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Effect of melatonin receptor gene polymorphism in body weight and dimension born local goats.

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ABSTRACT

Background this study was conducted on a sample of (42) pregnant local goats in the animal field of the Animal Production Department / College of Agriculture / University of Diyala for the period from (12/10/2024) to (10/2/2025).

Methods: The study aimed to extract genetic material (DNA), determine the Genotype of the melatonin receptor gene MTNR1A and its relationship to the growth characteristics of mothers and newborns. The polymerase chain reaction (PCR) technique was used, as the results of molecular analysis of the polymerase chain reaction (PCR) product showed the emergence of four genetic variations within Studied region. The first SNP is T22927C (TT=29, TC=3, CC=4), the second variation is G23011A GG=29), GA=5, AA=2), the third variation is C23195T CT=22), CT=12, TT=2), and the fourth variation is C23195T CT=22, CT=12, TT=2. A23362C (CC=19, AC=14, AA=3).

Results: the results of the current study showed significant differences in the studied variations in the weights of the newborns and the body dimensions of the newborns as well as the mother, where the genetic variation G23011A had a significant difference in the abdominal circumference of the mother, where the genotype AA was superior to the genotypes GG and GA, but as for the weight and length of the mother's body, the height of the forelock and the height of the rear, as well as the girth heart circumference, there were no significant differences, as for the genetic variations T22927C, (C23195T), and (A23362C), there were no significant differences in the weight and length of the mother's body, the height of the forelock and the rear, as well as the chest and abdominal circumference. Regarding the birth weaning weight and body dimensions of the newborns

Conclusions: The A23362C SNP had a significant effect on chest and abdominal circumferences of the newborns at weaning, with the AC genotype outperforming the CC and AA genotypes. No significant differences were found for the C23195T SNP in terms of birth and weaning weight and body dimensions of the newborn significant differences were found for the A23362C SNP in terms of weaning weight and body dimensions.

Introduction

Goats play a vital role in global livestock systems, especially in developing regions, where they contribute significantly to improving the livelihoods of small farmers through their milk and meat production[1]. Goats are considered one of the most adaptable animals due to their ability to adapt to living under harsh climatic conditions, and they are the most productive animals with poor nutrition and scarcity of fodder in pastures compared to cows and sheep[2]. Due to the increase in population around the world, the demand for animal products has increased, which prompted researchers to find ways to improve and increase the productivity of animals, including goats[3]. Local goat breeds are genetically different from other breeds and more suitable for genetic change, wich provides a good background for these breeds to improve them genetically and preserve them in the future[4]. Iraqi goats have high genetic diversity and adaptive immune genes, making them resistant to diseases and able to adapt to harsh environmental conditions, which enhances the value of Iraqi goats [5]. Iraqi goats are considered a primary genetic source adapted to local environmental conditions, as local goats can be crossed with foreign breeds to produce a goat breed capable of withstanding harsh environmental conditions and with high productivity [6]. The recent use of molecular genetics technologies has led to the discovery of genes that directly affect many important productive and economic traits, as well as the possibility of identifying The effect of these genes is determined by knowing the locations of the quantitative trait[7], which prompted researchers to seek more accurate, rapid, and efficient ways to improve these traits. Therefore, in 1990, researchers began studying the genes that primarily and directly affect these traits[8]. The productive performance of farm animals is affected by several factors, including diet, breed, environment, and lighting. Lighting is an essential element in the animal's environment, as the light period regulates the animal's biological rhythms and affects the secretion of many hormones within the body, especially melatonin, which regulates the secretion and release of many hormones through different pathways such as growth hormone, prolactin, and gonadotropin (GnRH)[9]. High levels of melatonin have a positive effect on reproduction for small ruminants. Melatonin functions through specific receptors located in different areas of the nervous system. Central, its circadian rhythm is mediated and its effects are mediated by specific receptors located on the pituitary and suprachiasmatic cells[10]. The number of chromosomes in goats is (60) chromosomes, i.e. (30) pairs, of which (29) pairs are autosomes and one pair is sex chromosomes [11].The melatonin receptor gene MTNR1A in goats is located on the long arm of chromosome number (27), specifically in the q14-15 region. This location was identified through a comparative study that used the fluorescence in situ hybridization (FISH) technique to determine the locations of three genes associated with fertility in goats, sheep, cows, and buffalo [12].The melatonin receptor MTNR1A consists of 350 amino acids[13] and two exons divided by approximately 8,000 base pairs (bp) of long introns [14]. The first exon shows a low degree of polymorphism [15]. The second exon is known to encode the MTNR1A gene for a multimeric MT1 receptor, so differences in receptor structure arise from changes in the second exon [16]. Given the importance of the light period in an animal's life, as it regulates its biological rhythms, it is necessary to study the relationship between the melatonin receptor A1 gene and pregnancy traits, milk production, and growth characteristics in goats, in addition to their extensive genetic diversity. Therefore, the study focused on:

1. Identifying the genotype of local goats raised in Iraq based on the frequencies and proportions of the melatonin receptor A1 gene genotypes.
2. Studying the effect of the melatonin receptor A1 gene polymorphisms the polymorphisms of the melatonin receptor A1 gene and animal performance and growth characteristics of mothers and offspring at birth and weaning.

Materials and Methods

The sample consisted of (42) goats. The laboratory work was conducted in the laboratory of the College of Agriculture / University of Diyala, during the period from (10/12/2024) to (2/10/2025), with the aim of extracting genetic material (DNA) and conducting electrophoresis, as well as conducting polymerase chain reaction (PCR) for the melatonin receptor A1 gene and its relationship to the growth characteristics of the mother and the offspring. The body dimensions and body weight of the mothers and the offspring (at birth and weaning) were measured. The measurements included (body length, hip height, hind hip height, abdominal circumference, chest circumference, and body weight). The dimensions were measured using a special measuring tape. The body weight of the mothers and the offspring was measured approximately 24 hours after birth using a 150 kg disc scale. The weight gain of the

young at weaning was also calculated. As for the blood samples, amounting to (42) samples, they were drawn from the jugular vein using a 10 ml medical syringe, and placed in tubes coated with the anticoagulant EDTA. The experiment used a device from the German company Gene Proof to extract genetic material (DNA Isolation Kit).

Table (1) Primers used to amplify the melatonin receptor gene A1, exon 2 [17]

Gene name	Sequence		fragment size (base pair)
MTNR1A	**Exon 2**	**F :** 5`-TGTGTTTGTGGTGAGCCTGG -3`	**824**
		R : 5`-ATGGAGAGGGTTTGCGTTTA -3`	

Then the program for amplifying the required fragment was determined using the PCR technique using the thermal cyclic reaction device, where the degree of binding of the primer (Annealing) to the complementary sequence in the template DNA for each region was determined as shown in Table (2), and the reaction volume was (23) microliters, as shown in Table (3).Then, the studied region of the melatonin receptor A1 gene for the second exon, with a size of 824 base pairs, was detected using the polymerase chain reaction (PCR) technique, with the aim of obtaining the polymerase chain reaction product, using the DNA extraction product, primers, and a PCR kit.

Table (2) Program used for molecular analysis using PCR technolog

Stages	Temperature Celsius	Time	Number of cycles
Initial denaturation	94	5 minutes	5
Denaturation	94	35 seconds	
Annealing	58	45 seconds	25
Elongation	72	45 seconds	
Final elongation	72	5 minutes	2
Final incubation	2	-	

Table (3) Materials used in the polymerase chain reaction (PCR)

Ingredients	Reaction volume (microliters)
Master Mix	12.5
Forward	1
Reverse	1
Distilled water	5.5
DNA	3
Final volume	23

Next, (5) µl of the PCR product was transferred to a 1% agar gel using a size marker (LEDR), and the voltage, current, and transfer time were set at 100 V for 20 minutes. The resulting images were then captured using a Gel Imaging System to ensure the replication of the target fragment. The bands appear bright orange with ethidium bromide staining, as shown in Figure (1). Subsequently, (20) µl of the PCR product was taken from each sample and sent to the Korean company Macrogen. After the results were obtained, the nucleotide sequence file was used to determine the presence or absence of variants, and the curves file was used to determine the apparent polymorphism of the four polymorphisms of the melatonin receptor A1 gene. The data were then statistically analyzed using SAS (2012) statistical software to determine the relationship between the geographic pattern of the melatonin receptor A1 gene and growth traits. Then, the test of significant differences between means was conducted using Duncan's multiple range test (Duncan, 1955).The mathematical model ($Yijm = \mu + Gi + eij$)

Yij = observation value due to the combination Genetic i.

µ = overall mean for the trait under study.

