

Single-Nucleotide Polymorphisms of Insulin-Like Growth Factor-1 (IGF1) Gene in Goat and Their Association with Growth Traits

Dela Ayu Lestari^{1,2}, Fatmawati Mustofa^{1,2}, Sutopo Sutopo¹, Dwi Wijayanti^{2,3}, Achiriah Febriana^{2,4}, Mamat Hamidi Kamalludin⁵, Asep Gunawan⁶, Asep Setiaji^{1,2*}

¹ Department of Animal Science, Faculty of Animal and Agricultural Sciences Universitas Diponegoro, Semarang 50275, Central Java, Indonesia

² Tropic Research on Productivity, Genetic Enhancement, and Conservation of Local Livestock (TROPICAL), Indonesia

³ Department of Animal Science, Perjuangan University of Tasikmalaya, Tasikmalaya, West Java, 46115, Indonesia

⁴ Indonesian Center for Livestock Training Batu (ICLT), Ministry of Agriculture of Indonesia, Batu 65301, Indonesia

⁵ Institute of Tropical Agriculture and Food Security, Universiti Putra Malaysia, Serdang, Selangor, 43400, Malaysia

⁶ Department of Animal Production and Technology, Faculty of Animal Science, IPB University, Bogor, 16680 Indonesia

ABSTRACT

Goat farming plays a vital role in sustaining the livelihoods of smallholder farmers worldwide, with improved growth performance being a primary objective of numerous breeding programs. The insulin-like growth factor-1 (*IGF1*) gene has been extensively studied as a key candidate gene due to its crucial involvement in regulating cell growth, differentiation, and metabolism, which underpin developmental processes. This systematic review synthesizes findings from 11 studies conducted between 2008 and 2024 across Asia and Africa, focusing on single nucleotide polymorphisms (SNPs) within the *IGF1* gene and their associations with growth traits in various goat populations. A range of genotyping techniques, including PCR-RFLP, sequencing, real-time PCR, and T-ARMS-PCR, were applied to both indigenous and crossbred goats. Multiple SNPs were identified, with the g.5752 locus consistently reported in three independent studies, indicating its potential utility as a marker-assisted selection (MAS). Genotypic frequencies varied from 0.00 to 0.91, and allelic frequencies ranged from 0.08 to 0.94, reflecting substantial genetic diversity among goat breeds. Although 79.9% of observations did not show statistically significant associations, 20.1% revealed notable links, particularly with body weight, body length, and body height. These findings suggest that while *IGF1* polymorphisms hold promise as molecular markers for growth traits, the phenotypic expression of growth in goats is likely influenced by complex polygenic inheritance and gene–environment interactions. Future research should focus on genome-wide association studies and breed-specific validation to enhance the application of *IGF1* SNPs in genetic improvement strategies for sustainable goat production.

Keywords

genetic variation, growth traits, *IGF1*, marker-assisted selection, SNPs

Received October 3, 2025, Revised November 17, 2025, Accepted February 7, 2026

Published online: April 15, 2026. *Correspondence to A. S: asepsetiaji@live.undip.ac.id

1. Introduction

Goat farming plays a vital role in global livestock production and is essential to the livelihoods of millions of smallholder farmers, particularly in the developing regions of Asia and Africa [1, 2]. Goats are among the most versatile domesticated species, valued for their ability to thrive in harsh environmental conditions, tolerate feed scarcity, and adapt to diverse agroecological systems [3, 4]. Their contributions extend beyond food production, as they provide meat, milk, fiber, leather, and manure and serve as a financial safety net for rural households. Given their economic, nutritional, and socio-cultural significance, improving goat productivity remains a strategic priority for ensuring food security and sustainable rural development in these regions [5, 6]. Among the various performance indicators in goats, growth traits, including body weight, average daily gain, body height, body length, and chest girth, are particularly important because they directly determine market value and profitability [7, 8, 9]. Rapid growth translates into shorter production cycles, lower maintenance costs, and increased returns on investment. However, growth traits are highly complex and are influenced by both non-genetic factors (nutrition, health management, climate, and housing) and genetic determinants. Traditional breeding programs based solely on phenotypic selection have contributed to some improvements but are often limited by long generation intervals, environmental variability, and the polygenic nature of growth [10, 11, 12]. This has led to growing interest in molecular genetics as a complementary tool for accelerating genetic improvement.

The *insulin-like growth factor-1 (IGF1)* gene has emerged as a promising target for genetic improvement. *IGF1* is a central regulator of postnatal growth and development and functions as a key mediator of the growth hormone (GH)-IGF axis [13, 14]. It plays an essential role in cell proliferation, differentiation, metabolism, and protein synthesis, thereby influencing skeletal and muscle growth. At the physiological level, *IGF1* affects both prenatal and postnatal growth processes, whereas at the molecular level, it activates multiple intracellular signaling cascades, including the PI3K-AKT and MAPK pathways, which regulate tissue development and metabolic efficiency [15, 16]. Because of its central role in growth biology, *IGF1* has been extensively studied in livestock, where polymorphisms in this gene are widely recognized as potential markers for growth-related traits. Furthermore, a deeper understanding of these variants may help support more efficient and targeted breeding programs [17, 18]. Single-nucleotide polymorphisms (SNPs), the most common form of genetic variation in animal genomes, provide a powerful means of exploring the relationship between genetic diversity and phenotypic traits. SNPs in the *IGF1* gene, distributed across exons, introns, and regulatory regions, can alter gene expression and protein function, ultimately influencing the growth performance of animals [19, 20]. Numerous SNPs have been reported in goats, with associations documented for body weight, body length, body height, and other morphometric traits. However, the findings of these studies are inconsistent, often varying according to breed, sample size, geographical region, and methodological approaches. Some studies have reported strong associations between specific SNPs and growth traits, whereas others have found weak or no significant effects. These inconsistencies create uncertainty regarding the practical application of *IGF1* polymorphisms as reliable markers for selection.

Given these discrepancies, a systematic review is needed to consolidate the available evidence, identify consistent associations, and highlight knowledge gaps. A critical synthesis of the literature will not only improve our understanding of *IGF1* genetic polymorphisms in goats but also provide a foundation for integrating molecular markers into breeding programs. Such efforts are particularly relevant for community-based and smallholder farming systems, in which marker-assisted selection (MAS) can complement traditional practices, accelerate genetic gain, and enhance the productivity of indigenous goat breeds. Therefore, this review aims to collect, evaluate, and synthesize scientific evidence on SNPs of the *IGF1* gene in goats and their reported

Please cite this article as

Lestari *et al.* Reviews in Agricultural Science, 14(2): 1–15, 2026

https://doi.org/10.7831/ras.12.2_1

associations with growth traits. This review aims to provide a consolidated framework for understanding the potential of *IGF1* polymorphisms as molecular markers, offering insights into future genetic improvement strategies to enhance goat growth performance.

2. Materials and Methods

2.1 Eligibility criteria

To ensure that only relevant and high-quality studies were included in this systematic review, specific inclusion and exclusion criteria were established before the literature search. These criteria were based on the PICOS framework [21] (population, intervention, comparison, outcomes, and study design) commonly used in systematic reviews.

