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Morphological diversity of kacang goats across southeast asian islands: evidence from body index analysis

Asep Setiaji
asepsetiaji93@gmail.com
Universitas Diponegoro Fakultas Peternakan dan Pertanian https://orcid.org/0000-0002-5505-7077
Fatmawati Mustofa
Universitas Diponegoro Fakultas Peternakan dan Pertanian
Dela Ayu Lestari
Universitas Diponegoro Fakultas Peternakan dan Pertanian
Sutopo Sutopo
Universitas Diponegoro Fakultas Peternakan dan Pertanian
Edy Kurnianto
Diponegoro University: Universitas Diponegoro
Muhammad Ihsan Andi Dagong
Universitas Hasanuddin Fakultas Peternakan
Sri Rachma Aprilita Bugiwati
Universitas Hasanuddin Fakultas Peternakan
Mamat Hamidi Kamalludin
Universiti Putra Malaysia
Mohd Adhan Ernie Muneerah
Universiti Putra Malaysia
Nurfaizin Nurfaizin
Ministry of Agriculture Republic of Indonesia: Kementerian Pertanian Republik Indonesia
Susanti Susanti
Lampung State Polytechnic: Politeknik Negeri Lampung
Procula Rudolf Matitaputty
Pusat Penelitian dan Pengembangan Peternakan

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Abstract

This study evaluated phenotypic variation in Kacang goats sampled from six geographic populations across Indonesian islands and the Malay Peninsula using body indexes and multivariate statistics. The dataset comprised 247 adult goats reared under traditional production systems. Body weight and five linear measurements were used to calculate seven body indexes. Stepwise discriminant analysis, Mahalanobis distance, canonical discriminant analysis, and cross-validation were applied separately by sex to identify discriminatory variables and assess morphological separation. The depth index showed the greatest discriminatory contribution (partial $R^2 = 0.726$ in the group reported as bucks and 0.512 in the group reported as ewes; $P < 0.001$). Mahalanobis distances ranged widely, with the largest reported distance between the Malay Peninsula and Sumatra populations (40.014) and the smallest between Celebes and Lombok (1.461). The first canonical function explained 53.9% and 64.9% of the variation in the two sex groups, respectively. Cross-validation indicated strong classification for some populations but substantial overlap for others, especially Celebes and Lombok. Therefore, the results support geographic variation in morphological profiles, not genetic differentiation, phylogenetic relationships, or demonstrated environmental adaptation. Molecular, pedigree, and environmental data are required to test the biological mechanisms underlying the observed patterns.

1. Introduction

Kacang goats are indigenous small ruminants with socioeconomic importance in Indonesia and the Malay Peninsula. Their small body size, ability to persist in low-input production systems, and contribution to local meat supply make them relevant to rural livelihoods (Sujarwanta et al., 2024). Previous studies have documented phenotypic and molecular variation among Southeast Asian goat populations, but morphometric and molecular evidence address different biological questions and should not be interpreted interchangeably (Ernie Muneerah et al., 2021; Lestari et al., 2024). Morphometric variation describes observable body form and may reflect multiple influences, including age, sex, nutrition, management, ancestry, and measurement conditions. It does not, by itself, demonstrate genetic purity, genetic divergence, or evolutionary history.

Body indexes summarize proportional relationships among linear measurements and can support phenotypic characterization when interpreted within the limits of the sampling design (Arandas et al., 2017; Melesse et al., 2022; Maksimović et al., 2023). Canonical discriminant analysis can identify combinations of indexes that best separate predefined geographic groups, while Mahalanobis distances quantify multivariate morphological dissimilarity. Hierarchical clustering based on these distances provides a descriptive dendrogram of phenotypic similarity. Such a dendrogram is not a phylogenetic tree and cannot be used to infer ancestry, gene flow, or evolutionary relationships without molecular evidence.

Accordingly, this study aimed to (1) quantify variation in seven body indexes among Kacang goat populations sampled from the Malay Peninsula, Sumatra, Java, Lombok, Celebes, and the Moluccas; (2) identify the indexes contributing most strongly to discrimination among sampled populations; (3) describe multivariate morphological distances and clustering; and (4) evaluate classification performance using cross-validation. We hypothesized that the distributions of body indexes would differ among sampled geographic populations and that classification accuracy would vary because some populations share overlapping morphological profiles. The study is positioned as a regional phenotypic characterization and does not test genetic differentiation or environmental adaptation.

2. Material and Methods

The study collected data on Kacang goats from five Indonesian islands and the Malaysian peninsula. To visually highlight these distinctions, maps of the research locations were meticulously crafted using QGIS 3.24 (QGIS Development Team 2022), enabling spatial analysis and contextual understanding. The detailed location as delineated in Fig. 1. were as follow: A. The Perak and Pahang states of Malaysia span from 3°31'60.00" to 4°48'26.3" north latitude and 100° 48'0.02" to 102°24'0.00" east longitude. B. Pringsewu Regency in Sumatra island span from 5°8'10"-5°34'27" south latitude and 104°45'25" to 105°8'42" east longitude. C. Grobogan Regency in Java island span from 7° to 7°30 south latitude and 110°15' to 111° 25' east longitude. D. Lombok island span from 8°33'54" to 8°56'5" south latitude and 116°21'04" to 116°35'1" east longitude E. Maros and Jeneponto regency in Cellebes island span from 40°45'-50°7' south latitude and 109°205' to 129°12' east longitude and 5°23'- 5°42' south latitude and 119°29' – 119°56' east longitude, respectively. F. Seram island span from 3°08' to 3.133° south latitude and 129°30' to 129.500° east longitude.

