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The Association of IGFBP7 Gene Polymorphism on Lamb Meat Quality in Javanese Thin-Tailed Sheep

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ABSTRACT

The insulin-like growth factor binding-protein 7 (IGFBP7) gene is one of the potential genes related to meat quality. The objective of the current study was to evaluate polymorphism of the IGFBP7 gene (g.72351183A>C) and its association with meat quality traits in the Javanese thin-tailed (JTT) sheep. A comprehensive analysis was conducted on 88 JTT male sheep to examine their fatty acid composition, carcass characteristics, carcass retail cuts, and the physical properties of lamb meat. The polymorphism was detected using the PCR-RFLP technique. The association between the IGFBP7 gene polymorphism and the observed variables of meat quality was evaluated using one-way analysis of variance (ANOVA). The study results indicated that the IGFBP7 gene was polymorphic in JTT sheep population, with the allele distribution conforming to Hardy-Weinberg equilibrium. The AA genotype was found to be predominant. The IGFBP7 gene variants were associated ($p<0.05$) with erucic acid, linoleic acid, eicosapentaenoic acid, and total polyunsaturated fatty acid (PUFA). Sheep possesing the CC genotype exhibited the highest levels of linoleic acid, eicosapentaenoic acid, and total PUFA in comparison to those with AA and AC genotypes. However, the IGFBP7 gene polymorphism was not associated with carcass characteristics, carcass retail cuts, and physical properties of meat. These findings suggest that the IGFBP7 gene is a promising candidate marker for improving fatty acid composition in JTT sheep.

Keywords: IGFBP7 gene; Javanese thin-tailed sheep; lamb meat quality

INTRODUCTION

Red meat, such as lamb, provides a crucial source of nutrients and protein for human health and body development (McNeill, 2014; Kausar *et al.*, 2019). The global production and demand for red meat have been steadily increasing (Zhang *et al.*, 2017; Parlasca & Qaim, 2022). This rising demand is primarily driven by population growth and increasing income levels (Parlasca & Qaim, 2022; Henchion *et al.*, 2014).

In Indonesia, sheep are a common livestock contributing substantially to meeting the demand for red meat. However, the sheep production is still predominantly from local sheep breeds raised by smallholders (Tiesnamurti *et al.*, 2020). The Javanese thin-tailed (JTT) sheep is a local breed commonly raised by farmers and significantly contributes to meat production (Ibrahim *et al.*, 2023; Harahap *et al.*, 2023). The production of local breeds is important for rural development and contributes to economic, social-culture, and religious activities (Nyam *et al.*, 2020). Gonzales-Barron *et al.* (2021) suggested that one of the strategies to maintain and also to improve local breed sheep production is enhancing meat quality.

The meat quality is a substantial factor influencing the perspective of customer purchase decisions (Li *et al.*, 2023). The quality of meat encompasses a wide range of attributes to meet customer's needs, including nutrional, commercial, sensory, safety, image, and technological properties (Prache *et al.*, 2022). Numerous factors influence meat quality, such as diet, genetics, slaughter age, muscle part, and ante-mortem and post-mortem conditions (Mwangi *et al.*, 2019). Meat quality traits have been shown to be heritable (Mortimer *et al.*, 2014). Therefore, meat quality traits had the potency to be improved through selection (Juárez *et al.*, 2021).

Several types of research have been conducted to recognize potential genes associated with meat quality in Indonesian local sheep, focusing on aspects such as fatty acid component, characteristics of carcass, and physical properties (Gunawan *et al.*, 2019; Abdillah *et al.*, 2021; Harahap *et al.*, 2021). Transcriptomic analysis identified that the insulin-like growth factor binding-protein 7 (IGFBP7) as one of the observed genes that re-

lated to tenderness in Indonesian improved local sheep breed (Listyarini *et al.,* 2023). Furthermore, the IGFBP7 gene has been reported to be linked to various meat quality attributes in small-tailed Han sheep and their crossbreeds with Mongolian sheep (Cheng *et al.,* 2020).

