INNSPUB

International Journal of Biosciences | IJB |
ISSN: 2220-6655 (Print), 2222-5234 (Online)
http://www.innspub.net
Vol. 14, No. 4, p. 15-25, 2019

RESEARCH PAPER OPEN ACCESS

# Genetic diversity of local chicken ecotypes in selected part of Central Tanzania

**Edward Moto[1*], Chrispinus C.D. Rubanza[2]**

[1]*Department of Biotechnology and Bioinformatics, P.O Box 338, University of Dodoma*

[2]*Department of Conservation Biology, P.O Box 338, University of Dodoma*

**Key words:** Microsatellite, Genetic Diversity, Tanzanian indigenous chickens, Conservation.

http://dx.doi.org/10.12692/ijb/14.4.15-25 Article published on April 15, 2019

## Abstract

This study was carried out to evaluate the genetic diversity of Central Tanzanian indigenous chicken. Chickens were collected from six different districts of Central part in Tanzania (Dodoma, Kondoa, Singida, Manyoni, Igunga and Tabora). Eighteen microsatellite markers recommended by International Society for Animal Genetics, Food and Agriculture Organization advisory group on animal genetic diversity were used to determine genetic variation. The microsatellite markers used were suitable for the measurement of the genetic diversity and relationship of Tanzanian chicken populations. Statistics related to genetic variation were estimated using GenALEx6. Genetic variation among population was 98% and 2% genetic variance was observed between the six populations. The least number of alleles was seven in MCW0111 locus and highly polymorphic locus was MCW0016 with 23 alleles with a grand mean heterozygosity of 0.779 ± 0.018 across the populations which indicate unlimited gene pool and high gene flow. Nei's genetic distance ranged from 0.203 (lowest) between population of Kondoa and Singida to 0.583 (highest) between population of Tabora and Kondoa suggesting their genetic relatedness and dissimilarity. Principal of Coordinate Analysis (PCoA) results revealed diverse genetic variation within six populations analyzed. The distribution patterns of the chickens showed no distinct group based on the location specific rather than intermixing of the genotypes was observed suggesting random mating of chickens. This study found a lot of genetic variation and relatedness within and among populations. The results from this study can therefore serve as an initial step to plan the conservation of indigenous chickens in Tanzania.

*** Corresponding Author:** Chrispinus C.D. Rubanza ✉ eddymotto@yahoo.co.uk

## Introduction

In Tanzania and Africa in general, indigenous chicken is one of the most important animal species which provides higher proportion of animal protein in the human diet. They produce meat which is usually preferred over exotic chickens due to their pigmentation, taste, flavour and leanness. Tanzania has a good number of local chicken and contributes about 94% of the traditional poultry farming in the country (Swai *et al.,* 2007). Tanzanians local chickens are found in almost every place where there is human settlement, although most of the indigenous chickens are kept in the central corridor regions of Tanzania (FAO, 2007; RDLC, 2010). Most of livestock keepers tend to migrate with their chickens as petty animals when shifting from place to another. Several studies have been conducted on chicken diversity, but most of these studies conducted on local chickens have centred on phenotypic characterization rather than on genetic diversity (Gueye, 1998; Msoffe *et al.,* 2001; Msoffe *et al.,* 2004). Phenotypically, there is an extensive diversity within indigenous domestic chicken and this should be used as a base of breeding for animals that are adapted to a wide range of local environments. However, industrialization and globalization of chicken in the 21st century have adversely affected distribution of chicken genetic resources limiting breed composition to industrial breeds. As a result, many chicken breeds are either extinct or seriously threatened with extinction. Therefore, a need to carry out genetic studies of the indigenous local chicken is of great importance for the purpose of conservation and breeding. Knowing the genotype of the local chicken will be a key point in breeding programs as it reduces the chance of inbreeding. Thus, chicken keepers or producers should not only rely on phenotypic characteristics, rather they should also consider the genotype.

Few studies have reported the genetic diversity of the local chickens in Tanzania (Wimmers *et al.,* 2000; Msoffe *et al.,* 2005; Marle-Koster and Nel, 2013; Lyimo *et al.,* 2013). Several methods of Deoxyribonucleic Acid (DNA) analysis have been employed to study genetic diversity in animals, but microsatellite DNA genotyping has provided better and reliable results (Marle-Koster and Nel, 2000; Wimmers *et al.,* 2000). DNA based typing methods provide a rapid and reliable method for differentiating individuals in a genetically diverse population (Bidwell, 1994; Parham and Ohta, 1996).

Microsatellites markers are highly polymorphic loci widely dispersed throughout animal genomes and consist of randomly repeated motifs or simple sequence repeats of nucleotide units (Tautz, 1989; Emara *et al.,* 2002). The variability of microsatellite loci is due to differences in the number of repeat units recognized as a major source of genetic variation (Weber and Wong, 1993).

Furthermore, microsatellites are useful in unveiling genetic diversity, individual identification, gene mapping, paternity analysis and the assessment of relatedness, and phylogenetic studies and as a means to measure inbreeding and differences among populations. Microsatellites have an instant rate of evolution making them mostly useful in working out the relationships among very closely related species. In addition, microsatellite markers also provide tools for study of linkages with quantitative trait loci (Zhou and Lamont, 1999).

Accurate determination of the animal genetic variations within animal species is a vital step towards conservation of the animal genetic resources (Oldenbroek, 1999). Thus, this study was carried out to provide information on genetic diversity of the indigenous chicken ecotypes in Central part of Tanzania that would be important in making effective selection and conservation strategies.

