

Alu Insertion / Deletion Polymorphisms in Yadava Population of Andhra Pradesh, South India

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KEYWORDS Alu insertion/deletion polymorphisms; Yadavas; Andhra Pradesh; South India; allele frequency; average heterozygosity; genetic distance

ABSTRACT Four Alu insertion/deletion polymorphisms (Alu TPA25, Alu ACE, Alu PV92 and Alu APO) were studied in Yadava population from Visakhapatnam, Andhra Pradesh. Blood samples were collected from fifty unrelated healthy donors. DNA was isolated and amplified by PCR and subjected to agarose gel electrophoresis. Gene frequencies were calculated and were used to calculate average heterozygosity. All the four loci are polymorphic in nature and showed high levels of heterozygosity. The average heterozygosity is recorded as 0.4945 to 0.4892. Genetic distance analysis of the present data with the available data of two Andhra Pradesh tribal populations revealed that Yadavas are closer to Konda Reddis when compared to Koya Doras.

INTRODUCTION

The Alu insertions are short interspersed nuclear elements (SINEs) present in the human genome. The insertion of an Alu-element at a particular locus can be regarded as a unique event as once inserted, most Alu elements, being stable genetic markers. Alu deletions are rare and even then the deletion leaves behind a foot print.

Alu insertion/deletion polymorphisms have gained importance in the study of genetic structure of human populations as they lack selection pressure. A number of populations in India and other parts of the world are found to be highly polymorphic for these markers. They have been used extensively in recent years to trace human history (Batzer et al. 1996; Stoneking et al. 1997; Majumder et al. 1999; Watkins et al. 2001).

In the present investigation, we present the allele frequencies of four Alu markers in Yadava population from Visakhapatnam, Andhra Pradesh, South India.

MATERIALS AND METHODS

Yadavas also called Gollas, are the great pastoral caste of the Telugu people. Fifty unrelated, healthy male and female donors, randomly selected from the Visakhapatnam city were investigated in the present study. About 5

ml of intravenous blood samples were collected in vials containing EDTA. DNA was extracted by using a simple, rapid, non enzymatic method (Lahiri and Nurnberger 1991) with little modifications. PCR amplification of the DNA samples was performed by using locus specific primers (Majumder et al, 1999). Electrophoresis of PCR products was done on 2% agarose gel (1.5% for Alu ACE) and the bands were visualized by ethidium bromide. ϕ X 174 Hae III marker was used for the allelic detection.

RESULTS AND DISCUSSION

All the four loci are found to be polymorphic in nature and showed high levels of heterozygosity. The allele frequencies and heterozygosities for the insertion/deletion alleles for the four loci studied in the Yadava population are given in table 1. The average heterozygosity is recorded as 0.4945 to 0.4892. It may be pertinent to point out here that Majumder et al (1999) reported consistently high levels of average heterozygosity in 14 populations from India ranging from 0.351 to 0.449. The present study population also exhibits high levels of heterozygosity.

Genetic distance is calculated as per Nei (1972) by comparing the present study with available data of 2 tribal populations from Andhra Pradesh, namely the Koya Doras and the Konda Reddis (Veerraju et al, 2001).

Table 1: Allele frequencies and heterozygosity at 4 polymorphic loci in Yadava population

<i>Locus</i>	<i>Insertion (+)</i>	<i>Deletion (-)</i>	<i>Heterozygosity</i>	<i>n</i>
Alu TPA 25	0.58	0.42	0.4872	50
Alu ACE	0.5312	0.4479	0.5173	48
Alu APO	0.6086	0.3913	0.4766	48
Alu PV 92	0.5405	0.4594	0.4969	37

n = number of individuals Average heterozygosity = 0.4945

Genetic distance between Yadavas and Koya Doras is recorded as 0.0337, while that between Yadavas and Konda Reddis is noted as 0.0164 to 0.0163. From this, we can come to the conclusion that Yadavas appear to be closer to Konda Reddis, when compared to Koya Doras.

Finally it may be concluded here with the observation made by Majumder et al. (1999) that consistent with the findings of classical markers, the Alu insertion/deletion markers show high levels of genomic diversity in Indian populations. Therefore, further studies are to be taken up on Alu markers in more Indian populations in near future.

ACKNOWLEDGEMENTS

We are thankful to Prof. T.Venkateswara Rao, Department of Human Genetics, Andhra University, Visakhapatnam-530 003 for his valuable suggestions.

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