P-ISSN: 2304-3075; E-ISSN: 2305-4360
International Journal of Veterinary Science
www.ijvets.com; editor@ijvets.com

Research Article https://doi.org/10.47278/journal.ijvs/2026.025

Genome Wide Association Study of Growth Traits in Saburai Goats

Akhmad Dakhlan [1,*], Purnama Edy Santosa [1], Dian Kurniawati [1] and Kusuma Adhianto [1]

[1]Department of Animal Husbandry, Faculty of Agriculture, Universitas Lampung Jl. Prof. Sumantri Brojonegoro no.1 Bandar Lampung 35145, Lampung, Indonesia
***Corresponding author:** akhmad.dakhlan@fp.unila.ac.id

Article History: 25-298 Received: 30-Oct-25 Revised: 27-Jan-26 Accepted: 30-Jan-26 Online First: 19-Feb-26

ABSTRACT

This study aims to identify specific genomic regions and potential genes that play a role in the growth traits of Saburai goats. Phenotypic trait including birth, weaning, and yearling weight of 100 male and female Saburai goat were used and analyzed in a mixed model using the animal model method using WOMBAT software to obtain the estimated breeding value for goat body weight. Residual data from mixed model analysis for each individual were used for association studies. Individual goats used in this study were genotyped using the Illumina Goat SNP52 BeadChip (Illumina Inc., San Diego, CA, USA). Regression of body weight residuals on SNP was carried out individually using a linear model. The result showed that there were 7, 5, and 24 significant SNPs associated with birth weight, weaning weight, and yearling weight, respectively. The single-nucleotide polymorphism (SNP) of snp14750-scaffold1594-1124587 located on chromosome 19 was the most significant SNP associated with all three traits. Furthermore, the study identified 24 candidate genes, including HDAC5, PCDH15, C15H11orf8, ARID1B, BEND4, CEP85L, and DDX43, which may contribute to body weight variation of Saburai goats. The study's findings provide valuable information for improving growth performance and can be applied to genomic selection in Saburai goats.

Key words: Body weight, Gene candidates, Genome-wide association study, Single-nucleotide polymorphism, Saburai goat.

INTRODUCTION

The Saburai goat, a local breed from Lampung, Indonesia, was officially recognized by the Indonesian Minister of Agriculture in 2015. It originated from a cross between Ettawa Grade (EG) does and Boer bucks, resulting in a genetic composition of approximately 25% EG and 75% Boer (Dakhlan et al. 2021a; Dakhlan et al. 2021b). Developed primarily for meat production, the Saburai goat has adapted well to Indonesia's tropical environment (Adhianto et al. 2022; Dakhlan et al. 2025). However, considerable variation in growth performance remains among individuals, indicating potential for further genetic improvement. Enhancing genetic quality through the selection of superior animals is therefore a promising strategy to increase productivity (Bisrat et al. 2025; Van Eenennaam 2025).

Body weight (BW) is a key selection criterion in meat-producing goats because it is directly associated with carcass yield, an economically important trait (Zhang et al. 2021; Tesema et al. 2023; Stanišić et al. 2025). Genetic variation among individuals leads to differences in body weight, which can be explored through genome-wide analyses. The increasing availability of genomic data, facilitated by commercial genotyping platforms such as Illumina, enables the implementation of genome-wide association studies (GWAS) to identify genomic regions and genes influencing complex traits like body weight (Abdalla et al. 2022; Wang et al. 2024; Wen et al. 2025). GWAS has become a powerful tool for dissecting the genetic architecture of quantitative traits, thereby supporting more accurate and rapid genetic improvement through genomic selection.

Advancements in single-nucleotide polymorphism (SNP) genotyping technologies have further strengthened the utility of GWAS in identifying genetic variants and candidate genes associated with economically important traits across animal species (Martin et al. 2016). Numerous studies have successfully applied GWAS in livestock, identifying quantitative trait loci (QTL) related to growth and performance traits in cattle (Igoshin et al. 2019; Yin and König 2019), horses (Nazari-Ghadikolaei et al. 2025; Šimon et al. 2025), pigs (Tang et al. 2019; Wang et al. 2022a; Zhao et al. 2022) and sheep (Dakhlan et al. 2017; Kominakis et al. 2017).

Cite This Article as: Dakhlan A, Santosa PE, Kurniawati D and Adhianto K, 2026. Genome wide association study of growth traits in saburai goats. International Journal of Veterinary Science 15(3): 815-823. https://doi.org/10.47278/journal.ijvs/2026.025

Despite the broad application of GWAS in livestock, studies focusing on body weight in goats remain limited. In sheep, the first GWAS on body weight was conducted by Jonas et al. (2009), who identified a gene on ovine chromosome 21 (OAR21) in an Awassi-Merino backcross population. Similarly, Al-Mamun et al. (2015) found 39 SNPs linked to body weight in Merino sheep and identified a significant QTL region on chromosome 6 (OAR6).

In goats, however, GWAS studies have primarily targeted traits other than growth. For instance, Nazari-Ghadikolaei et al. (2018) explored genes linked to coat color in Markhoz goats, while Mucha et al. (2018) investigated genes associated with milk production in a composite population of Saanen, Toggenburg and Alpine goats. Additionally, Simo et al. (2024) investigated prolificacy in Cameroon native goats (CNG), while Rahmatalla et al. (2018) and Luigi-Sierra et al. (2020) reported genes influencing body size and teat morphology in Sudanese and Murciano-Granadina goats, respectively. Recently, Moaeen-ud-Din et al. (2025) identified several potential SNP markers, such as those associated with BTAF1, NTM, GRID1, CEP78, ROBO1, ZFP36L2, SPTLC3, CTR9 and ZFHX3, for use in genomic selection targeting higher body weight in Pakistani Beetal goats.

Although research on goat body weight remains scarce, this trait continues to be of major interest due to its economic significance. Dakhlan et al. (2025) identified 2 SNPs associated with shoulder height, 7 with body length, and 14 with chest girth in Saburai goats, highlighting 14 genes potentially linked to body conformation traits. Similarly, Zhang et al. (2021) reported 21 SNPs related to body weight in Inner Mongolia Cashmere goats, while Selionova et al. (2022a) identified one SNP related to live body weight at birth and 33 SNPs at four months of age in Karachai goats. Notably, genes such as MSTN, HEG1, FGF10, FGF14, GHRH and SLAIN were found to have significant associations with early growth performance.

Given the limited genomic studies on body weight in goats, particularly local breeds such as the Saburai goat, further research is essential. Therefore, the present study aimed to identify genes associated with the body weight of Saburai goats at different growth stages, namely birth, 3 months, and 12 months of age, using GWAS. The findings are expected to contribute to the genetic improvement and breeding strategies of Saburai goats and support the application of genomic selection to enhance their productivity.

MATERIALS AND METHODS

Ethical approval

The study received ethical approval from the Faculty of Agriculture, University of Lampung and all experimental procedures were carried out in compliance with applicable animal welfare guidelines.