The IGFBP7 gene belongs to the IGFBP family gene (Kostecká *&* Blahovec**,** 2002). The IGFBP family genes itself have a function to regulate insulin-like growth factors (IGFs) activities and have substantial functions on the growth and differentiation of cells (Kostecká *&* Blahovec**,** 2002). The IGFBP7 gene has been reported to be associated with the deposition of subcutaneous fat in cattle (Hu *et al.,* 2021). However, to our knowledge, the molecular characterization of the IGFBP7 gene and its correlation with meat quality in Javanese thin-tailed sheep, particularly concerning fatty acid composition, carcass characteristics, carcass retail cuts, and physical properties, has not been previously studied. Hence, the current study had the objective to identify the IGFBP7 gene polymorphisms and investigate their relationship with meat quality in Javanese thin-tailed sheep.

MATERIALS AND METHODS

Animals

All treatments involving animals in the current study were permitted by the Institutional Animal Care and Use Committee of IPB University, with permit number 117-2018 IPB. The study utilized 88 males of Javanese thin-tailed (JTT) sheep. The sheep were raised under similar conditions and slaughtered at ages 10-12 months. The slaughtering method fulfilled animal welfare requirements and followed the Indonesian National Standard procedures number 99003-2018 (BSN, 2018). The observed variables of meat quality in the study were fatty acids composition, carcass characteristics, carcass retail cuts, and physical properties. Samples from the *longissimus dorsi* muscle were collected for analyses of fatty acid composition, physical properties, and DNA extraction. To note, the *longissimus dorsi* muscle is commonly used in many other studies on meat quality evaluation, as demonstrated in research by Cheng *et al*. (2020) and Chaves Lima *et al*. (2024). In addition, Bonny *et al*. (2018) and Mortensen *et al*. (2024) indicated that the *longismuss dorsi* muscle is the primary muscle for commercial meat yield; therefore, it is frequently utilized for meat quality assessment.

Fatty Acid Determination

The components of fatty acid were extracted and analyzed following the AOAC 969.333 method from a 100 g sample of the *longissimus dorsi* muscle (Latimer, 2012). The analysis was conducted using gas chromatography to determine the proportions of various fatty acid compositions. The analysis results encompassed total fat content and the fraction of the total fatty acids, including total saturated fatty acids (SFA), total monounsaturated fatty acids (MUFA), and total polyunsaturated fatty acids (PUFA).

Carcass Characteristic and Retail Cuts

The observed variables of carcass characteristics in the study were hot carcass weight, carcass percentage, and carcass length. The variables of carcass characteristics and the retail cut were according to Harahap *et al*. (2023). The weight of the hot carcass was the weight of the carcass immediately after the sheep was slaughtered and processed. The carcass percentage was determined by dividing the hot carcass weight by the live weight, which was expressed as a percentage. The carcass length was the distance from the shoulder point to the distal end of the tarsus.

Physical Properties

The observed variables for physical properties included pH, tenderness, cooking loss, and water holding capacity (WHC). The pH value (ultimate pH) was determined using a pH meter after storing the carcass for 24 hours (Listyarini *et al.,* 2023). The tenderness was assessed using the Warner-Blatzer shear force method (Listyarini *et al.,* 2023). The cooking loss was assessed by modifying the protocol described in Suliman *et al.* (2021) study, which involved determining the difference between the initial and final meat weights after the meat had been boiled until its internal temperature reached 80 °C. The WHC was evaluated according to Dagong *et al*. (2012) by assessing the quantity of weight lost from the initial meat weight after pressing it with a force of 2,250 g on filter paper for 5 minutes.

DNA Extraction and Genotyping

The *longissimus dorsi* muscle sample was taken for DNA extraction using a DNA kit (Geneaid Biotech, Taiwan). Specific primers were designed utilizing the Primer3 online application (https://primer3.ut.ee/). The amplification of the IGFBP7 gene used a sequence of forward primer 5′ -GCCTTATGCGTGCAAACTGT- 3′ and reverse 5′ -GGTGAAGGTGCTGAGCTGTA- 3′. The accession number for designing the primer was NC_019463.2. The primers flanked a DNA sequence of 426 bp. The PCR premix for each sample consisted of 2 μL of DNA, 6.1 μL of nuclease-free water, 7.5 μL of MyTaq Red Mix (Meridian Bioscience, USA), and 2 μL of each primer. The amplification began with a preliminary phase at 95 °C, lasting for a duration of 1 minute. Subsequently, 35 cycles were conducted, involving denaturation at 95 °C for 15 seconds, annealing of forward and reverse primers at 55 °C for 15 seconds, and elongation of DNA at 72 °C for 10 seconds in each cycle. The last step involved a 3-minute extension at 72 °C.

The polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) was employed for genotyping assessment, according to Gunawan *et al*. (2018). The mixture for digesting DNA amplicon contained 5 μL of the DNA amplicon, 0.7 μL of enzyme buffer, 0.3 μL of restriction enzyme (*Tsp*451), and 1 μL of nuclease-free water. After incubating at 37 °C for 54 hours, the mixture was visualized using 2% agarose

gel electrophoresis under a UV transilluminator (Alpha Imager, Alpha Innotech, Santa Clara, USA).

Data Analysis

The allele frequencies and the Hardy-Weinberg equilibrium were determined based on the methodologies outlined by Nei & Kumar (2000) and Hartl & Clark (1997), respectively. A one-way analysis of variance (ANOVA) was conducted to assess the association between IGFBP7 gene polymorphism and the observed variables using the following formula:

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

whereas Y_{ij} represents the observed variables (fatty acid composition, carcass characteristics, retail cuts, and physical properties), μ represents the overall mean, G_i represents the effect of genotype i, and e_{ij} represents the residual error. The Tukey test was employed to determine the differences between genotypes for observed variables if statistical significance was detected ($p<0.05$).

RESULTS

The IGFBP7 Gene Polymorphism

The PCR amplification of the IGFBP7 gene with SNP position g.72351183A>C yielded a 426 bp product, matching the expected size based on the primer pair simulation using the online program (https://primer3.ut.ee/). Subsequently, the *Tsp*451 restriction enzyme successfully digested the PCR amplicon, resulting in three genotypes of AA (426 bp), CC (147 and 279 bp), and AC (147, 279, and 426 bp), as was previously demonstrated in Komarudin *et al*. (2024). The AA genotype was predominant (n=69; 78%), followed by AC (n=17; 21%) and CC (n=2; 1%) genotype. Allele frequency analysis revealed that A allele was predominant, constituting 88% of the population, whereas C allele accounted for 12%. The calculation of allele distribution showed that the sheep population in the study was on the Hardy-Weinberg equilibrium (calculated chi-squre<3.84).

Association of IGFBP7 Gene with Fatty Acid Composition

The IGFBP7 gene variants showed significant associations ($p<0.05$) with erucic acid (C22:1n9), linoleic acid (C18:2n6c), eicosapentaenoic acid (C20:5n3), and total PUFA. However, this polymorphism did not show associations ($p>0.05$) with total fat content, total fatty acids, total SFA, total MUFA, and the majority components of SFA, MUFA, and PUFA (Table 1).

Association of IGFBP7 Gene with Carcass Characteristics and Retail Cuts

The IGFBP7 gene polymorphism was not significantly associated ($p>0.05$) with body live weight, hot carcass weight, carcass percentage, and carcass length (Table 2). The carcass percentage of JTT sheep in the study ranged from 39.07% to 41.88%. Furthermore, the IGFBP7 gene polymorphism was also not associated ($p>0.05$) with the retail cuts (Table 3).

Association of IGFBP7 Gene with Physical Properties

In the analysis of physical properties, the different genotypes of the IGFBP7 gene did not show significant differences ($p>0.05$) with pH, tenderness, cooking loss, and WHC (Table 4). The pH value in the study ranged from 5.65 to 5.72, tenderness from 3.10 to 3.96 kg/cm², cooking loss from 44.00% to 51.42%, and WHC from 28.14% to 29.48%, respectively.

DISCUSSION

The PCR-RLFP method was successfully employed to amplify and genotype the IGFBP7 variant (g.72351183A>C). The results revealed that the IGFBP7 gene was polymorphic in the Javanese thin-tailed (JTT) sheep population in the study, exhibiting three distinct genotypes (AA, AC, and CC). The A allele occurred more frequently than the C allele. However, the distribution of alleles in the JTT sheep population examined in the current study was on the Hardy-Weinberg equilibrium.