## Materials and methods

*Sampling*

Blood samples were collected from six districts in the central zone Tanzania. A total of 120 birds were collected from Manyoni (20), Singida (20), Igunga (20), Tabora (20), Kondoa (20) and Dodoma (20). Some of their phenotypic features were recorded including Frizzled, Normal feather, Feathered Shank,

Crested head, Bearded Black, Naked neck and Kuchi. Chickens were randomly sampled from each household, each household distanced by a minimum of 1km from the next household. All chickens sampled were free ranging indigenous chicken. Approximately two millilitres (2ml) of blood was drawn from their wing veins for every bird sampled and stored in serum tubes containing EDTA and were stored at -40°C . Laboratory analysis for the extraction of genomic DNA, its purification and PCR amplification was done at Molecular Biology laboratory, College of Veterinary Medicine and Biomedical Sciences – Sokoine University of Agriculture.

*DNA Extraction and Polymerase Chain Reaction*

The genomic DNA was extracted from blood following protocol by Quick-DNA MiniPrep plus Kit (Zymo Research – D4069 Epigenetics CO. Ltd). A total of 18 autosomal microsatellite loci which are among the 30 suggested markers by the International Society for Animal Genetics (ISAG), Food and Agricultural Organisation (FAO) project for surveying chicken biodiversity (FAO, 2012) were used for genotyping. All markers used and their sequences and annealing Temperature are shown in Table 1.

The Polymerase Chain Reaction (PCR) reactions were performed in a total reaction volume of 25µl containing 6.5µl of nuclease free water, 12.5µl of readymade PCR premix (ZymoBIOMICS, Epigenetics CO. Ltd) Primers, 0.5µl (10 pmol/ml) of Forward and Reverse primers and 5µl of template DNA.

The amplification was carried out in a Thermal Cycler (Takara Holdings Inc. Otsu, Shiga Japan). The cycling conditions were; initial temperature for denaturation was set at 95°C for 5 minutes followed by 30 cycles for denaturation at 94°C for 1 minute, annealing temperature was optimized for each marker, extension was 1 minute at 72°C and the final extension was done for 7 minutes at 72°C.

The PCR products were separated by electrophoresis at 100V through a 1.0% agarose-TAE gel for 40 minutes. Cyber safe staining was used for visualization under UV light followed by scoring of alleles using VisionCapt software (Vilber.de).

*Statistical analysis*

The data obtained were processed using GenAlEx6 (Genetic analysis in Excel version 6) which was used to show parameters of genetic diversity within and among populations.

The relationships among 6 chicken populations was estimated by using Nei's genetic distance (Nei, 1987). The analysed results were presented in form of tables, figures and pie chart.

*Genetic variability*

Allelic diversity and heterozygosity, Total number of alleles for individual markers (NA), mean number of alleles, number of private alleles by locus and by population, allelic patterns for across populations and genetic diversity were computed using GenAlEx software version 6.502 (Peakall and Smouse, 2012). The analysed results were presented in form of tables and figures.

*Genetic distances*

Nei's genetic distance and genetic identity per population were computed using GenAlEx software version 6.502 (Peakall and Smouse, 2012) where a population matrix was used to compare the distances between the different populations and indicate their relationships.

*Analysis of Molecular Variance (AMOVA)*

Analysis of molecular variance (AMOVA) was performed to describe variance components within and among populations using GenAlEx software version 6.502 (Peakall and Smouse, 2012) with 1000 permutations.

*Principal Coordinate Analysis (PCoA)*

The Principal co-ordinate analysis (PCoA) was carried out using GenAlEx 6.5 based on Nei's genetic estimations. The graph was viewed using the same software to show the distribution of each individual in a sampled population.

## Results and discussion

*Genetic diversity*

All the microsatellites used in this study were polymorphic. A total of 197 alleles were observed over the eighteen loci. The number of alleles ranged from 5.533 ± 0.322 to 8.200 ± 0.751, while the overall mean number of different alleles (Na) was 6.922 ± 0.459. Effective number of alleles (Ne) was 4.981 ± 0.354 and heterozygosity (He) was 0.779 ± 0.018 (Fig.1 and Table 3). This indicates that there is unlimited sample of gene pool and high gene flow in Tanzanian local chickens. Same study by Lyimo *et al.* (2013) reported mean number of alleles ranging from 5.10 ± 2.08 to 6.28 ± 2.24 in the Tanzanian population of indigenous chickens, which concur with the recent study, this implies that in Tanzanian indigenous chicken there is unrestricted gene pool and higher flow of gene.

