

Association of Growth Hormone Gene Polymorphisms (A1795>T and T1749>C) with Productive Performance and Egg Quality in Iraqi Indigenous Chickens

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Abstract

The Growth Hormone (GH) gene is a pivotal candidate marker for improving production traits in poultry due to its essential role in growth, metabolism, and reproduction. This study aimed to investigate the associations between two specific Single Nucleotide Polymorphisms (SNPs) in the GH gene (A1795>T and T1749>C) and the productive and physiological performance, as well as the metabolic status of Iraqi indigenous chicken. A total of 100 local hens were genotyped using PCR method amplification followed by Sanger sequencing. Productive traits included body weight at sexual maturity, egg production rate, egg mass, and feed conversion ratio (FCR), in addition to physiological indicators. Results sequence analysis revealed highly ($P \leq 0.01$) significant genetic variations. The A1795>T polymorphism was significantly ($P \leq 0.05$) associated with egg weight, certain egg quality traits, and FCR, with the AT genotype showing superior performance in these parameters. Furthermore, the T1749>C polymorphism exhibited a significant ($P \leq 0.05$) to highly significant ($P \leq 0.01$) effect on egg weight, egg production, egg mass, and FCR. Conversely, some other traits showed no significant differences, ($P \leq 0.05$) suggesting a neutral genetic role for these markers in specific production aspects. These findings indicate that the A1795>T and T1749>C SNPs in the GH gene can serve as effective molecular markers in Marker-Assisted Selection (MAS) programs to enhance the genetic potential of Iraqi indigenous poultry while maintaining their environmental adaptation.

Keywords: GH gene, SNPs, Sanger Sequencing, Iraqi local chicken, Egg production, Marker-Assisted Selection.

Introduction

The Growth Hormone (GH) gene is considered one of the most important candidate genes for production traits in poultry (1). The protein encoded by this gene is a major regulator of postnatal growth, muscle development, and lipid metabolism (2). Furthermore, the GH gene influences the reproductive axis by stimulating the production of Insulin-like Growth Factor-1 (IGF-1) which is essential for follicular development and egg production (3). Despite its importance, the genetic architecture of the GH gene in Iraqi local chicken remains insufficiently explored. Previous studies have indicated that polymorphisms in the intronic and exonic regions of the GH gene can significantly alter its expression or the functionality of the hormone (4). Among these, the A1795>T and T1749>C loci have been suggested as potential sites for genetic variation.

Therefore, this study was conducted to investigate the impact of A1795>T and T1749>C SNPs within the GH gene on the production performance and metabolic status of Iraqi indigenous poultry. The findings aim to establish a molecular basis for future breeding strategies to enhance the efficiency of local chicken production while preserving their unique environmental resilience. Targeting these regions is critical for understanding how the AA genotype at the 1795 locus provides late-

stage stability while the T1749>C locus serves as a dynamic marker for early growth.

By integrating PCR amplification, bidirectional Sanger sequencing utilizing the ABI 3730XL Genetic Analyzer, and General Linear Model (GLM) analysis, this study provides a robust framework for genetic discovery based on the monitoring of 100 indigenous Iraqi hens over a 100-day production period. The primary research objectives involve quantifying the influence of A1795>T and T1749>C SNPs on performance metrics such as body weight at sexual maturity, egg production rate, egg mass, and egg weight, while assessing the association between these genotypes and blood biochemical profiles including Glucose, Cholesterol, Triglycerides, and protein fractions. Ultimately, this work aims to evaluate the potential of the stable AA genotype at the A1795>T locus and the stage-specific TT/TC genotypes at the T1749>C locus as validated molecular markers for future high-precision selection programs.

Materials and Methods

1. Experimental Design and Housing A total of 100 indigenous Iraqi hens were utilized in this study. The experiment was conducted at the poultry research farm of the College of Agricultural Engineering Sciences, University of Baghdad, from September 20, 2023, to April 2, 2024. At 14 weeks of age (pre-sexual maturity), the hens were placed in individual cages under

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standardized environmental conditions. The monitoring period commenced at the age of sexual maturity and lasted for 100 days, divided into equal production periods.

2. Flock Management and Feeding Birds were managed according to standard commercial layer protocols. Feeding was based on National Research Council (NRC) recommendations (5), providing a diet that contained 17.5% Crude Protein and 2777.47 kcal/kg Metabolizable Energy during the production phase. Each bird received a restricted daily allowance of 100 grams of feed. A controlled lighting program was implemented according to the commercial management guide (6). The photoperiod was gradually increased from 8.5 hours at 18 weeks to 16 hours of light per day by the 28th week, which was maintained until the conclusion of the trial. Lighting intensity was standardized using 20-watt bulbs to ensure uniform distribution.

