



Research article

Genetic variations in somatostatin gene and their association with body weight and morphometric traits in two sheep breeds

Thamer R.S. Aljubouri*, Firas M. Al-Khafaji, Haider Alwan

Department of Animal Production, College of Agriculture, Al-Qasim Green University, Al-Qasim, Babil 51013, Iraq

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Abstract

Importance of Work: Somatostatin (SST) is a peptide hormone that regulates growth, metabolism and reproduction in sheep. Given the pronounced growth differences between the Awassi and Karakul breeds, investigating *SST*-related genetic variation may help explain these disparities.

Objectives: To identify polymorphisms in the *SST* gene and to evaluate their potential association with growth performance in Awassi and Karakul sheep.

Materials and Methods: In total, 175 sheep were evaluated, comprising 100 Awassi and 75 Karakul. Various growth trait indices were monitored in five successive time intervals, from birth to age 12 mth. Genotyping was performed using polymerase chain reaction–single-strand conformation polymorphism analysis, followed by electrophoretic identification of genotypes. The detected single nucleotide polymorphisms (SNPs) were confirmed based on Sanger sequencing. Genotype-phenotype associations were analyzed using a linear mixed model to account for repeated measures and the fixed effects of genotype, breed, sex and season.

Results: No polymorphism was detected in exon 2, whereas a novel silent SNP (154G>A; p.Q36=) was identified in exon 1. While no significant genotype differences were observed at birth for any measured traits, the 154G>A SNP showed significant associations ($p < 0.01$) with body weight, body length, and rump and wither heights from age 3 mth onward. Animals with the AA genotype had higher values for these traits than those with the GA and GG genotypes. In addition, the GA and AA genotypes occurred at higher frequencies in Karakul lambs than in Awassi lambs. The 154G>A SNP may serve as a potential marker for growth selection; however, the present findings, based on a moderate sample size and polygenic traits, require validation in larger and independent sheep populations.

Main Findings: The identified 154G>A SNP in the *SST* gene was associated strongly with postnatal growth performance in sheep and may serve as a useful molecular marker for selection programs. Its higher prevalence in Karakul sheep could partly explain the superior growth performance observed in this breed compared to Awassi sheep.

* Corresponding author.

E-mail address: thamerradhi@agre.uoqasim.edu.iq (T.R.S. Aljubouri)

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Introduction

Growth traits are among the several critical characteristics that influence the productivity of all breeds of sheep; thus, these traits are essential considerations for sheep breeders aiming to maximize ovine economic outputs, as several genes have been identified for their strong correlation with the comprehensive growth traits indices in lambs due to the various roles they play in reproductive physiology and metabolism of sheep (Li et al., 2024). One of the key hormones associated with growth trait regulation is somatostatin (Wańkowska et al., 2008). Primarily, this hormone is associated with inhibiting the secretion of several other hormones, including growth hormone, glucagon and insulin (Ampofo et al., 2020). This gene is part of a broader regulatory system that determines various physiological processes involving several types of transcriptional, post-transcriptional and post-translational control mechanisms. Usually, the complicated production of SST is aimed at ensuring its production in the right amounts at the right time to maintain a physiological balance between growth and metabolism (Lucey and Yamada, 1989). SST has a crucial involvement in livestock production due to its regulatory effects on growth, metabolism and reproductive functions. Among other key metabolic roles, numerous studies have indicated that any alteration in *SST* gene expression can substantially impact productivity and efficiency in various areas, including direct effects on the rate of animal growth and development (Low et al., 2001), meat production (Schanbacher, 1984) and the frequency of breeding cycles (McCosh et al., 2017). Hence, genetic polymorphism of *SST* can affect various aspects of sheep physiology and behavior, including the development of growth traits. *SST* gene polymorphism has substantially effects on productive performance due to the gene's role in regulating hormone secretion, particularly growth hormones (Eigler and Ben-Shlomo, 2014). These genetic polymorphisms can influence how the *SST* gene functions, leading to differences in growth rates, body composition and overall productivity. While the *SST* gene might be associated with growth development in puberty (Wańkowska, 2012), variations in the *SST* gene can impact various carcass characteristics such as fat content and deposition and body composition. These alterations may produce a wide range of effects on the growth rates and metabolic efficiency of sheep, making it a point of interest for genetic studies aimed at improving livestock production. Growth rates and overall reproductive performance can be increased greatly in various sheep populations by identifying

and selecting favorable *SST* alleles. Accordingly, the utilization of *SST* genetic markers may have the potential to accelerate selective breeding strategies, leading to improved growth-production capacity. While the importance has been explored of *SST* genetic diversity in shaping the growth traits in buffalo and cattle (Gao et al., 2011; Stafuzza et al., 2014), there remains a lack of studies investigating its correlations with growth traits in sheep.

The description available in the National Centre for Biotechnology Information (NCBI) of the *SST* gene in sheep indicates that this gene spans approximately 1,248 base pairs, extending from positions 200,453,333–200,454,581 on chromosome 2 (GenBank; NC_056054.1). The *SST* gene is made of only two exons that encode for a small polypeptide, which is made of 116 amino acid residues (Jin et al., 2011). Despite the versatile importance of *SST* in controlling a wide variety of physiological and metabolic pathways in the growth of sheep, attention has been restricted to somatostatin receptor (*SSTR*) polymorphisms in association with productive traits in various ovine breeds such as Hulum Buir sheep (Li et al., 2021) and New Zealand Romney sheep (Zhao et al., 2018). On the other hand, another study has demonstrated that Iranian Karakul lambs significantly outperformed Iraqi Awassi lambs in most growth trait measurements (Aljubouri et al., 2021). Irrespective of the phenotypic contribution of breed differences, this superiority has been attributed to various genetic factors (Aljubouri and Al-Shuhaib, 2023a; Alwan et al., 2024; Jassim et al., 2025). Based on these data, the primary aim of the present study was to identify the polymorphism variations in the *SST* gene and their potential association with body weight and body measurements in the Iraqi Awassi breed, compared with the Iranian Karakul breed. By comparing these two breeds, which differ in growth performance, the study aimed to clarify whether specific *SST* genotypes were linked to phenotypic differences in productivity-related traits. Establishing such a genotype-phenotype association may contribute to the identification of *SST* as a candidate molecular marker useful for future selection and breeding strategies in Middle Eastern sheep populations.

Materials and Methods

Sheep breeds

The research focus was on two well-known breeds of sheep that displayed major disparities in their growth trait indices,

namely Awassi (a sample of 100 sheep) and Karakul (using a sample of 75 sheep). In the Middle East, the most famous breed is Awassi, which is recognized for its ability to provide milk, meat and wool (Aljubouri and Al-Shuhaib, 2021). However, the geographical areas in which Awassi sheep are usually raised can have an impact on their profitability and growth trait qualities (Al-Jubouri et al., 2022). Another breed of fat-tailed sheep that is common throughout the Middle East is the Karakul, which stands out for being highly resilient to adverse conditions and having better growth characteristic indices than Awassi sheep (Alwan and Aljubouri, 2023). Primarily, the Karakul breed is used for the production of carcasses, wool and fleece (Aljubouri and Al-Shuhaib, 2025). The traits of these two breeds of sheep were monitored at the Barakat Abu al Fadhl Al-Abbas (Peace be upon him) Fields (BAFAS), where both breeds were raised. BAFAS is 32 m above sea level (32.6027°N; 44.0197°E) and situated in the Karbala Governorate of Iraq. On this station, All the sheep involved in the study were kept on BAFAS under uniform housing and management conditions, with routine feeding and care performed by the same trained staff.

