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Association of Liver X Receptor Alpha (LXRα) gene related to characteristic of carcass, meat quality and fatty acid composition in ducks

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ABSTRAK

Liver X Receptor Alpha (LXRα) merupakan gen reseptor inti yang berperan penting dalam meregulasi gen yang terlibat pada metabolisme lipid. Tujuan dari penelitian ini adalah mengidentifikasi keragaman dan asosiasi gen LXRα dengan karkas dan kualitas daging serta komposisi asam lemak menggunakan teknik Polymerase Chain Reaction-Restriction Fragment Length Polymorphism (PCR-RFLP). Total 98 ekor Itik Cihateup yang terdiri dari 57 betina dan 41 jantan umur 12 minggu digunakan pada penelitian ini. Ukuran produk amplikon adalah 661 bp. Frekuensi gen pada genotipe CC, GC dan GG masing-masing adalah 0.21, 0.55 dan 0.23. Hasil chi-kuadrat menunjukkan gen LXRα (g.3575 C>G) pada ekson 2 berada dalam kesetimbangan Hardy-Weinberg. SNP gen LXRα pada posisi g.3575 C>G berasosiasi ($P<0.05$) dengan kualitas daging itik dan kandungan asam lemak. Beberapa parameter yang berpengaruh ($P<0.05$) terhadap kualitas daging adalah bobot daging dada, persentase karkas dan persentase kepala, sedangkan untuk kandungan asam lemak adalah asam lemak jenuh (SFA) seperti asam palimat (C16:0); dan asam lemak tidak jenuh seperti asam γ-linolenat (C18:3n3); asam cis 11 eikosaenoat (C20:1) serta asam cis 11,14-eikosedinoat (C20:2). Dapat disimpulkan, gen LXRα berpotensi sebagai penanda genetik untuk mendapatkan kualitas daging yang baik serta asam lemak kaya asam lemak tidak jenuh.

Kata kunci: Asam lemak, karkas, kualitas daging, gen LXRα

ABSTRACT

Liver X Receptor Alpha (LXRα) is a nuclear receptor that play a crucial role in regulating of gene involvedin lipid metabolism. The aim of this research was to identify polymorphisms and association of LXRα gene with charateristic of carcass, meat quality and fatty acid composition in ducks using Polymerase Chain Reaction-Restriction Fragment Length Polymorphism (PCR-RFLP). A total sample of 98 Cihateup ducks consisted of 57 females and 41 males with age 12 weeks were used in this study. Product size is 661 bp amplicons. The genotype genes frequencies in CC, GC and GG were 0.21, 0.55 and 0.23 respectively. The chi-square test revealed that LXRα gene (g.3575 C>G) in exon 2 was in Hardy-Weinberg equilibrium. A SNP of LXRα gene in region g.3575 C>G was significantly associated ($P<0.05$) with duck meat quality and fatty acid content. Several parameters have significant affect ($P <0.05$) on meat quality in the breast meat weight, carcass percentage and head percentage, while associated fatty acids were saturated fatty acids (SFA) such as palimitic acid (C16:0); γ-and unsaturated fatty acids (UFA) such as linolenic acid (C18:3n3); cis 11 eicosenoic acid (C20:1) and 11.14 cis-eicosedenoic acid

(C20:2). In could be concluded that LXRα gene might be useful as genetic markers to select and produce meat with desirable unsaturated fatty acids.
Key words: Carcass, ducks, fatty acids, LXRα gene, meat quality

INTRODUCTION

Cihateup ducks are a local genetic resource of Indonesian livestock that has the potential to provide fulfillment of supply animal protein needs. The original distribution geographical region of Cihateup ducks mostly located in Tasikmalaya, West Java (Matitaputty *et al.,* 2015). Cihateup ducks have advantages in the size of the body such as the chest girth, breast meat and thighs have a high percentage so that it can indicate a potential better meat producer than the local ducks such as Cirebon, Mojosari and Alabio (Muzani *et al.,* 2005; Randa *et al.,* 2010). Anggraeni *et al.,* (2017b) reported that male Cihateup duck meat contains low content of unsaturated fatty acids (UFA) than females Cihateup duck meat. Production of meat with high polyunsatureted fatty acids (PUFA) and low saturated fatty acids (SFA) content is beneficial for human health and it is more in line with public health recommendation (Gunawan *et al.,* 2018).

