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Genetic Diversity and Adaptability Exist among Backyard Poultry Populations in Sri Lanka

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ABSTRACT: Data from 585 chickens and 298 households were recorded for the investigation of adaptability of backyard poultry to rough management and harsh environmental conditions in two geographically distinct sites in Sri Lanka. The molecular investigation using 20 microsatellite markers revealed a high and stable genetic diversity within populations but low genetic differentiation among populations. The management strategies that support this particular genetic structure could be attributed to the constant gene flow through exits from and entries to the flocks of backyard chickens among the villages, and a directional natural selection towards adaptability to local environmental conditions.
Keywords: Backyard poultry; Genetic diversity; Adaptability

Introduction

Backyard poultry rearing is one of the most common features among rural small scale livestock farmers in Sri Lanka (Gunaratne *et al*., 1993; Sanjeewa *et al*., 2011). The system is characterized by the rough management under harsh environment conditions, low input and indigenous non-descript chicken genotypes. The three key pillars that ensure the sustainability of backyard poultry system are the strong adaptability of birds, resource utilization efficiency of the system and minimal, but appropriate, management, of which the strong adaptability of the birds plays the most important role in sustaining the system (Gamage *et al*., 2013). High genetic variation present among the birds and populations is responsible for the adaptation to the harsh and varying environmental conditions. The present study is an attempt to investigate the role of system operations in preserving the high and stable genetic diversity among backyard poultry populations.

Materials and Methods

A repeated and cross sectional survey was conducted in two sites covering five villages in Sri Lanka under the GEF/UNEP supported project titled "Development and Application of Decision-support Tools to Conserve and Sustainably Use Genetic Diversity in Indigenous Livestock and Wild Relatives", implemented in four Asian countries (Bangladesh, Pakistan, Sri Lanka and Vietnam) by ILRI. The total number of households surveyed under initial in-depth survey, the first, second and third monitoring visits were 97, 70, 69 and 62, respectively. Monitoring visits were conducted in every two months. The samples were obtained from five populations within two sites based on the geographical locations (village). Both sites are located in dry zone of the country. The elevation is 89 m above the sea level and the mean annual rainfall and temperature are 1200-1900 mm and 28-30 ^{o}C, respectively, in site 1. Site 2 has an elevation at 40 m above the sea level and the mean annual rainfall and temperature of 600-1200 mm and 30-33 ^{o}C, respectively. The main occupation of farmers in the villages of the two sites is farming, especially paddy and shifting cultivation (*chena*).

Blood samples for molecular investigation, linear measurements and phenotypic characteristics of 585 birds were collected using a stratified sampling method among household clusters (50 m radius or 100 m diameter) derived from GPS positions that were recorded during initial in-depth survey. The rationale behind clustering was that animals/birds in free range systems rarely stick to individual household's boundaries and some of the mating systems are communal.

PCR amplification was carried out for chicken DNA using 20 microsatellite markers selected from ISAG–FAO recommended microsatellite markers (FAO, 2011). The genetic characteristics of each population were assessed by estimating the deviations from Hardy-Weinberg equilibrium (Genepop version 4.1.3), allelic frequency, mean number of alleles per locus and population (MNA), observed (H_O) and expected heterozygosity (H_E) as well as inbreeding coefficient (F_{IS}) within population (Microsatellite Toolkit version 3.1 and FSTAT version 2.9.3.2).

The data was captured and managed in MS Access and the quantitative data were analyzed using descriptive and inferential statistical procedures in STATA software. Tests of statistical significance or otherwise of particular comparisons were done with *Chi-square* (χ^2) test and *Marascuillo procedure* in Minitab for comparisons of multiple proportions.

Results and Discussion

In this study, the phenotypic and genetic diversity of indigenous chicken populations in five villages of two geographically distant sites in Sri Lanka was investigated. The full analysis of the molecular investigation done for this work has been presented elsewhere, but generally showed that there is a high allelic diversity, high MNA per

locus and also relatively high number of private alleles ranging from 2 to 9 in all populations, indicating a high genetic diversity present within the populations of backyard poultry. However, the low frequency of specific alleles indicated that there was a considerable level of migrations per population (Barton and Slatkin, 1986). Interestingly, relatively low Nei's standard genetic distances among populations, which are geographically close to each other, indicated the existence of interactions among populations with respect to the gene flow. A significant deficit of heterozygotes was another observation made in molecular analysis (Table 1). Accordingly, backyard poultry populations exhibited a high but stable genetic diversity across different populations.

Table 1. Deficit of heterozygotes indicated by F_{IS} estimated from 20 microsatellite loci for each population.

Site	Population no.	F_{IS}
1	1	0.036
	2	0.126
2	1	0.116
	2	0.088
	3	0.102

Considering the genetic structure depicted by the molecular analysis, we explore the possible backyard poultry management aspects that could have contributed to the observed genetic structure (*i.e.* high allelic diversity but low genetic distances) in backyard poultry populations. The two sites exhibited different trends in variation of flock structures as measured by the bird entries and exits. However, the trends of both entries and exists were not significantly different ($P > 0.05$), indicating the existence of a constant gene pool despite the frequent entries and exits (Figures 1 and 2). Since most of the exits and entries took place among young age categories and the major causes of exits (diseases and predation) benefited the selection for better fitness among the birds which survived, the directional natural selection towards the adaptability is as expected, very much evident under existing management conditions in backyard poultry.

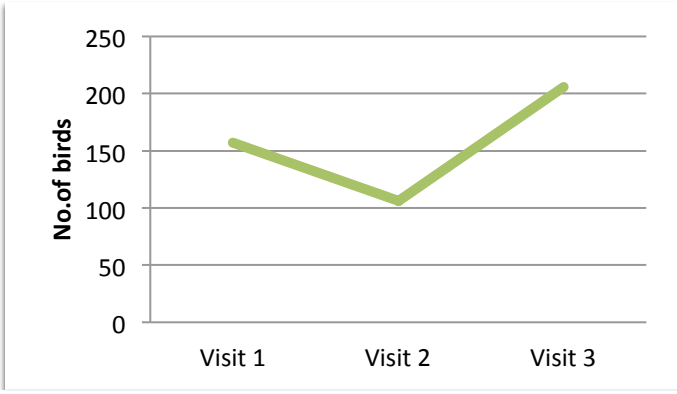

Figure 1: Trends in bird entry as captured by three visits

Figure 2: Trends in bird exits as captured by three visits

Conclusion

Existence of high and stable genetic diversity is a common feature among backyard poultry populations. The genetic diversity exhibited by the populations irrespective of the geographical locations is due to the common nature of inward and outward gene flow into and out of the populations that invariably facilitate a directional selection towards an improved adaptability of the backyard poultry at population level.

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