The dataset contained 247 goats reported to be 2 to 3 years old, comprisinnng of 161 bucks and 86 ewes and maintained under traditional farming systems. Animals were selected purposively in areas with relatively high goat density. Because the available field records did not document a probability-based farm-selection frame, pedigree relationships, molecular breed-purity verification, or repeated measurements for estimating observer error, the sample should be interpreted as representing the animals examined at the selected locations rather than the entire regional populations.

2.1. Data collection

Goats were selected purposively. Bucks were described as reproductively active, and ewes were reported as non-pregnant at measurement. Body weight (BW) and five morphometric traits were recorded: withers height (WH), body length (BL), chest depth (CD), chest width (CW), and chest girth (CG). Measurements were taken in kilograms or centimeters using a calibrated weighing device, ruler, measuring tape, and calipers as appropriate. The original field protocol did not report the number of farms, animals per farm, pedigree screening, blinding, duplicate measurements, inter-observer agreement, or technical error of measurement. These omissions limit assessment of representativeness and repeatability and are acknowledged explicitly in the interpretation.

An analysis of morphometric indices was conducted to assess the diverse characteristics and functionalities of the goat under investigation. These indexes provide insights body proportions and structural attributes for evaluating conformational differences. Seven key body indexes were selected, following the methodology of Khargharia et al. (2015) and Suryaka et al. (2024) as follow:

Length index (LI) = BL/WH x 100

Depth index (DI) = CD/WH x 100

Thoracic development (TD) = CG/WH x 100

Conformation index (CI) = (CG)2/ WH

Index of Body Weight (IBW) = BW/WH x 100

Body index (BI) = BL/CG x 100

Proportionality (Pr) = WH/BL x 100

2.2. Statistical Analyses

Descriptive statistics were calculated by sex. Comparisons were conducted using a t-test when distributional assumptions were considered adequate and a Wilcoxon test otherwise. Body-index differences among geographic populations were then examined, followed by sex-specific stepwise discriminant analysis to identify variables contributing to group separation. Canonical discriminant analysis summarized multivariate separation, squared Mahalanobis distances quantified pairwise morphological dissimilarity, and leave-one-out cross-validation assessed classification performance. Hierarchical clustering of the distance matrix was used only as a descriptive representation of morphological similarity. Analyses were performed using SAS OnDemand for Academics (SAS, 2021). Statistical significance was set at $P < 0.05$.

$$C = \mu + \mu_1 y_1 + \mu_2 y_2 + \mu_3 y_3 + \mu_4 y_4 + \mu_5 y_5 + \mu_6 y_6$$

The canonical discriminant function was expressed as C = a + b1X1 + b2X2 + ... + bpXp, where C is the canonical score, a is the intercept, b1 to bp are estimated canonical coefficients, and X1 to Xp are the selected body indexes. The analysis assumes independent observations, approximately multivariate-normal predictor distributions within groups, and sufficiently similar covariance structures. Formal diagnostics for multivariate normality, covariance homogeneity, influential observations, and independence were not available in the source analysis. Consequently, inferential results and classification rates should be interpreted cautiously, particularly for small or unequal group sizes.

3. Result

Table 1 summarizes body weight and linear measurements by the two reported sex groups. Mean body weight was similar between groups, whereas differences were more apparent in withers height, body length, and chest depth. Coefficients of variation were lower for withers height and chest girth than for chest width, indicating greater relative dispersion in chest width. These statistics describe the sampled animals and should not be generalized beyond the sampling frame.

Table 1
Descriptive statistic for body weight and body measurement of Kacang goat used in the study.

Traits	Buck (n = 161)		Ewe (n = 86)	
	Mean SE	CV	Mean SE	CV
Body weight (kg)	23.64 0.61	23.59	23.56 0.45	24.15
Withers height (cm)	58.96 0.55	8.71	56.16 0.41	9.25
Body length (cm)	62.68 0.83	12.29	59.82 0.51	10.82
Chest depth (cm)	27.81 0.57	19.19	29.47 0.39	17.11
Chest width (cm)	15.62 0.49	29.19	15.37 0.27	22.97
Chest girth (cm)	64.70 0.68	9.85	65.47 0.49	9.45

Table 2 shows geographic variation in body indexes. In the group reported as bucks, the Malay Peninsula had the highest depth index, Sumatra had the lowest depth and conformation indexes, and Celebes and the Moluccas had

relatively high length indexes. In the group reported as ewes, the Malay Peninsula again had the highest depth index, while several other indexes showed overlapping significance groups across populations. These patterns indicate differences in body proportions among the sampled locations but do not identify their genetic or environmental causes.

