

Breed Identification of Four Types Indonesian Native Cattle

(Identifikasi Bangsa dari Empat Tipe Sapi Potong Asli Indonesia)

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Abstrak

Penelitian untuk mengidentifikasi ukuran dan bentuk tengkorak, mempelajari efektifitas analisis multivariat, dan mengklarifikasi hubungan kekerabatan empat tipe sapi potong asli Indonesia, yaitu sapi Bali, sapi Madura, sapi Jawa dan sapi Peranakan Ongole telah dilakukan menggunakan 30 ukuran-ukuran kranium-mandibula dengan analisis komponen utama, analisis komponen diskriminan & analisis diskriminan kanonik. Hasil penelitian disajikan sebagai berikut : (1) Hasil analisis komponen utama menunjukkan bahwa ukuran kranium-mandibula terpanjang ada pada sapi Peranakan Ongole; dan terbesar pada sapi Madura. Ukuran-ukuran kranium-mandibula sapi Jawa dan Peranakan Ongole keduanya serupa dengan sapi Madura tetapi mempunyai bentuk yang lebih pendek dan tinggi; (2) Hasil analisis diskriminan menunjukkan keempat tipe sapi potong asli Indonesia tersebut mempunyai tingkat kesalahan sebesar 0% dalam pengelompokan bangsa sapi. Hal ini menunjukkan bahwa keempat tipe sapi potong tersebut diperoleh adanya perbedaan ukuran dan bentuk dari ukuran-ukuran kranium-mandibula secara jelas, dengan demikian analisis multivariat menggunakan ukuran-ukuran kranium-mandibula dapat digunakan secara akurat untuk mengidentifikasi bangsa sapi potong; (3) Hubungan kekerabatan atau jarak genetik bangsa sapi Jawa lebih dekat ke sapi Peranakan Ongole dan sapi Madura dibanding dengan sapi Bali. Sapi Bali mempunyai jarak genetik yang paling jauh terhadap sapi Peranakan Ongole.

Kata kunci : Identifikasi bangsa, sapi Indonesia, kranium, mandibula,

Introduction

The Bali cattle is assumed to be a breed domesticated from the Banteng, *Bos banteng* (*javanicus*), which inhabits some areas in eastern and western Java and Kalimantan (Payne and Rollinson, 1973). Hayashi *et al.* (1982) reported that the Bali cattle is nearest to that of the wild Banteng. This resemblance is not based on the skull-size but on the skull-shape. This result suggests that the Bali cattle may be minified form of the wild Banteng. Dwarfism is well known to have occurred frequently in the process of the domestication from the wild Banteng to the Bali cattle.

Namikawa and Widodo (1978) reported that the Hbb-X component of cattle haemoglobin was generally found in the blood of the indigenous

cattle of Southeast Asia and they suggested that the high incidence of Hbb-X in Southeast Asian cattle was the result of gene flow from Bali cattle.

On the other hand, it is historically known that Indian zebu cattle was introduced into Indonesia, and it is also assumed that some native cattle take their origin from the zebu cattle. The Ongole Crossbred is considered to be a direct descendant of the Ongole breed, one of the Indian zebu breeds (Sutopo *et al.*, 2001). The Madura cattle is a descendant from Bali cattle (Hardjosubroto and Astuti, 1980). The Java cattle is generally seen on the island of Java, for which it is named. It can be considered the same breed as the Madura (Rouse, 1976).

Biochemical methods for breed identification have been developed, but they are still too costly and laborious. It is important, alternatively, to use

another method that may be prove to be powerful. Multivariate analysis is a method for rapid and cheap to identification of cattle breeds.

Skeletal characters including craniomandible form reveal the highest heritability of all the quantitative traits. Therefore, we can identify a strain within an animal species and estimate closeness of relationships among different strain by application of an appropriate statistical analysis to the skeletal measurements (Goto *et al.*, 1991).

The first aim of the present study is to identify the size and shape skull of four types of Indonesian native cattle, *i.e.*, the Bali, Madura, Java, and Ongole Crossbred. The second aim to examine the effectiveness of multivariate analysis of cranial-mandibular measurements in attaining the objectives mentioned above. The third aim is to further clarify the genetic relationship among them.

Research Methods

Specimens and Measurements

The research was conducted by using purpose sampling. The number of specimens for Java, Bali, Madura, and Ongole Crossbred cattle were 17; 9; 12; and 12, respectively. They were collected and measured from slaughter houses in Brebes-Central Java, Denpasar-Bali, Bangkalan-Madura, and Semarang-Central Java respectively, on three islands in Indonesia (Figure 1.)

