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Association Between LMO4 Gene Polymorphism and Body Weight Traits in Iraqi Awassi Lambs

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Abstract: In 2023, 120 ewes of the indigenous, unimproved Awassi breed were used in the current investigation, which was carried out at a private sheep breeding facility in the center of Iraq. According to alleles resulting from single nucleotide polymorphism in both positions, the results indicated a significant difference (P≤0.01) in the sample distribution. At location 20782 of the LMO4 gene, two alleles with three genotypes—GG, GA, and AA—were found as a consequence of point mutation. Male Awassi lambs' body weight was greatly impacted by the LMO4 gene polymorphism; the lambs with the mutant genotype had the greatest birth weight, with a significant difference in birth weight (P≤0.05), 4.75 kg, whereas lambs with the hetero genotype weighed the least at 3.21 kg, and lambs with the wild type weighed the most at 4.27 kg. The LMO4 gene polymorphism had a significant (P≤ 0.05) impact on the birth and weaning weight of female lambs. The wild genotype lambs weighed the most, at 4.33 and 17.37 kg, respectively, while the heterogeneous lambs weighed the least, at 3.08 and 13.25 kg.

Keywords: *LMO4 Gene, Awassi Sheep, Body Weight.*

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I. INTRODUCTION

Since the majority of Iraqis favor mouton, Iraqi sheep breeds are quite significant, widely distributed throughout the nation, and highly adaptable. They are also regarded as the primary source of income for many households in desert regions or nations. The Awassi sheep breed is one of the most important and well-known in Iraq due to its advantageous traits and capacity to adapt to challenging agricultural conditions, such as poor pastures and heat stress in semi-tropical areas. [1].

Genetic and environmental influences both impact body weight of farm animals at different ages. These can be referred to as environmental factors in relation to the genotype of the animal. [2]. The fertility of the herd determines sheep productivity, and economically significant traits that are also crucial to production success are lambs' body weight at different age points. [3]. A reliable measure of production efficiency is lambs per ewe, which is influenced by both environmental and genetic components [4].

Several of these genetic markers have already been demonstrated in previous research to be valuable in selection and to increase or generate the performance of breeds. The LMO4 gene, for example, is a marker that is found on sheep chromosome 21 and contains two bases. It is regarded as a significant member of the cystein-rich protein-coding gene family [5].

According to recent studies, the LMO4 gene is one of several genes that are involved in muscular activities or functions that sustain body growth and development. It also regulates histon alteration during mitotic cell division [6].

Investigating the LMO4 gene single nucleotide polymorphism, its impact on sheep milk production, and using genotypes to select the best individuals through indirect selection are the main aims of the current study.

II. MATERIALS AND METHODS

120 Awassi ewes of the local, unimproved Awassi breed were used in the current study, which was carried out in 2023 at a private sheep breeding farm in the central region of Iraq.

Genetic sequencing at the time was carried out in the ASCO laboratory of Baghdad (AL-Harithya) to isolate DNA and determine genotypes for the cystein rich protein gene (LMO4) at position 20782.

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In accordance with the protocol of [7], blood samples were extracted from the jugular vein, and DNA was extracted using a Promega company supplement. The target area, which is found in the second exon, was amplified and detected using the primer:

- *GCCAGATTATGGGACTCAAG and TGCAAAGCCTGTGGTAAG*

908 bp was the product size, and the annealing temperature was around 60 c° for both forward and reverse processes.

Body weight was taken in birth and weaning for all lambs by balance with high accuracy.

A Quantus Fluorometer was used to evaluate the concentration of extracted DNA in order to assess the quality of samples for use in later procedures. One microliter of DNA was mixed with 200 microliters of diluted Quantifluor Dye. After five minutes of room temperature incubation, DNA concentration values were obtained.

PCR products were sent to Macrogen Corporation in Korea so they could be Sanger sequenced using the ABI3730XL, an automated DNA sequencer. Geneious software was used to examine the results when they were received via email.

Statistical analysis: Data were analyzed using SAS [8] computer and Chi- square test was used to determine the significant differences among phenotypes:

$$X^2 = \sum \frac{(Observed\ No. - Expected\ No.)^2}{Expected\ No.}.$$

According to the linear model below, the significant difference between groups that differed with genotypes (mutant, hetero, and wild) was ascertained using the Duncan multiple range test [9] and the analyses of variance technique in accordance with a totally randomized design:

Following model:

$Yijk = \mu + Ti + eijk$

Where: μ: the overall mean
Ti: effect of single nucleotide change
eijk : is a random error.

III. RESULTS AND DISCUSSION

The results showed a significant difference (P≤0.01) in the sample distribution based on alleles originating from single nucleotide polymorphism in both places (Table 1). At location 20782 of the LMO4 gene, two co-dominant alleles and three genotypes (GG, GA, and AA) were discovered. Point mutations that altered the nitrogen base from guanine (wild type) to adenine (mutant type) were the source of these.

The genotype rates for GG, GA, and AA were 54.17, 30.00, and 15.83%, respectively, whereas the allele frequencies for the G and A alleles were 0.704 and 0.296.

Table -1: Distribution of Genotypes and Allele Frequency of LMO4 Gene (20782 Position).

