

# Phenotypic diversity of five goat populations in tropical environment

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## ABSTRACT

Phenotype characteristic is observable traits such as morphology which is affected by genetic code, environment factor and their interaction. This study observed phenotypic diversity of five goat populations which are developed under Indonesian tropical environment. A total of 55 goats from five domesticated breeds have been used for morphological observation. They were Peranakan Etawa (PE) goat, Boer goat, Bligon (Jawa Randu) goat, Kacang goat, and crossbred Boer and Jawa Randu goat (abbreviated as Boerja). The phenotypic traits observed in this study were body weight (BW), chest girth (CG), body length (BL), withers height (WH), and coat color. Those data were analyzed using one-way analysis of variance (one-way ANOVA) with alpha at 5% level and Tukey's test was also performed to differentiate among goat breeds. Moreover, cluster analysis of k-means method was carried out to evaluate distribution pattern of phenotypic traits of five populations. The results showed that quantitative traits observed in this study were significantly different among goat breeds ( $P < 0.05$ ). PE, Boer and crossbred goats containing their DNA (Jawa Randu and Boerja) had higher BW, CG, BL, and WH than Kacang goats. Mix white and brown coat colors was found in most of Boer, Boerja, and Jawa Randu goat populations, on the other hand Kacang goat had mix black and brown coat color, and mix black and white coat color was found in PE goat population. In addition, BW was significantly correlated with CG, BL and WH traits. The Pearson correlations were 0.78, 0.67, and 0.44, respectively. In term of cluster analysis, WH and CG traits clearly clustered among goat populations. These results suggested that five goat populations developing in Indonesia were phenotypically diverse.

*Key words: Phenotypic diversity, Goat breed, Tropical environment, Cluster analysis*

## Introduction

Goat is one of the most popular domesticated animals which is favored to be raised in Indonesia. Batubara (2011) reported that domesticated goats have spread in several regions with different climates and have separated over a long period of time. Well-developed goat breeds in Indonesia

mostly classified into three groups, i.e. indigenous, imported, and well adapted breed which is mostly known as local breed. Various environments and selection methods of goat may cause genetic diversity among populations (Rout *et al.*, 2008). Cross-breeding between goat breeds, acclimatization, and isolation for long period of time in specific area may also generate specific population. In addition, goat

breed assimilated with other breed population may cause genetic diversity due to random genetic drift (Freeland, 2005). Leveque and Mounolou (2003) stated that other factors causing genetic variations are mutation, migration, and nonrandom mating. These processes trigger sustainable genetic diversity although genome in a species is almost the same. However, small changes in the genome may affect phenotypic traits, therefore every goat breed has different phenotypic characteristics. Phenotypic trait is composite of both qualitative and quantitative traits which are observable and important as marker. Qualitative trait is controlled by several genes with only small intervention of environment. On the other hand, quantitative trait is controlled by many genes (polygenic) and environment plays very important role (Leveque and Mounolou, 2003).

The study related to phenotypic diversity has been conducted with different approaches, however analysis of phenotypic diversity using cluster and principle component analyses in goat population does not found yet. The importance of cluster analysis and principle component analysis approaches is that the distribution patterns of phenotypic diversity clearly illustrated. Therefore, the objective of this study was to observe phenotypic diversity of five female goat populations which are developed under Indonesian tropical environment.

## Materials and Methods

### Goat population

A total of 55 goats have been used in this study. They were grouped into five breeds consisted of Peranakan Etawa (PE) goat, Boer goat, Bligon (Jawa Randu) goat, Kacang goat, and crossbred Boer and Jawa Randu goat (abbreviated as Boerja). The average age of goats was more than a year old based on its incisors. Each breed consisted of eleven heads of goat which are collected from several farms such as CV. Kambing Boerja, Sari Etawa Farm, CV. Sahabat Ternak, Bhumi Nararya Farm, Jatikuwung, Adhi Farm, and UD Sholeh. Purposive sampling method was applied to select animals.

### Observation of quantitative and qualitative traits

Both quantitative and qualitative traits have been observed in this study. Quantitative data observed were body weight (BW), chest girth (CG), body

length (BL), and withers height (WH). Goat was ensured standing with the correct posture before measurement. Body weight was scaled using analog body weight scale (Camry Scales, China). Body length and withers height were measured using ruler, while chest girth was measured using measuring tape. All data were in centimeter (cm). In addition, coat color pattern was also observed as representative of qualitative trait by directly observing coat color pattern.

