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Original article

Application of multivariate analysis in quantifying size and morphological traits of local chicken in central zone of Tigray

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ABSTRACT

The study was conducted in three districts of central zone of Tigray, with the aim, to assess the magnitude of genetic diversity and interdependence of morphological traits in varieties of indigenous chickens, an experiment was conducted using a total of 375 sexually matured randomly-selected female individuals' chickens. from 375 females were used with the weighting method of standardization. A total of 19 morphological measurable traits variables data was collected from selected locations in midland and highland chickens and were analyzed using Principal Component Analysis (PCA) procedure, discriminant analysis and cluster analysis. The PCA showed that five principal components' (PC) were extracted that accounted for 58.45% of the total variation. The first three principal components accounted for 47.24% of the total variation. The differentiation of the highland and midland chicken ecotypes populations was based on the weights of neck length, beak length, body length, wattle width, body weight, wattle length and height at back traits. Cluster analysis revealed that the pair wise squared Mahalanobis' distances between populations' shows smallest (3.00) and largest distances (29.01) between midland and highland chicken ecotypes, respectively This indicated that midland chicken share some phenotypic characters with other chicken types as a result farmers of these midland agro ecology often exchange cock/hen through different means with the fact that there existed genetic migration from one district to the next district chicken populations and gene flow is unregulated while the largest distance between highland chicken ecotypes indicates that higher heterogeneity within the breed type.

1. Introduction

The traditional poultry production system is characterized by small flock sizes, low input, low output, and periodic devastation of the flock by disease (Tadelle et al., 2003). With a number of challenges, backyard poultry production is still important in low-income, food-deficit production systems to supply the fast-growing human population with high demand for quality protein (Tadelle et al., 2003). Backyard poultry is also a source of employment for underprivileged groups in many local communities (Mengesha et al., 2008). According to Aklilu (2007), village poultry is the first step on the ladder for poor households to climb out of poverty and is a source of self-reliance for women, since poultry and egg sales are decided by women and provide women with an immediate income to meet household expenses.

Despite the importance of indigenous breeds in rendering income, posses' cultural value and source of nutrition for household, they are under threat due to various factors such as changing production systems and indiscriminate crossbreeding (Besbes, 2009).

Developing appropriate animal breeding programs for village conditions requires characterizing local chickens, defining the production environments and identifying the breeding practices, production objectives, and trait choices of rural farmers (Soelkner et al., 1998). Therefore, these existing chicken ecotypes have to be characterized for their overall merits and for subsequent improvement. Characterization is the initial step for long-term genetic improvement as it provides the basis for any other livestock development interventions and provides information for designing appropriate breeding programs.

The diversity in gene pool and influence of varied climatic conditions have given rise to different local populations of chicken which are repositories of unique genes that should be conserved for local and international future benefits (Adebambo, 2004). According to Groeneveld et al. (2010), identifying and understanding a unique genetic resource in a particular region and the development and proper use of the associated diversity is a global responsibility. Breed characterization has accordingly been recognized as the first approach to the sustainable use of animal genetic resource (Lanari et al., 2003).

It is believed that various breed characteristics provide to some extent reasonable economic indicators. Body size veryis important traits in broiler chickens. The characterization of local genetic resources depends on the knowledge of the variation of morphological traits, which have played a very fundamental role in classification of livestock based on size and shape (Yakubu et al., 2010)

Multivariate analyses were used to investigate the morphological structure and quantify differences among the sub-populations. From the correlation matrix, data were generated for the principal component factor analysis to transform the correlated quantitative traits to orthogonal quantitative traits (Everitt et al., 2001). Multi factorial analyses of morphological traits have proven to be suitable in assessing the variation within a population and can discriminate different population types when morphological variables are considered simultaneously (Yakubu et al., 2011). Various multivariate techniques such as Principal Component Analysis (PCA), cluster analysis, disccriminant analysis, canonical correlation analysis and others have been applied for multivariate variable data analysis in the field of animal science and other related fields. PCA is designed to transform original variables into new, uncorrelated variables (axes) called principal components which are linear combinations of the original variables (Shrestha et al., 2008). PCA has capacity to reduce the original variables measured into few components/factors to provide information on the most meaningful parameters which will describe a whole set affording data reduction with minimum loss of original information (Helena et al., 2000). In Ethiopia, there is little or no information on the interrelationships among morphometric traits of chicken using a multivariate approach.