2.2 Literature search

All authors conducted a literature search for relevant research publications using four databases Google Scholar, PubMed, ScienceDirect, and Web of Science, up to 15 April 2025. The following keywords were used in various combinations: “insulin-like growth factor-1 (*IGF1*)”, “single nucleotide polymorphisms”, “genetic effect”, “polymorphisms”, “genetic variations”, “growth traits”, and “goat”.

2.3 Inclusion criteria

Studies were considered eligible for inclusion if they met all of the following criteria:

- Population: Studies involving domestic goats (*Capra hircus*) of any breed or age group.
- Gene of Interest: Research focused specifically on the insulin-like growth factor-I (*IGF1*) gene, identifying and/or analyzing single-nucleotide polymorphisms (SNPs).
- Traits Studied: Studies reporting at least one measurable growth trait, such as body weight (at birth, weaning, or later stages), body length, height at withers, chest girth, average daily gain (ADG), or other indicators of growth performance.
- Genetic Analysis: The study must include molecular genotyping or sequencing techniques (e.g., PCR-RFLP, PCR-SSCP, DNA sequencing) used to identify SNPs within the *IGF1* gene.
- Association Analysis: The study should analyze associations between *IGF1* SNPs and growth traits using appropriate statistical or genetic models.
- Publication Type: Peer-reviewed original research articles published in English with full-text availability.
- Time Frame: No restriction on publication year was applied to capture both recent and historical studies.

2.4 Exclusion criteria

Studies were excluded from the review based on the following conditions:

- Species Mismatch: Articles focusing on species other than goats (e.g., cattle, sheep, pigs).
- Gene Irrelevance: Studies that did not involve the *IGF1* gene or did not analyze any SNPs within this gene.
- Non-growth Traits: Research that investigated *IGF1* gene polymorphisms related to reproductive, immune, milk production, or disease resistance traits only.

Please cite this article as

Lestari *et al.* Reviews in Agricultural Science, 14(2): 1–15, 2026

https://doi.org/10.7831/ras.12.2_1

Lack of Genotyping: Studies that discussed *IGF1* gene expression or protein levels without accompanying SNP analysis.

Non-original Articles: Review papers, meta-analyses, conference abstracts, theses, editorials, or letters. Articles lacking detailed methodology or statistical results on associations were also excluded.

Language Barrier: Studies published in languages other than English and without an available translated version.

2.5 Data extraction

The authors independently compiled the data from eligible studies. Extracted information from each article included details such as the first author's name, publication year, country of origin, goat breed, sample population size, the traits studied, and the genotyping techniques used.

2.6 Ethical consideration

All authors adhered to ethical standards by considering aspects such as plagiarism, research misconduct, informed consent, and the prevention of data fabrication and falsification.

3. Results

3.1 Characterization articles

This review compiled 11 studies conducted between 2008 and 2024 across Asia and Africa, focusing on the association between genetic markers and phenotypic traits in goats using various genotyping methods, predominantly PCR-RFLP and sequencing (Table 1). Four articles were from India, followed by two articles from Indonesia, two articles from China, and the remaining articles were from Iraq, Tunisia, and Pakistan.

Table 1: Characterization of included articles

Country	Breeds	N	Growth traits	Genotyping methods	References
India	Malabari	175	BW, BL, BH, CC, TC, BLI, CCI, TI	PCR-RFLP Sequencing	[22]
	Attapady black	102			
India	Malabari	50	BW	T-ARMS PCR	[23]
	Attappady black	50			
China	Liaoning cashmere	1180	BH, SH, OBL, CD, CW, HW, CC, CaC, WaH	PCR-Seq	[24]
Indonesia	Kejobong	35	BW, CW, HH, HW, HG	PCR-Seq	[25]
Iraq	Local Black	34	BWT, WWT, WG	PCR-Seq	[26]
Indonesia	Etawah grade	22	BW	PCR-RFLP	[27]
Tunisia	Arbi	144	BL, WH, EL, CG, CD, CW, TL, HL	SNP Genotyping (Real-Time PCR)	[28]
	Alpine	31			
	Boer	30			
	Damascus	21			
	Maltese	10			
	Boer x Damascus	17			
	Arbi x Damascus	10			
India	Assam hill	256	BW	PCR-RFLP	[29]
Pakistan	Beetal	60	BW, WH, BL, HG	PCR-RFLP	[30]
India	Sirohi	187	BW0, BW3, BW6, BW9	PCR-Seq	[31]
China	Nanjiang Huang	592	BW0, BW2, BW6, BW12, BL2, HG2, WH2, BL6, HG6, WH6, BL12, HG12, WH12	PCR-SSCP	[32]

Note:

BG: Body girth, BH: Body height, BL: Body length, BL2: Body length at 2 months, BL6: Body length at 6 months, BL12: Body length at 12 months, BLI: Body length index, BW: Body weight, BWT : Birth weight, BW0 : Body weight birth, BW2 : body weight

Please cite this article as

Lestari *et al.* Reviews in Agricultural Science, 14(2): 1–15, 2026
https://doi.org/10.7831/ras.12.2_1

at 2 months, BW3: Body weight at 3 months, BW6: Body weight at 6 months; BW9: Body weight at 9 months, BW12: Body weight at 12 months, CaC: Cannon circumference, CC: Chest circumference, CCI: Chest circumference index, CD: Chest depth, CG: Chest girth, CG2: Chest girth at 2 months, CG6: Chest girth at 6 months, CG12: Chest girth at 12 months, CW: Chest width, EL: Ear length, HG: Heart girth, HL: Head length, HW: Hip width, N: Total population, OBL: Oblique body length, SH: Sacral height, TC: Trunk circumference, TI: Trunk index, TL: Tail length, WG: Weight gain, WH: Withers height, WH2: Withers height at 2 months, WH6: Withers height at 6 months, WH12: Withers height at 12 months, WaH: Waist height, WWT: Weaning weight, x = cross

3.2 Distribution of the articles by years

The results revealed that eleven articles indicated the year of publication. The findings showed that the included articles were published in 2008, 2013, 2017, 2018, and 2019 (1 article each), 2022 (2 articles), 2023 (1 article), and 2024 (1 articles). The largest number of articles included was published in 2020 (2 articles).

3.3 Genotyping methods

The most frequently employed genotyping methods were PCR-RFLP and PCR coupled with sequencing. The combination of both approaches allows for rapid screening and precise nucleotide identification. DNA sequencing provided extensive genetic detail and enabled comparison across several exotic and indigenous breeds. Furthermore, one study employed real-time PCR (TaqMan SNP Genotyping), while another used T-ARMS-PCR.

3.4 Population and breed diversity

A wide range of goat breeds was studied, including indigenous and crossbreeds, reflecting regional biodiversity. India was the most represented country with four studies covering breeds such as Malabari, Attappady Black, Sirohi, and Assam Hill. Other countries included Indonesia (Kejobong and Etawah Grade), China (Liaoning Cashmere and Nanjiang Huang), Iraq (Local Black), Pakistan (Beetal), and Tunisia (Arbi, Boer, Damascus, Alpine, and their crosses), which studied both local and exotic breeds. Sample sizes varied from small populations (e.g., 22 Etawah Grade goats in [27]) to large-scale studies, such as the study of 1,180 Liaoning Cashmere goats conducted by [24].

