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Association between PROP1 gene polymorphism (g.748G>A) and growth traits in Assam hill goats

RAKESH KUMAR[1], DIPAK BHUYAN[2], MAHAK SINGH[3], MEENA DAS[4], RAHUL KATIYAR[4], P C CHANDRAN[1]✉, R K KAMAL[5], RAJNI KUMARI[1], SHANKAR DAYAL[1], RAGINI KUMARI[6]✉, AMITAVA DEY[1], P K RAY[1], JYOTI KUMAR[1], S K AHIRWAL[1], KAMAL SARMA[1] and ANUP DAS[1]

ICAR-Research Complex for Eastern Region (RCER), Patna 800 014 Bihar India

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ABSTRACT

PROP1 (Prophet of Pit-1) gene is a key transcription factor involved in pituitary development and regulation of growth-related hormones in livestock. This study investigated polymorphisms in the PROP1 gene and their association with growth traits in Assam Hill goats. Genomic DNA was extracted from blood samples collected from 147 unrelated Assam Hill goats. Primers targeting intron 1 and exon 1 of the PROP1 gene were designed using Primer3Plus, and genotyping was performed by PCR–RFLP. Population genetic parameters were estimated using PopGene version 1.32. A missense SNP, g.748G>A, was identified and genotyped using the restriction enzyme DrdI, which revealed three genotypes (GG, GA, and AA). The frequencies of alleles A and G were 0.53 and 0.47, respectively. The locus exhibited moderate polymorphism (PIC = 0.37) and moderate genetic diversity, with an effective number of alleles of 1.99 and an expected heterozygosity of 0.50. Association analysis revealed that animals carrying AA genotype tended to exhibit superior growth performance, with significantly greater body length and wither height at 6 months of age than those carrying the GG and GA genotypes ($P < 0.05$). These findings suggest that the PROP1 g.748G>A polymorphism might serve as a potential molecular marker for marker-assisted selection aimed at improving growth traits in Assam Hill goats. However, further validation in larger, independent, and genetically diverse goat populations is required before its practical application in breeding programmes.

Keywords: Assam Hill goat, Growth traits, PCR-RFLP, Polymorphism, PROP1 gene

Goat farming remains a cornerstone of smallholder and marginal livestock production systems worldwide (Meza-Herrera *et al.* 2024). Its importance has grown even more pronounced in the context of sustainable agriculture, particularly in developing countries (Devendra 2024; Modi *et al.* 2024). Despite the rapid transformations in global agriculture brought about by technological advancements, corporate consolidation, and globalization, the goat population has continued to increase (Nair *et al.* 2021; Bojovic and McGregor 2023). According to the 20th Livestock Census (2019), the goat population stood at 148.88 million, registering a 10.14% increase from 2012 and accounting for about 27.8% of the total livestock population. Their economic contribution is significant, accounting for approximately 3.36% of the country's total milk production and 15.5% of its meat production (BAHS 2019). Among India's diverse indigenous goat breeds, the Assam Hill Goat is well known for its prolificacy, early sexual maturity, and superior meat quality in hill and mountain agroecosystems and is considered an important genetic resource of the north-eastern region of India (Sarma *et al.* 2025).

In the context of breeding programs, traits related to growth, reproduction, and body conformation are key indicators of productivity and profitability. For instance, a study by Getachew *et al.* (2022) on community-based breeding programs in Ethiopia demonstrated that selecting for body weight and lactation milk yield over six months resulted in increased genetic gains and profitability. Furthermore, a systematic review by Ncube *et al.* (2025) emphasized the role of genomic advancements in assessing growth performance and carcass characteristics, facilitating more precise selection in breeding programs. In goats, Marker-Assisted Selection (MAS) has emerged as a powerful tool for genetic improvement, particularly because goats have smaller litter sizes compared to polytocous species, such as pigs (Hua *et al.* 2009; Chen *et al.*