### Data analyses

Phenotype data were filtered to eliminate incomplete and abnormal data before analyzed. In term of qualitative data, it was tabulated and proportionally calculated. Quantitative data was also tabulated and they were then calculated to know average values ( $\mu$ ) and their standard deviations. Furthermore, correlation between body weight and other body measurements were calculated using Pearson method by following formula:

$$r = \frac{\sum xy - \frac{(\sum x)(\sum y)}{n}}{\sqrt{\left(\sum x^2 - \frac{(\sum x)^2}{n}\right) \left(\sum y^2 - \frac{(\sum y)^2}{n}\right)}} \quad .. (1)$$

where  $r$  is correlation coefficient,  $x$  is variabel  $x$ ,  $y$  is variabel  $y$ .

Quantitative data was then analyzed using one-way analysis of variance (ANOVA) and 5% alpha was set. To differentiate variable tested among breeds, Tukey's test was applied.

$$Y_{ij} = \mu + T_i + \varepsilon_{ij} \quad .. (2)$$

$Y_{ij}$  is the value of observed variable,  $\mu$  is overall mean,  $\delta_i$  is the effect of  $i^{\text{th}}$  breed,  $\varepsilon_{ij}$  is random error.

The result of breed grouping based on quantitative data was furthermore analyzed using cluster k-means method with five dots (centroid). Data distribution pattern was also evaluated based on one trait distribution with other traits. Accuracy of cluster analysis was confirmed with correlation analysis.

$$\mu_k = \frac{1}{N_k} \sum_{q=1}^{N_k} x_q \quad .. (3)$$

where  $\mu_k$  is centroid dot of  $K^{\text{th}}$  cluster,  $N_k$  is the number of data of  $K^{\text{th}}$  cluster,  $x_q$  is  $Q^{\text{th}}$  data in the  $K^{\text{th}}$  cluster. To see percentage of diversity and distribution pattern of five different goat breeds was able to see by using principle component analysis.

$$\begin{aligned}
 Y_1 &= e'_1 X = e'_{11} X_1 + e'_{21} X_2 + \dots + e'_{p1} X_p \\
 Y_2 &= e'_2 X = e'_{12} X_1 + e'_{22} X_2 + \dots + e'_{p2} X_p \\
 &\vdots \\
 Y_p &= e'_p X = e'_{1p} X_1 + e'_{2p} X_2 + \dots + e'_{pp} X_p
 \end{aligned} \quad \dots (4)$$

$Y_1$  is first component,  $Y_2$  is second component,  $Y_p$  is  $p^{\text{th}}$  component,  $e'$  is Eigen vector,  $X_p$  is Random vector.

## Results and Discussion

### Quantitative traits

The highest average of body weight of five goat populations was statistically found in PE goat population following by Boer goat, and Boerja goat. Bligon and Kacang goat populations were identified as smaller goat breeds (Table 1). These results suggested that PE and Boer goats were considered as big goat breeds and Boerja goats as medium goat breed, on the other hand Bligon and Kacang breeds were categorized as small goat breeds. The body weight of adult PE goat is ranged from 34.03 to 40.20 kg (Pamungkas *et al.*, 2009; Hidayati *et al.*, 2015). In addition, body weight of adult Boer goat is ranged from 30 to 35 kg (Mirajuddin, 2006, Mahmilia and Tarigan, 2007; ABGA, 2019). Body weights of Bligon and Kacang goats which are considered as small goat breeds can reach 20 kg

(Pamungkas *et al.*, 2009).

Statistical analyses also showed that body measurement data including BL, WH, and CG were significantly different among goat breeds ( $P < 0.001$ ). PE goat was highest in BL, WH, and CG, on the other hand Kacang goat was smallest in BL, WH, and CG (Table 1). In addition, body measurement traits of crossbred goat population consisted of boerja (Boer and Bligon crosses), and Bligon (PE and Kacang crosses) showed average value of their parents (Table 1). These findings proved that five goat populations which are developed in Indonesian tropical climate were diverse. They can specifically be used to distinguish five goat breeds. Phenotypic diversity may be caused by genetic diversity in the goat populations. Body measurement traits without characteristics of a population which are able to describe a group of specific traits (uniqueness) of a goat breed (Suparyanto *et al.*, 1999; Zein *et al.*, 2012). Additionally, environment and activity differences of goat population response to different BW and body measurement traits (Cam *et al.*, 2010).

### Qualitative traits

Based on the observation, five goat populations displayed coat color pattern diversity (Table 2). Three major coat colors (white, brown, and black) and their combination were observed. PE, Boer, and Kacang goats represented pure breed, while Bligon and Boerja represented crossbred goats.

