

Research Article



A 19 bp Indel of the *PLAG1* as a Potential Marker for Growth Performance in Indonesian Ongole Cattle

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Abstract | This study investigated the association of *PLAG1* gene polymorphisms with growth-related traits in Indonesian Ongole cattle maintained at the Institute for Good Breeding Practice and Green Animal Fodders (BPTU-HPT) Sembawa, Indonesia. A total of 101 animals were genotyped for two *PLAG1* polymorphisms, g.48308C>T and a 19 bp insertion/deletion (g.32212). Genotype frequencies for g.48308C>T were CC (n = 16), CT (n = 50), and TT (n = 35), whereas those for the 19 bp indel were DD (n = 89) and ID (n = 12), with no II genotype detected. Association analysis revealed that the 19 bp indel was associated with chest girth (P = 0.042), with DD animals exhibiting greater chest girth (69.47 ± 0.48 cm) than ID animals (66.75 ± 1.35 cm). No significant associations were observed for the remaining growth traits. Similarly, the g.48308C>T polymorphism showed no significant association with any trait evaluated. Linkage disequilibrium analysis using Haploview indicated weak LD between the two loci (D' = 0.22; r² = 0.002), suggesting that they segregate largely independently in the studied population. These findings indicate a potential role of the *PLAG1* 19 bp indel in body measurement. However, the highly unbalanced genotype distribution and absence of the II genotype warrant cautious interpretation. Further validation in larger populations is required before this variant can be considered for marker-assisted selection in PO cattle.

Keywords | Chest girth, Growth traits, Indel, Indonesian Ongole, *PLAG1*, Beef cattle

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INTRODUCTION

Beef cattle production plays a strategic role in supporting national food security and meeting the increasing demand for animal-derived protein in Indonesia. Nevertheless, domestic beef production remains insufficient to satisfy national consumption requirements, resulting in a supply deficit of approximately 263 thousand tons annually (BPS, 2024). Enhancing the genetic merit

of local cattle populations is therefore considered one of the most sustainable long-term approaches for improving productivity, feed efficiency, carcass quality, and adaptation to tropical production environments (Azovtseva *et al.*, 2024). Recent advances in livestock genomics have further accelerated the implementation of genomic-assisted breeding strategies aimed at improving economically important traits in beef cattle under diverse environmental conditions (Li *et al.*, 2024).

Indonesian Ongole cattle, a *Bos indicus* derived breed widely distributed in Indonesia, are recognized for their adaptability to hot and humid climates, resistance to environmental stressors, and ability to survive under low-input production systems (Putri *et al.*, 2021; Irma *et al.*, 2025). Despite these adaptive advantages, PO cattle generally exhibit moderate growth performance and carcass productivity compared with specialized commercial beef breeds. Improvement of productive efficiency in PO cattle requires an integrated approach involving nutrition, management, and genetics. Among these factors, genetic background exerts substantial influence on body conformation, growth rate, carcass composition, and feed utilization efficiency (Zhou *et al.*, 2019; Borges *et al.*, 2025). Consequently, identification of functional genetic markers associated with growth-related phenotypes has become increasingly important for accelerating genetic improvement in Indonesian tropical cattle populations.

Molecular breeding approaches, particularly marker-assisted selection (MAS), enable the incorporation of DNA polymorphisms into conventional selection programs to improve breeding accuracy and shorten generation intervals (Lamido *et al.*, 2024). Among candidate genes associated with bovine growth traits, Pleomorphic adenoma gene 1 (*PLAG1*) has received considerable attention due to its pleiotropic effects on body size, carcass traits, and reproductive performance. The *PLAG1* gene, located on bovine chromosome 14 (BTA14), encodes a zinc-finger transcription factor involved in the regulation of insulin-like growth factor pathways, cellular proliferation, embryonic development, and skeletal growth (Takasuga, 2016; Fink *et al.*, 2017). Functional studies have demonstrated that *PLAG1* regulates growth-associated pathways through modulation of IGF2 expression and related endocrine mechanisms (D'Occhio *et al.*, 2024). Variants within or near *PLAG1* have consistently been identified as major quantitative trait loci (QTL) affecting stature, body weight, carcass composition, and puberty traits in cattle populations worldwide (Karim *et al.*, 2011; Fortes *et al.*, 2012; Engle and Hayes, 2022). In addition, recent evidence indicates that *PLAG1* may also contribute to muscle development, adipogenesis, and meat quality regulation through interactions with metabolic signaling pathways (Yu *et al.*, 2025).