3.5 Identified single nucleotide polymorphisms and genotype frequency

The identified SNPs and their corresponding genomic regions are summarized in Table 2. Analysis of the reviewed literature revealed that, among the 11 articles examined, 10 (90.9) reported the identification of SNPs. Notably, four studies consistently reported a GC SNP at the same position, g.5752G>C [24, 28, 29, 31]. Furthermore, analysis of the 11 studies revealed SNPs forming distinct genotypes, with note that one study did not report specific SNPs, but provided genotype data instead. The reported genotypic frequencies ranged from 0.00 to 0.91. For example, genotype distribution tended to be balanced in Attappady black [22], Assam Hill [29], Etawah Grade [27] and Nanjiang Huang [32] goat breeds, while the high proportion of heterozygotes (GC) at SNP g.5752G>C in Beetal (47%) and Assam Hill (49%) suggests that these populations still maintain a relatively high level of genetic diversity. Furthermore, certain SNPs also show breed-specific patterns.

For instance, in Kejobong goats, the CC genotype at SNP g.5752G>C occurs at the highest frequency (57%), while the GC genotype is not detected [25]. A similar pattern is observed in Malabari goats at SNP g.1617A>G, where the GG and AG genotypes are relatively common, whereas the AA genotype is absent [22]. Sirohi goats also demonstrate the dominance of specific genotypes; for SNP g.4700T>C, the TT genotype is predominant (0.851), and the CC genotype is found at a very low frequency (0.005). In contrast, for SNP g.5524C>T, the CC genotype is predominant (0.912), while the TT genotype is extremely rare (0.001) [31]. Furthermore, in Liaoning Cashmere

Please cite this article as

Lestari *et al.* Reviews in Agricultural Science, 14(2): 1–15, 2026

https://doi.org/10.7831/ras.12.2_1

goats, both rams and ewes based on g.5464C>T exhibit a predominant mm genotype (0.71–0.84), while the MM genotype is completely absent (0.00) [24]. In addition, the study by Chalbi *et al.* [28], reported the presence of a large number of SNPs (rs#) in various breeds such as Arbi, Alpine, Boer, Damascus, and Maltese, although without detailed reports on genotype frequencies.

Table 2: Identified single nucleotide polymorphisms

Identified SNPs	Genomic position*	Gen bank references	Breeds	Genotypic frequencies	References
A224G	g.1617A>G	HQ731040.1	Malabari	GG (0.51), AG (0.49), AA (0.00)	[22]
c.546+179170A.T	g.25752318A>T	NC030828.1	Attappady black	GG (0.82), AG (0.18), AA (0.00)	
C5464T	g.5464C>T	NC030812.1	Malabari	AA (0.40), TT (0.14), AT (0.44)	[23]
			Attappady black	AA (0.32), TT (0.28), AT (0.40)	
			Liaoning cashmere (ram)	MM (0.00), Mm (0.29), mm (0.71)	[24]
			Liaoning cashmere (ewe)	MM (0.00), Mm (0.16), mm (0.84)	
g5752G>C	g.5752G>C	D26119.2	Kejobong	GG (0.43), GC (0.00), CC (0.57)	[25]
A182G	g.1574A>G	HQ731040.1	Local Black	GG (0.91), AG (0.09), AA (0.00)	[26]
-	-	-	Etawah grade	AA (0.32), AB (0.50), BB (0.18)	[27]
rs669696004	g.64868083T>A	NC030812.1	Arbi, Alpine, Boer,	-	[28]
rs646819374	g.64882982T>C		Damascus,		
rs672362340	g.64884614A>G		Maltese,		
rs659298289	g.64885306T>C		Boer x Damascus,		
rs642422457	g.64902365G>A		Arbi x Damascus		
rs635891853	g.64920059A>G				
rs643504083	g.64937039C>T				
rs646704459	g.64938790T>C				
rs648452154	g.64939272T>C				
rs658505766	g.64940709A>G				
rs654055030	g.64941928T>G				
rs668949633	g.64943332C>A				
G5752C	g.5752G>C	D26119.2	Assam Hill	GG (0.19), GC (0.49), CC (0.32)*	[29]
g.5752G>C	g.5752G>C	D26119.2	Beetal	GG (0.39), GC (0.47), CC (0.09)*	[30]
g.4700T > C	g.4700T > C	D26119	Sirohi	CC (0.005), TC (0.142), TT (0.851)	[31]
g.5524C > T	g.5524C > T	D26119	Sirohi	CC (0.912), TC (0.084), TT (0.001)	
589 G>C	g.5752G>C	D26119.2	Nanjiang Huang	GG (0.36), GC (0.37), CC (0.27)	[32]

*The genotype nomenclature was adjusted because they originate from the same SNP position, and the consistency follows the format of Zhang *et al.* [32], the first researchers to report this SNP

3.6 Allelic Frequencies

Table 3 provides a summary of allelic frequencies reported in the reviewed literature. Among the 11 articles analyzed, allelic frequencies were explicitly reported in almost all studies, whereas one article reported frequencies differently by employing a minor allele frequency approach. The range of allelic frequencies observed across these studies ranged from 0.044 to 0.955.

The analysis of allele frequencies in various goat breeds revealed diverse patterns of genetic distribution. In Malabari goats, a predominance of the G allele (0.75) over A (0.25) was reported by Naicy *et al.* [22], as well as a distribution of A (0.62) and T (0.38) that reported by Alex *et al.* [23]. Differences in the SNP loci investigated produced variation in allele distribution; however, overall, Malabari goats still maintained a relatively good level of genetic diversity.

Please cite this article as

Lestari *et al.* Reviews in Agricultural Science, 14(2): 1–15, 2026

https://doi.org/10.7831/ras.12.2_1

In contrast to Malabari, Attappady Black goats displayed a more extreme pattern. Naicy *et al.* [22] reported a very high frequency of the G allele (0.91) compared to A (0.09), indicating allele fixation. However, a different result was reported by Alex *et al.* [23], who found a relatively balanced distribution of A (0.52) and T (0.48). These findings suggest that, at certain loci, the Attappady Black population experienced strong selective pressure, while at other loci, genetic diversity was preserved.

In Liaoning cashmere goats, allele distribution differences were observed based on sex. In rams, the frequency of allele M (0.14) was much lower compared to m (0.86), while in females, the proportion of M (0.08) and m (0.92) also showed a clear dominance of allele m [24]. This consistent pattern highlights the low genetic diversity at this locus in both sexes. Meanwhile, Sharma *et al.* [31] reported markedly contrasting allele frequency distributions at two loci identified in Sirohi goats. At the first locus, the T allele was overwhelmingly dominant (0.923), while the C allele occurred at a very low frequency (0.077). Conversely, at the second locus, the C allele showed a strong predominance (0.955), with the T allele being extremely rare (0.044). These findings highlight the presence of extreme allele frequency imbalances within the same population, suggesting that different selective forces or demographic factors may be acting independently across loci.

