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Research Article

Identification of Genetic Diversity of Bone Morphogenetic Protein (Bmp15) Genes in Senduro Goats and Boerawa Goats using Pcr-Sequencing

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Abstract | The first step to produce Marker Assisted Selection (MAS) in Senduro goats and Boerawa goats is to identify candidate genes related to litter size traits, one of which is the Bone Morphogenetic Protein (BMP15) gene. The study aimed to identify the genetic diversity of BMP15 exon 2 genes in Senduro goats and Boerawa goats in UPT PT-HMT Singosari, using PCR-Sequencing. This study used a survey method, sampling by means of purposive sampling, blood samples of Senduro and Boerawa goats were collected from UPT PT-HMT Singosari. The samples used were 27 samples of Senduro goats and 20 samples of Boerawa goats. DNA amplification was carried out at the Biotechnology Laboratory, Faculty of Animal Science, Brawijaya University, Malang. For the sequencing process, the PCr product were sent to 1st Base Laboratory (Genetica Science), Selangor Malaysia. The sequencing method used is the Sanger method, using the ABI Prims 3100-Avant Genetic Analyzer sequencer machine. Alignment the result of the sequencing in the form of chromatograms were analyzed using BioEdit and Mega X software. The association of genetic diversity of the BMP15 gene with litter size was carried out by T-test analysis. The sequencing results showed that the Boerawa goat sample (BC 11) experienced a mutation, there was a change in the base from Cytosine (C) to Guanine (G) at the position of 709 bp (C709G). In the Boerawa goat sample (BC 18) also mutated, there was a change in the base from Cytosine (C) to Guanine (G) at the position of 707 bp (C707G). No mutations were found in the Senduro goat samples because there was no change in the base for all Senduro goat samples. All samples of Senduro goats carry the base Cytosine (C). The results showed that the identification of the BMP15 exon 2 gene with Forward 5'-GACCCTTCTTCTCTTG-3' and Reverse 5'-CATCTCTGCTCCATACAC-3' primers along 990 bp in Senduro goats using PCR-sequencing was uniform (monomorphic). Identifying the BMP15-2 exon 2 gene for Boerawa goats is polymorphic, but cannot be associated with litter size.

Keywords | Senduro goat, Boerawa goat, BMP15, Genetic diversity, Sequencing

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INTRODUCTION

Senduro goats are a wealth of local Indonesian livestock genetic resources (SDG) which have been determined by the Decree of the Minister of Agriculture of the Republic of Indonesia Number 1055 / Kpts / SR.120 / 10/2014 concerning the Determination of Senduro Goat Strains. Senduro goats as dual-purpose livestock are milk produc-

ers and meat producers on people's farms. Senduro goats have advantages including adaptability and special maintenance patterns that are not needed, are resistant to disease, and produce more than one offspring per birth. According to Yulianto (2019), Senduro goats have an average litter size of 1.50±0.59 heads, and large jug-shaped udders can produce milk as much as 1.3 ± 0.5 liters per day (Susilorini and Kuswati, 2019).

Boerawa goats are the result of a cross between male Boer goats and PE goats. The birth weight of Boerawa goats from crosses is 3.23±0.70 kg (Nasution *et al*., 2014) when compared to the birth weight of PE goats of 2.57±0.72 kg and Boer goats of 2.71±0.70 kg. Boerawa goats have the advantages of a faster growth rate, weaning weight reaches 14-20 kg, 8 months of age reaches 40 kg, and produce more than one cub per birth, with an average litter size of 1.21.

The development of molecular technology makes DNA markers very likely to be used for conventional breeding activities. Studies of genetic and non-genetic diversity in the goat genome can be done with the latest molecular biology techniques. The discovery of many genes or polymorphic regions instead of genes is generated by gene mapping. Over the past 10 years, applications of molecular genetics have increased to reveal genetic variation.

Selection using DNA markers can be done with molecular technology, to accelerate genetic repair. Molecular selection for Senduro goats and Boerawa goats needs to be done to improve genetic quality. Nour El Huda *et al*. (2015), stated that the superior nature of livestock can be known on an accurate laboratory scale in a relatively fast time if using DNA characterization. Livestock productivity can be determined using gene-controlled litter size parameters. GH (Growth Hormone) is a growth gene, centesis, and secreted pituitary gland (Etherton and Bauman, 1998). GH has a role in regulating tissue growth, reproduction, lipid metabolism, lactation, and normal body growth in mammals (Amiri *et al*, 2018).