Gi = effect of the polymorphism of the melatonin receptor gene MTNR1A on the traits under study.

eij = random error, which is assumed to be randomly and normally distributed with a mean of zero and a variance of $\sigma^2 e$

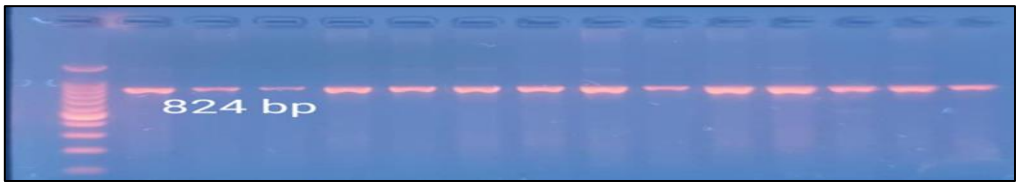

Figure (1) Transfer of the PCR results for the studied region of the melatonin receptor geneA1,exon 2.

Results and Discussion

The current research revealed the variations that occurred in the studied sample for a region of the melatonin receptor gene A1, the second exon, consisting of (824) nitrogenous bases. When conducting a sequence analysis of the nitrogenous bases, four snp were found, as shown in Figure (2, 3, 4, 5). All the snp that occurred did not change the amino acids, but rather the change was only in the nitrogenous bases. The first snp is T22927C with three genotype: TT, CC, and hybrid TC. The frequency of the dominant allele T was 0.84, while the mutant allele C was 0.16, and no change occurred in the amino acid. The second snp is G23011A with three genotype: GG, AA, and hybrid GA. The frequency of the dominant allele G was 0.88, while the mutant allele A was 0.12, and no change occurred in the amino acid. The third snp C23195T with three genotypes: CC, TT, and hybrid CT. The frequency of the dominant allele C was 0.75, while the frequency of the mutant allele T was 0.25, and no change occurred in the amino acid. The fourth snp, A23362C, with three genotypes: dominant CC, AA, and hybrid AC. The frequency of the dominant allele A was 0.19, while the frequency of the mutant allele C was 0.81. Also, no change occurred in the amino acid, as shown in Table (4) below. A highly significant superiority of the chi-square value ($P \leq 0.01$) was observed for all snp as follows: (59.71, 59.26, 26.21, 15.99), respectively.

Table (4) shows the number and percentages of genotype and allelic frequency of genetic variations in the melatonin receptor gene MTNR1A, exon 2.

Mutation	genotypes	number	observed	expected	chi-square value	allelic frequency
T*22927*C	TT	29	0.81	P^2=0.71	Total observed - expected)2/expected 59.71 P≤0.01	T=0.84 C=0.16
	TC	3	0.08	2pq=0.26		
	CC	4	0.11	q^2=0.03		
G*23011*A	GG	29	0.81	P^2=0.77	Total (observed - expected)2/expected 59.26 P≤0.01	G=0.88 A=0.12
	GA	5	0.13	2pq=0.21		
	AA	2	0.06	q^2=0.02		
C*23195*T	CC	22	0.61	P^2=0.56	Total (observed - expected)2/expected 26.21 P≤0.01	C=0.75 A=0.25
	CT	12	0.33	2pq=0.38		
	CC	2	0.06	q^2=0.06		
A*23362*C	CC	19	0.53	P^2=0.66	Total (observed - expected)2/expected 15.99 P≤0.01	C=0.81 A=0.19
	AC	14	0.39	2pq=0.31		
	AA	3	0.08	q^2=0.03		