The IGFBP7 gene polymorphism in the study showed significant associations ($p<0.05$) with erucic acid (C22:1n9), linoleic acid (C18:2n6c), eicosapentaenoic acid (C20:5n3), and total polyunsaturated fatty acid (PUFA). The IGFBP7 gene was essential to preadipocyte cell differentiation (Hu *et al*., 2021). Increased expression levels of IGFBP7 gene were observed alongside elevated mRNA expression levels of the C/EBPα, PPARγ, and LPL genes during the differentiation of progenitor cells in cattle (Hu *et al.,* 2021). The IGFBP7 gene seemed to interact with C/EBPα, PPARγ, and LPL since the protein expression pattern was similar to the mRNA expression (Hu *et al.,* 2021). The PPARγ and C/EBPα are the transcription factors that had important roles in promoting adipogenic differentiation (Hongfang *et al.,* 2022; Liu *et al.,* 2020). Likewise, a recent report by Geng *et al*. (2024) revealed a comparable pattern of IGFBP7 expression in chicken.

The IGFBP7 overexpression simulated the mRNA expression genes involved in lipogeneses such as C/EBPα, PPARγ, LPL, fatty acid binding protein 4 (FABP4), and fatty acid binding protein 5 (FABP5) during adipogenic differentiation and proliferation of preadipocytes in intramuscular tissue, providing strong evidence that the IGFBP7 gene plays a positive role in adipogenesis (Geng *et al.,* 2024). Xu *et al*. (2020) reported that the PPARγ gene expression on Tan sheep correlated with several fatty acids, including linoleic acid and eicosapentaenoic acid in the *longissimus dorsi* muscle. Additionally, they reported that the C/EBPα gene was linked to linolenic acid (C18:3n3) in the *longissimus dorsi* and eicosapentaenoic acid in the *triceps brachii* muscle. Meanwhile, the LPL gene was associated with linolenic acid and eicosapentaenoic acid in the *longissimus dorsi* muscle. The potential interaction between the IGFBP7 gene and the PPARγ, C/EBPα, and LPL genes might

Table 1. Association between IGFBP7 gene polymorphism with fatty acid composition