Phenotypes for association studies

The data for body weight was collected from 100 Saburai goats, comprising of 50 male goats and 50 female goats aged 1-1.5 years, which were the progeny of nine bucks and eleven dams. Birth weight, weaning weight (3 months of age), and yearling weight were obtained from their recorded data. The Saburai goats used in this study were obtained from the Saburai goat breeding center located in the Tanggamus district, Lampung province, Indonesia. The pedigree of each goat was traced back at least two generations.

Weaning weight was adjusted to 90 days of age (WW90) and calculated as follows.

$$\text{WW90} = \left(\frac{\text{Actual weight} - \text{Birth weight}}{\text{Weaning age in days}}\right) * 90 + \text{Birth weight}$$

Yearling weight was adjusted to 365 days of age (YW365) and calculated as follows.

$$\text{YW365} = \left(\frac{\text{Yearling weight} - \text{Weaning weight}}{\text{Yearling age} - \text{Weaning age in days}}\right) * 275 + \text{WW90}$$

We employed a mixed model, specifically the animal model method, using WOMBAT software (Meyer 2007; Meyer 2018) to obtain accurate body weight predictions (birth weight, weaning weight, and yearling weight) and residual data for each individual goat. The fixed effects in the animal model included year of birth (categorized into rainy and dry seasons), sex (male and female), birth type (single, twin, and triplet), and rearing location (Gisting and Sumberejo Districts), with dam age as a covariate variable. The random effects were the individual goat and the dam. Residual data from the mixed model analysis were then used for association studies. The mixed model is formulated as follows:

$$y = Xb + Z_1a + Z_2m + e$$

Where the vector of observations is represented by y, with b denoting the vector of fixed effects, a representing the vector of additive genetic effects, m the vector of maternal genetic effects, and e the vector of residual effects. X is the incidence matrix associated with the fixed effects, while Z_1 and Z_2 are incidence matrices linking the observations to the random effects of the animal (additive genetic) and the dam (maternal genetic), respectively.

Genotyping and association studies

Blood samples of 5mL from individual goat were collected and stored in ice box, and in the laboratory these samples were stored at -80ºC. DNA extraction was performed using the standard phenol-chloroform protocol (Sambrook and Russell 2006). Individual goats used in this study were genotyped using the Illumina Goat SNP52 BeadChip consisted of 53,347 SNPs (Illumina Inc., San Diego, CA, USA) and quality control was carried out before conducting an association study. SNPs were filtered out if they had call rates below 95%, minor allele frequencies (MAF) under 0.05, or P-values less than 0.001 for Hardy-Weinberg Equilibrium (HWE). After these quality control measures, 98 goats with 49,874 SNPs were retained for the association analysis. Body weight residual regression against SNP was carried out individually using a linear model in R (R Core Team 2023). SNP annotation used the genome reference of *Capra hircus* (assembly ARS1.2) provided by The National Center for Biotechnology Information (NCBI) (https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_001704415.2/). A 400-kb genomic region surrounding each

peak SNP was considered the candidate interval. Genes located within this interval were treated as candidate genes and subsequently identified and annotated.

Statistical analysis

The threshold value (P<0.05/52K) was determined for the GWAS significance by applying the Bonferroni correction (Kaler and Purcell 2019; Chen et al. 2021). The Manhattan -log10 plot and P-value distribution of the resulting GWAS analysis used the R-package qqman (Turner 2018).

RESULTS AND DISCUSSION

Birth weight

The Manhattan plot in Fig. 1 illustrates the P-values for all SNP markers associated with the birth weight of Saburai goats, providing a visual representation of the genome-wide association study (GWAS). This plot highlights the significant regions where SNPs are associated with birth weight across the genome. Complementing this, Fig. 2 presents the quantile-quantile (QQ) plot, which is a standard method to compare the distribution of observed P-values with those expected under the null hypothesis (Yang et al. 2011). The QQ plot helps to assess whether there is inflation in the test statistics or deviations from the expected distribution, which could indicate potential genetic associations (Purcell et al. 2007).

Table 1 lists the genome-wide significant SNPs identified for three key traits: birth weight, weaning weight, and yearling weight. Focusing on birth weight, seven SNPs reached high significance levels. These SNPs are located on chromosomes 6, 9, 14, 15, 19 and 26, with genomic positions ranging from 14.65 to 80.09Mb. Notably, the SNP labeled snp14750-scaffold1594-1124587, situated at 43.56Mb on chromosome 6, exhibited the strongest association with birth weight, with a P-value of 2.97×10^{-12}. This SNP stands out as a key genetic marker due to its highly significant association with birth weight, suggesting that it may play an important role in influencing this trait.

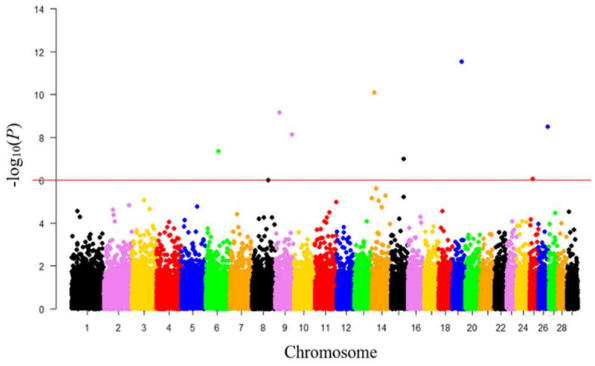

Fig. 1: Manhattan plot of genome-wide association analysis for birth weight of Saburai goat.

Fig. 2: Quantile-quantile plot of genome-wide association analysis for birth weight of Saburai goat.

Table 1: SNPs that have significant association with birth, weaning, and yearling weight

Chromosome	SNP Name	Position (BP)	P-value	Annotated Gene	Traits
6	CSN1S1-E-allele-1-2	85,995,008	9.86E-14	CSN1S1	YW
2	snp10686-scaffold138-297255	29,806,853	2.62E-08	TNS1	YW
14	snp11085-scaffold14-482393	21,520,797	6.51E-19	RIMS2	YW
19	snp14750-scaffold1594-1124587	43,563,475	8.79E-37	HDAC5	BW, WW, YW
7	snp20103-scaffold2-3959682	18,192,007	4.74E-10	LOC102179	YW
26	snp26621-scaffold278-501036	46,053,499	9.81E-16	PCDH15	BW, WW, YW
7	snp29825-scaffold323-3014209	41,699,831	2.27E-10	ITK	YW
15	snp34645-scaffold41-1766666	62,562,006	3.57E-09	C15H11orf8	BW, YW
9	snp36898-scaffold448-22063	80,093,901	2.92E-14	ARID1B	BW, YW
2	snp38148-scaffold477-592558	124,720,482	2.04E-14	ZNF804A	YW
25	snp38329-scaffold485-257787	17,001,938	4.66E-16	C25H16orf62	YW
28	snp39778-scaffold509-1759116	12,402,097	2.00E-08	KCNMA1	YW
6	snp40083-scaffold511-2344051	62,949,329	4.89E-09	KCTD8	YW
6	snp40114-scaffold511-3740135	61,559,529	9.33E-12	BEND4	BW, YW
1	snp414-scaffold1010-28033	137,123,894	2.65E-09	ACPP	YW
3	snp42099-scaffold55-2633854	59,028,955	4.51E-09	ADGRL2	YW
15	snp45777-scaffold628-1195006	39,029,468	1.23E-08	DENND5A	YW
9	snp462-scaffold1011-1266531	19,529,989	2.49E-20	CEP85L	BW, WW, YW
13	snp48676-scaffold691-1659135	60,244,108	2.98E-11	DEFB116	YW
25	snp52310-scaffold7764-82924	42,671,997	1.19E-07	PDGFA	YW
11	snp52855-scaffold793-6368	48,387,776	2.27E-09	POLR1A	YW
14	snp53157-scaffold8-343582	1,836,428	2.17E-19	SNX16	WW, YW
14	snp5331-scaffold1184-194029	14,654,159	8.83E-19	DDX43	BW, WW, YW
4	snp53936-scaffold820-966370	51,588,107	1.01E-07	HIBADH	YW