Problems regarding low interest of consumers towards the duck meat are due to the off-odors which are appreciated by the public. Unpleasent odour and flavour also were also found in other livestock namely boar taint in pig (Gunawan *et al.,* 2013a and 2013b) and mutton odor and flavour (Gunawan *et al.,* 2018). More intense smell nature distorted (off-odor) in the duck meat than off-odors in chicken meat is associated with the body's ability to deposit fat in the duck higher than poultry (Randa *et al.,* 2010; Anggraeni *et al.,* 2017b). About 60% of duck fat content is derived from unsaturated fatty acids (linoleic and arachidonic) easily oxidized and produce unpleasant aroma on meat or duck carcass (Suci *et al.,* 2012). Fat oxidation process produces free radicals which lead to the emergence of peroxide. These will decompose and produce compounds such as aldehydes, alcohols, ketones, carboxylic acids and hydrocarbons each with characteristic odor (Randa *et al.,* 2010).

Liver X Receptor Alpha (LXRα) is one of the important gene controlling fatty acids. LXRα is one of the receptors in the cell nucleus that regulate cholesterol metabolism (Ngadiarti *et al.,* 2014). Howell *et al.,* (2009) stated LXRα acts as a major regulator of lipid homeostasis through the activation of SREBP-1c regulatory elements. LXRα gene in duck lies in exon 2. The results of Zhang and Li (2014) reported that LXRα gene was associated with the quality of meat in the Cherry Valley (CV) duck. Cherry Valley (CV) duck have characteristics adaptable and can be nurtured with intensive and extensive systems in tropical environments such as Indonesia. Research related to LXRα gene associated with fatty acid composition mainly local ducks are still scarce. Therefore, this study was conducted to identify the polymorphism of LXRα gene using polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) and association with the fatty acids compositions in Cihateup ducks.

MATERIALS AND METHODS

Animals and Phenotypic

This study used 98 Cihateup ducks consisted of 57 females and 41 males and were kept at the Field Laboratory of Poultry, Department Animal Production and Technology, IPB University.All ducks used in the present research were kept in the same feeding and environmental conditions. Cihateup ducks were reared from the age of 1 day to 12 weeks. Feed given was the BR-511 commercial feed with ME nutritional composition of 2900 to 3000 kcal/kg, a protein of 21-23% and fat by 5%. The mean weight cut of 98 Cihateup duck consisted 41 male duscks at the age of 12 weeks was equal to 1458.7 ± 139.1 g, while the average weight cut Cihateup 57 female ducks of the same age of 1481.5 ± 96.7 g. The materials used for DNA extraction were blood samples which were taken from the brachial vein wing on Cihateup ducks. Meat quality and fatty acid content analysis were measured from breast muscle tissues.

Analysis of Carcass, Meat Quality and Fatty Acid Composition

Due to the limitations of meat samples of duck, we analyzed 60 samples for carcass and meat quality traits and 44 samples for fatty acid composition. Data of carcass and meat quality (pH, color, cooking, % free H2O (water holding

capacity), MDA/malonaldehyde, and TMA/trimethylamine) used the data analyzed and reported previously by Anggraeni et al. (2017a). While analysis of fatty acid composition (total fatty acids, saturated fatty acids, monounsaturated fatty acids, and polyunsaturated fatty acids) used the data analyzed and described previously by Anggraeni et al. (2017b).

DNA Extraction and PCR-RFLP Amplification

Extraction refers to the standard phenol-chloroform Sambrook and Russell (2001). DNA extraction was carried out blood sample taken from brachial vein. LXRα gene SNP refers to Zhang and Li (2014) with modifications SNP at position g.3575 C> G in exon 2. For PCR amplification, the forward (F: 5'- GGG AAG TGC AGA AGA ATG TC -3') and reverse (5 - R: 5'- GTC TCC TTA TTA CAC CAC CC -3') primers were designed from the exon 2 and the forward (5 -gacagcttccctgcagattc-3) and reverse (5 -ttcatcatgcccacttcgta-3) primers were designed from the intron 1 of duck LXRα genomic sequence using the Primer3 tool (Rozen and Skaletsky, 2000). DNA was extracted PCR inserted into the tube as much as 1 µL were added to the premix with a volume of 14 µL. Premix was made with a mixture of 0.4 µL of primer, 7.5 µL Green Master Mix and 6.1 µL distillation water. The mixture was incubated in a thermal cycler to the amplification process. Amplification process begins with predenaturation stage at 95 ºC for 5 minutes. The second phase consisted of 35 cycles, each cycle consisting of denaturation process at a temperature of 95 ºC. for 10 seconds, primer annealing at a temperature of 61 ºC for 20 seconds and DNA extraction at 72 ºC for 30 seconds. The final stage is the primary elongation at 72ºC for 5 minutes. The DNA amplification product was visualized by agarose gel 1.5%.

