

The Relation of IGF-1 Genotype with Weight in Etawah Grade Goats at Polewali Mandar Regency

Surya^{1,*} Andi Yulyani Fadwiwati¹ Muhammad Ihsan Andi Dagong²

¹ Agricultural Technology Research Center Gorontalo, Ministry of Agriculture, Gorontalo

² Department of Animal Production, Faculty of Animal Science, University of Hasanuddin

*Corresponding author. Email: aku.uyha@yahoo.com

ABSTRACT

A study was conducted to the relation of IGF-1 genotype with weight in Etawah Grade goats at Polewali Mandar Regency. The object of this research used 22 Etawah Grade goats that had been weighed and their blood was taken for DNA and PCR-RFLP extraction to determine the diversity of the IGF-1 genotype. The data then calculated the allele frequency and genotype frequency, a simple linear regression analysis, the correlation coefficient, and the coefficient of determination. The research results obtained were that AA, AB, and BB genotypes of IGF-1 gene with the most allele frequency and genotype frequency is allele A and AB genotype, simple linear regression equation $Y = 15,46 + 4,53X$ with a correlation coefficient of 0,67 and a coefficient of determination is 0,42. It was concluded that there was a strong the relationship of IGF-1 genotype diversity with weight in Etawah Grade goats.

Keywords: *IGF-1 genotype, weight, Etawah Grade goat*

1. INTRODUCTION

Goats is one of small ruminants have been developed in Indonesia Goats are one of the small ruminants that have been developed in Indonesia. Goats have the ability to adapt and survive the worst environmental conditions [1]. Goats can be classified into the kingdom: Animalia; phylum: Chordata, class: Mammalia; ordo: Artiodactyla; family: Bovidae; subfamily: Caprinae; genus: Capra; species: Capra aegagrus; and subspecies: Capra aegagrus hircus [2].

Indonesia's goat varieties, Etawah Grade goat, can produce meat, milk and skin. Etawah Grade goat is the result of a cross between *Kacang* goat and *Etawah* goat that can adapt to the conditions and habitats in Indonesia [3]. Goats have characteristics that are easy to breed, so that they have an important role as a genetic resource.

DNA or commonly referred to as deoxyribonucleic acid is located on the chromosome, seen in the form of double strands that twist each other long with the base groups, namely purines (Adenine and Guanine) and pyrimidines (Cytosine and Thymine), and have a function as a determinant of the type of protein to be synthesized [4]. Genes are

widely expressed, such as the growth hormone coding gene together with the IGF-1 gene expression, one which of present in the blood circulation [5].

The potential in Etawah Grade goats can be measured and observed through their weight characteristics. Weight is a trait that are controlled by two or more genes. One important gene that affect weight of goats is the growth hormone coding gene [6], as in the calpastatin gene [7], the IGF-1 gene [8], the leptin gene [9], the pituitary transcription factor-1 gene [10], etc. The IGF-1 gene are the candidates' gene it can be used that selection strategies for using DNA markers.

This study was conducted to the relationship of IGF-1 (Insulin-like Growth Factor-1) genotype diversity with weight in Etawah Grade goats at Polewali Mandar Regency.

2. METHODS

The research was conducted in May-June 2014 at the Biotechnology, Integrated Laboratory, Faculty of Animal Science, University of Hasanuddin, Makassar. This research used 22 Etawah Grade

female goats blood samples at Polewali Mandar Regency.

2.1. Research Procedure

The collected blood sample is then extracted with GeneJET Genomic DNA Extraction kit. Purified DNA using the spin column method and the DNA results were collected and stored at temperature of -20°C. Furthermore, PCR-RFLP amplification using IGF-1 exon 4 primers with DNA sequences (forward 5'-CACAGCGTATTATCCCAC-3' and reverse 5'-GACACTATGAGCCAGAAG-3'), annealing temperature of 60°C, and the restriction enzyme used was *HaeIII*. The PCR-RFLP product sample was then viewing and photographing the agarose gel with UV transilluminator (gel documentation system).

2.2. Data Analysis

2.2.1. Allele Frequency and Genotype Frequency

The allele frequency of the IGF-1 gene is the ratio of an allele in each individual in a population to the number of all individuals. The allele frequency is computed using the following formulas [11]:

$$X_1 = \frac{2N_{11} + N_{12}}{2N}$$

Information:

- X₁ = Allele frequencies A₁ or A₂
- N₁₁ = The number of samples in the genotype A₁₁ or A₂₁
- N₁₂ = The number of samples in the genotype A₁₁ or A₂₁
- N = Total sample from population

The genotype frequency, namely the ratio of certain genotypes in a population. The genotype frequency was calculated using the following formulas [11]:

$$X_{11} = \frac{N_{11}}{N}$$

Information:

- X₁₁ = Genotype frequency A₁₁ or A₂₁
- N₁₁ = The number of samples in the genotype A₁₁ or A₂₁
- N = Total sample from population

2.2.2. The Simple Linear Regression Model

When there is only one independent variable in the linear regression model, the model is generally termed as a simple linear regression model. A simple linear regression model can obtain using statistics according to Sugiyono [12]. A regression line has three possibilities which will describe a positive, negative linear relationship, and there is not a linear relationship.

