



Research Article

Detection of 15-bp Indel of HIAT1 Gene and Its Association with Morphometric Traits in Different Goat Populations of Bangladesh

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ARTICLE INFO	ABSTRACT
Article history Received: 21 December 2023 Accepted: 25 March 2024 Published: 31 March 2024 Keywords HIAT1 gene, Indel, Morphometric traits, Goat, Bangladesh Correspondence Mohammad Shamsul Alam Bhuiyan ✉: msabhuiyan.abg@bau.edu.bd OPEN ACCESS	Morphometrics are vital quantitative features for production performance and can affect body size. Hippocampus abundant transcript 1 (HIAT1) gene belongs to the major facilitator superfamily that has specific association with growth related traits in mammals including goat. This study was conducted to investigate possible association between 15-bp insertion/deletion (indel) polymorphism of HIAT1 gene and morphometric traits in different goat populations of Bangladesh. A total of 288 blood samples were collected from Black Bengal goat (BBG), Jamunapari (JP) and Black Bengal cross (BBC) populations. One pair of primer was used to amplify HIAT1 gene fragment that harboured 15-bp indel polymorphism. PCR amplification detected insertion (II), deletion (DD) and heterozygous (ID) genotypes. The II, ID, and DD genotype frequencies were 0.16, 0.44, and 0.40 respectively in BBG populations where the corresponding genotype frequencies were 0.00, 0.47, and 0.53 in JP and 0.11, 0.40, and 0.49 in BBC goat populations. Overall, both the DD and ID genotypes were predominant than II individuals in the studied goat populations. The studied morphometric traits differed significantly among the three goat populations ($P < 0.01$). However, rump width ($P < 0.001$) and rump length ($P < 0.01$) were significantly associated with 15-bp indel genotypes in BBG population and wither height and rump height were significantly ($P < 0.01$) associated in BBC. In conclusion, this study revealed the existence of 15-bp indel polymorphism in the studied goat populations and its influence on some morphometric traits was found.
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Introduction

In Bangladesh, the indigenous goat is raised largely for its meat and ranks second among the ruminant species. The total number of goats in Bangladesh is 26.94 million (DLS, 2022), of which Black Bengal goat (BBG) making up 90% of the total (Siddiky, 2017). BBG is found throughout Bangladesh, West Bengal, Assam and Odisha (Mason, 1996). This dwarf-type goat breed is well known around the world for its excellent meat and skin quality, adaptability to hot and humid conditions, earlier sexual maturity, higher fertility rate, and high prolificacy (Chowdhury et al., 2002). Irrespective of religion, creed and caste, goat meat (chevon) is popular to Bangladesh as special dish in the festivals. The typical daily gain ranges between 45 and 55 g which is the main obstacle for commercial BBG farming in Bangladesh (Amin et al., 2001). However, earlier studies

reported significant variation ($P < 0.05$) in production and fitness traits like birth weight, average daily gain, daily milk yield and parity wise litter size of BBG (Chowdhury et al., 2002; Faruque et al., 2017). Hence, within population selection could harness the existing variability of BBG through utilizing phenotypic performance data or genomic information.

Breeding through selection based on linear body measures is obvious for increasing animals' live weight and maximizing meat output. The correlations between linear body measurements (heart girth, body length, rump length and height etc.) and live weight are positive, and often used to predict the live weight of animal (Berhe, 2017). However, body measurements differ by sex, age, breed, and ecotype and this variability may be used to predict live weight and, consequently, the goats' economic worth (Jimmy et al.,