Lamb management

The dams were managed under semi-intensive conditions and fed *ad libitum* with seasonal pasture, supplemented daily with concentrate feed equivalent to approximately 2.5% of their live body weight. The concentrate consisted of barley (59%), wheat bran (40%) and salt (1%), with *ad libitum* access to clean drinking water. The lambs were managed following established husbandry guidelines. Immediately after birth, they were separated from their dams and housed in individual pens, where they received special care and close monitoring. Colostrum was provided during the first 2 wk to ensure adequate passive immunity and additional attention was given throughout the early weeks to support health, growth and adaptation. From age 3 wk, the lambs were gradually introduced to an oatmeal starter and alfalfa leaves. Weaning was carried out at age 3 mth.

The study was conducted during the autumn-winter lambing season (October–February), defined according to the local climatic calendar of central Iraq. This period corresponds to the main breeding and lambing season of indigenous sheep. Data were collected from lambs born in October ($n = 62$), November ($n = 47$) and December ($n = 66$) during 2023. The experimental population comprised both Karakul

(39 females, 36 males) and Awassi (48 females, 52 males) lambs, ensuring a balanced cohort for analysis. All experimental procedures were conducted in accordance with institutional guidelines for the care and management of livestock (Aljubouri et al., 2021) and were approved by the Ethical Committee for Animal Protection, Department of Animal Production, College of Agriculture, Al-Qasim Green University. (Ref. CAEC/0824/0058, dated; March 16, 2023).

Data collection

Different growth features were recorded for the Awassi and Karakul lambs under examination for 1 yr. The main characteristics assessed in both populations were body weight (BW), body length (BL), wither height (WH), rump height (RH), chest circumference (CC) and abdominal circumference (AC). Specifically, BW was recorded using a digital scale; BL was measured from the point of the shoulder to the base of the tail; WH and RH were measured using a measuring stick from the ground to the respective anatomical points; CC and AC were measured using a flexible measuring tape around the thoracic and abdominal regions, respectively. These records were taken when the sheep were standing in a relaxed state under similar conditions. Beginning at birth and continuing until age 1 yr, the growth parameters were recorded at regular 3 mth intervals (day of birth, ages 3 mth, 6 mth 9 mth, 12 mth). The descriptive data for the gathered variables under study, including the distribution and variability of growth traits in the examined lambs, are presented in Supplementary Material 1.

Genomic DNA extraction

Blood samples were collected from all lambs at the same intervals as the growth measurements, at the age of weaning. Blood samples were collected from the jugular veins of both breeds of sheep using a sterile needle and syringe. Peripheral blood samples were obtained carefully into tubes containing an anticoagulant (ethylenediaminetetraacetic acid, EDTA) to prevent clotting. Genomic DNA was extracted utilizing a rapid salting-out technique (Al-Shuhaib, 2018). The concentration used in the agarose gel electrophoresis was 0.8% (in $1 \times$ Tris-acetate-EDTA buffer) to evaluate the integrity of the isolated genomic DNA, while spectrophotometric evaluation, based on Nanodrop microvolume spectrometry, was used to determine the amount and quality of the genomic DNA (BioDrop Lite, BioDrop Ltd., UK).

Polymerase chain reaction primers design

Two polymerase chain reaction (PCR) oligonucleotide pairs were created to contain the complete two *SST* gene exons. Using NCBI's primer BLAST web server (Ye et al., 2012), the lengths of the proposed fragments were maintained within the optimum sensitivity ranges of the single-strand conformation polymorphism (SSCP) approach (Badi et al., 2021). Based on the NCBI gene annotation tool (GenBank NC_056054.1), the 248 bp (forward primer 5'-AGTTTGACCAACCGCACTCT-3' and 5'-CAAGGCGAGGGAAGGTTAGG-3') was designed to entirely cover exon 1. The second PCR fragment was designed to be 372 bp in length (with primers 5'-TCAAGCCAAGCTCTTCTGGTT-3' and 5'-GAGGGGTTAGGGAGGTGAGA-3'), completely covering exon 2.

Polymerase chain reaction conditions

Initially, gradient PCR thermocycling was used to determine the best annealing temperature for PCR amplification. Following the recommendations of the manufacturers (Catalogue no. K-2014, "Bioneer/Korea"), a 20 μ L PCR-ready PreMix was used for performing PCR. This PCR mixture consisted of Top DNA polymerase, a balanced mixture of the four dNTPs (250 μ M each), 1.5 mM $MgCl_2$ and a Tris-HCl/KCl reaction buffer system. The reaction was performed as: an initial denaturation step at 95°C for 5 min; 30 cycles of denaturation at 94°C for 30 s; annealing of the primer at 60°C for 45 s (for both amplicons); 45 s of polymerization at 72°C; and a final polymerization step at 74°C for 5 min. The PCR product sizes, as anticipated, were confirmed by applying 2% (w/v) agarose gel electrophoresis before conducting post-PCR genotyping.

Genotyping using polymerase chain reaction- single-strand conformation polymorphism

The PCR amplicons were genotyped using the PCR-SSCP method based on their exposure to heat denaturation at 95°C for 8 min, using a formamide-based SSCP denaturing loading buffer. Then, these PCR amplicons were frozen on ice immediately and loaded onto non-denatured polyacrylamide gels that were molded in a mini-wide polyacrylamide electrophoresis device (Cleaver Scientific, Rugby, UK), with samples being 10 cm in length, 20 cm in width and 0.10 mm in thickness. Subsequently, electrophoresis was performed using 200 mA and 100 V. After electrophoresis, the polyacrylamide

gels were stained with silver nitrate to identify the separated DNA bands, following a sensitive protocol described by Byun et al. (2009).

DNA Sequencing

The *SST* genotypes were identified electrophoretically and then Sanger dideoxy-sequencing was performed on them using the guidelines provided by the sequencing laboratory (Macrogen; Republic of South Korea). The obtained electropherograms of the PCR amplicons were annotated manually with the identified nucleotide variants using the SnapGene Viewer tool (<http://www.snapgene.com>). In accordance with the suggested technical parameters of the visualized electropherograms (Al-Shuhaib and Hashim, 2023), only the distinct nucleotide peaks of the representative genotypes were considered for the alignment with the *SST* genomic sequences, while other, less qualified, readings were disregarded. The single nucleotide polymorphisms (SNPs) detected in the coding nucleic acids were converted using ExPasy Translate (<https://web.expasy.org/translate/>) to the corresponding amino acid residues to evaluate their ultimate effects (Artimo et al., 2012). As per the recommended guidelines of the NCBI (Benson et al., 2018), the detected variations were submitted to the Bankit portal (<https://www.ncbi.nlm.nih.gov/WebSub/>) to confirm the annotations in the polymorphic regions of the *SST* gene sequences. The genotypes for the polymorphic regions of the *SST* gene were represented by unique GenBank identifiers that were acquired from NCBI.