Present address: [1]ICAR-Research Complex for Eastern Region (RCER), Patna-800 014, Bihar.[2]Assam Agricultural University, Goat Research Station, Byrnihat-793 101, Assam.[3]ICAR-Research Complex for North Eastern Hilly (NEH) Region, Nagaland Centre 797 106, Nagaland. [4]ICAR- Research Complex for North Eastern Hilly (NEH) Region, Umiam-793 103, Meghalaya.[5]ICAR-RCER, Farming System Research Centre for Hill and Plateau Region (FSRCHPR) Plandu, Ranchi-834 010, Jharkhand.[6]Animal and Fisheries Resources Department, Govt. of Bihar. ✉Corresponding author email: vetchandran@gmail.com; raginindri@gmail.com

Table 1. Primer pairs, amplicon sizes, and target regions of the PROP1 gene in goats.

Gene	Primer sequence (5′-3′)	Amplified region	Amplicon length (bp)	Annealing temperature Ta (°C)
PROP1	F: 5'-CCATGGACACAGAAGGGAGA-3' R: 5'-TCCCTCCAGCTCTCTTCCTC-3'	Intron 1 and exon 1	408	59.6

2025). One of the essential candidate genes in this regard is the PROP1 gene (Prophet of Pit-1), which plays a crucial regulatory role in the development of the anterior pituitary gland and the expression of growth and reproductive hormones such as growth hormone (GH), prolactin (PRL), thyroid-stimulating hormone (TSH), and others. Mutations or polymorphisms in the PROP1 gene are associated with growth hormone deficiencies and directly influence growth rates, reproductive performance, and developmental traits in various livestock species (Liu *et al.* 2015; Ma *et al.* 2017; Ekegbu *et al.* 2019). Therefore, PROP1 has been considered a promising candidate gene for marker-assisted selection in livestock breeding programmes.

Studies on small ruminants suggest that the PROP1 gene may be a key genetic factor influencing traits important to breeders such as body and weaning weights, daily growth rate, and litter size (Ekegbu *et al.* 2019). Due to its role in regulating hormonal pathways, PROP1 is a functional candidate gene for improving performance through molecular breeding approaches. In indigenous goat breeds, such as the Assam Hill goat, which is renowned for its robust growth and reproductive performance under low-input systems, investigating PROP1 gene polymorphisms can support the development of genomic selection strategies tailored to Indian agro-climatic conditions. Integrating PROP1 gene markers into selection indices could facilitate the early identification of genetically superior animals and improve selection accuracy in breeding herds. These programs can accelerate genetic gain and contribute to the long-term sustainability and productivity of goat populations, especially in marginal and climate-vulnerable regions. However, information regarding PROP1 gene polymorphism and its association with growth traits in Assam Hill goats is limited. Therefore, the present study was undertaken to identify polymorphism in the PROP1 gene and evaluate its association with growth traits in Assam Hill goats.

MATERIALS AND METHODS

Location and sampling of animals: Blood samples were collected from true-to-type, unrelated Assam Hill goats maintained in their native breeding tracts of Assam Hill goats in Meghalaya and Assam. During morphometric measurements, special care was taken to ensure that animals were positioned vertically on a flat surface. Morphometric traits were recorded according to the FAO (2012) guidelines for phenotypic characterization of animal genetic resources. The recorded traits included body weight (BW), body length (BL), wither height (WH), and chest girth (CG) at 3, 6, 9, and 12 months of age**.**

DNA isolation: Approximately 3–4 mL of blood was collected aseptically in EDTA-coated tubes and transported to the laboratory under chilled conditions. Genomic DNA was extracted using the Qiagen DNeasy Blood and Tissue Kit, and DNA concentration was adjusted to 50 ng/µL. DNA purity was assessed using a UV-visible spectrophotometer (Biophotometer Plus, Eppendorf), and integrity was checked by 1.3% agarose gel electrophoresis. The absorbance ratio (A260/A280) ranged from 1.8 to 2.0, indicating DNA of suitable quality for PCR amplification.

