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Research article

EARLY DETECTION OF CANDIDATE GENES FOR BODY WEIGHT IN INDONESIAN CATTLE BREEDS WITH GENOME-WIDE ASSOCIATION STUDY (GWAS)

Widya Pintaka Bayu PUTRA[1,2*], Hartati HARTATI[3], Mariyono MARIYONO[3], Ronny Rachman NOOR[4], Cece SUMANTRI[4], Endang Tri MARGAWATI[2]

[1]Bogor Agricultural University, Postgraduate School of Faculty Animal Science, Study Program of Animal Production and Technology Science, Bogor, Indonesia; [2]National Research and Innovation Agency (BRIN), Research Center for Applied Zoology, Bogor, Indonesia; [3]National Research and Innovation Agency (BRIN), Research Center for Animal Husbandry, Bogor, Indonesia; [4]Bogor Agricultural University, Faculty of Animal Science, Department of Animal Production and Technology, Bogor, Indonesia

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Genome-wide association study (GWAS) was used to detect candidate genes affecting economic traits in livestock. GWAS can detect single nucleotide polymorphisms (SNPs) in all chromosome regions. This study aimed to determine the genetic markers for body weight by GWAS in native cattle breeds of Indonesia. The Illumina Bovine 50K BeadChip was used to determine the candidate genes in three mixed-sex Indonesian cattle breeds of Bali (16 animals), Madura (16 animals), and Ongole grade (13 animals). All animals were raised at the Pasuruan Regency, East Java, Indonesia breeding station. The GWAS was performed in pooled sample of animals (45 animals) with the general linear model (GLM) method using SNP markers with minimum allele frequency (MAF) values more than 0.05 by TASSEL 5.0. software. Therefore, the body weight of cattle at 1 to 3 years of age was collected for each animal for computing Manhattan plot graphics. This research found that *SUGT1*, *SF3A3*, and *DSCAM* genes were detected as potential genetic markers for body weight in cattle breeds of Indonesia. The *SUGT1* and *DSCAM* genes were monomorphic in Bali cattle (*Bos javanicus*). In addition, both genes were significantly associated ($P<0.05$) with the body weight of Ongole-grade cattle (*Bos indicus*) at three years of age. However, the *SF3A3* gene was significantly ($P<0.05$) associated with body weight of Madura cattle (*Bos indicus*) at 2 and 3 years of age. In conclusion, the GWAS of pool animals reveals three candidate genes significantly associated with body weight in many cattle breeds of Indonesia. Further study to detect SNPs in candidate genes with sequencing method is essential to apply these findings practically.

Keywords: Body weight, genetic markers, GWAS, Indonesian cattle breeds.

*Corresponding author: e-mail: widya.putra.lipi@gmail.com

INTRODUCTION

Indonesia has many native cattle breeds for meat production. In 2022, Indonesia had 18,610,148 heads of cattle with 498,923.14 tons of beef production [1]. However, the total beef consumption in Indonesia in 2022 was about 440,706 tons [2]. Hence, a deficit of 58,217.14 tons (12%) was imported from other countries. Beef production can be increased by the selection of breeding programs in the native cattle breeds. Bali (*Bos javanicus*), Madura (*Bos indicus*), and Ongole grade (*Bos indicus*) cattle are three Indonesian native breeds that are kept for meat production purposes. Wiyatna [3] reported that carcasses obtained from Bali, Madura, and Ongole grade bulls reached weights of 182.68 kg, 138.26 kg, and 180.76 kg, respectively.

The genetic improvement in livestock can be assessed with the genome-wide association study (GWAS) method [4]. GWAS can detect many single nucleotide polymorphisms (SNP) in all chromosomes concerning economic traits, including body and carcass weights. The present report used the GWAS to detect the genetic markers for birth weight in Ongole grade [5] and Bali [6] cattle of Indonesia. Moreover, many previous studies reported the genetic markers for body weight with GWAS in Nellore (*Bos indicus*) [7,8], Braunvieh (*Bos taurus*) [9], and Charolais (*Bos taurus*) [10] cattle breeds.