Analyzing genetic diversity

To evaluate any possible deviations from the Hardy-Weinberg equilibrium (HWE) assumptions of the genotype distribution, the χ^2 test was used in the Pop_Gene32 software (version 1.32; Yeh FC, University of Alberta, Edmonton, AB, Canada). The same software was used to assess the values of observed heterozygosity (H_o) and expected heterozygosity (H_e), while the genotype frequencies were determined by direct counting.

Genotype-phenotype association analysis

The productive performance of the lambs was assessed from birth and every 3 mth until reaching age 1 yr. Statistical analysis was performed using the IBM, SPSS Statistics software

(version 26.0; IBM Corp.; USA), using a general linear mixed model. Any potential relationships between the genotypes and growth trait indices were assessed using Eq. (1):

$$\text{Trait}_{ijklm} = \mu + S_k(\text{Sex}) + T_i(\text{Season}) + \alpha_i(\text{Genotype}) + \beta_j(\text{Breed}) + (\alpha\beta)_{ij}(\text{Genotype} \times \text{Breed}) + \epsilon_{ijklm} \quad (1)$$

where Trait_{ijklm} denotes the traits' phenotypic value, μ is the overall mean, α_i is the fixed effect of the i th genotype (GG, GA and AA) for major homozygous, heterozygous and minor homozygous genotypes, β_j denotes the fixed effect of the j th breed (Karakul, Awassi), S_k is the fixed effect of sex (male, female), T_i is the fixed effect of season (where the term "season" refers specifically to the lambing season, i.e., the season in which each lamb was born, not the period of data collection), $(\alpha\beta)_{ij}$ indicates the calculated interaction between genotype and breed and ϵ_{ijklm} indicates each observation's random residual effect.

Several covariance structures (compound symmetry, AR (1) and unstructured) were evaluated and the best-fitting structure was selected based on the lowest Akaike information criterion) and Bayesian information criterion values to account for within-subject correlations. Post hoc pairwise comparisons

of least-square means ($\pm$ SE) were performed with Bonferroni adjustment and significance was declared at $p < 0.05$. Sex and birth month were retained as covariates (without interaction terms) to control for potential confounding and to improve the accuracy of the genotype and breed effect estimates.

Results

Single nucleotide polymorphism identification and annotation

The two amplicons were genotyped using the PCR-SSCP method to identify any possible polymorphism in the coding sequences of the *SST* gene. While the SSCP genotyping of the 372 bp PCR amplicons did not reveal any detectable variation in exon 2, the genotyping of 248 bp PCR amplicons of exon 1 exhibited clear genetic polymorphism by displaying three electrophoretic bands in the polyacrylamide gels. Sanger dideoxy sequencing demonstrated that the three electrophoretic banding changes found in the amplicons of 248 bp were caused by only one SNP. The detected SNP was given the identification 154G>A based on its position in these PCR products (Fig. 1).

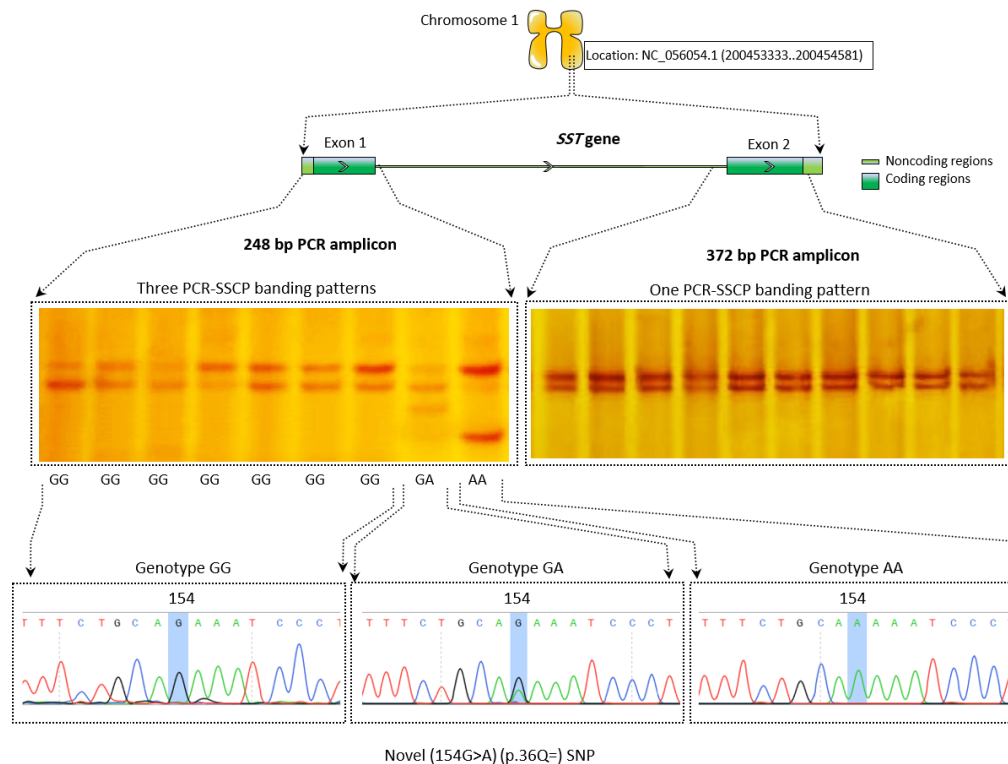


Fig. 1 Polymerase chain reaction (PCR)-single-strand conformation polymorphism (SSCP)-based genotyping of somatostatin (*SST*) gene in Awassi and Karakul sheep: (A) PCR primers designed for amplification and screening of exon 1, exon 2 and their flanking regions; (B) Representative PCR-SSCP banding patterns of the *SST* gene amplicons; (C) sequencing electropherograms showing the identified polymorphisms.

A major homozygous GG, a heterozygous GA and a minor homozygous AA were the three genotypes exhibited at this polymorphic locus. Upon examining the position of the 154G>A SNP in the NCBI database, this SNP was located at NC_056054.1;200453479G>A, which corresponds to the amino acid residue glutamine that is situated in the 36th position in the entire protein. Using the Expasy translate tool, the silent (synonymous) effect of the 154G>A SNP was revealed, namely p.Q36=. To determine if the observed synonymous SNP had already been deposited online, its position was analyzed within the *Ovis aries* database deposited in Ensembl Genome Browser 112 (<https://www.ensembl.org/index.html>). The identified synonymous SNP 154G>A was discovered in the variant table of the sheep *SST* gene, which had not yet been deposited in the Ensembl database. According to this annotation, the novelty of the detected SNP 154G>A was confirmed, as it has not been deposited in the *SST* gene Ensembl data (ENSOARG00020000243) to date. The detected three variations of the *SST* gene were uploaded to the NCBI server, along with three GenBank accession number identifiers (PQ227821, PQ227822 and PQ227823), which were issued for the polymorphic 248 bp amplicons to indicate the genotypes GG, GA and AA, respectively.