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2010). Growth traits are considered as complex quantitative traits since they may be adequately assessed using morphometric features and are impacted by a large number of candidate genes (Zang et al., 2019; Bi et al., 2020; Goa et al., 2020). Recently, a variety of naturally occurring genetic mutations associated to growth traits have been detected where hippocampus abundant transcript 1 (HIAT1) gene is noteworthy. HIAT1 is also known as major facilitator superfamily domain containing 14A (MFSD14A), has been anticipated to play significant roles at certain loci through transporter activity as well as in the control of mammalian growth, specifically in skeletal development (Wang et al., 2019). Importantly, influence of HIAT1 gene in meat goats is higher compared to breeds used for wool and dairy purpose (Zhang et al., 2018). Polymorphisms in this gene were significantly correlated with growth and morphometric traits in different goat breeds around the world (Zhang et al. 2018). In addition, association studies could provide candidate loci for marker-assisted breeding of domestic goats. The findings stated above suggest that, polymorphisms can be potential molecular markers for marker-assisted selection (MAS) program in order to improve the growth performance of goats. Recent studies reported indel polymorphism in the HIAT1 gene had significant association with morphometric and growth traits of Chinese goat populations (Gao et al., 2020). However, no investigation has not yet been carried out on the polymorphisms of the aforementioned gene involving morphometric traits of BBG. Here, previously reported 15-bp indel polymorphism of HIAT1 gene were investigated in BBG of Bangladesh and its possible association between the identified indel polymorphism and morphometric traits was performed.

Materials and Methods

Ethical Statement

All of the animals used in this study were handled in accordance with the standard guidelines for animal care approved by the Animal Ethics Committee of Bangladesh Livestock Research Institute, Savar, Dhaka (No. AECC/BLRI00104/2023). Additionally, the farmers who participated in this study were informed about the research activities and took their consent for using of the animals.

Animals and Phenotypes

Animals were selected randomly from both institutional and farmers' flocks. Institutional flocks included pure BBG and Jamunapari (JP) those were being selected from Bangladesh Livestock Research Institute (BLRI) headquarters and two regional stations of BLRI (Nikhongchhari, Bandarban and Godagari, Rajshahi). In

addition, BBG and Black Bengal derived crossbred (BBC) populations were selected from farmers' flocks of Mymensingh, Chuadanga, Meherpur and Kushtia districts. Animal's genotype was ascertained based on phenotypic features (ear length, ear orientation, coat color and body conformation), available pedigree information and in some cases interactions with animal owners. Usually, semi-intensive management was practiced to maintain the goats, either without or with supplementation of concentrate feed at the rate of 250 g per doe. The ingredients of concentrate feed were wheat bran, broken rice, soyabean meal and salt. Age of the selected animals varied from 1.5 to 2.5 years. Regular vaccination and deworming schedule were practiced in the studied goat populations. A total of ten morphometric data was recorded from 288 does according to the protocol of Gilbert et al. (1993). The investigated morphometric and phenotypic traits were mature body weight (BW), wither height (WH), rump height (RH), body length (BL), heart girth (HG), rump width (RW), rump length (RL), cannon circumference (CC), chest width (CW) and ear length (EL) and coat color.

Blood Sampling and DNA Extraction

Blood samples of selected animals were collected from the jugular vein using venoject tubes coated with K₂EDTA as anticoagulant. The collected blood samples were kept in icebox and carried to Animal Genomics and Breeding Lab, Department of Animal Breeding and Genetics, Bangladesh Agricultural University, Mymensingh and preserved at 4-6°C until DNA extraction. DNA extraction was performed by using AddPrep genomic DNA extraction kit, (ADD BIO INC., Daejeon, Republic of Korea) from the whole blood according to the manufacturer's instructions.

PCR Amplification and Genotyping

One pair of primers previously reported by Gao et al. (2020) were used for PCR amplification of the HIAT1 gene fragment that harbored 15-bp indel mutation in goat and the primer information is shown in Table 1. PCR amplification was performed by TECHNE thermocycler (Bibby Scientific, Leicestershire, UK) in a 10 µl reaction volume comprising 10 µM of each primer (Bionics, Daejeon, South Korea), 2x concentrated Add Taq master mix [20mM Tris-HCl (pH-8.8), 100mM KCl, 0.2% Triton® X-100, 4mM MgCl₂, protein stabilizer, sediment, loading dye and 0.5mM each of dATP, dCTP, dGTP and dTTP] (ADD BIO INC., Daejeon, Republic of Korea) and approximately 50 ng of genomic DNA. The thermal profile comprised initial denaturation at 95°C for 10 min followed by 37 cycles with denaturation at 95°C for 30 sec, annealing at 58°C for 30 sec and extension at 72°C for 30 seconds and final extension at 72°C for 10 minutes.