**Table 1.** List of microsatellite marker used for genotyping.

| Marker | Oligo Seq. | Chromosome location | Annealing Temperature (°C) | Allele range (bp) |
|---|---|---|---|---|
| ADL0268 | CTC CAC CCC TCT CAG AAC TA<br>CAA CTT CCC ATC TAC CTA CT | 1 | 60 | 102 - 116 |
| MCW0295 | ATC ACT ACA GAA CAC CCT CTC<br>TAT GTA TGC ACG CAG ATA TCC | 4 | 60 | 88 - 106 |
| MCW0081 | GTT GCT GAG AGC CTG GTG CAG<br>CCT GTA TGT GGA ATT ACT TCT C | 5 | 60 | 112 - 135 |
| MCW0014 | TAT TGG CTC TAG GAA CTG TC<br>GAA ATG AAG GTA AGA CTA GC | 6 | 55 | 162 - 182 |
| MCW0183 | ATC CCA GTG TCG AGT ATC CGA<br>TGA GAT TTA CTG GAG CCT GCC | 7 | 55 | 290 - 326 |
| ADL0278 | CCA GCA GTC TAC CTT CCT AT<br>TGT CAT CCA AGA ACA GTG TG | 8 | 50 | 114 - 126 |
| MCW0067 | GCA CTA CTG TGT GCT GCA GTT T<br>GAG ATG TAG TTG CCA CAT TCC GAC | 10 | 60 | 175 - 186 |
| MCW0123 | CCA CTA GAA AAG AAC ATC CTC<br>GGC TGA TGT AAG AAG GGA TGA | 14 | 50 | 75 - 100 |
| MCW0330 | TGG ACC TCA TCA GTC TGA CAG<br>AAT GTT CTC ATA GAG TTC CTG C | 17 | 50 | 256 - 300 |
| MCW0069 | GCA CTC GAG AAA ACT TCC TGC G<br>ATT GCT TCA GCA AGC ATG GGA GGA | 26 | 60 | 158 - 185 |
| MCW0248 | GTT GTT CAA AAG AAG ATG CAT G<br>TTG CAT TAA CTG GGC ACT TTC | 1 | 50 | 205 - 225 |
| MCW0111 | GCT CCA TGT GAA GTG GTT TA<br>ATG TCC ACT TGT CAA TGA TG | 1 | 50 | 96 - 120 |
| MCW0034 | TGC ACG CAC TTA CAT ACT TAG AGA<br>TGT CCT TCC AAT TAC ATT CAT GGG | 2 | 60 | 212 - 248 |
| LEI0234 | ATG CAT CAG ATT GGT ATT CAA<br>CGT GGC TGT GAA CAA ATA TG | 2 | 50 | 216 - 364 |
| MCW0016 | ATG GCG CAG AAG GCA AAG CGA TAT<br>TGG CTT CTG AAG CAG TTG CTA TGG | 3 | 60 | 155 - 206 |
| MCW0037 | ACC GGT GCC ATC AAT TAC CTA TTA<br>GAA AGC TCA CAT GAC ACT GCG AAA | 3 | 60 | 152 - 170 |
| LEI0094 | GAT CTC ACC AGT ATG AGC TGC<br>TCT CAC ACT GTA ACA CAG TGC | 4 | 50 | 247 - 287 |
| MCW0078 | CCA CAC GGA GAG GAG AAG GTC T<br>TAG CAT ATG AGT GTA CTG AGC TTC | 5 | 60 | 132 - 240 |

In contrast, Okumu *et al.* (2013) reported mean number of alleles over the 18 loci for each population ranged from 1.895 ± 0.072 to 2.00 with an average number of alleles across all loci in all the eight populations being 1.961 ± 0.018, which indicates limited gene pool and lower gene flow of Kenyan population of local chickens. Halima *et al.*, (2007) reported an average number of alleles across all populations in all loci to be 6.05 in the Ethiopian native chickens. Marle-Koster and Nel (2000) , reported a mean number of alleles ranging from 2.3 to 4.3 in five chicken lines representing the Fowls for Africa program. Wimmers *et al.,* (2000), reported a mean number of alleles ranging from 2 to 11 per locus for the local chickens from Africa, Asia and South America. Mtileni *et al.,* (2010), reported a higher mean number of alleles per locus ranging from 3.52 ± 1.09 to 6.62 ± 3.38 among the South African chickens. A similar higher mean number of alleles was observed in other free-ranging chickens reported by Muchadeyi *et al.,* (2007), in Zimbabwean, Malawian and Sudanese chicken populations.

These differences in heterozygosity values may be attributed by variation in geographical location, chicken types, sample sizes, laboratory and sources of microsatellites used. Expected heterozygosity value of < 0.5 may also be due to inbreeding and admixture as this occurrence is associated with population constrains and bottlenecks (Fariba, 2011).

**Table 2.** Total allelic patterns by populations.

| Population | Manyoni | Tabora | Igunga | Dodoma | Kondoa | Singida |
|---|---|---|---|---|---|---|
| Na | 122 | 83 | 123 | 101 | 96 | 98 |
| Na Freq. >= 5% | 105.000 | 83.000 | 79.000 | 101.000 | 96.000 | 98.000 |
| Ne | 32.000 | 9.000 | 17.000 | 5.000 | 2.000 | 0.000 |
| No. LComm Alleles (<=25%) | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| No. LComm Alleles (<=50%) | 23.000 | 16.000 | 31.000 | 22.000 | 24.000 | 27.000 |

Number of allele with frequency >=5%, Number of Locally Common alleles (frequency >=5%) found in <=25% and <=50% of populations.