Note: BW = birth weight, WW = weaning weight, YW = yearling weight.

The distribution of these highly significant SNPs across multiple chromosomes indicates that birth weight in Saburai goats is likely influenced by a variety of genetic regions (Ncube et al. 2025; Rong et al. 2025). Identifying the exact genes or regulatory elements near these SNPs could lead to a better understanding of the genetic architecture of growth traits in Saburai goats. These findings have important implications for selective breeding programs, as they provide valuable genetic markers that can be used to improve birth weight and related growth traits in this goat population (Shangguan et al. 2024).

There were 7 significant SNPs within 7 genes that span the region between 14.65 and 80.09Mb on different chromosome according to ARS1.2. These genes were HDAC5 (histone deacetylase 5 isoform X6), PCDH15 (protocadherin-15 isoform X1), C15H11orf8 (uncharacterized protein C11orf87 homolog isoform X1), ARID1B (AT-rich interactive domain-containing protein 1B isoform X1), BEND4 (BEN domain-containing protein 4), CEP85L (centrosomal protein of 85 kDa-like), and DDX43 (probable ATP-dependent RNA helicase DDX43) which are associated with birth weight in Saburai goat.

In the analysis of SNP associations with birth weight in Saburai goats, seven significant SNPs were identified within seven distinct genes spanning the region between 14.65 and 80.09Mb across different chromosomes based on the ARS1.2 reference genome. These genes, which are associated with birth weight, include HDAC5 (histone deacetylase 5 isoform X6), PCDH15 (protocadherin-15 isoform X1), C15H11orf8 (uncharacterized protein C11orf87 homolog isoform X1), ARID1B (AT-rich interactive domain-containing protein 1B isoform X1), BEND4 (BEN domain-containing protein 4), CEP85L (centrosomal protein of 85 kDa-like), and DDX43 (probable ATP-dependent RNA helicase DDX43).

Each of these genes plays a potential role in biological processes that may influence birth weight. For example, HDAC5 (histone deacetylase 5) gene which is involved in chromatin remodeling and transcriptional regulation by modifying the acetylation status of histones, which can impact gene expression and muscle development (Tian et al. 2020; Klymenko et al. 2020). The association of HDAC5 with birth weight suggests that epigenetic regulation may influence growth traits, potentially through the modulation of genes involved in development and metabolic processes (Li and Chen 2025).

Gene PCDH15 (protocadherin-15) is important for cell adhesion and signaling, particularly in neural and sensory systems (Alagramam et al. 2001). While this gene is primarily studied in the context of sensory functions, its involvement in birth weight suggests that cell communication and tissue development may also play roles in determining early growth. C15H11orf8 (uncharacterized protein C11orf87 homolog isoform X1) is an uncharacterized protein; the function of this gene remains largely unknown. However, the identification of SNPs in this region highlights the potential importance of previously unexplored genes in the regulation of birth weight and growth traits (Moaeen-ud-Din et al. 2022; Rong et al. 2025).

ARID1B, a component of the SWI/SNF chromatin-remodeling complex, has been linked to developmental regulation and body size traits (Moffat et al. 2019; Liu et al. 2022; Li et al. 2025). The specific function of ARID1B in ruminant growth is not detailed, but as an ARID (AT-rich interactive domain) family protein, it is known to be involved in chromatin remodeling and gene transcription, which are essential for development and growth.

The BEND4 (BEN domain-containing protein 4) gene is involved in gene regulation, particularly in DNA binding and chromatin organization (Abhiman et al. 2008). This gene's association with birth weight may reflect its role in regulating growth-related genes during development. CEP85L, essential for cell division and microtubule organization (Kodani et al. 2020; Huang et al. 2022), may influence fetal growth through effects on cell proliferation and mitotic processes. Finally, DDX43 encodes an RNA helicase implicated in RNA metabolism and germline cell regulation (Tutak et al. 2020). Its association with birth weight suggests that post-transcriptional regulation contributes to early growth processes.

The identification of these genes and their associations with birth weight in Saburai goats enhances understanding of the genetic factors influencing growth traits. Similar associations between HDAC5, ARID1B, and growth traits have been reported in other ruminants, supporting their conserved functional roles. These findings can inform genomic selection programs aimed at improving growth performance, emphasizing that both epigenetic mechanisms and fundamental cellular processes contribute to phenotypic variation in birth weight (Shangguan et al. 2024).

Weaning weight

Table 1 shows that there were 5 highly significant SNPs for weaning weight, and they were distributed on region on chromosomes 9, 14, 19, and 26 between 1.84 and 46.05 Mb. Among these SNPs, the most significant was snp14750-scaffold1594-1124587 ($P=4.19\times10^{-15}$), which was located at 43.56Mb. Manhattan plot of P-values for all SNP markers of weaning weight is shown in Fig. 3 and their quantile-quantile plots (QQ plot) for the GWAS result are shown in Fig. 4.

In the genomic study of weaning weight in Saburai goats, five significant SNPs were identified within five genes located between 1.84 and 46.05 Mb across different chromosomes, according to the ARS1.2 reference genome. These genes include HDAC5 (histone deacetylase 5 isoform X6), PCDH15 (protocadherin-15 isoform X1), CEP85L (centrosomal protein of 85 kDa-like), and DDX43 (probable ATP-dependent RNA helicase DDX43). Each of these genes is linked to biological processes that may influence weaning weight, a critical trait for growth performance in livestock.

The HDAC5 (histone deacetylase 5) gene is involved in chromatin remodeling through the deacetylation of histones, impacting gene expression and potentially affecting growth regulation. Given its role in epigenetic control, this gene may influence developmental pathways that determine the growth rate of goats prior to weaning, making it a candidate for genetic selection aimed at improving weaning weight (Kabra et al. 2016; Xu et al. 2023).

