

## Individual genomic loci in the caprine $\beta$ -lactoglobulin gene linked to mastitis incidence in Baladi goats

Yosra Abdel-Maksoud

Mohamed Fouda

Adel AbdElkhalek

Ahmed Ateya

# Individual Genomic Loci in the Caprine $\beta$ -lactoglobulin Gene Linked to Mastitis Incidence in Baladi Goats

Yosra Abdel-Maksoud <sup>a</sup>, Mohamed Fouada <sup>b</sup>, Adel Abdelkhalek <sup>c</sup>, Ahmed Ateya <sup>d,\*</sup>

<sup>a</sup> Department of Development of Animal Wealth, Faculty of Veterinary Medicine, Badr University in Cairo (BUC), Cairo, Egypt

<sup>b</sup> Department of Husbandry, Mansoura University, Mansoura, Egypt

<sup>c</sup> Food Safety, Hygiene and Technology Department, Faculty of Veterinary Medicine, Badr University in Cairo (BUC), Egypt

<sup>d</sup> Department of Development of Animal Wealth, Faculty of Veterinary Medicine, Mansoura University, Mansoura, Egypt

## Abstract

**BACKGROUND:** This study aimed to investigate genetic differences in the  $\beta$ -lactoglobulin ( $\beta$ -LG) gene and its effect on mastitis tolerance/susceptibility in Baladi goats.

**METHODS:** Blood samples were collected from 30 female Baladi goats to extract DNA and loaded into tubes containing the anticoagulant, disodium EDTA. PCR was performed to amplify the  $\beta$ -LG gene's 427 base pairs of the  $\beta$ -LG gene.

**RESULTS:** PCR-DNA sequencing analysis identified  $\beta$ -LG gene differences taking the form of C390A single-nucleotide polymorphism correlated with mastitis tolerance in Baladi goats (GenBank with accession numbers gb|PP265530| and gb|PP265531| for healthy and mastitis, respectively).

**CONCLUSION:** The  $\beta$ -LG gene may be an intriguing indicator of mastitis susceptibility or resistance in goats, allowing for marker-assisted selection of tolerant individuals.

**Keywords:** Baladi does, Individual genomic loci, Mastitis incidence,  $\beta$ -Lactoglobulin gene

## 1. Introduction

Globally, developing nations produce the vast majority of goat milk; thus, goat milk plays an important role in nourishing millions of people and serves as an important source of meat, milk, and fiber [1]. It was recently concluded that goats will continue to play an important role in challenging circumstances in the subtropical tropics, deserts, and Mediterranean regions [2]. Nevertheless, goats are recognized for their ability to adapt to harsh environments [3].

There are four main Egyptian goat breeds, three of which are extensively distributed throughout the country: Egyptian Baladi goats in the Delta, Saidi goats in Upper Egypt, and Barki goats in the Northern Coastal Zone of the Western Desert. The

fourth most significant breed is Zaraibi goats (Egyptian Nubian), which have a great reputation as a prospective milk-productive breed and are raised in the Northeast Delta. Other minor indigenous breeds include Wahati goats in the New Valley, Black Sinai goats located in the Sinai Peninsula, and Abouramada-Halaieb-Shalateen goats in the Halaieb-Shalateen triangle [4].

Mastitis minimizes milk production and quality because of the interaction between various factors, including animals, the environment, and microorganisms. Infection of the udder frequently occurs straight up through the teat canal [5]. Thus, numerous microorganisms can influence mammary epithelial cells and alveolar function, impairing milk quality and quantity and posing a severe public health risk [6,7].

Received 5 February 2024; revised 23 March 2024; accepted 23 March 2024.  
Available online 21 June 2024

\* Corresponding author at: Department of Development of Animal Wealth, Faculty of Veterinary Medicine, Mansoura University, Gomhoria Street, Mansoura, PO Box 35516, Egypt.  
E-mail address: [ahmed\\_ismail888@yahoo.com](mailto:ahmed_ismail888@yahoo.com) (A. Ateya).

<https://doi.org/10.35943/2682-2512.1233>

2682-2512/© 2024, The author. Published by Faculty of Veterinary Medicine Mansoura University. This is an open access article under the CC BY 4.0 Licence (<https://creativecommons.org/licenses/by/4.0/>).

