

# Assessing the morphological diversity of Ethiopian indigenous chicken populations using multivariate analysis of morphometric traits

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## Introduction

- Chickens are most widely distributed genetic resources in many rural regions of Africa and Asia [1].
- Due to their reproductive efficiency, and potential to adapt in a wide range of environments, they are considered the most suitable livestock species for smallholders.
- Chicken rearing has been reported to enhance food security through an increased supply of animal source products such as meat and eggs of high quality protein [2].
- Assessment of genetic characters of animal populations is a prerequisite for successful planning of genetic improvement programs [3].
- However, in regions where genetic characterization is not affordable, morphological studies have been used to explore the characteristics of local livestock populations.

## Materials and Methods

- Data were collected from 10 districts representing four zones: Sheka, Kaffa, Bale and Metekel.
- Three districts each from Kaffa and Sheka zones and 2 districts each from Bale and Metekel zones were proportionally selected.
- Collectively, 3069 chickens (959 males and 2110 females) were sampled from all zones.
- Traits scored were live weight (LW), body length (BL), breast circumference (BC), wingspan (WS), shank length (SL), shank circumference (SC), keel length (KL), back length (BkL), neck length (NL).
- A cluster and discriminant analysis was applied to identify combination of variables that best differentiate among chicken populations.

## References

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## Results

- Metekel chickens were characterized by higher LW, BL, KL and BkL and differed from other groups ( $p < 0.05$ ).
- Sheka chickens demonstrated the highest BC, WS, SL, SC and NL being different from others ( $p < 0.05$ ).

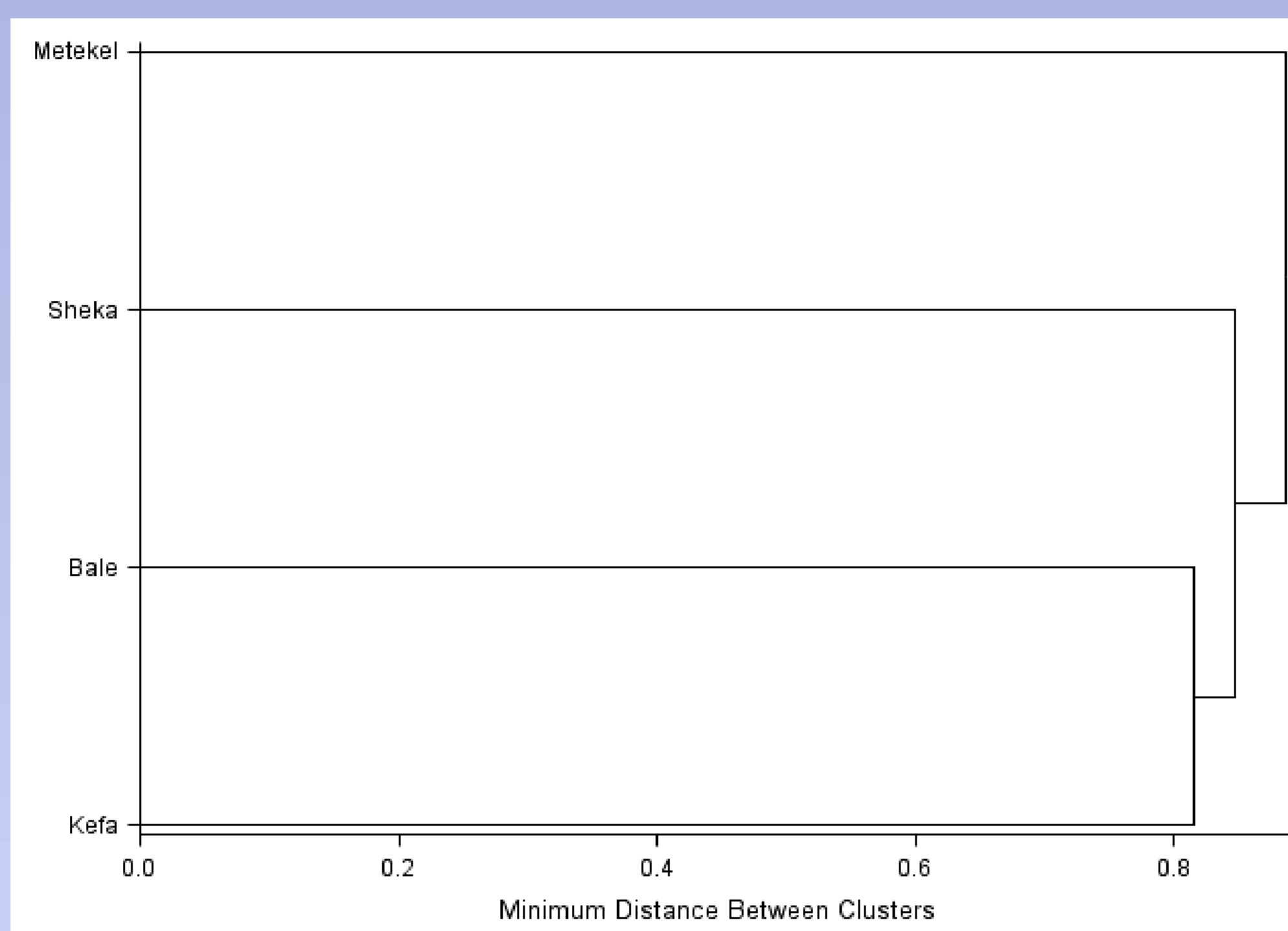


Fig. 1. Dendrogram of chicken populations

- Cluster analysis produced two distinct groups in which Bale and Sheka chickens were clustered in one group.
- Chickens of Metekel and Kaffa were grouped in another cluster each separated with sub-clusters (Fig 1).
- All Mahalanobis distances were significant being the shortest between Sheka and Bale chickens and the longest among those of Metekel and Bale (Table 1).