Primer design and PCR amplification: The complete sequence of the PROP1 gene in Capra hircus was retrieved from the NCBI database (GenBank accession number NC_030814.1). Primer3Plus software was used to design the primers, which were synthesized by Eurofins Genomics (India). The PROP1 gene region encompassing intron 1 and exon 1 was amplified using a single primer pair (Table 1). PCR amplification was carried out in a 25 µL reaction volume containing 50 ng genomic DNA, 0.5 µM of each primer, 12.5 µL DreamTaq Green PCR Master Mix (2×), and nuclease-free water. The PCR conditions consisted of an initial denaturation at 94°C for 3 min, followed by 34 cycles of denaturation at 94°C, annealing at 59.6°C for 35 s, and extension at 72°C for 1 min, with a final extension at 72°C for 7 min. Amplified products were resolved on 2% agarose gel prepared in 1× TAE buffer (Fig. 1). Representative PCR products were subjected to commercial Sanger sequencing to confirm the identified polymorphism, and sequence chromatograms were analysed using Chromas software.

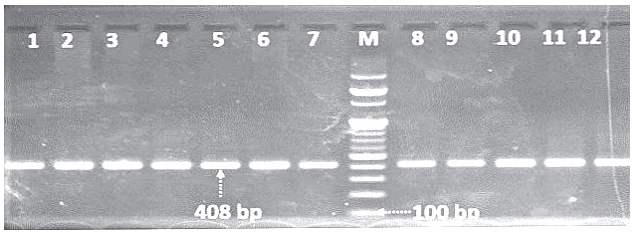


Fig. 1. Agarose gel electrophoresis of the PCR-amplified PROP1 gene fragment. M, 100 bp DNA ladder; lanes 1–12, representative PCR products.

Restriction digestion and SNP genotyping: Restriction enzyme analysis was performed using NEB cutter v2.0 to identify suitable enzymes for SNP genotyping. The g.748G>A polymorphism was genotyped in all animals by the PCR-RFLP assay. Following PCR amplification, the products were digested with 2 U of DrdI restriction enzyme at 37°C for 16 h. The digested fragments were separated on 2.8% agarose gel stained with ethidium bromide and visualized under a gel documentation system (Fig. 2).

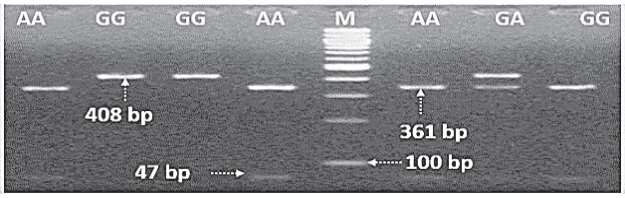


Fig. 2. PCR–RFLP patterns of the PROP1 gene following DrdI digestion. Homozygous GG genotype (408 bp), homozygous AA genotype (361 and 47 bp), and heterozygous GA genotype (408, 361 and 47 bp), M: 100 bp DNA ladder.

Statistical and bioinformatic analyses: PopGene version 1.32 (Yeh *et al.* 1999) was used to estimate genotype and allele frequencies, number of alleles, effective number of alleles, Shannon's information index, Nei's gene diversity, observed and expected heterozygosity, fixation index (FIS), polymorphism information content (PIC), and to assess deviation from Hardy–Weinberg equilibrium using chi-square (χ^2) test. To investigate the structural effects of the missense mutation, secondary structures of the wild-type and mutant PROP1 proteins were predicted using the SOPMA server. Three-dimensional protein models were generated and evaluated using SWISS-MODEL server.

Association between PROP1 genotypes and growth traits was analyzed using General Linear Model (GLM) procedure of SPSS software version 18.0 (IBM Corp., Armonk, NY, USA). A single model incorporating both genetic and non-genetic factors simultaneously was fitted as follows:

$$Y_{ijk} = \mu + G_i + B_j + P_k + e_{ijk}$$

where Y_{ijk} is the observation on a growth trait, μ is the overall mean, G_i is the fixed effect of genotype, B_j is the effect of birth type, P_k is the fixed effect of dam parity, and e_{ijk} is the random residual error. Least-square means were compared using Tukey's multiple comparison test, and means bearing different superscripts within a row differed significantly ($P < 0.05$).