PCR-RFLP was used for genotyping SNPs validation. PCR product and restriction enzymes namely BsaJI was incubated at 60 ºC for 4 hours (New England Biolabs, UK). The digested products were separated using 2.0% agarose gel which was stained with PeqGreen. The fragments were visualized under UV Transilluminator (Alpha Imager, Alpha Innotech, Santa Clara, USA).

Data Analysis

The genotypes obtained through PCR-RFLP, allele frequency, genotype frequencies and Hardy-Weinberg Equilibrium (HWE) value were calculated based on the following formula:

Genotype and Allele Frequencies (Nei and Kumar 2000)

$$x_{ii} = \frac{n_{ii}}{N} \qquad x_i = \frac{2n_{ii} + \sum n_{ij}}{2N}$$

Where : x_{ii} was frequency of genotype ii, x_{ii} was frequency of alel i, n_{ii} was total individuals with genotype ii, n_{ij} was total individuals with genotype ij and N was population size.

Hardy Weinberg Equlibrium (HWE) (Nei and Kumar 2000)

$$x^2 = \sum \frac{(O - E)^2}{E}$$

Where : χ^2 was chi-squared, O was the value of the observations and E was the expected value/ estimation.

Association Study

Association of LXRα gene related to fatty acid composition, carcass and meat quality analyses were performed using GLM procedure (SAS version 9.2, SAS Institute Inc., Cary, USA). The effects of genotype duck FAs, carcass and meat quality compounds were assessed by the fixed effect model (ANOVA) using GLM, then Duncan's Multiple Range Test was carried out. The model used according to Mattjik and Sumertajaya (2012).

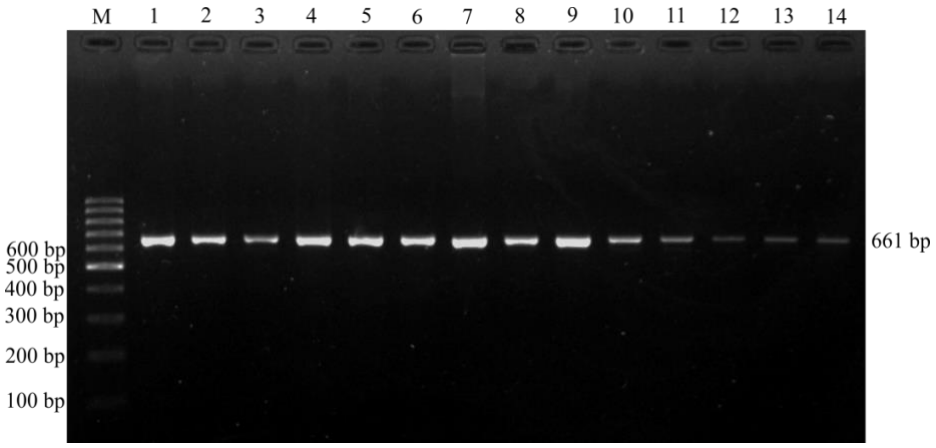
$$Yij = \mu + \text{genotype}i + \text{sex}j + eij$$

Where : Y_{ijk} was observed values genotype i, repetition j, µ was the population mean, genotipe_i was the fixed effect of i-th genotype (i = 1, 2, and 3), sex_j was the fixed effect of j-th sex (j = female/male), e_{ij} was the residual error.