Table 2
The least square means (LSM) standard errors (SE) of body indexes for Kacang goat among difference island

Indexes	Malay Peninsula	Sumatra	Java	Lombok	Celebes	Moluccas
Buck						
Length index	111.47 ± 8.34^{ab}	96.36 ± 1.66^{b}	99.21 ± 1.78^{b}	103.97 ± 2.28^{ab}	118.28 ± 3.24^{a}	116.49 ± 1.69^{a}
Depth index	64.31 ± 3.37^{a}	39.94 ± 0.64^{d}	51.87 ± 1.01^{b}	47.39 ± 0.55^{c}	45.49 ± 0.97^{c}	46.26 ± 0.93^{c}
Thoracic development	113.92 ± 8.19^{a}	101.03 ± 0.91^{b}	105.74 ± 1.73^{b}	117.99 ± 3.79^{a}	116.01 ± 2.08^{a}	115.51 ± 1.68^{a}
Conformation index	77.52 ± 7.89^{b}	62.02 ± 0.87^{d}	66.19 ± 1.86^{cd}	86.07 ± 3.87^{a}	72.71 ± 2.09^{bc}	78.42 ± 1.92^{ab}
Index of body weight	47.73 ± 3.97^{a}	32.41 ± 0.67^{c}	46.51 ± 1.26^{a}	36.20 ± 0.91^{bc}	38.06 ± 1.22^{b}	46.59 ± 1.83^{a}
Body index	105.46 ± 7.79^{a}	95.32 ± 1.22^{ab}	94.01 ± 1.75^{ab}	88.77 ± 2.73^{b}	102.18 ± 2.66^{ab}	101.06 ± 1.78 ^{ab}
Proportionality	92.32 ± 5.02^{cd}	104.44 ± 1.85^{a}	101.24 ± 1.90^{ab}	96.66 ± 2.21^{bc}	85.48 ± 2.14^{d}	86.08 ± 1.29^{d}
Ewe						
Length index	104.96 ± 1.82^{a}	103.73 ± 0.41^{a}	105.55 ± 2.05^{a}	109.64 ± 1.93^{a}	102.51 ± 2.96^{a}	117.78 ± 2.22^{b}
Depth index	67.55 ± 1.66^{a}	50.52 ± 0.82^{c}	55.09 ± 0.86^{b}	49.55 ± 0.76^{c}	48.33 ± 1.56^{c}	47.82 ± 0.82^{c}
Thoracic development	116.35 ± 2.47^{ab}	110.59 ± 1.37^{b}	114.81 ± 1.82^{ab}	118.28 ± 3.58^{ab}	120.21 ± 2.56^{a}	118.21 ± 1.68^{ab}
Conformation index	72.68 ± 2.70^{ab}	67.18 ± 1.11^{b}	76.66 ± 2.28^{ab}	84.11 ± 3.96^{a}	82.63 ± 2.51^{a}	75.88 ± 1.82^{ab}
Index of body weight	35.95 ± 1.54^{c}	37.83 ± 0.52^{bc}	53.37 ± 1.59^{a}	49.21 ± 2.07^{b}	42.78 ± 1.54^{b}	41.92 ± 0.81^{bc}
Body index	91.53 ± 2.71^{ab}	94.09 ± 1.13^{ab}	92.01 ± 1.48^{ab}	94.22 ± 3.14^{ab}	85.30 ± 1.43^{b}	99.99 ± 2.01^{a}
Proportionality	96.12 ± 1.69^{ab}	96.44 ± 0.38^{ab}	95.20 ± 1.82^{ab}	91.80 ± 1.79^{ab}	100.11 ± 2.21^{a}	85.82 ± 1.68^{b}

Lombok showed relatively high conformation and thoracic-development values in several comparisons, whereas Celebes and the Moluccas frequently showed higher length-related values. Java generally occupied an intermediate range for many indexes. Because management, nutrition, climate, genetic background, farm structure, and measurement conditions were not modeled, the observed geographic contrasts should be treated as descriptive phenotypic differences rather than evidence of local adaptation.

3.1. Discriminant power of body indexes

Stepwise discriminant analysis identified the depth index as the first and strongest discriminator in both reported sex groups (Table 3). Its partial R^2 was 0.726 in bucks and 0.512 in ewes, followed by proportionality in bucks and length index in ewes. Additional indexes improved discrimination incrementally. These statistics indicate which measured proportions contributed to separation among the predefined geographic groups; they do not establish biological causation or genetic divergence.