Table 1. Primers used in PCR amplification

Primer	Location	Primers	Primer Sequences (5'-3')	Length (bp)
rs665862918	Intron	Forward Reverse	AGAGCCTCAGTTTCGCTTATT GAGTTTATGAATCCAGCAGTTGT	183/198

In order to find the 15-bp indel mutation of the HIAT1 gene, a subset of samples (12) was sequenced both in forward and reverse directions using a genetic analyzer 3130xl (Applied Biosystems, Carlsbad, USA) by a commercial sequence service provider (Marcogen, Inc., Seoul, Republic of Korea). Alignment and editing of the generated sequences were performed using bioinformatic tools BioEdit and CLASTALW for detection of indel mutation and to ascertain the amplification of candidate HIAT1 gene fragment. Finally, genotyping of animals based on indel polymorphisms were performed by subjecting 5.0 µl of the PCR products to electrophoresis on 2.5% agarose gels.

Statistical Analysis

Genotypic and allelic frequencies were calculated manually according to Falconer and Mackay (1996). Single marker association analysis was carried out to evaluate the relationships between the resultant genotypes of HIAT1 indel and morphometric traits in goat populations using agricolae package in R (Mendiburu, 2023). Mean separation was tested using pastecs package in R (Grosjean et al., 2018). The genotype, management system, location and population were considered as fixed effect on morphometric traits where the effects were calculated according to the following model;

$$Y_{ijkl} = \mu + G_i + L_j + P_k + M_l + e_{ijkl}$$

Where, Y_{ijkl} = the dependent variable (morphometric traits);

μ = the overall mean;

G_i = the effect of i^{th} genotype;

L_j = the fixed effect of j^{th} location;

P_k = the fixed effect of k^{th} population;

M_l = the fixed effect of l^{th} management system;

e_{ijkl} = the random residual error.

Results

Effects of Genotypes on Morphometric Traits

The effects of genotypes on morphometric traits were highly significant ($P < 0.001$) among three goat populations of Bangladesh (Table 2). More particularly, JP goat had higher values irrespective of all traits followed by BBC and BBG. The body weight of JP goat (31.72 ± 1.45 kg) was significantly higher ($P < 0.001$) than BBC (23.76 ± 0.54 kg) and BBG (19.87 ± 0.28 kg). Likewise, the body length (cm) and heart girth (cm) of JP goat (63.79 ± 1.02 and 72.57 ± 1.06) were significantly higher than BBC (56.32 ± 0.46 and 67.92 ± 0.41) and BBG (52.97 ± 0.35 and 62.03 ± 0.35), respectively. Similar results were also found for other included traits such as wither height, rump height, rump width, rump length, cannon circumference, chest width, and ear length, where individuals of JP goat were larger in size compared to other two goat populations.

Table 2. Least-squares means (LSM) with standard errors (SE) of morphometric traits in different goat populations of Bangladesh

Traits ¹	Genotypes (Mean $\pm$ SE) ^{2,3}			Level of Significance
	BBG	JP	BBC	
BW	19.87 ^c $\pm$ 0.28 (165)	31.72 ^a $\pm$ 1.45 (14)	23.76 ^b $\pm$ 0.54 (68)	***
WH	49.67 ^c $\pm$ 0.25 (173)	69.29 ^a $\pm$ 0.95 (14)	59.45 ^b $\pm$ 0.54 (69)	***
RH	51.81 ^c $\pm$ 0.24 (174)	69.67 ^a $\pm$ 1.24 (15)	61.80 ^b $\pm$ 0.55 (70)	***
BL	52.97 ^c $\pm$ 0.35 (176)	63.79 ^a $\pm$ 1.02 (14)	56.32 ^b $\pm$ 0.46 (66)	***
HG	62.03 ^c $\pm$ 0.35 (174)	72.57 ^a $\pm$ 1.06 (14)	67.92 ^b $\pm$ 0.41 (64)	***
RW	12.16 ^c $\pm$ 0.12 (176)	15.83 ^a $\pm$ 0.24 (15)	12.59 ^b $\pm$ 0.15 (71)	***
RL	11.78 ^b $\pm$ 0.11 (167)	12.76 ^a $\pm$ 0.14 (13)	11.78 ^b $\pm$ 0.11 (71)	***
CC	7.01 ^c $\pm$ 0.04 (172)	8.17 ^a $\pm$ 0.25 (15)	7.36 ^b $\pm$ 0.07 (70)	***
CW	13.04 ^b $\pm$ 0.16 (171)	19.50 ^a $\pm$ 0.31 (14)	12.99 ^c $\pm$ 0.17 (68)	***
EL	12.08 ^c $\pm$ 0.08 (171)	23.46 ^a $\pm$ 0.46 (14)	15.52 ^b $\pm$ 0.22 (65)	***