Mastitis may be localized within a single gland or diffuse inflammation in one or more mammary glands. Mastitis affects the parenchymal tissue. It causes the release of toxic compounds, resulting in lesions varying from increasing the infiltration of leukocytes without visible alterations in milk to hyperemia due to high vascular permeability, which can lead to fibrosis, toxemia, and milk loss [8].

$\beta$ -Lactoglobulin ( $\beta$ -LG) is an important protein in mammalian milk. It has a substantial effect on milk quality.  $\beta$ -LG is a highly acid-resistant protein with a molecular weight of 36,000 Da. The complete amino acid arrangement of  $\beta$ -LG has been defined, and genetic variations in its sequence have been identified [9]. Previous studies have analyzed  $\beta$ -LG gene polymorphisms using restriction fragment length polymorphisms (RFLP). This study investigated the potential association between the  $\beta$ -LG gene and the incidence of mastitis in Baladi goats using PCR-DNA sequencing.

## 2. Materials and methods

### 2.1. Ethics statement

Sample collection and handling of the animals used in this investigation conformed to the experimental animal protocols published by the Research Ethics Committee, Faculty of Veterinary Medicine, Mansoura University (code M139).

### 2.2. Animals

The current study included 30 female Baladi goats (*Capra hircus*) obtained from a private farm in MitGhamr city, Dakahlia, Egypt. The does were housed in shaded, semi-open pens and nourished with 650 g of concentrate feed mixture and 650 g of alfalfa hay per head each day, with unlimited access to water. A thorough clinical examination was performed on the goats by previously described standard protocols [10]. Clinical mastitis was identified based on physical examination of the mammary glands through inspection, palpation, and evaluation of milk produced for aberrant color and consistency. Physical examination also determined body temperature, pulse, and respiratory rates. Based on the aforementioned criteria, the investigated animals were assigned to two equal groups: 15 healthy and 15 mastitic. Blood samples were collected in vacuum tubes containing anticoagulants (sodium fluoride or EDTA) for DNA extraction.

### 2.3. DNA extraction and polymerase chain reaction

DNA was extracted from whole blood using a Biospin Blood/Cell/Tissue Genomic DNA Extraction Kit (Cat. No. BSC47S1; Bioer Technology, Munich, Hamburg, Germany). Before further analysis, the concentration and purity of the extracted DNA were examined using a Nanodrop (Uv-Vis spectrophotometer Q5000/USA, Waltham, MA, USA).

PCR was carried out to amplify a noncoding fragment (427 bp) of  $\beta$ -LG gene using previously described primers [11].

F: 5'- CGGGAGCCTTGGCCCCTCTGG -3'  
R: 5'- CCTTTGTCGAGTTTGGGTGT -3'.

The reaction mixture of PCR was performed with a final volume of 50  $\mu$ l containing 3  $\mu$ l DNA, 0.5  $\mu$ l of each primer, 25  $\mu$ l PCR master mix (GENE-DIREX, Waltham, MA, USA), and 21  $\mu$ l H<sub>2</sub>O (d. d. water). The final reaction mixture was placed in Benchmark TC 9639 Gradient Thermal Cycler (Sayreville, New Jersey, USA) and exposed to initial denaturation 94 for 4 min, followed by 34 cycles of denaturation at 94 °C for 40 s, annealing at 60 °C for 1 min, extension at 72 °C for 2 min, and final extension at 72 °C for 10 min. PCR products were held at 4 °C and detected by agarose gel (2%) electrophoresis, then the fragment patterns were visualized under ultraviolet using a gel documentation system (Analytik Jena, Munich, Hamburg, Germany).

### 2.4. DNA sequencing

Before DNA sequencing, primer dimers, nonspecific bands, and other impurities were removed [12]. A PCR purification kit (Jena Bioscience # pp-201s/ Munich, Hamburg, Germany) was used to purify PCR products. To guarantee acceptable quantities and purity of the PCR products, they were quantified using Nanodrop (NanoDrop One/OneC UV-Vis; Thermo Fisher Scientific, Munich, Hamburg, Germany) [13]. The results of PCR-containing target bands in all studied does (15 healthy and 15 mastitic) were submitted for forward and reverse DNA sequencing using an ABI 3730XL DNA sequencer (Applied Biosystems, Munich, Hamburg, Germany).