Variables (%)	Population of sheep			The genotype of IGFBP7 gene (x̄±SEM)			p-value
	x̄±SEM	min	max	AA (n=69)	AC (n=17)	CC (n=2)	
Fat content	6.00±0.42	1.02	14.23	6.13±0.47	5.76±1.02	3.54±2.00	0.64^{ns}
Total saturated fatty acid	43.64±0.39	27.83	52.65	43.87±0.45	42.71±0.79	43.74±1.30	0.50^{ns}
Caprylic acid, C8:0	0.17±0.04	0.00	2.99	0.16±0.05	0.22±0.11	0.00±0.00	0.73^{ns}
Capric acid, C10:0	0.12±0.01	0.03	0.39	0.12±0.01	0.12±0.02	0.09±0.02	0.75^{ns}
Lauric acid, C12:0	0.28±0.03	0.06	1.45	0.28±0.03	0.29±0.06	0.19±0.06	0.88^{ns}
Tridecanoic acid, C13:0	0.02±0.00	0.00	0.07	0.01±0.00	0.02±0.00	0.03±0.01	0.14^{ns}
Myristic acid, C14:0	2.58±0.11	1.14	5.86	2.60±0.12	2.50±0.27	2.53±0.81	0.94^{ns}
Pentacyclic acid, C15:0	0.58±0.02	0.00	0.99	0.57±0.02	0.59±0.03	0.85±0.15	0.08^{ns}
Palmitic acid, C16:0	20.25±0.24	14.00	24.86	20.36±0.28	19.88±0.44	19.69±1.10	0.68^{ns}
Margaric acid, C17:0	0.87±0.04	0.05	1.92	0.90±0.04	0.76±0.09	0.63±0.38	0.24^{ns}
Stearic acid, C18:0	16.86±0.29	9.86	23.65	16.92±0.32	16.30±0.69	19.48±2.64	0.28^{ns}
Arachidic acid, C20:0	1.63±0.18	0.00	6.24	1.66±0.20	1.70±0.49	0.11±0.11	0.46^{ns}
Heneicosylic acid, C21:0	0.23±0.03	0.00	1.06	0.23±0.04	0.26±0.09	0.09±0.01	0.75^{ns}
Behenic acid, C22:0	0.03±0.00	0.00	0.11	0.03±0.00	0.03±0.01	0.03±0.03	0.64^{ns}
Tricosylic acid, C23:0	0.02±0.00	0.00	0.13	0.02±0.00	0.03±0.01	0.03±0.03	0.65^{ns}
Lignoceric acid, C24:0	0.01±0.00	0.00	0.06	0.01±0.00	0.01±0.00	0.01±0.01	0.76^{ns}
Total MUFA	34.97±0.40	22.20	50.99	35.04±0.48	34.94±0.77	32.82±0.65	0.72^{ns}
Myristoleic acid, C14:1	0.10±0.01	0.00	0.33	0.10±0.01	0.11±0.02	0.06±0.06	0.47^{ns}
Palmitoleic acid, C16:1	1.50±0.06	0.09	2.79	1.57±0.07	1.29±0.17	0.88±0.06	0.07^{ns}
Ginkgoleic acid, C17:1	0.29±0.03	0.00	1.15	0.30±0.04	0.25±0.07	0.03±0.01	0.39^{ns}
Oleic acid, C18:1n9c	30.26±0.33	19.40	42.84	30.33±0.39	30.24±0.66	27.94±1.32	0.57^{ns}
Elaidic acid, C18:1n9t	2.66±0.15	0.00	6.21	2.58±0.18	2.82±0.20	3.90±0.15	0.35^{ns}
Paullinic acid, C20:1	0.10±0.03	0.00	1.49	0.10±0.04	0.10±0.06	0.00±0.00	0.89^{ns}
Erucic acid, C22:1n9	0.04±0.01	0.00	0.71	0.03±0.01^{b}	0.10±0.04^{a}	0.02±0.01^{b}	0.02*
Nervonic acid, C24:1	0.02±0.00	0.00	0.11	0.02±0.00	0.02±0.01	0.00±0.00	0.55^{ns}
Total PUFA	3.03±0.17	0.69	7.21	2.86±0.18^{b}	3.34±0.37^{b}	6.43±0.78^{a}	0.00**
Linoleic acid, C18:2n6c	1.36±0.14	0.00	4.48	1.25±0.14^{b}	1.52±0.34^{b}	3.52±0.46^{a}	0.04*
Linolelaidic acid, C18:2n9t	0.26±0.02	0.00	1.18	0.25±0.03	0.30±0.05	0.28±0.09	0.67^{ns}
y-Linoleic acid, C18:3n6	0.08±0.01	0.00	0.36	0.08±0.01	0.09±0.02	0.01±0.01	0.45^{ns}
a-Linolenic acid, C18:3n3	0.42±0.03	0.00	1.11	0.43±0.04	0.35±0.07	0.80±0.22	0.12^{ns}
Eicosadienoic acid, C20:2	0.04±0.00	0.00	0.15	0.04±0.00	0.04±0.01	0.08±0.03	0.17^{ns}
Dihomo-y-linolenic acid, C20:3n6	0.04±0.00	0.00	0.17	0.04±0.00	0.05±0.01	0.09±0.02	0.13^{ns}
Arachidonic acid, C20:4n6	0.43±0.04	0.00	1.80	0.41±0.03	0.47±0.12	0.76±0.23	0.32^{ns}
Docosadienoic acid, C22:2	0.00±0.00	0.00	0.08	0.00±0.00	0.01±0.00	0.02±0.02	0.14^{ns}
Eicosapentaenoic acid, C20:5n3	0.35±0.04	0.00	1.97	0.31±0.03^{b}	0.47±0.13^{b}	0.77±0.15^{a}	0.04*
Cervonic acid, C22:6n3	0.05±0.01	0.00	0.37	0.05±0.01	0.05±0.02	0.12±0.00	0.31^{ns}
Total unsaturated fatty acid	38.00±0.40	26.92	56.55	37.89±0.47	38.28±0.79	39.25±1.43	0.83^{ns}
Total fatty acid	81.64±0.63	54.75	109.20	81.77±0.76	80.98±1.02	82.98±0.13	0.84^{ns}

Note: x̄= mean, SEM= standard error of mean, ns= not significant, *= mean in the same row with different superscripts differ significantly at p<0.05, **= mean in the same row with different superscripts differ significantly at p<0.01.