Table 3
Summary of stepwise discriminant analysis for body indexes of Kacang Goats with discriminating power

Step	Variable entered	Partial R-Square	Pr > F	Wilks' Lambda	Pr < Lambda	ASCC	Pr >ASCC
Buck							
1	Depth index	0.726	< .0001	0.273	< .0001	0.145	< .0001
2	Proportionality	0.516	< .0001	0.132	< .0001	0.245	< .0001
3	Conformation index	0.388	< .0001	0.081	< .0001	0.308	< .0001
4	Index of body weight	0.378	< .0001	0.050	< .0001	0.379	< .0001
5	Body index	0.350	< .0001	0.033	< .0001	0.429	< .0001
Ewe							
1	Depth index	0.512	< .0001	0.488	< .0001	0.102	< .0001
2	Length index	0.391	< .0001	0.298	< .0001	0.157	< .0001
3	Index of body weight	0.304	< .0001	0.207	< .0001	0.216	< .0001
4	Conformation index	0.181	< .0001	0.169	< .0001	0.247	< .0001
5	Body index	0.213	< .0001	0.133	< .0001	0.288	< .0001
6	Proportionality	0.136	0.0005	0.115	< .0001	0.311	< .0001
7	Thoracic development	0.122	0.0015	0.101	< .0001	0.325	< .0001

3.2. Mahalanobis distances among kacang goat populations

The Mahalanobis distance analysis in Table 4 highlights significant morphological differences among Kacang goat populations across Southeast Asian islands. The Malay Peninsula consistently exhibits the greatest distances from other populations, indicating its distinctiveness in body indexes. Conversely, Celebes, Lombok, and Moluccas show relatively small distances, suggesting a high degree of similarity and forming a closely related eastern group.

Western populations like Sumatra and Java also display shorter distances between each other, reflecting closer morphological relationships. These patterns are generally consistent for both bucks (above diagonal) and (Buck above diagonal) ewe below the diagonal.

Table 4
Mahalanobis distance among Kacang goat Population Across Southeast Asian Islands

Malay Peninsula	**Malay Peninsula**	**Sumatra**	**Java**	**Lombok**	**Celebes**	**Moluccas**
		40.014	**16.522**	**18.712**	**33.597**	**29.083**
Sumatra	8.385		12.647	12.098	7.819	11.951
Java	11.208	5.359		15.727	13.139	10.161
Lombok	14.285	5.255	5.765		9.856	9.827
Celebes	11.629	3.248	3.497	1.461		3.045
Moluccas	16.896	2.969	8.097	2.935	4.194	

The Mahalanobis distance matrix (Table 4) indicates heterogeneous degrees of morphological separation. In the group reported as bucks, the largest distance occurred between the Malay Peninsula and Sumatra (40.014), whereas several eastern-population comparisons were smaller. In the group reported as ewes, the smallest distance was between Celebes and Lombok (1.461). Figures 2 and 3 display hierarchical clustering based on these distances. The clusters summarize similarity in the selected body indexes only and must not be interpreted as lineages, phylogenies, shared ancestry, or evidence of gene flow.

3.3. Key Results of canonical structure

Table 5 summarizes the canonical discriminant functions. The first function had the largest eigenvalue and explained 53.9% of the variation in bucks and 64.9% in ewes. The first two functions together accounted for 76.9% and 84.6% of the variation, respectively. The reported likelihood-ratio tests were significant, indicating statistical separation among group centroids in the fitted model. Because diagnostic tests for multivariate normality and covariance homogeneity were not reported, the magnitude and stability of this separation require cautious interpretation. Later canonical functions contributed progressively less to separation. The high adjusted canonical correlations for the first function indicate useful discrimination within this dataset, but they do not imply complete separation among populations. Interpretation should therefore consider the cross-validation results and the visible overlap in the canonical plots rather than relying only on statistical significance.

Table 5
Summary of canonical correlation, eigen-values and likelihood ratios

Functions	Adjusted canonical correlations	Eigen-values			Likelihood Ratio	Approximate F-value	Pr > F
		Eigenvalues	Proportion	Cumulative			
Buck							
CAN 1	0.879	3.399	0.539	0.539	0.033	17.15	< .0001
CAN 2	0.769	1.454	0.230	0.769	0.144	13.05	< .0001
CAN 3	0.732	1.157	0.183	0.952	0.353	11.25	< .0001
CAN 4	0.455	0.261	0.041	0.994	0.763	5.73	0.0002
Ewe							
CAN 1	0.813	1.947	0.649	0.649	0.141	15.64	< .0001
CAN 2	0.609	0.589	0.197	0.846	0.415	9.70	< .0001
CAN 3	0.474	0.290	0.097	0.942	0.659	7.72	< .0001
CAN 4	0.373	0.162	0.054	0.996	0.851	6.47	< .0001

3.4. Cross-validation accuracy and canonical representation

Cross-validation results (Table 6) varied markedly among populations. Correct classification was high for some groups, including Sumatra and Java, but substantially lower for Celebes and for the group reported as Lombok ewes. For example, correct classification for Celebes was 58.82% in bucks and 46.51% in ewes, while the reported Lombok-ewe value was 50.00%. These errors show appreciable overlap in body-index profiles and do not support a claim of uniformly strong geographic differentiation.

