Morphometric Differentiation of Indigenous Chicken Populations of Ethiopia Using Discriminant Analysis

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Introduction

The livestock population of Ethiopia is believed to be one of the largest in Africa comprising of 56.7 million cattle, 29.3 million sheep, 29.1 million goats and 56.9 million poultry (FAOSTAT, 2016). This sector has been contributing considerable portion to the economy of the country, and still promising to rally round the economic development (NABC, 2010). Poultry production is one of integral parts of livestock farming activities in the country, where chickens are the most widespread with almost every rural family owns chicken that contribute greatly to the supply of eggs and meat (Alemu, Y. and Tadelle D., 1997, Tadelle, D., 2003, Aklilu, H.A., 2007).

Despite the large number of the country's livestock &/or poultry population, the productivity per unit of animal and the contribution of this sector to the national economy is relatively low. This may be due to different factors such as poor nutrition, prevalence of diseases, lack of appropriate breed and breeding strategies and poor understanding of the production system as a whole.

A number of studies have been carried out on the performance characteristics of various ecotypes of chicken in the country (Duguma R., 2010, Halima, H.M., 2007, Aberra, M. and Tegene N., 2011, Mengesha, M. and Tsega W. 2011). However, there is still little information available on the diversity of different chicken populations. Moreover, no real efforts have been made so far to conserve these chicken genetic resources. One of the important reasons to conserve indigenous chicken genetic resources is to keep genetic variation within and among them. The present and future improvement and sustainable utilization of indigenous chickens are dependent upon the availability of these genetic resources and variations (Benitez, F., 2002).

Characterization work (some phenotypic and very few genetic) are being carried out in Ethiopia to generate useful information towards conservation and utilization of animal genetic resources, but these works are mostly on ruminants rather than on chicken. Genetic characterization based on molecular assessment is reported to be most common and used method to evaluate genetic diversity among and within livestock breeds; however it needs high technology and cost (Wimmers, K., et. al. 2000, Romanov, M.N. and S. Weigend, 2001, Hillel, J.M.A., et al., 2003).

Researchers have used a characterization method based on morphological traits that are easy to measure, low cost and provide valuable information (Duguma, R., 2010, Halima, H.M., 2007). Hence, the purpose of this study was to use discriminant analysis for differentiation of indigenous chicken population in Ethiopia by taking quantitative morphological traits into consideration.

Material and Methods

Study area location: The study was conducted in three districts (Gobusayo, Bakotibe and Danno) of Oromia Region, Ethiopia. Gobusayo is found in east Wollegga that is located between 09°5'N latitude and 35°45'E longitudes at about 263km far from Addis Ababa. The district has an altitude ranging from 1500 to 1750m.a.s.l. The mean annual temperature of the district ranges between 15-21°C whereas the mean annual rain fall is about 2000mm. Bakotibe is found in west Showa that is located between 08°59'N latitude and 37°29'E longitudes at about 251km away from Addis Ababa. The area has an altitude of 1650m.a.s.l. The district receives an average of 1242 mm rainfall and temperature ranges from 13.3-27.9°C. Danno is found in west Showa that is located between 08°45'N latitude and 37°15'E longitudes at a distance of 217km away from Addis Ababa. The district has an altitude ranging from 1400-2500m.a.s.l. and it receives on the average 900-1400mm annual rain fall and the annual temperature ranges from 15-30°C.

Data collection: A total number of 711 chickens (162 males and 548 females) of age >8 months were selected randomly from sampled households in the three districts for data collection. Body weight (BW) and LBMs i.e., *back-length (BaL), beak-length (BeL), body-length (BoL), breast-circumference (BC), comb-height (CH), comb-length (CL), keel-length (KL), neck-length (NL), shank-circumference (SC), shank-length (SL), wattle-length (WL), wattle-width (WW), and wing-span (WS))* were taken following FAO (2012) recommendations on each bird from December 2014 to April 2015. A spring balance and measuring tape were used to record the respective traits. All measurements were taken by the same person early in the morning before the birds were fed.

Data analysis: SAS-program version 9.4 (2014) was used for all statistical analysis in this study.

Univariate Analysis: The general linear model procedure (PROC GLM) of SAS was employed for quantitative variables to detect statistical differences among sampled chicken populations.

Multivariate Analysis: Stepwise discriminant (PROC STEPDISC), canonical discriminant (PROC CANDISC) and discriminant function (PROC DISCRIM) analyses were employed to ascertain the existence of population level phenotypic differences among the chicken populations sampled from the three districts. In order to avoid potential sampling bias due to low number of males, only female birds were considered in this analysis.

Results and Discussion

Univariate Analysis: Results from PROC GLM showed significant (p<0.05) sex and district effects on the traits. Male chickens had significant higher values than females for all the traits. The chickens from Danno district had for most of the traits the highest LSMEANS values followed by Bakotibe and Gobusayo.

Multivariate Analysis: Stepwise discriminant analysis was carried out on the traits recorded to assess the significance of the traits in discriminating the chicken populations sampled from the three districts in a stepwise fashion. At each step, the significance of already entered traits was evaluated based on the significance for staying (p-value: 0.15) criterion, and the significance of newly entering traits was evaluated based on the significance for entering (p-value: 0.15) criterion. When no traits could be removed or entered, the stepwise selection procedure stopped.