3. Measurement of Productive Traits The productive performance was monitored individually for each hen throughout the 100-day experimental period. The following traits were evaluated:

- I. Body Weight at Sexual Maturity (BWSM): Recorded for each hen on the day of her first egg using a sensitive digital balance (accuracy ± 0.1 g).
- II. Egg Production Rate (HDP%): Calculated based on Hen-Day Production using the formula: $HDP\% = (\text{Total number of eggs produced} / \text{Number of days in the period}) \times 100$.
- III. Egg Weight (EW): Each egg was weighed daily to calculate the average egg weight for each genotype.
- IV. Total Egg Mass (EM): Calculated daily (g/hen/day) using the formula: $\text{Egg Mass} = (\text{Egg Production Percentage} \times \text{Average Egg Weight}) / 100$.
- V. Feed Conversion Ratio (FCR): Determined weekly and for the total period based on the efficiency of feed utilization for egg production: $FCR = \text{Total Feed Intake (g)} / \text{Total Egg Mass (g)}$.

4. Blood Sampling and Biochemical Analysis Blood samples (2 mL per bird) were collected from the brachial vein using sterilized syringes containing EDTA for DNA extraction and without anticoagulant for serum separation. The non-anticoagulated blood was allowed to clot at room temperature and then centrifuged at 3000 rpm for 15 minutes to obtain the serum. Serum samples were stored at -20°C until analysis. The biochemical traits, including Glucose, Total Protein, Albumin, Cholesterol, and Triglycerides, were measured using specialized commercial diagnostic kits and a spectrophotometer according to the manufacturer's instructions. Genomic DNA was extracted from the

whole blood using a specialized DNA Purification Kit (Geneaid, Taiwan) following the manufacturer's protocol to ensure high purity and yield.

5. Primer Design and PCR Amplification A specific pair of primers was designed to amplify a 429 bp fragment of the Growth Hormone (GH) gene. The nucleotide sequences of the primers used were:

Forward Primer (F):

5'-GAGCCATCGCTGCTACAGAT-3'

Reverse Primer (R):

5'-CGTCAAGCTGGAGGAGTTCT-3'

The PCR reaction was conducted in a total volume of 25 μL , consisting of 12.5 μL of 2X Master Mix, 1 μL of Forward Primer (10 pmol), 1 μL of Reverse Primer (10 pmol), 3 μL of Template DNA, and 7.5 μL of Nuclease-free water. The PCR programming included an initial denaturation at 94°C for 5 min, followed by 35 cycles of denaturation at 94°C for 30 sec, annealing at 56°C for 30 sec, and extension at 72°C for 30 sec, with a final extension at 72°C for 7 min. PCR products were verified by 1.5% agarose gel electrophoresis and visualized under a UV transilluminator.

6. Genotyping and Sanger Sequencing The PCR products were purified and subjected to bidirectional sequencing using the Sanger Method (ABI 3730XL Genetic Analyzer). The resulting sequences were analyzed and aligned with the Gallus gallus (GeneID-378781) reference sequence using BioEdit and MEGA software to identify the Single Nucleotide Polymorphisms (SNPs) at positions A1795>T and T1749>C.

7. Statistical Analysis Data were analyzed using the General Linear Model (GLM) procedure of SAS software (7). For traits measured once (e.g., body weight at sexual maturity), a simple one-way model was used: $Y_{ij} = \mu + G_i + e_{ij}$. Experiments including animals were performed in accordance with the principles and specific guidelines presented in local legislation on the care and use of animals in research, and the protocol was formally approved by the institutional animal ethics committee.

RESULTS AND DISCUSSION

1. Analysis of GH Gene Polymorphisms

The PCR amplification of the target region in the GH gene yielded a specific fragment of 429 bp. Sequence analysis of this fragment in 100 Iraqi indigenous hens revealed the presence of two mutations: a transversion (A1795>T) and a transition (T1749>C), as shown in Figures 2 and 3.