**Table 3.** Mean and standard errors of the different genetic diversity parameters estimated for six local chickens populations.

| Population | | Na | Na Freq.>=5% | Ne | I | No. Private Alleles | He |
|---|---|---|---|---|---|---|---|
| Manyoni | Mean | 8.133 | 7.000 | 5.594 | 1.836 | 2.133 | 0.798 |
| | SE | 0.723 | 0.775 | 0.555 | 0.094 | 0.646 | 0.018 |
| Tabora | Mean | 5.533 | 5.533 | 4.463 | 1.554 | 0.600 | 0.748 |
| | SE | 0.322 | 0.322 | 0.350 | 0.080 | 0.190 | 0.028 |
| Igunga | Mean | 8.200 | 5.267 | 5.248 | 1.795 | 1.133 | 0.784 |
| | SE | 0.751 | 0.284 | 0.570 | 0.092 | 0.274 | 0.019 |
| Dodoma | Mean | 6.733 | 6.733 | 4.888 | 1.681 | 0.333 | 0.778 |
| | SE | 0.452 | 0.452 | 0.366 | 0.072 | 0.159 | 0.017 |
| Kondoa | Mean | 6.400 | 6.400 | 4.891 | 1.691 | 0.133 | 0.788 |
| | SE | 0.235 | 0.235 | 0.226 | 0.045 | 0.091 | 0.011 |
| Singida | Mean | 6.533 | 6.533 | 4.804 | 1.683 | 0.000 | 0.777 |
| | SE | 0.274 | 0.274 | 0.317 | 0.056 | 0.000 | 0.017 |

Total allelic patterns by populations are summarised in Table 2 and Mean and standard errors of the different genetic diversity parameters estimated for six local chickens populations are summarised in Table 3. Briefly, total number of different alleles identified was higher in Igunga (N=123) and lower in Tabora (N=83). The effective number of alleles was higher in Manyoni (N=32) and lower in Singida (N=0.00) as shown in Table 2.

The number of alleles and allele's frequency identified in each locus are shown in Fig. 2. The least number of

alleles was seven in MCW0111 Locus and highly polymorphic locus was MCW0016 with twenty three alleles. The mean number of information index, private alleles and heterozygosity was higher in Manyoni populations with mean average of 1.836 ± 0.094, 2.133 ± 0.646 and 0.798 ± 0.018, respectively (Fig. 1 & Table 3). The summary of private alleles at specific loci and their frequencies in all six populations are shown on table 4.

**Table 4.** Summary of numbers of private alleles at specific loci and their frequencies.

| Population | Private alleles (N) | Locus | Alleles | Frequency |
|---|---|---|---|---|
| | | MCW0295 | 89 | 0.125 |
| | | MCW0295 | 92 | 0.063 |
| | | MCW0295 | 95 | 0.063 |
| | | MCW0081 | 121 | 0.050 |
| | | MCW0081 | 126 | 0.050 |
| | | MCW0016 | 157 | 0.118 |
| | | MCW0016 | 158 | 0.059 |
| | | MCW0016 | 166 | 0.059 |
| Manyoni | 32 | MCW0016 | 174 | 0.059 |
| | | MCW0016 | 176 | 0.059 |
| | | MCW0016 | 183 | 0.059 |
| | | MCW0016 | 191 | 0.059 |
| | | MCW0016 | 204 | 0.059 |
| | | MCW0034 | 218 | 0.118 |
| | | MCW0034 | 247 | 0.059 |
| | | MCW0034 | 248 | 0.059 |
| | | MCW0078 | 132 | 0.053 |
| | | MCW0078 | 228 | 0.053 |
| | | MCW0069 | 162 | 0.045 |
| | | MCW0069 | 164 | 0.045 |
| | | MCW0069 | 166 | 0.045 |
| | | MCW0069 | 168 | 0.045 |
| | | MCW0069 | 169 | 0.045 |
| | | MCW0069 | 184 | 0.045 |
| | | MCW0183 | 323 | 0.100 |
| | | MCW0183 | 325 | 0.050 |
| | | MCW0123 | 75 | 0.045 |
| | | MCW0123 | 82 | 0.045 |
| | | MCW0123 | 83 | 0.095 |
| | | MCW0123 | 84 | 0.048 |
| | | MCW0123 | 85 | 0.048 |
| | | MCW0248 | 214 | 0.095 |
| | | ADL0268 | 111 | 0.222 |
| | | ADL0268 | 112 | 0.222 |
| Tabora | 9 | MCW0081 | 128 | 0.125 |
| | | MCW0016 | 198 | 0.125 |
| | | MCW0034 | 212 | 0.111 |
| | | MCW0034 | 242 | 0.111 |
| | | MCW0078 | 139 | 0.111 |
| | | MCW0069 | 173 | 0.091 |
| | | MCW0330 | 297 | 0.100 |
| | | ADL0268 | 106 | 0.040 |
| | | MCW0081 | 118 | 0.043 |
| | | MCW0081 | 119 | 0.083 |
| | | MCW0081 | 134 | 0.083 |
| Igunga | 17 | MCW0016 | 168 | 0.040 |
| | | MCW0016 | 185 | 0.040 |
| | | MCW0016 | 205 | 0.080 |
| | | MCW0034 | 234 | 0.038 |
| | | MCW0034 | 245 | 0.038 |
| | | MCW0078 | 136 | 0.043 |
| | | MCW0078 | 240 | 0.043 |
| | | MCW0067 | 175 | 0.038 |
| | | MCW0037 | 156 | 0.083 |
| | | MCW0037 | 168 | 0.043 |
| | | MCW0183 | 312 | 0.037 |
| | | MCW0123 | 98 | 0.036 |
| | | LEI0234 | 252 | 0.037 |
| | | MCW0081 | 206 | 0.059 |
| Dodoma | 5 | MCW0034 | 219 | 0.063 |
| | | MCW0034 | 232 | 0.063 |
| | | MCW0067 | 182 | 0.053 |
| | | MCW0037 | 170 | 0.056 |
| Kondoa | 2 | MCW0123 | 96 | 0.059 |
| | | MCW0248 | 211 | 0.176 |

**Table 5.** Analysis of Molecular Variance (AMOVA) table showing the percentage variations among populations and within populations.