Unfortunately, no studies are reporting the new candidate genes for body weight in native cattle breeds of Indonesia by utilization of GWAS. Hence, exploring the new genetic markers is essential to obtain new candidate genes controlling the economic traits of cattle. This study aimed to determine the genetic markers for body weight of Indonesian native cattle at 1 to 3 years of age using Illumina Bovine 50K BeadChip. The results of the present study are essential for developing a molecular selection program in the native cattle of Indonesia based on genomic information.

MATERIAL AND METHODS

Ethical approval

The study was approved by the Animal Ethics Committee of the Indonesian Agency for Agricultural Research and Development (Balitbangtan/Lolitsapi/Rm/ll/2018).

Animals and research site

Fourty-five (45) animals of mixed-sex cattle, including Bali (n=16), Madura (n=16), and Ongole grade (n=13) breeds were used for the genomic analysis. The cattle were raised at the breeding station (previously *Loka Penelitian Sapi Potong*), Grati District, Pasuruan Regency, East Java Province of Indonesia. This place is located at latitude 7.30'-8.30' S and 112°30'-113°30' E and at 4-5 m asl. This area has climatological parameters of 25-31 °C air temperature, 70% relative humidity, and 1000-1400 mm/year of rainfall.

Management of animals

The animals were kept in the barn with a natural mating system. The ratio of 1 bull and 15 to 20 cows per stall was achieved. Forage feed was given at about 3-5 kg/ head consisting of Elephant grass (*Pennisetum purpureum*) and *ad libitum* rice straw. The standard nutritional content of 9-10% of crude protein (CP), 58-60% of total digestible nutrient (TDN), and 19-22% of crude fiber (CF) were given to the cattle from birth to the weaning period. The standard nutritional content of 10-11% of CP, 58-60% of TDN, and 17-19% of CF was given to cattle from weaning to adulthood. About 30% of concentrate (3% of body weight) and 70% of forages were combined in the feed ration while fresh water was given *ad libitum*. Regular medical examinations and vaccinations were carried out. The composition of concentrate feed that was used for the animals during the study is shown in Table 1.

Table 1. Composition of the concentrate feed

Composition	Percent (%)
Chalk	1.89
Salt	1.89
Rice bran	24.75
Slamper corn	20.51
Coffee peel	4.98
Palm kernel cake	9.70
Copra cake	10.16
Cassava flour	10.16
Destillers dried grains with soluble	7.98
Corn gluten feed	7.98

Body weight

The body weights of the animals at one year of age (BW1), two years of age (BW2), and three years of age (BW3) were collected using a digital weighing scale (Sonic NI-7, China). The average of body weight in the experimental animals is presented in Table 2. The correction factor of sex was performed for the body weight of female animals using a mathematical formula [11] :

$$\mathbf{CF}_{sex} = \frac{\overline{\mathbf{X}}_{male}}{\overline{\mathbf{X}}_{female}}$$

$$\mathbf{BW}_c = \mathbf{BW} \times \mathbf{CF}_{sex}$$

Where CF_{sex} is the correction factor of sex, BW_c is the corrected body weight, BW is the actual body weight, X_{male} is the average body weight in males, X_{female} is the average body weight in females.

Table 2. Average body weight in three cattle breeds of Indonesia

Breed	N	BW1	BW2	BW3
Bali	16	116.62±27.82a	221.76±55.97a	323.30±57.26a
Madura	16	100.30±24.48a	189.39±58.23a	271.53±94.73a
Ongole grade	13	193.37±53.45b	357.35±68.12b	478.01±91.61b
Total	45	132.99±53.01	249.42±92.30	349.59±117.49

N: number of animals; **BW1:** body weight (kg) at one year of age; **BW2:** body weight (kg) at two years of age; **BW3:** body weight (kg) at three years of age. Superscripts in the different column related to significant differences ($P<0.05$)

Genomic analysis

An amount of 5 µL of the blood sample was collected from each animal by jugular venepuncture using venoject and vacutainer tubes containing EDTA (BD Vacutainer, USA). Thus, the DNA samples were extracted from the collected blood samples with a DNA Extraction Kit (Geneaid, Taiwan) following the manufacturer's protocols. The DNA samples with the clarity (260/280 nm) of 1.8-2.0 were selected for genome analysis with Illumina Bovine 50K BeadChip (Macrogen, South Korea).