Bone morphogenetic protein (BMP) belongs to the superfamily transforming growth factor b (TGFb). The BMP15 gene known as FecX is located on the X chromosome and is only expressed in oocytes (Hasan *et al*., 2011). The BMP15 gene is expressed in developing ovarian cells (Damayanti and Sri Rahayu, 2013). BMP-15 regulates granulosa cell proliferation and differentiation (Ireland *et al*., 2007), extracellular matrix deposition, and apoptosis (Massague & Chen (2007), by promoting cell mitosis, suppressing FSH (Follicle Stimulating Hormone) receptor expression and stimulating Kit ligand expression, all of which play a role in female mammalian fertility (Otsuka *et al*., 2000). BMP15 plays a role in follicular maturation and development as a homodimer, then forms a heterodimer with GDF9 (Dube *et al*., 1998). In late primary follicles, BMP15 is more expressed and unexpressed in small primary follicles. BMP15 transcription has been translated In the early stages of folliculogenesis, BMP15 transcription has been translated.

Barzegari, *et al*. (2010) stated that the gene encoding BMP15 was shown to affect the productivity of ewes. Many studies have been conducted on different races to investigate the relationship between mutations in the BMP15 gene and fertility. The BMP-15 gene is a fecundity gene of economic value in the field of sheep and ruminant reproduction (Dong *et al*., 1996; Polley *et al*., 2009). The BMP-15 gene is a candidate gene that affects goat reproductive traits (Ahlawat *et al*., 2015). According to Polley *et al*. (2009), genes that have an important role in the ovulation process and natural mutations are BMP15, Bone morphogenetic protein receptor 1B, and GDF9 genes. Litter size will increase if the three genes undergo ovulation processes and natural mutations. The secretion of FSH (Follicle Stimulating Hormone) hormone at the time of folliculogenesis and a large number of eggs ovulated each cycle will affect litter size (Hamdan *et al*., 2012).

Genetic diversity from 50 female goat samples (17 Boers, 16 Beans, and 17 Boerka) has identified 2 polymorphic SNPs using PCR-sequencing methods and BMP15 gene amplification resulting in fragments with a length of 141 bp (Coal *et al*., 2016). Coal *et al*. (2016) reported that there was a mutation between adenine bases (A) and guanine (G) and found genotypes GG, GA, and AA in the BMP15 gene. Mishra *et al*. (2017) have found polymorphic BMP15 genes in exon 2 segments and reported to affect litter size. Hakim (2019) reported the discovery of BMP15 gene polymorphism in PE goats in BPT-HPT Pelaihari, South Kalimantan, SNP which was found to be used as a determinant of livestock genotype but could not yet be used as a selection tool. Similar research results were reported by Hidayat (2015) that there is a correlation between FecXG gene polymorphism to the prolific nature of local goats, resulting in each genotype having differences in litter size. Shaha *et al*. (2022) reported that there were three SNPs identified namely G616T, G735A, and G811A at the BMP15 locus that the locus at BMP15 was quite polymorphic (PIC ≥0.25) in Jamunapari goats and crossbred goats in Bangladesh. In contrast to the results of Rahayu's (2011) study which reported that there was no BMP15 gene polymorphism in 5 samples of peanut goats. Farag *et al*. (2013) also reported that no polymorphism of the FecXI locus (BMP15) was found in local Egyptian goats.

This study aims to identify the genetic diversity of BMP15 genes in Senduro goats and Boerawa goats and to examine the association of the genetic diversity of BMP15 genes

with litter size in Senduro goats and Boerawa goats.

MATERIALS AND METHODS

Time and place of research

The research will be conducted from August 2022 to March 2023. The field research conducted was the blood sampling of Senduro goats from UPT-HMT Singosari, Malang Regency. DNA amplification was carried out at the Biotechnology Laboratory, Faculty of Animal Husbandry, Brawijaya University, Malang.

