

# Multi Variate Analyses on Morphological Traits of Local Chicken Ecotypes of Benishangul-Gumuz Region, Western Ethiopia

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**Key words:** Benishangul Gumuz, chicken ecotype, discriminant analysis, morphological variation, characterization

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# Abstract: This study was conducted in four districts of Benishangul Gumuz regional state Western Ethiopia to characterize local chicken population based on morphological variation using multi variate discriminant analyses. A total of 847 matured local chickens (619 females and 228 males) were randomly sampled from the study are and twenty morphometric traits were measured. Based on a discriminant analysis, sample chicken populations were classified into their respective ecotypes with overall hitting rate of (85.73%) for females and (87.85%) for males. Step wise discriminant analysis identified back length, beak length, wing span and neck length to have more discriminating power causing morphological variation among female chicken ecotypes. Similarly, best variables that discriminated male sample chicken ecotypes were back length, neck length and beak length and breast circumference. The study revealed that most of the parameters measured revealed distinctive variations among ecotypes. The present phenotypic information will be the basis for further characterization, conservation and selection strategies for the local chicken population in the study area.

## **INTRODUCTION**

Ethiopia possesses huge number of chicken population in Eastern Africa. According to CSA<sup>[1]</sup> chicken population in the country estimated to be 56.87 million of which 96% are indigenous chicken ecotypes. Characterization of livestock breeds is the first approach to a sustainable use of its animal Genetic resources<sup>[2, 3]</sup>. The first step of the characterization of local Genetic resources is based on the knowledge of variation in the morphological traits<sup>[4]</sup>. Morphometric measurements have been used to evaluate the characteristics of various breeds of animals and could provide useful information on the suitability of animals for selection<sup>[5-9]</sup>. Previous efforts on the phenotypic characterization of breeds of livestock have been restricted to the use of analysis of variance whereas the current trend in livestock classification involves the use of multi variate statistical tools<sup>[10]</sup>. This

is because univariate statistical analysis, analyze each variable separately and do not explain how the populations under investigations differ when all measured morphological variables are considered jointly<sup>[11-13]</sup>.

Multifactorial discriminant analyses have been found to be more suitable in assessing variation within a population and can discriminate different population types when all measured morphological variables are considered jointly. The objective of the study is to characterize local chicken population of Benishangul-Gumuz Regional state western Ethiopia based on morphological variation using multi variate discriminant analyses which could help in proper management, conservation and genetic improvement of the local chicken population.

## MATERIALS AND METHODS

**Description of the study areas:** The study was conducted in four districts (Bambassi, Kamashi, Homosha and Maokomo) of Benishangulgumuzregional state. Assosa town is located at 670 km West of Addis Ababa, capital city of Ethiopia. Bambasi is located 45 km East of Assosa town whereas Kamashi, Homosha and Maokomo are located 225 km North East, 35 km West and 105 km South West of Assosa town, respectively.

Benishangul Gumuz regional state is located between geographical coordinates of 9° 30-110 39'N latitude and 34°, 20-36°30'E longitude with altitude ranging from 1272-1573 masl. Mean annual rainfall and temperature of the region lies between 700-1450 mm and 21-35°C, respectively<sup>[14]</sup>.

**Phenotypic measurements:** Linear body measurements were measured and from 847 chickens, comprising of 228 males and 619 females. The measurement was taken from matured local chicken >6 months of age by asking chicken owners. Measurements were taken early in the morning to avoid the effect of feeding and watering on the chicken size and conformation. The twenty morphometric traits measured were body weight (kg), body length, wing span, wing length shank length, breast circumference, wattle length, wattle width, keel length, beaklength, back length, comp length, comb width, toe to back length, tail length, earlobes length, earlobes width, neck length, back length and height were measured using spring balance and centimetre (cm) in the nearest two 0.5 digits using breed characterization manual (FAO, 2012).