RESULTS AND DISCUSSION

Identification of the PROP1 polymorphism and allele frequencies: Genotyping of the g.748G>A locus of the PROP1 gene using the DrdI restriction enzyme revealed three genotypes (GG, GA, and AA) in the Assam Hill goat population. Among these, the AA genotype exhibited highest frequency, with allele A (0.53) slightly more prevalent than allele G (0.47), indicating the predominance of the A allele in the studied population.

Genetic diversity parameters and Hardy–Weinberg equilibrium (HWE): At the g.748G>A locus, allele frequencies of 0.53 and 0.47 were observed for alleles A and G, respectively (Table 2). The locus deviated significantly from Hardy–Weinberg equilibrium ($\chi^2 = 53.68$; $P < 0.05$), which might reflect of the effects of selection, genetic drift, non-random mating, or population structure. The locus exhibited moderate polymorphism with a PIC value of 0.37. The effective number of alleles, Shannon's information index, and expected heterozygosity were 1.99, 0.69, and 0.50, respectively, indicating moderate genetic diversity in the studied population and suggesting the potential usefulness of this locus for genetic improvement programmes.

Protein structure prediction: A missense mutation at the g-748 G>A locus of the PROP1 gene resulted in an amino acid substitution from glycine to arginine. Secondary structure prediction using SOPMA revealed that the wild-type PROP1 protein comprised of 24.59% α-helices, 13.11% extended strands, and 62.30% random coils. The mutant protein exhibited a similar distribution of secondary structural elements. Furthermore, the three-dimensional structure model developed using SWISS-MODEL and evaluated by QMEAN indicated no obvious alterations in the predicted overall protein conformation between the wild-type and mutant proteins (Fig. 3a and 3b).

Association of PROP1 genotypes with growth traits: The association of the g.748G>A polymorphism in the PROP1 gene with growth traits was evaluated in Assam Hill goats possessing GG, GA, and AA genotypes (Table 3). Animals carrying the AA genotype generally exhibited superior growth performance compared with those carrying GG and GA genotypes. At 3, 6, 9, and 12 month of age, body weight differed numerically among genotypes; however, differences were not statistically significant ($P<0.05$). Among body measurements, a significant effect ($P < 0.05$) of genotype was observed on body length at 6 months of age, with AA animals exhibiting significantly greater body length (47.63±0.18 cm) than GG (45.52±0.38 cm) and GA (45.81±0.24 cm) animals. Likewise, wither

Table 2. Genotype and allele frequencies and genetic diversity parameters of the PROP1 gene in Assam hill goats

Gene	Genotype frequency		Allele frequency		n_a	Ne	I	Nei	Obs_ Hom	Obs_ Het	Exp_ Hom	Exp_ Het	Ave_ Het	Fis	PIC	χ^2 (HWE)
SNP1	AA	AG	A	G	2.0	1.99	0.69	0.50	0.80	0.20	0.50	0.50	0.50	0.60	0.37	53.68
	GG		0.53	0.47												
	0.43															
	0.20	0.37														

(*na*, number of alleles; *Ne*, effective number of alleles; *I*, Shannon's information index; *Nei*, Nei's gene diversity (expected heterozygosity); *Obs_Hom*, observed homozygosity; *Obs_Het*, observed heterozygosity; *Exp_Hom*, expected homozygosity; *Exp_Het*, expected heterozygosity; *Ave_Het*, average heterozygosity; *Fis*, fixation index; *PIC*, polymorphism information content; and *χ^2 (HWE)*, chi-square value for the Hardy-Weinberg equilibrium test.)