Bioinformatics

Two PLINK format ped and map files were obtained from the GWAS in pool animals through GenomeStudio software (Illumina, USA) [12]. The quality control for total SNP markers (53,218 sites) was performed by TASSEL 5.0 software (The Buckler Lab at Cornell University, USA) [13]. The SNP markers with a minimum allele frequency (MAF) value of less than 5% were not used for the genome analysis [14]. This study selected 24,347 SNP markers (MAF>5%) for analysis. The quantile-quantile plots (QQ-plots) and Manhattan plots graphics of three traits (BW1, BW2, BW3) were computed with the general linear model (GLM) method using TASSEL 5.0 software. In addition, the SNP marker with the highest Bonferroni threshold value was described as the best SNP marker for the evaluated traits. Referring to Becker [15], detection of the candidate genes was performed using the Bos taurus genome sequence (assembly: Btau_4.6.1 and Btau_5.0.1) that was accessed at National Center for Biotechnology Information (NCBI) website (https://www.ncbi.nlm.nih.gov). Moreover, the gene interaction network among candidate genes was performed using STRING v.11 software (Global Core Biodata Resource, USA) [16].

Data analysis

The genetic diversity of selected SNP markers such as genotype frequency, allele frequency, observed heterozygosity (Ho), expected heterozygosity (He), number of

effective alleles (n_e), polymorphic informative content (PIC), and Chi-square (χ^2) values [17-20] was analyzed. The data records of body weight were used for the association study with SPSS 16.0 software [21] using a mathematical formula:

$$\mathbf{Y}_{ijk} = \mu + \mathbf{G}_i + \mathbf{B}_j + \mathfrak{E}_{ijk}$$

Where Y_{ijk} is the observed traits, μ is the overall mean, G_i is the effect of i^{th} genotype, B_j is the effect of j^{th} breed, and $\mathfrak{E}_{ijk}$ is the experimental error.

RESULTS

The QQ-plots of the BW2 trait were spread under the threshold line. While the QQ-plots of BW1 and BW3 traits were spread upper the threshold line (Figure 1). However, many SNP marker plots in the BW1 were spread under the threshold line. In addition, the significance of SNP markers (P<0.0001) in each trait was determined with the P-value of $4.4E^{-3.5}$ (BW2), $3.8E10^{-4}$ (BW1), and $4.4E10^{-6}$ (BW3). Therefore, the Manhattan plots of body weights reveal the maximum Bonferroni corrected threshold of 4.0 (BW1), 3.6 (BW2), and 6.0 (BW3), as shown in Figure 2. Hence, three SNP markers of ARS-BFGL-NGS-114401 (BTA12), ARS-BFGL-NGS-43764 (BTA3), and ARS-BFGL-NGS-39460 (BTA1) were selected as the three potential SNP markers for body weight in animal under study because of highest – Log_{10}(P) value.

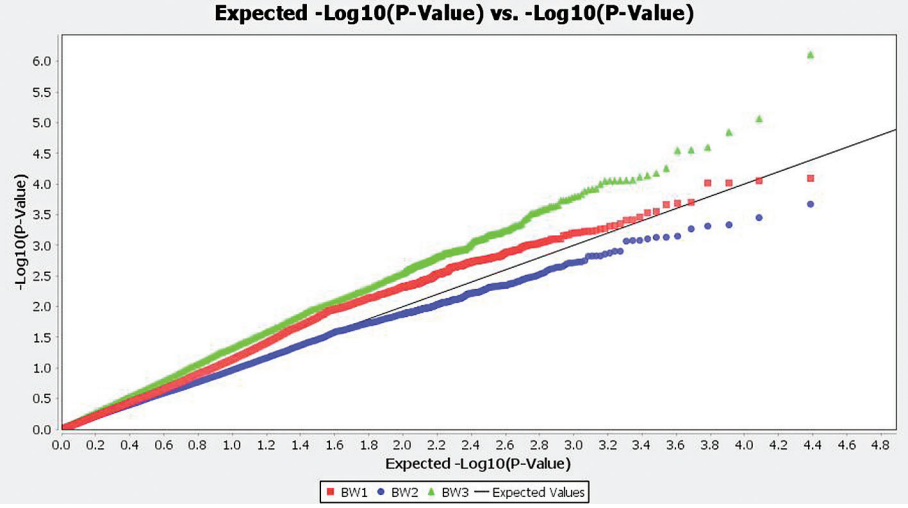

Figure 1. QQ-plots of body weight at one year **(BW1)**, two years **(BW2)**, and three years **(BW3)** of age in the pooled animals. Dots indicate -Log_{10} (p) values for individual SNPs. The line indicates the expected values when confirming the null hypothesis of the absence of associations.