For analysis of DNA sequencing data, Blast 2.0 and chromas 1.45 (<http://www.technelysium.com.au>) were utilized [14]. Single-nucleotide polymorphisms (SNPs) have been detected in PCR products of the  $\beta$ -LG gene in all animals analyzed and GenBank-based reference sequences. Furthermore, a neighbor-

joining phylogenetic tree was constructed to clarify the grouping between the DNA sequence under investigation and the reference sequence obtained from GenBank [15].

### 3. Results

#### 3.1. Clinical findings

Clinically, healthy Baladi produce typical, regular milk and do not have any mammary anomalies. Patients with mastitis have swollen, heated, hard, and extremely painful udder. Milk production was drastically reduced and the milk was dense and yellow. Respiratory and rectal temperatures in this group increased. The mean rectal temperature in this group was 41.5 °C.

#### 3.2. Association between nucleotide sequence variation in $\beta$ -lactoglobulin gene and mastitis susceptibility

PCR-DNA sequencing revealed SNP differences in amplified nucleotide sequences linked to mastitis incidence in healthy and affected animals for the  $\beta$ -LG (427 bp) gene (submitted to GenBank with accession numbers gb|PP265530| and gb|PP265531| for healthy and mastitis does). Among the 30 analyzed does (15 healthy and 15 mastitic), nine healthy ones had the A390C SNP (Fig. 1). The identified SNP was validated using representative DNA sequence variations between the  $\beta$ -LG gene analyzed in the investigated does and the reference gene nucleotide sequence obtained from GenBank (Fig. 2).

According to the SNP Fisher's exact test, the  $\beta$ -LG gene was shown to be significantly different in both normal and mastitis-affected does ( $P < 0.01$ ). As illustrated in Fig. 3, the neighbor-joining phylogenetic tree of the representative sequenced samples, when compared to the GenBank reference accession number gb|KM817769.1|, revealed that healthy animals exhibiting the discovered SNP were located in one cluster, and the remaining animals were in a different cluster.

### 4. Discussion

Genetics plays a vital role in milk production, quality, and disease resistance. Genetic polymorphisms could be used in marker-assisted selection for various target traits [16], especially mastitis resistance and milk production traits in small ruminants [17]. Current methods for controlling mastitis rely on prophylactic and antibiotic treatments. Identifying a genetic marker that allows the inclusion of mastitis resistance in selection

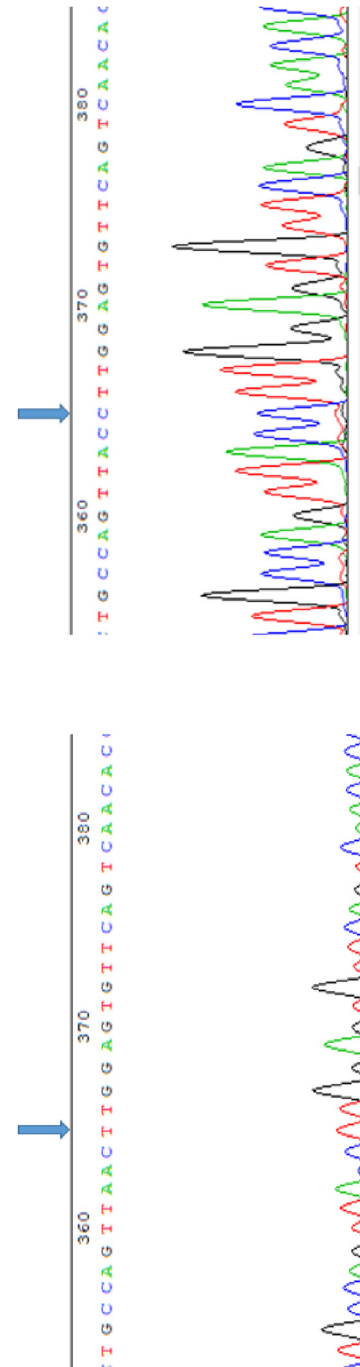


Fig. 1. Partial chromatograph of  $\beta$ -LG gene (427 bp) between healthy (H) and mastitis (M) does indicating T/C SNP.  $\beta$ -LG,  $\beta$ -lactoglobulin; SNP, single-nucleotide polymorphism.