This study was aimed to determine the most important characters causing variation and to ascertain the magnitude of genetic diversity in varieties of highland and midland chickens for genetic and breeding purposes.

2. Materials and methods

2.1. Description of study area

The study was conducted in three rural districts of the central zone of Tigray: Laelay Maichew, Ahferom and Adwa (Fig. 1). The Central Tigray zone is bordered by Eritrea in the north, East Tigray zone in the East and south east Tigray, West Tigray zone in the west and Amhara National Regional State in the south. The central zone of Tigray covers about 9741 km^2 with a total population of 1,132,229 of which 51% are female.

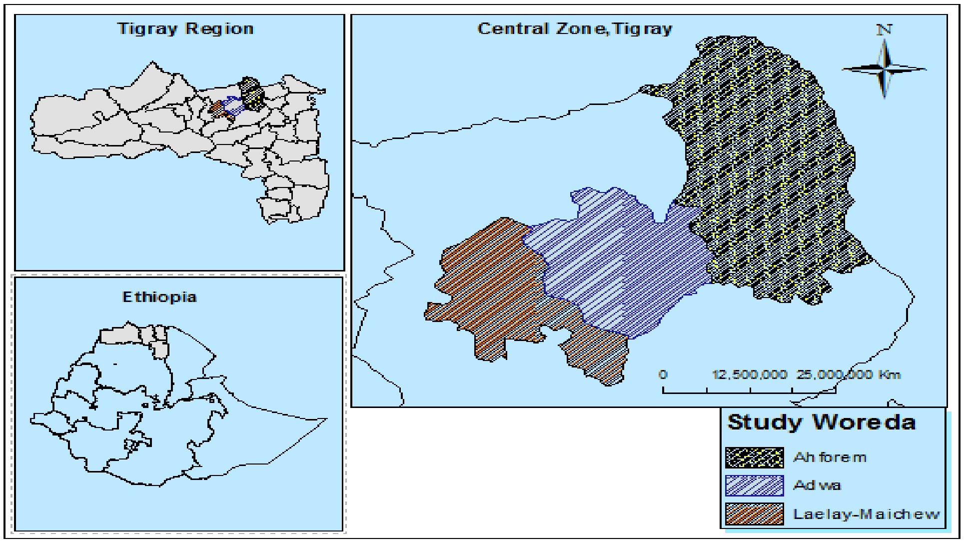

Fig. 1. Map of the study area.

2.1.1. Topography and climate

The Central zone of Tigray extends between 13^{o}15’ and 14^{o}39’ North latitude, and 38^o 34’ and 39^{o}25’ East longitude. The larger part of the zone receives mean annual rainfall ranging from 400 to 800mm. The mean monthly maximum and minimum temperatures of the zone are 30^{o}C and 10^{o}C, respectively (National Meteorological Service Agency of Ethiopia, 1996). The selected districts vary in biophysical conditions including agro-ecological zoning, elevation, rainfall pattern and amount, temperature, land use and soil types. The selected zone was categorized as Dry Weina Dega in Laelay-maichew and Adwa districts followed by Dega in the highlands of Ahferom. The elevation of the study districts ranges from 1920 to 2921 masl. Annual rainfall is variable within a range of 540-850mm. Temperature ranges from 14 to 22°C. Most of the lands are cultivated with some patchy grazing bottomlands and degraded hilly sites (Gebremedhin et al., 2013).

2.2. Sampling method, sample size and data collection

Stratified sampling technique was employed to stratify kebeles (smallest administrative unit in Ethiopia) of the three districts in to midland or waina dega (1500-2500masl) and highland or dega (>2500masl) (EARO, 2000). Ahferom (Sefo and Mayqeyah kebeles) was represented highland, Laelaymaichew (Dura and Medego kebeles) and Adwa (Mariam Shewito and Bete Yohannes kebles) was represented as midlands.