¹BW: body weight; WH: wither height; RH: rump height; BL: body length; HG: heart girth; RW: rump width; RL: rump length; CC: cannon circumference; CW: chest width and EL: ear length.

²Values in the parentheses represent the number of samples under respective breed/population.

³The different superscripts in the same row differ significantly at $P < 0.001$.

Detection of 15-bp Indel within Goat HIAT1 Gene

Multiple sequence alignment using CLUSTALW and BLAST analysis confirmed the generated sequence fragment of HIAT1 gene and is presented in Figure 1. Red triangular indicates the existence 15-bp insertion in the studied samples. PCR amplification showed a size of 183/198 bp fragments that depicted the primer specific amplification (Figure 2). Three different genotypes were

detected based on the amplified fragments of 15-bp indel of HIAT1 gene. The homozygous insertion (II), homozygous deletion (DD) and heterozygous (ID) genotypes possessed 198 bp/198 bp, 183 bp/183 bp and 183 bp/198 bp, respectively (Figure 1) as revealed by the agarose gel documentation. Finally, 288 DNA samples were successfully genotyped based on 15-bp indel.

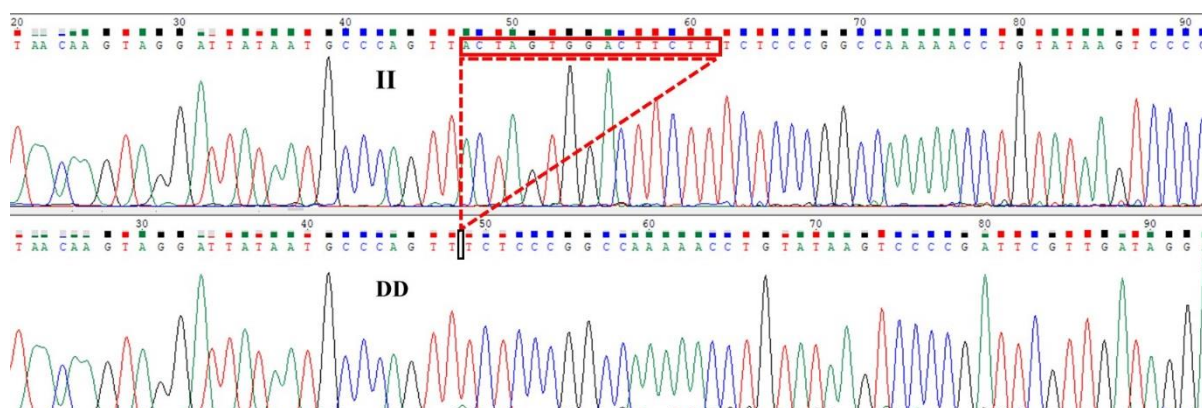


Figure 1. Sequencing chromatograms of the detected 15bp indel of the HIAT1 gene in BBG; II=Insertion type, DD=Deletion type.