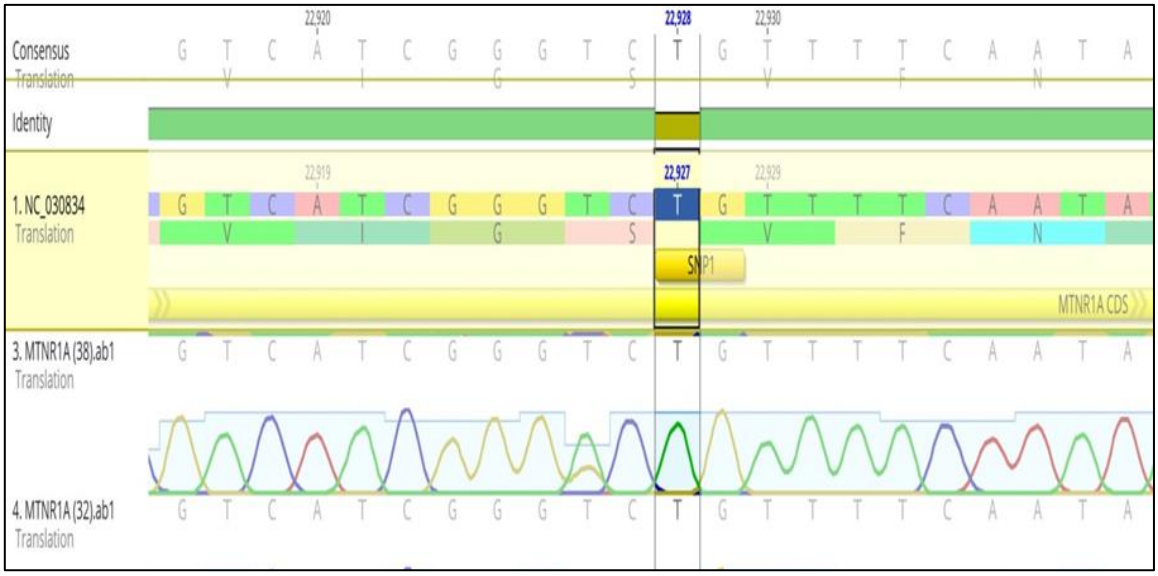

Figure (2) shows the location of the variation (T22927C) in the melatonin receptor gene

MTNR1A,Exon2.

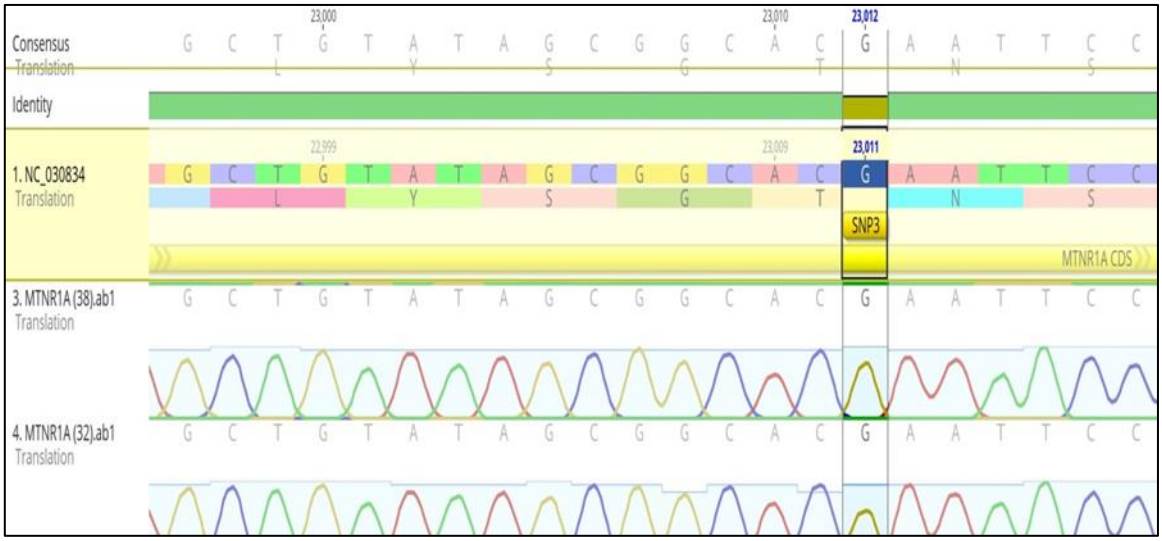

Figure (3) shows the location of the variation (G23011A) in the melatonin receptor gene MTNR1A Exon2.

