Identification of Locus GH/Alu Polymorphisms of Kuantan and Pesisir Cattle

Hidayati* and Robbana Saragih
Breeding and Reproduction Laboratory, Faculty of Agricultural and Animal Science, UIN Sultan Syarif Kasim Riau, Pekanbaru, 28292, Indonesia

ABSTRACT

Kuantan cattle is a local beef cattle of Riau Province that adaptive and breed well along the Kuantan river flow, found in Indragiri Hulu Regency and Kuantan Singingi Regency. The highest population of Kuantan cattle (Figure 1) was found in Indragiri Hulu Regency with a total of 5,959 heads and in Kuantan Singingi Regency was 2,386 heads (Department of Animal Husbandry Riau Province, 2011). The morphometric of Kuantan cattle was relative to differences in year to year.

Qualitatively and morphometrically, the cattle have a variety of coat color, horn shape, and morphometrics. The results of Zulfikar (2018) showed that the coat color variations of male and female adult cattle high significantly to differences in the size of chest circumference, body length, shoulder height, hip height, hip width and circumference of the scrotum (male), where cows with light coat color have morphometrics higher than the dark coat color of Kuantan cattle. Kuantan cattle have relatively small body size and bodyweight compared to Bali cattle breeds and are relatively the same as Pesisir cattle (Decree of The Minister of Agricultural Number: 2908/Kpts/OT.140/6/2011). The morphometric of the bull i.e height of shoulder is 99.28 cm, the body length is 103.78 cm and the chest circumference is 126.22 cm with a bodyweight of about 138 kg while for the cows i.e the height of shoulder is 99.19 cm, the body length is 102.35 cm and the chest circumference is 123.27 cm with the weight the body is only around 132.18 kg (Decree of The Minister of Agricultural Number, 1052/Kpts/SR.120/10/2014).

Growth is a process of deposition, transfer of the substance of cells and an increase in the size and number of cells at different levels and points in a certain time that is influenced by growth hormones (Lawrence and Fowler, 2002). Growth in cattle is controlled by a complex system that is through the presence of somatotropic hormones (growth hormones). The existence of somatic hormones is regulated...
through the presence of genes that encode the hormones responsible for growth. Gene that have a relationship with postnatal growth is Growth Hormone (GH) which has an impact on bone and muscle growth after birth, anabolism such as bone growth and protein synthesis. GH is also needed for tissue growth, fat metabolism, normal growth (Etherton and Bauman, 1998), superovulation response, ovulation rate, fertility rate and embryo quality (Sumantri et al., 2011). GH consists of 191 amino acid sequences that are synthesized and secreted by the anterior pituitary gland under hypothalamic control, the two hormones it produces are GH RH (GH Releasing Hormone) and SRIF (Somatotrophin Releasing Inhibiting Factor) (Silveira et al., 2008). GH is encoded by the GH gene consisting of 5 exons and 4 introns found at 19q26qter on the bovine chromosome (Hediger et al., 1990).

Polymorphisms of GH/AluI genes as growth markers in cattle has been reported by several researchers, namely in Sahiwal cattle (Biswas et al., 2003), Pesisir cattle (Jakaria et al., 2007), Bali cattle, PO cattle, SIMPO cattle, LIMPO cattle (Mu'in, 2008), FH cattle (Muin and Zurahmah, 2009), Limousin cattle (Jakaria et al., 2009), Limura cattle (Volkan et al., 2013), and FH cattle (Volkan et al., 2013) and there have been no reports for Kuantan cattle. The AluI mutation point is at position 2141 (C>G) of the bovine GH gene, converts the amino acid Leucine to Valine on the 127th sequence of proteins (Volkan et al., 2013).