Several polymorphisms within *PLAG1*, including single nucleotide polymorphisms (SNPs) and insertion/deletion (indel) variants, have been associated with economically important growth traits across *Bos taurus* and *Bos indicus* breeds. Previous studies reported significant associations between *PLAG1* variants and body measurements in Brahman cattle (Trilaksono *et al.*, 2024), body weight in Madura and Bali cattle (Hartati *et al.*, 2026), and

skeletal development traits in Chinese cattle populations (Xu *et al.*, 2018; Zhong *et al.*, 2019). However, despite the economic and genetic importance of PO cattle, information regarding *PLAG1* polymorphisms and their association with growth performance in this breed remains limited. Furthermore, the effects of *PLAG1* variants appear to be breed-dependent, likely due to differences in genetic background, linkage disequilibrium structure, and environmental adaptation (Kowalewska *et al.*, 2024; Trilaksono *et al.*, 2024). Therefore, the present study aimed to evaluate the association of two *PLAG1* polymorphisms, namely g.48308C>T and the g.32212 19 bp indel, with growth-related traits in Indonesian Ongole cattle. The findings of this study are expected to provide additional insight into the genetic architecture of growth traits in Indonesian cattle and support the future implementation of *PLAG1*-based molecular markers in tropical beef cattle breeding programs.

MATERIALS AND METHODS

ANIMALS, MANAGEMENT, AND PHENOTYPIC DATA

A total of 101 Indonesian Ongole cattle maintained at the Institute for Good Breeding Practice and Green Animal Fodders (BPTU-HPT) Sembawa, Indonesia, were included in this study. All animals were clinically healthy and managed under a semi-intensive production system. The daily ration consisted of approximately 3 kg of commercial concentrate and 30 kg of fresh forage grass per animal.

Phenotypic records included birth weight, body length, withers height, chest girth, hip height, corrected body weight at 750 days, mature body weight, and average daily gain (ADG). Morphometric traits were recorded according to the routine performance recording protocol of BPTU-HPT Sembawa at standardized ages, thereby minimizing age-related variation among animals. These measurements were selected because they are widely used indicators of growth performance, skeletal development, and carcass production potential in beef cattle.

DNA EXTRACTION

Genomic DNA was isolated from whole blood samples using a commercial extraction kit (Geneaid Biotech Ltd., Taiwan) following the manufacturer's instructions with slight optimization. Approximately 300 µL of blood was transferred into a 1.5 mL microtube and mixed with three volumes of red blood cell (RBC) lysis buffer. The suspension was allowed to stand for 10 minutes at room temperature and then centrifuged at 3,000 rpm for 5 minutes to remove the supernatant. The resulting pellet was resuspended in 100 µL of RBC lysis buffer and mixed with 200 µL of GB buffer to lyse the cells

completely. The tube was incubated at 60°C for 10 minutes with gentle inversion every few minutes. Afterward, 200 µL of absolute ethanol was added to the lysate and vortexed briefly before being transferred to a GD spin column placed in a 2 mL collection tube. The column was centrifuged at 14,000–16,000 rpm for 5 minutes to bind DNA to the membrane. The column was then washed twice, first with 400 µL of W1 buffer and then with 600 µL of wash buffer, each followed by short centrifugation to remove impurities. To ensure complete removal of ethanol, the column was centrifuged again for 3 minutes at maximum speed. Finally, the column was placed in a new 1.5 mL microtube, and 100 µL of pre-warmed elution buffer (60°C) was added to release the DNA. After a 3-minute incubation, the tube was centrifuged at 14,000 rpm for 30 seconds. The purified genomic DNA was then stored at –20°C for downstream analyses, including PCR amplification and genotyping.