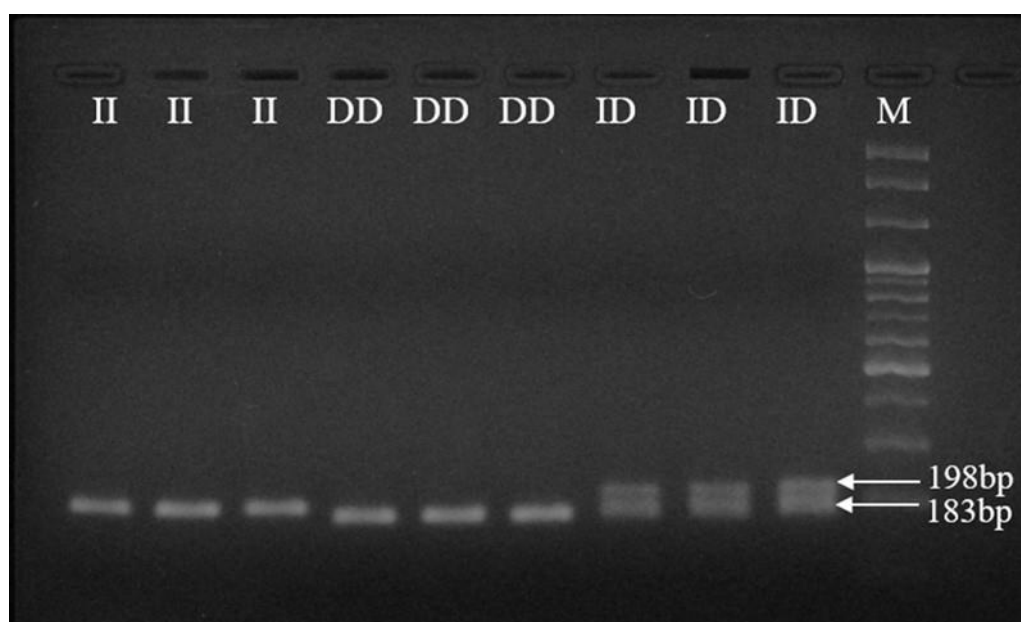


Figure 2. Electrophoresis assay of the 15bp indel sequence of the HIAT1 gene fragment of BBG. M=100bp DNA marker, II=Insertion type (198bp), DD=Deletion type (183bp) and ID=heterozygous (183/198bp).

Genotypic and Allelic Frequencies

Table 3 describes genotype and allele frequency based on 15-bp Indel polymorphism of HIAT1 gene. In BBG population, 44% of heterozygous ID, 40% of homozygous DD whereas only 16% of the population was found homozygous II type. On the other hand, 47% ID and 53% DD type individuals were found in JP goat breed without II types. Genotype frequency of II, ID and DD genotypes in BBC were 11%, 40% and 49%,

respectively. The predominant D allele frequency in BBG, JP and BBC were 62%, 77% and 69% respectively and the corresponding I allele frequencies were 38%, 23% and 31% respectively. Overall, DD and ID genotypes were equally (43%) present in the studied goat populations of Bangladesh, where II individuals were only 14% and the corresponding D and I allele frequencies were 65% and 35%, respectively.

Association of the 15-bp Indel Genotypes with Morphometric Traits of BBG and BBC

Table 4 and 5 explain the association between morphometric traits of BBG and BBC with three identified genotypes (II, ID, DD) deduced from 15-bp Indel of HIAT1 gene. The indel genotypes had effects only on the rump width and rump length traits of BBG (Table 5). Rump width and rump length (12.45 ± 0.21 and 12.03 ± 0.18 cm, respectively) of the individuals of DD genotype of BBG was significantly higher than II genotype (11.57 ± 0.27 and 11.22 ± 0.23 cm) but individuals of ID genotype (12.12 ± 0.16 and 11.74 ± 0.16

cm) varied insignificantly with them. On the other hand, wither height, rump height and ear length traits varied significantly ($P < 0.05$) among the resultant genotypes of HIAT1 gene in BBC (Table 5). The DD (60.24 ± 0.81 and 62.65 ± 0.87 cm) and ID (54.75 ± 0.70 and 61.96 ± 0.72 cm) genotypes had significantly higher ($P < 0.01$) wither and rump height than the individuals with II genotype (59.86 ± 1.39 and 57.63 ± 1.15 cm). Similarly, higher ear lengths were observed in DD (15.77 ± 0.33 cm) and ID (15.59 ± 0.30 cm) individuals compared to II (14.07 ± 0.64 cm) genotype.

