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Characterization in Two Indonesian *Bos indicus* Cattle Breeds Based on Morphometrical Measurements

Widya Pintaka Bayu Putra[1] Fiqy Hilmawan[2] Johar Arifin[3]

[1] *Indonesian Institute of Science, Bogor, West Java, Indonesia*
[2] *South Kalimantan Assessment Institute for Agricultural Technology, Banjarbaru, South Kalimantan, Indonesia*
[3] *Faculty of Animal Science, Padjajaran University, Jatinangor, West Java, Indonesia.*

Correspondence: *Widya Pintaka Bayu Putra* (*widya.putra.lipi@gmail.com*)

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ABSTRACT

Objective: The aim of this study was carried out to obtain the discriminant variables between Pasundan and Ongole bulls through morphometrical measurements.

Materials and Methods: Six morphometric traits of chest girth (CG), withers height (WH), body length (BL), chest depth (CD), hip height (HH) and rump width (RW) were performed in this study. Total of 110 bulls (72 Pasundan and 38 Ongole) from West Java Province of Indonesia were used in this study.

Results: The stepwise discriminant analysis showed that three morphometrical measurements of CG, BL and CD had strong discriminating power to characterize of both breeds. The discriminant function obtained correctly classified 87.5% for Pasundan and 100% for Ongole (with canonical correlation of 0.81).

Discussion: Pasundan and Ongole bulls can be characterized using discriminant analysis with at least three morphometrical measurements of CG, BL and CD. Therefore, about 12.5% of morphological characteristics in Pasundan bulls was closed to Ongole bulls.

Keywords: *Bos indicus, Discriminant analysis, Morphometrical measurements, Indonesia*

INTRODUCTION

Pasundan and Ongole cattle were included of *Bos indicus* breed that adapted well in Indonesia. Both cattle were kept by the farmers as beef cattle. Selection program in both cattle can be started with breed characterization. Breed characterization is important to evaluate livestock performance for developing breed standard in the future. Breed characterization can be performed based on molecular genetic and morphometric. Hartatik et al. (2019) reported that Pasundan and Bali cattle (*Bos javanicus*) had similar of Cytochrome-b gene (mtDNA) sequence. According to Cytochrome Oxidase Sub-unit 1 (COI) gene (mtDNA) Pasundan cattle closed to Madura (*Bos indicus*) cattle (Wulandari et al., 2019). Thus, Agung et al. (2019) reported the genetic distance of Pasundan cattle was closed to the Madura (0.89) and followed by Ongole (1.96) based on microsatellite markers. However, the characterization of livestock must be supported by morphometric analysis. Breed characterization using morphometrical measurements is easily and cheaply to apply in the smallholds.

Breed characterization by morphometrical measurements can be performed with many statistical analyses such as multivariate analysis (cluster analysis), principal component anaysis (PCA) and canonical discriminant analysis (Carneiro et al., 2010). The morphometrical measurements has been widely used for breed characterization of livestock (Cazar, 2003). Hence, the discriminant analysis is one of statistical method has been proved to be assessing the variation within population or breed and can characterize of different population or breed based on morphomerical measurements (Boujenane et al., 2016).

Previous studies worked with morphometrical measurements to characterize breeds of ruminant livestock i.e. cattle (Pundir et al., 2015; Yakubu et al., 2014), goat (Bolaceli et al., 2017; Hamdan et al., 2018), sheep (Carneiro et al., 2010; Asamoah-Boaheng and Sam, 2016; Dauda et al., 2018) and buffalo (Rezende et al., 2017). Recently, study of breed characterization among Indonesian native cattle based on morphometrical measurements was not reported. Therefore, the aim of this study was to obtain morphological characterization in two *Bos indicus* cattle breeds of Indonesia (Pasundan and Ongole) using discriminant analysis. The results of this study can be used as supported information for phylogenetic studies in Indonesian native cattle in the future.

MATERIALS and METHODS

Data collection

Data used in this study were obtained from 110 *Bos indicus* bulls consisted of 72 Pasundan and 38 Ongole bulls (Figure 1). The morphometric data of Ongole bulls and 15 Pasundan bulls were collected from breeding station (BPPIB-SP Ciamis, West Java). This station located at longitude 108°20′ to 108°40′ E and latitude 7°40′20″ to 7°41′20″ S with 20-500 above the sea level. The air temperature about 25-35°C with air humidity 45-80% and rainfall intensity about 1,680 mm/year. Meanwhile, morphometric data of the other Pasundan bulls were collected from smallholders. In addition, all animals had 2 or 3 pairs permanent incisors.