Mapping expenditure was done before the main survey, to validate the geographical distribution, concentration and populations of local chicken ecotypes, the kebeles of each sample districts and to gate sampling framework from which sampling of district was taken. Multi-stage sampling technique was employed to select both sample kebeles and respondents. Six sample kebeles were selected purposively to represent midland and highland (four kebele from midland and two kebele from highland agro ecology) based on the village poultry population density, chicken production potential, road accessibility and agro-ecological representation. A total of 464 six-month or older chicken (279 from midland and 185 from highland agro ecology) were selected randomly for the study and the numbers of chickens per midland and highland agro ecology were determined by proportionate sampling technique based on the chicken flock size.

2.3. Data analyses

Stepwise discriminate procedure was applied using PROCSTEPDISC to determine which morphological traits have more discriminate power than the others or to gain information about traits particularly important in the separation of sub-populations for eventual use in cluster analysis. Canonical discriminant analysis using CANDISC procedure was employed to calculate the Mahanobis distance between chickens of the agro-ecology and to obtain the function of all traits necessary for the separation of sub-populations. The degree of morphological similarity or divergence between the chicken were determined using wards option of PROC CUSTER procedures. Hierarchical cluster methods were used to group morphological similarity or divergence of the local chickens of the agro-ecology with the aid of dendrogram. The analyses were performed by taking individual birds as a unit. In order to avoid potential sampling bias due to low number of males in the study, only female birds were considered in discriminant analysis.

3. Results and discussion

Multivariate analysis techniques are usually used to explore the factors of dissimilarity within a population, and eventually reorganize a heterogeneous set of observation units into relatively more homogenous groups from the total population ((Minitab, 1998). For this study, the unit of analysis was the population of mature female chicken at each site characterized by the mean of the continuous variables. Mature females were selected because it is customary to describe a breed by a description of the females because they usually exist in larger numbers. The variables selected to describe the mature female chicken included continuous variables like body weights, breast width, spur length, thigh circumference, chest circumference, shank length, neck length, body length, wing length, wing span, wattle width, wattle length, earlobe width, beak length, beak width, earlobe length, comb length, comb width and height at back.

3.1. Principal component analysis (PCA) of different quantitative traits of local chicken

In this study to perform PCA a total of 19 variables from 375 female individuals' chickens were used with the weighting method of standardization. Five principal components' (PC) were extracted that accounted for 58.45% of the total variation (Table 1, Figure2). The first 5 of these PC accounted for 27.204% of the variance in the 19 variables (PC1 = 27.204%, PC2 = 12.132%, PC3 = 7.91%, PC4 = 5.665%, PC5 = 5.54%).

Table 1
Eigen values, proportion of variability and cumulative variability explained by the first five principal components.

	Initial Eigen values		
Components	**Total**	**% of Variance**	**Cumulative %**
1	5.169	27.204	27.204
2	2.305	12.132	39.336
3	1.504	7.913	47.249
4	1.076	5.665	52.914
5	1.052	5.539	58.454

The correlation between the original traits and the first principal component were all positive (Table 2). Principal component one was most strongly influenced by wattle length, wattle width comb width, body weight comb length, wing span, chest circumference, earlobe length and height at back. Principal component 2 was most strongly associated with neck length, thigh circumference and height at back. Principal component 3 was closely related to chest circumference, wing length wing span beak width and beak length. Principal component 4 was highly related with shank length, neck length, wattle width, wing span and beak length and principal component 5 was highly related with spur length, thigh circumference and wattle length.

Based on their associated eigenvalue seven variables from PC1, PC2, PC3, PC4 and PC5 were selected (Table 2). This reduces the variables from 19 to 7 and these were quite satisfactory for the analysis (Sneath and Sokal, 1973; Pimental, 1979). The first five PCs (Table 2) that display weight on the Scree plot profile (Fig. 2) and explained 58.45% of the total variation were selected for classification.