AMPLIFICATION AND GENOTYPING OF *PLAG1* POLYMORPHISMS

Two polymorphic loci within the *PLAG1* gene, namely g.48308C>T and g.32212 (19 bp indel), were amplified using the primer pairs listed in Table 1. Polymerase chain reactions (PCR) were performed in a final volume of 25 µL containing 12.5 µL of 2× MyTaq HS Red Mix (Bioline, UK), 1 µL of each primer, 1 µL of genomic DNA, and 9.5 µL of nuclease-free water (Promega, USA). Amplification

was carried out in a MiniAmp® Thermal Cycler (Thermo Fisher Scientific, Singapore) under the following conditions: Initial denaturation at 95°C for 5 min; 35 cycles of 95°C for 30 s, 60°C for 30 s, and 72°C for 30 s; followed by a final extension at 72°C for 10 min. PCR products were separated on 1.5% agarose gels prepared in 1× TAE buffer, stained with FluoroSafe, and visualized under ultraviolet illumination. Fragment sizes were estimated using a 100 bp DNA ladder (Figure 1).

Genotyping was performed using PCR–restriction fragment length polymorphism (PCR–RFLP) and fragment size analysis. For the g.32212 (19 bp indel), the insertion (I) allele generated a 142 bp fragment, whereas the deletion (D) allele generated a 123 bp fragment (Figure 1A). Consequently, the DD genotype was identified by a single 123 bp band, the ID genotype by two bands (142 and 123 bp), and the II genotype by a single 142 bp band (Figure 1B).

For the g.48308C>T polymorphism, the 628 bp PCR product was digested with *SacII* (Figure 2A). The CC genotype produced two fragments of 522 and 106 bp, the TT genotype remained undigested and yielded a single 628 bp fragment, whereas the CT genotype displayed three fragments of 628, 522, and 106 bp (Figure 2B). Genotypes were assigned according to the resulting electrophoretic patterns.

Table 1: Primer pairs targeting two polymorphisms of *PLAG1*.

Polymorphism	Location	Primer (5' to 3')	Annealing (°C/sec.)	Amplicon (bp)	Restriction enzyme
g.48308 C>T	3' UTR	F: GCGCGTATCAGTCAGGACAT R: CCTTTGCCTGTTGCTTTCCC	58/45	628	<i>SacII</i>
g.32212 (19 bp indel)	Intron 3	F: TCCGAACAACAGGTGAGGGAGAAAT R: CCACTTCAGGGGTGCTCTAGGTTTG	60/30	142/123	-

UTR is an untranslated region.