Furthermore, several populations showed relatively balanced allele distributions. Kejobong goats had G (0.43) and C (0.57) [25], while Etawah Grade goats showed A (0.57) and B (0.43) [27]. Likewise, Assam Hill goats displayed G (0.43) and C (0.57) [29], and Beetal goats showed G (0.65) and C (0.35) [30]. Nanjiang Huang goats also exhibited a balanced allele frequency distribution, with G (0.546) and C (0.454) [32]. These five populations indicate that genetic diversity remains preserved, offering potential advantages in terms of adaptive capacity as well as opportunities for marker-assisted breeding. Conversely, Local Black goats demonstrated a strong dominance of the G allele (0.94) compared to A (0.06) [26]. This pattern indicates allele fixation, which may reduce the population's adaptive capacity to environmental changes or disease challenges. On the other hand, broader research by Chalbi *et al.* [28] reported the presence of numerous SNPs (rs#) across breeds such as Arbi, Alpine, Boer, Damascus, Maltese, and their crossbreeds. The reported allele frequencies were highly variable, for instance T:A (0.08), C:T (0.31), A:G (0.32), and T:C (0.37). Although no detailed data on genotype distribution were provided, this variation underscores the high level of genetic diversity in these breeds.

Table 3: Allelic frequencies

Breeds	Allelic frequencies	References
Malabari	G (0.75), A (0.25)	[22]
Attapady Black	G (0.91), A (0.09)	[23]
Attapady Black	A (0.52), T (0.48)	
Malabari	A (0.62), T (0.38)	[24]
Liaoning cashmere (Ram)	M (0.14), m (0.86)	
Liaoning cashmere (Ewe)	M (0.08), m (0.92)	[25]
Kejobong	G (0.43), C (0.57)	
Local Black	G (0.94), A (0.06)	[26]
Etawah Grade	A (0.57), B (0.43)	[27]
Arbi, Alpine, Boer, Damascus, Maltese,	T:A (0.08), C:T (0.31), A:G (0.32), T:C (0.37), G:A (0.49), G:A (0.28),	[28]
Boer x Damascus, Arbi x Damascus	C:T (0.15), T:C (0.15), T:C (0.33), A:G (0.22), G:T (0.33), C:A (0.15)	
Assam Hill	G (0.43), C (0.57)*	[29]
Beetal	G (0.65), C (0.35)*	[30]
Sirohi	T (0.923), C (0.077)	[31]
Sirohi	C (0.955), T (0.044)	[32]
Nanjiang Huang	G (0.546), C (0.454)	

*The allele nomenclature was adjusted because they originate from the same SNP position, and the consistency follows the format of Zhang *et al.* [32], the first researchers to report this SNP.

3.7 Association between identified SNP's genotypes and growth traits

Based on Table 4, the reviewed studies demonstrated that the association between *IGF1* polymorphisms and growth traits in goats varies across breeds and specific SNPs. Several breeds, including Attappady Black, Malabari, Kejobong, Local Black goats, Sirohi, Nanjiang Huang, and Etawah Grade, show significant relationships between *IGF1* variants and body weight. *IGF1* polymorphisms have also been linked to body size traits in multiple populations, with notable associations observed for morphometric measurements such as body height, body length, chest depth, chest width, and withers height. Additionally, some studies have highlighted specific SNPs that influence particular traits, indicating that *IGF1* may play breed-dependent roles in shaping growth performance and body conformation. These findings suggest that *IGF1* may serve as a valuable candidate marker for genetic improvement. However, the variability among breeds emphasizes the need for further validation in diverse goat populations.

Table 4: Association between SNP and growth traits

Breeds	SNPs	Genotypes	Growth traits**	Sig	References
Malabari	A224G	GG (0.51), AG (0.49), AA (0.00)	BW, BL, BH, CC, TC, BLI, CCI, TI	Ns	[22]
Attappady Black		GG (0.82), AG (0.18), AA (0.00)	BW, BH, CC BL, TC, BLI, CCI, TI	Sig Ns	
Malabari	c.546+ 179170A > T	AA (0.40), TT (0.14), AT (0.44)	BW0, BW3 BW6	Sig Ns	[23]
Attappady Black		AA (0.32), TT (0.28), AT (0.40)	BW0, BW3, BW6	Sig	
Liaoning cashmere (ram)	C5464T	CC (0.00), CT (0.29), TT (0.71)	BH, SH, OBL, CD, CW, CaC, WaH HW, CC	Sig Ns	[24]
Liaoning cashmere (ewe)		CC (0.00), CT (0.16), TT (0.84)	BH, SH, WaH OBL, CD, CW, HW, CC, CaC	Sig Ns	
Kejobong	g5752G>C	GG (0.43), GC (0.00), CC (0.57)	BW7, BW8, BCW7, CW8, HH4, HH7, HW4, HW7, HW8, HG2, HG4, HG5, HG7, HG8 BW1, BW2, BW3, BW4, BW5, BW6, CW1, CW2, CW4, CW5, CW6, HH1, HH2, HH3, HH5, HH6, HH8, HW1, HW2, HW3, HW5, HW6, HG1, HG3, HG6	Sig Ns	[25]
Local Black Goat	A182G	GG (0.91), AG (0.09), AA (0.00)	WWT BWT, WG	Sig Ns	[26]
Etawah Grade	-	AA (0.32), AB (0.50), BB (0.18)	BW	SC	[27]
Arbi,	rs669696004	-	BL, WH, EL, CG, CD, CW, TL, HL	Ns	[28]
Alpine,	rs646819374	-	BL, WH, EL, CG, CD, CW, TL, HL	Ns	
Boer,	rs672362340	-	BL	Sig	
Damascus,			WH, EL, CG, CD, CW, TL, HL	Ns	
Maltese,	rs659298289	-	BL, TL, EL	Sig	
Boer×Damascus			WH, CG, CD, CW, HL	Ns	
Arbi×Damascus	rs642422457	-	BL, WH, EL, CG, CD, CW, TL, HL	Ns	
	rs635891853	-	BL, WH, EL, CG, CD, CW, TL, HL	Ns	
	rs643504083	-	BL	Sig	
			WH, EL, CG, CD, CW, TL, HL	Ns	
	rs646704459	-	BL, WH, EL, CG, CD, CW, TL, HL	Ns	
	rs648452154	-	BL	Sig	
			WH, EL, CG, CD, CW, TL, HL	Ns	
	rs658505766	-	BL	Sig	
			WH, EL, CG, CD, CW, TL, HL	Ns	
	rs654055030	-	CD	Sig	

Please cite this article as

Lestari *et al.* Reviews in Agricultural Science, 14(2): 1–15, 2026

https://doi.org/10.7831/ras.12.2_1

	rs668949633	-	BL, WH, EL, CG, CW, TL, HL TL	Ns Sig	
Assam hill goats	G5752C	GG (0.19), GC (0.49), CC (0.33)*	BL, WH, EL, CG, CD, CW, HL BW0, BW3, BW9, BW12	Ns Ns	[29]
Beetal	g.5752G>C	GG (0.65), GC (0.47), CC (0.09)*	BL WH, BL, HG	Sig Ns	[30]
Sirohi	g.4700T > C	CC (0.005), TC (0.142), TT (0.851)	BW0, BW3, BW6, BW9	Sig	[31]
Sirohi	g.5524C > T	CC (0.912), TC (0.084), TT (0.001)	BW6, BW9 BW0, BW3	Sig Ns	
Nanjiang Huang	g.5752G>C	GG (0.36), GC (0.37), CC (0.27)	BW0, BW6, BW12, CG2, CG12, BL6, WH6, WH12 BW2, BL2, BL12, CG6, WH2	Sig Ns	[32]