Biodiversity of 154G>A single nucleotide polymorphism

The observed allelic distributions of the detected 154G>A SNP showed that allele G had greater frequencies (0.88 and 0.71) than allele A (0.12 and 0.29) in the Awassi and Karakul lambs, respectively. The main homozygous (GG) genotype had the greatest frequencies (0.83 and 0.59, respectively), followed by the heterozygous (GA; 0.10 and 0.24, respectively)

and minor homozygous (AA; 0.07 and 0.17, respectively) genotypes. It was concluded that both populations had a high likelihood of inbreeding, as shown by the observed heterozygosity (H_o) values (0.100 and 0.240) being lower than the expected heterozygosity (H_e) values (0.212 and 0.417) in Awassi and Karakul lambs, respectively. The values from the χ^2 analysis showed that both the Awassi (29.061) and Karakul (13.805) breeds were not within HWE (Table 1).

Association of 154G>A single nucleotide polymorphism with growth traits

Various parameters were tracked related to growth traits over an age span from birth to 1 yr in both Awassi and Karakul breeds. On the day of birth, the effect of the breed was limited. From 3 mth onward, breed had a significant influence on most of the productive traits measured. Based on most growth parameters evaluated, the impact of this SNP was significant ($p < 0.05$) and highly significant ($p < 0.01$). At age 12 mth, there were confirmed significant differences between the Awassi and Karakul breeds in terms of BL, BW, RH and WH. Compared to the Awassi breed, Karakul lambs consistently had more growth trait continuity, showing that they dominated over the Awassi breed at all times recorded (Table 2). No significant sex differences were observed at birth ($p \geq 0.05$). However, from 3 mth onward, males consistently had higher BW and body size traits than females ($p < 0.05$), with differences in LSMeans $\pm$ SE becoming more pronounced by age 12 mth (48.06 $\pm$ 0.43 kg versus 44.75 $\pm$ 0.56 kg; $p < 0.001$). These findings indicated that sex exerted a significant influence on postnatal growth performance, favoring males throughout the fattening stages (Table 3).

Table 1 Genotype and allele frequencies and genetic diversity parameters for the somatostatin *SST* gene in Awassi and Karakul breeds

Breed	Genotype (n)			Genotype frequency			Allele frequency		H_o	H_e	c
	GG	GA	AA	GG	GA	AA	G	A			
Awassi	83	10	7	0.83	0.10	0.07	0.88	0.12	0.100	0.212	29.061
Karakul	44	18	13	0.59	0.24	0.17	0.71	0.29	0.240	0.417	13.805

Table 2 Measured effects of breed on growth traits in studied populations of Awassi breed ($n=100$) and Karakul breed ($n=75$)

Age (mth)	Measured parameter	Karakul ($n=75$)	Awassi ($n=100$)	Significance
0 (at birth)	Body weight (kg)	4.27 $\pm$ 0.07	4.37 $\pm$ 0.09	0.84
	Body length (cm)	31.26 $\pm$ 0.39	31.52 $\pm$ 0.29	0.57
	Wither height (cm)	40.25 $\pm$ 0.42	40.17 $\pm$ 0.30	0.34
	Rump height (cm)	40.56 $\pm$ 0.35	40.77 $\pm$ 0.27	0.45
	Chest circumference (cm)	42.19 $\pm$ 0.40	42.05 $\pm$ 0.30	0.63
	Abdominal circumference (cm)	43.72 $\pm$ 0.45	43.02 $\pm$ 0.34	0.51
3	Body weight (kg)	25.90 $\pm$ 0.45 ^a	24.76 $\pm$ 0.34 ^b	0.01
	Body length (cm)	64.48 $\pm$ 0.83 ^a	62.35 $\pm$ 0.63 ^b	0.01
	Wither height (cm)	65.01 $\pm$ 0.38 ^a	64.49 $\pm$ 0.30 ^b	0.01
	Rump height (cm)	65.28 $\pm$ 0.53 ^a	64.81 $\pm$ 0.40 ^b	0.01
	Chest circumference (cm)	81.88 $\pm$ 0.83 ^a	78.33 $\pm$ 0.63 ^b	0.01
	Abdominal circumference (cm)	90.52 $\pm$ 0.88 ^a	86.73 $\pm$ 0.67 ^b	0.01

Table 2 Continued

Age (mth)	Measured parameter	Karakul (n=75)	Awassi (n=100)	Significance
6	Body weight (kg)	34.71±0.41 ^a	32.24±0.54 ^b	0.01
	Body length (cm)	73.48±0.47 ^a	69.80±0.62 ^b	0.01
	Wither height (cm)	71.72±0.32 ^a	69.26±0.39 ^b	0.01
	Rump height (cm)	72.02±0.38 ^a	70.04±0.50 ^b	0.01
	Chest circumference (cm)	96.11±1.15 ^a	91.09±0.87 ^b	0.01
	Abdominal circumference (cm)	106.16±1.12 ^a	102.36±0.85 ^b	0.01
9	Body weight (kg)	41.07±0.43 ^a	37.94±0.57 ^b	0.01
	Body length (cm)	75.97±0.37 ^a	71.75±0.49 ^b	0.01
	Wither height (cm)	74.24±0.55 ^a	71.84±0.50 ^b	0.01
	Rump height (cm)	74.70±0.43 ^a	72.15±0.32 ^b	0.01
	Chest circumference (cm)	105.74±1.21 ^a	100.41±0.92 ^b	0.01
	Abdominal circumference (cm)	115.00±1.30 ^a	112.16±0.99 ^b	0.01
12	Body weight (kg)	47.73±0.63 ^a	45.09±0.48 ^b	0.01
	Body length (cm)	77.34±0.34 ^a	73.72±0.44 ^b	0.01
	Wither height (cm)	76.05±0.42 ^a	74.01±0.40 ^b	0.01
	Rump height (cm)	76.18±0.40 ^a	73.96±0.31 ^b	0.01
	Chest circumference (cm)	111.17±1.11 ^a	108.02±0.84 ^b	0.01
	Abdominal circumference (cm)	123.16±1.17 ^a	119.65±0.89 ^b	0.01

Values are presented as least-square means (LSMeans) ± standard errors (SE). Means within the same row with different lowercase superscripts indicate significant differences ($p < 0.05$), with p-values provided for clarity.