Table 6
Percent of cross validation for individual goats into their respective island based on body indexes (value in the bracket are number of goats)

Islands	Malay Peninsula	Sumatra	Java	Lombok	Celebes	Moluccas	Total
Buck							
Malay Peninsula	75.00(6)	0.00(0)	0.00(0)	12.50(1)	0.00(0)	12.50(1)	100.00(8)
Sumatra	0.00(0)	90.91(20)	0.00(0)	0.00(0)	9.09(2)	0.00(0)	100.00(22)
Java	7.40(1)	0.00(0)	85.71(12)	0.00(0)	0.00(0)	7.14(1)	100.00(14)
Lombok	0.00(0)	0.00(0)	0.00(0)	90.91(10)	0.00(0)	9.09(1)	100.00(11)
Celebes	0.00(0)	5.88(1)	0.00(0)	17.65(3)	58.82(10)	17.65(3)	100.00(17)
Molucas	0.00(0)	0.00(0)	0.00(0)	7.14(1)	28.57(4)	64.29(9)	100.00(14)
Ewe							
Malay Peninsula	80.00(24)	6.67(2)	0.00(0)	10.00(3)	3.33(1)	0.00(0)	100.00(30)
Sumatra	0.00(0)	91.67(22)	0.00(0)	4.17(1)	0.00(0)	4.17(1)	100.00(24)
Java	0.00(0)	7.14(1)	92.86(13)	0.00(0)	0.00(0)	0.00(0)	100.00(14)
Lombok	0.00(0)	5.00(1)	10.00(2)	50.00(10)	15.00(3)	20.00(4)	100.00(20)
Celebes	4.65(2)	13.95(6)	13.95(6)	4.65(2)	46.51(20)	16.28(7)	100.00(43)
Molucas	0.00(0)	10.00(3)	0.00(0)	16.67(5)	10.00(3)	63.33(19)	100.00(30)

The canonical plots in Figs. 4 and 5 are consistent with the cross-validation results: some groups show displacement along the first two canonical axes, while central and eastern populations overlap. The plots should be interpreted as descriptive visualization of the fitted discriminant space. Overlap may arise from within-population variation, similar body proportions, unequal group sizes, management effects, shared ancestry, or other unmeasured factors; the present data cannot distinguish among these explanations.

4. Discussion

The study demonstrates measurable variation in body proportions among the sampled Kacang goat populations. Depth index contributed most strongly to discrimination in both reported sex groups, while proportionality, length index, conformation index, body-weight index, and body index provided additional information. This agrees with the broader use of morphometric traits and discriminant methods for phenotypic characterization of local goats (Arandas et al., 2017; Melesse et al., 2022; Maksimović et al., 2023). The contribution of the present work is primarily geographic: it compares six Southeast Asian island and peninsula populations within a common body-index framework rather than introducing a new analytical method.

Differences in body indexes may reflect a combination of biological and non-biological factors. Nutrition, production system, age assessment, reproductive status, ancestry, and measurement procedures can influence body size and proportion. Although geographic variation is compatible with differences in local production

environments, the study did not measure feed resources, climate at farm level, health status, or management intensity. It therefore cannot attribute the observed morphology to environmental adaptation or localized selection. Such explanations remain hypotheses for future testing.

Mahalanobis distances and hierarchical dendrograms revealed both separation and similarity. The relatively large distance between the Malay Peninsula and Sumatra in one reported sex group contrasts with the small distance between Celebes and Lombok in the other. These patterns provide a concise description of multivariate phenotypic resemblance, but the dendrograms are not phylogenetic reconstructions. Morphological proximity can result from convergent body form or shared management, while morphological distance can arise without deep genetic divergence. Molecular markers and explicit population-genetic models would be required to evaluate ancestry, gene flow, or genetic structure (Colli et al., 2018; Ernie Muneerah et al., 2021).

The canonical analysis identified statistically significant group separation, but statistical significance should not be equated with complete biological differentiation. Classification performance provides a more direct assessment of practical separability. High rates for Sumatra and Java indicate relatively distinctive profiles in this dataset, whereas the lower rates for Celebes, Lombok, and the Moluccas demonstrate considerable overlap. Unequal or small subgroup sizes may also affect the stability of discriminant functions and cross-validation estimates.

Several limitations affect reproducibility and inference. Sampling was purposive, farm-selection criteria were incompletely documented, breed purity was not verified molecularly, relatedness among animals was unknown, and observer repeatability was not quantified. In addition, formal diagnostics for multivariate normality, covariance homogeneity, influential observations, and independence were not reported. The apparent conflict in sex-specific sample totals across tables must also be resolved from the source dataset. These limitations do not invalidate the descriptive patterns, but they restrict generalization and preclude strong claims about genetic differentiation, phylogeny, adaptation, or region-specific breeding value.

5. Conclusion

Kacang goats sampled from six Southeast Asian geographic populations differed in several body indexes, and the depth index contributed most strongly to discrimination in both reported sex groups. Mahalanobis distances and canonical discriminant analysis summarized variation in multivariate morphological profiles, while cross-validation showed that classification was strong for some populations but weak to moderate for others. The findings therefore support geographic variation with partial morphological overlap. They do not demonstrate genetic differentiation, phylogenetic relationships, environmental adaptation, or superior breeding value. Future studies should use probability-based and well-documented farm sampling, verify breed identity and relatedness, quantify measurement repeatability, test multivariate assumptions, and integrate genomic, pedigree, management, and environmental data before conservation or breeding recommendations are made.