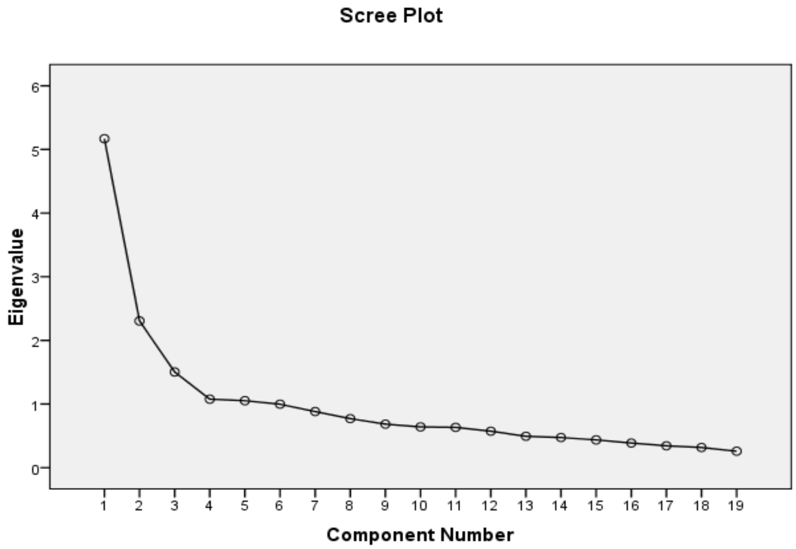

Fig. 2. Scree plot of eigenvalue to component number.

Table 2
Correlation between principal component analysis and qualitative traits of chicken.

	Principal component				
Traits	**1**	**2**	**3**	**4**	**5**
BWTkg	0.809	-0.079	0.177	-0.142	-0.053
Brwth	0.461	-0.013	0.152	-0.572	0.076
SpL	0.251	0.072	-0.481	0.241	0.370
TC	0.303	0.608	-0.200	-0.288	0.262
Cc	0.589	-0.092	0.331	-0.043	-0.306
SL	0.562	0.445	0.165	0.280	-0.118
NL	0.156	0.761	-0.099	0.201	-0.073
BL	0.499	0.286	0.202	-0.358	0.140
WL	0.163	-0.138	0.360	0.020	0.634
WS	0.488	0.000	0.442	0.226	-0.082
WW	0.660	-0.041	-0.175	0.268	-0.217
WAL	0.739	-0.139	-0.254	0.183	-0.043
EAW	0.603	-0.384	-0.151	-0.092	-0.123
BKL	0.209	0.188	0.308	0.361	0.412
BKW	0.146	-0.586	0.436	0.192	0.092
EAL	0.532	-0.407	-0.264	-0.071	0.083
CL	0.653	-0.099	-0.300	0.007	0.121
CW	0.742	-0.204	-0.247	0.000	0.095
HB	0.525	0.522	0.204	-0.038	-0.158

Note: BWT was in Kg and the others in cm

3.2. Discriminant analysis

Discriminate analysis model was used to prove variations among the sampled populations. Discriminate functions have relatively higher trait coefficients which functions are termed as discriminate trait functions. The results on discriminate analysis of the study chicken ecotypes using nineteen linear traits are presented in Table 3.

Table 3
Linear discriminate function coefficients for each chicken eco type population.

Variable	Midland chicken	Highland chicken
Sample size	172	185
Constant	-215.92	-223.54
Body weight	-49.19	-51.07
Breast width	3.16	3.23
Spur length	2.54	2.70
Thigh circumference	2.49	2.53
Chest circumference	2.86	2.93
Shank length	6.27	6.47
Neck length	1.17	1.43
Body length	2.75	2.65
Wing length	1.96	1.88
Wing span	2.02	2.05
Wattle width	-1.22	-0.97
Wattle length	-3.78	-3.32
Earlobe width	0.93	0.61
Beak length	7.73	7.59
Beak width	17.11	18.01
Earlobe length	10.85	11.19
Comb length	-3.31	-3.18
Comb width	-0.85	-0.96
Height at back	1.49	1.55

Discriminate function was classified by using all the data and functions in the form of classification matrix of all chicken populations. In this result the following discriminant function models were extracted (Table 3).