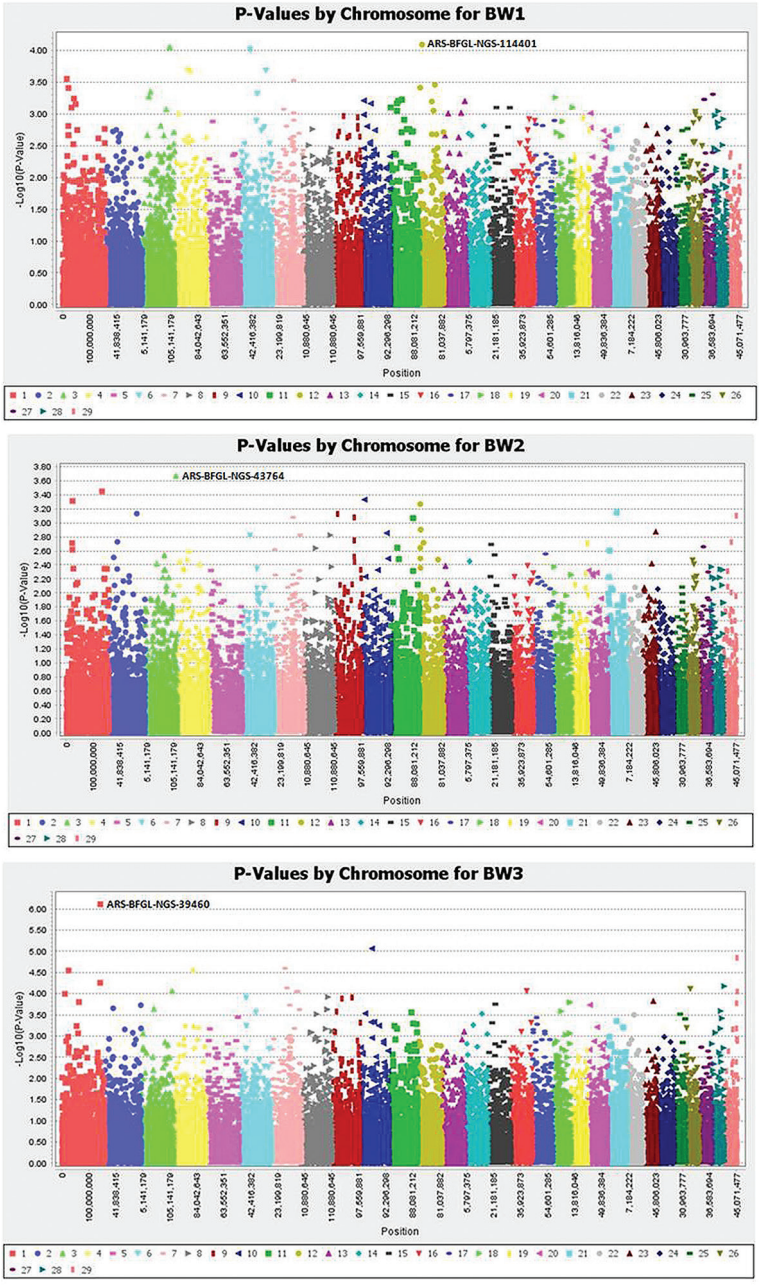

Figure 2. The best SNP markers in Manhattan plot for body weight at one year **(BW1)**, two years **(BW2)**, and three years **(BW3)** of age in pool animals. The X-axis shows chromosomal positions. The Y-axis shows – Log_{10}(p) values. The colored dots indicate the SNP markers at different chromosomes.