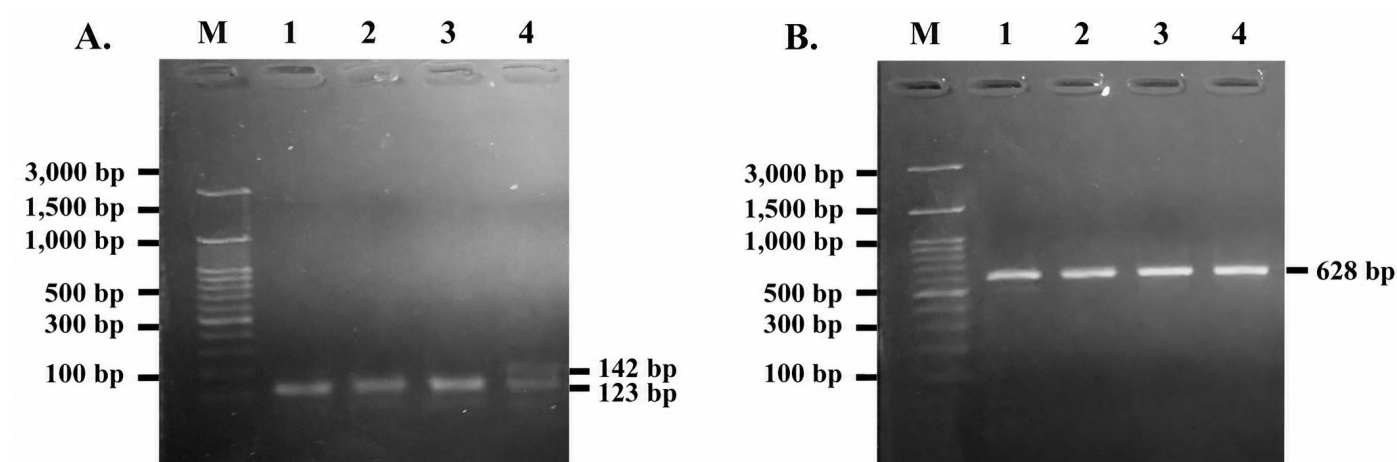


Figure 1: Agarose gel electrophoresis of PCR products targeting two *PLAG1* polymorphisms. A: PCR product targeting g.48308C>T SNP; B: PCR product targeting g.32212 (19 bp indel). M = 100 bp DNA ladder; lanes 1–4 represent PO cattle samples.

Pairwise linkage disequilibrium (LD) between the g.48308C>T SNP and the g.32212 (19 bp indel) was estimated using Haploview version 4.2 (Barrett *et al.*, 2005). LD was quantified using Lewontin's standardized disequilibrium coefficient (D') and the squared correlation coefficient (r^2).

STATISTICAL ANALYSIS

Allele and genotype frequencies were calculated according to Nei and Kumar (2000), and deviations from Hardy-Weinberg equilibrium (HWE) were assessed using the chi-square (χ^2) test.

Associations between *PLAG1* genotypes and growth traits were evaluated using the following mixed linear model implemented in MINITAB 19.1:

$$Y_{ij} = \mu + G_i + S_j + e_{ij}$$

Where Y_{ij} is the observed phenotypic value, μ is the overall mean, G_i is the fixed effect of genotype, S_j is the random effect of sire, and e_{ij} is the random residual error.

Morphometric traits were recorded within a standardized age range under the institutional performance recording system. Therefore, age at measurement was not included as a covariate. Statistical significance was declared at $P < 0.05$, and differences among least-squares means were compared

using Tukey's honestly significant difference (HSD) test.

Because the g.32212 (19 bp indel) locus exhibited a highly unbalanced genotype distribution, a post-hoc power analysis was conducted for chest girth based on the observed effect size. The difference between DD and ID genotypes (2.72 cm) corresponded to a large standardized effect (Cohen's $d \approx 0.80$). Under unequal sample sizes ($n = 89$ and $n = 12$) and $\alpha = 0.05$, the estimated statistical power ranged from 0.70 to 0.75. Although sufficient to detect moderate-to-large effects, this power remained below the conventional threshold of 0.80 and therefore warrants cautious interpretation of the observed association.

RESULTS

PLAG1 GENOTYPING OUTCOMES

Genotyping successfully identified polymorphisms at two loci of the *PLAG1* in PO cattle population. For the g.48308C>T locus, three genotypes were detected, CC ($n = 16$), CT ($n = 50$), and TT ($n = 35$), while for the g.32212 (19 bp indel) locus, two genotypes were observed, DD ($n = 89$) and ID ($n = 12$) (Table 2). The g.48308C>T locus exhibited moderate genetic variation, as indicated by the balanced distribution among homozygous and heterozygous genotypes. In contrast, the g.32212 locus showed a predominance of the DD genotype, suggesting a lower level of polymorphism.

Table 2: Allele and genotype frequencies for *PLAG1* polymorphisms.