The ages of specimens were determined by the status of eruption and wearing of the incisor teeth. 15 cranial and 15 mandibular measurements used in the present study are defined by Driesch, 1976 (Hayashi *et al.*, 1982). Figure 2 shows these measurements, including the important measuring points. All measurements were taken with sliding or spreading calipers and were recorded to the nearest 0.1 millimeters. Table 1 shows the variables name of cranial-mandibular measurements.

Statistical Analysis

Multivariate analysis is carried out in order to discover how closely the shape of the cranium-mandibular resembled each other in the strain, the related strains and unrelated strain. Principal Component Analysis (PCA) : PCA is used to examine relationships among several quantitative variables. Discriminant Component Analysis (DCA) : DCA is used to compute various discriminant function for classifying observation into two to more groups on basis of one or more quantitative variables. Canonical Discriminant Analysis (CDA) : CDA is used to show probability that an individual is a member of each group and classify all individuals into the group with the largest probability of group membership.

Canonical discriminant analysis is a method of extracting a few axes which describe the positions among *n* groups on a two-dimensional plane clearly. The SAS (1990) was applied multivariate analysis approaches. Estimation of genetic distance based on the Mahalanobis distance values. From the matrix of the genetic distance values, a dendrogram presenting the genetic relationship was drawn by the unweight-pair group method (UPGMA) by software MEGA version 3.1 (Kumar *et al.*, 2004).

Results and Discussion

Morphometrical Observations on Cattle Cranium-Mandibular

Table 2 shows the eigenvalue and its contribution in each principal component (PC).

Eigenvalues are analogous to variances, whereas eigenvectors are principal axes at right angles of scattergram. As result, it was indicating that 75.44% of cumulative contribution ratios from the 1st (PC1) to the 3rd (PC3) principal components. This means that the first three PCs extracted account for more than 75% of morphometrical variation information.

In the morphometrical applications of the principal component analysis, the first component is acceptable as a "size" factor, and the second one as a "shape" factor (Hayashi *et al.*, 1982).

The chart in Figure 3 is constructed by the components derived from the correlation matrix. Figure 3 shows the scattering diagrams of four breeds on constructed by PC₁, and PC₂. As shown in Figure 3, a clear separation was found among the Indonesian native cattle breeds. According to the above interpretation for each PC, the Ongole Crossbred has higher value than other breeds. An observation located on the upper right side of figures indicates a large and long size type. The opposite, an observation on the lower left side of figures indicate a small and short size type. This means that the longest cranium was belong to Ongole Crossbred, subsequently followed by Madura, Java, and Bali cattle. In the other hand, the Madura cattle showing comparatively large PC₂ in the figures. This means that the cranial shape of Madura cattle was largest, followed by Bali, Java, and Ongole Crossbred cattle.

Breed Identification Using Morphometrical Measurements

Table 3 shows the results of identification 4 types native cattle breeds by the aid of the analysis. Using Canonical Discriminant Analysis for classifying four types native cattle breeds resulted in high accuracy as indicated by the low probability of erroneous discrimination. The accuracy accounted was 100%, and the rate of misclassification was 0%. As shown in Table 3, all cattle are identified correctly. It was possible

to discriminate all the breeds from one another with high probability. The results of this investigation suggest that cranium-mandibular analysis is applicable to discriminate of four types native cattle breed.

Table 1. Variables name of the cranial-mandibular measurements (Driesch, 1976 in Nishida *et al.*, 1983)

No	Variables Name
1	Profile / total length
2	Median frontal length
3	The greatest length of the nasals
4	Rhinion-Prosthion
5	Basal length
6	Basion-Staphylion
7	Median palatal length
8	Least breadth between the bases of the horncores
9	Least frontal breadth
10	Greatest breadth of the skull
11	Least breadth between the orbits
12	Least breadth between the supraorbital foramina
13	Facial breadth between the infraorbital foramina
14	The greatest height of the occipital region
15	Height of the nasal region/ Nasion-Staphylion
16	Length from the angle
17	Length from the condyle
18	Aboral height of the vertical ramus
19	Middle height of the vertical ramus
20	Length of the median section of the body
21	Gonion laterale-Gonion laterale
22	M3-M3
23	P2-P2
24	Length of the premolar row
25	Length of the pMolar row
26	Length of the cheektooth row
27	Height of the mandible in front
28	Height of the mandible behind M3
29	Length of the horizontal ramus
30	Gonion caudale aboral border of the alveolus of M3

Table 2. Eigenvalue and its contribution in each principal component (PC)