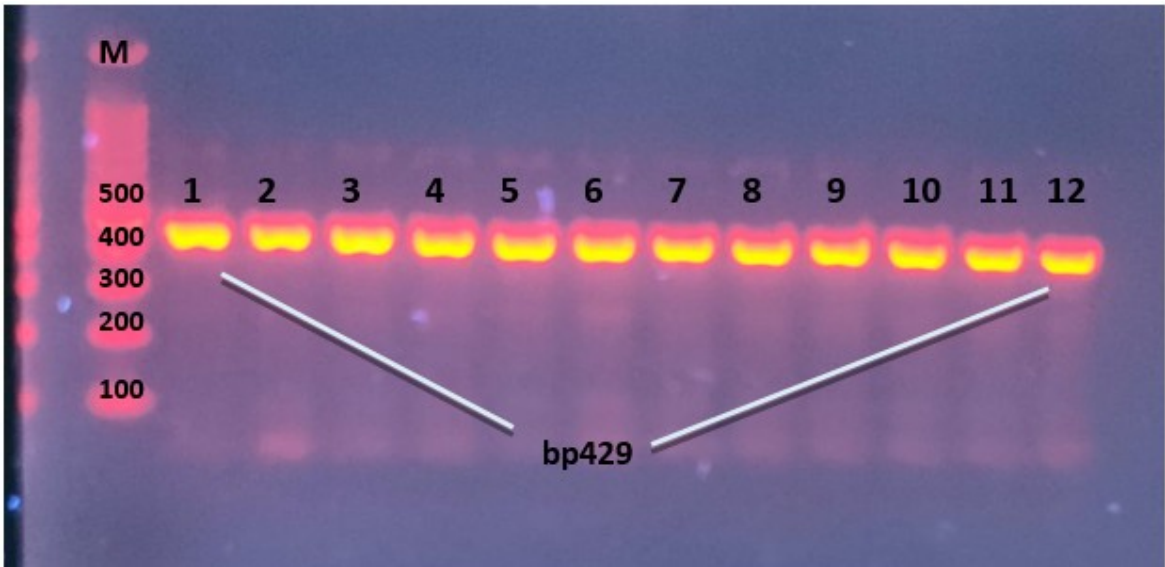


Figure 1. Agarose gel electrophoresis (1.5%) showing the specific PCR amplification products of the target region of (GH) gene

Lane M: DNA ladder (100–1000 bp) used as a molecular weight standard. .

Lane M: 100–1000 bp DNA ladder; Lanes 1–12: Amplified genomic fragments from Iraqi indigenous chicken samples, showing a sharp, consistent band at the expected size of 429 bp with no non-specific products or primer dimers. These confirmed amplicons were utilized for subsequent downstream Sanger sequencing.

Sequence Analysis of the Growth Hormone (GH) Gene

Following PCR amplification, the products were resolved by electrophoresis on a 1.5% agarose gel at 5

V/cm for one hour. A 100–1000 bp DNA ladder was loaded into the first well to determine the molecular weight of the resulting bands. The gel was stained with ethidium bromide and visualized under an ultraviolet (UV) transilluminator for documentation (**Figure 1-1**). For sequence analysis, the confirmed PCR amplicons (429 bp) were subjected to bidirectional Sanger sequencing utilizing the ABI 3730XL Genetic Analyzer. The resulting electropherograms were then analyzed to identify the targeted Single nucleotide Polymorphisms (**A1795>T** and **T1749>C**).

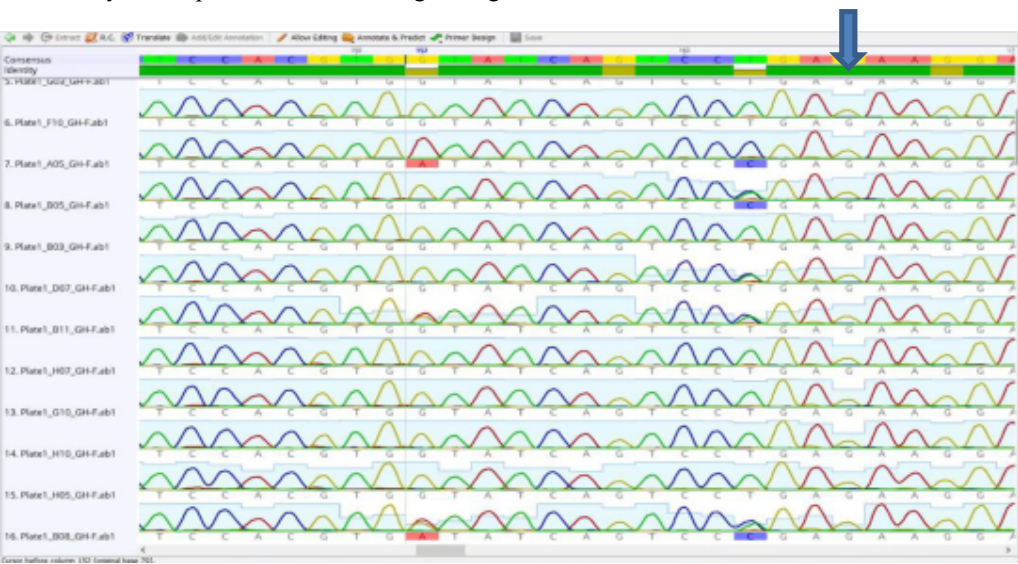


Figure 2. Representative DNA sequence chromatograms of the GH gene (T1749>C) locus in Iraqi local chicken using Sanger sequencing

The figure displays the electropherograms obtained from bidirectional Sanger sequencing, illustrating the genetic polymorphism at the (T1749>C) position. The high-quality, distinct peaks confirm the accuracy of the genotyping

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process. Three distinct patterns are observed: Homozygous Wild-type (TT), represented by a single red peak (e.g., Samples 5, 6, and 9); Homozygous Mutant (CC), represented by a single blue peak (e.g., Samples 7 and 16), indicating the substitution of Thymine with Cytosine; and Heterozygous (TC), clearly identified by the presence of overlapping red and blue dual-peaks at the same locus (e.g., Samples 8, 10, and 11), confirming the presence of both alleles in these individuals.