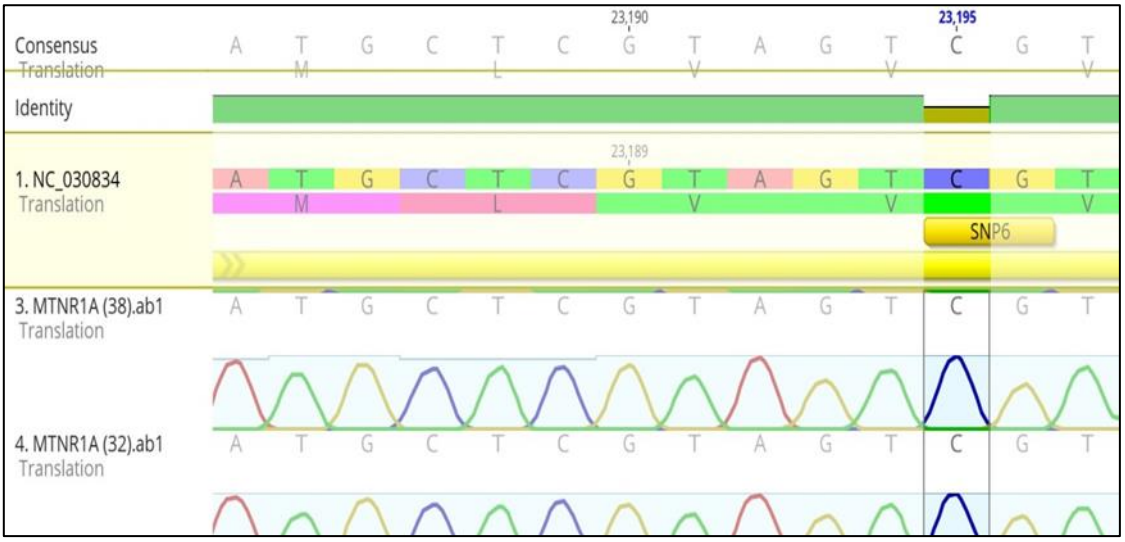

Figure (4) shows the location of the variation ((C23195T) in the melatonin receptor gene MTNR1A Exon2.

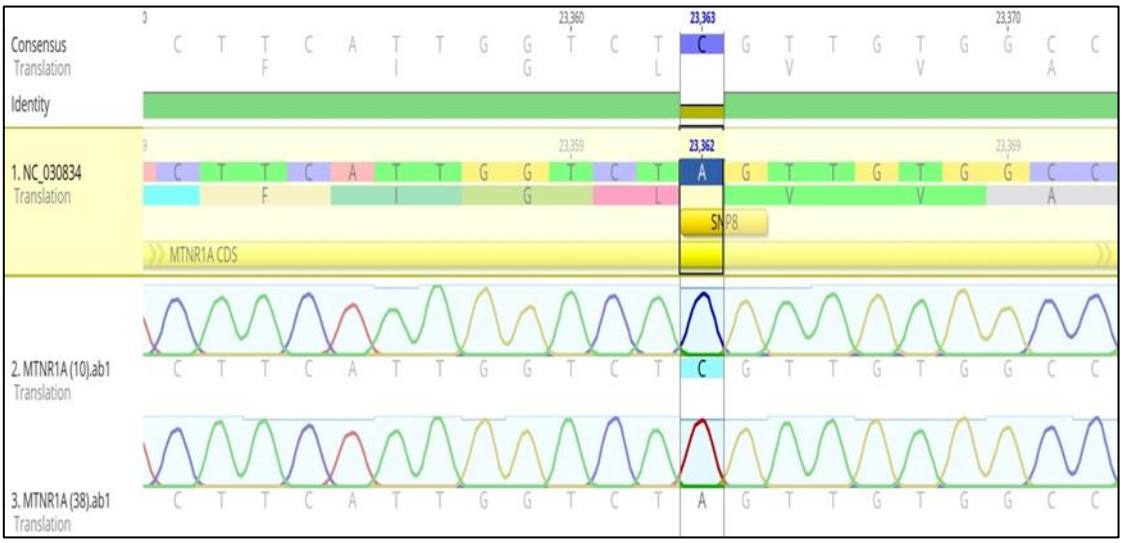

Figure (5) shows the location of the variations (A23362C) in the melatonin receptor gene MTNR1A Exon2.

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The effect of the studied genetic variants of the melatonin receptor gene MTNR1A, exon 2, on maternal weight and body dimensions at birth.

The results of the current study showed no significant differences between the genetic variants T22927C, C23195T, and A23362C in maternal body weight and length, fore- and hindquarter height, as well as chest and abdominal circumference. However, the genetic variant G23011A had a significant difference (P≤0.01) in abdominal circumference, with the AA genotype outperforming the GG and GA genotypes, with averages of 104.0%, 84.63%, and 82.60%, respectively. However, there were no significant differences in maternal body weight and length, fore- and hindquarter height, and chest circumference, as shown in Table (5).

Table (5) The effect of the studied genetic variations of the melatonin receptor gene MTNR1A, exon 2, on the weight and body dimensions of the mother at birth.