Table 3. Genotypic and allelic frequencies for the 15-bp Indel of HIAT1 gene in three goat populations of Bangladesh

Population	Sample Size	Genotype Frequency ^{1,2}			Gene Frequency	
		II	ID	DD	I	D
BBG	201	0.16 (32)	0.44 (87)	0.40 (80)	0.38	0.62
JP	15	0.00 (00)	0.47 (07)	0.53 (08)	0.23	0.77
BBC	72	0.11 (08)	0.40 (29)	0.49 (35)	0.31	0.69
Overall	288	0.14 (201)	0.43 (15)	0.43 (72)	0.35	0.65

¹Homozygous II genotype, heterozygous ID genotype, homozygous DD genotype.

²Values in the parentheses represent the number of samples under respective genotype.

Table 4. Association of the 15-bp Indel of HIAT1 gene with morphometric traits of BBG

Traits ¹	Genotype (Mean $\pm$ SE) ^{2,3}			Level of Significance ⁴
	DD	ID	II	
BW	19.87 $\pm$ 0.52 (64)	19.34 $\pm$ 0.39 (71)	19.98 $\pm$ 0.61 (27)	NS
WH	49.48 $\pm$ 0.37 (69)	49.99 $\pm$ 0.41 (74)	49.26 $\pm$ 0.68 (27)	NS
RH	51.99 $\pm$ 0.35 (69)	51.86 $\pm$ 0.40 (74)	51.30 $\pm$ 0.60 (28)	NS
BL	52.62 $\pm$ 0.56 (71)	53.05 $\pm$ 0.53 (74)	53.21 $\pm$ 0.90 (28)	NS
HG	62.39 $\pm$ 0.61 (70)	61.80 $\pm$ 0.53 (73)	61.71 $\pm$ 0.79 (28)	NS
RW	12.45 ^a $\pm$ 0.21 (72)	12.12 ^{ab} $\pm$ 0.16 (73)	11.57 ^b $\pm$ 0.27 (28)	***
RL	12.03 ^a $\pm$ 0.18 (67)	11.74 ^{ab} $\pm$ 0.16 (70)	11.22 ^b $\pm$ 0.23 (27)	**
CC	6.95 $\pm$ 0.07 (71)	7.00 $\pm$ 0.06 (72)	7.13 $\pm$ 0.10 (26)	NS
CW	13.18 $\pm$ 0.26 (68)	12.97 $\pm$ 0.25 (72)	12.86 $\pm$ 0.40 (28)	NS
EL	12.10 $\pm$ 0.11 (69)	12.13 $\pm$ 0.12 (71)	12.00 $\pm$ 0.20 (28)	NS
BW	19.87 $\pm$ 0.52 (64)	19.34 $\pm$ 0.39 (71)	19.98 $\pm$ 0.61 (27)	NS

¹BW: body weight; WH: wither height; RH: rump height; BL: body length; HG: heart girth; RW: rump width; RL: rump length; CC: cannon circumference; CW: chest width and EL: ear length.

²Values in the parentheses represent the number of samples under respective genotype within BBG.

³The different superscripts in the same row differ significantly at $P < 0.001$ or $P < 0.01$.