Figure 3. Representative DNA sequence chromatograms (electropherograms) of the GH gene (A1795>T) locus in Iraqi local chicken

The alignment illustrates the genetic variation at the A1795>T position within a 429 bp fragment of the GH gene. The chromatograms reveal two distinct genotypes at this locus: Homozygous Wild-type (AA), observed in samples 22, 23, and 25, characterized by a single sharp green peak; and Heterozygous (AT), observed in samples 24 and 26, evidenced by the presence of overlapping green (Adenine) and red (Thymine) dual-peaks. The high signal-to-noise ratio and the clarity of the peaks confirm the high quality of the Sanger sequencing and the successful identification of the targeted SNP.

2. Genotypic and Allelic Frequencies of A1795>T and T1749>C SNPs

The distribution of genotypes and allele frequencies for the two studied SNPs (A1795>T and T1749>C) in the GH gene of Iraqi indigenous chicken is summarized in Table 1.

Table 1. Combined genotypic and allelic frequencies of GH gene SNPs (n = 96)

SNP Locus	Genotype	Observed (n)	Frequency (%)	Allele	Frequency	X ²
A1795>T	AA	80	83.33	A	0.92	42.667
	AT	16	16.67	T	0.08	
	TT	0	0.00			
T1749>C	TT	57	59.38	T	0.74	61.062
	TC	29	30.21	C	0.26	
	CC	10	10.42			
Footnote: SNPs = Single Nucleotide Polymorphisms; HWE = Hardy-Weinberg Equilibrium χ^2 = Chi-square						

In both loci a clear dominance of one allele was observed allele A (0.92) for the first site and allele T (0.74) for the second. Notably, the homozygous recessive genotype (TT) was entirely absent in the A1795>T locus. Such fixation or high frequency of a single allele is common in indigenous breeds and is often attributed to long-term natural selection for survival in specific environments (8). Similar trends have been reported previously (3), where certain GH polymorphisms become conserved in local populations to maintain metabolic homeostasis.

3. Deviation from Hardy-Weinberg Equilibrium (HWE) Both SNPs exhibited high and significant Chi-square (χ^2) values (42.667 and 61.062, respectively), indicating a substantial deviation from Hardy-Weinberg Equilibrium. This disequilibrium suggests that the GH gene is under intense selection pressure, either natural or artificial (4, 9). Such deviations in indigenous poultry are frequently linked to the gene's association with vital production traits and adaptation mechanisms, where specific genotypes like AA and TT offer a selective advantage under heat stress or limited nutritional

resources (9, 11). This selection potential often leads to the manifestation of heterosis in crossbred or varied populations, enhancing overall fitness and productivity.

The higher frequency of the C allele (0.26) and the presence of the CC genotype (10.42%) in the T1749>C locus make it a more dynamic and actionable marker for genetic improvement. Previous studies demonstrated that polymorphisms in the GH gene's regulatory or intronic regions can significantly modulate IGF-1 levels, which directly impacts egg production and mass (1).

In the specific context of Iraqi local chicken populations, this deviation strongly reflects the impact of prolonged natural selection under the region's unique environmental pressures. The harsh climate, characterized by extreme summer heat and fluctuating nutritional resources, has likely favored the conservation of specific alleles that enhance metabolic efficiency and survival resilience. For instance, the high frequency or fixation of certain alleles at the studied loci, such as the A allele, indicates that these variants provide a functional selective advantage, allowing the birds to maintain physiological stability and production persistence in the Iraqi environment. This reinforces the conclusion that the GH gene in these indigenous breeds has undergone a strategic genetic adaptation to the local agro-ecological conditions rather than being subject to random genetic drift.

4. Effect of the Growth Hormone Gene A1795>T and T1749>C Polymorphisms on Weekly Egg Weight The results revealed a distinct statistical and physiological variation in egg weight response to the studied growth hormone (GH) gene polymorphisms. Regarding the A1795>T SNP, although no significant differences were observed during the early production phases, the AA genotype exhibited a highly significant superiority ($P \leq 0.01$) during the late stages (Weeks 13 and 14), achieving a mean weight of 51.84 g. This enhancement is attributed to the role of the GH gene in maintaining the efficiency of the shell gland and albumin deposition via the activation of the GH-IGF-1 somatotrophic axis (16, 1).

In contrast, the second SNP, T1749>C, demonstrated a significant localized impact. Statistical analysis showed a clear significant difference ($P \leq 0.05$) during Weeks 4 and 5, which reached a highly significant level ($P \leq 0.01$) by Week 11 in favor of the TT genotype. This fluctuated significance suggests a temporal interaction between GH gene expression, peak production periods, and environmental factors such as photoperiod and nutrition (12). Although this SNP did not show a significant effect on the overall mean egg weight, these periodic significant variations align with previous findings (13), which noted that the impact of specific SNPs is highly dependent on the genetic background of the strain and the production season.