Note:

*The genotype nomenclature was adjusted because they originate from the same SNP position, and the consistency follows the format of Zhang *et al.* [32], the first researchers to report this SNP

**BG: Body girth, BH: Body height, BL: Body length, BL2: Body length at 2 months, BL6: Body length at 6 months, BL12: Body length at 12 months, BLI: Body length index, BW: Body weight, BW0: Body weight birth, BW2: body weight at 2 months, BW3: Body weight at 3 months, BW6: Body weight at 6 months; BW9: Body weight at 9 months, BW12: Body weight at 12 months, BWT: Birth weight, CaC: Cannon circumference, CC: Chest circumference, CCI: Chest circumference index, CD: Chest depth, CG: Chest girth, CG2: Chest girth at 2 months, CG6: Chest girth at 6 months, CG12: Chest girth at 12 months, CW: Chest width, EL: Ear length, HG: Heart girth, HL: Head length, HW: Hip width, OBL: Oblique body length, SH: Sacral height, TC: Trunk circumference, TI: Trunk index, TL: Tail length, WG: Weight gain, WH: Withers height, WH2: Withers height at 2 months, WH6: Withers height at 6 months, WH12: Withers height at 12 months, WaH: Waist height, WWT: Weaning weight.

Ns: Non-Significant, SC: Strong association, Sig: Significant

4. Discussion

Growth traits, including body weight, average daily gain, body length, and chest girth, are critical measurable parameters that directly impact goat production efficiency and profitability. These growth traits not only determine the market value of animals but also influence the reproductive performance, adaptability, and long-term sustainability of goat farming systems [3–33]. In developing countries, particularly in Asia and Africa, where goats play a central role in the livelihoods of smallholder farmers, growth performance is closely linked to household food security, income generation, and cultural practices. Therefore, improving these traits using modern genetic tools and breeding approaches is of high practical relevance. Among the numerous genes implicated in growth regulation, *IGF1* has received significant scientific attention. The *IGF1* gene is prominent because of its fundamental role in regulating cell proliferation, differentiation, and metabolism, all of which are essential for skeletal and muscular development [33, 34, 35]. *IGF1* is a key component of the growth hormone (GH), IGF axis, acting as a mediator of GH signaling. After GH binds to its receptor, *IGF1* is synthesized mainly in the liver and transported via the bloodstream to various target tissues. In muscles, it stimulates hypertrophy and protein synthesis, whereas in bones, it promotes chondrocyte proliferation and differentiation, leading to longitudinal bone growth. At the cellular level, *IGF1* activates intracellular signaling pathways, such as PI3K-AKT and MAPK, which govern processes essential for both prenatal and postnatal growth [37, 38]. Owing to these wide-ranging functions, polymorphisms in the *IGF1* gene can have direct and indirect effects on phenotypic traits related to animal productivity.

Understanding the influence of *IGF1* gene polymorphisms on growth traits in goats is particularly important for designing effective breeding and management strategies aimed at improving productivity via marker-assisted selection (MAS) [13]. Traditional breeding strategies that rely solely on phenotypic selection are often slow,

Please cite this article as

Lestari *et al.* Reviews in Agricultural Science, 14(2): 1–15, 2026

https://doi.org/10.7831/ras.12.2_1

labor-intensive, and affected by environmental noise. In contrast, MAS enables breeders to select animals carrying favorable alleles at an early age, thereby shortening generation intervals and accelerating genetic gain [39, 40]. To further this understanding, it is essential to review existing research exploring the genetic association between *IGF1* polymorphisms and economically important growth traits in goats. Consistent with this, Table 1 summarizes 11 studies conducted from 2008 to 2024 across Asia and Africa, highlighting rapid advancements in genetic marker utilization to elucidate associations between single nucleotide polymorphisms (SNPs) and phenotypic traits in goats. These studies span multiple breeds and production environments, underscoring the global interest in leveraging *IGF1* polymorphisms to improve goats. Most of these studies employed PCR-RFLP and sequencing methods, which facilitate the rapid and precise identification of genetic variations. Polymerase chain reaction–restriction fragment length polymorphism (PCR-RFLP) is particularly cost-effective and has been widely adopted in resource-limited research contexts [41, 42]. Direct sequencing, on the other hand, provides detailed information about nucleotide changes, thereby allowing the identification of both known and novel SNPs [43].

The diversity of genotyping techniques including the use of real-time PCR (rt-PCR) and the Tetra-Primer Amplification Refractory Mutation System (T-ARMS-PCR), demonstrates the adaptability of molecular tools across different research contexts, whether involving small or large populations. For instance, RT-PCR provides high sensitivity and allows quantification of allele-specific amplification, whereas T-ARMS-PCR enables rapid screening of SNP genotypes in large numbers of animals at a relatively low cost. The increasing adoption of these techniques reflects a trend toward precision and scalability in goat molecular genetics. A notable finding from this review is that 90.9% of the studies successfully identified SNPs, with four studies consistently reporting a SNP at position g.5752 [25, 29, 30, 32]. This consistency suggests that this SNP may hold strong potential as a candidate marker for growth traits in goats, thereby serving as the basis for MAS, which can accelerate genetic improvement compared with traditional phenotypic selection. Identification of consistent genetic markers, such as SNP g.5752, also has the potential to reduce production costs through accelerated genetic improvement, increased feed efficiency, and reduced failure rates in selection that commonly occur in traditional breeding systems. The repeated detection of g.5752 across diverse breeds further indicates its stability and possible universal applicability as a marker for MAS. However, the magnitude of its phenotypic effect and its interaction with other loci remain areas that require further study.

Furthermore, the distribution of genotypic frequencies (ranging from 0.00 to 0.91) and allelic frequencies (ranging from 0.044 to 0.955) formed by SNPs in the *IGF1* gene reflects genetic variation among populations, as shown in Tables 2 and 3. This wide range suggests that differences in genotype and allele distribution may be influenced by factors such as breed, sample size, and breeding history. The distribution pattern indicates that homozygous genotypes dominate at extreme frequencies, both high and low frequencies. For instance, Ali and Mahdi [26] reported that the GG genotype had a frequency of 0.91, whereas the AA genotype was absent (0.00), consistent with the findings of Naicy *et al.* [22], Liu *et al.* [24], and Sharma *et al.* [31]. In contrast, heterozygous genotypes tend to appear at intermediate frequencies. This pattern may indicate the influence of selection pressure, either natural or artificial, which maintains major alleles in the homozygous state at high frequencies owing to their adaptive or productive advantages. Conversely, the presence of homozygotes at low frequencies may represent rare minor alleles persisting in the population as a result of weak selection or mutation–selection balance [44]. Moreover, the prevalence of heterozygotes at intermediate frequencies could reflect the heterozygote advantage or balancing selection that promotes genetic diversity within the population [45]. Such genetic diversity is crucial for long-term population resilience and adaptability, as it ensures that goats can

Please cite this article as

Lestari *et al.* Reviews in Agricultural Science, 14(2): 1–15, 2026
https://doi.org/10.7831/ras.12.2_1

respond to environmental changes and emerging diseases. Importantly, minor alleles with low frequencies remain relevant, as they may exert significant effects on specific traits despite their limited occurrence. In contrast, major alleles found at high frequencies, such as the G allele reported by Naicy *et al.* [22] and Ali and Mahdi [26], the m allele described by Liu *et al.* [24] and C and T alleles reported by Sharma *et al.* [31], illustrate the outcomes of long-term natural or artificial selection. These insights are valuable for designing breeding programs in which major alleles are maintained for trait stability, while beneficial minor alleles can be increased through targeted selection. From an applied perspective, integrating this genetic knowledge is especially valuable for community-based breeding programs (CBBPs) in local goat populations, thereby supporting sustainable goat production systems tailored to smallholder farming. The CBBPs often implemented in regions with limited infrastructure [46], can benefit from simple genotyping tools to identify animals carrying favorable alleles, thereby improving herd productivity and conserving genetic diversity.