⁴NS: $P > 0.05$; **: $P < 0.01$; ***: $P < 0.001$

Table 5. Association of the 15-bp Indel of HIAT1 gene with morphometric traits of BBC

Traits ¹	Genotype (Mean $\pm$ SE) ^{2,3}			Level of Significance ⁴
	DD	ID	II	
BW	24.36 $\pm$ 0.74 (33)	23.91 $\pm$ 0.91 (28)	20.31 $\pm$ 1.02 (7)	NS
WH	60.24 ^a $\pm$ 0.81 (33)	54.75 ^a $\pm$ 0.70 (28)	59.86 ^b $\pm$ 1.39 (8)	**
RH	62.65 ^a $\pm$ 0.87 (34)	61.96 ^a $\pm$ 0.72 (28)	57.63 ^b $\pm$ 1.15 (8)	**
BL	56.30 $\pm$ 0.72 (33)	56.96 $\pm$ 0.60 (26)	54.00 $\pm$ 1.33 (7)	NS
HG	68.40 $\pm$ 0.57 (30)	67.67 $\pm$ 0.66 (27)	66.86 $\pm$ 1.16 (7)	NS
RW	12.71 $\pm$ 0.24 (35)	12.61 $\pm$ 0.21 (28)	12.00 $\pm$ 0.46 (8)	NS
RL	12.84 $\pm$ 0.23 (35)	12.77 $\pm$ 0.35 (28)	12.38 $\pm$ 0.28 (8)	NS
CC	7.44 $\pm$ 0.11 (34)	7.32 $\pm$ 0.19 (28)	7.13 $\pm$ 0.12 (8)	NS
CW	13.04 $\pm$ 0.24 (34)	12.81 $\pm$ 0.26 (26)	13.31 $\pm$ 0.62 (8)	NS
EL	15.77 ^a $\pm$ 0.33 (31)	15.59 ^a $\pm$ 0.30 (27)	14.07 ^b $\pm$ 0.64 (7)	*

¹BW: body weight; WH: wither height; RH: rump height; BL: body length; HG: heart girth; RW: rump width; RL: rump length; CC: cannon circumference; CW: chest width and EL: ear length.

²Values in the parentheses represent the number of samples under respective genotype within Black Bengal Cross.

³The different superscripts in the same row differ significantly at $P < 0.001$ or $P < 0.01$.

⁴NS: $P > 0.05$; *: $P < 0.05$; **: $P < 0.01$.

Discussion

Earlier studies showed genetic variations with growth-related features in goats. Indel mutations in candidate genes like GDF9 (Wang et al., 2017), PITX2 (Yan et al., 2018), KDM6A (Wang et al., 2019), PRLR (Liu et al., 2020), HIAT1 (Gao et al., 2020), and PLAG1 (Wei et al., 2021) have been revealed impact on goat growth and morphology. Likewise, Luo et al. (2023) evaluated both the high mRNA expression profile and genetic variants of the HIAT1 gene in Chinese sheep populations, discovering that a 9-bp Indel was strongly connected with growth features in Luxi black-headed sheep (LXBH) and Guiqian semi-fine wool sheep (GSFW).

This study resulted highly significant effects ($P<0.001$) on all considered morphometric traits in different goat populations of Bangladesh. Similar to the current study, goat breeds had significant differences on productive, morphometric and reproductive traits (Bilal et al., 2018). Miah et al. (2016) stated that BBG performed higher than JP under semi-intensive conditions considering the productive and reproductive aspects, while birth weight and mature weight were non-significant, but birth type showed a significance difference ($P<0.05$) between the breeds. However, Khandaker et al. (2017) observed no statistically significant differences in the three investigated breeds where BBG within breed showed significantly varying body length and body height. Bhowmik et al. (2013) showed that the BBG had lower average birth weights than crossbred goats, which was statistically significant ($P<0.05$). Choudhury et al. (2012) found significant differences among the coat color variants of BBG for morphometric (body weight, body length, chest girth, wither height and ear length) and production traits which partially agrees with the present study. Hossain et al. (2020) investigated the comparative performance of three coat color variants of BBG under semi-intensive management, finding that the three-color variants performed nearly identically. Contrasting to the present findings, Akthar et al. (2021) also reported that color phenotypes in BBG were not a determinant of body measurements and there were no major morphological variations observed among the BBG populations from different places and coat color variants. BBG possessed variations for body size, morphometric features, coat color and beard pattern and supports this finding (Rakib et al., 2022).