Locus	Genotype frequency	Allele frequency	Chi-Square (χ^2) Test
g.48308C>T	CC= 0.158, CT= 0.495, TT= 0.346	C = 0.406 T = 0.594	$\chi^2 = 0.0746$, $df = 1$, $p > 0.05$, Expected: CC = 0.3067, CT = 0.494, TT = 0.199
g.32212 (19 bp indel)	DD= 0.881, ID= 0.119, II= 0	I = 0.059 D = 0.941	$\chi^2 = 0.408$, $df = 1$, $p > 0.05$, Expected: DD = 0.885, ID = 0.111, II = 0.0035

Table 3: Association of *PLAG1* polymorphism g.48308C>T with growth traits in PO cattle population.

Variable	g.48308C>T			P value
	CC (16)	CT (50)	TT (35)	
Birth weight (kg)	31.13±1.09	30.62±0.52	29.57±0.39	0.235
Body length (cm)	60.31±0.82	60.42±0.60	59.74±0.59	0.691
Withers height (cm)	73.88±0.63	73.00±0.48	73.26±0.57	0.675
Chest girth (cm)	69.13±1.05	69.70±0.72	68.37±0.69	0.315
Hip height (cm)	77.94±0.66	77.40±0.45	76.97±0.53	0.545
Corrected body weight at 750 days (kg)	281.30±11.70	274.22±5.98	266.46±7.73	0.719
Mature body weight (kg)	281.00±11.40	273.74±6.11	265.03±7.72	0.658
Mature body length (cm)	123.06±1.53	122.08±0.85	121.40±0.94	0.775
Mature withers height (cm)	125.69±1.08	126.04±0.56	125.63±0.63	0.906
Mature chest girth (cm)	155.50±2.43	155.10±1.33	155.49±1.63	0.984
Mature hip height (cm)	132.60±1.25	133.43±0.60	133.00±0.73	0.766
Average daily gain (kg)	0.32±0.02	0.31±0.01	0.29±0.02	0.766

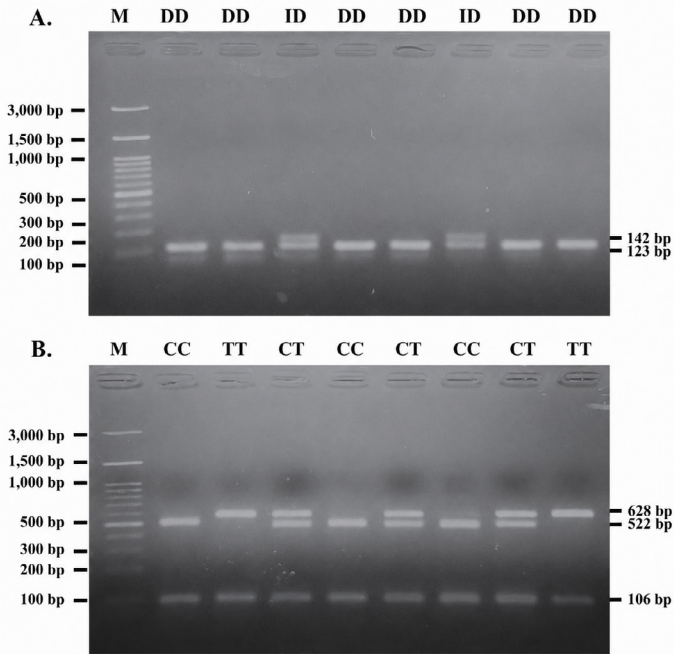


Figure 2: Genotypes of two *PLAG1* polymorphisms. A: PCR-RFLP product targeting g.48308C>T SNP using the restriction enzyme *Sac*II; B: Genotypes of g.32212 (19 bp indel). M = 100 bp DNA ladder; CC, CT and TT are genotypes of g.48308C>T SNP; DD and ID are genotypes of g.32212 (19 bp indel).

ASSOCIATION OF THE G.48308C>T POLYMORPHISM WITH GROWTH TRAITS

The association between the g.48308C>T polymorphism of the *PLAG1* and growth-related traits is presented in Table 3. Statistical analysis revealed no significant differences ($P > 0.05$) among genotypes (CC, CT, and TT) for any of the evaluated phenotypic traits.