As shown in Table 4, the compiled results indicate that out of 208 observations on growth traits across various goat breeds, only 27.9% showed a significant association between the *IGF1* gene and growth traits, whereas the remaining 72.1% did not. Among these significant associations, 31 % pertained to body weight, with the remainder related to other measurements. Notably, significant associations between the *IGF1* gene and body weight (BW) have been reported in several goat breeds, including Attappady Black [22, 23], Malabari [22], Kejobong [25], Local Black goat [26], Etawah Grade [27], Assam hill goats [29] and Sirohi [31] all of which demonstrated a strong association with the *IGF1*. In addition to BW, body length (BL) was significantly associated with *IGF1* in studies by Chalbi *et al.* [28] and Shareef *et al.* [30], while body height (BH) showed significant associations in Attappady Black [22] and Liaoning Cashmere goats [24]. These findings suggest that although *IGF1* has been extensively studied as a candidate marker, its influence on growth traits in goats appears inconsistent and may vary depending on the breed, population structure, environmental conditions, or specific SNPs analyzed. The relatively low proportion of significant associations implies that, despite *IGF1* 's important biological role in regulating growth through cell proliferation, differentiation, and metabolism, the phenotypic expression of growth traits in goats is likely governed by a complex interplay of multiple genes (polygenic inheritance) as well as non-genetic factors such as nutrition and management practices [47, 48].

This underscores the need for comprehensive studies employing genome-wide approaches and considering gene environment interactions to elucidate the genetic basis of growth performance in goats. Approaches such as genome-wide association studies (GWAS), transcriptomic profiling, and integrative bioinformatics can identify novel loci beyond *IGF1* that contribute to growth. Furthermore, studies involving larger and more diverse populations are required to improve the statistical power and reliability of the association results [49]. The variability in association results across breeds highlights the importance of validating candidate gene markers, such as *IGF1*, in diverse goat populations before their application in breeding programs [50]. In addition to improving productivity, research on *IGF1* in various local goat populations is also important for maintaining genetic diversity. Marker-assisted breeding can be directed not only toward enhancing performance but also toward preserving unique traits that contribute to local adaptability. This aligns with global agendas such as the Sustainable Development Goals (SDGs), particularly the targets related to food security (SDG 2) and poverty alleviation (SDG 1), since marker-assisted goat breeding can enhance the productivity of smallholder farmers in developing countries [51, 52]. Such validation is critical to ensure the effectiveness and genetic relevance of marker-assisted selection strategies tailored to the specific genetic backgrounds of the target goat populations. Breeds differ in their genetic architecture owing to their long histories of adaptation, natural selection, and

Please cite this article as

Lestari *et al.* Reviews in Agricultural Science, 14(2): 1–15, 2026
https://doi.org/10.7831/ras.12.2_1

human-driven breeding practices. Therefore, a marker that is strongly associated with growth traits in one breed may not have similar effects in another.

5. Conclusion

The *IGF1* gene represents a promising candidate marker for growth traits in goats, with several SNPs, particularly the g.5752 locus, consistently identified across multiple breeds. While most reported associations lacked statistical significance, significant associations were observed between *IGF1* polymorphisms and body weight, body length, and body height. These findings suggest that goat growth is influenced by both genetic and environmental factors, indicating that *IGF1* can serve as a complementary marker but cannot replace polygenic approaches in goat breeding programs. To optimize the practical application of *IGF1* in marker-assisted selection, further validation studies across diverse breeds and integration with genome-wide association studies are essential. Such approaches will prospectively enhance the accuracy and effectiveness of breeding strategies aimed at sustainable goat production.

CRedit authorship contribution statement

Asep Setiaji: Conceptualization, writing – review & editing. **Dela Ayu Lestari, Sutopo, Dwi Wijayanti, Achiriah Febriana:** Methodology & writing original draft. **Dela Ayu Lestari, Fatmawati Mustofa:** Formal analysis & data curation. **Mamat Hamidi Kamalludin, Asep Gunawan:** Supervision.

Acknowledgements

The authors gratefully acknowledge the financial support from Universitas Diponegoro, Indonesia, through Grant No. 222-043/UN.7. D2/PP/IV/2025.

CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

REFERENCES

- [1] Boyazoglu J, Hatziminaoglou I and Morand-Fehr P (2005) The role of the goat in society: Past, present and perspectives for the future. *Small Rumin. Res.*, 60(1-2): 13–23. <https://doi.org/10.1016/j.smallrumres.2005.06.003>
- [2] Skapetas B and Bampidis V (2016) Goat production in the world: present situation and trends. *Livest. Res. Rural. Dev.*, 28(11): 200. <https://www.lrrd.cipav.org.co/lrrd28/11/skap28200.htm>
- [3] Peacock C and Sherman DM (2010) Sustainable goat production—Some global perspectives. *Small Rumin. Res.*, 89 (2-3): 70–80. <https://doi.org/10.1016/j.smallrumres.2009.12.029>
- [4] Nair MRR, Sejian V, Silpa MV, Fonsêca VFC, de Melo Costa CC, Devaraj C, Krishnan G, Bagath M, Nameer PO and Bhatta R (2021) Goat as the ideal climate-resilient animal model in tropical environment: revisiting advantages over other livestock species. *Int. J. Biometeorol.*, 65(12): 2229–2240. <https://doi.org/10.1007/s00484-021-02179-w>
- [5] Dubeuf JP, Genis JC, Morand-Fehr P and Morales FDAR (2023) The contribution of goats in the future redesigning of livestock activities and value chains. *Small Rumin. Res.*, 227: 107065. <https://doi.org/10.1016/j.smallrumres.2023.107065>
- [6] Lu CD (2023) The role of goats in the world: Society, science, and sustainability. *Small Rumin. Res.*, 227: 107056. <https://doi.org/10.1016/j.smallrumres.2023.107056>
- [7] Rout PK and Behera BK (2021) Goat and sheep farming. In *Sustainability in ruminant livestock: Management and marketing* (pp. 33–76). Singapore: Springer Singapore.
- [8] Madikadike MK and Tyasi TL (2024) Growth traits as predictors of body weight in sheep: A review. *World Vet J.*, 14(2): 284–292. <https://doi.org/10.54203/scil.2024.wvj35>

