The Variability of Growth Hormone Gene Associated with Ultrasound Imaging of *Longissimus dorsi* Muscle and Perirenal Fat in Rabbits

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\textasteriskcentered\textsuperscript{Received 03-03-2014; Reviewed 21-03-2014; Accepted 28-04-2014}

**ABSTRACT**

Identification of genes in rabbits correlated to economic traits were intended to improve and develop their genetic quality. The objective of this research was to analyze the variability of growth hormone gene (GH) in three rabbit breeds, i.e. Rex, Satin, and Reza (Rex and Satin crosses) then was associated with ultrasound imaging of *Longissimus dorsi* muscle and perirenal fat thickness. Identification of the variability of growth hormone gene was analyzed using PCR RFLP technique from blood samples of 33 mature male rabbits in Indonesian Research Institute for Animal Production (IRIAP). Thickness of *Longissimus dorsi* muscle and perirenal fat were imaged and measured by using ultrasound unit at 2\textsuperscript{nd} to 3\textsuperscript{rd} lumbar vertebrae in the left body side. PCR product of GH gene fragment (231 base pair /bp) was digested with restriction enzyme *Bsh1236I*. PCR-RFLP patterns were allele T resulted in an undigested fragment of 231 bp; allele C resulted in fragment of 169 bp and 62 bp. The result showed that *Bsh1236I* GH gene had three genotypes, i.e. CC, TT, and CT. There were significant association of *Longissimus dorsi* muscle thickness between rabbit breed (P<0.05). There was no significant association between GH *Bsh1236I* gene polymorphism and imaging ultrasound of *Longissimus dorsi* muscle and perirenal fat thickness. The association of characteristic genotype of GH|*Bsh1236I* gene with measurement phenotype was not significant, however it had potency as marker assisted selection (MAS).

**Key words:** growth hormone gene, *Longissimus dorsi*, perirenal fat, rabbit, ultrasound

**ABSTRAK**


**Kata kunci:** gen hormon pertumbuhan, *Longissimus dorsi*, lemak perirenal, kelinci, ultrasonografi

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INTRODUCTION

Rabbits have several advantages besides as pets, laboratory animals, may also serve to produce meat and leather-fur (Rogel-Gaillard et al., 2009). Rabbit is potential livestock that produces meat. The rabbit meat product in Indonesia is not as popular as in other countries. The world’s largest rabbit meat production was reported in China with an estimated annual production 550,000–600,000 tons of carcass each year (Lebas, 2009). Rabbit populations in Indonesia at 2011 reached 915,140 heads and spreaded in 12 provinces (Ditjen PKH, 2011). Along with change the way the community views the rabbit meat, this can increase the need for seed broiler rabbits. However, rabbit meat consumption in Indonesia is relatively still low due to the less supply. Rabbit meat has different characteristics from beef, chicken, pork, or lamb. Rabbit meat is white meat, has a smooth and soft fiber and higher protein with cholesterol and low fat (Rogel-Gaillard et al., 2009).

Rex, Satin, and Reza (crosses Rex and Satin) are rabbit developed breed in IRIAP which germplasm rabbit meat in Indonesia. Currently, the existence of selection and crossbreeding conducted on the rabbits with potential for meat and leather-fur had only seen from phenotypic aspects include performance and productivity, while the genetic aspects (gene) has not been done. Identification of genes related to the economic trait were needed for improvement and development of the quality of rabbit genetic.

Target gene used was growth hormone gene (GH) having an important role in growth and development. Effects of the GH gene on the growth are observed in several tissues (Akers, 2006). Polymorphisms in this gene have been used as a genetic marker associated with different performances and productions traits such as body weight, birth weight and weaning weight in goat (Wickramaratne et al., 2010; Supakorn Pralomkarn, 2013), milk yield and body weight in cattle (Jakaria et al., 2007; Katoh et al., 2008; Misrianti et al., 2012), sheep (Adams & Briegel, 2005), carcass traits in pig (de Faria et al., 2002; Schroder & Staufenbiel, 2006), cattle (Wall et al., 2013), milk yield and body weight in cattle (Jakaria et al., 2007; Katoh et al., 2008; Misrianti et al., 2012), sheep (Adams & Briegel, 2005), carcass traits in pig (de Faria et al., 2002). The rabbit GH gene has been already amplified with Wallis & Wallis (1995) and has been investigated as a gene associated with market weight on commercial rabbit (Fontanesi et al., 2012).