In conclusion, while the AA genotype at the A1795>T locus appears to be the most stable genetic marker for improving egg weight in local Iraqi chickens (14), the T1749>C site serves as a complementary genetic driver whose significance is tied to specific physiological stages and environmental interactions (15), as shown in Table 2.

Table 2. Effect of growth hormone (GH) gene polymorphisms (A1795>T and T1749>C) on weekly egg weight (g) in Iraqi local chickens (Means $\pm$ SE)

Association of Growth Hormone Gene Polymorphisms (A1795>T and T1749>C) with Productive Performance and Egg Quality in Iraqi Indigenous Chickens

Week	Genotype: A1795>T (AA)										Genotype: T1749>C (TT)										Significance
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
1	4	7	.	6	6	±	7	.	2	3	47.81±5.59	N.S	4	8	.						
2	5	0	.	7	0	±	5	.	3	8	51.31±5.66	N.S	5	1	.						
3	5	0	.	8	7	±	4	.	6	2	50.06±5.93	N.S	5	1	.						
4	5	1	.	0	7	±	4	.	4	7	48.79±5.86	N.S	5	0	.						
5	5	1	.	1	4	±	4	.	0	4	50.32±5.22	N.S	5	1	.						

5. Effect of the Growth Hormone Gene A1795>T and T1749>C Polymorphisms on Weekly Egg Mass The polymorphisms of the GH gene and their effect on weekly egg mass are illustrated in Table 3. For the A1795>T site, the AA genotype demonstrated a clear statistical superiority during the late production phase (Weeks 11, 13, and 14) at a significant level ($P \leq 0.05$). This superiority suggests that the AA pattern not only enhances egg weight but also supports high production persistence. These results are consistent with previous findings (14, 1), which emphasized the role of the GH gene in optimizing metabolic efficiency and partitioning nutrients toward the oviduct.

Conversely, the T1749>C polymorphism exerted its most substantial influence during the early and peak production stages (Weeks 4, 5, and 11), specifically favoring the TT genotype ($P \leq 0.05$; $P \leq 0.01$). However, this significant effect diminished as the trial progressed toward the final stages. Such variation suggests that the T1749>C locus is closely associated with physiological maturation and the onset of peak laying. This period coincides with the zenith of growth hormone secretion, which plays a pivotal role in stimulating folliculogenesis and sustaining early reproductive performance.

Table 3. Effect of growth hormone gene SNPs (A1795>T and T1749>C) on egg mass in Iraqi local chickens (Means ± SE)

Week	Genotype: T1749>C (CC)	T1749>C (TC)	T1749>C (TT)	Significance (1)	Genotype: A1795>T (AA)	A1795>T (AT)	Significance (2)
1	86.32 ± 47.19	104.3 ± 55.87	113.5 ± 57.59	N.S	110.2 ± 57.61	96.51 ± 48.51	N.S
2	95.37 ± 109.9 ^b	86.96 ± 150.9 ^{ab}	99.11 ± 187.0 ^a	*	166.0 ± 99.73	178.3 ± 88.92	N.S

Association of Growth Hormone Gene Polymorphisms (A1795>T and T1749>C) with Productive Performance and Egg Quality in Iraqi Indigenous Chickens

							S
							.
3	84.60 ± 169.7		N	190.2 ± 79.74	183.2 ± 104.6	N	.
	188.8 ± 66.99	192.6 ± 91.86	.			.	.
			.			.	.
4	189.2 ± 79.56		N	210.1 ± 91.26	218.8 ± 88.65	N	.
	201.2 ± 75.66	220.7 ± 98.80	.			.	.
			.			.	.
5	178.2 ± 87.16		N	205.8 ± 99.14	170.8 ± 91.59	N	.
	188.1 ± 92.48	209.8 ± 103.2	.			.	.
			.			.	.
6	170.1 ± 103.8		N	205.9 ± 108.3	193.8 ± 112.1	N	.
	108.2 ± 186.1	218.9 ± 108.4	.			.	.
			.			.	.
7	62.96 ± 57.30		N	297.8 ± 142.5	81.05 ± 61.88	N	.
	97.79 ± 64.77	349.4 ± 161.9	.			.	.
			.			.	.
8	88.41 ± 136.3 ^a		*	193.4 ± 118.4	206.7 ± 108.7	N	.
	115.5 ± 212.3 ^b	119.5 ± 197.5 ^{ab}	*			.	.
			.			.	.
9	255.6 ± 137.2		N	244.1 ± 117.8	251.3 ± 110.7	N	.
	267.5 ± 102.4	232.2 ± 119.0	.			.	.
			.			.	.
10	214.7 ± 141.6		N	253.9 ± 126.5	235.0 ± 140.8	N	.
	266.9 ± 117.2	248.8 ± 132.3	.			.	.
			.			.	.
11	180.7 ± 110.8		N	220.2 ± 123.2	172.4 ± 136.6	N	.
	213.3 ± 132.2	217.2 ± 126.6	.			.	.
			.			.	.
12	260.3 ± 72.69		N	259.5 ± 117.5	248.6 ± 130.9	N	.
	287.9 ± 99.15	241.8 ± 132.6	.			.	.
			.			.	.
13	170.4 ± 102.1		N	198.0 ± 106.6	172.3 ± 147.1	N	.
	199.8 ± 102.0	194.7 ± 122.5	.			.	.
			.			.	.
14	95.55 ± 256.4 ^b		N	298.4 ± 126.1	282.4 ± 152.8	N	.
	111.4 ± 350.9 ^a	137.0 ± 274.5 ^b	.			.	.
			.			.	.
T	2441 ± 683.7		N	2898 ± 919.9	2691 ± 1132	N	.
o			.			.	.
t	2916 ± 736.4	2911 ± 1079	S			S	.
a			.			.	.
l			.			.	.
*Means with different superscripts within the same row differ significantly (P ≤ 0.05).							
**Means with different superscripts within the same row differ highly significantly (P ≤ 0.01).							
NS: No significant difference.							