Genotype	No.	%	Allele frequency	
GG	65	54.17	G	A
CA	39	30.0	0.704	0.296
AA	16	15.83		
Chi-square	54.4667**			

**(P≤0.01)

The findings indicated that in male Awassi lambs, the LMO4 gene polymorphism had a substantial impact on body weight (Fig. 1), and that the LMO4 genotype (site 20782) significantly affected the birth weight (BW) (P≤0.05). Lambs with the mutant genotype (GG) weighed the most at birth (4.75 kg), while lambs with the hetero genotype (CG) weighed the least (3.21 kg), and lambs with the wild type (CC) weighed the moderate amount (4.27 kg).

The LMO4 gene polymorphism also caused a substantial difference in weaning weight; the lambs with the mutant genotype had the greatest body weight at weaning (WW), while the lambs with the hetero genotype had the lowest weight, 20.65 and 11.14 kg, respectively.

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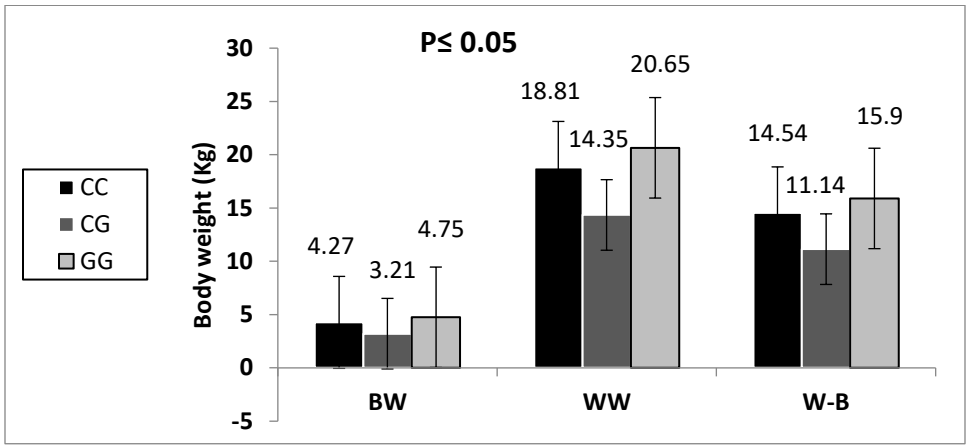

Fig. 1: Relationship of LMO4 Gene Polymorphism with Body Weight in Male Awassi Lambs

The body gain from birth to weaning (W-B) in male Awassi lambs was differed significantly (P0.05), the highest body weight gain was recorded in lambs with mutant genotype (15.9 kg) while the body weight gain was 14.54 and 11.14 kg for both lambs with wild and hetero genotypes respectively.

Female lambs at birth and weaning age are substantially (P≤ 0.05) impacted by the LMO4 gene polymorphism (Fig.2). The female lambs with hetero genotype (CG) had the lowest birth and weaning weights, 3.08 and 13.25 kg, respectively, whereas the lambs with wild genotype (CC) had the greatest weights, 4.33 and 17.37 kg, respectively.

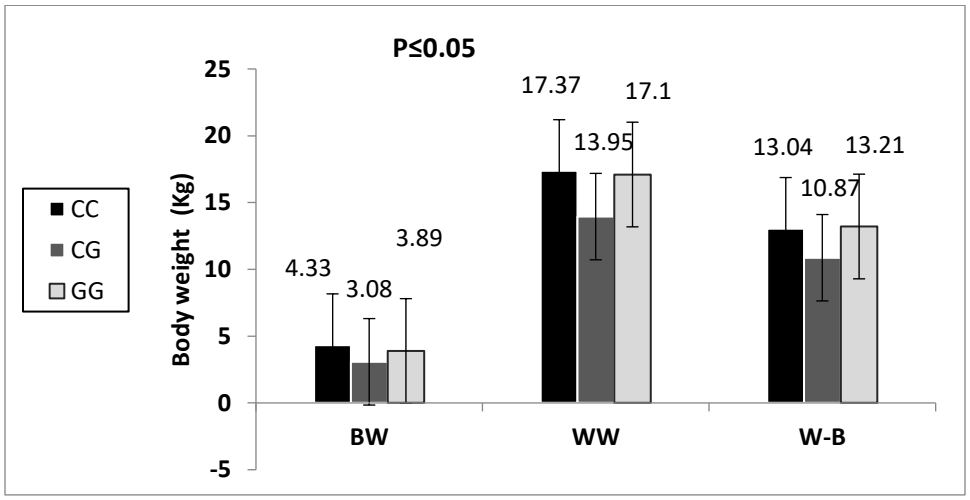

Fig. 2: Relationship of LMO4 gene polymorphism with body weight in female Awassi lambs

The present study's findings were consistent and corroborated several other investigations that suggested this gene or related genes had a major impact on sheep performance in numerous global locations. According to [10,11,12,13], genetic variables impact milk yield or composition to varying degrees. A few genes that affect sheep milk performance will be examined for their important roles, including those in the gene family.

Many past studies indicated that the LMO4 gene play a real role in body development in many mammalian species such as sheep [14] and the action of this gene is related with many genes leading to combined effects in many physiological path ways inside the body which reflexes positively in productive performance and development. STAT3, a key downstream target of LMO4, is crucial in controlling the antiapoptotic signaling in cisplatin ototoxicity[17]. LMO4 also functions as a scaffold for protein complexes and binds with a number of transcription factors and coregulators that encourage the transcription of anti-apoptotic genes [15,16].

IV. CONCLUSION

In conclusion, LMO4 gene is one of the important genes with a wide effects on body growth and dairy production in sheep and we can use it for indirect selection to improve the sheep performance through choosing or select the good individuals with stabile genotypes and depend on this gene in selection programs.

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