Materials and Tools

This research has been approved by the research ethics commission with an ethical clearance number 054-KEP-UB-2023. The research material used in this study was 27 samples of Senduro goat blood and 20 Boerawa goat blood samples from UPT-HMT Singosari, Malang Regency. The materials used are genomics DNA Mini Kit, agarose, alcohol 70%, Diamond Nucleic Acid Dye, ethanol absolute, TBE buffer, Green Master Mix, blue dye, Nuclease Free Water, and a pair of primers for each gene BMP15 gene (access number ENSCHIG00000015206) with Forwarding (5'-GACCCTTCTCTTCTCTTG-3') and Reverse (5'-CATCTCTCTCTTCTCCATACAC-3') along 990 bp. The research tools used include Ethylene Diamine Tetraacetic Acid (EDTA) anti-coagulant vacuum tube, tube holder, cool box, 1.5 ml tube, beaker glass (IWAKI), micropipette (Select BioProducts), GD Column, tip (Axygen scientific 301-03-051), centrifuge (HETTICH Mikro 185), tube rack, PCR machine (BioRad T100 Thermal Cycler), microcentrifuges (Forcemini SBC-140-3), microwave (Panasonic NN-SM32HM), electrophoresis device (Bio-Rad Mupid-Exu), Gel Doc (Gite 965GW).

Research Methods

Blood draw: Blood samples of Senduro goats are collected in the jugular vein in the neck of goats.

B. DNA isolation: DNA isolation is separating DNA present in the blood from other organic components. The method used in DNA isolation is the Phenol-chloroform extraction method according to Sambrook *et al.* (1989), modified using the Geneaid Extraction Kit (Genomics DNA Mini Kit for Blood).

DNA amplification: According to the PCR Kit, DNA amplification with Polymerase Chain Reaction (PCR) premix composition of 30 µl for BMP15 gene sequencing analysis includes 0.3 µl forward primer, 0.3 µl reverse primer, Green Master Mix Promega 15 µl and DW (Nuclease free water) 4.4 µl. Incubation of the mixture using a Biorad PCR machine with PCR conditions, namely: stage I includes initial denaturation at 95°C for 5 minutes, stage II includes denaturation at 95°C for 15 seconds, annealing at 54°C for 30 seconds, and elongation at 72°C for 45 seconds, carried out as many as 35 cycles, stage III is post-elongation at 72°C during 5 minutes.

BMP15 gene PCR Product Visualization: Visualization of PCR products with electrophoresis aims to observe amplification results in the form of DNA bands /bands that show the size and number of base pairs. BMP15 gene PCR product electrophoresis in 1.5% agarose gel, voltage 100volt for 30 min. When the electrophoresis process is complete, visualization is carried out using a UV-transilluminator. We will see the length of the target DNA band that appears, compare it with the marker, then save the image in a file.

Sequence Data Analysis

PCR product sequencing analysis was carried out by a commercial company (1st BASE, Malaysia) using the Sanger method, using an ABI Prism 3100-Avant Genetic Analyzer sequencing machine. The chromatogram shape was then edited using BioEdit software version 7.0.0, after which it was aligned with the nucleotide sequence of the BMP15 gene in Capra hircus access number (ENSCHIG00000015206) using Mega software version X (Kumar *et al.*, 2018).

BMP15 Gene Allele Frequency

Allele frequency and genotype frequency according to Nei and Kumar (2000) as follows:

Allele Frequency Formula:

$$X_i = \frac{2n_{ii} + \sum n_{ij}}{2N}$$

Information:
Xi = I-th allele frequency
n_{ii} = Number of individuals with genotype I
n_{ij} = Number of individuals with the IJ genotype
N = number of individual samples

Genotive Frequency Formula:

$$X_{ii} = \frac{n_{ii}}{N}$$

Information:
X_{ii} = I-th genotypic frequency
n_{ii} = Number of individuals with genotype I
N = Number of individuals with genotype I

The value of observed heterozygosity (Ho) can be calculated by the following formula:

$$Ho = \sum_{i \neq j} \frac{n_{ij}}{N}$$

Information:
H_o = frequency of heterozygosity of observations
n_{ij} = number of heterozygosity individuals at the 1st locus
N = number of individuals analyzed

The value of expectation heterozygosity (He) can be calculated by the following formula:

$$He = 1 - \sum_{i \neq j}^{n} x_i^2$$

Information:
H_e = Heterozygosity and expectations among populations
X_i^2 = Allele frequency
n = number of alleles

Polymorphic Informative Content (PIC) Value
The information level of an allele is calculated by the polymorphic informative content (Bostein, *et al*., 1980):

$$(PIC)\ value\ approach: PIC = 1 - \sum_{i=1}^{n} pi^2 - \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} 2pi^2 pj^2$$