Table 3. Genetic diversity of three selected SNP markers in three cattle breeds of Indonesia

SNP marker	Parameter	Cattle breed (N)		
		Bali (16)	Madura (16)	Ongole grade (13)
ARS-BFGL-NGS-114401	Frequency of CC genotype	0.00	0.00	0.00
	Frequency of TT genotype	1.00	0.81	0.62
	Frequency of CT genotype	0.00	0.19	0.38
	C allele frequency	0.00	0.09	0.19
	T allele frequency	1.00	0.91	0.81
	Observed heterozygosity (Ho)	0.00	0.19	0.38
	Expected heterozygosity (He)	0.00	0.17	0.31
	Number of effective alleles (ne)	1.00	1.20	1.45
	Polymorphic informative content (PIC)	0.00	0.16	0.26
	Chi-square ($\chi 2$)	-	0.17	0.74
ARS-BFGL-NGS-43764	Frequency of AA genotype	0.69	0.75	0.38
	Frequency of GG genotype	0.00	0.00	0.00
	Frequency of AG genotype	0.31	0.25	0.62
	An allele frequency	0.84	0.87	0.69
	G allele frequency	0.16	0.13	0.31
	Observed heterozygosity (Ho)	0.31	0.25	0.61
	Expected heterozygosity (He)	0.26	0.22	0.43
	Number of effective alleles (ne)	1.36	1.28	1.74
	Polymorphic informative content (PIC)	0.23	0.19	0.33
	Chi-square ($\chi 2$)	0.55	0.33	2.57
ARS-BFGL-NGS-39460	Frequency of CC genotype	0.00	0.00	0.15
	Frequency of TT genotype	1.00	0.69	0.15
	Frequency of CT genotype	0.00	0.31	0.70
	C allele frequency	0.00	0.84	0.23
	T allele frequency	1.00	0.16	0.77
	Observed heterozygosity (Ho)	0.00	0.31	0.15
	Expected heterozygosity (He)	0.00	0.26	0.35
	Number of effective alleles (ne)	1.00	1.36	1.55
	Polymorphic informative content (PIC)	0.00	0.23	0.29
	Chi-square ($\chi 2$)	-	0.55	4.17

N: number of animals

Two SNP markers of ARS-BFGL-NGS-114401 and ARS-BFGL-NGS-39460 were monomorphic in Bali cattle (Table 3). A SNP marker of ARS-BFGL-NGS-114401 was polymorphic in animals under study with the PIC value of 0.16 (Madura) and

0.26 (Ongole grade), respectively. A SNP marker of ARS-BFGL-NGS-43764 was polymorphic in all cattle breeds with the PIC value of 0.23 (Bali), 0.19 (Madura) and 0.33 (Ongole grade). In addition, a SNP marker of ARS-BFGL-NGS-39460 was polymorphic in animals under study with the PIC value of 0.23 (Madura) and 0.29 (Ongole grade). Generally, three selected SNP markers in the present study were in a genetic equilibrium (χ^2<5.99).

According to the bovine genome database (assembly: Btau_4.6.1 and Btau_5.0.1), three selected SNP markers were located at the intron 1 of *SUGT1* (*SGT1 Homolog, MIS12 Kinetochore Complex Assembly Cochaperone*) gene for ARS-BFGL-NGS-114401; intron 2 of *SF3A3* (*Splicing Factor 3A Subunit 3*) gene for ARS-BFGL-NGS-43764 and intron 23 of *DSCAM* (*Down Syndrome Cell Adhesion Molecule*) gene for BFGL-NGS-39460 (Table 4). Therefore, those genes had a related interaction, as shown in Figure 3. At least five genes of *HSP90AA1* (*Heat Shock Protein 90 Alpha Family Class A Member 1*), *BCAS2* (*Breast Carcinoma-Amplified Sequence 2*), *CD2BP2* (*CD2 Antigen Cytoplasmic Tail-binding Protein 2*), *ASCC3* (*Activating Signal Cointegrator 1 Complex Subunit 3*) and *UNC5C* (*Unc-5 Netrin Receptor C*) have related interaction with *SUGT1, SF3A3* and *DSCAM* genes.