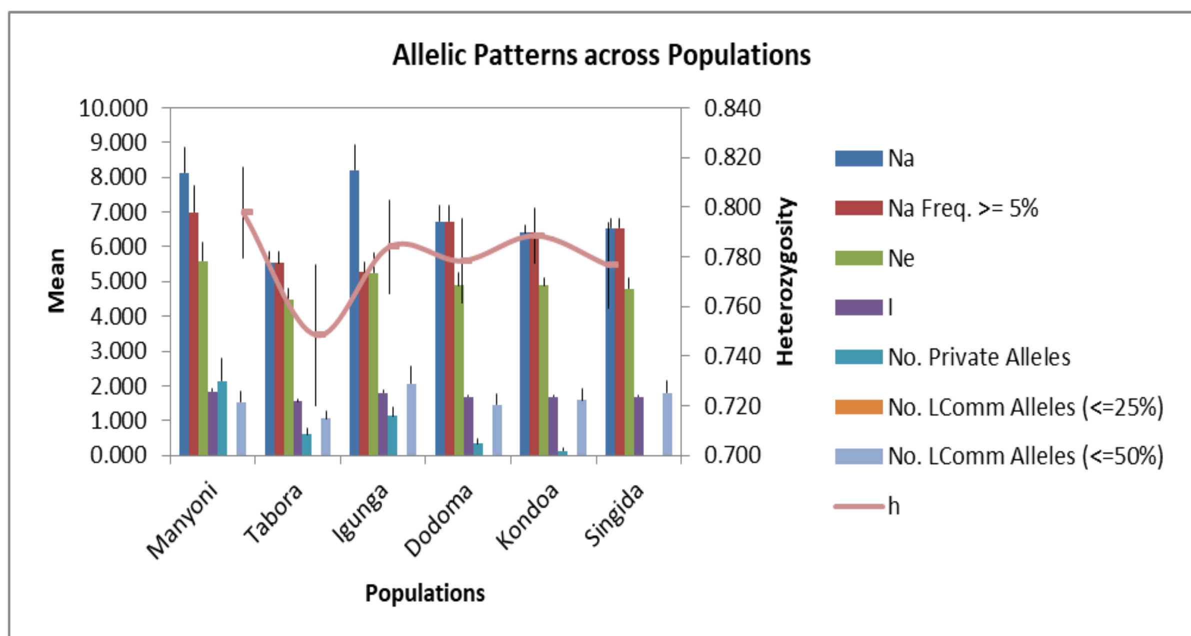
| Source | df | SS | MS | Est. Var. | % |
|---|---|---|---|---|---|
| Among Pops | 5 | 41.838 | 8.368 | 0.109 | 2% |
| Within Pops | 114 | 709.739 | 6.226 | 6.226 | 98% |
| Total | 119 | 751.577 | | 6.334 | 100% |

**Table 6.** Pairwise Population Matrix of Nei Genetic Distance.

| Manyoni | Tabora | Igunga | Dodoma | Kondoa | Singida | |
|---|---|---|---|---|---|---|
| 0.000 | | | | | | Manyoni |
| 0.359 | 0.000 | | | | | Tabora |
| 0.286 | 0.308 | 0.000 | | | | Igunga |
| 0.350 | 0.451 | 0.281 | 0.000 | | | Dodoma |
| 0.421 | 0.583 | 0.462 | 0.250 | 0.000 | | Kondoa |
| 0.327 | 0.474 | 0.378 | 0.248 | 0.203 | 0.000 | Singida |

*Principal Coordinate Analysis (PCoA)*

PCoA were used to determine the distribution of the populations and the genetic relatedness among the population genotypes (Fig. 3). Majority of the chickens from Igunga and Tabora were clustered together with chickens from Manyoni on the first and second quadrant showing their genetic relatedness. Majority of the chickens from Kondoa were clustered on the right side of axis 1 on the fourth quadrant while the remaining populations from Dodoma and Singida were distributed uniformly in all four quadrants. Generally, PCoA did not clearly group genotypes based on the location specific. But intermixing of the genotypes across the coordinates was observed. However, some distinct genotypes from Manyoni, Igunga and Kondoa were inclined to stay on the quadrant 1 and IV respectively indicating their genetic identity and dissimilarity. Lyimo *et al.*, (2013) did a plot of the principal component and the ecotypes studied were grouped into three clusters with axis 1 showing more variation than other clusters.




Number of alleles (Na), Number of allele with frequency >=5%, Effective number of alleles, information index (I) and Number of private alleles.

**Fig. 1.** Mean values, Heterozygosity and Allelic patterns across six populations.

*Analysis of Molecular Variance (AMOVA)*

AMOVA was used to examine the partitioning of genetic variation (Table 5). Analysis of the 120 Local chickens from 6 different populations showed that within-group genetic differences accounted for 98% of the total variations indicating panmictic populations, there are no mating restrictions of individuals within population. Only 2% variations among populations were observed, indicating individuals from different populations are genetically more closely related than within population (Fig. 4).