Information:
pi = Allele frequency to i
pj = allele frequency to j
n = Number of alleles per marker

Hardy-Weinberg Equilibrium
The Hardy-Weinberg equilibrium was tested with the X^2 test (Hart *et al*., 1997):

$$x^2 = \sum \frac{(obs - \exp)^2}{exp}$$

Information:
X^2 = Chi-Square Test
Obs = Number of genitive observations to I
Exp = Number of Expectations of the Genotype to I

Association of genetic diversity of BMP15 gene with litter size
The association of the genetic diversity of BMP15 genes with litter size was performed by T-test analysis.
The mathematical model used:

$$t_{hit} = \frac{M_1 - M_2}{\sqrt{\frac{SS_1+SS_2}{n_1+n_2-2}\left(\frac{1}{n_1}+\frac{1}{n_2}\right)}}$$

Keterangan :
M_1 = rata-rata skor kelompok 1
M_2 = rata-rata skor kelompok 2
SS_1 = *sum of square* kelompok 1
SS_2 = *sum of square* kelompok 2
n_1 = jumlah subjek/sample kelompok 1
n_2 = jumlah subjek/sample kelompok 2
Dimana :

$$M_1 = \frac{\sum X_1}{n_1} \qquad SS_1 = \sum X_1^2 - \frac{(\sum X_1)^2}{n_1}$$

$$M_2 = \frac{\sum X_2}{n_2} \qquad SS_2 = \sum X_2^2 - \frac{(\sum X_2)^2}{n_2}$$

Information:
M1 = average group 1
M2 = average group 1
SS1 = Sum of Square Group 1
SS2 = Sum of Square Group 2
N1 = Number of Subject/Sample Group 1
N2 = Number of Subject/Sample Group 2

RESULTS AND DISCUSSION

PCR amplification of the BMP15 gene in Senduro and Boerawa goats with primer BMP15

BMP15 amplicon fragments (exon 2) in Senduro and Boerawa goats of 990 bp can be seen in the PCR results of Figure 1 and Figure 2. DNA sequencing conducted in this study was 27 samples of Senduro goats and 20 samples of Boerawa goats, each consisting of forward and reverse. After alignment sequencing was carried out on Senduro goats (MP) and Boerawa goats (BC) using BioEdit software and alignment using Mega ver X software (Kumar *et al*., 2018)., it can be seen that there are mutations in Boerawa goat samples (BC 11 and BC 18). In Senduro goats no mutations were found, it was because there was no change in the base for all Senduro samples. From Figure 3. Showed that the results of sequencing the BMP15 gene in Boerawa goats (BC) mutated in samples BC 11 and BC 18 were found double peak, while other Boerawa goat samples all carried base C at position 709 bp (Figure 3c) and position 707 bp (Figure 3d). Sample BC 11 (Figure 3a) underwent a base change from Cytosine (C) to Guanine (G) at position 709 bp (C709G). The BC 18 sample (Figure 3b) also underwent a base change from Cytosine (C) to Guanine (G), at position 707 bp (C707G). In the Senduro goat samples, no mutations were found, because there was no change in base for all Senduro goat samples. All Senduro goat samples carried the base Cytosine (C) at position 704 bp (Figure 3g) and at position 706 bp (Figure 3f). The results of this study are different from the results of Chu *et al* (2007) research that BMP15 gene mutations occur in sheep causing changes in Cytosine (C) bases to Thymine (T). Similar research results have also been reported by Davis (2005), there has been a mutation of the BMP15 gene that causes amino acid changes (CAG = Glutamine-TAG = stop codon).

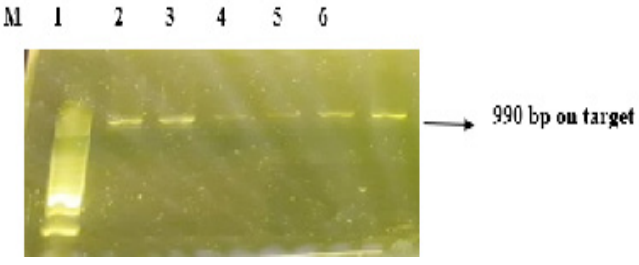

Figure 1: BMP15 Gene PCR results with the second primer in Senduro goats Description:
M = DNA marker, 1-6 = Senduro goat sample