ASSOCIATION OF THE G.32212 (19 BP INDEL) POLYMORPHISM WITH GROWTH TRAITS

The association analysis of the g.32212 (19 bp indel) polymorphism with growth traits is summarized in Table 4. A nominally significant association ($P = 0.042$) was observed between the g.32212 (19 bp indel) and chest girth, with DD genotypes showing larger mean values than ID genotypes. Given the highly unbalanced genotype frequencies, this result should be interpreted as suggestive rather than definitive. Other traits, including birth weight, withers height, hip height, corrected body weight at 750 days, mature body weight, body length, and ADG, did not differ significantly ($P > 0.05$) between genotypes.

LINKAGE DISEQUILIBRIUM BETWEEN *PLAG1* POLYMORPHISMS

Pairwise LD analysis performed using Haploview revealed weak linkage disequilibrium between the g.48308C>T SNP and the g.32212 (19 bp indel), with D' and r^2 values of 0.22 and 0.002, respectively (Figure 3). These results

indicate a low degree of non-random association and virtually no correlation between the two loci, suggesting that they segregate largely independently in the PO cattle population.

Table 4: Association of g.32212 (19 bp indel) of the *PLAG1* with growth traits in PO cattle population.

Variable	g.32212 (19 bp indel)		P value
	DD (89)	ID (12)	
Birth weight (kg)	30.55±0.35	28.75±1.19	0.088
Body length (cm)	60.44±0.40	58.17±0.98	0.051
Withers height (cm)	73.30±0.34	72.67±1.02	0.501
Chest girth (cm)	69.47 ^a ±0.48	66.75 ^b ±1.35	0.042
Hip height (cm)	77.44±0.32	76.58±0.98	0.336
Corrected body weight at 750 days (kg)	272.47±4.61	274.00±14.60	0.780
Mature body weight (kg)	271.65±4.58	273.50±15.50	0.779
Mature body length (cm)	121.89±0.63	122.83±1.64	0.488
Mature withers height (cm)	125.71±0.41	126.83±1.17	0.331
Mature chest girth (cm)	155.40±1.02	154.50±2.44	0.751
Mature hip height (cm)	133.00±0.46	134.27±1.38	0.358
Average daily gain (kg)	0.31±0.01	0.27±0.04	0.302

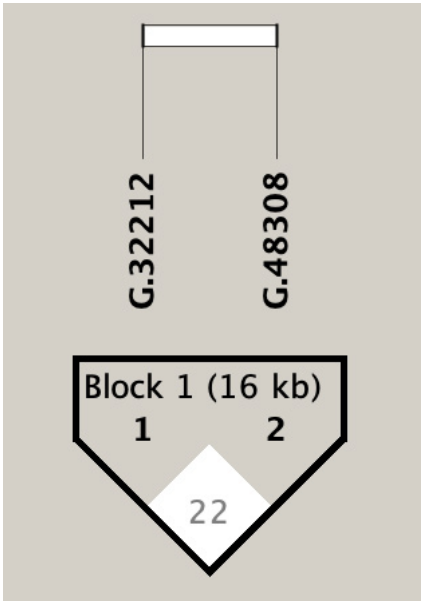


Figure 3: Pairwise linkage disequilibrium (LD) between the g.48308C>T SNP and the g.32212 (19 bp indel).

DISCUSSION

The Pleomorphic adenoma gene 1 (*PLAG1*) encodes a zinc-finger transcription factor involved in the regulation of growth, development, somatic cell proliferation, and skeletal formation (Wang *et al.*, 2022). Variants within or near *PLAG1* have been consistently associated with economically important traits, including body size, carcass composition, and reproductive performance across

livestock species (Li *et al.*, 2019; Zhong *et al.*, 2019; Mia *et al.*, 2022). Given its pleiotropic role, *PLAG1* has emerged as one of the most important candidate genes influencing growth-related traits in cattle.