**Statistical analysis:** The stepwise discriminant analysis procedure (PROC STEPDISC) was run to rank the quantitative morphological traits by their discriminating power SAS.,<sup>[15]</sup> version 9.2. Selected significant traits

from PROC STEPDISC were then subjected to canonical discriminant analysis (PROC CANDISC)<sup>[15]</sup> version 9.2 and discriminant function analysis (PROC DISCRIM) SAS.,<sup>[15]</sup> Version 9.2 to ascertain the existence of population level phenotypic differences between the districts/ecotypes. The analysis was done using individual birds as a unit of classification.

## **RESULTS AND DISCUSSION**

Discriminant analysis: Thevalidity of discriminant analysis procedure was assessed by means of reclassification statistics for female and male sampled populations and indicated in Table 1 and 2. The correct classification for female chicken sample population into their respective ecotypes ranged from 71.72-100%. The overall average error count estimate was 14.27% for all observations and 85.73% of the female chicken samples were correctly classified. Concerning male sample chicken population, the correct classification ranged from 73.85-100%. The overall average error count estimate was 12.15% for all observations and 87.85% of the male chicken samples were correctly classified. Females and males indigenous chicken sample populations from Kamashi district were more homogeneous on the quantitative variables as it can be witnessed from their respective high hit ratios.

Canonical discriminant analysis: Pair-wise squared Mahalanobis distance between ecotypes for the female sample populations is shown in Table 3. The pair-wise squared Mahalanobi's distances among ecotypesfor female chicken sample populations were highly significant (p < 0.001). This shows that female populations from each ecotype have distinct and measurable differences from other sampled populations. The shortest distance (1.02) was measured between Bambassi and Homosha ecotypes and the longest distance (5.32) was measured between Bambassi and Kamashi ecotypes. This indicates that sample populations from Bambassi and Homosha ecotypes were not much different in the group quantitative features under consideration. The squared Mahalanobis distances for male sample populations from canonical discriminant analysis Table 3. The shortest distance (2.01) was observed between Bambassi and Homoshaecotypes and the longest distance was between Kamashi and Bambassi ecotypes with a value of (10.75) standard units. The distances expressed here between sample populations are due to distinct phenotypic differences between ecotypes for quantitative traits.

**Stepwise discriminant analysis:** Result of the stepwise discriminant analysis is presented in Table 4 and 5. All 20 quantitative variables for both sexes were separately

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From district/ecotypes	Bambassi	Kamashi	Mao-komo	Hmosha	Total	
Bambassi	90(72.58)	0(0.00)	0(0.00)	34(27.42)	124(100)	
Kamashi	0(0.00)	206(100)	0(0.00)	0(0.00)	206(100)	
Mao-Komo	1(0.69)	0(0.00)	142(98.61)	1(0.69)	144(100)	
Hmosha	41(28.28)	0(0.00)	0(0.00)	104(71.72)	145(100)	
Total	132(21.32)	206(33.28)	142(22.46)	139(22.46)	619(100)	
Error count estimates for	districts/ecotypes		0.1427			

Table 1: Correctly classified for female chicken sample population using discriminant analysis

Table 2: Correctly classified for male sample population using discriminant analysis

From district/ecotype	Bambassi	Kamashi	Mao-komo	Hmosha	Total	
Bambassi	48(73.85)	0(0.00)	0(0.00)	17(26.15)	65(100.)	
Kamashi	0(0.00)	61(100)	0(0.00)	0(0.00)	61(100)	
Mao-komo	0(0.00)	0(0.00)	53(100)	0(0.00)	53(100)	
Hmosha	11(22.45)	0(0.00)	0(0.00)	38(77.55)	49(100.00)	
Total	59(25.88)	61(26.75)	53(23.25)	55(24.12)	228(100)	
Error count estimates for	districts/ecotypes		0.1215			

Number of observations and percent (in bracket)

Table 3: Squared Mahalanobis distance between ecotypes for the males above diagonal and for females below diagonal indigenous chicken sampled populations

From ecotypes	Bambassi	Homosha	Kamashi	Mao-komo
Bambassi	***	2.01791	10.75121	3.31827
Hmosha	1.02446	***	8.02063	2.30023
Kamashi	5.32326	5.14703	***	7.79402
Mao-komo	1.46943	1.86005	4.81481	***