Please cite this article as

Lestari *et al.* Reviews in Agricultural Science, 14(2): 1–15, 2026

https://doi.org/10.7831/ras.12.2_1

- [9] Zewdie B and Welday K (2015) Reproductive performance and breeding strategies for genetic improvement of goat in Ethiopia: a review. *Greener J Agric Sci.*, 5 (1): 23–33. <http://doi.org/10.15580/GJAS.2015.1.080614317>
- [10] Carolino N, Vicente A and Carolino I (2017) Genetic improvement of local goats. In: Simões J, Gutiérrez C (eds). *Sustainable goat production in adverse environments: Volume I*. Springer, Cham. https://doi.org/10.1007/978-3-319-71855-2_8
- [11] Fortes MR, Li Y, Collis E, Zhang Y and Hawken RJ (2013) The *IGF 1* pathway genes and their association with age of puberty in cattle. *Anim. Genet.*, 44 (1): 91–95. <https://doi.org/10.1111/j.1365-2052.2012.02367.x>
- [12] Biscarini F, Nicolazzi EL, Stella A, Boettcher PJ and Gandini G (2015) Challenges and opportunities in genetic improvement of local livestock breeds. *Frontiers in genetics*, 6: 33. <https://doi.org/10.3389/fgene.2015.00033>
- [13] Kumar S, Dahiya SP, Magotra A, Ratwan P and Bangar Y (2023) Influence of single nucleotide polymorphism in the *IGF-1* gene on performance and conformation traits in Munjal sheep. *Zygote.*, 31 (1): 70–77. <https://doi.org/10.1017/S0967199422000545>
- [14] Flores-Encinas LA, Rodríguez-Almeida FA, Felix-Portillo M, Jahuey-Martínez FJ and Martínez-Quintana JA (2022) A variant associated to *IGF-1* mRNA and protein expression in sheep. *Anim. Biotechnol.*, 33 (6): 1086–1094. <https://doi.org/10.1080/10495398.2020.1869561>
- [15] Cannata D, Vijayakumar A, Fierz Y and LeRoith D (2010) The GH/IGF-1 axis in growth and development: new insights derived from animal models. *Adv. Pediatr.*, 57(1): 331–351. <https://doi.org/10.1016/j.yapd.2010.09.003>
- [16] Wang L, Li L, Wang B and Zhang H (2011) Postnatal development of *IGF-I* and *IGF-II* genes in goat skeletal. *J. Anim. Vet. Adv.*, 10(20): 2745–2750. <https://doi.org/10.3923/javaa.2011.2745.2750>
- [17] Valencia CPL, Franco LÁÁ and Herrera DH (2022) Association of single nucleotide polymorphisms in the CAPN, CAST, LEP, GH, and *IGF-1* genes with growth parameters and ultrasound characteristics of the Longissimus dorsi muscle in Colombian hair sheep. *Trop. Anim. Health. Prod.*, 54 (1): 82. <https://doi.org/10.1007/s11250-022-03086-x>
- [18] El-Magd MA, Saleh AA, Nafeaa AA, El-Komy SM and Afifi MA (2017) Polymorphisms of the *IGF-1* gene and their association with growth traits, serum concentration and expression rate of IGF1 and IGF1R in buffalo. *J. Zhejiang. Univ. Sci. B.*, 18 (12): 1064–1074. <https://doi.org/10.1631/jzus.B1600573>
- [19] Martinez R, Rocha JF, Bejarano D, Gomez Y, Abuabara Y and Gallego J (2016) Identification of SNPs in growth-related genes in Colombian creole cattle. *Genet. Mol. Res.*, 15 (3): 1–16. <http://dx.doi.org/10.4238/gmr.15038762>
- [20] Gerasimov NP, Dzhulamanov KM, Lebedev SV and Kolpakov VI (2023) Effect of *IGF-1* C472T, GH C2141G, and GHR T914A polymorphisms on growth performance and feed efficiency in young Kazakh white-headed cattle. *Vet. World.*, 16 (8): 1584–1592. <https://doi.org/10.14202/vetworld.2023.1584-1592>
- [21] Ede T and Parsons TD (2023) Cognitive tasks as measures of pig welfare: a systematic review. *Front. Vet. Sci.* 10:1251070. <https://doi.org/10.3389/fvets.2023.1251070>
- [22] Naicy T, Venkatachalapathy RT, Aravindakshan TV and Kurian E (2017) Association of a Cac8I polymorphism in the *IGF-1* gene with growth traits in Indian goats. *J. Genet. Eng. Biotechnol.*, 15 (1): 7–11. <https://doi.org/10.1016/j.jgeb.2017.04.002>
- [23] Alex P, Kanakkaparambil R, Gopalakrishnan R, Ramasamy C and Thazhathuveetil A (2023) The effect of insulin-like growth factor 1 receptor gene single nucleotide polymorphism on growth and milk production traits in two native Indian tropical goat breeds. *Anim. Biotechnol.*, 34(9): 4828–4836. <https://doi.org/10.1080/10495398.2023.2197468>
- [24] Liu Y, Kong L, Li S, Nie L, Gao J, Li S, Pan Y, Liu Q and Wang Z (2024) Correlation and regression analysis of GH and *IGF-1* genes in Liaoning cashmere goats with body size and other production performance. *J. Genet. Eng. Biotechnol.*, 22(4): 100440. <https://doi.org/10.1016/j.jgeb.2024.100440>
- [25] Lestari DA, Oikawa T, Sutopo S, Purbowati E, Setiaji A and Kurnianto E (2020) Effect of insulin-like growth factor 1 gene on growth traits of Kejobong goat and its growth analysis. *Vet. World*, 13(1): 127–133. <https://doi.org/10.14202/vetworld.2020.127-133>
- [26] Ali RN and Mahdi ZM (2022) Relationship of polymorphism of untranslated region (5'-UTR) of the insulin-like growth factor (*IGF-1*) gene with milk production and growth traits in local black goats. *Int. J. Health. Sci.*, 6 (S3): 12366–12375. <https://doi.org/10.53730/ijhs.v6nS3.9481>
- [27] Surya AYT, Ihsan M and Dagong A (2021) The relation of *IGF-1* genotype with weight in Etawah Grade goats at Polewali Mandar Regency. In *KOBICINC-20 Proceedings*. Atlantis Press. <https://doi.org/10.2991/absr.k.210621.069>
- [28] Chalbi S, Dettori ML, Djemali M, Vacca GM, Petretto E, Pazzola M and Bedhiaf-Romdhani S (2023) Haplotype structure of MSTN, *IGF-1*, and BMP2 genes in Tunisian goats (*Capra hircus*) and their association with morphometric traits. *Trop. Anim. Health Prod.*, 55: 2. <https://doi.org/10.1007/s11250-022-03403-4>

