DETERMINATION OF GENETIC STRUCTURE OF MALAWI LOCAL CHICKENS USING MICROSATELLITE MARKERS

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Summary
A determination of the genetic structure of 60 phenotypically diverse chickens in Malawi using 29 microsatellites showed presence of 171 alleles (5.9 ± 2.97) and slight inbreeding (F_{IS} = 0.09; P = 0.0018). Both phylogenetics and cluster analysis indicated absence of sub-structuring. Therefore, these chickens are a single phenotypically heterogenous population. Conservation of chicken phenotypes must improve mating systems to minimise inbreeding.

Key words
Chickens, genetic structure, biodiversity, Malawi

Introduction
Rural poultry, kept under extensive systems of production, constitutes over 80 % of the total poultry population in Malawi [2]. Local chickens exist in a wide range of phenotypes such as different plumage colours, body conformation and feather distribution. Limited information on the degree to which the different phenotypes represent unique populations poses a problem in choosing a representative sample of chickens for conservation. Polymorphism exhibited by microsatellites can be used to estimate average genetic relatedness of individuals within and among populations [5]. The objective of the present study was to determine the genetic structure of Malawi local chickens using microsatellite markers.

Materials and methods
Sixty local chicken blood samples were collected from three rural locations and one research station covering a 50 km radius in Lilongwe, District of Central Malawi. The chickens consisted of the naked neck (n = 9), dwarf (n = 8), rumpless (n = 6) and crested (n = 10), while the rest (n = 27) had normal feathering and none of the mentioned major genes. DNA polymorphism was determined using a set of 29 microsatellite markers.
The total number of alleles, observed and expected heterozygosity, and F_{IS} values were calculated using the F STAT procedure [3]. The negative logarithm of the proportion of shared alleles (-lnPSA) genetic distances was performed using MICROSAT [4]. A -lnPSA genetic distance matrix based unrooted neighbour joining tree was constructed using the PHYLIP programme [1]. A cluster analysis was performed with STRUCTURE programme using models with $2 \leq k \leq 5$ clusters.

Results and discussion
A total of 171 alleles were observed across the 29 loci. The average number of alleles per loci was 5.9 ± 2.97. Romanov and Weigend [5], for example, reported more alleles, an observation which could be attributed to the evaluation of more populations. The polymorphic information

content for the 29 loci averaged 55 percent. Expected heterozygosity across loci was 0.6 ± 0.03. Inbreeding, a major cause of allele fixation was evident in this population and resulted in a number of loci being deficient in heterozygosity. The small but significant level of inbreeding (0.09) could be attributed to the sharing of a single cock among a number of households [2] in the absence of performance and pedigree records. Although local chickens grouped into 4 clusters (Figure 1), the partitioning of variation within and among clusters indicated an insignificant level of among sub-population diversity (Table 1). In conformity to this observation, the cluster analysis using STRUCTURE indicated absence of population sub-structure (Figure 2).

Table 1: Partitioning of variation within and among subpopulations

Sub-structuring category	**F_{IS} (SE)**	**F_{ST}(SE)**	**F_{IT}(SE)**
Plumage colour	0. 078* (0.030)	0.006^{NS} (0.005)	0.084* (0.030)
Major gene	0.082* (0.027)	0.009^{NS} (0.007)	0.090* (0.029)
Proportion of shared alleles clusters	0.059^{NS} (0.028)	0.041^{NS} (0.08)	0.098^{NS} (0.029)

**Significantly greater than zero at 95 % confidence interval; ^{NS} not significantly greater than zero at 95% confidence interval*

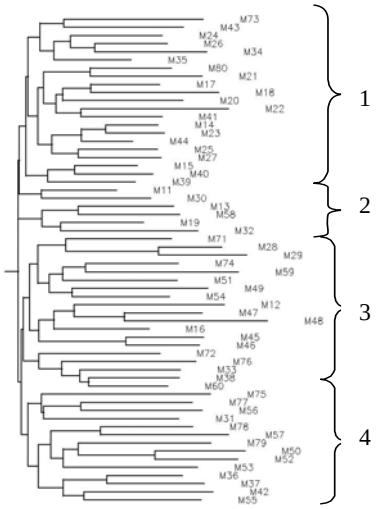

Figure 1: –lnPSA generated dendrogram

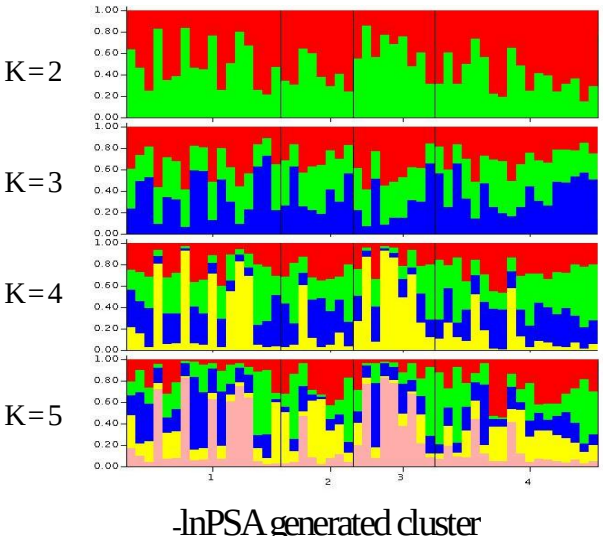

Figure 2: STRUCTURE based clustering

Conclusion

Local chickens in Lilongwe District of Malawi are a single population, characterised by phenotypic heterogeneity. A conservation programme can sample any of the chicken phenotypes and focus on improving the mating systems to minimise inbreeding.

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