Table 4. The candidate genes for body weight of pooled cattle based on the best SNP markers

Trait	SNP marker	BTA	Position	Allele	MAF	Gene	Region	Range
BW1	ARS-BFGL-NGS-114401	12	9,728,887	C/T	0.09	*SUGT1*	intron 1	9,727,256 – 9,768,013[a]
BW2	ARS-BFGL-NGS-43764	3	114,170,005	A/G	0.20	*SF3A3*	intron 2	114,168,834 – 114,195,151[a]
BW3	ARS-BFGL-NGS-39460	1	142,475,932	C/T	0.20	*DSCAM*	intron 23	142.190.688 – 142,524,692[b]

[a]**assembly**: Btau_4.6.1 (GCF_000003205.5); [b]**assembly**: Btau_5.0.1 (GCF_000003205.7);BTA: Bos taurus autosome; MAF: minimum allele frequency; **BW1**: body weight (kg) at 1 year of age; **BW2**: body weight (kg) at 2 years of age; **BW3**: body weight (kg) at 3 years of age

The SNP marker of ARS-BFGL-NGS-114401 (SUGT1 gene) was significantly associated (P<0.05) with the BW2 trait of Madura cattle and the BW3 trait of Ongole grade cattle (Table 5). The SNP marker of ARS-BFGL-NGS-43764 (SF3A3 gene) was significantly associated (P<0.05) with BW2 and BW3 traits of Madura cattle. In comparison, the SNP marker of BFGL-NGS-39460 (DSCAM gene) was significantly associated (P<0.05) with the BW3 trait of Ongole grade cattle. The heterozygous animals in the SUGT1 and SF3A3 genes commonly have higher body weight than homozygous animals. Interestingly, three genotypes were observed in the Ongole grade cattle by SNP marker of ARS-BFGL-NGS-39460.

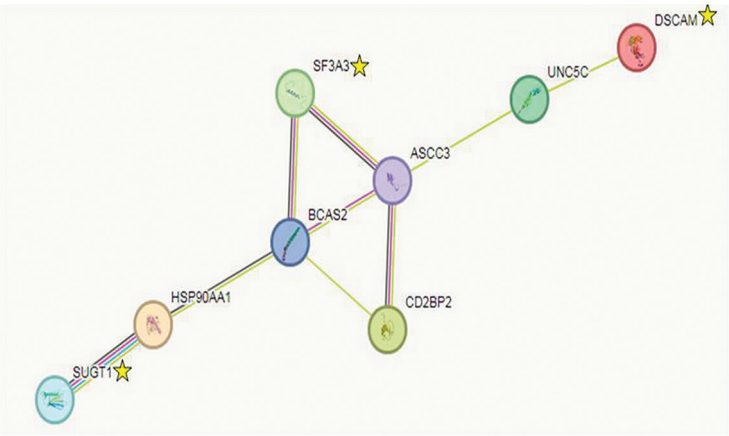

Figure 3. Gene interaction network between the candidate genes under study (star symbol) and other related genes

Table 5. Association between the three selected SNP markers and body weight in three cattle breeds of Indonesia

Breed	SNP marker	Genotype (N)	BW1	BW2	BW3
Bali	ARS-BFGL-NGS-43764	AA (11)	110.30±24.49	196.83±42.18	304.73±55.45
		AG (5)	130.52±32.42	276.62±42.74	364.16±39.66
Madura	ARS-BFGL-NGS-114401	TT (13)	96.34±22.16	173.29±32.93^{a}	244.70±67.56
		CT (3)	117.47±31.72	259.17±99.71^{b}	387.82±122.26
	ARS-BFGL-NGS-43764	AA (11)	93.47±21.49	172.20±35.16^{a}	241.10±49.71^{a}
		AG (5)	115.32±26.14	227.22±83.82^{b}	338.49±139.00^{b}
	ARS-BFGL-NGS-39460	TT (11)	105.95±20.90	182.09±47.32	255.05±80.47
		CT (5)	87.86±29.58	205.46±81.55	307.80±122.76
Ongole grade	ARS-BFGL-NGS-114401	TT (8)	190.29±61.63	342.55±80.43	426.64±78.19^{a}
		CT (5)	198.30±43.28	381.02±38.24	560.20±27.51^{b}
	ARS-BFGL-NGS-43764	AA (5)	175.34±66.87	321.18±59.45	400.12±63.24
		AG (8)	204.64±44.33	379.95±66.47	526.69±71.14
	ARS-BFGL-NGS-39460	CC (2)	140.40±72.83	303.15±85.77	415.80±111.02^{a}
		CT (9)	191.31±42.98	360.31±69.86	484.06±96.24^{ab}
		TT (2)	255.60±28.28	398.20±1.70	513.00±61.38^{b}

N: number of animals; **BW1:** body weight (kg) at one year of age; **BW2:** body weight (kg) at two years of age; **BW3:** body weight (kg) at three years of age. Superscripts in the same column differ significantly ($P<0.05$)