Studied traits

Six morphometrical measures were taken from each animals i.e. chest girth (CG) withers height (WH), body length (BL), chest depth (CD), hip height (HH) and rump width (RW). CG was measured with a tape measure as circumference of the chest just behind the foreleg (fourth *os costa*). WH was measured from the behind of *os scapulla* at dorsal point to the ground. BL was measured from from *tuber humerus* to *tuber ischium.* CD was measured from from the behind of *os scapulla* at dorsal to ventral points. HH was measured from from *os coxae* or *tuber coxae* to the ground. RW was measured from left and right of the *tuber coxae.* All measurements were taken by measuring stick and taken from the right side of the animal.

Statistical analysis

Canonical discriminant analysis were used to obtain some variable as the discriminator variable based on the canonical structure or canonical correlation values. This analysis has been used for the genetic distance estimation between livestock populations or breeds through Mahalanobis distance analysis (Hamdan et al., 2018). The genetic distance of Mahalanobis as the minimum quadratic square distance (D^2) and can be presented in the following model:

$$D^2 = \left(\overline{X}_i - \overline{X}_j\right) C^{-1} \left(\overline{X}_i - \overline{X}_j\right)$$

In this model, $\overline{X}_i$ is the vector of average observation for i^{th} group in each variable; $\overline{X}_j$ is the vector of average observation for j^{th} group in each variable and C^{-1} is the inverse matrix of variance-covariance between variables (Nei, 1987). Each discriminant function consisted of a linear combination (Z) of the independent variable (Y_i) in order to maximize the correlation between Z and Y_i. Linear combination of a discriminant function can be represented in the following model:

$$Z = \mu_0+\mu_1 Y_1+\mu_2 Y_2+\mu_3 Y_3+......+\mu_i Y_i$$

In this model, μ_i is the estimated canonical coefficient for the i^{th} data and Y_i is the independent variables of i^{th} data (Arandas et al., 2017). Discriminant analysis has been used to characterize species into statistically different groups based on morphometric traits. The canonical discriminant analysis was performed in this study using SPSS 16.0 statistical package.

RESULTS AND DISCUSSION

The average of CG, CD, HH and RW of Ongole bulls were higher than Pasundan bulls but not significantly different as presented in Table 1. The stepwise discriminant analysis showed that CD, BL and CG were the most discriminating variables between Pasundan and Ongole bulls (Table 2). When the three most important morphometrical measurements for discriminating the two cattle breeds were selected, Wilk's Lambda (λ) and Mahalanobis distance (D^2) dropped to 0.37 and 7.30 respectively with a significant difference between the two cattle breeds (F = 9.49). The unstandardized stepwise discriminant function was used to classify individual cattle. The three discriminating variables variables earlier extracted were the variables included in the discriminant (D) equation: D = -

5.06+0.05(CG)-0.05(BL)+0.10(CD) as presented in Table 3. Hence, the canonical correlation in this study was 0.81 (very high category). While 100% of Ongole bulls were classified into their source population.

Table 1. Descriptive statistic of the morphometric traits of Pasundan and Ongole bulls

Morphometric (cm)	**Pasundan (Mean±SD)**	**Ongole (Mean±SD)**
Chest girth	135.20±9.71	154.13±11.97
Withers height	125.31±6.56	124.74±6.70
Body length	128.46±11.02	123.97±11.58
Chest depth	39.69±8.28	58.37±5.16
Hip height	128.49±6.54	130.82±6.39
Rump width	31.07±3.44	33.42±3.57

Table 2. Morphometrical characters selected by stepwise discriminant analysis to characterize Pasundan and Ongole bulls

Step	**Variables entered**	**Tolerance**	**F-remove**	**Min. D Squared**	**Wilk's Lambda (λ)**
1	Chest depth	0.67	30.42	5.52	0.44
2	Body length	0.74	16.40	6.64	0.40
3	Chest girth	0.52	9.49	7.30	0.37

