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Relationship of MyoD1 (myogenic) gene polymorphism with production performance of for Pekin ducks raised in Iraq

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Abstract

This study was conducted in the education hall of the Animal Production Field at the Faculty of Agriculture at the University of Basra from 10-10-2025 to 5-12-2025 and this study aimed at the relationship between genetic polymorphism of the MyoD1 gene and some productive traits of the Raised Pekin ducks in Iraq, and the use of 100 unnaturalized ducklings at the age of one day with an average weight of 45 grams and distributed. The birds were randomly measured inside the breeding hall and then the weights of the birds were measured at the ages of (2, 4, 6, 8) weeks and both weight gain, feed conversion efficiency, amount of feed consumed and live body weight were calculated, and 65 samples of bird blood were collected at the age of 8 weeks before slaughter in order to complete the work of the genetic aspect of the study, which includes DNA extraction and detection of the genetic formations of the MyoD1 gene and its relationship with Yielding and carcass traits where the results showed that there is heterogeneity in the nitrogenous base of Adnine A and the thymine base at the site of A>T260 in the second segment of the first axon of the MyoD1 gene and resulted in three genetic formations that led to significant differences ($p < 0.05$.) at the ages (2, 4, 6, 8) weeks of overweight, feed conversion efficiency, amount of feed consumed and body weight, as the highest averages were reached in the genetic polymorphism AA followed by AT TT, in each of the productive traits that were calculated as well as.

Keywords: MyoD1, myogenic, polymorphism, production performance

Introduction

Ducks rank second in the world in terms of the abundance of domesticated poultry species, after chickens (Bello *et al.*, 2022) ^[4]. Ducks are characterized by their ease of breeding and their low susceptibility to many common diseases in poultry (Abo Ghanima., 2020 (Global production of duck meat and eggs has been increasing in recent years, with Asia being the main producer and China leading the way as the largest contributor to this sector.) ^[2] Huang *et al.*, 2012; Zeng *et al.*, 2016) ^[7]. Genetic improvement programs for ducks for meat production have significantly enhanced their production performance (Fouad *et al.*, 2018) ^[18]. The MyoD1 gene is a key gene in the process of muscle formation (Myogenesis) and encodes a protein that acts as a transcription factor that regulates muscle gene expression and plays a crucial role in the transformation of stem cells into muscle cells (Xinyang Dong *et al.*, 2019). The duck MyoD1 gene was found to be located on the fifth chromosome and contains three exons, and the gene length (61603575- 61606523 (NCBL) and the structure of the introns differ in sequence of the MyoD1 gene by species (Wu *et al.*, 2012) ^[15]. (Baylies, 2001) ^[3]. Several studies have shown that birds and mammals have one copy of the MyoD1 gene (Session *et al.*, 2016) ^[13]. Many fish have been found to have more than one copy of the MyoD1 gene (Fisher *et al.*, 2003) ^[6]. This may be due to the occurrence of complete genome duplication (WGD) in bony fish (Macqueen, 2008; Aase-Remedios, 2020) ^[10, 1].

The aim of this study is to determine the best genetic makeup in terms of production performance to be used as an electoral marker in genetic improvement programs for domestic ducks.

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Materials & Procedures

This study was conducted in a hall of the Animal Production Field at the Faculty of Agriculture at the University of Basra from 10-10-2025 to 5-12-2025. Ducklings were raised under traditional conditions and in this study, 100 birds of local ducks with a lifespan of one day to 8 weeks were used and the birds were fed freely on two ready-made feeders, the first one containing (18% protein and energy represented 2900 kcal/kg) and continued. The brood was introduced to 3 weeks of the bird's life, while the second brood was a growth brood containing (20% crude protein and an energy of 3100 kcal/kg) up to 8 weeks of the bird's life (N.R.C.1994) and the birds were also free to access the water continuously, and the lighting program was applied during the study period and 65 blood samples were collected

before slaughtering them at the age of 8 weeks, and the blood samples were kept in vacuum tubes containing an anticoagulant agent (EDTA) and tubes were shaken to mix the blood with an anticoagulant, and then the samples were transported in a refrigerated container and the blood samples were preserved in the laboratory at a temperature of (-18) °C, after which the DNA extraction procedure was performed. The use of ARMS PCR technology for a piece of the first exon, and through the use of NCBI. The presence of heterogeneity in the wild allele was detected in this piece of the first exon of this gene and the ARMS PCR technique was worked on, through which the location of the heterogeneity at the site of 260 bp was known, and using the Electrophoresis technique of the samples, the genetic polymorphism of each sample was detected and known.