Declarations

Competing Interest

The authors declare that they have no competing interests.

Data Availability Statement

The data supporting the findings of this study are available from the corresponding author upon reasonable request.

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Figures

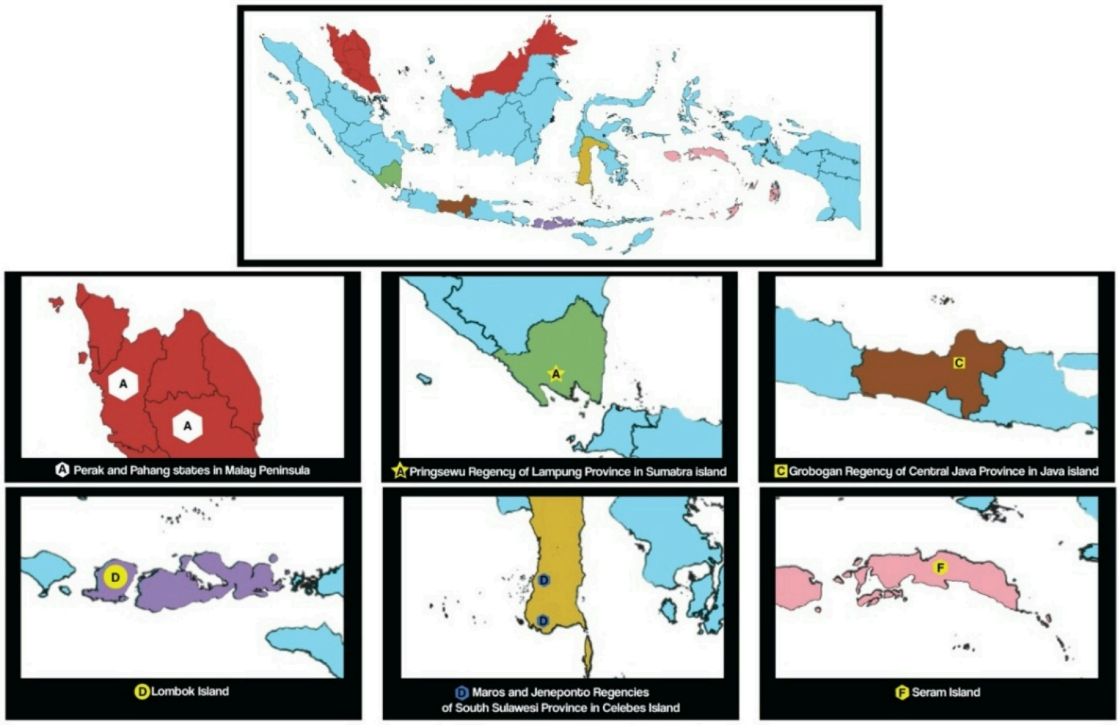


Figure 1

Location of the research: A. Perak and Pahang states in Malay Peninsula, B. Pringsewu regency of Lampung Province in Sumatra island, C. Grobogan Regency of Central Java Province in Java island, D. Lombok Island, E. Maros and Jeneponto Regencies of South Sulawesi Province in Celebes Island, and F. Seram Island of Moluccas Province

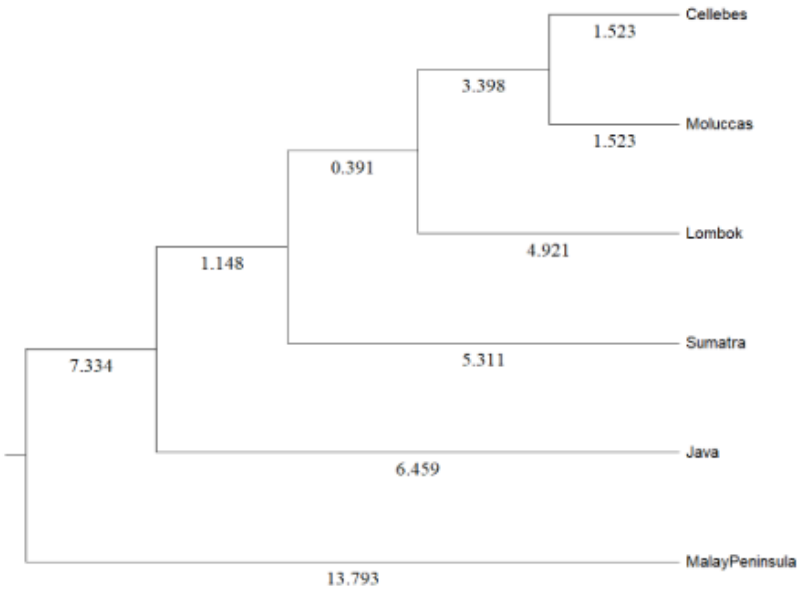


Figure 2

Hierarchical dendrogram based on Mahalanobis distances among geographic populations for the group reported as bucks.