Though PCDH15 (protocadherin-15) are typically associated with cell adhesion and signaling in neural tissues, their involvement in growth traits like weaning weight suggests a broader role in tissue development

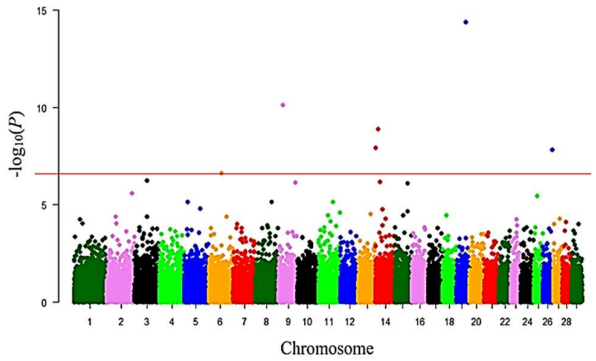

Fig. 3: Manhattan plot of genome-wide association analysis for weaning weight of Saburai goat

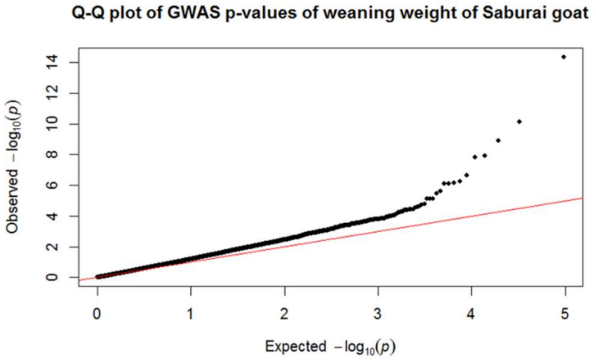

Fig. 4: Quantile-quantile plot of genome-wide association analysis for weaning weight of Saburai goat

and intercellular communication during early growth stages. The significance of PCDH15 in this context may point to the importance of cellular interactions and structural development in determining growth rates (Pancho et al. 2020; Zhen et al. 2022).

CEP85L (centrosomal protein of 85 kDa-like) which is integral to cell division and proliferation. Its association with weaning weight suggests that efficient cell division and growth factor signaling are critical during the pre-weaning period when rapid body growth and development are necessary for survival and future productivity (Kodani et al. 2020; Duan et al. 2025).

The role of DDX43 (probable ATP-dependent RNA helicase DDX43) gene in RNA metabolism, including RNA splicing and translation, is essential for regulating gene expression. Variations in this gene may influence key growth-regulating pathways, potentially affecting protein synthesis and overall growth rates leading up to weaning. This highlights the role of post-transcriptional regulation in determining growth outcomes (Tan et al. 2023).

The identification of these significant SNPs provides valuable insight into the genetic factors influencing weaning weight in Saburai goats. These genes are involved in crucial biological functions such as epigenetic regulation, cell division, and RNA processing, all of which are fundamental to growth and development. Understanding the genetic basis of weaning weight not only enhances our knowledge of the molecular mechanisms driving early growth but also offers practical applications in selective breeding programs (Husien et al. 2024; Visser 2025). By targeting these specific genetic markers, breeders could potentially improve weaning weight and overall growth performance in Saburai goats, leading to increased productivity and better management of genetic resources.

Furthermore, the overlap between some genes associated with both birth weight and weaning weight, such as HDAC5 and DDX43, suggests that these genes may play a consistent role throughout different stages of early development. This consistency across developmental stages emphasizes the importance of these genes in regulating growth processes from birth to weaning, making them key targets for further research and potential genetic selection strategies.

Yearling weight

The Manhattan plot of P-values for all SNP markers of yearling weight is depicted in Fig. 5. Furthermore, the GWAS result's quantile-quantile plots (QQ plot) are shown in Fig. 6. The Table 1 reveals that 24 SNPs were significant for yearling weight, and they were distributed in the regions of chromosomes 1, 2, 4, 6, 7, 9, 11, 13, 14, 15, 19, 25, 26, and 28 between 1.84 and 137.12 Mb. Of the 24 significant SNPs, the most noteworthy SNP was snp14750-scaffold1594-1124587 ($P = 8.79 \times 10^{-37}$), situated at 43.56Mb.

The study identified 24 significant SNPs corresponding to 24 genes located across various chromosomes within the 1.84 to 137.12Mb region, based on the ARS1.2 reference genome, with HDAC5 (histone deacetylase 5 isoform X6) having the most pronounced impact on yearling weight in Saburai goats. This result aligns with previous studies by Easa et al. (2022) and Selionova et al. (2022b), which also found significant SNPs associated with body weight and meat productivity in Karachai goats, notably SNP40083-scaffold511-2344051 on chromosome 6. Other SNPs, such as SNP38426-scaffold486-2412676 and SNP1448-scaffold104-1147808 on chromosomes 5, 6, and 10, were linked to body weight in Karachai goats.

Comparatively, Moaeen-ud-Din et al. (2022) reported different SNPs and genes related to body weight in goats, such as SNP24590-scaffold25-1223464 and the gene LOC108636659 on chromosome 8, indicating that genetic determinants of body weight can vary between goat breeds. Similarly, Selionova et al. (2022a) identified SNPs associated with live body weight in Karachai goats across numerous chromosomes, including 1, 2, 3, 5, 6, and 16, highlighting the genomic diversity influencing growth traits in goats. These findings underscore the variability in the genetic architecture of body weight across different goat populations, emphasizing that each breed may possess unique sets of SNPs contributing to growth traits.

Although there is limited research specifically focusing on the functions of the genes identified in this study, some candidate genes have been reported in earlier studies. For instance, CSN1S1 (casein alpha s1) has been shown to regulate both milk production and body development in mammals (Zhang et al. 2019; Guan et al. 2020), which suggests its potential role in influencing growth traits. TNS1, another gene identified in the study, is known to regulate cell adhesion, migration, and proliferation in mammals (Bruns and Lo 2020; Wang et al. 2022b), processes that are crucial for growth and tissue development.

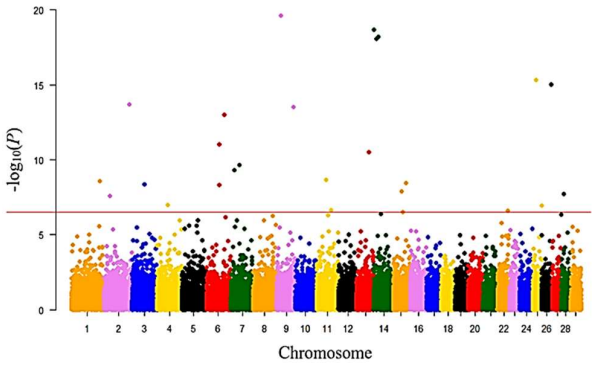

Fig. 5: Manhattan plot of genome-wide association analysis for yearling weight of Saburai goat

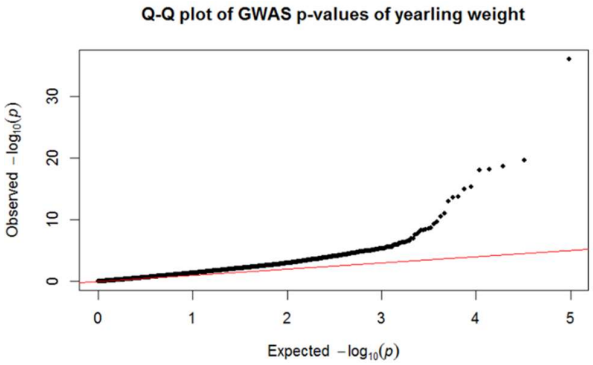

Fig. 6: Quantile-quantile plot of genome-wide association analysis for yearling weight of Saburai goat

The gene's involvement in cell migration and proliferation also suggests a possible role in the regulation of muscle development and growth, which could impact yearling weight in goats.