RESULTS

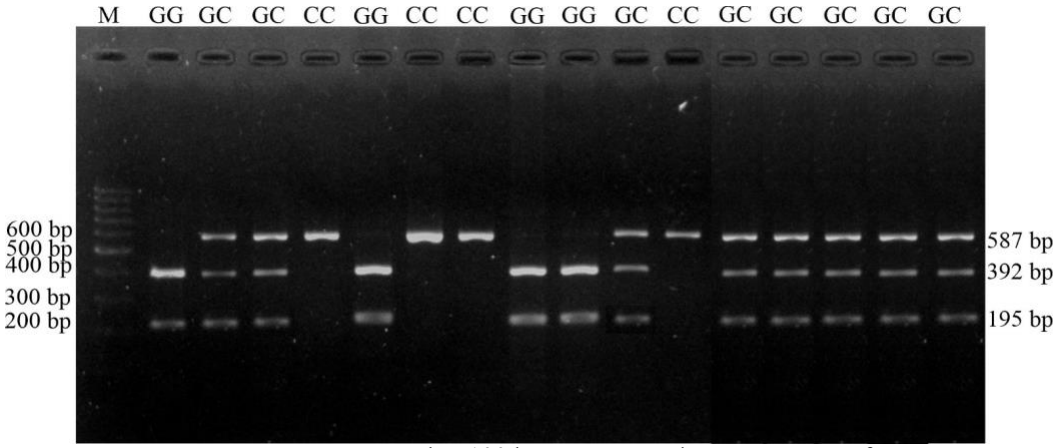
Identification of SNP and genotyping

Identification a nonsynonymous SNP in LXRα with a target position g.3575 C>G in exon 2 in Cihateup ducks using PCR-RFLP method was confirmed (Figure 1). PCR product was cut with a length of 661 bp sequences using BsaJI enzymes and produced 3 kinds of genotypes of two kinds of combinations of alleles C and G. Genotype CC has only one fragment with a length of 587 bp product, GG have two fragments with a length of 392 bp product and 195 bp, and GC as a combined genotype previously had three fragments with a length of 587 bp product, 392 bp and 195 bp (Figure 2). Results of the analysis showed that the allele frequency of G allele is



Note: M: DNA Marker 100 bp; Samples 1-14 LXRα gene amplification product

Figure 1 Results LXRα gene amplification on 1.5% agarose gel



Note: M: DNA Marker 100 bp; CC, GC and GG: genotype of LXRα gene

Figure 2. Visualization cutting fragment of LXRα gene|BsaJI on 2% agarose gel

dominant allele and has a value of 0.51, while the C allele had a frequency value of 0.49 (Table 1).

Gene frequency of LXRα (g.3575 C>G) was in Hardy-Weinberg Equilibrium (Table 1).

Table 1. Frequency of genotype, allele frequencies and Hardy-Weinberg Equilibrium LXRα|BsaJI on Cihateup ducks

Population	N	Genotype frequencies			allele frequency		Chi Square	Chi Square Table
		CC	GC	GG	C	G	(χ^2)	(χ^2)
Cihateup ducks	98	0.21 (21)	0.55 (54)	0.23 (23)	0.49	0.51	1.03*	3.84

Note: n = N: many samples (...) = many samples of genotype CC, GC and GG, * = Significantly different (χ^2 0.05= 3.841)

Association carcass and meat quality in exon 2 of LXRα gene

The results showed that LXRα gene was significantly associated (P<0.05) with several parameters carcass characteristics including the carcass percentage, breast and head percentage Cihateup ducks (Table 2). Genotype CC was dominant or higher in breast muscle and carcass percentage than another genotype, but lower in head percentage. The results showed the gene LXRα obtained was not significant on meat quality on color brightness (L*), redness (a*), the yellowish color (b*), pH, cooking loss and drip loss.

Table 2. Genotype and association analysis of LXRα gene with duck carcass characteristic

Traits	Genotype (μ ± S.E)		
	CC	GC	GG
	(n=11)	(n=35)	(n=14)
Carcass traits			
Body weight (g)	1453.09 ± 142.51	1472.97 ± 116.92	1465.36 ± 117.18
Carcass weight (g)	964.36 ± 161,74	938 ± 116.22	895.71 ± 83.99
Carcass (%)	66.05 ± 5.98a	63.62 ± 5.20ab	61.11 ± 2.66b
Breast (g)	267.27 ± 59.56a	241.60 ± 55.59ab	224.78 ± 34.72b
Breast (%)	27.84 ± 4.60	25.70 ± 4.70	25.27 ± 4.26
Head (g)	80.82 ± 7.64	84.43 ± 7.4	85.5 ± 9.39
Head (%)	1.48 ± 2.55b	2.91 ± 3.05ab	4.01 ± 3.11a
Neck (g)	79.1 ± 10.45	82.54 ± 10.26	81.29 ± 9.84
Shank (g)	45.73 ± 6.99	49.77 ± 9.7	46.71 ± 4.79
Wings (g)	126.82 ± 14.63	134.86 ± 12.33	129.07 ± 9.95
Foot (g)	238.36 ± 38.19	233.74 ± 29.96	232 ± 26.81
Meat quality			
L (brightness)	38.66 ± 1.41	34.79 ± 12.73	36.32 ± 10.59
a (redness)	19.21 ± 1.59	16.67 ± 6.24	17.27 ± 5.05
b (yellowish)	3.47 ± 0.49	2.79 ± 1.15	2.86 ± 1.05
pH	5.51 ± 0.13	5.20 ± 1.31	5.43 ± 0.16
Cooking loss	46.57 ± 4.52	40.28 ± 12.43	46.63 ± 3.35
Drip loss	26.64 ± 1.75	25.76 ± 6.97	27.08 ± 2.24