Table 3 Least-squares mean ± SE values for effects of sex on growth traits in sheep based on linear mixed model

Age (mth)	Measured parameter	Sex		Significance
		Female (n=87)	Male (n=88)	
0 (at birth)	Body weight (kg)	4.28±0.08	4.37±0.06	0.89
	Body length (cm)	30.97±0.35	31.80±0.27	0.17
	Wither height (cm)	39.85±0.35	40.06±0.27	0.06
	Rump height (cm)	40.41±0.32	40.92±0.24	0.16
	Chest circumference (cm)	41.95±0.36	42.29±0.27	0.60
	Abdominal circumference (cm)	43.16±0.40	43.57±0.31	0.61
3	Body weight (kg)	24.44±0.4 ^b	26.22±0.31 ^a	0.00
	Body length (cm)	63.24±0.75	63.59±0.57	0.51
	Wither height (cm)	64.10±0.49 ^b	65.40±0.38 ^a	0.01
	Rump height (cm)	64.33±0.47 ^b	65.77±0.36 ^a	0.01
	Chest circumference (cm)	78.81±0.74 ^b	81.40±0.57 ^a	0.01
	Abdominal circumference (cm)	86.98±0.79 ^b	90.27±0.60 ^a	0.00
6	Body weight (kg)	32.23±0.49 ^b	34.72±0.37 ^a	0.00
	Body length (cm)	70.94±0.55 ^b	72.34±0.42 ^a	0.04
	Wither height (cm)	69.82±0.45 ^b	71.16±0.34 ^a	0.01
	Rump height (cm)	70.47±0.45 ^b	71.59±0.34 ^a	0.02
	Chest circumference (cm)	92.58±1.03 ^b	94.62±0.79 ^a	0.02
	Abdominal circumference (cm)	102.95±1.00	105.57±0.77	0.07
9	Body weight (kg)	38.18±0.51 ^b	40.84±0.39 ^a	0.00
	Body length (cm)	73.34±0.44	74.37±0.34	0.07
	Wither height (cm)	72.46±0.36 ^b	73.63±0.28 ^a	0.02
	Rump height (cm)	72.84±0.38 ^b	74.01±0.29 ^a	0.02
	Chest circumference (cm)	101.77±1.09 ^b	104.37±0.83 ^a	0.03
	Abdominal circumference (cm)	112.91±1.17	114.25±0.90	0.20
12	Body weight (kg)	44.75±0.56 ^b	48.06±0.43 ^a	0.00
	Body length (cm)	74.58±0.40 ^b	76.48±0.31 ^a	0.00
	Wither height (cm)	74.14±0.38 ^b	75.91±0.29 ^a	0.01
	Rump height (cm)	74.28±0.36 ^b	75.86±0.28 ^a	0.01
	Chest circumference (cm)	108.06±0.99 ^b	111.13±0.76 ^a	0.02
	Abdominal circumference (cm)	119.89±1.05 ^b	122.93±0.81 ^a	0.04

Values are presented as least-square means (LSMeans) ± standard errors (SE). Means within the same row with different lowercase superscripts indicate significant differences ($p < 0.05$), with p-values provided for clarity.

The identified 154G>A genotypes were evaluated for potential associations with growth traits to determine whether the genetic factor was the cause of these variations. At age 3 mth, there was a highly significant correlation between the 154G>A SNP and all growth trait indicators, while no significant association was detected at birth. On the other hand, it was deduced that lambs with an altered AA genotype appeared to have higher values in most of the growth rate indices (BL, BW, RH, WH, AC) than those with GA and GG genotypes, respectively. The observed higher growth traits of lambs with the AA genotype continued to be significant to highly significant at age 3 mth and onward (Table 4).

The interaction between breed and the 154G>A genotype showed limited effects on growth traits. No significant differences were detected at birth ($p \geq 0.05$). At age 3 mth, the Awassi lambs carrying the GG genotype had lower wither and rump heights than the other genotypes ($p < 0.05$). However, across subsequent ages (6–12 mth), the genotype $\times$ breed interaction was generally not significant ($p \geq 0.05$), indicating that the SNP effect on growth performance was largely consistent across breeds (Table 5).

Table 4 Effect of detected 154G>A singular nucleotide polymorphism of somatostatin *SST* gene on growth traits of entire studied population of Awassi and Karakul lambs

Age (mth)	Measured parameter	AA (n=20)	GA (n=28)	GG (n=127)	Significance
0 (at birth)	Body weight (kg)	4.45 $\pm$ 0.13	4.29 $\pm$ 0.11	4.23 $\pm$ 0.05	0.97
	Body length (cm)	32.29 $\pm$ 0.54	31.17 $\pm$ 0.45	30.70 $\pm$ 0.21	0.20
	Wither height (cm)	40.57 $\pm$ 0.55	39.99 $\pm$ 0.45	40.06 $\pm$ 0.21	0.70
	Rump height (cm)	41.06 $\pm$ 0.49	40.57 $\pm$ 0.41	40.37 $\pm$ 0.19	0.67
	Chest circumference (cm)	43.02 $\pm$ 0.56	41.66 $\pm$ 0.46	41.68 $\pm$ 0.22	0.58
	Abdominal circumference (cm)	43.98 $\pm$ 0.62	42.81 $\pm$ 0.52	43.31 $\pm$ 0.24	0.71
3	Body weight (kg)	27.84 $\pm$ 0.63 ^a	25.74 $\pm$ 0.53 ^a	22.41 $\pm$ 0.25 ^b	0.00
	Body length (cm)	67.09 $\pm$ 1.16 ^a	62.69 $\pm$ 0.97 ^b	60.47 $\pm$ 0.46 ^c	0.00
	Wither height (cm)	66.39 $\pm$ 0.77 ^a	64.96 $\pm$ 0.64 ^a	62.90 $\pm$ 0.30 ^b	0.00
	Rump height (cm)	66.55 $\pm$ 0.74 ^a	65.31 $\pm$ 0.62 ^a	63.28 $\pm$ 0.29 ^b	0.00
	Chest circumference (cm)	82.12 $\pm$ 1.15 ^a	80.73 $\pm$ 0.96 ^a	77.46 $\pm$ 0.45 ^b	0.01
	Abdominal circumference (cm)	91.45 $\pm$ 1.23 ^a	88.94 $\pm$ 1.02 ^a	85.49 $\pm$ 0.48 ^b	0.00
6	Body weight (kg)	35.73 $\pm$ 0.76 ^a	34.40 $\pm$ 0.63 ^a	30.29 $\pm$ 0.30 ^b	0.00
	Body length (cm)	73.81 $\pm$ 0.86 ^a	72.11 $\pm$ 0.72 ^a	68.99 $\pm$ 0.34 ^b	0.00
	Wither height (cm)	71.48 $\pm$ 0.70 ^a	71.06 $\pm$ 0.58 ^a	68.93 $\pm$ 0.27 ^b	0.00
	Rump height (cm)	72.25 $\pm$ 0.70 ^a	71.47 $\pm$ 0.58 ^a	69.36 $\pm$ 0.27 ^b	0.00
	Chest circumference (cm)	98.12 $\pm$ 1.60 ^a	91.39 $\pm$ 1.34 ^b	91.29 $\pm$ 0.63 ^b	0.00
	Abdominal circumference (cm)	108.00 $\pm$ 1.56 ^a	103.16 $\pm$ 1.30 ^b	101.62 $\pm$ 0.6 ^{bc}	0.00
9	Body weight (kg)	41.77 $\pm$ 0.80 ^a	40.45 $\pm$ 0.66 ^a	36.30 $\pm$ 0.31 ^b	0.00
	Body length (cm)	76.35 $\pm$ 0.68 ^a	72.51 $\pm$ 0.57 ^b	72.71 $\pm$ 0.27 ^b	0.00
	Wither height (cm)	76.11 $\pm$ 0.56 ^a	71.39 $\pm$ 0.47 ^b	71.63 $\pm$ 0.22 ^b	0.00
	Rump height (cm)	76.25 $\pm$ 0.60 ^a	71.96 $\pm$ 0.50 ^b	72.06 $\pm$ 0.23 ^b	0.00
	Chest circumference (cm)	106.57 $\pm$ 1.70 ^a	102.79 $\pm$ 1.42 ^b	99.85 $\pm$ 0.66 ^c	0.00
	Abdominal circumference (cm)	117.91 $\pm$ 1.82 ^a	112.38 $\pm$ 1.52 ^b	110.45 $\pm$ 0.71 ^{bc}	0.00
12	Body weight (kg)	49.51 $\pm$ 0.88 ^a	47.27 $\pm$ 0.73 ^a	42.44 $\pm$ 0.34 ^b	0.00
	Body length (cm)	78.52 $\pm$ 0.62 ^a	74.08 $\pm$ 0.52 ^b	73.99 $\pm$ 0.24 ^b	0.00
	Wither height (cm)	77.44 $\pm$ 0.59 ^a	74.07 $\pm$ 0.49 ^b	73.57 $\pm$ 0.23 ^b	0.00
	Rump height (cm)	77.69 $\pm$ 0.56 ^a	73.74 $\pm$ 0.47 ^b	73.77 $\pm$ 0.22 ^b	0.00
	Chest circumference (cm)	112.19 $\pm$ 1.55 ^a	108.88 $\pm$ 1.29 ^{ab}	107.72 $\pm$ 0.60 ^b	0.02
	Abdominal circumference (cm)	125.44 $\pm$ 1.64 ^a	120.73 $\pm$ 1.37 ^{ab}	118.06 $\pm$ 0.64 ^b	0.00

