GENETIC CHARACTERIZATION OF JAFFNA LOCAL SHEEP IN SRI LANKA

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Introduction

Jaffna Local sheep (JL) is the only indigenous sheep type present in Sri Lanka. They are reared under traditional management system unique to the specific cultural practices in the area. The farming system where JL sheep are reared could be described as a mixed crop-livestock system operated predominantly in large scale under free-range arrangement. The origin of the JL sheep is not well documented. According to Ravindran *et al*. (1983), they are believed to be brought from South India several hundred years ago by traders, and as a result of isolated breeding, the population remains with its unique characteristics. It also has been reported that a cross breeding program was started in 1960 to improve Jaffna Local sheep, but it was not continued owing to various reasons (Premasundara and Silva, 2004). No attention has been paid on investigating the genetic potential of indigenous sheep breed, except for the performance evaluation conducted by Ravindran et al. (1983). The present study is an attempt to evaluate the genetic specificity of Jaffna Local sheep compared to selected reference sheep breeds.

Materials and Methods

A laboratory investigation was carried out as a preliminary step of characterizing the local sheep using molecular markers. DNA was extracted from 39 blood samples of JL sheep and seven samples of reference exotic sheep (Dorset-3, Red Madras-3, Bikaneri-1) using Salting out protocol. Six microsatellite loci (BM757, BM827, BM6526, BM8125, OarCP34, and OarFCB48) were used for evaluating the diversity as described by Mukesh *et al*. (2006). Microsatellite Tool Kit and PHYLIP (neighbor- joining approach) computer software was used for molecular data analysis.

Results

A total of 43 alleles were detected across the six loci screened in this study. The total number of alleles found in JL, Bikaneri, Red Madras and Dorset individuals were 39, 10, 17 and 16, respectively. On average 7.17 alleles per locus were observed among JL individuals. There were fourteen unique alleles found in four loci (OARFCB48, BM827, BM6526 andBM8125) in JL sheep population describing the distinctiveness of the indigenous sheep breed. The genetic characteristics of the four sheep populations as depicted by the six marker loci are given Table1. The dendogram developed by PHYLIP (neighbor- joining approach) analysis shows two distinct sub clusters, C1 and C2 (Figure 1).

Table 1: Genetic composition of Jaffa Local sheep and three reference sheep breeds.

Population	Sample size	Loci typed	Expected Heterozygosity (H_e)	Observed Heterozygosity (H_e)	No Alleles
Jaffna Local	39	6	0.66 ± 0.06	0.67 ± 0.03	6.50 ± 2.26
Bikaneri	1	6	0.67 ± 0.21	0.67 ± 0.19	1.67 ± 0.52
Red Madras	3	6	0.70 ± 0.05	0.78 ± 0.10	2.83 ± 0.75
Dorset	3	6	0.68 ± 0.15	0.83 ± 0.09	2.67 ± 1.21
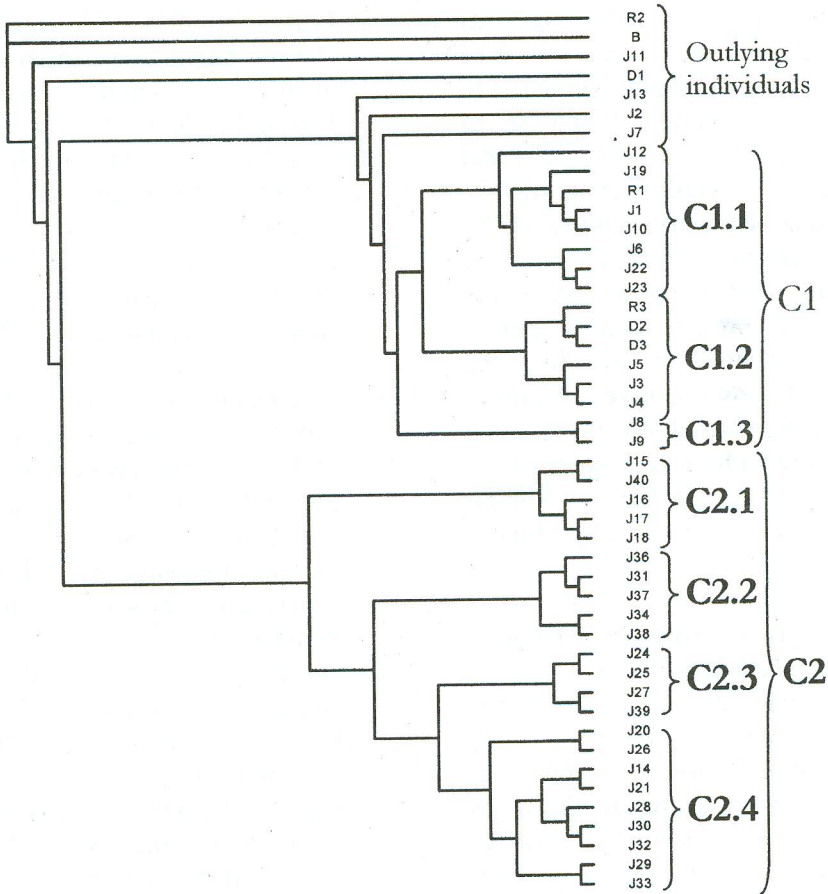
Figure 1: Dendogram showing the clustering pattern of the Jaffna Local (J) sheep samples (C2) and reference sheep samples (C1). (B= Bikaneri, D= Dorset   and R= Red Madras)

Discussion

The high values of H_o and H_e in JL sheep were comparable to those values reported for Indian sheep breeds (Chokla, H_o=0.64 and Nali, H_o = 0.65) by Mukesh et al. (2006) and by Arora and Bhatia (2003) on Muzzafarnagri sheep (H_o = 0.65, H_e = 0.70). The high mean heterozygosity values could be attributed to low level of selection pressure and high allelic polymorphism observed in indigenous population. Overall mean of 7.17 alleles per locus is higher compared to the values for different Indian sheep breeds Chokla (5.63), Nali (6.27) and Garole (5.63) by Mukesh et al., (2006), and for Muzzafarnagri sheep (5.04) by Arora and Bhatia, (2003). This may be attributable to the sampling procedure adopted in the present study to capture the high variation by avoiding the sampling of close relatives. Majority of the markers used for the present study reported a high polymorphism in reference sheep populations. Similar observation has been made by Mukesh et al. (2006).

The dendogram showed a separation of two main clusters; C1 and C2. C1 cluster includes all the sheep breeds alone with few JL sheep and C2 cluster contains only JL sheep. This observation indicates that JL sheep has a clear separation from the reference breeds. However, there is a possible admixture effect due to crossbreeding in the past.

Conclusions

The Jaffna local sheep is a unique population with high diversity. The population showed a possible admixture effect in the past.

References

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