Note: Figures with different letters in the same row shows the results significantly different (P<0.05) using Duncan test

Association LXRα gene with fatty acid composition

Statistical analysis LXRα gene in the base sequence g.3575 C> G showed a significant association (P<0.05) to some of the fatty acid composition such as saturated fatty acids (SFA) including palmitic acid (C16:0), Monounsaturated fatty acids (MUFA) including γ-linolenic acid (C18:3n6), cis 11 eikosenoic acid (C20:1) and polyunsaturated fatty acid including cis 11, 14-eikosedenoic acid (C20:2). CC genotype had significant results (P<0.05) to lower saturated fatty acid composition (SFA) and palmitic acid (C16:0). Composition of γ-linolenic acid (C18:3n6) and acid cis 11, 14-eikosedinoic acid (C20:2) significantly affected in the CC genotype, it had the highest value (0.06 ± 0:02) in the γ-linolenic acid of the total increase in PUFAs (19.25±1.25), but genotype GG has the highest value (0.14±0.03) on cis acid 11, 14-eikosedenoic acid. CC genotype was also found to have significant results (P<0.05) to the high cis 11 eikosenoic acid (Table 3).

Table 3. Genotype and association analysis of LXRα gene with fatty acid composition

Traits	Genotype (μ ± S.E)		
	CC (n=7)	GC (n=23)	GG (n=14)
SFA	31.33 ± 2.48b	33.02 ± 1.86a	33.81 ± 1.75a
Lauric acid (C12:0)	0.06 ± 0.02	0.10 ± 0.07	0.09 ± 0.07
Myristic acid (C14:0)	0.49 ± 0.04	0.52 ± 0.05	0.53 ± 0.03
Pentadecanoic acid (C15:0)	0.04 ± 0.005	0.05 ± 0.008	0.05 ± 0.01
Palmitic acid (C16:0)	25.86 ± 1.76b	27.45 ± 1.72a	27.86 ± 1.91a
Heptadecanoic acid (C17:0)	0.10 ± 0.01	0.12 ± 0.11	0.08 ± 0.02
Stearic acid (C18:0)	4.35 ± 0.59	4.38 ± 0.77	4.79 ± 0.61
Arachidic acid (C20:0)	0.21 ± 0.07	0.23 ± 0.05	0.23 ± 0.05
MUFA	48.63 ± 2.05	47.20 ± 3.00	46.25 ± 2.65
Palmitoleic acid (C16:1)	2.39 ± 0.35	2.23 ± 0.59	2.02 ± 0.49
Oleic acid (C18: 1n9c)	45.32 ± 2.28	44.10 ± 2.61	43.47 ± 2.52
Cis 11 eicosenoic acid (C20:1)	0.81 ± 0.15a	0.75 ± 0.11a	0.63 ± 0.11b
PUFA	19.25 ± 1.45	18.68 ± 1.07	18.77 ± 1.46
Elaidic acid (C18:1n9t)	0.12 ± 0.03	0.11 ± 0.03	0.12 ± 0.04
Linoleic acid (C18:2n6c)	18.85 ± 1.48	18.24 ± 1.07	18.30 ± 1.46
γ-linolenic acid (C18:3n6)	0.06 ± 0.02a	0.04 ± 0.01ab	0.04 ± 0.01b
Cis 11, 14-eikosedinoic acid (C20:2)	0.14 ± 0.03b	0.17 ± 0.06ab	0.20 ± 0.06a
Arachidonic acid (C20:4n6)	0.13 ± 0.06	0.16 ± 0.06	0.19 ± 0.18