**Table 1.** Quantitative Traits of Five Goat Breed Populations

Breed	BW (kg)	BL (cm)	WH (cm)	CG (cm)
PE	46.90 <sup>a</sup>	75.31 <sup>a</sup>	74.36 <sup>a</sup>	80.90 <sup>a</sup>
Boer	38.54 <sup>b</sup>	67.50 <sup>b</sup>	64.63 <sup>b</sup>	77.22 <sup>ab</sup>
Kacang	24.63 <sup>d</sup>	60.27 <sup>c</sup>	62.27 <sup>b</sup>	69.27 <sup>c</sup>
Bligon	28.31 <sup>cd</sup>	62.63 <sup>bc</sup>	73.54 <sup>a</sup>	72.90 <sup>c</sup>
Boerja	31.77 <sup>c</sup>	66.13 <sup>bc</sup>	64.68 <sup>b</sup>	69.10 <sup>bc</sup>

<sup>a,b,c,d</sup> Different superscript in the same column indicates highly significant differences among goat breeds ( $P < 0.001$ )

**Table 2.** Coat Color Pattern of Five Goat Populations (%).

Breed	W	L	B	W-L	L-B	W-B	W-L-B
PE	0	0	0	63.6	0	36.4	0
Boer	0	0	0	0	0	100	0
Kacang	0	0	18.2	0	36.4	18.2	27.3
Bligon	9.1	0	18.2	18.2	0	45.4	9.1
Boerja	0	0	9.1	27.3	0	63.4	0

W is white; L is black; B is brown; W-L is combination of white and black, L-B is combination of black and brown; W-B is combination of white and brown; and W-L-B is combination of white, black and brown.

PE goat in this study was mostly combination of white and black (W-L). White and brown coat color was also found in PE population (Table 2). This result was similar to Hidayati *et al.* (2015) that PE goat is dominantly white coat color with black and brown in some parts of its body. Purebred PE can be found in Kaligesing District of Central Java. Combination of white-black and white-brown is the most combination (Pamungkas *et al.*, 2009; Hidayati *et al.*, 2015). Coat color of Boer breed was a hundred percent uniform with white and brown combination. This result is similar to previous study that states Boer goat generally white in its body and brown (brick red) is found in neck and head (Mirajuddin, 2006; Mahmilia and Tarigan, 2007; ABGA, 2019). Kacang goat observed in this study was varied with black and combination of white, black, and brown (W-L-B) which are similar to Pamungkas *et al.* (2009) and Batubara (2011).

In term of crossbred goat populations, their coat color was also varied. Their coat colors were affected by their parents since it is well-known inherited. Bligon coat color represented its parental (PE and Kacang) likewise Boerja which created by three goat breeds (Boer, PE and Kacang goats). Diversity of coat color in five goat populations can be used as phenotype characteristic of each breed.

### Correlation among quantitative traits in five goat populations

Correlation analysis has been conducted between body weight and body measurement traits in five goat populations. Body weight was significantly correlated with BL, WH, and CG (Table 3). The highest coefficient correlation was found between BW and CG in all populations, i.e. 0.78. Chest girth is directly associated with chest and abdomen cavity where most of body weight donated by chest to hip, therefore higher chest girth produces higher body weight. Chest girth has the best accuracy which is indicated by high coefficient correlation than body length and withers height (Raja *et al.*, 2013). It may be due to digestive tract in the abdomen contributes 10 to 25% of live body weight in ruminant animals (Dalton, 1984). Previous studies reported that chest girth was tightly correlated with body weight in Bligon goat, Donggala sheep, and Yakansa sheep (Malewa, 2009; Basbeth *et al.*, 2015; Afolayan *et al.*, 2006).

Body weight was also significantly correlated with body length in goat population in Indonesia.

**Table 3.** Coefficient correlation between body weight and body measurement traits in five goat populations

Goat Breed	BL	WH	CG
Peranakan Etawa	0.20	0.36	0.81*
Boer	0.20	0.66*	0.74*
Kacang	0.54*	0.35	0.83*
Bligon	0.81*	0.25*	0.24
Boerja	0.68*	0.60*	0.30
All breeds	0.67*	0.44*	0.78*

\*Different superscript in the same column indicates significant correlation ( $P < 0.05$ )

Previous studies reported that body length was closely correlated with body weight (Pesmen and Yardimici, 2008). In addition, Adeyinka and Mohammed (2006) described that coefficient correlation between body weight and body length was 0.88 in North Nigeria goat population. Positive correlation between body length and body weight was also found in Iranian Macoei sheep and male sheep in Nigeria (Shirzeyli *et al.*, 2013; Mahmud *et al.*, 2014).

Withers height was also found to be positively correlated with body weight of five goat populations. However, the coefficient correlation was quite small and less than 0.5. Raja *et al.* (2013) stated that withers height does not directly contribute to abdominal cavity where foot bone structure plays a role in body movement.