KM817769.1	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
PP265530	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
M2	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
M3	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
M4	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
M5	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
M6	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
M7	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
M8	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
M9	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
M10	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
M11	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
M12	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
M13	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
M14	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
M15	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
H10	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
H11	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
H12	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
H13	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
H14	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
H115	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
PP265531	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
H2	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
H3	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
H4	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
H5	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
H6	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
H7	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
H8	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
H9	CGGGAGCCTTGGCCCCCTCTGGGGACAGACGACGTACCCCCGCCTCCCCATCAGGGGGA	60
	*****	
KM817769.1	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
PP265530	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
M2	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
M3	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
M4	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
M5	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
M6	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
M7	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
M8	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
M9	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
M10	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
M11	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
M12	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
M13	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
M14	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
M15	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
H10	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
H11	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
H12	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
H13	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
H14	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
H115	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
PP265531	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
H2	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
H3	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
H4	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
H5	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
H6	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
H7	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
H8	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
H9	CCAGGAGGGACCGGGACCGCGGTACCTCTCTCTGGGACCCAGGCCCTCCAGGCCCTCC	120
	*****	

Fig. 2 Representative DNA sequence alignment of  $\beta$ -LG gene (427-bp) between healthy (H) and mastitis (M) does and reference sequence available in GenBank gb|KM817769.1|. Asterisks represent similarity.  $\beta$ -LG,  $\beta$ -lactoglobulin.





KM817769.1	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
PP265530	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
M2	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
M3	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
M4	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
M5	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
M6	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
M7	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
M8	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
M9	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
M10	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
M11	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
M12	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
M13	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
M14	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
M15	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
H10	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
H11	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
H12	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
H13	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
H14	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
H115	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
PP265531	AGGGACTCAGCAGAGATATCTGCCAGTTACCTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
H2	AGGGACTCAGCAGAGATATCTGCCAGTTAACTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
H3	AGGGACTCAGCAGAGATATCTGCCAGTTAACTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
H4	AGGGACTCAGCAGAGATATCTGCCAGTTAACTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
H5	AGGGACTCAGCAGAGATATCTGCCAGTTAACTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
H6	AGGGACTCAGCAGAGATATCTGCCAGTTAACTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
H7	AGGGACTCAGCAGAGATATCTGCCAGTTAACTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
H8	AGGGACTCAGCAGAGATATCTGCCAGTTAACTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
H9	AGGGACTCAGCAGAGATATCTGCCAGTTAACTTGGAGTGTTCAAGTCAACACCCAAACTCG	420
	*****	
KM817769.1	ACAAAGG	427
PP265530	ACAAAGG	427
M2	ACAAAGG	427
M3	ACAAAGG	427
M4	ACAAAGG	427
M5	ACAAAGG	427
M6	ACAAAGG	427
M7	ACAAAGG	427
M8	ACAAAGG	427
M9	ACAAAGG	427
M10	ACAAAGG	427
M11	ACAAAGG	427
M12	ACAAAGG	427
M13	ACAAAGG	427
M14	ACAAAGG	427
M15	ACAAAGG	427
H10	ACAAAGG	427
H11	ACAAAGG	427
H12	ACAAAGG	427
H13	ACAAAGG	427
H14	ACAAAGG	427
H115	ACAAAGG	427
PP265531	ACAAAGG	427
H2	ACAAAGG	427
H3	ACAAAGG	427
H4	ACAAAGG	427
H5	ACAAAGG	427
H6	ACAAAGG	427
H7	ACAAAGG	427
H8	ACAAAGG	427
H9	ACAAAGG	427
	*****	

Fig. 2 (continued).

programs would help reduce the economic impact of the disease as well as the use of antibiotics.

Mastitis has low heritability, making it challenging to select mastitis-resistant animals. Therefore, selective breeding can lower mastitis incidence in goats, using suitable candidate genes associated with mastitis resistance as  $\beta$ -LG gene [18]. This study aimed to detect nucleotide sequence variations in  $\beta$ -LG gene sequence as a possible genetic marker of mastitis resistance in Baladi goats using PCR-DNA sequencing. In this context, PCR-DNA sequencing was carried out for the molecular characterization of a 427-bp fragment of  $\beta$ -LG gene in Baladi goats exposed to environmental conditions in Egypt.