Please cite this article as

Lestari *et al.* Reviews in Agricultural Science, 14(2): 1–15, 2026

https://doi.org/10.7831/ras.12.2_1

- [29] Sarmah RG, Laskar S, Nahardeka N, Borah P, Das B and Borkalita L (2019) Polymorphism of insulin-like growth factor -1 gene and their association with weight at different age in Assam hill goats. J. Entomol. Zool. Stud., 7 (6): 759–762.
- [30] Shareef M, Basheer A, Zahoor I and Anjum AA (2018) Polymorphisms in growth hormone (GH) and insulin-like growth factor-1 (*IGF-1*) gene and their association with growth traits in Beetal goat. Pak. J. Agri. Sci., 55 (3): 713–720.
<https://doi.org/10.21162/PAKJAS/18.7166>
- [31] Sharma A, Dutt G, Sivalingam J, Singh MK, Pathodiya OP, Khadda BS and Dixit SP (2013) Novel SNPs in *IGF1*, *GHR* and *IGFBP-3* genes reveal significant association with growth traits in Indian goat breeds, Small Rumin. Res., 115: 7–14.
<https://doi.org/10.1016/j.smallrumres.2013.08.001>
- [32] Zhang C, Zhang W, Luo H, Yue W, Gao M and Jia Z (2008) A new single nucleotide polymorphism in the *IGF-1* gene and its association with growth traits in the Nanjiang Huang goat, Anim. Biosci., 21(8): 1073–1079.
<https://doi.org/10.5713/ajas.2008.70673>
- [33] Sejian V, Silpa MV, Chauhan SS, Bagath M, Devaraj C, Krishnan G, Nair MR *et al.* (2021) Eco-intensified breeding strategies for improving climate resilience in goats. In Ecological Intensification of Natural Resources for Sustainable Agriculture. Springer: Berlin/Heidelberg, Germany, pp. 627–655
- [34] Schiaffino S and Mammucari C (2011) Regulation of skeletal muscle growth by the *IGF-1*-Akt/PKB pathway: insights from genetic models. Skelet Muscle, 1(1): 4. <https://doi.org/10.1186/2044-5040-1-4>
- [35] Yoshida T and Delafontaine P (2020) Mechanisms of *IGF-1*-mediated regulation of skeletal muscle hypertrophy and Atrophy. Cells, 9(9): 1970. <https://doi.org/10.3390/cells9091970>.
- [36] Guan X, Yan Q, Wang D, Du G and Zhou J (2022) IGF-1 signaling regulates mitochondrial remodeling during myogenic differentiation. Nutrients, 14(6): 1249. <https://doi.org/10.3390/nu14061249>.
- [37] Arjunan A, Sah DK, Woo M and Song J (2023) Identification of the molecular mechanism of insulin-like growth factor-1 (*IGF-1*): a promising therapeutic target for neurodegenerative diseases associated with metabolic syndrome. Cell & Bioscience, 13(1), 16. <https://doi.org/10.1186/s13578-023-00966-z>
- [38] Cheng Y, Li W, Gui R, Wang C, Song J, Wang Z, Wang X *et al.* (2021) Dual characters of GH-IGF1 signaling pathways in radiotherapy and post-radio therapy repair of cancers. Front. Cell Dev. Biol., 9: 671247.
<https://doi.org/10.3389/fcell.2021.671247>
- [39] Wakchaure R, Ganguly S, Praveen PK, Kumar A, Sharma S and Mahajan T (2015) Marker assisted selection (MAS) in animal breeding: a review. J. Drug. Metab. Toxicol., 6(5) e127. <https://doi.org/10.4172/2157-7609.1000e127>
- [40] Visscher PM, Van der Beek S and Haley CS (2021) Marker assisted selection. In Animal breeding (pp. 119–136). Routledge.
- [41] Evans J, Swart M, Soko N, Wonkam A, Huzair F and Dandara C (2015) A global health diagnostic for personalized medicine in resource-constrained world settings: a simple PCR-RFLP method for genotyping CYP2B6 g. 15582C> T and science and policy relevance for optimal use of antiretroviral drug efavirenz. OMICS: A Journal of Integrative Biology, 19(6): 332–338.
<https://doi.org/10.1089/omi.2015.0039>
- [42] Yalley AK, Ahiatrogah S, Kafintu-Kwashie AA, Amegatcher G, Prah D, Botwe AK, Adusei-Poku MA, Obodai E and Nii-Trebi NI (2022) A Systematic Review on Suitability of Molecular Techniques for Diagnosis and Research into Infectious Diseases of Concern in Resource-Limited Settings. Curr. Issues Mol. Biol. 44(10): 4367–4385. <https://doi.org/10.3390/cimb44100300>
- [43] Etter PD, Bassham S, Hohenlohe PA, Johnson EA and Cresko WA (2011) SNP discovery and genotyping for evolutionary genetics using RAD sequencing. Methods in molecular biology (Clifton, N.J.), 772: 157–178.
https://doi.org/10.1007/978-1-61779-228-1_9
- [44] Desai MM and Fisher DS (2007) Beneficial mutation selection balance and the effect of linkage on positive selection. Genetics, 176(3): 1759–1798. <https://doi.org/10.1534/genetics.106.067678>
- [45] Charlesworth B (2013) Encyclopedia of Biodiversity (second edition) Chapter: Population Genetics.
<https://doi.org/10.1016/B978-0-12-384719-5.00116-7>
- [46] Haile A, Getachew T, Rekik M, Abebe A, Abate Z, Jimma A, Mwacharo JM *et al.* (2023) How to succeed in implementing community-based breeding programs: Lessons from the field in Eastern and Southern Africa. Front. Genet., 14: 1119024.
<https://doi.org/10.3389/fgene.2023.1119024>
- [47] Triantaphyllopoulos KA, Ikononopoulos I and Bannister AJ (2016) Epigenetics and inheritance of phenotype variation in livestock. Epigenetics Chromatin, 9: 31. <https://doi.org/10.1186/s13072-016-0081-5>

Please cite this article as

Lestari *et al.* Reviews in Agricultural Science, 14(2): 1–15, 2026
https://doi.org/10.7831/ras.12.2_1

- [48] Huang J (2024) Quantitative genetics in livestock breeding: principles and applications, *Animal Molecular Breeding*, 14(4): 252–261. <https://doi.org/10.5376/amb.2024.14.0026>
- [49] Lashmar SF, Visser C, van Marle-Köster E (2016) SNP-based genetic diversity of South African commercial dairy and fiber goat breeds. *Small Rumin. Res.*, 136: 65–71. <https://doi.org/10.1016/j.smallrumres.2016.01.006>
- [50] Brito LF, Kijas JW, Ventura RV, Sargolzaei M, Porto-Neto LR, Cánovas A, Feng Z *et al.* (2017) Genetic diversity and signatures of selection in various goat breeds revealed by genome-wide SNP markers. *BMC genomics*, 18(1): 229. <https://doi.org/10.1186/s12864-017-3610-0>
- [51] Jembere T, Rischkowsky B, Dessie T, Kebede K, Okeyo AM, Mirkena T and Haile A (2019) Genetic and economic evaluation of alternative breeding scenarios for community based productivity improvements of three indigenous goat breeds in Ethiopia. *Small Rumin Res.*, 178: 46–54. <https://doi.org/10.1016/j.smallrumres.2019.07.017>
- [52] Ncube KT, Nephawe KA, Mpofu TJ, Monareng NJ, Mofokeng MM and Mtileni B (2025) Genomic advancements in assessing growth performance, meat quality, and carcass characteristics of goats in Sub-Saharan Africa: A systematic review. *Int. J. Mol. Sci.*, 26(5): 2323. <https://doi.org/10.3390/ijms26052323>