Genotype frequency and allele frequency of BMP15-2 gene

Putri *et al*. (2021) stated that the selection process and mar

Table 1: Primary Information and anneling temperature

Primary Name	Primary sequence (5' →3')	Annealing temperature (°C)	Product Size (bp)
BMP15-2	F (5'-GACCCTTCTCTTCTCTTG-3')	60°C	990 bp
	R (5'-CATCTCTGCTCCATACAC-3')		

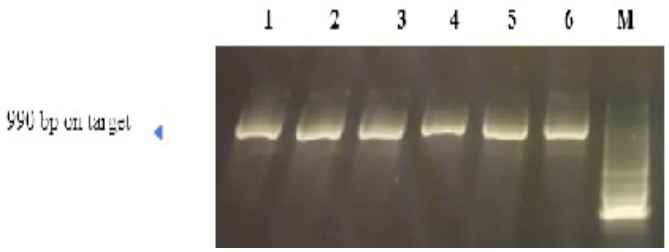

Figure 2: PCR results of BMP15 gene with the second primer in Boerawa goats
Information: M = Marker DNA, 1-6 = Boerawa goat samples

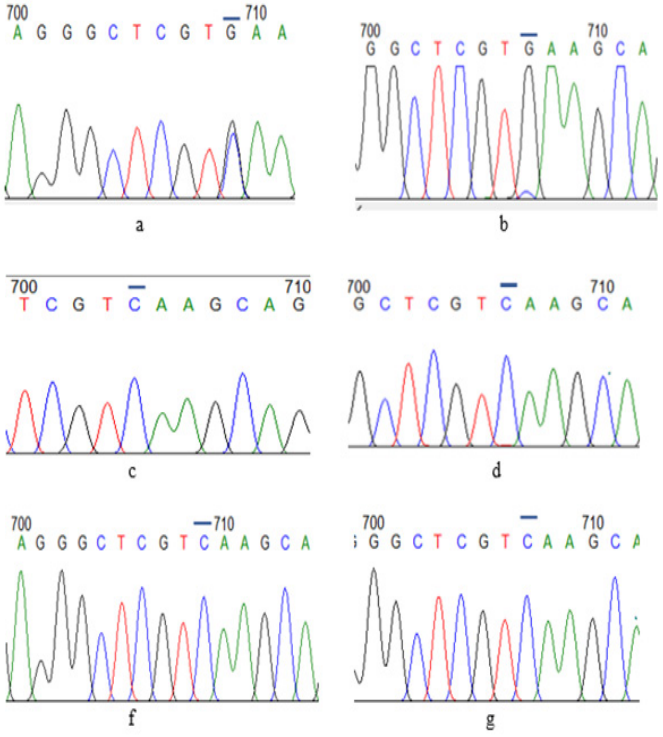

Figure 3: Boerawa goats BMP-15 gene sequences (a. BC 11 and b. BC 18 double peak), (c. BC 1 and d. BC 5 one peak) and Senduro goats BMP-15 gene sequences (e.MP4 and f. MP16)

riage arrangements can be arranged to increase the chances of the emergence of the desired genotype and also reduce the chance of the emergence of unwanted genotypes. This is in line with Noor (2010) stating that selection is a process that uses power in determining which livestock will breed in the next generation. From the sequencing results, two genotypes of the BMP15-2 gene were obtained in Boerawa goats, namely CC and CG. All samples of Senduro goats carry a C base, so they only have one genotype, namely CC. The frequency of the CC genotype is 0.9 and the frequency of the CG genotype is 0.1, while the frequency of the C allele is 0.95 and the frequency of the G allele is 0.05. Genotype Frequency and Allele Frequency can be seen in Table 2.

Table 2: Genotype Frequency and Allele of BMP15 -2 Gene Boerawa goat and Senduro goat

	Genotype Frequency			Allele Frequency	
	CC	CG	GG	C	G
Boerawa goat	0,9	0,1	0	0,95	0,05
Senduro goat	1	0	0	1	0