PC	Sex	Eigenvalue	Contribution ratio (%)	Cumulative Contribution ratio (%)
1 st	Male	32.07	51.97	51.97
2 st	Male	9.78	15.84	67.82
3 st	Male	4.71	7.63	75.45

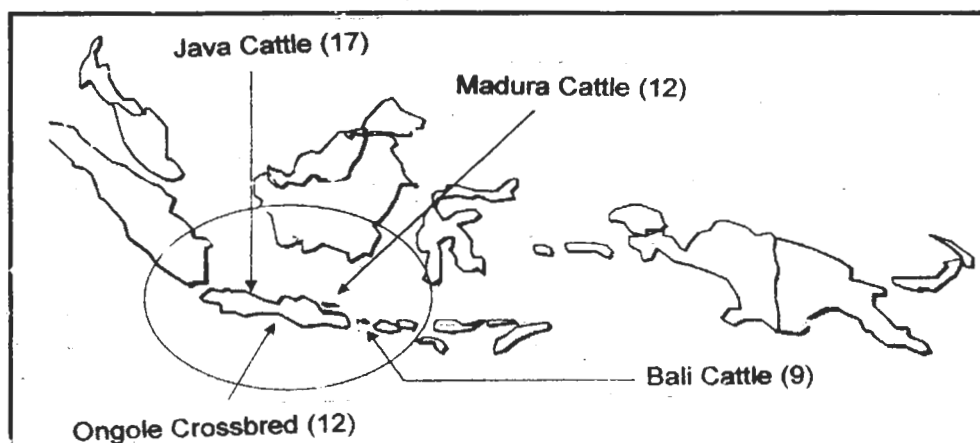


Figure 1. Map of part of Indonesia showing the islands on which cattle were surveyed. The number in parentheses is the number of specimens samples were obtained.

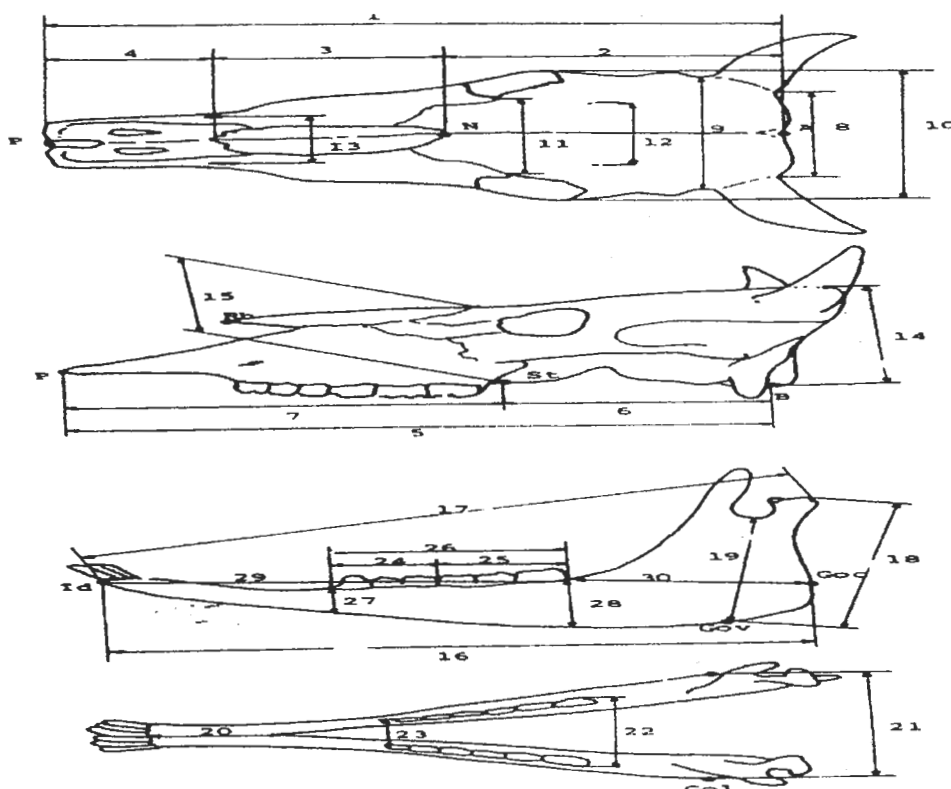


Figure 2. Measurements of the skull of *Bos* (Driesch, 1976 in Hayashi *et al.*, 1982)