Increasing the productivity of Kuantan cattle could be done through selection and crossbreeding. Conventional selection requires high costs, a long time and a large population. Application of marker assisted selection through identification of GH/AluI gene polymorphisms, is one solution that could be done. Identification of gene diversity at the DNA level allows early detection of genetic potential in the early growth phase (Curi et al., 2005; Dekkers, 2004). Identification of locus polymorphisms of DNA can also be used as genetic markers to increase livestock production if polymorphic is found, and can also be used to assist conservation efforts if found monomorphic.

Materials and Methods

Sampling and DNA extraction

Fifty-four samples of Kuantan cattle bloods consist of 25 samples from Indragiri Hulu Regency (Figure 1) and 29 samples from Kuantan Singiringi Regency and 25 Pesisir cattle from BPTU-HPT Padang Mengatas West Sumatra were used in this study. Blood collection using a 5 mL syringe on vena jugularis vein, 4-5 mL blood was collected in the EDTA vacuum tube and carried in a cool box for DNA isolation. The process of DNA isolation was carried out at the Animal Molecular Genetic Laboratory of Faculty of Animal Science, IPB Bogor using Phenol Chloroform Method (Sambrook and Russel, 2001). The isolated DNA was then tested using agarose gel electrophoresis 1.5% and a random sampling using a spectrophotometer to calculate the concentration and purity of DNA.

GH gene amplification using the polymerase chain reaction method

DNA amplification was carried out at a total volume of 50 µL consisting of 4 µL (25-50 ng) template DNA, each 0.4 µL oligonucleotida forward and reverse (10 ng), 25 µL dream tag green master mix a and ddH2O up to 50 µL volume. The condition of the PCR thermocycler was 94°C predenaturation for 5 minutes, 94°C denaturation for 30 seconds, annealing 65°C for 1 minute, 72°C extension for 50 seconds and 72°C final extension for 5 minutes. Stages 2-5 of the PCR process were repeated 34 times. The success of PCR was tested agarose gel electrophoresis with a gel concentration of 2% in 1 x TAE shown by appearing a single band at the position of 211 bp (PCR product), using Bio Rad Documentation Gel. The DNA marker used is 50 bp. PCR amplification and AluI restriction process were done in Reproduction and Breeding Laboratory of UIN Suska Riau, Pekanbaru.

Identification of polymorphisms GH gene used Restriction Fragment Length Polymorphisms technique

The PCR product which was successfully amplified, then incubated the AluI enzyme (AG^CT) at 37°C for 3 hours. RFLP mixture consist of 6 µL PCR products, 0.4 µL Alu enzymes (4 units) added, 2.4 µL 10 x buffer and 15.2 µL ddH2O. Diversity visualization was performed on agarose gel 3% in 1 x TAE using Bio Rad Documentation Gel. The cutting site refers to Reis et al. (2001), LL genotype (two bands at 52 bp and 159 bp), LV genotype (three bands at 52 bp, 159 bp, and 211 bp) and VV genotype (one band 211 bp).
Data analysis
Analysis of genotype and allele frequency of GH/AluI locus in Kuantan and Pesisir cattle according to Nei (1987) and Hardy-Weinberg equilibrium (Guo and Thomson, 1992).

Results and Discussion
Concentration and purity of DNA isolation
The success of DNA isolation was carried out agarose gel of 1.5% in 1 x TAE qualitatively, determined by the appearance of a single band that was bright and clear and was above the marker (Figure 2). The average concentration and purity of isolated DNA were presented in Table 1. The concentration of DNA produced in this study ranged from 4.85 - 15.90 ng/µL indicated a relatively low range. Hidayati et al. (2016) reported that the concentration of DNA of Kuantan cattle in the same isolation method ranged from 27.45 - 121.45 ng/µL. Nsubaga et al. (2004) states that damage to the sample as a source of DNA material could affected the concentration of DNA produced. Factors causing damage to the source of DNA material are a long storage time, high environmental temperature so that it can damage the DNA hydrogen bonds so that it becomes irreversible and damaged purine and pyrimidine bonds from DNA, and the presence or number of cells (Hidayati and Aulawi, 2016). The lower the DNA concentration, the more volume is needed in the PCR process. DNA concentrations commonly used for the PCR process are in the range of 25-50 ng/µL (Hidayati et al., 2016).