In this present study, 15-bp indel of the HIAT1 gene was detected in different goat populations of Bangladesh and its association study with morphometric traits was also performed. The analysis revealed significant association of rump width ($P<0.001$) and rump length ($P<0.01$) in BBG whereas wither height, rump height

($P<0.01$) and ear length ($P<0.05$) in BBC. This indel polymorphism of HIAT1 gene was reported at first by Gao et al. (2020) in Chinese Shaanbei White Cashmere goats. Individuals of DD genotype was predominant in this study than the II genotype that supports the findings of Gao et al. (2020) who reported the DD genotype (63%) was found to be predominant and II genotype (4%) was negligible. In contrast to this study, frequencies of II genotype in Shaanbei White Cashmere goat, Inner Mongolia White Cashmere goat, and Guanzhong Dairy goat (80.5%, 69.5% and 94.4%, respectively) were higher than DD individuals (Wei et al., 2021). Similarly, higher frequency of II individuals (76.9%) than ID individuals (21%) and DD individuals (2.1%) were also observed by Wang et al. (2019) in Shaanbei White Cashmere goat and contradicts with the results of current study. Genotypic and allelic frequency are population specific that depends mostly on genetic constitution of a population, sample size, sampling strategy etc.

The DD individuals of BBG and BBC were significantly higher than II individuals considering rump width, rump length and wither height, rump height, ear length respectively. Gao et al. (2020) reported reverse orientation of genotypes where morphometric traits (chest width, chest depth, heart girth, body length and height at hip cross) associated with the genotype II were significantly higher than those of genotypes ID and DD ($P<0.01$ or $P<0.05$) in Shaanbei White Cashmere goat population. Similarly, Wei et al. (2021) revealed that II genotypes of Shaanbei White Cashmere goat and Hainan Black goat were dominant than ID genotypes, having better phenotypes such as body weight ($P<0.01$), body height ($P<0.05$), chest circumference ($P<0.05$) and body index ($P<0.05$) respectively. According to Wang et al. (2017), individuals of II genotypes (58.07 ± 0.29), DD genotypes (57.46 ± 0.25) of Shaanbei White Cashmere goat also resulted in higher ($P<0.01$) body height than ID (56.97 ± 0.17) individuals. Earlier studies reported significant association between Indel genotypes of candidate genes and morphometric and growth traits in different goat populations. More particularly, 15-bp indel of PLAG1 (Wei et al., 2021), 16-bp indel of KDM6A (Wang et al., 2019), 14-bp indel of SPAG17 (Zhang et al., 2019) and 17-bp indel of CHCHD7 gene (Li et al., 2020) had significant association with different morphometric traits in goats and supports the present findings. Wang et al. (2019) also worked with Shaanbei White Cashmere goat and investigated the 16-bp indel within the KDM6A gene and reported that this indel was strongly associated with growth traits such as body height, chest width, height across the hip, body length and chest circumference ($P<0.05$) and supports our Indel based association study. Li et al. (2020) discovered that the individuals of II genotypes within 17-bp indel of

CHCHD7 gene were mostly greater ($P < 0.01$) body length, heart girth, hip width, height at hip cross, cannon circumference, chest depth in Shaanbei White Cashmere goat (adults) and higher ($P < 0.05$) body height, height at hip cross in Inner Mongolia White Cashmere (weaner) than the individuals of ID genotypes. Altogether, most of the studied traits of this study didn't reach at the significance level and one of the possible reasons is the existence of large variation within the population for a particular trait of interest. Hence, it warrants to include large number of samples in association studies for making valid conclusion.

Conclusion

All of the investigated morphometric traits differed significantly among BBG, JP and BBC goat populations. The coat color variants of BBG also had significant association with morphometric traits. Sequence analysis revealed the existence of 15-bp indel of HIAT1 gene in BBG. The overall genotype frequencies of II, ID, and DD genotypes were 0.14, 0.43, and 0.43, respectively. There was a significant association of 15-bp indel polymorphism with rump width and rump length in BBG and wither height, rump height and ear length in BBC of Bangladesh. Taken together, the 15-bp indel derived genotypic information could be employed in goat breeding program to accelerate genetic gain particularly for morphometric traits.

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