Values are presented as least-square means (LSMeans) $\pm$ standard errors (SE). Means within the same row with different lowercase superscripts indicate significant differences ($p < 0.05$), with p-values provided for clarity.

Table 5 Least squares mean $\pm$ SE values for interaction effects of I54G>A (p.Q36=) genotypes (GG, GA, AA) with breed (Karakul and Awassi) on growth traits.

Age (mth)	Measured parameter	Karakul breed			Awassi breed			Significance
		AA (n=13)	GA (n=18)	GG (n=44)	AA (n=7)	GA (n=10)	GG (n=83)	
0 (at birth)	Body weight (kg)	4.29 $\pm$ 0.15	4.36 $\pm$ 0.13	4.18 $\pm$ 0.08	4.60 $\pm$ 0.21	4.23 $\pm$ 0.18	4.28 $\pm$ 0.06	0.40
	Body length (cm)	31.82 $\pm$ 0.64	31.43 $\pm$ 0.52	30.51 $\pm$ 0.34	32.76 $\pm$ 0.85	30.91 $\pm$ 0.74	30.88 $\pm$ 0.25	0.55
	Wither height (cm)	40.60 $\pm$ 0.64	39.76 $\pm$ 0.53	40.38 $\pm$ 0.34	40.55 $\pm$ 0.86	40.22 $\pm$ 0.74	39.74 $\pm$ 0.25	0.51
	Rump height (cm)	40.85 $\pm$ 0.58	40.13 $\pm$ 0.48	40.71 $\pm$ 0.31	41.27 $\pm$ 0.77	41.01 $\pm$ 0.67	40.04 $\pm$ 0.23	0.16
	Chest circumference (cm)	43.47 $\pm$ 0.66	41.08 $\pm$ 0.54	42.03 $\pm$ 0.35	42.58 $\pm$ 0.88	42.24 $\pm$ 0.76	41.34 $\pm$ 0.25	0.18
	Abdominal circumference (cm)	44.81 $\pm$ 0.74	42.73 $\pm$ 0.61	43.62 $\pm$ 0.39	43.15 $\pm$ 0.98	42.89 $\pm$ 0.85	43.00 $\pm$ 0.29	0.53
3	Body weight (kg)	27.81 $\pm$ 0.75	26.25 $\pm$ 0.61	23.63 $\pm$ 0.40	27.88 $\pm$ 1.00	25.22 $\pm$ 0.87	21.19 $\pm$ 0.29	0.11
	Body length (cm)	66.86 $\pm$ 1.37	63.86 $\pm$ 1.13	62.72 $\pm$ 0.73	67.32 $\pm$ 1.83	61.52 $\pm$ 1.59	58.22 $\pm$ 0.53	0.10
	Wither height (cm)	65.32 $\pm$ 0.91 ^a	65.40 $\pm$ 0.75 ^a	64.30 $\pm$ 0.48 ^a	67.46 $\pm$ 1.21 ^a	64.51 $\pm$ 1.05 ^a	61.50 $\pm$ 0.35 ^b	0.01
	Rump height (cm)	65.50 $\pm$ 0.87 ^a	65.72 $\pm$ 0.72 ^a	64.63 $\pm$ 0.46 ^a	67.61 $\pm$ 1.16 ^a	64.89 $\pm$ 1.01 ^a	61.94 $\pm$ 0.34 ^b	0.02
	Chest circumference (cm)	83.69 $\pm$ 1.36	83.25 $\pm$ 1.12	78.70 $\pm$ 0.72	80.54 $\pm$ 1.82	78.21 $\pm$ 1.58	76.22 $\pm$ 0.53	0.48
	Abdominal circumference (cm)	92.60 $\pm$ 1.44	91.99 $\pm$ 1.19	86.98 $\pm$ 0.77	90.30 $\pm$ 1.93	85.88 $\pm$ 1.67	84.00 $\pm$ 0.56	0.34
6	Body weight (kg)	36.01 $\pm$ 0.89	36.28 $\pm$ 0.73	31.84 $\pm$ 0.47	35.44 $\pm$ 1.19	32.53 $\pm$ 1.04	28.74 $\pm$ 0.35	0.22
	Body length (cm)	75.07 $\pm$ 1.01	74.99 $\pm$ 0.83	70.37 $\pm$ 0.54	72.54 $\pm$ 1.35	69.23 $\pm$ 1.17	67.62 $\pm$ 0.39	0.15
	Wither height (cm)	72.46 $\pm$ 0.82	72.77 $\pm$ 0.67	69.93 $\pm$ 0.44	70.50 $\pm$ 1.09	69.35 $\pm$ 0.95	67.93 $\pm$ 0.32	0.53
	Rump height (cm)	72.79 $\pm$ 0.82	72.98 $\pm$ 0.67	70.28 $\pm$ 0.44	71.72 $\pm$ 1.09	69.96 $\pm$ 0.95	68.43 $\pm$ 0.32	0.52
	Chest circumference (cm)	102.45 $\pm$ 1.89	93.03 $\pm$ 1.55	92.84 $\pm$ 1.00	93.79 $\pm$ 2.52	89.75 $\pm$ 2.19	89.73 $\pm$ 0.73	0.25
	Abdominal circumference (cm)	109.94 $\pm$ 1.83	104.51 $\pm$ 1.51	104.02 $\pm$ 0.97	106.06 $\pm$ 2.45	101.81 $\pm$ 2.13	99.21 $\pm$ 0.71	0.75
9	Body weight (kg)	42.57 $\pm$ 0.94	42.63 $\pm$ 0.77	38.01 $\pm$ 0.50	40.96 $\pm$ 1.25	38.26 $\pm$ 1.09	34.60 $\pm$ 0.36	0.40
	Body length (cm)	78.33 $\pm$ 0.80	74.77 $\pm$ 0.66	74.80 $\pm$ 0.43	74.38 $\pm$ 1.07	70.24 $\pm$ 0.93	70.62 $\pm$ 0.31	0.94
	Wither height (cm)	76.86 $\pm$ 0.66	73.13 $\pm$ 0.54	72.74 $\pm$ 0.35	75.37 $\pm$ 0.88	69.65 $\pm$ 0.77	70.51 $\pm$ 0.26	0.35
	Rump height (cm)	77.14 $\pm$ 0.70	73.83 $\pm$ 0.58	73.11 $\pm$ 0.37	75.35 $\pm$ 0.94	70.08 $\pm$ 0.81	71.01 $\pm$ 0.27	0.29
	Chest circumference (cm)	110.11 $\pm$ 2.00	104.98 $\pm$ 1.64	102.11 $\pm$ 1.06	103.03 $\pm$ 2.67	100.60 $\pm$ 2.32	97.59 $\pm$ 0.77	0.76
	Abdominal circumference (cm)	117.56 $\pm$ 2.14	114.38 $\pm$ 1.77	113.06 $\pm$ 1.14	118.26 $\pm$ 2.87	110.38 $\pm$ 2.49	107.83 $\pm$ 0.83	0.29
12	Body weight (kg)	50.32 $\pm$ 1.03	49.14 $\pm$ 0.85	43.72 $\pm$ 0.55	48.71 $\pm$ 1.38	45.39 $\pm$ 1.20	41.16 $\pm$ 0.40	0.63
	Body length (cm)	80.14 $\pm$ 0.73	76.36 $\pm$ 0.60	75.53 $\pm$ 0.39	76.91 $\pm$ 0.97	71.80 $\pm$ 0.85	72.44 $\pm$ 0.28	0.44
	Wither height (cm)	78.20 $\pm$ 0.69	75.55 $\pm$ 0.57	74.40 $\pm$ 0.37	76.69 $\pm$ 0.92	72.59 $\pm$ 0.80	72.73 $\pm$ 0.27	0.47
	Rump height (cm)	78.50 $\pm$ 0.66	75.37 $\pm$ 0.55	74.65 $\pm$ 0.35	76.89 $\pm$ 0.88	72.11 $\pm$ 0.77	72.90 $\pm$ 0.26	0.33
	Chest circumference (cm)	113.19 $\pm$ 1.82	110.30 $\pm$ 1.50	110.02 $\pm$ 0.97	111.18 $\pm$ 2.43	107.45 $\pm$ 2.11	105.43 $\pm$ 0.71	0.64
	Abdominal circumference (cm)	125.50 $\pm$ 1.93	123.56 $\pm$ 1.59	120.43 $\pm$ 1.03	125.38 $\pm$ 2.58	117.90 $\pm$ 2.24	115.69 $\pm$ 0.75	0.36