RIMS2, identified in humans, regulates synaptic membrane exocytosis (Mechaussier et al. 2020), while HDAC5 in mice muscle cells is involved in glucose transporter transcription (Klymenko et al. 2020). Although these genes are primarily studied in other species, their roles in fundamental cellular processes, such as metabolism and cell signaling, suggest that they may play similar roles in influencing growth traits like yearling weight in goats. Additionally, PCDH15 is crucial for hair cell function in the ear (Nie et al. 2016; Kaushik et al. 2025), but its association with growth in goats could indicate its involvement in cell signaling pathways beyond its known sensory functions.

Other notable genes include ITK, which encodes a tyrosine kinase involved in the immune response, and ZNF804A, associated with neurodevelopment and gene regulation, which may have indirect effects on growth through their roles in regulating immune function and brain development (Bernstein et al. 2014). The potassium channel-related gene KCTD8 and the DENND5A gene involved in membrane trafficking in humans (Han et al. 2016) further illustrate the diversity of biological processes potentially contributing to growth traits in goats. These findings suggest that growth traits such as yearling weight are influenced by a complex network of genes with varied functions.

The identification of significant SNPs and associated genes offers valuable insights into the genetic underpinnings of growth in Saburai goats, providing potential markers for future breeding programs aimed at improving growth traits. However, it is important to recognize that these findings represent only part of the broader genetic framework influencing growth. Growth traits are highly polygenic, and the SNPs and genes identified in this study are likely just a subset of the larger genomic architecture. Future research should continue exploring additional loci and gene-gene interactions to provide a more comprehensive understanding of the genetic factors driving growth in goats.

Moreover, while some genes, such as HDAC5 and TNS1, have well-characterized roles in regulating growth-related processes, the functions of many other genes, particularly in the context of goats, remain less understood. As genomic technologies advance and more data become available, further functional studies are needed to unravel the roles of these genes in goat physiology and development. This will be essential for translating genetic findings into practical applications in goat breeding and management, ultimately enhancing growth performance and productivity in goat populations.

Conclusion

This genome-wide association study identified genomic regions and candidate genes influencing growth traits in Saburai goats at birth, weaning and yearling weight. A total of 7, 5, and 24 significant SNPs were associated with birth, weaning, and yearling weight, respectively, highlighting the polygenic nature of growth traits. The SNP snp14750-scaffold1594-1124587 on chromosome 19 (candidate gene of HDAC5) showed consistent and strong associations across all traits, indicating its key role in growth regulation. Additional candidate genes, including PCDH15, ARID1B, CEP85L, and DDX43, were also implicated. These findings provide valuable molecular markers to support genomic selection and genetic improvement programs for Saburai goats.

DECLARATIONS

Funding: This research was funded by the Directorate General of Higher Education of the Ministry of Education, Culture, Research, and Technology of the Republic of Indonesia via the national competitive of basic research scheme with contract number 114/E5/PG.02.00PT/2022; 027/E5/PG.02.00.PL/2023; 057/E5/PG.02.00.PL/2024.

Acknowledgement: We thank the livestock group in Saburai goat breeding center for their help in collecting the data. We also thank the Directorate General of Higher Education of the Ministry of Education, Research and Technology of the Republic of Indonesia for funding this research.

Conflict of Interest: The authors stated that they have no conflicts of interest to declare.

Data Availability: The data that support this study's findings are available in this article. There is no other supporting data.

Ethics Statement: All animal procedures related to data collections of Saburai goats were conducted in accordance with the Institute for Research and Community Service (LPPM), University of Lampung No. 2152/UN26.21/PN/2022.

Author's Contribution: AD: responsible for the research design, initial manuscript preparation, and statistical analysis. PES: oversaw the methodology and provided supervision. DK: handled data collection and conducted the literature review. KA: provided critical revisions of the manuscript. All authors reviewed and approved the final version of the paper.

Generative AI Statement: The authors declare that no Gen AI/DeepSeek was used in the writing/creation of this manuscript.

Publisher's Note: All claims stated in this article are exclusively those of the authors and do not necessarily represent those of their affiliated organizations or those of the publisher, the editors, and the reviewers. Any product that may be evaluated/assessed in this article or claimed by its manufacturer is not guaranteed or endorsed by the publisher/editors.

REFERENCES

Abdalla EAE, Makanjuola BO, Wood BJ and Baes CF, 2022. Genome-wide association study reveals candidate genes relevant to body weight in female turkeys (Meleagris gallopavo). PLoS One 17(3): e0264838. https://doi.org/10.1371/journal.pone.0264838

Abhiman S, Iyer LM and Aravind L, 2008. BEN: a novel domain in chromatin factors and DNA viral proteins. Bioinformatics 24(4): 458-461. https://doi.org/10.1093/bioinformatics/btn007

Adhianto K, Lenanto SI, Dakhlan A and Hamdani MDI, 2022. Genetic and phenotypic correlation of weaning and yearling weight of female Saburai goats in Sumberejo District, Tanggamus Regency, Lampung Province, Indonesia. Advances in Animal and Veterinary Sciences 10(2): 421-426. http://dx.doi.org/10.17582/journal.aavs/2022/10.2.421.426

Alagramam KN, Yuan H, Kuehn MH, Murcia CL, Wayne S, Srisailpathy CRS, Lowry RB, Knaus R, Laer LV, Bernier FP, Schwartz S, Lee C, Morton CC, Mullins RF, Ramesh A, Camp GV, Hagemen GS, Woychik RP and Smith RJH, 2001. Mutations in the novel protocadherin *PCDH15* cause Usher syndrome type 1F. Human Molecular Genetics 10(16): 1709–1718. https://doi.org/10.1093/hmg/10.16.1709

Al-Mamun HA, Kwan P, Clark SA, Ferdosi MH, Tellam R and Gondro C, 2015. Genome-wide association study of body weight in Australian Merino sheep reveals an orthologous region on OAR6 to human and bovine genomic regions affecting height and weight. Genetics Selection Evolution 47(1):1–11. https://doi.org/10.1186/s12711-015-0142-4

Bernstein HG, Steiner J, Dobrowolny H and Bogerts B, 2014. ZNF804A protein is widely expressed in human brain neurons: possible implications on normal brain structure and pathomorphologic changes in schizophrenia. Schizophrenia Bulletin 40(3): 499–500. https://doi.org/10.1093/schbul/sbt237