6. Effect of the Growth Hormone Gene A1795>T and T1749>C Polymorphisms on Egg Quality Traits

The effects of the studied GH gene polymorphisms on egg quality traits are presented in Table 4. Eggshell weight exhibited a significant difference ($P \leq 0.05$) in favor of the AA genotype, suggesting that the GH gene may indirectly contribute to calcium deposition by influencing the IGF-1 hormone, which interacts with shell gland cell receptors (8). This finding is consistent with previous results (24), which linked GH stimulation to the activity of eggshell-secreting cells and increased shell hardness.

Furthermore, highly significant differences ($P \leq 0.01$) were observed favoring the AA genotype in terms of Haugh Unit (HU) values, a primary indicator of superior albumin quality and relative height. This result aligns with reports (10, 32) confirming that GH gene mutations are positively associated with higher HU values due to the hormone's pivotal role in maintaining protein equilibrium within the albumin during the egg formation process.

Table 4. Association of growth hormone (GH) gene genotypes with internal and external egg quality traits in Iraqi local chickens (Means $\pm$ SE)

Egg Quality Traits														
S	h	e	l	l		T	h	i	e	k	n	e	s	s
Y		o		I		k			w		e		i	
Y		o		I		k		h	e	i	g	h	t	
A		l	b	u	m	i	n		H	e	i	g	h	t
A		l	b	u	m	i	n		W	e	i	g	h	t
S		h	e	l	l			W	e	i	g	h	t	
H		a		u		g	h		U		n	i	t	(

7. Effect of the Growth Hormone Gene A1795>T and T1749>C Polymorphisms on Feed Conversion Ratio The study indicates that GH gene polymorphisms exert a stage-specific influence on FCR. The A1795>T locus (genotype AA) showed highly significant superiority ($P \leq 0.01$) during the 5th week, recording the best feed conversion efficiency (1.701) compared to the AT genotype (2.815). This is likely due to the stability of the wild-type allele (A) in this region, which optimizes metabolic sensitivity during production peaks.

Conversely, the T1749>C locus influenced early growth (Week 2), where the TT and TC genotypes demonstrated superior feed efficiency (2.711 and 3.081, respectively). This reflects the peak activity of the GH-IGF-1 axis during rapid protein deposition stages. Collectively, these findings suggest that the GH gene acts as a temporal metabolic regulator throughout the birds' developmental stages.

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The significant impact of the A1795>T and T1749>C polymorphisms on production traits, presumably mediated by the GH-IGF-1 axis, requires further molecular functional classification. If these SNPs are located within the exonic regions, they may act as missense mutations, potentially altering the amino acid sequence and structural conformation of the GH protein, thereby affecting its binding affinity to target receptors. Conversely, if located in the intronic or regulatory regions, these variations could influence mRNA splicing efficiency, mRNA stability, or transcription rates (1) .

In either case, the resultant modulation in circulating GH and IGF-1 levels directly impacts nutrient partitioning toward the oviduct, explaining the observed variations in egg weight and FCR.

Table 5. Effect of growth hormone gene SNPs (A1795>T and T1749>C) on feed conversion ratio in Iraqi local chickens (Means $\pm$ SE)