Analysis of genetic variation that associated with measurement of phenotypic was determined by using ultrasound imaging of Longissimus dorsi muscle and perirenal fat thickness. Ultrasonography is one of the most widely used techniques for in vivo prediction of carcass in swine, sheep and cattle (Moloney et al., 2002; Schroder & Staufenbiel, 2006; McEvoy et al., 2007). Some reports have also shown the suitability of this technique for the evaluation of body composition in rabbits (Pascual et al., 2010; Cardinali et al., 2008), estimated of Longissimus muscle in sheep (Sahin et al., 2008; Esquivelzeta et al., 2012), cattle (Wall et al., 2004; Yokoo et al., 2008), pig (Micklander et al., 2005). Taking imaging with ultrasound does not interfere of livestock, low cost and useful method to evaluate subcutaneous and visceral adipose tissue in anatomy and different metabolic conditions (Stouffer, 2004).

Percentage of perirenal fat depot (PFD) is a predictor of percentage fat in whole carcass (Blasco & Ouhayun, 1993). PFD in rabbit very sensitive to variation of feed and can increase to 40% in rabbit with high diet. Using of USG is practical method to predict carcass traits included Longissimus dorsi muscle and perirenal fat (Silva et al., 2012).

This research therefore was aimed to analyze the GH/Bsh1236I gene polymorphism in Rex, Satin and Reza rabbit breed that associated with ultrasound imaging of Longissimus dorsi muscle and perirenal fat thickness to improve genetic potential through molecular selection.

MATERIALS AND METHODS

Sample Sources

Total 33 blood samples of adult male rabbits were collected from 3 breeds, consisting of Rex (11 samples), Satin (11 samples), and Reza (11 samples) at Indonesian Research Institute for Animal Production (IRIAP). Blood samples were already extracted as DNA collections at the Animal Molecular Genetic Laboratory, Faculty of Animal Science, Bogor Agricultural University.

DNA Extraction

About 5 mL of blood samples were collected from each rabbit in non anticoagulant polypropylene tubes. Blood samples were then mixed with 96% ethanol. The process of DNA isolation used phenol-chloroform method (Sambrook et al., 1989) that was modified by Andreas et al. (2010). Genomic DNA was stored at -20°C until amplification with polymerase chain reaction (PCR).

Polymerase Chain Reaction (PCR)

Amplification of PCR was carried out by using specific primer (Fontanesi et al., 2012) for parts of the 5′-flanking region and 5′untranslated region, exon 1 and with method of two step gradient cycle PCR (Lopez & Prezioso, 2001; Xiong, 2004). Primers used were for forward 5′- GTATAGTGGGATGGGGTTGG -3 ' and reverse 5′-TTACGCTCCCCATTCAGAGC -3 ' (Gen Bank access number Z28137). The PCR was performed in a final volume of 15 µL for each reaction containing 1 µL of DNA sample, 9.35 µL distilled water, 0.3 µL primers, 0.05 µL Taq polymerase, buffer 3 µL, 0.3 µL dNTPs, and 1 µL MgCl₂. The reaction mixture was subjected to an initial 5 min of denaturation 95 °C, followed by first 15 cycles of denaturation 95 °C for 30 s, annealing 30 s at 68 °C, extension 30 s at 72 °C, then second of 15 cycles of denaturation at 95 °C for 30 s, annealing 30 s at 68 °C, extension 30 s at 72 °C, and final extension for 5 min at 72°C.