Abdominal circumference	Chest circumference	buttock height	Front rise	Body length	Mother's weight at birth	number	Geno types
First genetic SNP (T22927C)							
1.28±84.63	1.23±80.26	0.98±72.00	1.08±67.03	2.12±63.36	1.19±36.80	30	TT
3.71±87.33	3.28±78.33	2.96±69.66	2.00±65.00	2.00±62.00	3.84±31.66	3	TC
8.23±89.75	4.02±80.25	2.10±69.50	0.64±65.50	5.29±61.25	4.06±36.75	4	CC
N.S	N.S	N.S	N.S	N.S	N.S	Signifacant level	
Second genetic SNP (G23011A)							
±84.63 b1.28	1.23±80.26	0.98±72.00	1.08±67.03	2.12±63.36	1.19±36.80	30	GG
±82.60 b3.54	2.67±76.80	1.88±68.80	1.14±65.00	2.60±58.60	2.39±31.20	5	GA
±104.0 a1.00	1.00±86.00	3.5±71.5	1.00±66.00	6.00±69.00	3.00±43.00	2	AA
**	N.S	N.S	N.S	N.S	N.S	Signifacant level	
Third genetic SNP (C23195T)							
1.80±86.08	1.10±79.69	1.11±71.13	0.91±66.86	2.10±63.43	1.63±36.17	23	CC
2.03±83.83	2.65±81.08	1.60±71.91	2.19±66.08	3.89±62.33	1.15±37.58	12	CT
±87.00 10.00	4.00±79.00	1.00±74.00	1.50±68.50	4.50±62.50	0.50±31.50	2	TT
N.S	N.S	N.S	N.S	N.S	N.S	Signifacant level	
The fourth genetic SNP (A23362C)							
2.26±85.40	1.25±78.55	1.05±70.40	1.14±65.05	3.06±64.35	1.12±35.65	20	CC
1.49±84.85	2.12±82.50	1.61±72.57	1.44±68.14	1.88±61.64	2.37±37.71	14	AC
3.51±88.00	2.84±79.33	1.66±74.33	3.05±71.00	1.76±60.66	2.64±35.00	3	AA
N.S	N.S	N.S	N.S	N.S	N.S	Signifacant level	
** Different letters indicate a significant difference at a level of (P≤0.01). N.S indicates no significant differences.							

The effect of the studied genetic SNP of the melatonin receptor gene MTNR1A exon 2 on the birth weight and body dimensions of the newborn.

The current study showed significant differences for the studied genetic variation (T22927C) in birth weight and rump height. The TC genotype outperformed the TT and CC genotypes in terms of birth weight, reaching (4.01, 3.10, and 2.94%), respectively. As for rump height, the TC genotype outperformed the CC and TT genotypes, reaching (38.00, 34.16, and 32.12%), respectively, as shown in Table (6). As for the AA genotype at the SNP site (G23011A), a

significant difference was found in forelimb and rump height, with the AA genotype outperforming the GA and GG genotypes, reaching (36.33, 33.20, 31.48% for foreleg height, while the hindleg height reached (38.00, 33.10, 32.12%), respectively, for the same genotypes. This result is partially consistent with what [18] reached through an analysis of genetic polymorphisms of the melatonin receptor gene and their association with reproductive performance criteria for two breeds of Mediterranean sheep. The study showed three genotypes: GG, GA, and AA. No significant difference was detected between the three genotypes, as the fertility of the ewes and the size of the offspring were not affected. However, the ewes with the AA genotype gave birth to offspring with a higher weight than the GG and GA genotypes of one of the breeds. While no significant differences were found for the genetic SNP (C23195T), this result is inconsistent with the results of [19] in their study on Han short-tailed sheep of five breeds, where polymorphisms at five gene loci of the second exon of the MTNR1A gene were associated with birth size. The results of the association analysis within five gene loci and birth size in sheep with the TT genotype showed larger birth size than those with the CC and CT genotypes at other gene loci. The genetic SNP (A23362C) also caused any significant difference in birth weight and body dimensions of the offspring. This result is consistent with the what (12) has found [20]in their study on Iraqi local goats, where they found three genotypes: CC, AA, and CA. No relationship was found between birth weight, sex, and birth type (single or twin) with the genetic analysis model of the MTNR1A gene in goats. These results can be taken into account in goat selection programs to improve reproductive genetic traits in the future.