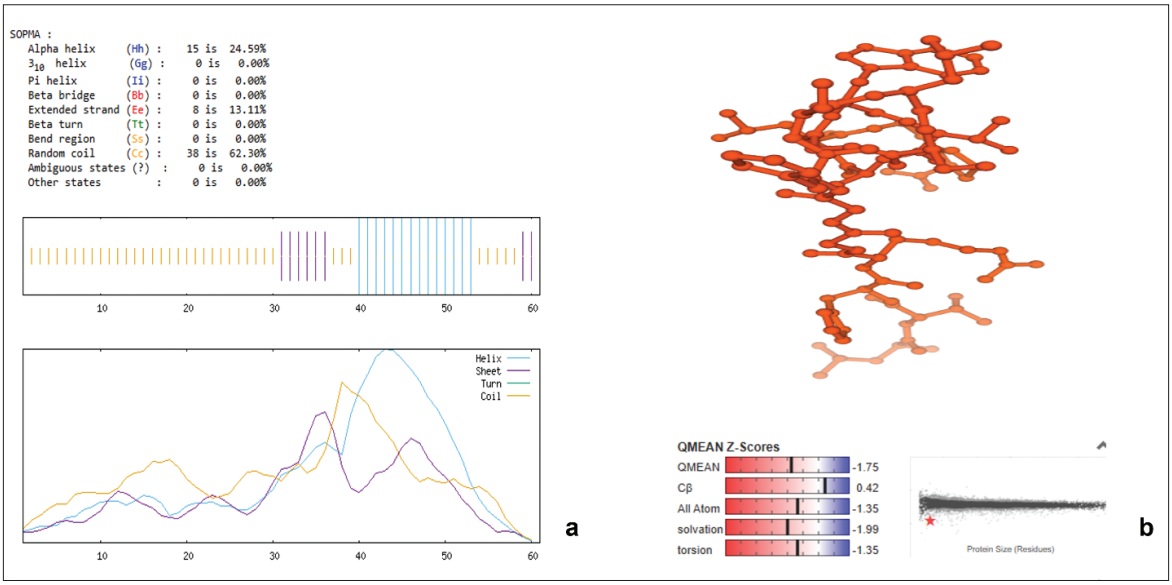


Fig. 3. Predicted secondary structure (a) and three-dimensional structure (b) of the caprine PROP1 protein carrying the g.748G>A SNP. The three-dimensional model is shown with its corresponding QMEAN score

Table 3. Association of the g.748G>A polymorphism in the PROP1 gene with growth traits in Assam hill goats (LSMean ± SE)

Traits	Genotypes at the g.748G>A			
	GG	GA	AA	P-value
		Body weight (kg)		
3-month BW	5.24 ± 0.18	5.87 ± 0.42	6.08 ± 0.39	0.958
6-month BW	9.08 ± 0.31	8.74 ± 0.28	9.70 ± 0.22	0.760
9-month BW	11.12 ± 0.52	11.84 ± 0.60	11.24 ± 0.68	0.176
12-month BW	13.31 ± 0.36	13.61 ± 0.31	14.02 ± 0.20	0.089
		Body length (cm)		
3-month BL	30.48 ± 0.68	30.48 ± 0.58	31.48 ± 0.42	0.612
6-month BL	45.52 ± 0.38^{a}	45.81 ± 0.24^{a}	47.63 ± 0.18^{b}	0.046
9-month BL	54.70 ± 0.35	54.14 ± 0.40	55.08 ± 0.17	0.615
12-month BL	60.23 ± 0.22	60.81 ± 0.28	61.12 ± 0.39	0.354
		Wither height (cm)		
3-month WH	26.23 ± 0.55	26.86 ± 0.62	26.95 ± 0.31	0.456
6-month WH	37.28 ± 0.37^{a}	38.06 ± 0.15^{a}	40.14 ± 0.22^{b}	0.041
9-month WH	44.01 ± 0.18	45.36 ± 0.63	46.74 ± 0.22	0.358
12-month WH	50.16 ± 0.31	51.38 ± 0.66	52.51 ± 0.71	0.777
		Chest girth (cm)		
3-month CG	29.26 ± 0.54	28.47 ± 0.78	29.76 ± 0.69	0.787
6-month CG	44.13 ± 0.41	43.82 ± 0.48	44.20 ± 0.57	0.575
9-month CG	51.74 ± 0.46	50.38 ± 0.67	50.69 ± 0.49	0.893
12-month CG	55.24 ± 0.47	54.12 ± 0.69	55.78 ± 0.53	0.662

LSMean, least-square mean; SE, standard error. Means within a row bearing different superscripts differ significantly according to Tukey's multiple comparison test ($P < 0.05$).

height at 6 months differed significantly ($P < 0.05$) among genotypes, with AA animals showing significant higher values (40.14±0.22 cm) than GG (37.28±0.37 cm), and GA (38.06±0.15 cm) animals. No significant differences were observed for chest girth and other growth traits among the genotypes. Overall, the findings indicated that the AA genotype at the g.748G>A locus is associated with improved growth performance, particularly with respect to body length and wither height at 6 months of age, suggesting that it could serve as a potential molecular

marker after further validation.