PCR - RFLP Analysis

Visualization of amplification was analyzed on Agarose gel 1.5% that containing 2.5 µL EtBr (ethidium bromide), 0.5X TBE buffer (1M Tris, 0.9 M Boric acid, 0.01 M EDTA pH 8.0) with a 100 bp ladder as a molecu-
lar weight marker for confirmation of the length of PCR product. Digestion by using enzyme and determination of RFLP, 5 μL of PCR products was added to 0.3 μL Bsh1236I enzyme, 1 μL distilled water, and 0.7 μL R buffer. The mixture was then incubated at 37 °C for 16 h. The digestion products were separated by horizontal electrophoresis (100 volts, 40 min) in 2% agarose gel in 0.5 X TBE and 2.5 μL ethidium bromide visualized on UV transiluminator.

Ultrasound Measurement

Images were obtained with an ultrasound unit (SonoDop® 55, PT Karindo Alkestron, Indonesia), equipped with a transducer micro-convex with frequency 7.5 MHz. Scanning sites for Longissimus dorsi Muscle (LM) and perirenal fat (PF) were located by physical palpation at 2nd to 3rd lumbar vertebrae in the left body side. Ultrasound gel was applied to the scanning sites area. The transducer was always placed in the same position. The images taken were digitalized and ultrasound measurements determined image analysis by using NIH Image J software (ImageJ®, NIH, USA).

Data Analysis

PCR-RFLP data were analyzed by allele calculating and genotype frequencies (Nei & Kumar, 2000). Genotype frequency, determined by the calculation of the ratio of a specific genotype of each population, was calculated by the following formula:

\[ x_i = n_{ii} / N \]

Allele frequency was calculated as ratio of a certain allele to the overall alleles at a certain locus in a population. Allele frequency of GH gene|Bsh1236I was calculated by the following formula:

\[ x = (2n_{ii} + \sum n_{ij})/2N \]

where \( x_i \) is frequency of genotype AiAi, \( x_j \) is frequency of allele A, \( n_{ii} \) is number of genotype AiAi, \( n_{ij} \) is number of genotype AiAj, and \( N \) is total samples.

Information content of allele was calculated by PIC values using method described by Botstein et al. (1980) and Nagy et al. (2012).

\[ PIC = 1 - \sum_{i=1}^{n} P_i^2 - \sum_{i=1}^{n} \sum_{j=i+1}^{n} 2P_i^2P_j^2 \]

where \( P_i \) and \( P_j \) stand for frequency of band i and band j respectively in one population; \( n \) is the number of alleles from a certain locus.

Characteristic phenotypic data of each rabbit breed were analyzed using the General Linear Model (GLM) with the model (Steel & Torrie 1995):

\[ Y_{ij} = \mu + \alpha_i + \beta X_{ij} + \epsilon_{ij} \]

where \( Y_{ij} \) is the observed value, \( \mu \) is overall mean, \( \alpha_i \) is effect for breed i, \( \beta \) is coefficient of linear regression; \( X_{ij} \) is covarian (rabbit breeds), and \( \epsilon_{ij} \) is the random error associated with \( Y_{ij} \) experimental unit.

RESULTS AND DISCUSSION

GH Gene Amplification

Genetic polymorphism of the GH gene was done by Polymerase Chain Reaction–Restriction Fragment Length Polymorphism (PCR-RFLP) method using Bsh1236I restriction enzyme. This enzyme recognized and cut at nucleotides of CG/CG sites. RFLP process resulted in two fragments with the base lengths of 231 and 169 bp.

Results from the PCR-RFLP analysis shows there were three genotypes identified, namely CC, TT, and CT genotypes that were derived from two alleles, namely C and T alleles (Figure 3). Genotyping the GH gene|Bsh1236I showed for the resulted one fragment of 231 bp for the CT genotype; one fragment of 169 bp for the CC genotype; and two fragments of 231 and 169 bp for the CT genotype. Identification of the GH gene polymorphism in rabbit has been done by PCR-RFLP using Bsh1236I restriction enzyme by Fontanesi et al. (2012) who reported the presence of two types of alleles, namely C and T alleles with three kinds of genotypes, namely CC, TT, and CT genotypes.