Table 4: Step	wise sele	ection sum	narv for i	female cł	nicken p	opulation

Stepw	Stepwise selection summary										
Steps	Variable entered	Partial R <sup>2</sup>	f-values	Pr>F	Wilk's lambda	Pr <lambda< th=""><th>Average squared canonical correlation</th><th>Pr&gt;ASCC</th></lambda<>	Average squared canonical correlation	Pr>ASCC			
1	BaL	0.3299	100.93	< 0.0001	0.67009647	< 0.0001	0.10996784	< 0.0001			
2	BeL	0.1001	22.78	< 0.0001	0.60298799	< 0.0001	0.13974707	< 0.0001			
3	WS	0.0828	18.44	< 0.0001	0.55307824	< 0.0001	0.16385805	< 0.0001			
4	NL	0.0597	12.95	< 0.0001	0.52006570	< 0.0001	0.17732032	< 0.0001			
5	Н	0.0885	19.78	< 0.0001	0.47402750	< 0.0001	0.19698293	< 0.0001			
6	ToBL	0.0807	17.85	< 0.0001	0.43576450	< 0.0001	0.21250476	< 0.0001			
7	BC	0.0454	9.65	< 0.0001	0.41599376	< 0.0001	0.22597902	< 0.0001			
8	WgL	0.0185	3.83	0.0098	0.40827964	< 0.0001	0.23103492	< 0.0001			
9	BL	0.0166	3.41	0.0174	0.40151905	< 0.0001	0.23552701	< 0.0001			
10	BW	0.0162	3.32	0.0196	0.39503335	< 0.0001	0.23890405	<0.0001			

Table 5: Step wise selection summary for male chicken population

Stepwise selection summary

Step	Variable entered	Partial R <sup>2</sup>	f value	Pr>F	Wilk's lambda	Pr <lambda< th=""><th>Average squared canonical correlation</th><th>Pr&gt;ASCC</th></lambda<>	Average squared canonical correlation	Pr>ASCC
1	BaL	0.3441	39.18	< 0.0001	0.65586596	< 0.0001	0.11471135	< 0.0001
2	NL	0.1146	9.62	< 0.0001	0.58073519	< 0.0001	0.13994936	< 0.0001
3	BeL	0.0799	6.42	0.0003	0.53434911	< 0.0001	0.16400268	< 0.0001
4	BC	0.0546	4.25	0.0060	0.50517792	< 0.0001	0.17822221	< 0.0001
5	Bw	0.0561	4.36	0.0052	0.47681320	< 0.0001	0.19469242	< 0.0001
6	BL	0.0571	4.42	0.0049	0.44959989	< 0.0001	0.21005690	< 0.0001
7	ELW	0.0542	4.16	0.0068	0.42523256	< 0.0001	0.22625385	< 0.0001

Where CL= Comb Length; CW = Comb Width; WL = Wattle Length; WW = Wattle length; BeL = Beak Length; BeW = Beak Width; WgL = Wing Length; WS = Wing Span BL= Body Length; BaL= Back Length; EalL = Earlobes Length; EaW = Earlobes Width; SL= Shank Length; BC = Breast Circumference; TL = Tail Length, ToBL = Toe to Back Length; H = Height, BW = Bod Weight; NL = Neck Length

subjected to the STEPDISC procedure of SAS<sup>[15]</sup> and 17 variables for both sexes were identified as best discriminating variables on Stepwise selection summary. Wilk's lambda test shows that all the traits considered were highly significant (p<0.01) contributors to discrimination of the total population in to separate groups. As depicted by the, respective, partial  $R^2$  and

f-values the variables with the highest discriminating powers on the female population in the four ecotypes were back length, beak length, wing span and neck length in descending order. Similarly, best variables that discriminated the sample male chicken population were back length, neck length and beak length and breast circumference.

#### CONCLUSION

Indigenous chicken population in the study area had distinct physical variations under consideration for quantitative traits in traditional management system. This shows that female and male chicken populations from each districts/ecotype have distinct and measurable differences from other sampled populations. This phenotypic variability caused by both genetic and environmental factors. The high phenotypic diversity in indigenous chicken is major evidence for the existence of high genetic variability in the study area. This variability may provide an opportunity for future selection and breeding improvement strategies.

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