Bisrat A, Besufkad S, Abebe A, Goshme S, Abebe A, Zewdie T, Areaya A, Tesema Z, Demis C, Yitagesu E, Wondifra Y, Asfaw T, Alemnew E, Gizaw S, Getachew T, Rischkowsky B, Rekik M, Belay B and Haile A, 2025. Genetic evaluation of growth rate and efficiency-related traits in Menz sheep. PLoS One 20(12): e0337718. https://doi.org/10.1371/journal.pone.0337718

Bruns AN and Lo SH, 2020. Tensin regulates pharyngeal pumping in *Caenorhabditis elegans*. Biochemical and Biophysical Research Communication 522(3): 599–603. https://doi.org/10.1016/j.bbrc.2019.11.153

Chen Z, Boehnke M, Wen X and Mukherjee B, 2021. Revisiting the genome-wide significance threshold for common variant GWAS. Genes Genomes Genetics (G3) 11(2): jkaa056. https://doi.org/10.1093/g3journal/jkaa056

Dakhlan A, Santosa PE and Kurniawati D, 2025. Genome-wide association study of body measurements in Saburai goat. International Journal of Veterinary Science 14(5): 876-881. https://doi.org/10.47278/journal.ijvs/2025.030

Dakhlan A, Qisthon A and Hamdani MDI, 2021a. Predicting body weight based on body measurements at different ages and sex in Saburai goat. Advances in Animal and Veterinary Sciences 9(11): 1791–1799. https://doi.org/10.17582/journal.aavs/2021/9.11.1791.1799

Dakhlan A, Hamdani MDI, Putri DR, Sulastri and Qisthon A, 2021b. Short communication: Prediction of body weight based on body measurements in female saburai goat. Biodiversitas. 22(3): 1391–1396. https://doi.org/10.13057/biodiv/d220341

Dakhlan A, Moghaddar N, Gondro C and Van der Werf JHJ, 2017. Gene by birth type interaction in Merino lamb. In: Proceeding of the Association for the Advancement of Animal Breeding and Genetics (AAABG) 22 Vol. 22. Townsville, Australia; p. 45–48. http://www.aaabg.org/aaabghome/AAABG22papers/10Dakhlan22045.pdf

Duan S, Liu X, Liu W, Dou Y, Xu G, Zhang F, Geng K, Xiong Q and Chen M, 2025. Exploration of the mechanism of a novel enhancer on buffalo muscle development. Genomics 117(4): 111071. https://doi.org/10.1016/j.ygeno.2025.111071

Easa AA, Selionova M, Aibazov M, Mamontova T, Sermyagin A, Belous A, Abdelmanova A, Deniskova T and Zinovieva N, 2022. Identification of genomic regions and candidate genes associated with body weight and body conformation traits in Karachai goats. Genes (Basel). 13(10): 1–18. https://doi.org/10.3390/genes13101773

Guan D, Landi V, Luigi-Sierra MG, Delgado JV, Such X, Castelló A, Cabrera B, Mármol-Sánchez E, Fernández-Alvarez J, de la Torre Casañas JLR, Martinez A, Jordana J and Amills M, 2020. Analyzing the genomic and transcriptomic architecture of milk traits in Murciano-Granadina goats. Journal of Animal Science and Biotechnology 11(35). https://doi.org/10.1186/s40104-020-00435-4

Han C, Alkhate R, Froukh T, Minassian AG, Galati M, Liu RH, Fotouhi M, Sommerfeld J, Alfrook AJ, Marshall C, Walker S, Bauer P, Scherer SW, Riess O, Buchert R, Minassian BA and McPherson PS, 2016. Epileptic encephalopathy caused by mutations in the guanine nucleotide exchange factor DENND5A. The American Journal of Human Genetics 99(6): 1359–1367. https://doi.org/10.1016/j.ajhg.2016.10.006

Huang L, Peng Y, Tao X, Ding X, Li R, Jiang Y and Zuo W, 2022. Microtubule organization is essential for maintaining cellular morphology and function. Oxidative Medicine and Cellular Longevity 2022: 1623181. https://doi.org/10.1155/2022/1623181

Husien HM, Saleh AA, Hassanine NNAM, Rashad AMA, Sharaby MA, Mohamed AZ, Abdelhalim H, Hafez EE, Essa MOA, Adam SY, Chen N and Wang M, 2024. The Evolution and role of molecular tools in measuring diversity and genomic selection in livestock populations (traditional and up-to-date insights): a comprehensive exploration. Veterinary Sciences 11(12): 627. https://doi.org/10.3390/vetsci11120627

Igoshin AV, Yudin NS, Belonogova NM and Larkin DM, 2019. Genome-wide association study for body weight in cattle populations from Siberia. Animal Genetics 50(3): 250–253. https://doi.org/10.1111/age.12786

Jonas E, Thomson PC and Raadsma HW, 2009. Genome-wide association study and fine mapping of QTL on OAR 21 for body weight in sheep. In: Proceeding of World Congress on Genetics Applied to Livestock Production. Leipzig, Germany: WCGALP. pp. 0–3. http://wcgalp.org/system/files/proceedings/2010/genome-wide-association-study-and-fine-mapping-qtl-oar-21-body-weight-sheep.pdf

Kabra DG, Pfuhlmann K, García-Cáceres C, Schriever SC, Casquero García V, Kebede AF, Fuente-Martin E, Trivedi C, Heppner K, Uhlenhaut NH, Legutko B, Kabra UD, Gao Y, Yi CX, Quarta C, Clemmensen C, Finan B, Müller TD, Meyer CW, Paez-Pereda M, Stemmer K, Woods SC, Perez-Tilve D, Schneider R, Olson EN, Tschöp MH and Pfluger PT, 2016. Hypothalamic leptin action is mediated by histone deacetylase 5. Natural Communication 7: 10782. https://doi.org/10.1038/ncomms10782

Kaler AS and Purcell LC, 2019. Estimation of a significance threshold for genome-wide association studies. BMC Genomics 20(618): 1-8. https://doi.org/10.1186/s12864-019-5992-7

Kaushik R, Pandey S, Prakash A, Ganatra F, Abe T, Kiyonari H and Ladher RK, 2025. Role of Pcdh15 in the development of intrinsic polarity of inner ear hair cells. PLoS Genetics 21(8): e1011825. https://doi.org/10.1371/journal.pgen.1011825

Klymenko O, Brecklinghaus T, Dille M, Springer C, de Wendt C, Altenhofen D, Binsch C, Knebel B, Scheller J, Hardt C, Herwig R, Chadt A, Pfluger PT, Al-Hasani H and Kabra DG, 2020. Histone deacetylase 5 regulates interleukin 6 secretion and insulin action in skeletal muscle. Molecular Metabolism 42: 101062. https://doi.org/10.1016/j.molmet.2020.101062