Table 3. Canonical discriminant function coefficients

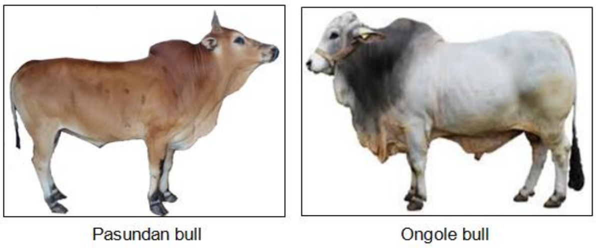
Parameter	**Function 1**
Constant	-5.06
Chest girth	0.05
Body length	-0.05
Chest depth	0.10

Table 4. Percentage (%) of individual classification per breed based on discriminant analysis

Breed	**Predicted group membership (N)**		**Total (N)**
	Pasundan	**Ongole**	
Pasundan	87.5 (63)	12.5 (9)	100.0 (72)
Ongole	0.0 (0)	100.0 (38)	100.0 (38)

N: number of animal

In Pasundan bulls, 87.5% of the individuals (63 animals) were classified into their origin populational, and 12.5% were classed as individuals of Ongole bulls (9 animals) as presented in Table 4. According to discriminant score (D), the breed characterization in this study was obtained two groups with positive D score for Ongole breed and negative D scores for Pasundan breed (Figure 2).


Pasundan bull

Ongole bull

Figure 1. Two *Bos indicus* cattle breeds of Indonesia

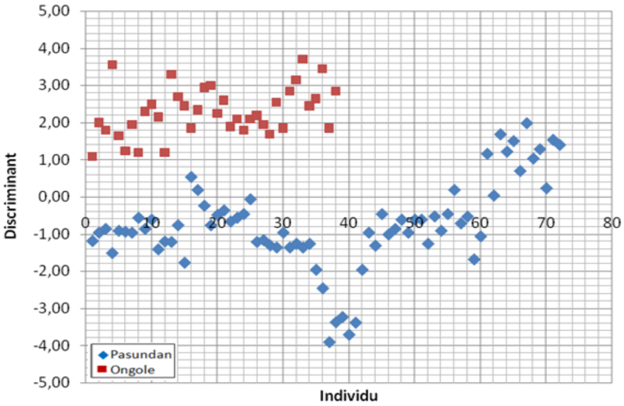


Figure 2. Canonical discriminant plot in the morphological characterization between Pasundan and Ongole bulls

Three morphological measurements of CD, BL and CG were important variable to characterize Pasundan and Ongole bulls. Yakubu et al. (2010) obtained three morphometrical measurements of RW, WH and face length (FL) as the strong variables to characterize Bunaji and Sokoto Gudali cattle. Pundir et al. (2015) obtained 6 morphometrical measurements of WH, BL, FL, ear length (EL), tail length (TL) and paunch girth (PG) as the strong variables to characterize Tripura, Mizoram and Manipur cattle. Dauda et al. (2018) obtained canonical correlation of 0.71 (high category) with 14 morphometrical measurments to characterize Balomi, Karoji, Uda and Yankasa sheeps. Nafti et al. (2014) obtained canonical correlation of 0.51 (moderate) with six morphometrical measurements to characterize Arbi and Serti goats. Asamoah-Boaheng and Sam (2016) obtained canonical correlation of 0.89 (very high) with 16 morphometrical measurements to characterize Djallonke, Sahel and crosses sheeps. In addition, Yakubu et al. (2010) obtained the D^2 value of 7.19 between Bunaji and Sokoto Gudali cattle and close to this study. Pundir et al. (2015) obtained the D^2

value among three Indian cattle breeds about 9.73 (Tripura-Mizoram), 5.72 (Tripura-Manipur) and 4.65 (Mizoram-Manipur) using eight variables. In addition, Rezende et al. (2017) obtained the D^2 value among three Bralizian buffalo breeds that lower than in this study i.e. 4.48 (Jafarabadi-Murrah), 3.31 (Jafarabadi-Mediterranean) and 0.37 (Murrah-Mediterranean) using 11 variables. The tolerance values obtained in the present study were greater than 0.1 and indicated no collinearity problem among discriminator variables (Yakubu et al., 2010) among discriminator variables. The three discriminator variables extracted were sufficiently to characterize two cattle breeds. The morphometrical measurements may considerably increase the reliability of the classification of different cattle breeds. In addition, Yakubu et al. (2010) obtained 85.48% (Bunaji) and 96.55% (Sokoto Gudali) of individual cattle into their different groups. Pundir et al. (2015) used discriminant analysis to classify Tripura (84.13%), Mizoram (82.09%) and Manipur (79.87%) cattle in their source population. Nine Pasundan bulls in this study showed misclassification and can be caused by genetic flow from Ongole cattle as reported by Agung et al. (2019).