Our results revealed nucleotide sequence variations among the enrolled does associated with

mastitis susceptibility (submitted to GenBank with accession numbers gb|PP265530| and gb|PP265531| for healthy and mastitic does). Interestingly, the denoted SNP was considered novel compared to the GenBank reference sequence. In contrast to earlier studies, this study investigated polymorphisms using SNP genetic markers, a more accurate method than RFLP, to compare the prevalence of mastitis in healthy and mastitic individuals. SNP genetic markers have revolutionized breed genetic classification, biodiversity assessment, and conservation decision-making [19]. Compared with other markers, SNP studies may provide a more precise picture of the evolution of European cattle [20,21]. In addition, SNPs are believed to be particularly significant when attempting to find links between a



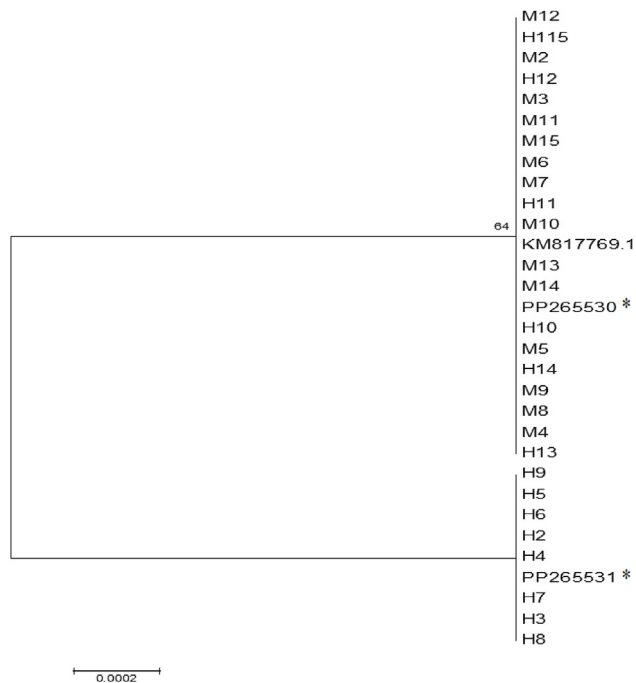


Fig. 3. Representative neighbor-joining phylogenetic tree of  $\beta$ -LG gene between the healthy (H) (GenBank accession number PP265531) and mastitis (M) (GenBank accession number PP265530). Goats compared with the reference accession number gb|KM817769.1|.  $\beta$ -LG,  $\beta$ -lactoglobulin.

marker at an unknown gene locus and a known location in the genome. The search for such associations is crucial because it is possible to evaluate phenotypic effects by comprehending their genetic foundation [22,23].

According to the findings of our study, the  $\beta$ -LG gene (427-bp) contains a SNP, C390A. The modified mutant base in the buffalo database is preserved based on the results of the basal local alignment search algorithm (BLAST) (GenBank accession number JF274007.1). Furthermore, a database with a modified mutant base for cattle (GenBank accession number DQ489319.1) has been preserved. The close relationship among ruminant species, for whom genetic resource conservation initiatives help boost numbers and preserve important gene reservoirs, may cause the conservation behavior in the modified bases [24].

$\beta$ -LG gene plays a significant role in mastitis resistance and tolerance in cattle [25]. This gene has bactericidal and bacteriostatic actions against pathogenic agents of mastitis. Previous studies have investigated the relationship between the  $\beta$ -LG gene and milk composition via RFLP.  $\beta$ -LG gene appears to greatly impact on milk yield and composition (fat and protein) [26,27]. Interestingly, there is previous information on the association between  $\beta$ -LG gene and mastitis resistance in ruminants, including

cattle [28–31] and sheep [32]; however, there is little information about the relationship between  $\beta$ -LG gene and mastitis resistance in goats.

Certain challenges to this study that should be considered in the future. First, a larger number of animals should be considered. Furthermore, several goat breeds should be investigated. Finally, PCR-DNA sequencing should be performed on different potential genes related to mastitis resistance or susceptibility.

## 5. Conclusion

PCR-DNA sequencing of the  $\beta$ -LG gene in 30 animals of the Baladi goat breed (15 healthy and 15 mastitic) demonstrated nucleotide sequence variations (SNPs) between healthy and mastitic goats. These functional differences offer a viable way to reduce the incidence of mastitis using genetic markers alongside regular goat selection. Therefore, the gene investigated in this study provides a useful management strategy for goat mastitis.