The stepwise discriminant analysis identified eleven traits (namely: WS, BaL, BC, WW, BW, CH, NL, BeL, WL, CL and SC) to have more discriminating power in assessing morphological variation among the chicken populations sampled. These eleven traits were thus used in further analysis of canonical discriminant and discriminant function analyses.

Canonical discriminant analysis: The univariate ANOVA results indicate that highly significant district effect exist for all the traits (Table 1).

Table 1. Univariate test statistics

Nr.	Trait	Between STD	R-Square	F Value	P-Value
1	*Wing-span*	0.9076	0.5501	**333.20**	<.0001
2	*Back-length*	0.7042	0.3312	134.92	<.0001
3	*Breast-circumference*	0.5007	0.1675	54.81	<.0001
4	*Wattle-width*	0.4083	0.1113	34.13	<.0001
5	*Body-weight*	0.3594	0.0863	25.73	<.0001
6	*Comb-height*	0.3241	0.0701	20.55	<.0001
7	*Neck-length*	0.2310	0.0266	10.07	<.0001
8	*Beak-length*	0.1995	0.0261	7.44	0.0007
9	*Wattle-length*	0.1977	0.1113	7.30	0.0007
10	*Comb-length*	0.1653	0.0183	5.07	0.0066
11	*Shank-circumference*	0.1359	0.0123	**3.40**	0.0340

By comparing the F- and P-value statistics for each significant trait, we can conclude that "wing-span" has the highest amount of significant discriminative power, while "shank-circumference" has the least amount of discriminative power in differentiating the chicken populations sampled. The relatively large significant p-values obtained for the traits (Table 1) indicate the fact that these traits have high discriminatory power in classifying the chicken populations.

Table 2. Correlations and eigenvalues

	Canonical correlation	Squared canonical correlation	Eigen value	Difference	Proportion	p-value
CAN1	0.7932	0.6292	1.6971	1.3411	0.8266	<.0001
CAN2	0.5124	0.2625	0.3560		0.1734	<.0001

The correlation between CAN1 and districts is high (>0.8), and about 63% of the variation in the first canonical variable can be attributed to the differences among the three chicken populations. The first eigenvalue measures the variability in CAN1 and accounts for 83% of the variability among the chicken populations in the traits (Table 2).

Discriminant function analysis: The Mahalanobis distance between Gobusayo and Bakotibe, Gobusayo and Danno and Bakotibe and Danno were respectively 8.93, 7.85 and 2.05. These distances were all significant (p-value: <0.0001). Table 3 lists the misclassified observations based on the posterior probability estimates computed by the quadratic function via cross-validation.

Table 3. Classification results

From District	Gobusayo	Bakotibe	Danno	Total
Gobusayo	**169 (92.35)**	11 (6.01)	3 (1.64)	183 (100.00)
Bakotibe	15 (8.24)	**142 (78.02)**	25 (13.74)	182 (100.00)
Danno	10 (5.46)	38 (20.77)	**135 (73.77)**	183 (100.00)
Total	195 (35.58)	190 (34.67)	163 (29.74)	548 (100.00)
Error rate	0.0765	0.2198	0.2623	0.1862

Numbers before the parenthesis indicate the number of observation

The standardized canonical scores and the structure leadings are used in two-dimensional biplot to aid visual interpretation of the district difference. Interrelationships among the traits and the discrimination of the three chicken populations are presented in Figure 1.
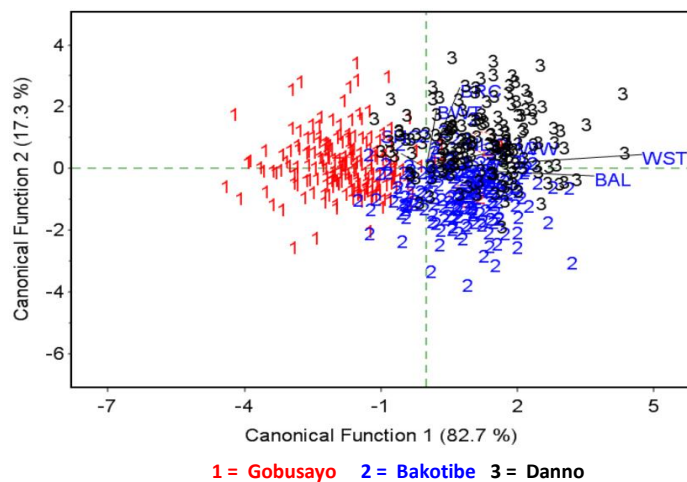

1 = Gobusayo   2 = Bakotibe   3 = Danno

Figure 1. Biplot display of canonical discriminant functions and structure leadings

Conclusions and Outlook

In this study significant morphological variations were detected among the chicken ecotypes from the three districts. The high diversity in indigenous chicken ecotypes is a major evidence for the existence of high genetic variability among them. Thus, further work on indigenous chicken ecotypes need to be carried out at molecular level to assert the advantage of maintaining genetic diversity and adaptability.

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