Week (Feed Conversion n)	CC (C>1749T)	TC (C>1749T)	TT (C>1749T)	Sig. (C>1749T)	AA (A1795>T)	AT (A1795>T)	Sig. (A1795>T)
1	9.458 $\pm$ 5.783	8.390 $\pm$ 4.680	7.397 $\pm$ 4.740	N.S	7.852 $\pm$ 4.976	8.209 $\pm$ 4.169	N.S
2	5.974 $\pm$ 7.876 a	3.081 $\pm$ 4.766 b	2.711 $\pm$ 4.035 b	*	4.650 $\pm$ 3.493	4.471 $\pm$ 2.903	N.S
3	4.482 $\pm$ 3.203	3.926 $\pm$ 2.077	3.693 $\pm$ 2.093	N.S	3.793 $\pm$ 2.077	4.136 $\pm$ 2.858	N.S
4	3.388 $\pm$ 1.056	4.209 $\pm$ 2.803	3.708 $\pm$ 3.239	N.S	3.677 $\pm$ 2.444	4.579 $\pm$ 4.678	N.S
5	3.647 $\pm$ 1.519	4.068 $\pm$ 2.260	3.401 $\pm$ 1.866	N.S	1.701 $\pm$ 3.434 b	2.815 $\pm$ 4.593 a	**
6	5.181 $\pm$ 4.506	4.956 $\pm$ 3.780	3.607 $\pm$ 3.146	N.S	4.010 $\pm$ 3.328	5.045 $\pm$ 4.402	N.S
7	8.945 $\pm$ 3.969	6.606 $\pm$ 3.070	6.466 $\pm$ 3.975	N.S	6.867 $\pm$ 3.911	5.870 $\pm$ 2.402	N.S
8	4.359 $\pm$ 1.462	3.197 $\pm$ 1.471	3.932 $\pm$ 2.943	N.S	3.850 $\pm$ 2.638	3.261 $\pm$ 1.379	N.S
9	3.639 $\pm$ 4.079	2.794 $\pm$ 2.055	3.202 $\pm$ 1.155	N.S	3.248 $\pm$ 2.558	2.456 $\pm$ 0.423	N.S
10	4.545 $\pm$ 3.971	2.867 $\pm$ 1.549	3.124 $\pm$ 2.625	N.S	3.255 $\pm$ 2.628	2.836 $\pm$ 1.969	N.S
11	4.774 $\pm$ 3.690	4.405 $\pm$ 3.995	3.771 $\pm$ 2.569	N.S	4.011 $\pm$ 3.289	4.388 $\pm$ 2.403	N.S
12	2.859 $\pm$ 0.877	2.616 $\pm$ 1.420	3.807 $\pm$ 3.453	N.S	3.132 $\pm$ 2.259	4.324 $\pm$ 4.665	N.S
13	5.253 $\pm$ 4.748	3.943 $\pm$ 2.409	4.021 $\pm$ 3.119	N.S	4.157 $\pm$ 3.073	3.935 $\pm$ 3.482	N.S
14	4.020 $\pm$ 1.922	2.552 $\pm$ 0.732	4.055 $\pm$ 3.485	N.S	3.417 $\pm$ 2.435	4.456 $\pm$ 4.346	N.S
total	4.231 $\pm$ 1.221	3.796 $\pm$ 2.513	6.428 $\pm$ 12.260	N.S	5.217 $\pm$ 9.891	6.339 $\pm$ 8.259	N.S
*Means with different superscripts within the same row differ significantly ($P \leq 0.05$).							
**Means with different superscripts within the same row differ highly significantly ($P \leq 0.01$).							
NS: No significant difference.							

Table (5) reveals significant differences ($P \leq 0.05$) in the Feed Conversion Ratio (FCR) during the second week only among the genotypes of the GH gene T1749>C polymorphism. The TT and TC genotypes demonstrated superior feed efficiency (lower FCR) compared to the CC genotype, whereas no significant differences were recorded during the remaining weeks. These findings suggest that the impact of this genomic region is stage-specific, predominantly influencing the early growth phase. This period is characterized by peak GH gene expression levels during the initial weeks of the bird's life, which gradually decline with advancing age, consistent with the findings of (19).

8. Effect of the Growth Hormone Gene A1795>T and T1749>C Polymorphisms on Blood Biochemical Traits The results indicated a lack of significant differences (NS) between the AA and AT genotypes at the A1795>T locus, as well as among the TT, TC, and CC genotypes at the T1749>C locus, across all studied blood biochemical traits. This lack of significance suggests a state of physiological homeostasis, indicating that these metabolites are regulated by complex interactions involving multiple hormonal axes, such as insulin, glucagon, and thyroxin, rather than the isolated effect of a single gene. These findings align with previous reports noting the limited isolated genetic effect of the GH gene on serum profiles in the absence of physiological stressors (3, 16).

Furthermore, the results suggest that biochemical traits are often polygenic and influenced by various homeostatic mechanisms regulating their secretion (3). It is possible that significant results could be obtained if multiple genes were studied simultaneously to account for the statistical interactions between different genetic variants.

Furthermore, to fully elucidate the adaptive significance of these SNPs, it is highly recommended that future investigations evaluate their impact under environmental stressors. Specifically, studying these genetic variants under conditions of high ambient temperatures a common challenge in the Iraqi climate could reveal latent associations between the GH gene and blood biochemical profiles that are not apparent under the state of physiological homeostasis maintained during standard management conditions, as summarized in Table 6.