Table (6) Effect of the studied mutations in the melatonin gene MTNR1A exon 2 on the birth weight and body dimensions of the

Abdominal circumference	**Chest circumference**	**buttock height**	**Front rise**	**Body length**	**birth weight**	**number**	**Geno types**
First genetic SNP (T22927C)							
0.73±37.54	0.64±36.33	±32.12 b0.58	0.65±31.48	1.16±29.91	±3.10 b0.11	33	TT
5.50±37.50	2.00±37.00	±38.00 a2.00	2.00±36.00	1.50±34.50	±4.01 a0.59	2	TC
0.61±35.66	0.61±34.33	±34.16 ab2.24	1.27±33.83	2.82±29.83	±2.94 b0.26	6	CC
N.S	N.S	*	N.S	N.S	**	Significant level	
Second genetic SNP (G23011A)							
0.73±37.54	0.64±36.33	±32.12 b0.58	±31.48 b0.65	1.16±29.91	0.11±3.10	33	GG
1.80±36.60	1.20±34.80	±33.10 b2.27	±33.20 ab1.35	2.65±28.40	0.46±3.09	5	GA
1.20±35.33	0.33±35.33	±38.00 a2.51	±36.33 a1.20	2.72±35.33	0.11±3.40	3	AA
N.S	N.S	*	*	N.S	N.S	Significant level	
Third genetic SNP (C23195T)							
0.79±36.70	0.64±35.88	±33.11 0.75	0.73±32.00	1.38±30.19	0.13±3.13	27	CC
1.22±38.50	1.15±36.41	±32.25 1.13	1.19±32.25	1.59±30.00	0.19±3.15	12	CT
1.50±37.50	1.50±36.50	±30.00 2.00	1.50±31.50	5.00±30.00	0.44±2.76	2	TT
N.S	N.S	N.S	N.S	N.S	N.S	Significant level	
The fourth genetic SNP (A23362C)							

0.83±36.76	0.69±35.40	±32.00 0.79	0.74±31.72	1.01±30.32	0.11±2.84	25	CC
1.12±37.92	0.93±37.21	±33.64 1.00	1.11±32.57	2.46±29.87	0.17±3.57	14	AC
0±39.00	0.50±36.50	±35.00 1.00	0.50±32.50	0.50±29.50	0.14±3.48	2	AA
N.S	N.S	N.S	N.S	N.S	N.S	Significant level	
* Different letters within a single column differ significantly from each other at a significance level of (P≤0.05) according to Duncan's test. ** Different letters indicate a significant difference at a level of (P≤0.01). N.S indicates no significant differences.							

The effect of the studied genetic variations of the melatonin receptor gene MTNR1A exon 2 on the weight and body dimensions of the newborn at weaning.

The current study showed no significant differences between the four studied SNP (T22927C, G23011A, C23195T, and A23362C) in weaning weight, total weight gain, body length, and forelimb height, as shown in Table (7). However, the TT genotype at the T22927C snp site showed a higher significant difference than the TC and CC genotypes in hindquarter height, reaching (44.87%), 40.50%, and 39.33%, respectively. The GG genotype at the snp site (G23011A) also showed a significantly higher difference than the AA and GA genotypes in rump height (44.83, 40.00, and 39.66%), respectively. heterozygous geno type (AC) At the site (A23362C) showed a significantly higher difference than the CC and AA genotypes at the chest circumference (51.30, 48.11, and 44.50%), respectively, and abdominal circumference (54.50, 51.76, and 49.00%), respectively. The C23195T genotype did not show any significant differences in weaning weight, total weight gain, body length, fore-hind height, and chest and abdominal circumference of the newborns at weaning.

Table (7) The effect of the studied genetic SNP of the melatonin receptor gene MTNR1A, exon 2, on the weight and body dimensions of the newborn at weaning.

Abdominal circumference	**Chest circumference**	**buttock height**	**Front rise**	**Body length**	**Total weight gain**	**Weaning weight**	**number**	**Geno types**
First genetic SNP (T22927C)								
±52.20 0.72	±48.83 0.77	±44.87 a0.71	0.65±42.04	±43.58 0.69	0.31±5.19	±8.28 0.28	25	TT
±55.00 1.00	0±50.00	±40.50 ab2.50	1.50±40.50	±46.50 1.50	0.36±4.76	±8.77 0.23	2	TC
±53.33 1.66	±49.33 0.66	±39.33 b1.33	1.20±38.33	±44.00 1.00	0.75±5.22	±8.56 0.88	3	CC
	N.S	**	N.S	N.S	N.S	N.S	Significant level	
Second genetic SNP (G23011A)								
±52.20 0.72	0.77±48,83	±44.83a 0.77	0.65±42.04	±43.58 0.67	0.31±5.19	±8.28 0.38	25	GG
±55.00 0.57	0±50.00	±39.66 b1.66	1.00±40.00	±46.00 1.00	0.28±4.56	±8.30 0.48	3	GA
±52.50 2.50	1.00±49.00	±40.00 ab2.00	2.00±38.00	±43.50 1.50	0.95±5.75	±9.15 1.15	2	AA
N.S	N.S	**	N.S	N.S	N.S	N.S	Significant level	
Third genetic SNP (C23195T)								
±52.26	0.71±48.57	±44.10	0.71±42.94	±44.05	0.33±5.22	±8.14	20	CC