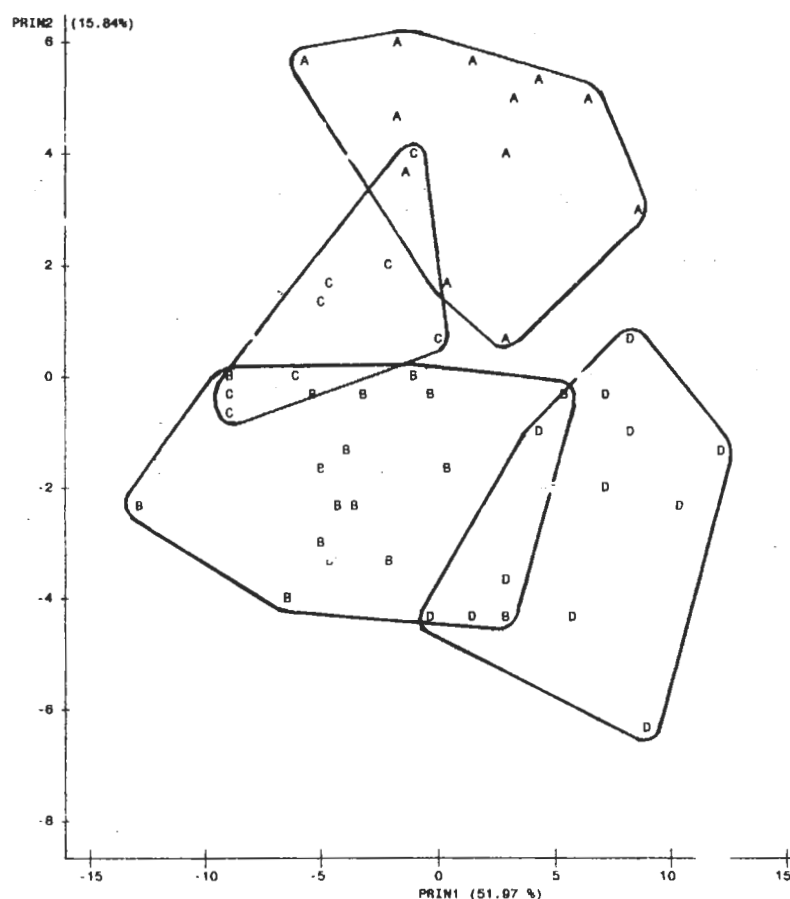


Figure 3. Principal component chart of the first two transformed variables from 30 cranialmandibular variables for four breeds male native cattle.

A:Madura, B:Java, C:Bali, D:Ongole Crossbred

Note : 1 Obs hidden

Table 3. Number of observations and percent classified into breed

From breed					Total	Probability*)	
	Madura	Java	Bali	Ongole Crossbred		Means	SD
Madura	12	0	0	0	12	1.00	0.00
	100.00	0.00	0.00	0.00	100.00		
Java	0	17	0	0	17	1.00	0.00
	0.00	100.00	0.00	0.00	100.00		
Bali	0	0	9	0	9	1.00	0.00
	0.00	0.00	100.00	0.00	100.00		
Ongole Crossbred	0	0	0	12	12	1.00	0.00
	0.00	0.00	0.00	100.00	100.00		
Total	12	17	9	12	50	1.00	0.00
Percent	24.00	34.00	18.00	24.00	100.00		
Priors	0.24	0.34	0.18	0.24			
Error Count Estimates for breed :							
	Madura	Java	Bali	Ongole Crossbred	Total		
Rate	0.00	0.00	0.00	0.00	0.00		
Priors	0.24	0.34	0.18	0.24			

*) Probability associated with the largest discriminant function

Relationship Among 4 Types Indonesian Native Cattle

Table 4 shows the contribution ratio of z_k , which was applied to the cranial-mandibular measurements of all the 4 breeds in this analysis.

Figure 4 shows the position of the breeds on the two dimensional plane as determined by z_1 and z_2 . As is clear from these figures, the breeds were mapped closer to one another than they were to other breeds.

In conducting the discriminant analysis, the Mahalanobis distances based on the 30 measurements were calculated between 4 breeds. Because the cranium-mandibular size and shape are highly heritable traits, the distance may reflect the genetic distance between breeds. Table 5 shows the Mahalanobis distance among 4 types Indonesian native cattle breeds.

The Madura and Ongole Crossbred seen separate clearly from Java cattle. The Ongole Crossbred is a direct descendant of the Ongole breed with Java cattle, and Madura cattle is a descendant of the Shinala breed. Both of them were introduced into Indonesia in order to increase the body size and productivity on the local cattle (Hardjosubroto, 1994; Sutopo *et al.*, 2001).