Furthermore, a correlation coefficient analysis was carried out to measure a relation between X and Y. The mathematical formula for computing *r* and magnitude value of correlation coefficient can provide an interpretation using statistics according to Sugiyono [12].

Value of a correlation coefficient, which ranges from -1 to +1. The + and - signs are used to positive and negative linear correlations based on criteria [12].

A coefficient of determination can be used to determine the ability a model explained variation in the dependent variable [13]. The coefficient of determination analysis using statistics according to Sugiyono [12].

3. RESULT AND DISCUSSION

3.1. Allele Frequencies and Genotype Frequencies

The allele and genotype frequencies differed in results. Frequency results were obtained based on the IGF-1 gene band pattern of exon 4 using the restriction enzyme *HaeIII*, as in Figure 1.

Figure 1 shows the results of the UV visualization of the transilluminator on PCR-RFLP for the IGF-1 exon 4 gene band pattern using the restriction enzyme *HaeIII* in the blood sample in Etawah Grade goats to produce genotypes AA (363 bp), AB (363, 264 and 99 bp), and BB (264 and 99 bp). The results of RFLP analysis are commonly used to detect the diversity in genes related to economic characteristics, such as milk production and quality [14]. Furthermore, stated that the PCR-RFLP method is one of the methods to continue the analysis of PCR products [15]. The PCR method uses nucleotide sequences which will later be recognized by restriction enzymes which are also known as restriction sites.

The IGF-1|*HaeIII* gene in Etawah Grade goats at Polewali Mandar Regency is polymorphic. This is in

line with Tunnisa [16] research on *Kacang* goat and according to research that the IGF-1 gene in goats is polymorphic [17]. The same was true for *Xinjiang* goats

and *Nanjiang* goats where there were three genotypes [18].

The allele frequency and genotype frequency values in Etawah Grade goats at Polewali Mandar Regency as in Table 1.

The allele frequencies A (0.57) and B (0.43), as well as the genotypic frequencies of AA (0.32), AB (0.50), and BB (0.18) shown in Table 1, show the characteristics in Etawah Grade goats at Polewali Mandar Regency, where the allele A and AB genotype frequencies are the most frequent. The study by Arisuryanti [19] showed that the peculiarities of a population can be seen based on the frequency of genes and the frequency of their genotypes. Furthermore, the allele frequency and genotype frequency can change, this can be due to

evolution, for example, mutations, migration, gene flow, genetic drift, and natural selection [20].

The results of the research on allele frequency and genotype frequency resulted in 2 (two) types of alleles and three (three) types of genotypes. The difference in allele frequency and genotype frequency values indicates a change in a population due to an indication of microevolution, namely the occurrence of small evolution at the gene level. Based on the results of the genotype frequency, it can describe simple functions of allele frequency. The frequencies of different genes influence by mutation, selection, sudden changes in genetic frequency, as well as factors in the occurrence of *in-breeding* and *out-breeding* [21].

3.2. The Simple Linear Regression Model

The simple linear regression model that shows the relationship of IGF-1|*HaeIII* locus in Etawah Grade goats, as in Figure 2.

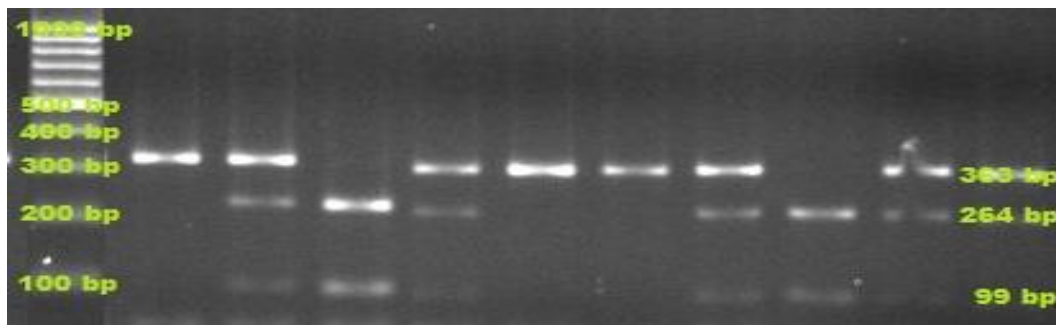


Figure 1. Ex-4 IGF-1 Gene Band Patterns on Agarose 2% with the *HaeIII* Restriction Enzyme. AA genotype: 363 bp; AB genotype: 363, 264 and 99 bp; BB genotype: 264 and 99