### Cluster analyses

Cluster analysis is addressed to evaluate group plotting of body weight and body measurement traits of five goat populations in tropical area. Handoyo *et al.* (2014) explains that k-means clustering determines cluster according to centroid of desired cluster, the nearest value to centroid forms a cluster, so the new data set is formed according to centroid and the number of clusters. Previously, a number of studies using body measurements to estimate genetic distance in five Andalusian goats (Herera *et al.*, 1996), local goat in Burkina Faso (Traore *et al.*, 2008), Indonesian local goat (Suparyanto *et al.*, 1999; Sumantri *et al.*, 2007; Batubara, 2011) have been reported.

The accuracy of original data with cluster data reached 71.25% in overall population. In details, the accuracies were 59.09% in Boer goat population indicated by black dots, 52.63% in Boerja goat indicated by dark blue dots, 76.47% in Kacang goat (red

dots), 100% in PE goat (light blue dots), and 68.1% in Bligon goat (green dots), respectively (Fig. 1). Five clusters have been created by using BW, BL, WH, and CG data. They were mixed in Kacang goat cluster, Boer cluster, Boerja cluster, and Bligon cluster. It may be due to their body weight and body measurement traits were identical and also their blood composition was also closed which is resulted as compensation of crossbreeding among them. Unrelated goat breeds have high genetic distance (Zein *et al.*, 2012). In this study, PE and Kacang goat populations were completely separated and unrelated each other. It may be caused by the big differences of quantitative trait values observed in this study. On the other hand, crossbred goats were mixed each other based on quantitative traits because their phenotypic characters inherited by parents which are literally different breeds. Sumantri *et al.* (2007) reported that the proportion of mixture value affecting similarity of a goat breed or cluster may be based on similarity of phenotypic traits, especially body measurements.

In Figure 2, cluster analysis of overall data (both quantitative and qualitative data) showed that 84.97% of data were varied. This result also showed that there was high variation of observed traits from five goat populations. However, the clusters formed in this study were not completely separated. They were still linked each other suggested there were similarity in the diversity of five goat population

developing in Indonesian tropical area.

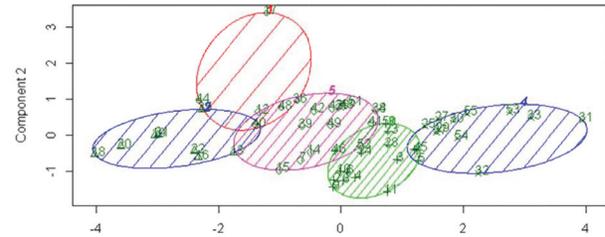


Fig. 2. Diversity and Clustering of Five Goat Populations Resulted by the Principle Component Analysis

**Conclusion**

In conclusion, phenotypic characteristics of five goat populations in Indonesia consisted of PE, Boer, Kacang, Bligon and Boerja goats were varied by 84.97% based on quantitative data and coat color pattern. This value showed phenotypic traits can be used to identify goat breeds. Further study may be needed using much more data.

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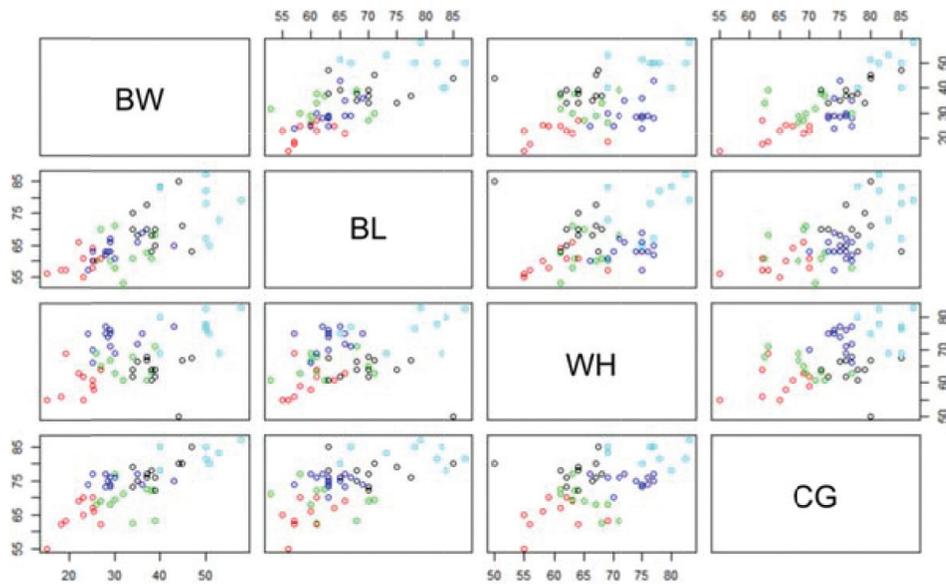


Fig. 1. Plotting Pattern of Quantitative Traits using Cluster K-Means in Five Goat Population

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