Table 1: The primer used for the first AX1 fragment of the first exon segment of the Myod1 gene

Product Size		Prefixes	Gene
476 Base Pairs	Outer F	CTTCTCTGTCCCTGGTCATTTAGCTGA	Myod1
	Outer R	AGCAAGTGGCTGAAAGTACTCATTGTG	
226 Base Pairs	inner primer (A allele):	GATAAAAATACATTCTCTCGGCAACTGAT	ARMS-PCR
307 Base Pairs	inner primer (T allele):	ATGCAAAACATGGTTTAAAGACTGGGGT	

Results and discussion

The results of electrophoresis amplify the MyoD1 gene and detect Nitrogenous bases in the nitrogenous bases. The results of electrolysis on an agarose gel with a concentration of 1.5% showed the appearance of a bundle with a size of

476 base pairs, the appearance of a bundle of 226 base pairs (for allele A), as well as the appearance of a bundle of 307 base pairs (for the T allele) in addition to the genetic genotype. The mixture is AT, as shown in Figure (1).



Fig 1: Results of the first exon segment of the MyoD1 gene amplification on agarose gel at a concentration of 1.5%.

As in figure 2, the presence of a substitution of the nitrogenous base adenine (A) with the thymine base (T) at the A>T260 site of the first exon segment of the MyoD1

gene of the amplified segment by aligning the nucleic acid sequence using the BioEdit program of the first exon fragment.

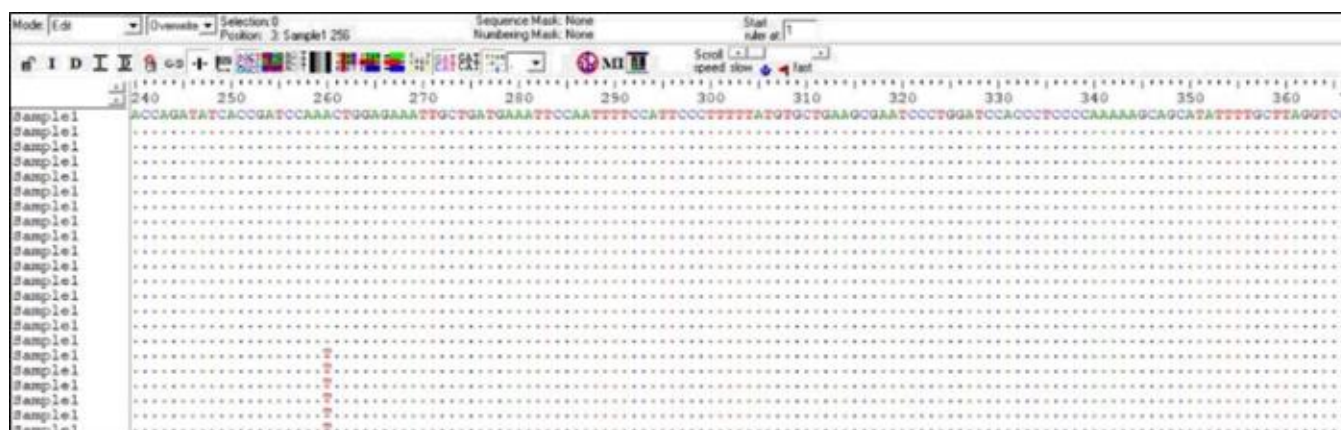


Fig 2: Results Sequence alignment of the first exon segment of the MyoD1 gene

Table 2: Effect of genetic polymorphism of the first exon segment of the MyoD1 gene on the amount of feed consumed