Absorbance ratio values of 260/280 and 260/230 are used to assess the level of purity of DNA from the isolation. The value of DNA purity range (260/280) ranges between 1.49-2.97 and the value of DNA purity (260/230) is 0.07 - 0.20 (Table 1). The results showed that based on the ratio of absorbance values of 260/280, 32% (n = 8) samples had a good purity because they had a purity value between 1.8-2.0, 4% (n = 1) had a purity below 1, 8 and the remaining 64% (n = 16) have above 2.0 (Figure 3). Maximum absorbance of DNA occurs at a wavelength of 260 nm and protein at a wavelength of 280 nm (Boyer, 2005). Purity values (260/280) indicate the purity of DNA from protein contaminants (Widiarthi et al., 2014; Qomar et al., 2017). The variation in absorbance ratio values of 260/280 was influenced by DNA pH, wavelength accuracy, composition of nucleotide bases (A; T; G; C). Efforts can be made to increase the purity of DNA from protein contaminants, according to Qomar et al. (2017), with an increase in Proteinase K (Prot K) and Washing Blood Cell repeatedly.

Figure 2. Qualitative Test of DNA Isolation, 1-15 = Sample Code, M = DNA Leader 100 bp.

Table 1. Average value of DNA concentration and purity of isolated DNA

<table>
<thead>
<tr>
<th>Variables</th>
<th>Average ± Stdev</th>
<th>Maximum</th>
<th>Minimum</th>
</tr>
</thead>
<tbody>
<tr>
<td>Concentration (ng/µL)</td>
<td>9.76 ± 2.87</td>
<td>15.90</td>
<td>4.85</td>
</tr>
<tr>
<td>Purity 260/280</td>
<td>2.15 ± 0.33</td>
<td>2.97</td>
<td>1.49</td>
</tr>
<tr>
<td>Purity 260/230</td>
<td>0.13 ± 0.04</td>
<td>0.20</td>
<td>0.07</td>
</tr>
</tbody>
</table>
phenol contaminants added to the DNA isolation process in the form of compounds phenol chloroform.

**Amplification GH gene and restricted fragment length polymorphisms with AluI enzyme on Kuantan and Pesisir cattle**

Amplification of the GH gene of Kuantan and Pesisir cattle samples were carried out at annealing temperature of 65°C for one minute. The results showed that the PCR product along 211 bp flanking intron 4 and exon 5, and the results of the RFLP by AluI enzyme were presented in Figure 4. AluI enzyme cutting sites on PCR products at 52 bp and 159 bp were formed the LL genotype (Leucine-Leucine). LL genotype of the GH/AluI locus was a common genotype that appears in cattle with small body sizes or light beef type such as Kuantan cattle. The LL genotype of Kuantan cattle can be used to assist conservation efforts in the future. Jakaria et al. (2007) the same reported in Pesisir cattle from the Regency of Pesisir Selatan and Padang Pariaman, West Sumatra Province were LL genotypes. LL genotype was the dominant genotype in Pesisir cattle with LL, LV and VV genotypes were 0.985, 0.015 and 0.000 respectively. GH/AluI loci of Madura cattle were monomorphic with LL genotype and polymorphic in Limura cattle with LL, LV and VV genotypes were 0.985, 0.015 and 0.000 respectively (Hidayati et al., 2016). Bos indicus was group of cattle that have a dominant LL genotype compared to LV and VV genotypes (Biswas et al., 2003; Jakaria et al., 2007; Mu'in, 2008; Volkandari et al., 2013), as well as Bos sundaicus (Bali cattle) (Mu'in, 2008) and buffaloes (Biswas et al., 2003).