## Declaration

### Ethical approval

The authors confirm the ethical policies of the journal, as noted on the journal's author guidelines page, with approval number (code M139) obtained from the Research Ethics Committee, Faculty of Veterinary Medicine, Mansoura University, Egypt.

### Authors' contributions

AA Writing – review & editing, Writing – original draft, Methodology, Data curation, Conceptualization. YA Writing – original draft, Methodology. MF and AK Writing – original draft, Data curation.

### Funding

The authors (s) received no financial support for the research, authorship, and/or publication of this article.

### Data availability

The data supporting the findings of this study are available from the corresponding author upon reasonable request.

### Conflicts of interest

The authors declare no conflicts of interest.

### Informed consent

The owner of the private farm has been informed of the nature of the project and agreed to participate in the research project.

### Acknowledgements

We gratefully acknowledge all members of the Department of Animal Wealth Development, Faculty of Veterinary Medicine, Mansoura University for their help and support. We also want to acknowledge the Veterinary Medicine School of Badr University in Cairo for their assistance.

### References

- [1] Mureithi S, Wambugu S, Huho J. Determinants of spatial variation and adoption of dairy goat farming in nyeri county. *J Env Sust Adv Res* 2022;8:57–65.
- [2] Silanikove N, Koluman N. Impact of climate change on the dairy industry in temperate zones: predications on the overall negative impact and on the positive role of dairy goats in adaptation to earth warming. *Small Rumin Res* 2015; 123:27–34.
- [3] Silanikove N. Effects of heat stress on the welfare of extensively managed domestic ruminants. *Livest Prod Sci* 2000;67: 1–18.
- [4] De Pauw E, Rischkowsky B, Abou-Naga A, Ansari-Renani H, Boujen I, Gursoy O. Using production environment description and GIS tools to identify potential natural environments for animal genetic resources. Aleppo, Syria: ICARDA Technical Document; 2011.
- [5] Abu A, Mhomga L, Akogwu E. Assessment of udder characteristics of West African Dwarf (WAD) goats reared under different management systems in Makurdi, Benue State, Nigeria. *Afr J Agric Res* 2013;8:3255–8.
- [6] Lee J-W, O'Brien CN, Guidry AJ, Paape MJ, Shafer-Weaver KA, Zhao X. Effect of a trivalent vaccine against *Staphylococcus aureus* mastitis lymphocyte subpopulations, antibody production, and neutrophil phagocytosis. *Can J Vet Res* 2005;69:11.
- [7] Addis MF, Cubeddu T, Pilicchi Y, Rocca S, Piccinini R. Chronic intramammary infection by *Listeria monocytogenes* in a clinically healthy goat—a case report. *BMC Vet Res* 2019; 15:1–7.
- [8] Ahmed YF, Ezzo OH, Mansour S. Some udder problems associated with productivity in goats. *Egypt J Vet Sci* 2020;51: 1–9.
- [9] Rachagani S, Gupta ID, Gupta N, Gupta S. Genotyping of  $\beta$ -Lactoglobulin gene by PCR-RFLP in Sahiwal and Tharparkar cattle breeds. *BMC Genet* 2006;7:1–4.
- [10] Pugh DG, Baird NN. *Sheep & Goat Medicine-E-Book*. Elsevier/Saunders: Maryland Heights, MO, USA; 2012.
- [11] Isik R, Bilgen G, Kosum N, Kandemir Ç, Taskin T, editors. Polymorphism in Exon 7 of  $\beta$ -Lactoglobulin ( $\beta$ -LG) Gene and Its Association with Milk Yield in Saanen Goats. *Tekirdağ Ziraat Fakültesi Dergisi. The Special Issue of 2<sup>nd</sup> International Balkan Agriculture Congress* May 16–18, 2017.
- [12] Boom R, Sol C, Salimans M, Jansen C, Wertheim-van Dillen P, Van der Noordaa J. Rapid and simple method for purification of nucleic acids. *J Clin Microbiol* 1990;28:495–503.