Values are presented as least-square means (LSMeans) $\pm$ standard errors (SE). Means within the same row with different lowercase superscripts indicate significant differences ($p < 0.05$), with p-values provided for clarity.

Discussion

This study investigated the potential association between genetic variation in the *SST* gene and growth traits in two important Middle Eastern sheep breeds using various morphological productivity parameters. The relatively lower growth performance observed in the Awassi breed compared to the Karakul breed provided the primary motivation for conducting this association analysis. Notably, SNPs potentially associated with these phenotypic differences have already been reported in previous studies (Aljubouri et al., 2020).

Accordingly, this study genotyped the *SST* gene using the PCR-SSCP method due to its being less expensive, with a high rate of processing and the ability to detect more variations than other commonly used post-PCR techniques (Kakavas, 2021). The entire *SST* gene's coding regions were genotyped in this research due to the substantial and straightforward effect of the missense SNPs on the structure, function, stability and interaction of the protein (Bayraktar et al., 2023; Abuzahra et al., 2024). However, based on the results of the present study, the *SST* gene exerts its effect by having a synonymous instead of a non-synonymous effect on the 3D structure of somatostatin. The present results were consistent with those reported by Kijas et al. (2006), who found more than 70% of synonymous SNPs in the overall detected variants in 120 gene orthologs compared with only 14–17% of non-synonymous substitutions in sheep. Given that non-coding SNPs are known to exist at higher frequencies than coding sequences (Vignal et al., 2002; Capriotti et al., 2013), the discovery of synonymous SNPs was not unusual.

It was observed that the breed had a major impact on the measured growth characteristics. This could be attributed to the fact that, compared to the Awassi breed, the Karakul breed has notably higher values across a wide spectrum of growth indices (Alwan and Aljubouri, 2023; Aljubouri and Al-Shuhaib, 2023b). However, the present findings indicated that both the investigated populations were not consistent with HWE due to the extensive exposure of both breeds to a wide range of breeding programs for meat production over successive generations (Aljubouri et al., 2020; Khazaal et al., 2023).

The present study revealed that the differences between the Awassi and Karakul breeds were not attributable to only the non-genetic factors. Instead, the significant contribution of *SST* genetic polymorphism played a critical role in this arena due to the discovery of a synonymous SNP (154G>A) with a strong correlation with various growth traits in both assessed

populations. The genetic polymorphism of the 154G>A SNP interacted significantly with lamb breed in determining the final situation of genotype-phenotype association. This could be attributed, irrespective of the breed being studied, to the presence of a strong correlation among the GG, GA and AA genotypes and growth traits. Due to this association, lambs having the AA genotype generally exhibited better growth performance than lambs with GA or GG genotypes, beginning from age 3 mth. Such was the case for BW, as well as BL, WH and RH, with the AA genotype consistently giving the highest values, followed by the GA and GG genotypes. Based on the data, the SNP effect increased with sheep age. Although no significant differences were evident at birth across the genotypes for all measured traits, significant distinctions were apparent by 3 mth, when a trend emerged of greater disparities in most of the characteristics. This trend continued through 6 mth, 9 mth and 12 mth, suggesting that the SNP may have a delayed effect that becomes more noticeable as the animals mature. Therefore, the effect of the now-identified 154G>A SNP may act in combination with the breed under study.