Bos taurus such as Friesien Holstein (Biswas et al., 2003; Muin and Zurahmah, 2009; Hartatik et al., 2015), Karan Fries (Aruna et al., 2004), Brazilian Canchim (Silveira et al., 2008), Podolian cattle (Dario et al., 2005), and Limousin (Jakaria et al., 2009) were polymorphic, the frequency of L allele was not more than 0.99. Crosses Bos taurus X Bos indicus have produced polymorphic cattle at GH/AluI gene locus such as in Limousin X Madura (Volkandari et al., 2013), Simmental x PO (Mu'in, 2008) and Limousin x PO (Mu'in, 2008). The LV genotype has better growth compared to LL genotype on SIMPO calf (Mu'in, 2008). Reis et al. (2001) also reported that LV genotypes from local Portuguese beef cattle i.e Alentejana, Marinha and Preta breeds have greater bodyweight than other breeds (Arouquesa, Barossã, Maronesa, Mertolenga and Mirandesa).

**Genotype frequency and allele frequency of GH/AluI gene locus in Kuantan and Pesisir cattle**

Genotype and allele frequency of Kuantan and Pesisir cattle of GH/AluI gene locus are presented in Table 2. The results showed that the GH/AluI gene locus in Kuantan and Pesisir cattle showed monomorphic (LL genotype). The GH/AluI

![Figure 4](image)

Figure 4 : 1st Well = 50 bp DNA Leader, 2nd – 5th Well (PCR Product of Kuantan Cattle sample code: 10, 24, 30, 51), 6th – 7th Well (PCR Product of Pesisir cattle, sample code: 4863, 4856), 8th – 15th Well (RFLP of Kuantan cattle, sample code: 10, 24, 30, 51 and Pesisir cattle, sample code: 4863, 4856, 4858, 4819), were formed LL genotype.

<table>
<thead>
<tr>
<th>Breed</th>
<th>Genotype Frequency</th>
<th>Allele Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>LL</td>
<td>LV</td>
</tr>
<tr>
<td>Kuantan Cattle</td>
<td></td>
<td></td>
</tr>
<tr>
<td>a. Indragiri Hulu Regency (n= 25)</td>
<td>1.00</td>
<td>0.00</td>
</tr>
<tr>
<td>b. Kuantan Singingi Regency (n=29)</td>
<td>1.00</td>
<td>0.00</td>
</tr>
<tr>
<td>Total</td>
<td>1.00</td>
<td>0.00</td>
</tr>
<tr>
<td>Pesisir Cattle</td>
<td></td>
<td></td>
</tr>
<tr>
<td>BPTU-HPT Padang Mengatas (n=25)</td>
<td>1.00</td>
<td>0.00</td>
</tr>
</tbody>
</table>
gene locus could not be used as one genetic markers of body growth genes in Kuantan cattle, but can be used to their conservation effort. A monomorphic allele if the allele frequency is equal to or less than 0.01 (Nei, 1987). In this study the frequency of L allele in Kuantan and Pesisir cattle was equal to 1.00, so that the Kuantan and Pesisir cattle don’t mutated at the GH/AluI gene locus. One effort to bring up variations of the GH/AluI gene locus in Kuantan and Pesisir cattle through crossing with Bos taurus (Simmental, Limousin and FH) that have a VV or LV genotype. The results of Hardy Weinberg’s equilibrium analysis were the population of Kuantan and Pesisir cattle wasn’t in equilibrium, the value of chi square >1. This can be caused by the relatively small size of sample used in this study. Research using a larger sample size is recommended for further research.

Conclusions

The locus of the GH/AluI gene in Kuantan (n = 54) and Pesisir cattle (n = 25) were monomorphic with the LL genotype (1.00) so that the GH/AluI gene locus could not be used as one genetic markers of growth body but used to conservation effort in the future.

Acknowledgment

We would like to thank the Research and Development Institute of UIN Suska Riau for funding this research with contract number 282 / Un.04 / L.1 / TL.01 / 2019.

References


Hidayati and Robbana Saragih
Identification of Locus GH/Alui Polymorphisms of Kuantan and Pesisir Cattle