$$\begin{aligned}Midland\ chicken = {} & -49.19 * Bwt + 3.16 * Brwth + 2.54 * SPl + 2.49 * TC + 2.86 * Cc + \\ & 6.27 * SL + 1.17 * NL + 2.75 * BL + 1.96 * WL + 2.02 * WS + \\ & -1.22 * WAW + -3.78 * WAL + 0.93 * EAW + 7.73 * BKL + \\ & 17.11 * BKW + 10.85 * EAL + -3.31 * CL + -0.85 * CW + 1.49 * HB + -215.92\end{aligned}$$

$$\begin{aligned}Highland\ chicken = {} & -51.07 * Bwt + 3.23 * Brwth + 2.70 * SPl + 2.53 * TC + 2.93 Cc + \\ & 6.47 * SL + 1.43 * NL + 2.65 * BL + 1.88 * WL + 2.05 * WS + \\ & -0.97 * WAW + -3.32 * WAL + 0.61 * EAW + 7.59 * BKL + \\ & 18.01 * BKW + 11.19 * EAL + -0.96 * CL + -3.18 * CW + 1.55 * HB + -223.54\end{aligned}$$

Where:-

Bwt= body weights, Brwth= breast width, SPl= spur length, TC= thigh circumference, Cc= chest circumference SL= shank length, NL= neck length, BL= body length, WL= wing length, WS= wing span, WAW= wattle width, WAL= wattle length, EAW= earlobe width, BKL= beak length, BKW= beak width, EAL= earlobe length, CL= comb length, CW= comb width, HB= height at back.

3.2.1. Canonical discriminate analysis

Canonical discriminate analysis measures the strength of the overall relationship between the linear composite of the predictor set of variables (Minitab, 1998). In this analysis the predictor is the canonical variants and the criterion is the ecotype. Canonical discriminant functions evaluated group means to discriminant distributions and graphic representations of the homogeneity of the two chicken ecotypes and were normally distributed from centroids of their multivariate means (group centroids).

Table 4 presents the total-sample standardized canonical coefficients and total variation explained by each canonical variable. The total sample standardized canonical coefficients indicate the partial contribution of each variable to the discriminant function, controlling for other attributes entered in the equation. Accordingly, the total sample standardized canonical coefficients given in the table indicate that the explanatory variables, beak length, wattle length, earlobe length, neck length, wattle width, shank length, spur length and comb length contributed significantly in that order to the first canonical variable (CAN1). The correlation between CAN1 and the chicken populations sampled from midland and highland agro ecology was moderate -0.518 and 0.346, respectively.

Table 4
Total sample standardized canonical coefficients and canonical correlation.

Variable	Can1
Body weight	-2.180
Breast width	0.083
Spur length	0.191
Thigh circumference	0.050
Chest circumference	0.080
Shank length	0.236
Neck length	0.297
Body length	-0.114
Wing length	-0.098
Wing span	0.039
Wattle width	0.289
Wattle length	0.524
Earlobe width	-0.368
Beak length	-0.159
Beak width	1.037
Earlobe length	0.397
Comb length	0.155
Comb width	-0.123
Height at back	0.062
High land	-0.518
Midland	0.346

The significant ($p>0.001$) differences between means of neck length, beak width, body length wattle width, body weight, wattle length, height at back producing high F values (Table 5) indicated that these variants have high discriminating power and better ability to differentiate the groups. The result was in agreements with finding of Deeve et al. (2013) reported that similar observation. These variables can be used to characterize and differentiate between isolated populations of local chickens.

Stepwise discriminate analysis was the most important techniques for discriminating the investigated ecotypes (Minitab, 1998). The result of the stepwise discriminant analysis is presented in Table 5. Seven standard canonical discriminant traits were extracted in the study.

The significance of the discriminant function as indicated by wilks lambda is present in Table 5. Wilks lambda text indicated that traits like neck length, beak width, body length wattle width, body weight, wattle length and height at back was highly significant ($p< 0.0001$) to provide the validity for the canonical discriminant analysis.