Table 2. Association between IGFBP7 gene polymorphism with carcass characteristics

Variables	Population of sheep			The genotype of IGFBP7 gene (x̄±SEM)			p-value
	x̄±SEM	min	max	AA (n=69)	AC (n=17)	CC (n=2)	
Live weight (kg)	25.42±0.50	18.52	38.00	25.51±0.59	24.89±1.03	26.97±1.82	0.80^{ns}
Hot carcass (kg)	10.44±0.27	6.96	17.97	10.43±0.31	10.49±0.58	10.48±0.11	0.99^{ns}
Percentage of carcass (%)	40.84±0.42	34.39	52.60	40.64±0.48	41.88±0.86	39.07±3.03	0.41^{ns}
Length of carcass (cm)	61.36±0.67	49.00	75.00	61.03±0.75	61.94±1.52	68.00±5.00	0.28^{ns}

Note: n=number of sample, x̄= mean, SEM= standard error of mean, ns= not significant.

regulate fatty acids, which had been significant with the IGFBP7 polymorphism in the study.

Sheep with the CC genotype exhibited lower levels of erucic acid (C22:1n9) compared to those with the AC genotype. However, the total MUFA between genotypes was not differ (p>0.05). Sheep possessing the CC genotype had the highest levels (p<0.05) of linoleic acid, eicosapentaenoic acid, and total PUFA compared

Table 3. Association between IGFBP7 gene polymorphism with carcass retail cuts

Variables (g)	Population of sheep			The genotype of IGFBP7 gene (x̄±SEM)			p-value
	x̄±SEM	min	max	AA (n=69)	AC (n=17)	CC (n=2)	
Leg	1,694.65±36.22	998.50	2,513.30	1,688.65±41.43	1,701.01±84.30	1,847.40±47.90	0.81^{ns}
Loin	457.70±18.52	211.10	1,027.70	457.24±21.88	467.16±36.70	393.05±43.15	0.85^{ns}
Flank	171.63±8.33	77.50	450.30	172.98±10.10	168.70±13.70	148.75±18.05	0.90^{ns}
Shoulder	894.43±27.99	456.90	1,766.50	903.48±32.72	854.59±58.56	920.85±67.25	0.79^{ns}
Rack	431.99±12.92	229.70	787.10	426.61±14.58	448.52±31.47	477.15±11.55	0.70^{ns}
Breast	482.44±15.20	266.90	952.80	482.92±18.40	478.03±25.43	503.40±37.20	0.97^{ns}
Shank	411.74±10.09	239.50	669.80	411.23±11.40	413.76±24.63	412.15±47.25	0.99^{ns}
Neck	497.41±17.70	202.30	1,003.70	492.88±20.19	516.26±41.86	493.35±1.75	0.88^{ns}

Note: n=number of sample, x̄= mean, SEM= standard error of mean, ns= not significant.

Table 4. Association between IGFBP7 gene polymorphism with physical properties

Variables	Population of sheep			The genotype of IGFBP7 gene (x̄±SEM)			p-value
	x̄±SEM	min	max	AA (n= 69)	AC (n=17)	CC (n= 2)	
pH	5.70±0.02	5.28	6.48	5.69 ± 0.03	5.72 ± 0.07	5.65 ± 0.04	0.88^{ns}
Tenderness (kg/cm^3)	3.85±0.06	2.30	4.90	3.84 ± 0.07	3.96 ± 0.14	3.10 ± 0.05	0.14^{ns}
Cooking loss (%)	45.67±0.89	25.71	62.50	45.92 ± 1.02	44.00 ± 1.97	51.42 ± 1.02	0.44^{ns}
WHC (%)	28.41±0.35	21.15	39.52	28.14 ± 0.39	29.48 ± 0.85	28.86 ± 0.46	0.31^{ns}

Note: n=number of sample, x̄= mean, SEM= standard error of mean, ns= not significant, WHC= water holding capacity.

to sheep with the AA and AC genotypes. Meat with higher PUFA is crucial for improving meat quality and also human health (Gunawan *et al*., 2021). PUFA has an important role in many cellular and biological functions such as maintaining cell membrane integrity and fluidity, regulating blood pressure, supporting the nervous system function, modulating inflammatory responses, and regulating skeletal muscle metabolism (Kapoor *et al*., 2021). Increased PUFA consumption could reduce the incidence of cardiac diseases (Marangoni *et al*., 2020; Ooi *et al*., 2015) and is important for brain development and cognitive functions (Van Dael, 2021; Djuricic *et al*., 2021).