Java cattle was nearer in the genetic relationship to Ongole Crossbred and Madura cattle compared to Bali cattle. Bali cattle was the farthest to Ongole Crossbred cattle. Result of this research is similar with Sutopo's *et al.* (2001) which used the blood protein polymorphisms at 25 loci. Figure 5 shows the dendrogram presenting the genetic relationship among four types Indonesian native cattle breeds.

Table 4. Eigenvalue and its contributions

Canonical variate	Sex	Eigenvalue	Contribution ratio (%)	Cumulative (%)
1 st	Male	14.55	48.57	48.57
2 nd	Male	9.09	30.36	78.93
3 rd	Male	6.31	21.07	100.00

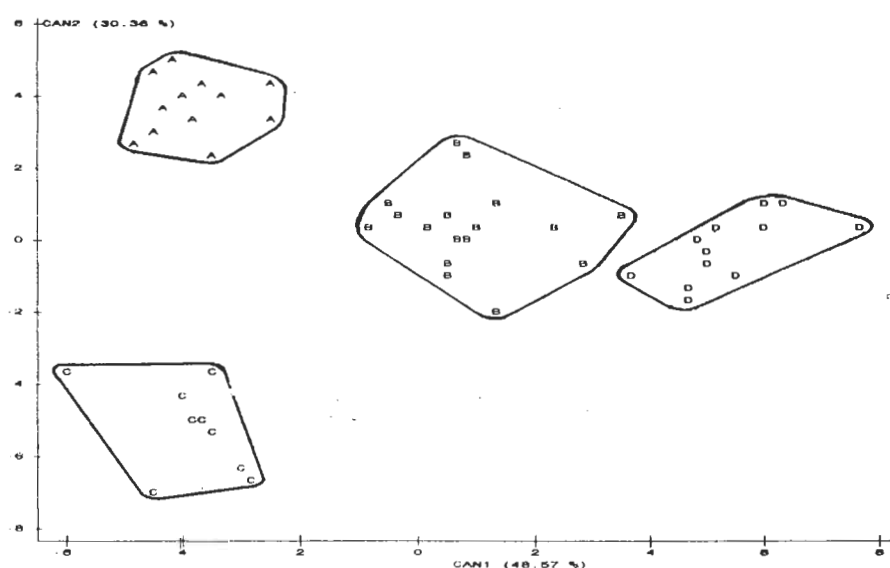


Figure 4. Scattering diagram of 4 breeds on two-dimensional plane z_1 - z_2 as determined by canonical discriminant analysis. A:Madura, B:Java, C:Bali, D:Ongole Crossbred

Table 5. Mahalanobis distances between breeds

Breed	Sex	Breed			
		Madura	Java	Bali	Ongole Crossbred
Madura	Male	-	57.35	81.14	101.00
Java	Male		-	71.90	52.66
Bali	Male			-	112.41
Ongole Crossbred	Male				-

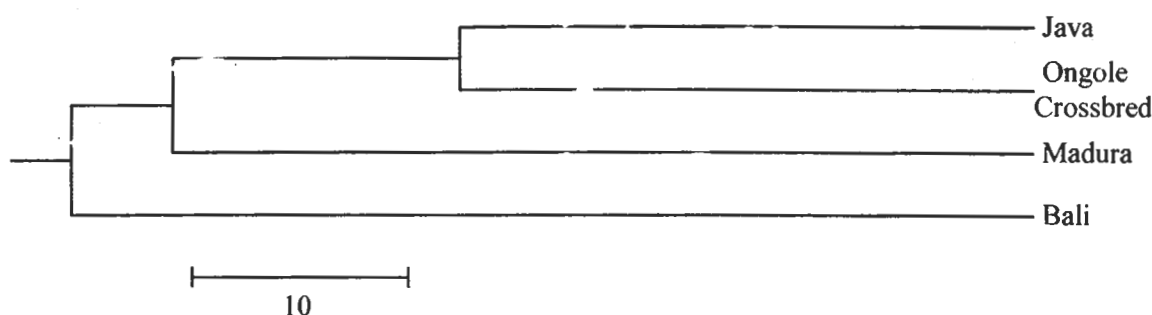


Figure 5. Dendrogram presenting the genetic relationship among four types of Indonesian native cattle breeds based on 30 cranial-mandibular measurements and the UPGMA

Conclusion

The longest cranium was belong to Ongole Crossbred cattle; and the cranial shape of Madura cattle was largest. Multivariate analysis can be used to identify and clarify a strain within an animal species and estimate closeness of relationships among different strains to the skull measurements. Java cattle was near in the genetic relationship to Ongole Crossbred and Madura cattle compared to Bali cattle. Bali cattle was the farthest to Ongole Crossbred cattle.

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