Kodani A, Kenny C, Lai A, Gonzalez DM, Stronge E, Sejourne GM, Isacco L, Partlow JN, O'Donnell A, McWalter K, Byrne AB, Barkovich AJ, Yang E, Hill RS, Gawlinski P, Wiszniewski W, Cohen JS, Fatemi SA, Baranano KW, Sahin M, Vossler DG, Yuskaitis CJ and Walsh CA, 2020. Posterior neocortex-specific regulation of neuronal migration by CEP85L identifies maternal centriole-dependent activation of CDK5. Neuron 106(2): 246-255.e6. https://doi.org/10.1016/j.neuron.2020.01.030

Kominakis A, Hager-Theodorides AL, Zoidis E, Saridaki A, Antonakos G and Tsiamis G, 2017. Combined GWAS and 'guilt by association'-based prioritization analysis identifies functional candidate genes for body size in sheep. Genetics Selection Evolution 49(1): 1–16. https://doi.org/10.1186/s12711-017-0316-3

Li JY and Chen MY, 2025. Epigenetic regulation of growth and feather development in ducks. Animal Molecular Breeding 15(2): 60-71 https://doi.org/10.5376amb.2025.15.0007

Liu Z, Zhou T and Gao D, 2022. Genetic and epigenetic regulation of growth, reproduction, disease resistance and stress responses in aquaculture. Frontiers in Genetics 13: 994471. https://doi.org/10.3389/fgene.2022.994471

Luigi-Sierra MG, Landi V, Guan D, Delgado JV, Castelló A, Cabrera B, Mármol-Sánchez E, Alvarez JF, Gómez-Carpio M, Martínez A, Such X, Jordana J and Amills M, 2020. A genome-wide association analysis for body, udder, and leg conformation traits recorded in Murciano-Granadina goats. Journal of Dairy Science 103(12): 11605–11617. https://doi.org/10.3168/jds.2020-18461

Martin PM, Palhière I, Ricard A, Tosser-Klopp G and Rupp R, 2016. Genome Wide Association Study Identifies New Loci Associated with Undesired Coat Color Phenotypes in Saanen Goats. PLoS One 11(3): e0152426. https://doi.org/10.1371/journal.pone.0152426

Mechaussier S, Almoallem B, Zeitz C, Van Schil K, Jeddawi L, Van Dorpe J, Dueñas Rey A, Condroyer C, Pelle O, Polak M, Boddaert N, Bahi-Buisson N, Cavallin M, Bacquet JL, Mouallem_Beziere A, Zambrowski O, Sahel JA, Audo I, Kaplan J, Rozet JM, Baere ED and Perrault I, 2020. Loss of function of RIMS2 causes a syndromic congenital cone-rod synaptic disease with neurodevelopmental and pancreatic involvement. The American Journal of Human Genetics 106(6): 859–871. https://doi.org/10.1016/j.ajhg.2020.04.018

Meyer K, 2007. WOMBAT: a tool for mixed model analyses in quantitative genetics by restricted maximum likelihood (REML). Journal of Zhejiang University Science B 8(11): 815–821. https://doi.org/10.1631/jzus.2007.B0815

Meyer K, 2018. WOMBAT [Internet]. [accessed 2020 Nov 10]. http://didgeridoo.une.edu.au/km/wombat.php

Moaeen-ud-Din M, Khan MS, Muner RD and Reecy JM, 2025. Potential SNPs and candidate genes influencing growth characteristics in Pakistani Beetal goat identified by GWAS analysis. The Journal of Basic and Applied Zoology 86: 18. https://doi.org/10.1186/s41936-025-00437-6

Moaeen-ud-Din M, Danish Muner R and Khan MS, 2022. Genome wide association study identifies novel candidate genes for growth and body conformation traits in goats. Scientific Report 12(1): 1–12. https://doi.org/10.1038/s41598-022-14018-y

Mucha S, Mrode R, Coffey M, Kizilaslan M, Desire S and Conington J, 2018. Genome-wide association study of conformation and milk yield in mixed-breed dairy goats. Journal of Dairy Science 101(3): 2213–2225. https://doi.org/10.3168/jds.2017-12919

Moffat JJ, Jung EM, Ka M, Smith AL, Jeon BT, Santen GWE and Kim WY, 2019. The role of ARID1B, a BAF chromatin remodeling complex subunit, in neural development and behavior. Prog Neuropsychopharmacol Biol Psychiatry 89: 30-38. https://doi.org/10.1016/j.pnpbp.2018.08.021

Nazari-Ghadikolaei A, Mehrabani-Yeganeh H, Miarei-Aashtiani SR, Staiger EA, Rashidi A and Huson HJ, 2018. Genome-wide association studies identify candidate genes for coat color and mohair traits in the Iranian Markhoz Goat. Frontiers in Genetics 9(APR): 1–15. https://doi.org/10.3389/fgene.2018.00105

Nazari-Ghadikolaei A, Fikse WF, Viklund AG, Mikko S and Eriksson S, 2025. Single-Step Genome-wide association study of factors for evaluated and linearly scored traits in Swedish warmblood horses. Journal of Animal Breeding and Genetics 142: 499–512. https://doi.org/10.1111/jbg.12923

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. International Journal of Molecular Sciences 26(5): 2323. https://doi.org/10.3390/ijms26052323

Nie H, Liu Y, Yin X, Cao H, Wang Y, Xiong W, Lin Y and Xu Z, 2016. Plasma membrane targeting of protocadherin 15 is regulated by the golgi-associated chaperone protein PIST. Neural Plasticity 2016: 1–10. https://doi.org/10.1155/2016/8580675

Pancho A, Aerts T, Mitsogiannis MD and Seuntjens E, 2020. Protocadherins at the crossroad of signaling pathways. Frontiers in Molecular Neuroscience 13: 117. https://doi.org/10.3389/fnmol.2020.00117

Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MA, Bender D, Maller J, Sklar P, de Bakker PI, Daly MJ and Sham PC, 2007. PLINK: A tool set for whole-genome association and population-based linkage analyses. American Journal of Human Genetics 81(3): 559-75. https://doi.org/10.1086/519795

R Core Team, 2023. R: A Language and Environment for Statistical Computing, Vienna, Austria [Internet]. https://www.r-project.org/

Rahmatalla SA, Arends D, Reissmann M, Wimmers K, Reyer H

and Brockmann GA, 2018. Genome-wide association study of body morphological traits in Sudanese goats. Animal Genetics 49(5): 478–482. https://doi.org/10.1111/age.12686

Rong Y, Ao X, Guo F, Wang X, Han M, Zhang L, Xia Q, Shang F, Lv Q, Wang Z, Su R, Zhao Y, Zhang Y and Wang R, 2025. Genome-wide association analysis revealed candidate genes related to early growth traits in inner Mongolia Cashmere Goats. Veterinary Sciences 12(3): 192. https://doi.org/10.3390/vetsci12030192

Sambrook J and Russell DW, 2006. Purification of nucleic acids by extraction with phenol:chloroform. Cold Spring Harbor Protocols 2006(1): pdb.prot4455. https://doi.org/10.1101/pdb.prot4455

Selionova M, Aibazov M, Mamontova T, Malorodov V, Sermyagin A, Zinovyeva N and Easa AA, 2022a. Genome-wide association study of live body weight and body conformation traits in young Karachai goats. Small Ruminant Research 216(September): 106836. https://doi.org/10.1016/j.smallrumres.2022.106836