Table 1. The Allele Frequency and Genotype Frequency Values at the IGF-1|*HaeIII* Locus in *Etawah Grade* goats at Polewali Mandar Regency

Frequency	
Allele	Score
A	0.57
B	0.43
Genotype	Score
AA	7 (0,32)
AB	11 (0,50)
BB	4 (0,18)

Source: Processed data, 2020.

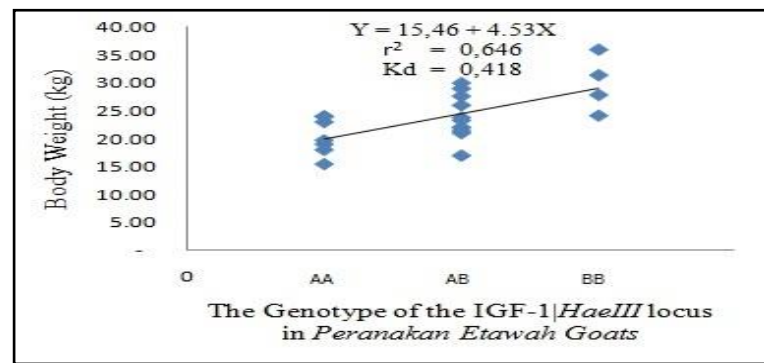


Figure 2. The Simple Linear Regression Analysis, the Correlation Coefficient, and the Coefficient of Determination of the relationship of IGF-1|HaeIII Locus with Weight in Etawah Grade goats at Polewali Mandar Regency.

Figure 2 shows results in simple linear regression following an equation $Y = 15,46 + 4,53X$, where the regression coefficient of the genotype variable for the IGF-1|HaeIII locus is 4,53 meaning that every addition to the genotype variable for the IGF-1|HaeIII locus, there will be an increase in weight of body amounted to 4,53. This shows that there is a positive (unidirectional) influence between the genotype of the IGF-1|HaeIII locus with weight in Etawah Grade goats at Polewali Mandar Regency. The genotype BB has a higher weight compared to the AA and AB genotypes. Thus, IGF is an important growth factor involved in a variety of physiological processes including cell differentiation, embryogenesis, lactation, metabolism, reproduction, and growth. The study by Misitahari [15] showed that growth hormone (GH) gene through the IGF-1 induction plays an important role part of a wide network of growth factors and its derivatives [22].

The correlation is defined as the relationship between two variables. The results obtained show a correlation coefficient $r > 0$ of 0,646, it means that the data is a strong linear relationship of IGF-1|HaeIII locus with weight in Etawah Grade goats at Polewali Mandar Regency. This strong relationship is seen based on the performance in Etawah Grade goats by measuring their weight. The study Curi [23] showed that the GH and IGF-I are important regulators of bone and muscle growth of livestock.

Furthermore, coefficient of determination should be used to determine the percentage the influence genotypes of IGF-1|HaeIII locus with weight in Etawah Grade goats at Polewali Mandar Regency. The coefficient of determination obtained was 0,418, meaning that the genotype of the IGF-1|HaeIII locus affected weight in Etawah Grade goat by 41,8 % and

the rest was influenced by other variables. The study Nawawi [24] shows a proportion for diversity of a variable will be explained by the predictor variable or power from independent variables to explain dependent variables. Other studies related to growth hormone (GH) coding genes regarding the diversity of the GH HaeIII gene haplotype in Boer goats [25], regulation of the IGF-1 to animal growth [26], the relationship the IGF-1 gene with growth in Nanjiang Huang goat [27]. The IGF-1 gene of local mediators of the GH action, is used of potential marker genes related to weight traits [28]. This is because the IGF-1 gene is a growth factor that stimulates cell proliferation and differentiation [26].

4. CONCLUSION

The results obtained were that AA, AB, and BB genotypes of IGF-1 gene with the most allele frequency and genotype frequency is allele A and AB genotype, simple linear regression equation $Y = 15,46 + 4,53X$ with a correlation coefficient of 0,67 and a coefficient of determination is 0,42. It was concluded that there was a strong the relationship of IGF-1 genotype diversity with weight in Etawah Grade goats.

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