0.72		0.85		0.74		0.42		
±53.55 1.25	1.40±50.00	±43.55 1.47	1.19±40.55	±43.22 1.03	0.48±5.19	±8.95 0.54	9	CT
48.00	47.00	46.00	43.00	45.00	3.80	7.00	1	TT
N.S	N.S	N.S	N.S	N.S	N.S	N.S	Signifacant level	
The fourth genetic SNP (A23362C)								
±51.76 ab0.74	±48.11 ab0.66	±44.11 1.07	0.84±41.58	±43.64 0.69	0.39±5.22	±8.18 0.38	17	CC
±54.50 a1.03	±51.30 a1.02	±43.80 0.99	0.82±41.90	±44.60 1.16	0.37±5.34	±8.78 0.67	11	AC
±49.00 b1.00	±44.50 b2.50	±44.00 2.00	3.50±39.50	±41.50 1.50	0.58±3.80	±7.28 0.72	2	AA
*	**	N.S	N.S	N.S	N.S	N.S	Signifacant level	

* Different letters within a single column differ significantly from each other at a significance level of (P≤0.05) according to Duncan's test.
** Different letters indicate a significant difference at a level of (P≤0.01).
N.S indicates no significant differences.

Conclusions

The study results showed the presence of four genetic SNP within the studied region in exon 2, the first variation was T22927C, the second was G23011A, the third was C23195T, and the fourth was A23362C. There was a significant effect on the mother's body dimensions at birth with regard to abdominal circumference. There was also a significant effect on birth weight, weaning weight, total weight gain, and body dimensions of the newborns at birth and weaning. Therefore, more studies should be conducted on the melatonin receptor A1 gene and on a larger number of samples, as it affects the amount of replication of the desired gene and its relationship to growth traits in mothers and newborns

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Declaration of interests

The authors declare that they have no conflicts of interest.

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Data and material availability

All data generated and analyzed during this study are included in this published article.

Author contribution

Researchers' contribution in choosing the title, laboratory work, data analysis and writing.

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تأثير تعدد أشكال جين مستقبل الميلاتونين على وزن الجسم وأبعاده للمواليد في الماعز المحلي

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الملخص

نفذت هذه الدراسة على عينة مكونة من (42) معزة محلية حامل في الحقل الحيواني التابع لقسم الانتاج الحيواني / كلية الزراعة / جامعة ديالى للفترة من (1 / 10 / 2024) ولغاية (10 / 2 / 2025)، وكان الهدف منها استخلاص المادة الوراثية (DNA)، وتحديد التراكيب الوراثية لجين مستقبل الميلاتونين MTNR1A وعلاقته بصفات النمو للامهات والمواليد،

طرائق العمل وبينت نتائج التحليل الجزيئي لناتج (PCR) ظهور اربعة تغايرات وراثية ضمن المنطقة المدروسة، التغاير الاول هو T22927C (TT=29 ، TC=3 ، CC=4)، والتغايرالثاني هو G23011A (GG=29 ، GA=5 ، AA=2) والتغايرالثالث هو C23195T (CT=22 ، CT=12 ، TT=2)، والتغاير الرابع A23362C (CC=19 ، AC=14 ، AA=3)،

النتائج واظهرت نتائج الدراسة الحالية عن وجود فروقات معنوية للتغايرات المدروسة في اوزان المواليد الصغار وقياسات ابعاد الجسم للمواليد وكذلك الام، حيث كان للتغاير الوراثي (G23011A) فرق معنوي في محيط البطن للام ، حيث تفوق التركيب الوراثي AA على التركيبين الوراثيين GG و GA ، اما بالنسبة لوزن وطول جسم الام وارتفاع المقدمة وارتفاع المؤخرة وكذلك محيط الصدر لايوجد فروقات معنوية ،

الاستنتاجات: الطفرة الوراثية A23362C تأثيرٌ ملحوظ على محيط الصدر والبطن لدى المواليد عند الفطام، حيث تفوق النمط الجيني AC على النمطين الجينيين CC و .AA لم تُلاحظ فروقٌ ذات تأثير معنوي بالنسبة للطفرة الوراثية C23195T من حيث وزن المواليد عند الولادة والفطام وأبعاد ألجسم .

الكلمات المفتاحية: الصفات، الماعز المحلي، جين MTNR1A.