DISCUSSION

The Bonferroni corrected threshold value of 3.8 to 6.0 was used to select the SNP marker of body weight in the animals under study. Previous studies reported that GWAS can determine the genetic marker of body weight with the Bonferroni corrected threshold of $-\text{Log}_{10}$ (p) = 4.0 to 5.0 in Nellore [8], Charolais [22] and Braunvieh [23] beef cattle. The GWAS in Russian cattle reveals the Bonferroni corrected threshold of $-\text{Log}_{10}$ = 5.0 to 6.0 of the body weight [24]. The Bonferroni corrected threshold can be affected by statistical analysis models used to select SNP markers [25]. The SNP markers with the highest Bonferroni corrected value also indicate the most significant makers of observed traits. In this study, the best SNP markers for the body weight of Indonesian native cattle were located at BTA1, BTA3, and BTA12. According to previous studies, BTA12 has the SNP markers significantly associated with body weight gain [8] and yearling height [26] of cattle. Many SNP markers for the weight of cattle were determined from BTA3 of Nellore cattle [8], BTA11, BTA22, and BTA27 of Braunvieh and Canchim cattle [23,27], BTA 5 of Russian cattle [25], and BTA14 of European cattle [28]. In Charolais cattle, mostly the SNP markers for yearling weight (BW1) were determined from BTA6 [10]. Moreover, the BTA1 and BTA21 of Brahman cattle have the SNP markers associated with weaning and yearling weights, respectively [29]. In *Bos taurus* cattle, many SNP markers in the BTA1 (ARS-BFGL NGS-103884, ARS-BFGL-NGS-118725, ARS-BFGL-NGS-94206), BTA3 (Hapmap43441 BTA-103289) and BTA12 (ARS-BFGL-NGS-40668) are the genetic markers for weaning weight [30].

This study obtained three novel candidate genes of *SUGT1*, *SF3A3*, and *DSCAM* genes based on GWAS. The *SUGT1* gene is essential to the immune response [31]. According to the BTA12 sequence (GenBank: NC_037339.1), the length of the bovine *SUGT1* geneis 41,878 bp with 14 exons. In cattle, the genetic mutation in the *SUGT1* gene (g.11102143A>G) is associated with embryonic mortality rate with the G allele is undesirable [32]. The *SF3A3* gene is essential in the pre-mRNA splicing or transcriptional control [33]. According to the BTA3 sequence (GenBank: NC_037330.1), the length of bovine *SF3A3* is 26,317 bp with 17 exons. In humans, the genetic mutation in the *SF3A3* gene can influence the risk of ovarian cancer [34]. Therefore, the *DSCAM* gene plays a role in neuronal self-avoidance and promotes repulsion between specific neuronal processes of either the same cell or the same subtype of cells [35]. According to the BTA1 sequence (GenBank: NC_037328.1), the bovine DSCAM gene has a length of 690,467 bp with 33 exons. In humans, the genetic mutation in the DSCAM gene can affect Hirschsprung disease [36]. In mice, the genetic mutation in the *DSCAM* gene affects the nervous system formation and several neurological defects, such as ataxia and seizures [37]. On the other hand, the *DSCAM* has also been implicated in cell migration of embryonic cephalic cells destined to become neuroectoderm in zebrafish [38].

Three candidate genes for body weight in animals under study are survival-related genes that play essential roles in survivability traits (immune response, transcriptional activity, and nervous system). Interestingly, *SUGT1*, *SF3A3,* and *DSCAM* genes can express the related protein by involving many related genes for interaction. *SUGT1*and *HSP90AA1* are immune-associated genes with related protein expression [39]. In general, the *Heat Shock* family genes can interact with the *BCAS2* gene to regulate the protein stability of cells [40]. *DSCAM* and *UNC5C* are crucial genes for developing the nervous system and neuronal growth [41]. In general, the PIC value in *SUGT1*, *SF3A3,* and *DSCAM* genes in Indonesian cattle is under the moderate to high category. Hence, the genetic diversity of these genes are high and possible to improve the body weight of cattle with molecular selection. The PIC value can be categorized into low (<0.10), moderate (0.11-0.30), and high (>0.30) categories [18].