In the present study, the g.32212 (19 bp indel) polymorphism was significantly associated with chest girth in PO cattle, with animals carrying the DD genotype exhibiting larger chest girth than those with the ID genotype. Chest girth is an important indicator of thoracic development, body capacity, and carcass production potential (Buchanan *et al.*, 2002). This finding agrees with previous studies reporting associations between *PLAG1* polymorphisms and growth-related traits in cattle. For example, Trilaksono *et al.* (2024) reported significant effects of the g.48308C>T SNP and the 19 bp indel on body weight and chest girth in Brahman cattle, whereas Cahyadi *et al.* (2022) demonstrated that an intronic *PLAG1* variant influenced body length in Bali cattle. Collectively, these findings support the involvement of *PLAG1* in skeletal growth and body conformation in Indonesian cattle breeds.

The biological relevance of the 19 bp indel is further supported by studies conducted in other cattle populations. Xu *et al.* (2018) identified the same indel in multiple Chinese cattle breeds and reported significant associations with growth traits, suggesting that this variant, or a closely linked functional mutation, may contribute to skeletal development. Similarly, Zhou *et al.* (2019) demonstrated that the 19 bp indel was widely distributed across 37 Chinese native breeds and significantly associated with body height and chest circumference. Together with the present results, these studies indicate that the *PLAG1* 19 bp indel may represent a conserved source of genetic variation influencing body size in cattle.

Despite the observed association, the results should be interpreted cautiously due to the highly unbalanced genotype distribution at the g.32212 locus, characterized by the absence of the II genotype and the low frequency of heterozygotes. The insertion allele frequency was only 0.059, yielding an expected II genotype frequency of approximately 0.35% under Hardy–Weinberg equilibrium. Consequently, fewer than one II individual would be expected in the sampled population, indicating that the absence of this genotype is likely attributable to low allele frequency and limited sample size rather than biological lethality or strong negative selection. Similar genotype distributions have been reported in *Bos indicus*-derived cattle populations carrying the same polymorphism (Xu *et al.*, 2018; Trilaksono *et al.*, 2024).

The skewed genotype distribution may also reduce statistical power and increase susceptibility to Type I

error, particularly in association studies involving low-frequency variants (Edwards *et al.*, 2005; Serdar *et al.*, 2021). Nevertheless, post-hoc analysis indicated that the observed association with chest girth was accompanied by a relatively large effect size (Cohen's $d \approx 0.80$), partially compensating for the reduced power associated with unequal sample sizes. Moreover, consistent associations of the same 19 bp indel with growth- and body size-related traits across independent cattle populations provide additional biological support for the observed relationship (Xu *et al.*, 2018; Zhou *et al.*, 2019; Mia *et al.*, 2022). Nonetheless, validation in larger populations remains necessary before this variant can be confidently incorporated into marker-assisted selection programs.

In contrast, no significant association was detected between the g.48308C>T SNP and any of the evaluated growth traits. This discrepancy may be explained, at least in part, by the weak linkage disequilibrium observed between the two *PLAG1* polymorphisms ($D' = 0.22$; $r^2 = 0.002$). Although both variants are located within the same gene, the extremely low r^2 value indicates that the 3' UTR SNP does not effectively tag the 19 bp indel in the studied population. Therefore, the association observed for the indel is unlikely to be attributable to linkage with the g.48308C>T SNP and more likely reflects an independent genetic signal or linkage with another functional variant within the *PLAG1* region.

Several genomic studies provide additional support for the role of *PLAG1* in growth regulation. Song *et al.* (2016) identified a pleiotropic quantitative trait nucleotide within the *PLAG1-CHCHD7* region that explained a substantial proportion of variation in multiple carcass traits in Simmental cattle. Furthermore, Li *et al.* (2019) reported genotype-dependent differences in *PLAG1* mRNA expression among tissues and developmental stages, suggesting that sequence variation within this region may influence growth through transcriptional regulation. Likewise, Hou *et al.* (2020) demonstrated associations between *PLAG1* variants and adult body height in Chinese cattle, supporting the notion that *PLAG1* exerts stronger effects on skeletal development and mature body size than on early-life growth traits.