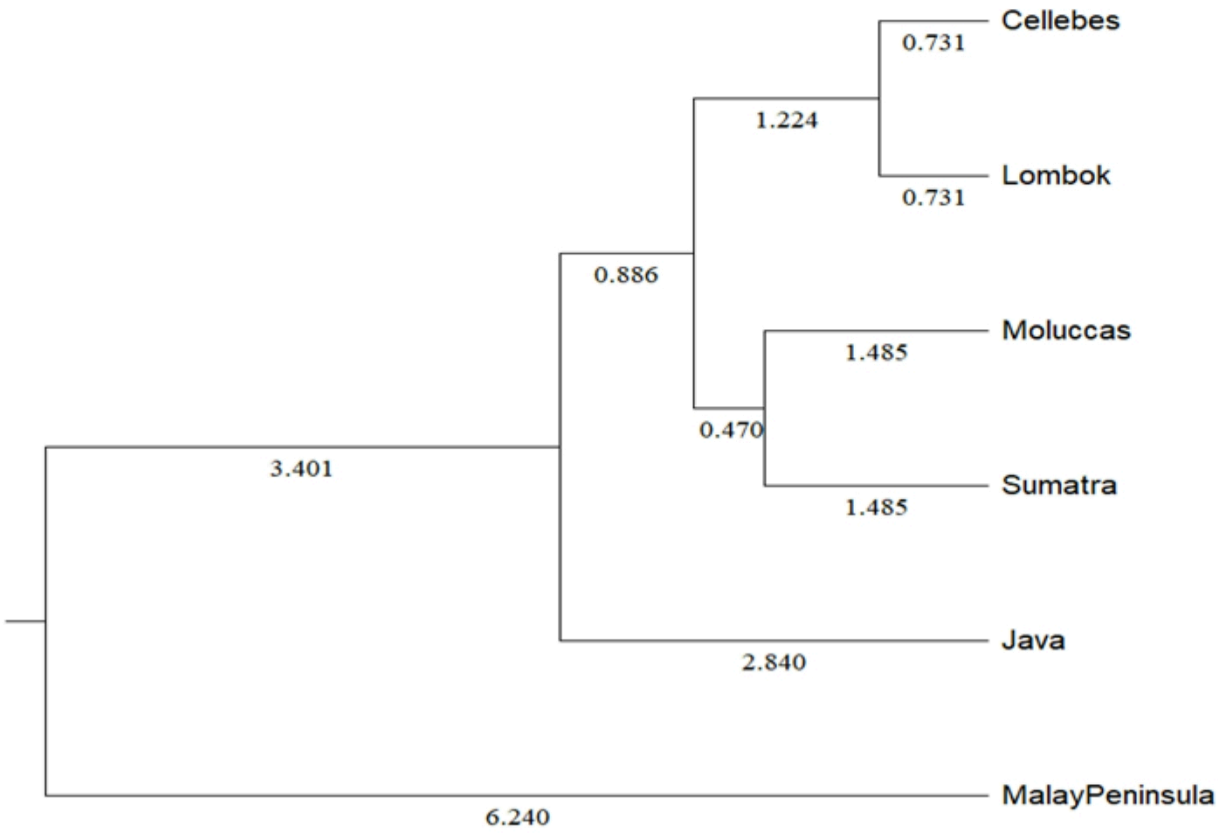


Figure 3

Hierarchical dendrogram based on Mahalanobis distances among geographic populations for the group reported as ewes.