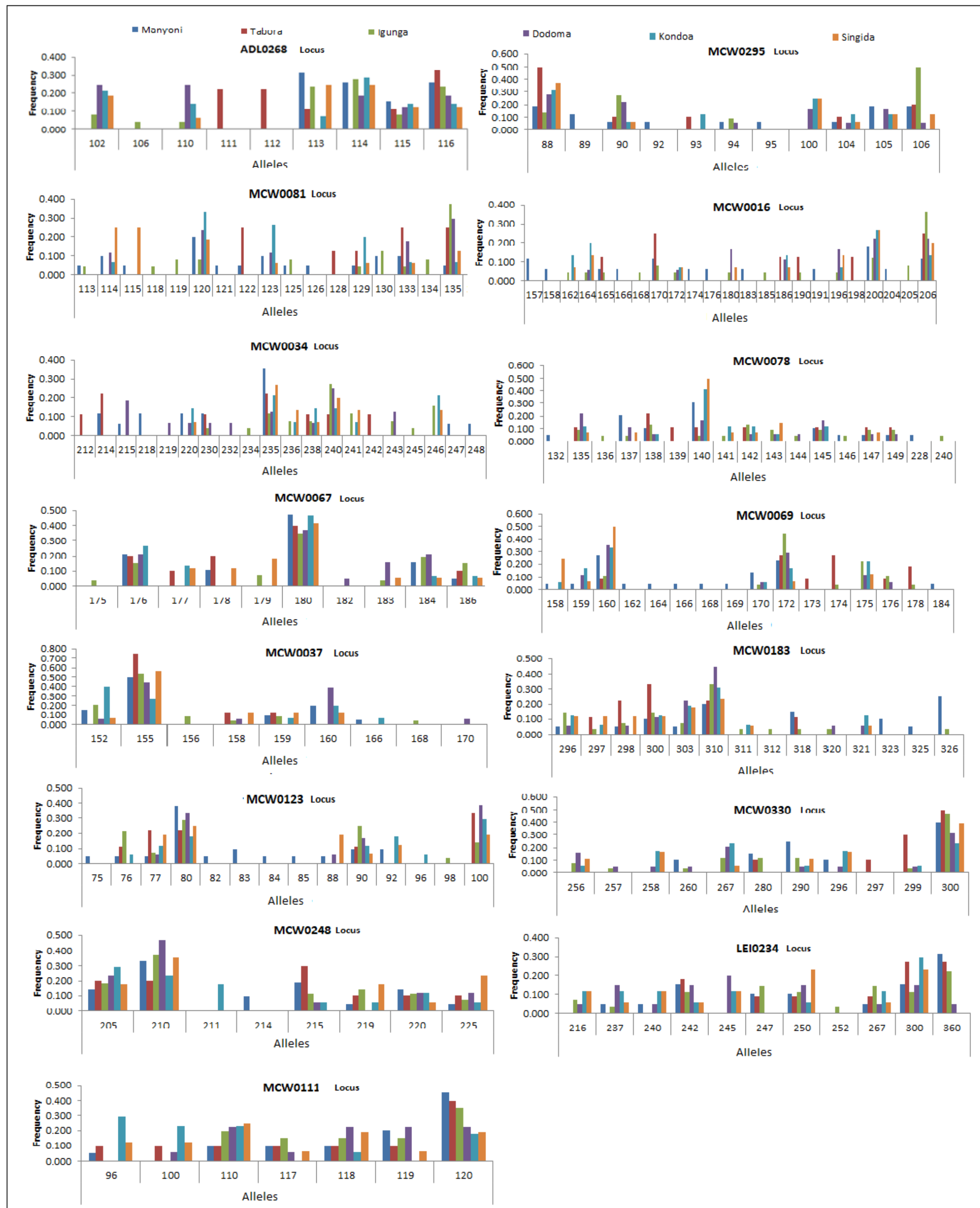



**Fig. 2.** Number of alleles and allele's frequency identified in each locus. Least number of alleles was seven in MCW0111 Locus and highly polymorphic locus was MCW0016 with twenty three alleles.

Nei's genetic distance was estimated between six populations (Table 6). The pairwise Nei's genetic distance ranged from 0.203 (lowest) between population of Kondoa and Singida to 0.583 (highest) between population of Tabora and Kondoa (Table 6) suggesting their genetic relatedness and dissimilarity. Tanzanian indigenous chickens are therefore closely related to one another compare to their counterparts of Ethiopia. This could be due to the cultural practices and admixture. Halima *et al.,* (2007), studied the genetic variation in the 147 native chickens (seven populations) from northwest Ethiopia, and reported the smallest and largest genetic distance of 0.073 and 1.3, respectively. Vanhala *et al.,* (1998) evaluated the genetic variability and genetic distances between eight chicken lines using microsatellites and reported the smallest and the largest genetic distances of 0.117 and 1.17, respectively.