Elucidating the genetic architecture underlying growth traits in goats is a major objective of caprine breeding programs aimed at improving productive performance and economic efficiency (Shi *et al.* 2025). Body weight, body length, wither height, and chest girth are important indicators of growth and productivity and are closely associated with meat production, reproductive efficiency, and overall fitness (Akounda *et al.* 2023, Tanvi *et al.* 2024, Mathapo *et al.* 2025). Marker-assisted selection based on functional candidate genes provides an effective strategy for accelerating genetic improvement in livestock populations. Among the candidate genes, PROP1 (prophet of PIT1) plays a crucial role in pituitary development and endocrine regulation by controlling the differentiation of growth hormone-producing cells and thereby influencing postnatal growth (de Moraes *et al.* 2012). Previous studies have reported associations between PROP1 polymorphisms and growth and reproductive traits in goats and other livestock species (Lan *et al.* 2013; Zhou *et al.* 2016; Ekegbu *et al.* 2019; Wajid *et al.* 2022).

In the present study, the g.748G>A polymorphism of the PROP1 gene was identified and its association with growth traits was evaluated in Assam Hill goats. The present findings demonstrated that animals carrying the AA genotype tended to exhibit superior growth performance than those with the GG and GA genotypes. Significant differences ($P < 0.05$) were observed for body length and wither height at 6 months of age, with AA animals, showing higher values than the other genotypes. Although body weight and some body measurements tended to be numerically higher in AA animals the difference were not statistically significant, except for body length and wither hight at 6 months. These findings were consistent with earlier reports demonstrating the influence of PROP1 polymorphisms on growth and productive traits in livestock (Ekegbu *et al.* 2019, Lan *et al.* 2009, Jafari *et al.* 2014). Similar observations were reported by Kumar *et al.* (2026), who identified significant associations between the PROP1 gene polymorphism (g.1860C>T) and growth traits in Assam Hill goats, suggesting that genetic variations within PROP1 may contribute to growth performance in this breed. The genetic diversity parameters obtained in the present study indicated moderate polymorphism at the investigated locus, with a PIC value of 0.37. The expected heterozygosity and Shannon's information index further indicated the presence of considerable genetic variability within the Assam Hill goat population. Such diversity is important for maintaining favourable alleles and sustaining long-term genetic improvement while minimizing the risk of inbreeding depression (Botstein *et al.* 1980, Tosser-Klopp *et al.* 2016, Zhang *et al.* 2025).

A missense mutation resulting in a glycine-to-arginine substitution at the g.748G>A locus of the PROP1 gene may influence the functional activity of the encoded protein. However, secondary and tertiary structure predictions using SOPMA and SWISS-MODEL indicated no apparent alterations in the overall protein conformation between the wild-type and mutant proteins. Nevertheless, subtle amino acid substitutions may affect DNA-binding affinity and transcriptional activity, thereby influencing growth-related pathways (Liu *et al.* 2019). Similar observations have been reported in sheep and goats, where PROP1 polymorphisms have been associated with variation in growth and production traits (Ekegbu *et al.* 2019, Zhou *et al.* 2016, Wajid *et al.* 2022).

In conclusion, a missense SNP (g.748G>A) was identified in the PROP1 gene of Assam Hill goats, exhibiting moderate polymorphism and genetic diversity. Animals carrying the AA genotype showed superior growth performance, with significant effects observed for body length and wither height at 6 months of age. These findings suggest that the PROP1 g.748G>A polymorphism may serve as a potential molecular marker for improving growth traits in Assam Hill goats. However, further validation in larger, independent, and genetically diverse goat populations is required before its application in marker-assisted breeding programmes.