The variants of the IGFBP7 gene variants did not exhibit any association (p>0.05) with carcass characteristics and retail cuts. The previous studies on sheep have demonstrated varying results in the association of the IGFBP7 gene with carcass characteristics or retail cuts. Cheng *et al*. (2020) reported a weak association between IGFBP7 gene and carcass characteristics, whereas Armstrong *et al*. (2020) did not identify IGFBP7 as a gene significantly associated with those traits. In contrast, major sheep genes reported to be associated with these traits include Callipyge, Carwell, Calpain, Calpastatin, Myostatin, and Leptin genes (Gebreselassie *et al*., 2019; Talebi *et al*., 2022; Meira *et al*., 2018). The contribution of IGFBP7 gene to carcass characteristics might be minor, if any, in which it modulates the fatty acid content through adipogenesis rate. Nevertheless, this was not significant enough to affect the overall properties of the carcass. Notably, the major component of the carcass is protein, for which its biosynthesis may not be highly associated with the role of IGFBP7 gene. Typically, hot carcass weight and percentage of carcass had a high positive correlation with live weight (Bautista-Díaz *et al*., 2020; Gurgel *et al*., 2021). The comparable live weights observed among genotypes in the study may also have contributed to the similar hot carcass weights and carcass percentages. The percentage of carcass in the study was similar to the findings by Purbowati *et al*. (2021) in Indonesian local sheep.

The variation of the IGFBP7 gene in the study was not significantly associated (p>0.05) with the pH, tenderness, cooking loss, and WHC of lamb meat. According to Hu *et al*. (2021) and Geng *et al*. (2024), the roles of IGFBP7 are mostly associated with lipid biosynthesis in the tissue. On the other hand, it is known that muscle proteins are the main factor influencing tenderness (Thu, 2006), cooking loss (Purslow *et al*., 2016), and WHC (Huff-Lonergan & Lonergan, 2005; Bowker & Zhuang, 2015). Therefore, finding no association between IGFBP7 and those parameters might be acceptable. Meanwhile, the pH of the muscle represents the rate of degradation of muscle glucose or glycogen (Álvarez *et al*., 2019). Accordingly, it is unlikely that IGFBP7 is associated with the pH changes in the meat.

The pH is a crucial parameter of meat quality (Geletu *et al*., 2021). The range of pH in our study observed fell within the range value associated with high meat quality, indicating the absence of meat quality issues such as DFD (dark, firm, dry) meat, as defined by Poznyakosvkiy *et al*. (2015) and Ijaz *et al*. (2020). The ultimate pH value in the study was similar to prior lamb research (Ekiz *et al*., 2019; Gallo *et al*., 2019).

Tenderness values observed in the study were classified as indicative of high edible quality, based on the threshold of hard meat by Aksoy & Ulutaş (2016) and Listyarini *et al*. (2023). The tenderness values observed in the study were lower than those reported by Setyaningrum *et al*. (2015) for thin-tailed lambs. The

cooking loss in the study was slightly elevated compared to previous studies on lamb by Aksoy *et al*. (2019) and Wang *et al*. (2021), which could potentially be influenced by breed differences and cooking temperatures. Vaskoska *et al*. (2020) demonstrated that meat cooking loss increases with higher cooking temperatures.

CONCLUSION

The IGFBP7 gene (g.72351183 A>C) was found to be polymorphic in the Javanese thin-tailed (JTT) sheep population in the current study. The polymorphism was associated with erucic acid, linoleic acid, eicosapentaenoic acid, and total PUFA. Nevertheless, the IGFBP7 gene polymorphism was not associated with carcass characteristics, retail cuts, and the physical properties of lamb meat. Among the genotypes, the CC genotype appeared to be the most favorable due to its highest total PUFA content. It is proposed that the IGFBP7 gene appears to be a promising candidate for improving the fatty acid composition in JTT sheep.

CONFLICT OF INTERESTS

C. Budiman, C. Sumantri, & A. Gunawan serve as editors of the Tropical Animal Science Journal but have no role in the decision to publish this article. The authors also declare that they have no conflict of interest related to the experiment and the manuscript.

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