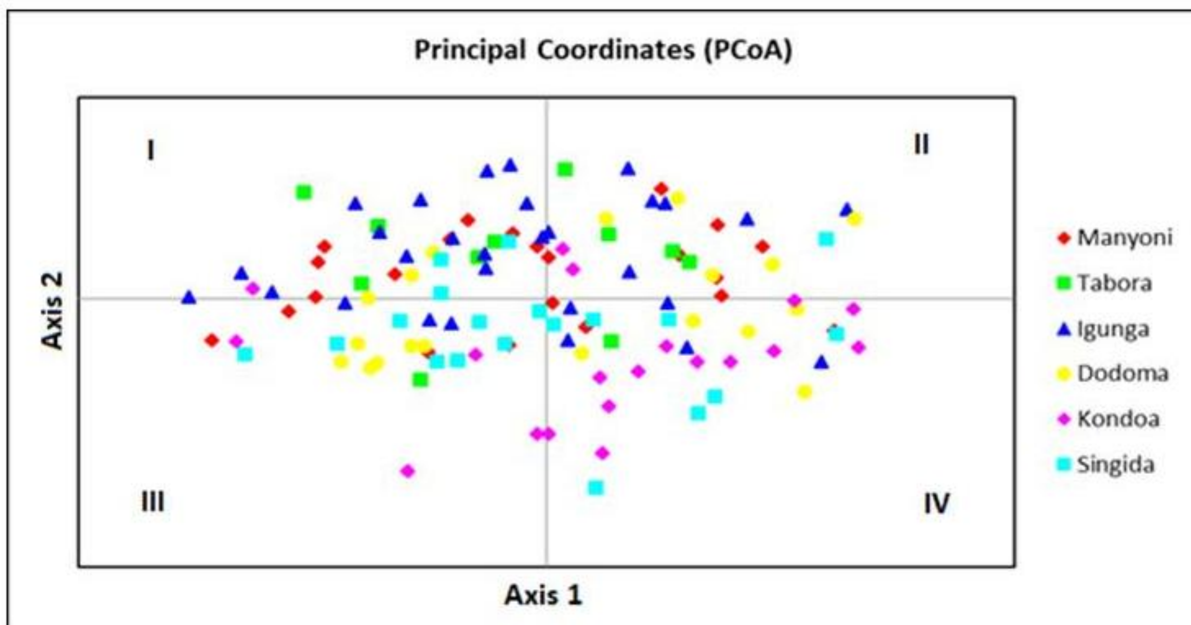



**Fig. 3.** Scatter diagram showing principal coordinate analysis for 6 local chickens populations collected from Central zone in Tanzania.

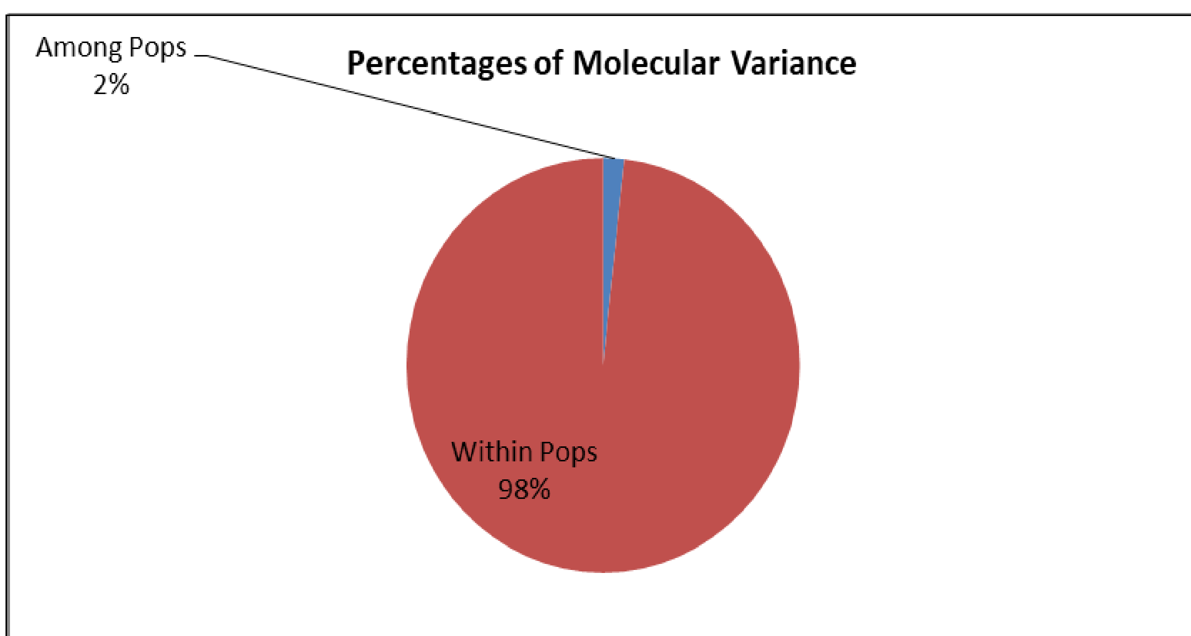



**Fig. 4.** Pie chart showing the percentage variations among populations and within populations.

## Conclusion

The results revealed diverse genetic variation within six populations analyzed. The distribution patterns of the chickens show no distinct group based on the location specific. Intermixing of the genotypes is observed suggesting random mating of chickens. However, more extensive sample size required from different sites to draw firm conclusion about genetic diversity of local chickens within populations in central zone. The preliminary findings obtained from this study may provide background for future studies of identification of the genetic uniqueness of Tanzanian native chicken breeds, breeding programmes and development of conservation strategies.

## Competing interests

The authors declare that they have no competing interests

## Funding

This study was sponsored by the University of Dodoma under the 10th Anniversary of University of Dodoma. The fund covered all costs of study from data collection, laboratory work, data analysis and interpretation and manuscript preparation.

## Acknowledgments

This study was supported by University of Dodoma (UDOM) under the UDOM 10th Anniversary. The authors are grateful for the support. Sokoine University of Agriculture (SUA) is thanked for giving us an opportunity to use the molecular laboratory during the study. Special thanks to Mr. Elisa Mwega for his assistance in laboratory work and data analysis.

## References

**Bidwell J.** 1994. Advances in DNA-based HLA-typing methods. Immunology Today **15,** 303-307.

**Emara MG, Kim H, Zhu J, Lapierre RR, Lakshmanan N, Lillehojt HS.** 2002. Genetic diversity at the major histocompatibility complex (B) and microsatellite loci in three commercial broiler pure lines. Poultry Science **81,** 1609–1617.