Note: Figures with different letters in the same row shows the results significantly different (P<0.05) at 5% level using Duncan test

DISCUSSION

This study showed that relationship between the LXRα gene and carcass characteristic (carcass percentage, breast muscle and head percentage) and fatty acids content (SFA, palmitic acid, γ-linolenic acid, cis 11 eikosenoic acid and cis 11, 14-eikosedenoic acid). LXRα is a member of Liver X receptors (LXRs) gene which form heterodimers of the retinoid X receptor family (RXR). RXR including LXRα was transcription factor in peroxisome proliferator-activated receptors (PPARs) signaling pathway which play an important role in the regulation of adipocyte tissue development, lipogenesis, and skeletal muscle lipid metabolism (Berger and Moeler, 2002). Peroxisome proliferator-activated receptors (PPARs) are nuclear hormone receptors that are activated by fatty acids and their derivatives such characteristic of meat production. LXRα is the most significantly overrepresented in pathway involved in fatty acid composition and skeletal muscle including carcass and meat quality, suggesting that LXRα would also play a key role in controlling fatty acid metabolism and meat quality traits. Some LXRα diversity is significantly related to the quality of meat and fatty acid in other livestock. Previous research reported by Yu *et al.*, (2006) explained the significant associations in the loin area and total fat in Berkshire and Yorkshire pig. Huang *et al.*, (2010) reported the finding of his research that a mutation in the sequence of bases g.1530 T>C in exon 2 LXRα genes were significant effect on

backfat thickness, carcass length and marbling score in Qinchuan cattle. In the study of Zhang *et al.,* (2015), there was an association of the LXRα gene at the locus position 53 G>A from White Muscovy duck in meat quality characteristic. Birds with AA genotype were higher values than BB genotype at intramuscular fat (IMF), polyunsaturated fatty acid (PUFA) and unsaturated fatty acid (UFA).

LXRα can be discovered in some tissues such as brown adipose tissue, lung and intestine, submandibular gland and thyroid gland but the expression of genes LXRα dominant on the metabolism of lipids are in the liver, intestines, kidneys, adrenals and adipose tissue (Annicote *et al.,* 2004; Schulman 2017). LXRα is one of the genes that regulate the homeostasis of cholesterol and is a member of a transcription factor that is activated by ligand in the nucleus, activation causes the modulation of the expression of genes involved in the homeostasis of cholesterol, including the ATP-binding cassette transporter A1 (ABCA1), which plays an important role in the formation of plasma high-density lipoprotein cholesterol (HDL-C) (Kazeminasab *et al.,* 2013).

Genotype CC was a dominant or higher in breast muscle and carcass percentage than another genotype, but lower in head percentage (Table 2). These results are in accordance with Gunawan *et al.,* (2018a) reported that Cihateup duck breast weights ranged 233.60-312.30 g. The difference between the weight of the breast muscles showed that the characteristics of the muscle fibers belonging to the essential components of the quality of the meat. Deposition of meat on the breast occur relatively slowly in ducks development. Breast and leg meat weight were formed from the speed of meat fibers in poultry that was recommended by the aerobic capacity (Turner and Butler 1988). The percentage of carcasses resulting from the research significant effect was dominated with a range of outcomes (61.11-66.05)%. Some genotype results of this study is in accordance with Anggraeni *et al.,* (2017a) who reported that the percentage of carcasses in Cihateup ducks range (63.64±4.90)% and in accordance with the standards of local ducks percentage (54-62%). The percentage of the carcass can be used as a yardstick to judge the production of meat.

The results showed that LXRα gene obtained is not significant on meat quality (Table 2). These results were different with the Anggraeni *et al.,* (2017a) which had significant results in redness (a*), pH, cooking loss and drip loss. Differences redness which are affected by differences in levels of Fe or haematin then the microstructure of the matrix protein, while the levels of brightness can be affected by differences in muscle composition of duck or structures that influence the refraction of light, the state of chemical myoglobin or diffusion of oxygen can be possible be other factors that affect the quality of the meat (Swatland 2012; Mateo *et al.* 2017). Cooking loss has a higher number than Cherry Valley duck which has a span ranging from 34.5% to 35.6% (Qiao *et al.,* 2017). The high cooking loss results of the literature indicate a higher proportion of oxidative fibers associated with the water-holding capacity of duck meat (Ali *et al.,* 2017). It could be speculated that the analysis of the characteristics and quality of the meat carcass can be used as a reference to characterize the carcass and meat quality standards more precise clump of local ducks in Indonesia, especially Cihateup ducks.