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REFERENCES

Akounda B, Ouedraogo D, Soudre A, Burger P A, Rosen B D, Van Tassell C P and Solkner J. 2023. Morphometric characterization of local goat breeds in two agroecological zones of Burkina Faso, West Africa. *Animals* **13**: 1931.

BAHS. 2019. Basic Animal Husbandry Statistics. Department of Animal Husbandry and Dairying, Ministry of Fisheries, Animal Husbandry and Dairying, Government of India, New Delhi.

Bojovic M and McGregor A. 2023. A review of megatrends in the global dairy sector: what are the socioecological implications? *Agriculture and Human Values* **40**: 373–394. https://doi.org/10.1007/s10460-022-10338-x

Botstein D, White R L, Skolnick M and Davis R W. 1980. Construction of a genetic linkage map in man using restriction fragment length polymorphisms. *American Journal of Human Genetics* **32**: 314–331.

Chen W, Han Y, Chen Y, Liu X, Liang H, Wang C and Khan M Z. 2025. Potential candidate genes associated with litter size in goats: A review. *Animals* **15**: 82. https://doi.org/10.3390/ani15010082

de Moraes D C, Vaisman M, Conceição F L and Ortiga-Carvalho T M. 2012. Pituitary development: a complex, temporally regulated process dependent on specific transcriptional factors. *Journal of Endocrinology* **215**(2): 239–45. doi:10.1530/JOE-12-0229

Devendra C. 2024. Transforming small ruminant systems in Asia: Pathways to sustainability and productivity. *Asian-*

Australasian Journal of Animal Sciences **37**(2): 151–163.

Ekegbu U J, Burrows L, Amirpour-Najafabadi H, Zhou H and Hickford J G H. 2019. Gene polymorphisms in PROP1 associated with growth traits in sheep. *Gene* **683**: 41–46.

FAO. 2012. Phenotypic characterization of animal genetic resources. FAO Animal Production and Health Guidelines No. 11. Rome.

Getachew T, Rischkowsky B, Rekik M, Mueller J, Tessema T, Solomon D and Haile A. 2022. Optimizing breeding structures and related management in community-based goat breeding programs in the Borana pastoral system of Ethiopia. *Livestock Science* **256**: 104819.

Hua G H, Chen S L, Yu J N, Cai K L, Wu C J, Li Q L, Zhang C Y, Liang A X, Han L, Geng L Y, Shen Z, Xu D Q and Yang L G. 2009. Polymorphism of the growth hormone gene and its association with growth traits in Boer goat bucks. *Meat Science* **81**: 391–395.

Jafari Z, Miraei Ashtiani S R and Sadeghi M. 2014. A PCRRFLP investigation on *PROP1* gene polymorphism and its association with milk production and growth traits in Mahabadi goats. *Journal of Livestock Science and Technology* **2**(1): 43–48.

Kumar R, Das M, Chandran P C, Kumari R, Dayal S, Kamal R K and Das A. 2026. Association of PROP1 Gene Polymorphism (g.1860C>T) with growth traits in Assam Hill Goats. *Indian Journal of Animal Research* 1–9. https://doi.org/10.18805/IJAR.B-5665.

Lan X Y, Pan C Y, Zhang L Z, Zhao M, Zhang C L, Lei C Z and Chen H. 2009. A novel missense (A79V) mutation of goat *PROP1* gene and its association with production traits. *Molecular Biology Reports* **36**(8): 2069–2073.

Lan X Y, Penagaricano F, DeJung L, Weigel K A and Khatib H. 2013. Short communication: A missense mutation in the *PROP1* gene affects male fertility and milk production traits in the US Holstein population. *Journal of Dairy Science* **96**(2): 1255–1257.

Liu Q, Geng C, Chu M, Chen H, Jin M, Zhang Y, Di R, Feng T and Li N. 2015. Polymorphism of Prophet of Pit-1 gene and its relationship with litter size of Small Tail Han sheep. *Journal of Genetics* **94**: e27–e30.