Total Feed Consumed	Age/Week				Genetic makeup
	8	6	4	2	
5804.6a+ -	2021.634a+ -	1719.487a+ -	1422.804a+ -	640.756a+ -	AA
53.198	19.282	20.768	11.662	7.308	
5084.0b	1705.454b	1527.363b	1305.272b	545.909b	AT
+	+	+	+	+	
-	-	-	-	-	
18.787	14.258	6.991	5.346	2.858	
4674.0c	1509.600c	1406.700c	1289.100c	468.600c	TT
+	+	+	+	+	
-	-	-	-	-	
17.181	9.447	5.011	6.181	4.664	
*	*	*	*	*	Significant

Feed consumption and feed conversion efficiency are economically important traits in ducks Table (2) the results showed significant differences ($P<0.05$) between the genetic polymorphisms. AA genetic polymorphism was superior in the amount of feed consumed at the age of two weeks (640.756) g, and the superiority continued until 8 weeks of age in favor of AA genetic polymorphism, as the feed consumption (g/bird) reached (2021.634) g, and results are consistent with (Zhang *et al.* 2017), The average amount of feed consumed for Peking ducks was 5773.26 gm during

the age period of 42 days, close to the results of AA genetic polymorphism in this study, which was 5804.6 g. The results of the current study were similar to the findings of Li GS *et al.* (2020) ^[17, 9], where the average total amount of feed consumed was 5.36 kg/bird, and a positive and strong genetic correlation was observed between the amount of feed consumed and the final body weight, where the correlation reached within the range of (0.40 – 0.91) at 42 days of age, and growth and the body's food need (Zhang *et al.*, 2017) ^[17].

Table 3: Effect of genetic polymorphism in the first exon segment of the MyoD1 gene on weight gain in ducks

Total weight gain	Age in week				Genetic makeup
	6-8	4-6	2-4	0-2	
2120.243^a + -3.237	534.195^a + -2.019	592.365^a + -5.250	548.829^a + -1.329	444.853^a + -2.694	AA
1996.727^b + -4.081	495.181^b + -3.269	582.090^b + -1.268	520.090^b + -1.090	399.363^b + -2.899	AT
1852.40^c + -	460.900^c + -	535.700^c + -	503.200^c + -	352.600^c + -	TT
5.23	1.642	1.813	1.339	5.371	
*	*	*	*	*	Significant

Table (3) shows significant differences ($p<0.050$) in weight gain across different age periods. The genotype of the first segment of the MyoD1 gene, AA, achieved the highest weight gain during the period (0-2 weeks), reaching 444.852 g. For the AT and TT genotypes, the weight gain during the period (0-2 weeks) was 503.200 and 520.090 g, respectively. Weight gain continued in favor of the AA genotype, followed by the AT and TT genotypes, until the age of 8 weeks. As)Al-Fayyad and Naji 1989) demonstrated, birds exhibit a high rate of weight gain during their early ages, which then gradually decreases with age. Furthermore,

Zhang and Wu (2012) indicated that genetic polymorphisms in the second intron of the MyoD1 gene are significantly associated with body weight at 8 weeks of age. Many carcass traits, such as breast weight, thigh muscle weight, and dressing percentage. The results showed that the MyoD1 gene contributes to the process of regulating muscle growth, which positively affects weight gain, and also confirms the possibility of using it as a candidate gene that can be used in genetic selection programs to improve growth traits in ducks.

Table 4: Effect of genetic polymorphism in the first exon segment of the MyoD1 gene on average feed conversion efficiency (g/g weight gain) of ducks

Total Nutrient Conversion Efficiency	Age/Week				Genetic makeup
	8	6	4	2	
2.737a+ -0.240	3.786a+ -0.391	2.908a+ -0.362	2.593+ -0.218	1.442a+ -0.185	AA
2.546b+ -0.115	3.446b+ -0.407	2.624b+ -0.148	2.510+ -0.139	1.367ba+ -0.126	AT
2.523b+ -0.094	3.275c+ -0.257	2.626b+ -0.158	2.561+ -0.163	1.331b+ -0.210	TT
*	*	*	N	*	Significant