The results showed that for Boerawa goats the frequency of the CC genotype was greater than the frequency of the CG genotype. The frequency of the C allele is higher than the frequency of the G allele. The difference in the value of allele frequency and genotype frequency in this study shows that there is genetic diversity (polymorphic). This is by following fer under Nei and Kumar (2000) who state that a gene is polymorphic if it has an allele frequency value whose value is greater than 1% in the population. BMP15 gene polymorphisms found in Boer, Bean, and Boerka goats resulting in GG, GA, and AA genotypes have been reported by Coal *et al.* (2016). Palai *et al.* (2012) have reported similar studies on Raighar goats, Beetal, Jakhrana, Barbari, Black Bengal, Ganjam, Osmanabadi, Sangamneri goats (Ahlawat *et al.*, 2016), Jining Grey goats, Inner Mongolia Cashmere, Hechuan White, Dazu Black, Boer, and Nubian (Guang *et al.*, 2016). Three genotype variants of the BMP15 gene namely BB, BM, and MM with genotype frequencies of 0.46, 0.43, and 0.11 in Anglo-Nubian goats have been reported Abdel-Rahman *et al.* (2013).

Hardy-Weinberg Degree of Equilibrium, Heterozygosity and Polymorphic Informative Content (PIC)

The enactment requirements of the Hardy-Weinberg decree law are that the number of individuals or chromosomes in a population is always large and eliminates the selection and mutation process in genetic algorithms (Panggabean, 2016). If both genotype frequency and allele frequency are constant from generation to generation due to random gamete mergers in a large population, the population can be expressed as being in equilibrium (Allendorf *et al* (2012). Noor (2010) states that a large enough population will not change from generation to generation if there is no selection, mutation, or genetic drift.

The He value of this study was 0.1, while the Ho value was 0.095. This He value is higher than the Ho value. From the chi-square results (X2), observational heterozygosity values (Ho), expectation heterozygosity values (He), and Polymorphic Informative Content (PIC) values show that the genotype frequency of the BMP15-2 exon 2 gene fragment is in Hardy-Weinberg equilibrium in Boerawa goats (Table 3). The BMP15 gene fragment in Senduro goats is monomorphic (uniform). This is evidenced by the discovery of only 1 genotype in Senduro goats, namely the CC genotype. The population of Senduro goats and Boerawa goats in UPT-PT HMT Singosari Malang Regency is in a balanced state according to the Hardy-Weinberg balance, it is likely due to intensive livestock maintenance and controlled mating patterns, females mate naturally only with males in UPT PT-HMT Singosari, namely for Senduro males 4 males, while Boerawa goats 2 males.

Table 3: Test results of chi-square (χ2), heterozygosity, and Polymorphic Informative Content (PIC) BMP15-2 gene in Boerawa goats

Gene	(χ2)	He	Ho	PIC
BMP15-2	0,0054	0,1	0,095	0,045

Information: χ2: Chi-square (0,05: Df 1= 3,84), * no real difference (χ2 calculate < χ2 table) Balanced Ho: Observed heterozygosity, He: Heterozygosity of expectations, PIC: *Polymorphic Informative Content*.

The ideal index for measuring allele fragment polymorphism is with PIC values. The PIC value is used to evaluate genetic markers from PCR-amplified DNA bands. Carson *et al*. (2014), there are three classes of PIC values, namely: 1) PIC>0.5 = very informative, 2) 0.25>PIC>0.5 = medium, and 3) PIC < 0.25 = low. Zhang *et al*. (2011), stated that the PIC≥0.5 value is an informative primer. Primers that have increasingly large PIC values are the best primers that can be used as molecular markers. The PIC value of the BMP15 gene in Boerawa goats is 0.045. From the PIC category, it is known that the PIC value in this study is included in the low category, with only two alleles found in this study. This is supported by Sihombing *et al*. (2019) who state that the PIC value will be high if more than two alleles are found and the frequency value is not conspicuous.

Association of BMP15 Gene Genotype to Litter Size

The association of the BMP15 gene to litter size in Boerawa goats at UPT Breeding Livestock and Forage Animal Feed (PT-HMT) Singosari, Malang Regency was analyzed with an Independent Sample t-test using IBM Windows SPSS software version 26.0 (IBM Corporation). The average litter size of Boerawa goats can be seen in Table 4. The average litter size of the CC genotype of Boerawa goats in this study was 1.23±0.15, while the average litter size of the CG genotype was 1.45±0.07. The discovery of mutations in Boerawa goat samples (BC11 and BC18) shows that the BMP15 gene in Boerawa goats is polymorphic (diverse) but cannot be associated with litter size. A similar study was reported by Abdel-Rahman *et al* (2013), which stated that there are three variants of the BMP15 gene genotype, namely BB, BM, and MM with genotype frequencies of 0.46, 0.43, and 0.11 in Anglo-Nubian goats, whose BB genotype has a higher litter size than BM and MM.