Liu Y, Liu J, Chen T, Zhang J and Wang D. 2019. Structural insights into transcription factor–DNA interactions: Implications for disease-associated mutations. *Journal of Molecular Biology* **431**(10): 1998–2012. https://doi.org/10.1016/j.jmb.2019.02.010

Ma L, Qin Q, Yang Q, Zhang M, Zhao H, Pan C, Lei C, Chen H and Lan X. 2017. Associations of six SNPs of POU1F1-PROP1-PITX1-SIX3 pathway genes with growth traits in two Chinese indigenous goat breeds. *Annals of Animal Science* **17**(2): 399–411.

Mathapo M C, Tyasi T L and Thinawanga J. 2025. Prediction of body weight from linear body measurement traits of Nguni goats in the Limpopo province. *Journal of Applied Animal Research* **53**(1): 2462581.

Meza-Herrera C A, Navarrete-Molina C, Macias-Cruz U, Arellano-Rodriguez G, De Santiago-Miramontes A, Sarinana-Navarrete M A, Marin-Tinoco R I and Perez-Marin C C. 2024. Dairy goat production systems: A Comprehensive analysis to reframe their global diversity. *Animals* **14**(24): 3717.

Modi R J, Patel N M, Patel Y G, Islam M M and Nayak J B. 2024. Goat farming: A boon for economic upliftment. *Trends in Clinical Diseases, Production and Management of Goats* **1**: 51–62.

Nair M R R, Sejian V, Silpa M V, Fonseca V F C, de Melo Costa C C, Devaraj C, Krishnan G, Bagath M, Nameer P O and Bhatta R. 2021. Goat as the ideal climate-resilient animal model in tropical environment: Revisiting advantages over other livestock species. *International Journal of Biometeorology* **65**: 2179. https://doi.org/10.1007/s00484-021-02179-w.

Ncube K T, Nephawe K A, Mpofu T J, Monareng N J, Mofokeng M M and Mtileni B. 2025. Genomic advancements in assessing growth performance, meat quality, and carcass characteristics of goats in Sub-Saharan Africa: A systematic review. *International Journal of Molecular Sciences* **26**: 2323. https://doi.org/10.3390/ijms26052323

Sarma O, Das B, Phookan A and Gogoi A. 2025. Animal genetic resources and biodiversity in the north-eastern state of Assam, India: An overview. *Uttar Pradesh Journal of Zoology* **46**(5): 140–152.

Shi Y, Liu Y, Qi Y, Rong Y, Ao X, Zhang M, Xia Q, Zhang Y and Wang R. 2025. Estimation of genetic parameters of growth traits in the Inner Mongolia White Cashmere goat (Erlangshan type). *Animals* **15**(11): 1652.

Tanvi T Z, Ferdous M, Bahar F and Ferdous Z. 2024. Morphometric attributes and structural indices of Jamunapari goat available in Chattagram District, Bangladesh. *Indian Journal of Veterinary Public Health* **10**(1): 87–94.

Tosser-Klopp G, Bardou P, Bouchez O, Cabau C, Crooijmans R, Dong Y, Donnadieu-Tonon C, Eggen A, Heuven H, Jamli S. 2016. Design and characterization of a 52K SNP chip for goats. *PLOS ONE* **11**(1): e0151053.

Wajid C, Baloch A H, Khosa A N, Kaleri H A, Bangulzai N, Fazlani S A, Sadia H, Kalsoom S, Arain M B and Vistro W A. 2022. *PROP1* gene: a selective marker of wool production in sheep breeds of Balochistan, Pakistan. *Journal of Animal Health and Production* **10**(2): 238–244.

Yeh F C, Yang R C and Boyle T. 1999. POPGENE Version 1.32: Microsoft Windows-based freeware for population genetic analysis. University of Alberta, Edmonton, Canada.

Zhang X, Yang F, Zhang J, Zhu T, Zhao X, Liu Y, Wen J, Gu H, Wang G, Ren X, Chen A and Qu L. 2025. Genomic variation responding to artificial selection on different lines of Pekin duck. *Poultry Science* **104**(2): 104785

Zhou F, Yang Q, Lei C, Chen H and Lan X. 2016. Relationship between genetic variants of POU1F1, PROP1, IGFBP3 genes and milk performance in Guanzhong dairy goats. *Small Ruminant Research* **140**: 40–45.