- [13] Boesenberg-Smith KA, Pessaraki MM, Wolk DM. Assessment of DNA yield and purity: an overlooked detail of pcr troubleshooting. *Clin Microbiol Newsl* 2012;34:1–6.
- [14] Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. Basic local alignment search tool. *J Mol Biol* 1990;215:403–10.
- [15] Tamura K, Stecher G, Kumar S. MEGA11: molecular evolutionary genetics analysis version 11. *Mol Biol Evol* 2021; 38:3022–7.
- [16] Fragomeni B, Lourenco D, Legarra A, VanRaden P, Misztal I. Alternative SNP weighting for single-step genomic best linear unbiased predictor evaluation of stature in US Holsteins in the presence of selected sequence variants. *J Dairy Sci* 2019;102:10012–9.
- [17] Akhatayeva Z, Bi Y, He Y, Khan R, Li J, Li H, et al. Survey of the relationship between polymorphisms within the BMP1B gene and sheep reproductive traits. *Anim Biotechnol* 2023;34:718–27.
- [18] Cai Z, Guldbbrandtsen B, Lund MS, Sahana G. Prioritizing candidate genes post-GWAS using multiple sources of data for mastitis resistance in dairy cattle. *BMC Genom* 2018;19: 1–11.
- [19] Groeneveld LF, Lenstra JA, Eding H, Toro MA, Scherf B, Pilling D, et al. Genetic diversity in farm animals – a review. *Anim Genet* 2010;41(s1):6–31.
- [20] Gautier M, Faraut T, Moazami-Goudarzi K, Navratil V, Foglio M, Grohs C, et al. Genetic and haplotypic structure in 14 European and African cattle breeds. *Genetics* 2007;177: 1059–70.
- [21] McKay SD, Schnabel RD, Murdoch BM, Matukumalli LK, Aerts J, Coppieters W, et al. An assessment of population structure in eight breeds of cattle using a whole genome SNP panel. *BMC Genet* 2008;9:37.
- [22] Svensson EM, Anderung C, Baubliene J, Persson P, Malmström H, Smith C, et al. Tracing genetic change over time using nuclear SNPs in ancient and modern cattle. *Anim Genet* 2007;38:378–83.
- [23] Socol CT, Iacob L, Mihalca I, Criste FL. Molecular and population genetics tools for farm animal genetic resources conservation: brief overview. *Sci Papers Anim Sci Biotechnol* 2015;48:1.
- [24] kasprzak-Filipek K, Sawicka-Zugaj W, Litwińczuk Z, Chabuz W, Šveistienė R, Bulla J. Assessment of the genetic structure of Central European cattle breeds based on functional gene polymorphism. *Glob Ecol Conser* 2019;17:e00525.
- [25] Fang L, Sahana G, Ma P, Su G, Yu Y, Zhang S, et al. Exploring the genetic architecture and improving genomic prediction accuracy for mastitis and milk production traits in dairy cattle by mapping variants to hepatic transcriptomic regions responsive to intra-mammary infection. *Genet Sel Evol* 2017;49:1–18.
- [26] de Sousa Rego R, Jangarelli M, Soares MAM, de Melo ALP, Rodrigues MT, de Oliveira HR, et al. Polymorphism in  $\beta$ -lactoglobulin gene and its association with dairy goats' production traits. *Small Rumin Res* 2022;216:106834.
- [27] Raja G, Mahmood A, Saqlain R, Zafar M, Raja A, Shaiq P, et al. B allele of b-lactoglobulin as a marker of dairy traits in pakistani goat breeds. *J Anim Plant Sci* 2020;30:18–24.
- [28] Chaneton L, Sáez JP, Bussmann LE. Antimicrobial activity of bovine  $\beta$ -lactoglobulin against mastitis-causing bacteria. *J Dairy Sci* 2011;94:138–45.
- [29] Tarbal DC, Jung'a JO, Bett RC. *Int J Agric Res* March-April 2020;6(2):203–12.
- [30] Luhar R, Patel R, Singh K. Studies on the possible association of beta-lactoglobulin genotype with mastitis in dairy cows. *Indian J Dairy Sci* 2006;59:155.
- [31] Machira BW, Pacho VQ. Relationship between lactoferrin and Beta-lactoglobulin genes with the milk quality traits and somatic cell counts in crossbred dairy cattle genotypes. *Int J Environ Agric Res* 2022;8:60–7.
- [32] Gigli I, Riggio V, Monteleone G, Cacioppo D, Rosa A, Maizon D. Relationship between beta lactoglobulin and subclinical mastitis in Valle del Belice sheep breed. *Ital J Anim Sci* 2007;6(sup1):140–2.