The significant of the discriminant traits tested with the minimization of wilks' lambda (lambda= 0.93, 0.91, 0.90, 0.89, 0.88, 0.87 and 0.87 for discriminant neck length, beak width, body length wattle width, body weight, wattle length and height at back) provided the validity for the canonical discriminant analysis. By comparing the F-value and the P-value statistics for each significant explanatory variable, we can conclude that 'neck length' has the highest amount of significant discriminative potential, while 'height at back has the least significant discriminative power in differentiating the chicken populations sampled from the two agro ecology.

Therefore, the differentiation of those two populations, highland and midland was based on the weights of neck length, beak length, body length, wattle width, body weight, wattle length and height at back traits. These traits were very important both to discriminate and to classify populations. This result was almost similar with reports of Reddish and Lilburn (2004) and Rosario et al. (2008) who reported that average live weight was the most important trait to cluster many chicken populations and strains.

The result is also in agreements with finding of Abdelqader et al. (2007) who indicated that body weight, body length, heart girth and height at back showed the largest discriminatory power between three Jordanian chicken genotypes.

Table 5
Summary of discriminate stepwise selection among midland and highland ecotypes.

Step	Traits	Partial R^2	F-statistics	Significant	Wilki λ	Pr< λ
1	Neck length	0.06	22.72	<.0001	0.93	<.0001
2	Beak width	0.02	8.05	0.0048	0.91	<.0001
3	Body length	0.01	4.81	0.0290	0.90	<.0001
4	Wattle width	0.01	6.29	0.0126	0.89	<.0001
5	Body weight	0.007	2.48	0.1163	0.88	<.0001
6	Wattle length	0.011	4.04	0.0452	0.87	<.0001
7	Height at back	0.011	4.04	0.0452	0.87	<.0001

3.3. Cluster analysis

The first 5 principal components, accounting for 58.45% of the total variance, were considered to develop the classification by cluster analysis. The set of three observations against those principal components was clustered by hierarchical technique. The Mahalanobis distance was the similarity coefficient used to develop the classification tree from which the desired number of clusters was obtained. The dendogram shows three distinct groups (cluster) of chicken populations (Fig. 3). In general, a cluster with a high similarity percentage is more compact than one with a small similarity percentage (Minitab, 1998).

In the present study, the pair wise squared Mahalanobis' distances between populations' shows smallest and largest distances between midland and highland chicken ecotypes, respectively (Fig. 3). Based on their pair wise squared Mahalanobis' distances the three clusters, cluster1 and cluster2 formed by the midland agro ecologies of the two district populations and cluster3 were formed by highland agro ecologies chicken population (Table 6).

The closeness of cluster1 and cluster2 was explained by the fact that both clusters have been fund with in the same midland agro ecologies with a short distance between the districts, as a result farmers of these two districts often exchange cock/hen through different means with the fact that there existed genetic migration from one district to the next district chicken populations and gene flow is unregulated.

Table 6
Squared distance between clusters centroids (Mahalanobis distance).

Cluster	Cluster1	Cluster2	Cluster3
Cluster1	-	6.31	7.69
Cluster2	6.31	-	5.87
Cluste3	7.69	5.87	-
Midland	2.00	1.00	3.00
Highland	29.01	10.95	1.96
Similarity	99.99	98.94	97.89

Result of the study shows that, the greatest distance were observed between cluster1 and 3 (7.69) followed by cluster1 and 2 (6.31) (Table 6). The distance between agro ecologies and cluster shows that greatest distance were observed between cluster1 and highland (29.01) followed by cluster2 (10.95), whereas midland agro ecologies shows greatest distance with cluster3 (3.00)