Table 6. Effect of growth hormone (GH) gene polymorphisms (A1795>T and T1749>C) on blood biochemical traits in Iraqi local chickens (Means $\pm$ SE)

Traits (Unit)	Site A1795>T (AA)	Site A1795>T (AT)	Site T1749>C (CC)	Site T1749>C (TC)	Site T1749>C (TT)	Sig. 2
Glucose (mg/dl)	238.0±32.13	239.6±27.52	N.S	224.8±14.84	238.3±22.88	240.7±32.84 N.S
Cholesterol (mg/dl)	163.0±48.21	157.8±45.30	N.S	172.6±48.07	152.2±39.13	165.3±51.15 N.S
Triglycerides (mg/dl)	548.2±27.84	541.9±58.11	N.S	551.7±10.26	553.9±15.67	542.9±42.69 N.S
HDL (mg/dl)	51.33±11.39	54.93±10.42	N.S	53.40±12.45	53.13±10.56	51.07±11.52 N.S
LDL (mg/dl)	23.12±8.869	21.62±4.814	N.S	22.20±6.957	22.48±8.728	23.19±8.460 N.S
VLDL (mg/dl)	92.15±41.10	81.25±37.29	N.S	97.00±34.65	77.55±33.22	95.66±43.79 N.S
Total Protein (g/dl)	5.377±0.542	5.434±0.596	N.S	5.177±0.443	5.364±0.658	5.434±0.503 N.S
Globulin (g/dl)	2.989±0.528	3.012±0.510	N.S	2.804±0.453	2.952±0.621	3.047±0.476 N.S
Albumin (g/dl)	2.416±0.264	2.421±0.161	N.S	2.473±0.343	2.421±0.224	2.404±0.246 N.S
NS: No significant difference (P > 0.05).						

Conclusion

In light of the aforementioned findings, it is evident that the Growth Hormone (GH) gene serves as a temporal metabolic regulator, exerting stage-specific influences throughout the birds' developmental and physiological phases. This study demonstrates that the identified Single Nucleotide Polymorphisms (A1795>T and T1749>C) possess a significant directional impact on production performance, particularly regarding the Feed Conversion Ratio (FCR) and egg quality traits. Such genetic variations reflect a flexible metabolic response in Iraqi indigenous poultry, enabling a functional balance between high production demands and physiological homeostasis.

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ارتباط تعدد أشكال جين هرمون النمو (A1795>T و T1749>C) بالأداء الإنتاجي وجودة البيض في الدجاج العراقي المحلي

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بسام ج.م. الخطيب

يُعدّ جين هرمون النمو (GH) مؤشراً رئيسياً لتحسين الصفات الإنتاجية في الدواجن نظراً لدوره الأساسي في النمو والتمثيل الغذائي والتكاثر. هدفت هذه الدراسة إلى بحث العلاقة بين نوعين محددين من تعدد أشكال النوكليوتيدات المفردة (SNPs) في جين هرمون النمو (A1795>T و T1749>C) والأداء الإنتاجي والفسولوجي، بالإضافة إلى الحالة الأيضية للدجاج العراقي المحلي. تم تحديد النمط الجيني لـ 100 دجاجة محلية باستخدام تقنية تفاعل البوليميراز المتسلسل (PCR) متبوعةً بتسلسل سانجر. شملت الصفات الإنتاجية وزن الجسم عند النضج الجنسي، ومعدل إنتاج البيض، وكتلة البيض، ومعامل تحويل العلف (FCR)، بالإضافة إلى المؤشرات الفسيولوجية. كشف تحليل التسلسل عن اختلافات جينية ذات دلالة إحصائية عالية ($P \leq 0.01$) ارتبطت تعدد الأشكال A1795>T ارتباطاً وثيقاً ($P \leq 0.05$) بوزن البيض، وبعض صفات جودة البيض، ومعامل تحويل العلف، حيث أظهر النمط الجيني AT أداءً متفوقاً في هذه المعايير. علاوة على ذلك، أظهر تعدد الأشكال T1749>C تأثيراً معنوياً للغاية ($P \leq 0.05$) و ($P \leq 0.01$) على وزن البيض، وإنتاج البيض، وكتلة البيض، ومعامل تحويل العلف. في المقابل، لم تُظهر بعض الصفات الأخرى فروقاً معنوية ($P \leq 0.05$)، مما يشير إلى دور وراثي محايد لهذه المؤشرات في جوانب إنتاجية محددة. تشير هذه النتائج إلى أن تعدد الأشكال النوكليوتيدية المفردة A1795>T و T1749>C في جين هرمون النمو يمكن أن تُستخدم كمؤشرات جينية فعالة في برامج الانتقاء المدعوم بالعلامات الجينية لتعزيز الإمكانات الوراثية للدواجن العراقية المحلية مع الحفاظ على تكيفها البيئي.

الكلمات المفتاحية: جين هرمون النمو، تعدد الأشكال النوكليوتيدية المفردة، تحليل التسلسل، الدجاج العراقي المحلي، إنتاج البيض، الانتقاء المدعوم بالعلامات الجينية.