The early investigation with a limited sample revealed that three survival-related genes in this study could influence the body weight of the animal under study. In the tropical climate, the survival-related genes in Bali, Madura, and Ongole grades can influence growth traits. A study in Bali cattle revealed that the *HSP70* gene affects the body weight and body measurements traits [42]. Additionally, the *Interleukin-2* gene is one of the immune-related genes that can affect cattle's milk production [43]. Hence, survival-related genes can indirectly influence the growth traits of tropical cattle breeds.

CONCLUSION

Three survival-related genes of *SUGT1, SF3A3,* and *DSCAM* were significantly associated with body weight in native cattle of Indonesia. These genes have the moderate to high category of PIC value. Therefore, the survival-related genes under study have the potency for the candidate genes of growth traits in tropical cattle of Indonesia. Hence, designing of specific primer pairs for detecting of SNP marker with sequencing analysis is important to manage a molecular selection with low cost and easily. However, in-depth research involving large samples is essential to obtain several candidate genes for growth traits accurately.

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Authors' contributions

WPBP and HH conducted the field study design and conception, data acquisition, analysis and interpretation of data. MM formulated the feed ration. HH, MM, RRN, CS and ETM revised the manuscript draft All authors read and approved the final manuscript.

Declaration of conflicting interests

The author(s) declared no potential conflicts of interest with respect to the research, authorship, and/or publication of this article.

ORCID iDs

Widya Pintaka Bayu Putra https://orcid.org/0000-0002-1102-6447
Hartati Hartati https://orcid.org/0000-0002-6396-6801
Mariyono Mariyono https://orcid.org/0000-0003-4668-6768
Ronny Rachman Noor https://orcid.org/0000-0001-8795-2992
Cece Sumantri https://orcid.org/0000-0002-5729-1254
Endang Tri Margawati https://orcid.org/0000-0002-4679-6783

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RANO OTKRIVANJE GENA POTENCIJALNO ODGOVORNIH ZA TELESNU TEŽINU INDONEZIJSKIH RASA GOVEDA POMOĆU GENOMSKE STUDIJE (GWAS)

Widya Pintaka Bayu PUTRA, Hartati HARTATI, Mariyono MARIYONO, Ronny Rachman NOOR, Cece SUMANTRI, Endang Tri MARGAWATI

Studija asocijacije na nivou genoma (GWAS) je korišćena za otkrivanje gena kandidata koji utiču na ekonomske osobine. GWAS može otkriti polimorfizme pojedinačnih nukleotida (SNP) u svim regionima hromozoma. Ova studija je imala za cilj da odredi genetske markere za telesnu težinu autohtonih rasa goveda Indonezije pomoću GWAS-a. *Illumina Bovine 50K BeadChip* je korišćen za određivanje gena kandidata u tri mešovite indonežanske rase goveda Bali (16 životinja), Madura (16 životinja) i Ongole (13 životinja). Sve životinje su uzgajane u Pasuruan Regency, Istočna Java, Indonezija. GWAS je izveden u objedinjenom uzorku životinja (45 životinja) metodom opšteg linearnog modela (GLM) korišćenjem SNP markera sa vrednostima minimalne frekvencije alela (MAF) više od 0,05 prema TASSEL 5,0. softveru. U tom cilju je zabeležena telesna težina goveda u dobi od 1 do 3 godine, prikupljena za svaku životinju za potrebe izračunavanje *Manhattana* grafikona. Ovo istraživanje je otkrilo da su geni SUGT1, SF3A3 i DSCAM otkriveni kao potencijalni genetski markeri za telesnu težinu Bali, Madura i Ongole goveda u Indoneziji. Geni SUGT1 i DSCAM bili su monomorfni kod balijskog goveda (*Bos javanicus*). Pored toga, oba gena su bila značajno povezana ($P<0,05$) sa telesnom težinom Ongole goveda (*Bos indicus*) u dobi od tri godine. Međutim, gen SF3A3 je bio značajno ($P<0,05$) povezan sa telesnom težinom Madura goveda (*Bos indicus*) u dobi od 2 i 3 godine. U zaključku, GWAS kod životinja otkriva tri gena kandidata značajno povezana sa telesnom težinom kod mnogih rasa goveda u Indoneziji. Dalja studija za otkrivanje SNP-a u genima metodom sekvenciranja je od suštinskog značaja za praktičnu primenu ovih nalaza.