Rex rabbit breed had frequency of genotype CC highest than Satin and Reza rabbit breeds. Satin rabbit breed had the highest frequency of genotype CT. Rex and Satin breeds were rabbit with good fur and Reza (Rex and Satin crosses) mostly influenced by Satin rabbit in this case that frequency of genotype TT same with CT (Table 1). Reza rabbit breed created by crossing between Rex and Satin rabbit with Mendel law did not work in the F2 based on Prasetyo (2007).
Phenotypic of Rabbit Breeds

Phenotypic studies included measurement of body weight and ultrasound imaging (USG) to measure the Longissimus dorsi muscle and perirenal fat thickness in every breed of rabbits. Ultrasound imaging of Longissimus dorsi muscle and perirenal fat in rabbits are shown in Figure 4. Perirenal fat visible white (hyper-echoic) curved shape on the wall of the stomach, while the muscle was part black gray (hypo-echoic) measured from under the skin. This measurement was performed transversely.

Phenotypic measurement of Longissimus dorsi muscle in every rabbit breeds showed significant association (P<0.05). Measurement analysis of muscle thickness from

Table 1. Estimating of polymorphic informative content (PIC) value on Rex, Satin, and Reza rabbit breeds

<table>
<thead>
<tr>
<th>Breed</th>
<th>n</th>
<th>PIC</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rex</td>
<td>11</td>
<td>0.207</td>
</tr>
<tr>
<td>Satin</td>
<td>11</td>
<td>0.375</td>
</tr>
<tr>
<td>Reza</td>
<td>11</td>
<td>0.373</td>
</tr>
</tbody>
</table>

Note: $n=$ number of samples.
Association of GH Gene Polymorphsm with Ultrasound Imaging of Perirenal Fat and Longissimus dorsi Muscle

Polymorphism of GH\(Bsh1236I\) gene with ultrasound imaging of perirenal fat and Longissimus dorsi muscle thickness at Rex, Satin and Reza rabbit showed that rabbit with CT genotype had thickness of Longissimus dorsi muscle higher than CC and TT genotype, although had no significantly different (\(P<0.05\)) (Table 5).

It seems that at rabbit with homozygous genotype, rabbit with CC genotype had Longissimus dorsi thickness muscle higher than rabbit with TT genotype. It was related to the thickness of fat that was inversely with the thickness of muscle, and could be associated with sexual maturity rate. Animal with late-maturing had a greater proportion of muscle with less fat (Irshad et al., 2012).

Table 5. Measurement of ultrasound imaging with different genotype for gene fragment of GH\(Bsh1236I\)

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Genotype</th>
<th>Perirenal Fat (cm)(\text{n=15})</th>
<th>Longissimus dorsi muscle (cm)(\text{n=10})</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>1.71 ± 0.40</td>
<td>1.78 ± 0.36</td>
</tr>
<tr>
<td></td>
<td>CC(\text{n=15})</td>
<td>1.91 ± 0.26</td>
<td>1.68 ± 0.21</td>
</tr>
<tr>
<td></td>
<td>TT(\text{n=8})</td>
<td>1.81 ± 0.32</td>
<td>1.86 ± 0.20</td>
</tr>
<tr>
<td></td>
<td>CT(\text{n=10})</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Note: \(n=\) number of samples; ns= non significant.

CONCLUSION

PCR-RFLP analysis of the GH\(Bsh1236I\) gene segments are high polymorphism in Rex, Satin, and Reza rabbit breeds. There are significant association between rabbit breed with Longissimus dorsi muscle thickness. The association of characteristic genotype of GH\(Bsh1236I\) gene with measurement phenotype is not significant, however it has a potency as marker assisted selection (MAS).

ACKNOWLEDGEMENT

Sincerely thanks is addressed to Dr. Ir. Bram Brahmaniyo, MSi. from Indonesian Research Institute for Animal Production (IRIAP) Ciawi Bogor, Indonesian Ministry of Education and Culture – Directorate General of Higher Education for BU (Beasiswa Unggulan) 2012, and special thanks to Mokhamad Fakhirul Ulum, DVM MSi. for ultrasound measurement.

REFERENCES