Selionova MI, Aibazov AMM, Sermyagin AA, Belous AA and Zinovieva NA, 2022b. Genome-wide analysis in the search for candidate genes associated with meat productivity traits in meat-and-dairy goats. Theory and Practice of Meat Processing 7(4): 288–295. https://doi.org/10.21323/2414-438X-2022-7-4-288-295

Shangguan A, Xiang C, Deng Z, Zhang N, Yu M, Zhang F, Suo X, Chen M, Chen C, Tao H and Xiong Q, 2024. Genome-wide association study of growth and reproductive traits based on low-coverage whole-genome sequencing in a Chubao black-head goat population. Gene 931: 148891. https://doi.org/10.1016/j.gene.2024.148891

Simo JK, Meutchieye F, Wouobeng P, Tarekegn GM, Mutai C, Nandolo W, Pelle R, Djikeng A and Manjeli Y, 2024. Genome-wide association study for the level of prolificacy in Cameroon's native goat. Journal of Applied Animal Research 52(1): 2291472. https://doi.org/10.1080/09712119.2023.2291472

Šimon M, Bogićević S, Kaić A, Luštrek B and Potočnik K, 2025. Exploring Genetic Influences on Equine Meat Quality: A Bioinformatics Approach. Foods 14(3): 533. https://doi.org/10.3390/foods14030533

Stanišić N, Cekić B, Maksimović N, Petričević M, Delić N, Stajić S and Keškić T, 2025. Carcass traits and meat quality in Balkan goats: A multivariate evaluation of crossbreeding and slaughter weight effects. Czech Journal of Animal Science 70(10): 438-449. https://doi.org/10.17221/53/2025-CJAS

Tan H, Wang W, Zhou C, Wang Y, Zhang S, Yang P and Zheng K, 2023. Single-cell RNA-seq uncovers dynamic processes orchestrated by RNA-binding protein DDX43 in chromatin remodeling during spermiogenesis. Nature Communications 14(1): 2499. https://doi.org/10.1038/s41467-023-38199-w

Tang Z, Xu J, Yin L, Yin D, Zhu M, Yu M, Li X, Zhao S and Liu X, 2019. Genome-wide association study reveals candidate genes for growth relevant traits in pigs. Frontiers in Genetics 10: 302. https://doi.org/10.3389/fgene.2019.00302

Tesema Z, Tilahun M, Yizengaw L and Zegeye A, 2023. Relationship of body mass index with meat production and energy reserves in yearling bucks. Small Ruminant Research 225: 107000. https://doi.org/10.1016/j.smallrumres.2023.107000

Tian H, Liu S, Ren J, Lee JKW, Wang R and Chen P, 2020. Role of histone deacetylases in skeletal muscle physiology and systemic energy homeostasis: implications for metabolic diseases and therapy. Frontiers in Physiology 11: 949. https://doi.org/10.3389/fphys.2020.00949

Turner SD, 2018. qqman: an R package for visualizing GWAS results using Q-Q and manhattan plots. The Journal of Open Source Software 3(25): 731. https://doi.org/10.21105/joss.00731

Tutak K and Rozwadowska N, 2020. Discrete roles of RNA helicases in human male germline and spermatogenesis. Journal of Applied Genetics 61(3): 415-419. https://doi.org/10.1007/s13353-020-00558-4

Van Eenennaam AL, 2025. Current and future uses of genetic improvement technologies in livestock breeding programs. Animal Frontiers 15(1): 80-90. https://doi.org/10.1093/af/vfae042

Visser C, 2025. The impact of genetic selection for increased production on fitness traits of small ruminants. Small Ruminant Research 247: 107491. https://doi.org/10.1016/j.smallrumres.2025.107491

Wang B, Li P, Hou L, Zhou W, Tao W, Liu C, Liu K, Niu P, Zhang Z, Li Q, Su G and Huang R, 2022a. Genome-wide association study and genomic prediction for intramuscular fat content in Suhuai pigs using imputed whole-genome sequencing data. Evolutionary Application (February): 1–13. https://doi.org/10.1111/eva.13496

Wang Z, Ye J, Dong F, Cao L, Wang M and Sun G, 2022b. Emerging Insights into Its Domain Function, Biological Roles, and Tumors. Biology (Basel). 11(11): 157. https://doi.org/10.3390/biology11111571

Wang S, Liu M, Zhang H, He S, Li W and Liang L, 2024. Genome-wide association study of body weight traits in Texel and Kazakh crossbred sheep. Genes 15(12): 1521. https://doi.org/10.3390/genes15121521

Wen J, Zheng M, Wang Z, Hu X and Li Z, 2025. Genome-wide association study and meta-analysis uncovers key candidate genes for body weight traits in chickens. Genes (Basel) 16(8): 945. https://doi.org/10.3390/genes16080945

Xu J, Li C and Kang X, 2023. The epigenetic regulatory effect of histone acetylation and deacetylation on skeletal muscle metabolism-a review. Frontiers in Physiology 14: 1267456. https://doi.org/10.3389/fphys.2023.1267456

Yang J, Lee SH, Goddard ME and Visscher PM. 2011 GCTA: A tool for genome-wide complex trait analysis. American Journal of Human Genetics 88(1): 76-82. https://doi.org/10.1016/j.ajhg.2010.11.011

Yin T and König S, 2019. Genome-wide associations and detection of potential candidate genes for direct genetic and maternal genetic effects influencing dairy cattle body weight at different ages. Genetics Selection Evolution 103(8): 7222–7237. https://doi.org/10.3168/jds.2019-18010

Zhang L, Wang F, Gao G, Yan X, Liu H, Liu Z, Wang Zhixin, He L, Lv Q, Wang Zhiying, Wang R, Zhang Y, Li J and Su R, 2021. Genome-Wide Association Study of Body Weight Traits in Inner Mongolia Cashmere Goats. Frontiers in Veterinar Science 8(752746): 1–9. https://doi.org/10.3389/fvets.2021.752746

Zhang Y, Wang K, Liu J, Zhu H, Qu L, Chen H, Lan X, Pan C and Song X, 2019. An 11-bP indel polymorphism within the CSN1S1 gene is associated with milk performance and body measurement traits in Chinese goats. Animals 9(12): 1–11. https://doi.org/10.3390/ani9121114

Zhao YX, Gao GX, Zhou Y, Guo CX, Li B, El-Ashram S and Li ZL, 2022. Genome-wide association studies uncover genes associated with litter traits in the pig. Animal 16(2022):100672. https://doi.org/10.1016/j.animal.2022.100672

Zhen Y, Cullen CL, Ricci R, Summers BS, Rehman S, Ahmed ZM, Foster AY, Emery B, Gasperini R and Young KM, 2022. Protocadherin 15 suppresses oligodendrocyte progenitor cell proliferation and promotes motility through distinct signalling pathways. Communications Biology 5(1): 511. https://doi.org/10.1038/s42003-022-03470-1