Palmitic acid has the dominant result (25.86±1.76) for the low total SFA (31.33±2.48) on the CC genotype (Table 3). These results are consistent with studies Weiss *et al.,* (2011) which states that the palmitic acid (C16:0) decreased significantly in female mice by treatment LXR, RAR and RXR. Palmitic acid was considered to have a positive effect in reducing bad cholesterol, reduce fat deposition in blood vessels and the formation of clots and maintain concentration and repartition of certain tissues in the classification of lipid metabolism that requires good regulation. Palmitic acid represents 20-30% of total fatty acids in the membrane phospholipids and adipose triacylglycerol (Carta *et al.,* 2015). The research result from Carta *et al.* (2017) showed the distribution and metabolism of palmitic acid in tissues is strictly controlled.

Composition of γ-linolenic acid (C18:3n6) and acid cis 11, 14-eikosedenoic acid (C20:2) significantly affected in the CC genotype (Table 4). Firestein *et al.,* (2013 stated that the γ-linolenic acid is formed by PPARγ through phosphorylation and translocation stimulant towards LXRα gene targets. γ-linolenic acid (Gamma Linolenic Acid/GLA) was produced in animals through Δ6 desaturation linolenic acid. GLA has significance in the medical and pharmaceutical, among others to lower low density lipoprotein cholesterol (LDL) for patients with hypercholesterolemia, treatment of premenstrual syndrome, atopic eczema.

Deficiency of linolenic acid and its derivatives may decrease the ability of reproduction, growth disorders and susceptible to infection (Iskandar *et al.,* 2010). The increase in total MUFA dominated by cis 11 eikosenoic acid (C20: 1) is also generated by the CC genotype. Eicosenoic acid and its derivatives have a great advantage in the process of inflammatory mediators and medical raw materials (Pinchaud *et al.,* 2018). These results are in accordance with previous study published by Han *et al.,* (2012), which showed a significant correlation ($P<0.05$) LXRα genes with increased concentrations of cis 11 eikosenoic acid (C20:1) at the intersection of steer Canadian commercial cattle.

Parameters that are commonly used to assess the nutritional quantity of meat can through total ratio (PUFA: SFA) (Enser *et al.,* 1998) in addition, the ratio of PUFA:SFA is an important factor that affects the cardiovascular disease (Yousefi *et al.,* 2012). Results ΣPUFA and ΣSFA ratio obtained in genotype CC, GC and GG respectively by 0.62, 0.57 and 0.56 but the ratio was only affected ($P<0.05$) in CC genotype. The ratio of the three genotypes according to Horcada *et al.,* (2012) which states that ΣPUFA / ΣSFA recommended for the meat should be more than 0.45, but lower than the Peking duck that has a value of 0.806 (Onk *et al.,* 2018). DFA (desirable fatty acids) is another parameter that was used to assess nutritional lipid profile desired for the health of consumers (Chen *et al.,* 2016). DFA obtained from the sum of stearic acid, MUFA and PUFA. The results showed that the CC genotype had the highest DFA value (72.24%) than the GC genotype (70.27%) and GG (69.80%). Association result on fatty acids are diverse and appropriate for the consumers into consideration gene LXRα particularly in Cihateup ducks CC ducks might be used as a genetic marker in the selection of duck that has a low content of saturated fatty acids and contains higher unsaturated fatty acids.

CONCLUSION

The LXRα gene was polymorphic in base sequence g.3575 G>C in Cihateup ducks. Several parameters carcass characteristics were associated including the carcass percentage, breast and head percentage Cihateup ducks. Furthermore, LXRα gene is significantly associated with a lower SFA in palmitic acid (C16:0), the high PUFA on γ-linolenic acid (C18:3n6) and cis 11,14-eicosedinoic acid (C20:2) and the association of the high MUFA at cis 11 eicosenoic acid (C20:1). LXRα gene might be useful as genetic markers to select and produce meat with desirable unsaturated fatty acids.

CONFLICT OF INTEREST

The authors declare that they have no competing interest with any financial, support, or other relationships with other personal or organization related to the material discussed in the manuscript

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