Table 1. Mahalanobis distances between chicken populations of the four zones

Zones	Kaffa	Sheka	Bale	Metekel
Kaffa	0	7.08***	9.12***	9.37***
Sheka		0	4.39***	19.2***
Bale			0	23.9***
Metekel				0

- Three statistically significant canonical variables (CAN) were extracted.
- CAN1 and CAN2 accounted for 73.2 and 14.6% of the total variations.

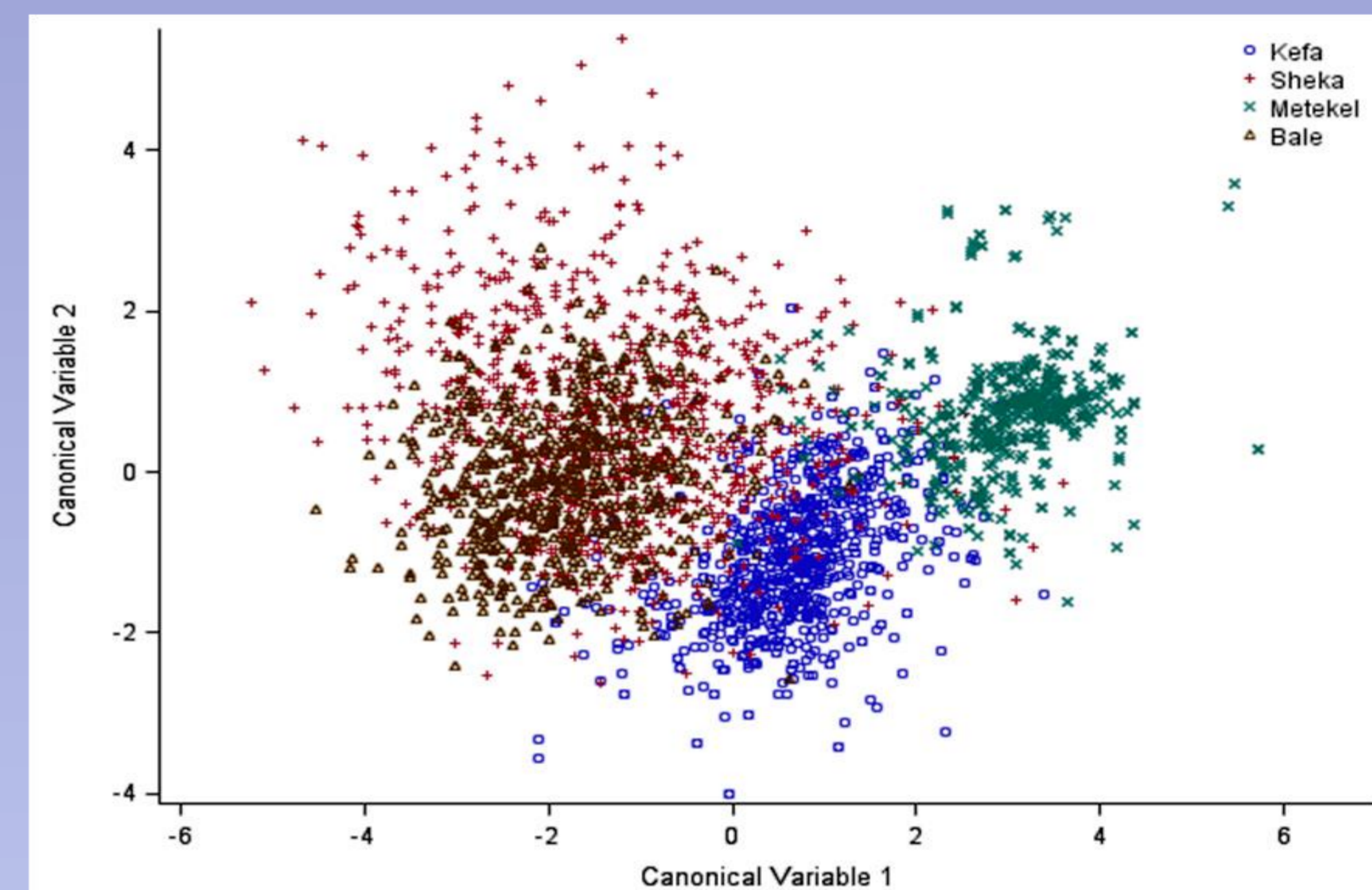


Fig. 2. Canonical representation of indigenous chicken populations across the four zones

- Scatter plot showed that CAN1 effectively discriminated between chickens of Metekel and Kaffa (Fig. 2).
- However, CAN2 discriminated against those of Bale and Sheka.
- About 95, 95, 92, and 82% of Metekel, Bale, Kaffa, and Sheka chickens were correctly classified into their origin population, respectively (Table 2).

Table 2. Percent of chickens classified into their respective zones (values in number)

Zones	Kaffa	Sheka	Bale	Metekel	Total
Kaffa	92.3 (683)	4.57 (41)	0.67 (6)	2.45 (22)	100 (898)
Sheka	6.28 (53)	82.2 (694)	10.2 (86)	1.30 (11)	100 (844)
Bale	0.83 (6)	4.17 (30)	94.9 (683)	0.14 (1)	100 (720)
Metekel	1.50 (9)	3.0 (18)	0.17 (1)	95.3 (572)	100 (600)

## Conclusions

- Distinct differentiation reflected the existence of high genetic variability among chicken populations.
- About 91% of chickens were classified into their origin population indicating genetic homogeneity within population.
- It is recommended that these findings could be validated through molecular-based genetic characterization studies.

## Acknowledgements

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