Table (4) The results show that there are significant differences ($p<0.05$) between the genetic structures of the first exon fragment of the MyoD1 gene and the averages of feed conversion efficiency (g / g of overweight), where the best genotype (TT) was achieved in the efficiency of food conversion at the age of two weeks, where the average of (1.331) g / g feed/g weight gain was achieved, while the average genotype was 1.442 (AA) The average of the two was (1.367) g/g feed/g weight gain, and at 4 weeks of age,

there were no significant differences ($P>0.05$) between the genetic polymorphisms because the efficiency of food conversion is considered one of the quantitative traits (QTL) that are controlled by many genes and in addition, are affected by many environmental and administrative factors.)Li *et al.*, 2022) ^[8] while the AT genotype achieved the lowest value in the efficiency of feed conversion at 6 weeks of age, amounting to (2.624) g feed, followed by TT and AA, which reached (2.626, 2.908) g / g overweight, and

the superiority continued in favor of the TT genotype, as the efficiency of dietary conversion at 8 weeks of age reached (3.275) g / g feed/g weight gain, followed by the genetic makeup AT and These results of TT genotype at 6 weeks of age were consistent with the results of Li *et al.* (2020) ^[9], where the efficiency of food conversion at the age of 21 to 42 days was (2.61) kg in Peking ducks, as it was shown in

their study that the efficiency of food conversion is considered one of the traits with high heritability, which confirms that it can be improved through genetic selection programs. Zhang *et al.* (2017) ^[17] also indicated that when studying the efficiency of feed conversion, it was an average at the age of (15-42) at 2.53 g of feed/g weight gain.

Table 5: Effect of genetic polymorphism in the first exon segment of the MyoD1 gene on the average body weight of ducks

Final Body Weight	Age/Week				Genetic makeup
	8	6	4	2	
2165.243a+ - 3.237	2165.243a+ - 3.237	1631.048a+ - 4.838	1038.682a+ - 2.435	489.853a+ - 2.694	AA
2041.727b+ - 4.081	2041.727b+ - 4.081	1546.545b+ - 2.465	964.454b+ - 2.559	444.363b+ - 2.899	AT
1897.400c+ - 5.232	1897.400c+ - 5.232	1436.500c+ - 5.055	900.800c+ - 4.649	397.600c+ - 5.371	TT
*	*	*	*	*	Significant

Table (5) shows that there are significant differences ($p < 0.05$) between the genetic polymorphisms of the first exon segment of the MyoD1 gene *in vivo* weight between individuals. At genotype age of 2 weeks, the AA genotype significantly outperformed, achieving a better mean (489.853) g compared to the rest of the other genetic polymorphisms, and at the age of 4 weeks, the superiority in favor of the AA genotype continued until the eighth week. As explained by (Zhang, Wu ana 2012) when studying three breeds of ducks (Cherry Valley, Muscovy, and Jingjiang), the results showed that the presence of a mutation at the A359T site in the second intron of the MyoD1 gene has a significant effect ($p < 0.05$) on body weight at the age of [8] weeks, where the highest average body weight was the AA genotype (3038.67 g), while the genotype of AT (2916.56) was recorded as an average between the compositions (AA and AT) genotype for the Cherry Valley ducks, and the highest average body weight (1946.85) g at the age of 8 weeks for the TT genotype was significantly superior to the genetic makeup of AA and AT for Muscovy ducks and Jingjiang ducks. No significant differences were observed *in vivo* weight ($p > 0.05$) for the genetic structure (AA, AT, TT) genotype, and the reason may be attributed to the genetic background of the strain, the small effect of the A359T mutation in this strain, or the genetic influence. The results showed that individuals carrying the AA genotype of the MyoD1 gene recorded the highest weight and had higher levels of the gene expression of the MyoD1 gene at the site of (G.2967A>G, g.3044G>A) as shown by (Bhuiyan *et al.*, 2009) ^[5] when studying the detection of nucleotide polymorphism (SNPs) in the MyoD1 gene. The results showed that the mutation in the g.1274G>A site in the first intron was significantly related to body weight and carcass weight in Korean cows.

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