lines, suggesting its potential advantages for meat production. In contrast, white quails demonstrate the lowest weights for these traits, particularly in the thigh, neck, and back. The yield of the breast and thigh is influenced by several factors, including slaughter age, genetic line, and sex (Chartrin *et al.,* 2018). Additionally, Al-Kafajy *et al.,* (2018) reported significant effects of genetic lines on various carcass characteristics in Japanese quails, including heart, thigh, breast, and back weights, with no notable differences in neck and wing weights. Similarly, Rehman *et al.,* (2021) found significant differences ($p \leq 0.05$) in breast and thigh yield among three genetic groups of Japanese quails, along with significant variations ($p \leq 0.05$) in heart and gizzard percentages, while liver percentages remained consistent across groups ($p > 0.05$). Previous studies, such as Minvielle *et al.,* (2005) and Yilmaz & Çaglayan, (2008), reported that white-line quails generally have lower body weights compared to brown-line quails, whereas, Tarhyel *et al.,* (2012) observed higher breast and thigh meat percentages in white-line quails. These results indicate that both genetic line and sex significantly influence growth and carcass composition in Kurdish quails. On the other hand, Ahmad *et al.,* (2018) found no significant differences in carcass yield among four closely bred Japanese quail flocks, though sex-based differences were noted in traits like thigh, feet, liver, and gizzard percentages. Bongiorno *et al.,* (2022) identified substantial differences in slaughter performance and meat quality between two Italian chicken breeds, Bionda Piemontese and Bianca di Saluzzo, showing that breed and gender significantly influenced carcass, breast, and thigh yields ($p \leq 0.001$). Additionally, Dewanti *et al.,* (2019) observed that females had higher percentages of thoracic meat and wings compared to males. Abdel-Halim *et al., (*2024) identified a notable interaction between line and sex regarding the weights of edible carcass parts, including the heart, liver, giblets, and gizzard, among six hybrid quail lines.

The relationship between specific genotypes of the *GH* and *IGF-1* genes and carcass yield characteristics reveals significant variations across different lines and genotypes. Ahmed & Al-Barzinji, (2022; 2020) found a strong link between RFLP patterns and essential growth traits, including live weight at six months, carcass weight, and dressing percentage in local quails. Moreover, Anh *et al.,* (2015) discovered a potential connection between polymorphisms in the *GH* and *IGF-1* genes and traits such as dressing percentage, body weight at hatching, and breast and wing muscle percentages at various ages (2, 4, and 6 weeks) in four populations of Thai broilers. Promwatee *et al.,* (2011) reported a significant correlation between the *IGF-1* gene and both body

weight (BW) and average daily gain (ADG) in Thai native chickens (Chee). Nasirifar *et al.*, (2018) indicated that the growth hormone gene is crucial for enhancing economically important traits and is a promising candidate for marker-assisted selection in Japanese quails. Additionally, Hosnedlova *et al.*, (2020) demonstrated that single nucleotide polymorphisms (SNPs) in the *IGF1*, *IGFBP2*, and *TGFß3* genes are significantly associated ($p \leq 0.05$) with growth performance traits in broiler chickens, such as body weight, average daily gain, and carcass characteristics. These findings highlight the significance of genetic markers, especially in the *GH* and *IGF-1* genes, in influencing carcass traits and growth performance. This underscores their potential as valuable tools for marker-assisted selection and genetic improvement programs in poultry.

Conclusion

The presented study illustrated significant genetic and phenotypic differences among the desert, brown, and white Kurdish quail lines. The results indicate that the desert quail line exhibits superior carcass traits, including higher weights for breast, thigh, neck, heart and abdominal fat than the brown and white lines. Genetic analyses identified distinct *GH* and *IGF-1* genotypes associated with these traits. The results highlight the effectiveness of using genetic markers for improving quail breeding programs and suggest that targeting specific genotypes could enhance growth performance and carcass quality.

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