However, compared with the non-synonymous SNPs, the impact of this synonymous SNP was difficult to observe because of its indirect effect on somatostatin activity, making it difficult to identify. Nonetheless, the significant effect of the silent SNP can be considered as a contributing factor in many metabolic changes in the cell (Komar, 2007). The silent SNP may modify substrate specificity, which may result in different protein kinetics (Kirchner et al., 2017; Sukhumsirichart, 2018). While synonymous substitutions are generally considered silent, such mechanisms remain speculative in the absence of experimental validation. Nevertheless, the results of the present study may provide additional support for the suggested crucial role that synonymous SNPs may play in a variety of ovine genes in relation to a wide spectrum of productive and reproductive traits (Girmay et al., 2022; Skorykh et al., 2023; Cao et al., 2024).

Apart from our SNP, genetic growth traits in Chinese cattle have been reported to be strongly associated with *SST* gene polymorphisms (Gao et al., 2011). This was also apparent in the sequences of exon 1, while exon 2 did not exhibit any detectable polymorphism. Though these results have not been observed in sheep yet, these bovine-based data were in agreement with the present results that showed the polymorphic nature of the exon 1 in the ovine *SST*. In contrast to the present study, there were no differences in the coding sequences of the caprine *SST* gene, with all detected variations occurring only in intron 1. These intronic variations were significantly associated with

caprine body length and height (Jin et al., 2011). However, other than these studies, our results cannot be compared with any research in sheep because no published studies have reported a potential association between the *SST* gene and productive traits in sheep. The reason for this lack in the literature may be attributed to the critical importance of the *SST* receptor in terms of its high level of association with variable productive traits in sheep (Zhao et al., 2018).

Due to the novelty of the 154G>A SNP in the Ensembl database, the association of this SNP with growth traits, as well as other productivity traits, has not been shown in any breed (sheep or other domestic animals). Analysis of the present association results revealed that lambs with the modified AA genotype had greater growth trait indices than lambs with the GA and GG genotypes. These changes could be related to nucleic acid substitution in exon 2 of the *SST* gene. Lambs of the minor homozygous, AA genotype performed better than those of the heterozygous GA and major homozygous GG genotypes, since the 154G>A SNP was involved in the attributes that were assessed. With the homozygous advantage, more than the other two genotypes, it can be assumed that the discovered SNP had a positive impact. The Karakul breed had substantially greater frequencies of GA and AA genotypes than the Awassi breed, which might offer a plausible explanation for the slower growth characteristic values observed in the Awassi breed. Therefore, the present findings support the significance of the 154G>A SNP in marker-assisted selection, given its crucial involvement in altering the lambs' productivity potential. However, the limited number of samples investigated may not give a sufficient impression of its actual frequency. This point may represent the main limitation behind this study, as this investigation needs to conduct a large-scale association analysis to add another layer of confirmation to the current findings. Even though the present study has demonstrated a strong correlation between the 154G>A SNP and the Karakul breed's higher productive potential, more research is necessary to comprehend the mechanisms underlying this SNP's profound influence on the *SST* gene's mRNA transcripts.

Based on the publications available, the present research was the first to show a connection between this SNP and sheep growth characteristics. Taking this information into account, the present findings on *SST* variations could improve the evaluation of growth traits in the breeds being studied through marker-assisted selection and may also be applied to other breeds that have lower potential for growth productivity.

The identification of the 154G>A SNP in the *SST* gene and its association with postnatal growth traits provides an

opportunity for its application in marker-assisted selection programs. Through screening of young lambs of this variant, breeders would be able to select at will those that contain the desirable AA genotype that has always been linked to good BW, body length and skeletal frame size at the age of 3 mth. This may accelerate genetic progress by enabling earlier and more accurate identification of animals with higher growth potential, particularly in breeds with traditionally lower productivity, such as the Awassi sheep. In addition, the higher frequency of favorable genotypes in Karakul sheep suggests that this breed may serve as a valuable genetic reservoir for introgression programs aimed at improving growth performance across other sheep populations (Aljubouri et al., 2020b).

While the identified 154G>A SNP in the *SST* gene showed significant associations with postnatal growth traits, notably, growth and body size are polygenic and environmentally influenced traits. This observation indicates that if even a single SNP exhibited a significant effect, this effect is only part of a much larger genetic and physiological network that determines growth performance. Although the identified SNP in the *SST* gene is synonymous and does not change the amino acid sequence, accumulating evidence indicates that such variants can still have functional consequences on gene expression and phenotype. Synonymous substitutions may influence mRNA secondary structure, codon usage bias or translation kinetics, which can affect mRNA stability and co-translational protein folding, ultimately modifying the efficiency of gene expression without altering the encoded protein (Wang et al., 2021; Lin et al., 2023). Furthermore, another study in livestock has shown that synonymous variants could influence gene expression and biological traits, including growth and immune responses (Darwish et al., 2025). Given the critical role of *SST* in regulating growth hormone secretion and energy metabolism, such molecular effects may plausibly underlie the observed associations between this SNP and body weight or morphometric traits in sheep.

Furthermore, the relatively small sample size of 175 animals across two breeds represents a limitation of the present study. While significant associations were observed between the 154G>A SNP and growth traits, the limited number of individuals may have affected the robustness and generalizability of these findings. To strengthen confidence in the results, future studies should validate this SNP in larger and independent populations, ideally including additional breeds and diverse environmental conditions. Such validation would help to confirm the utility of the 154G>A SNP as a reliable molecular marker for marker-assisted selection programs.

While the identified 154G>A SNP showed a significant association with growth traits in these breeds, the effect of this SNP may vary across different genetic backgrounds and environmental conditions. Therefore, validation in larger, independent populations, including diverse breeds with varying growth potentials, is necessary to confirm the broader applicability of this marker. Such studies would also help to determine whether the observed genotype-phenotype associations are consistent across breeds or influenced by breed-specific factors.

Thus, the results obtained can be regarded as an initial pointer rather than a definite growth predictor. The higher frequency of the Karakul sheep with GA and AA genotypes, combined with their superior growth traits, suggests that the effect of the SNP may be influenced by genetic background. However, the present study was not designed to fully disentangle genotype effects within each breed independently, due to sample size constraints. Accordingly, it can be stated that larger and balanced breed-specific populations would be required to define whether the SNP has the same effect in all breeds or whether its influence is breed-specific

Conclusions

This investigation found a unique SNP (154G>A) in the *SST* gene, which showed significant association with several growth traits in the Awassi and Karakul breeds. Lambs with the AA genotype (minor homozygosity) displayed greater growth trait values compared to the GA and GG genotypes. The higher frequencies of the A allele in the Karakul breed may partially explain the better growth characteristics observed in this breed than in the Awassi breed. However, these findings are preliminary and the potential use of this SNP in marker-assisted selection should be interpreted with caution. Further studies, including functional assays and validation in larger and more diverse sheep populations, are necessary to confirm the practical utility of this SNP.

Conflict of interest

The authors declare that they have no conflict of interest and that no funding or other forms of financial assistance were obtained to prepare this manuscript.

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