Recent evidence also indicates that *PLAG1* influences traits beyond body size. Engle and Hayes (2022), using genomic data from 2,839 Australian Brahman cows, reported significant associations between *PLAG1* variants and both growth and fertility traits, suggesting that the gene contributes to endocrine pathways affecting somatic and reproductive development. In addition, Wang *et al.* (2023) showed that *PLAG1* copy number variations were associated with body size traits in goats, highlighting

the conserved biological role of *PLAG1* across ruminant species and emphasizing the potential importance of structural variants, including indels, in regulating growth-related phenotypes.

The absence of association for the g.48308C>T SNP may reflect limited statistical power, breed-specific linkage disequilibrium patterns, or interactions between genetic background and environmental conditions. Previous studies have demonstrated that the phenotypic effects of *PLAG1* variants vary among cattle breeds and production systems (Engle and Hayes, 2022). Furthermore, *PLAG1* generally exerts stronger effects on mature stature and skeletal dimensions than on juvenile growth traits (Karim et al., 2011; Fortes et al., 2012), which may explain the lack of detectable effects for several traits evaluated in the present study.

Overall, the results suggest that the *PLAG1* g.32212 (19 bp indel) polymorphism may contribute to variation in chest girth in PO cattle. Combined with evidence from Brahman, Bali, and Chinese cattle populations, the findings further support the role of *PLAG1* as an important growth-related gene in cattle. However, because of the limited sample size and highly unbalanced genotype distribution, the observed association should be regarded as preliminary until confirmed in larger populations. Future studies incorporating larger datasets, genome-wide association analyses, and functional genomic approaches will be valuable for elucidating the molecular mechanisms through which *PLAG1* influences growth, body conformation, and production traits in tropical cattle.

CONCLUSIONS

This study confirmed polymorphisms at two *PLAG1* loci in PO cattle. The g.32212 (19 bp indel) variant showed a significant association with chest girth in PO cattle, indicating potential relevance to body measurement. However, due to limited genotype balance, this finding should be considered preliminary and requires validation in larger populations before application in breeding programs. Further study using larger populations, additional *PLAG1* variants, and whole-genome association approaches (GWAS) is recommended to validate these findings.

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(BPTU-HPT Sembawa), Indonesia, for their valuable assistance during blood sample collection and phenotypic data recording. Their technical expertise and dedication were essential to the successful completion of this study.

NOVELTY STATEMENT

This study is the first to evaluate the effects and linkage disequilibrium of the *PLAG1* g.48308C>T SNP and the 19 bp indel in Indonesian Ongole cattle. It demonstrates a breed-specific association of the 19 bp indel with chest girth and provides new genetic evidence supporting the potential application of *PLAG1* in marker-assisted selection for beef cattle breed.

AUTHORS CONTRIBUTION

DDP: Writing original draft, investigation, formal analysis, data curation. AERM: Methodology, Formal analysis. WP: Writing review and editing, validation, funding acquisition, supervision. YY: Validation, funding acquisition, formal analysis. SS: Validation, funding acquisition, formal analysis. HK: Investigation, data curation. MI: Investigation, data curation. MC: Writing review and editing, validation, methodology, funding acquisition, conceptualization, supervision.

ETHICAL APPROVAL

All animal procedures related to blood collection were reviewed and approved by the Research Ethics Commission of the National Research and Innovation Agency (BRIN), Indonesia, under approval number 81/Klirens/X/2021.

GENERATIVE AI AND AI ASSISTED TECHNOLOGY STATEMENT

The authors declare that no generative AI and AI assisted technology was used in the creation of this manuscript.

CONFLICT OF INTEREST

The authors have declared no conflict of interest.

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