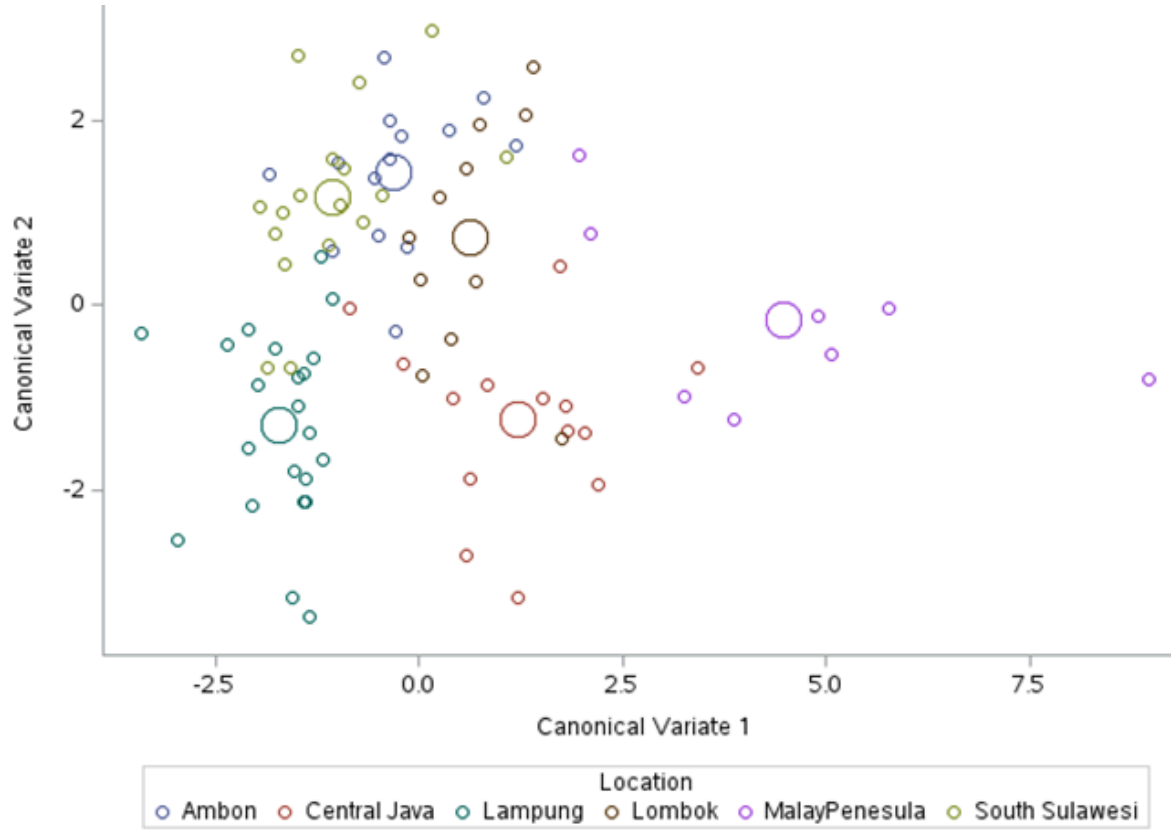


Figure 4

Canonical representation of the geographic populations for the group reported as bucks based on body indexes.

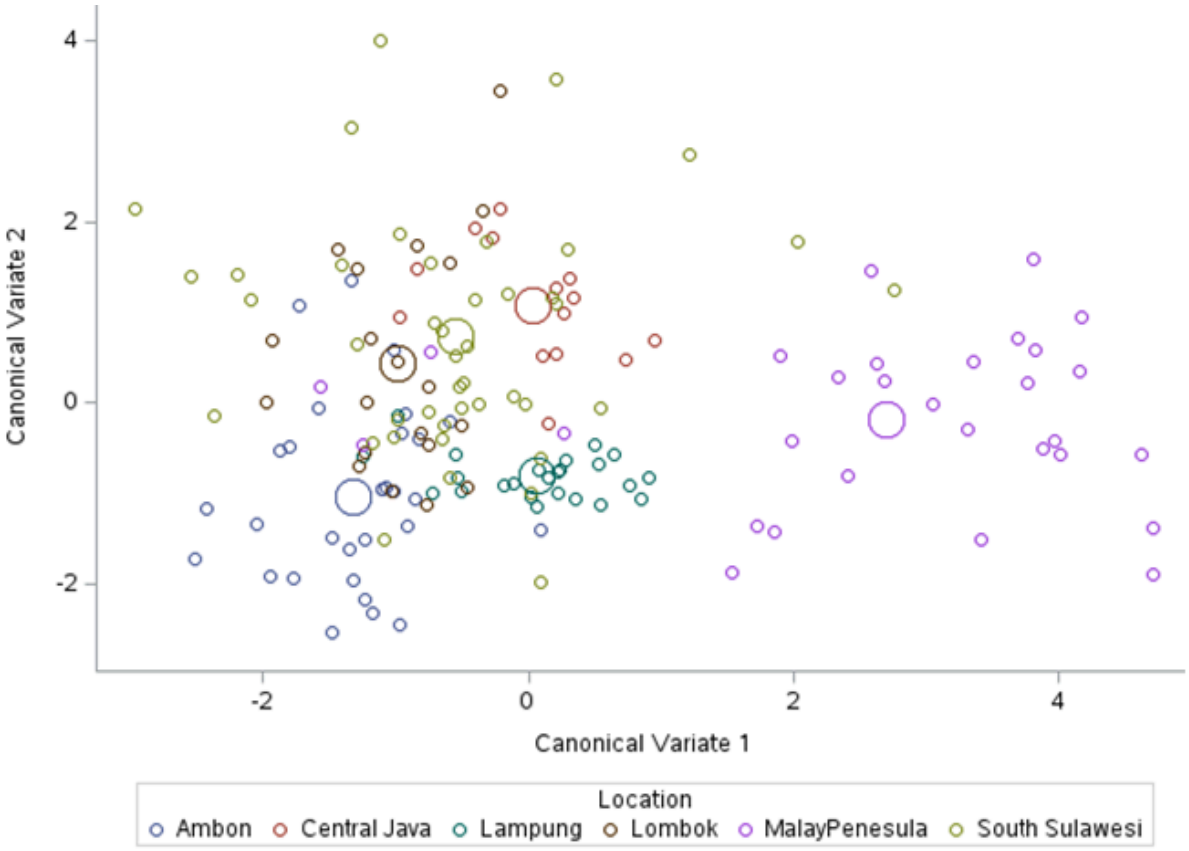


Figure 5

Canonical representation of the geographic populations for the group reported as ewes based on body indexes.