Table 4: Average Litter Size of Boerawa goats by Genotype

BMP15 gene	Number of Boerawa Goats	Flat Litter Size
CC	18	1,23±0,15
CG	2	1,45±0,07

The results of research by Mishra *et al*. (2017) have found polymorphic BMP15 genes in exon 2 segments and reportedly affect litter size. The mutated FecXG gene resulted in BMP15 gene polymorphism in local goats (Hidayat, *et al*., 2015). There are two genotypes produced, namely ++ (homozygous wild type) and G + (heterozygous). Similar research results have also been reported by Maskur and Arman (2010) that fat-tailed Lombok sheep carry FecXG mutase from the BMP15 gene. The results of BMP15 gene analysis locus 2 for Senduro goat samples are monomorphic (uniform) and cannot be associated with litter size. The results of this study are similar to Farag *et al*. (2013) in that there was no finding of FecXI locus polymorphism (BMP15) in Egyptian goats. Rahayu (2011) has also reported that no polymorphisms of BMP15 and GDF9 genes were found in Kacang goats. The results of Mulyono *et al*'s (2019) research showed that the results of BMP15 research (exon 1) are monomorphic (uniform) and cannot be associated with litter size. Hakim (2019) reported the discovery of BMP15 gene polymorphism in PE goats in BPT-HPT Pelaihari, South Kalimantan, SNP which was found to be used as a determinant of livestock genotype but could not yet be used as a selection tool. Similar research results were reported by Hidayat (2015) that there is a correlation between FecXG gene polymorphism to the prolific nature of local goats, resulting in each genotype having differences in litter size.

The results of the BMP15 gene locus 2 showed mutations in the BMP15 gene in Boerawa goats (BC11 and BC18) causing changes in amino acid bases (TCA = Serine - TGA = stop codon) which produced the G allele. Mutations in the BMP15 gene namely stop codon in the 239th amino acid (Q239R) have been reported by Chu *et al*. (2007) and produce the G allele has been reported Maskur and Arman (2010). Mutations in the BMP15 gene are due to changes in the base Cytosine (C) to Thymine (T) at position 718

(Chu *et al*., 2007). Similar research results have also been reported by Davis (2005), there has been a mutation of the BMP15 gene that causes amino acid changes (CAG = Glutamine-TAG = stop codon). It is further stated that changes in amino acids cause BMP15 to lose function in inhibiting the expression of FSH (Follicle Stimulating Hormone) receptors in granulosa cells experienced, which consequently opens up opportunities for increased FSH sensitivity and increases BMP15 gene expression. Fabre *et al*. (2006) reported that the relationship between BMP15 mutations with ovulation rate is to increase reduced BMP15 activity, ovulation rate increases, but if BMP15 levels are too low it results in total dysfunction. The fecundity gene that controls this prolific trait is the BMP15 gene. Chu *et al*. (2007) stated that there are differences in gene control patterns on the proliferation mechanism in goat and sheep breeds, but still controlled by the BMP15 gene.

CONCLUSION

In the Boerawa goat sample (BC 11) mutated, there was a change in the base from Cytosine (C) to Guanine (G) at the position of 709 bp (C709G). In the Boerawa goat sample (BC 18) also mutated, there was a change in the base from Cytosine (C) to Guanine (G) at the position of 707 bp (C707G). In the Senduro goat samples, no mutations were found, because there was no change in base for all Senduro goat samples. All samples of Senduro goats carry the base Cytosine (C). From the identification of the BMP15 gene in Senduro goats from UPT PT-HMT Singosari, Malang Regency is uniform (monomorphic). The identification of the BMP15 gene for Boerawa goats is polymorphic, but cannot be associated with litter size.

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NOVELTY STATEMENT

The genes and restriction enzymes used in this research are commonly used by other researchers, however this study observes different loci.

AUTHORS CONTRIBUTION

Heri Damayanti conceived the study, collected and analyzed data, interpreted the results, and drafted the manuscript, formatted it, and approved the final manuscript. W. A. Septian, G. Prasetyo, A. Z. Efendi, A. Ardiantoro, and N. Hidayah conceived the study, conducted the statistical analysis and interpreted the results. T. E. Susilorini and Suyadi conceived the original idea and approved the final manuscript.

Coflict of Interest

Authors declare no conflict of interest.

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