**FAO.** 2007. Poultry Sector Country Review-Tanzania. FAO Animal Production and Health Division. ftp://ftp.fao.org/docrep/fao/011/ai349e/ai349e00.pdf.

**Fariba IS.** 2011. A Molecular Genetic Survey of Immune Response Genes and Biodiversity of Industrial and Non-Industrial Chickens. Electronic Theses and Dissertations (ETDs) 2008+. University of British Columbia.

**Guèye EF.** 1998. Village egg and fowl meat production in Africa. World's Poultry Science Journal, **54,** 73-86.

**Halima H, Neser FWC, De-Kock A, MKE Van.** 2007. Study on the genetic diversity of native chickens in northwest Ethiopia using microsatellite markers, African Journal of Biotechnology **8,** 1347–1353.

**Lyimo CM, Weigend A, Janben-Tapken U, Msoffe PL, Samianer H, Weigend S.** 2013. Assessing the genetic diversity of five Tanzanian chicken ecotypes using molecular tools, South African Journal of Animal Science **4,** 43.

**Marle-Koster EVM, Nel ELH.** 2000. Genetic characterization of native southern African chicken population: evaluation and selection of polymorphic microsatellite markers, South Africa Journal Animal Science **30,** 1–6.

**Msoffe PL, Minga UM, Olsen JE, Yongolo MGS, Juul-Madsen HR, Gwakisa PS, Mtambo MMA.** 2001. Phenotypes including immunocompetence in scavenging local chicken ecotypes in Tanzania. Tropical Animal Health Production **33(4),** 341-54.

**Msoffe PLM, Mtambo MMA, Minga UM, Olsen JE, Juul-Madsen HR, Gwakisa PS, Mutayoba**

**SK, Katule AM.** 2004. Productivity and reproductive performance of the free-range local domestic fowl ecotypes in Tanzania. Livestock Research for Rural Development **16(9),** http://www.lrrd.org/lrrd16/9/msof16067.htm.

**Msoffe PLM, Mtambo MMA, Minga UM, Juul-Madsen HR, Gwakisa PS.** 2005. Genetic structure among local chicken ecotypes of Tanzania based on microsatellite DNA typing. African Journal of Biotechnology **4(8),** 768-771.

**Mtileni BJ, Muchadeyi FC, Maiwashe A, Groeneveld E, Groeneveld LF, Dzama K, Weigend S.** 2010. Genetic diversity and conservation of South Africa n indigenous chicken populations, Journal of Animal Breed Genetics **128,** 209 – 218.

**Muchadeyi Eding FCH, Wollny CBA, Groeneveld E, Makuza SM, Shamseldin R, Simianer H, Weigend S.** 2007. Absence of population sub-structuring in Zimbabwe chicken ecotypes inferred using microsatellite analysis, Animal Genetics. **38**: 332–339.

**Nei M.** 1987. Molecular Evolutionary Genetics, Columbia University Press, New York, USA.

**Okumu ON, Ngeranwa Binepal JJN, Kahi YS, Bramwel AK, Ateya WW, Wekesa FC.** 2017. Genetic diversity of indigenous chickens from selected areas in Kenya using microsatellite markers. Journal of Genetic Engineering and Biotechnology, **15,** 489–495 http://dx.doi.org/10.1016/j.jgeb.2017.04.007.

**Oldenbroek JK.** 1999. Introduction. In: Genebanks and Conservation of Farm Animal Genetic Resource, DLO, Institute for Animal Science, Lelystad, the Netherlands, p 1-9.

**Parham P, Ohta T.** 1996. Population biology of antigen presentation by MHC class I molecules. Science **272,** 67-74.

**Peakall R, Smouse PE.** 2012. GenAlEx 6.5: Genetic Analysis in Excel. Population Genetic Software for Teaching and Research - An Update. Bioinformatics Application Note **28,** 2537-2539. http://dx.doi.org/10.1093/bioinformatics/bts460.

**RLDC,** 2010. Changing Poultry keeping into a commercial rural activity. Rural Livelihood Development Company (RLDC) Annual Report. Prepared with inter-cooperation of Swiss Agency for Development and Cooperation. http://www.rldp.org/reports/annual-report-2010.pdf.

**Swai ES, Karimuribo ED, Kyakaisho PF, Mtui PF.** 2007. Free-range village chickens on the humid coastal belt of Tanga, Tanzania: their roles, husbandry and health status. Livestock Research for Rural Development. **19(8).** www.lrrd.org/lrrd19/8/swai19104.htm.

**Tautz D.** 1989. Hypervariability of simple sequences as a general source for polymorphic marker, Nucleic Acids Research. **17,** 6463–6471. https://doi.org/10.1093/nar/17.16.6463.

**Vanhala T, Tuiskula-Haavisto M, Elo K, Vilkki J, Maki-Tanila ASO.** 1998. Evaluation of genetic variability and genetic distances between eight chicken lines using microsatellite markers, Poultry Science **77,** 783–790.

**Weber J, Wong C.** 1993. Mutation of human short tandem repeats, Human Molecular Genetics **2,** 1123–1128.

**Wimmers K, Ponsuksili S, Hardge T, Valle-Zerate A, Marthur PK, Horst P.** 2000. Genetic distinctness of African, Asian and South American local chickens, Animal Genetics **31,** 159–165.

**Zhou H, Lamont SJ.** 1999. Genetic characterization of biodiversity in highly inbred chicken lines by microsatellite markers, Animal Genetics **30,** 256–264.