CONCLUSION

Pasundan and Ongole bulls can be characterized using discriminant analysis with at least three morphometrical measurements of CG, BL and CD. Therefore, about 12.5% of morphological characteristics in Pasundan bulls was closed to Ongole bulls. The morphometrical measurements in this study can be used for field assessment, management and conservation in both cattle breeds to obtain phenotypically pure local genetic resources and breeding improvement strategies in the future.

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REFERENCES

Agung PP, Saputra F, Zein MSA, Wulandari AS, Putra WPB, Said S, *et al*. Genetic diversity of Indonesian cattle breeds based on microsatellite markers. *Asian-Australas J Anim Sci* 2019; 32:467-476.

Arandas JKG, da Silva NMV, Nascimento RB, Filho ECP, Brasil LHA, Ribeiro MN. Multivariate analysis as a tool for phenotypic characterization of an endangered breed. J Appl Anim Res 2017; 45:152-158.

Asamoah-Boaheng M, Sam EK. Morphological characterization of breeds of sheep: a discriminant analysis approach. *SpringerPlus* 2016; 5:69.

Bolacali M, Ozturk, Y, Yilmaz O, Kucuk M, Karsli MA. Investigation of some morphological traits of Boer x Hair F1 crossbred and pure hair goat kids raised in semi-intensive conditions. Int J Morphol 2017; 35:1502-1511.

Boujenane I, Derqaoui L, Nouamane G. Morphological differentiation between two Marocco goat breeds. *J Livest Sci Tech* 2016; 4:31-38.

Carneiro H, Louvandini H, Paiva SR, Macedo F, Mernies B, McManus C. Morphological characterization of sheep breeds in Brazil, Uruguay and Colombia. *Small Rum Res* 2010; 94:58-65.

Cazar RA. An exercise on chemometrics for a quantitative analysis course. *J Chem Edu* 2003; 80:1026-1029.

Dauda A, Abbaya HY, Ebegbulem, V.N. Application of multifactorial discriminant analysis of morphostructural differentiation of sheep. *J Genet Eng* 2018; 2:11-16.

Hamdan, Saputra H, Mirwandhono E, Hasnudi, Sembiring I, Umar S, *et al*. Genetic distance estimate and variable factors distinguishing between goat Kacang, Muara and Samosir. *Earth Env Sci* 2018; 122:012130.

Hartatik T, Hariyono DNH, Adinata Y. Genetic diversity and phylogenetic analysis of two Indonesian local cattle breeds based on cytochrome-b gene sequences. *Biodiversitas* 2019; 20:17-22.

Nafti M, Khaldi Z, Haddad B. Multivariate characterization of morphological traits in local Tunisian oases goats. *Anim Genet Res* 2014; 55:29-38.

Nei M. Molecular Evolutionary Genetic. New York, NY: Columbia University Press; 1987.

Pundir RK, Singh PK, Sadana DK. Multivariate analysis of morphometric traits of three different indigenous cattle populations from north east states of India. *JITV* 2015; 20:79-86.

Rezende MPG, Ferraz PC, Carneiro PLS, Malhado CHM. Phenotypic diversity in buffalo cows of the Jafarabadi, Murrah and Mediterranean breeds. *Pesq Agr Bras* 2017; 52:663-669.

Wulandari A, Nurgiartiningsih, VMA, Kuswati, Susilorini TE, Agung PP. Kinship of several Indonesian local cattle by using DNA mitochondrial COI (Cytochrome Oxidase Sub-unit I). *Int Res J Adv Eng Sci* 2019; 4:165-167.

Yakubu A, Idahor KO, Haruna HS, Wheto M, Amusan S. Multivariate anaysis of phenotypic differentiation in Bunaji and Sokoto Gudali cattle. *Acta Agric Slov* 2014: 96:75-80.

Yakubu A, Salako AE, Imumorin IG, Ige AO, Akinyemi MO. Discriminant analysis of morphometric differentiation in the West African Dwarf and Red Sokoto goats. *South African J Anim Sci* 2010: 40:381-387.