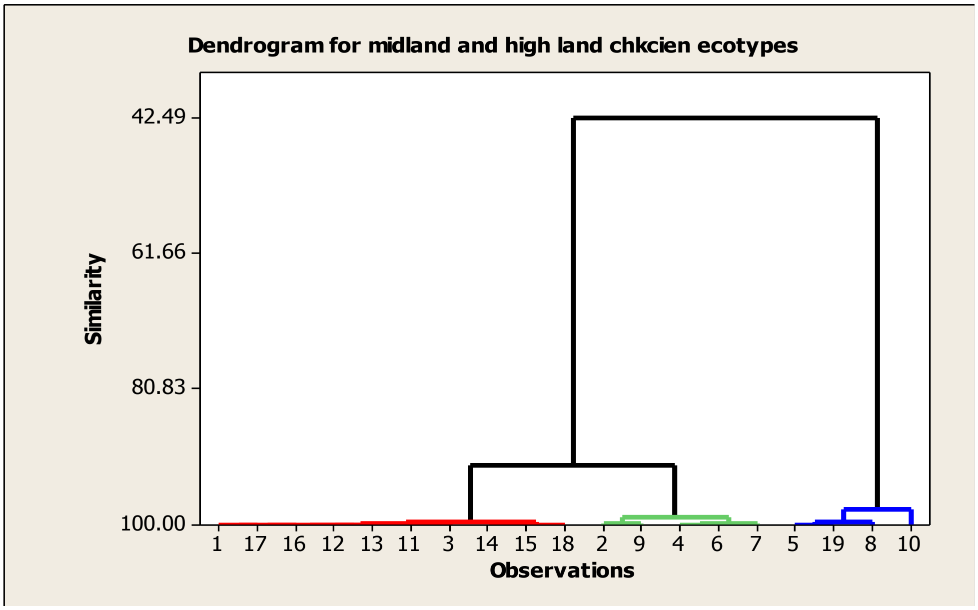

Fig. 3. Clustering of chicken in midland and highland agro ecologies by using dendrogram.

Number 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18 and 19 represents Bwt, Brwth, SPl, TC, Cc, SL, NL, BL, WL, WS, WAW, WAL, EAW, BKL, BKW, EAL, CL, CW and HB.

The formation of two large groups seen in Fig.3 showed that the distribution of the populations influence by agro ecology. Therefore, the current result of the study was in agreement with findings of Tunon et al. (1989) who reported that classification of populations should take into account not only the genetic aspect, but also the ecological, morphological and productive aspects.

Cluster1 have highest (99.9%) similarity level and was considered as highly compact and closet followed by cluster2 (98.94%). While cluster 3 has lowest similarity level as comparatively 97.89% (Fig. 3) exhibited the slackness of the cluster. The relatively large size of similarity level (91.56%) of the midland chicken indicated that midland chicken share some phenotypic characters with other chicken types. Similarly, the intra-cluster similarity level of highland chicken type with other clusters, as indicated by the similarity 42.49% indicated higher heterogeneity within the breed type (Fig. 3).

The study reviles that traits like body weight, comb length, earlobe length, wattle length, earlobe width, wattle width, spur length beak length and comb width measurements are similar with similarity level 99.82% in both agro ecologies formed cluster1. Similarly traits like breast width, wing length, thigh circumference, shank length and neck length are similar with similarity level of 99.90% combine into one and formed cluster2. While chest circumference, height at back, body length and wing span are similar in both agro ecologies formed custer3.

4. Conclusion

Multivariate analysis result showed that five PC were extracted that accounted for 58.45% of the total variation. Most important variable for discriminating between the ecotypes was the neck length, beak length and body length with partial R^2 0.060, 0.22 and 0.013.

Greatest distance were observed between cluster1 and 3 (7.69) followed by cluster1 and 2 (6.31). The distance between agro ecologies and cluster shows that greatest distance were observed between cluster1 and highland (29.01) followed by cluster2 (10.95).

In the present study, the pair wise squared Mahalanobis' distances between populations shows the smallest and largest distances between highland and midland chicken ecotypes. The three clusters, cluster1 and cluster2 formed by the midland agro ecologies of the two district populations and cluster3 were formed by highland agro ecologies chicken population.

The closeness of cluster1 and cluster2 was explained by the fact that both clusters have been fund with in the same midland agro ecologies with a short distance between the districts, as a result farmers of these two districts often exchange cock/hen through different means with the fact that there existed genetic migration from one district to the next district chicken populations and gene flow is unregulated.

Recommendations

The findings of this study demonstrate that there are diverse indigenous chicken ecotypes in phenotype but there is a need to study variability at molecular levels that will further clarify the genetic similarity and diversity among the ecotypes in order to record and registered these breeds internationally.

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