

A Study on Telugu – Speaking Immigrants of Tamil Nadu, South India

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ABSTRACT *Alu* insertion/deletion polymorphisms (*Alu* ACE, *Alu* PV92 and *Alu* APO) were studied in three Telugu – speaking immigrants of Tamil Nadu, to understand their affinities with Andhra Pradesh population. Gene frequencies and average heterozygosity were calculated. All the three loci are polymorphic in nature and showed high levels of heterozygosity. Phylogenetic analysis of the present data with the available data of two Tamil Nadu caste population and Yadavar of Andhra Pradesh revealed that all the three immigrant populations did not show closeness with the Andhra Yadavar.

INTRODUCTION

Alu elements are a family of short interspersed elements (SINEs) with about 500,000 members distributed throughout the primate genome (Batzer et al. 1994). The human-specific *Alu* InDels are highly polymorphic in most human populations, and since their ancestral states are known, these InDels are particularly useful in tracing the ancestry through phylogenetic trees more effectively (Perna et al. 1992; Batzer et al. 1994, 1995, 1996). *Alu* insertions do not occur multiple times at the same chromosomal location; therefore, the sharing of *Alu* elements is necessarily because of common ancestry. This fact makes the *Alu* elements useful markers for various population genetic studies (Batzer et al. 1994; Stoneking et al. 1997).

Tamil Nadu, one of the Southern States of India, known to have received continuous gene flow from different caste and linguistic groups of other regions of India. Many of the immigrant linguistic groups while maintaining their biological identity to a great extent adopted many cultural aspects of the local people and also the language. Thereby, the biological status of the present-day groups can be considered to be “immigrants” at varying periods of time. Many of the caste groups have subcastes, maintaining endogamous status to some extent (Singh 1998).

In the present investigation, we have attempted to study the affinities of three Telugu - speaking immigrants of Tamil Nadu with an Andhra population, South India using *Alu* insertion – deletion polymorphism.

Yadava is a pastoral community of Andhra Pradesh; they are popularly called a Golla. They are also living in Tamil Nadu, Karnataka and Kerala. They are medium or below medium in stature, dolichocephalic and exhibit broader facial profile with a long and moderately broad nasal shape. Thurston (1909) said, “Yadava, meaning descendants of King Yadu, from whom Krishna was descended, has been recorded. Idaiyan and Golla are synonyms for Yadava and their titles are Konar and Pillai. They speak Telugu and Tamil with their kin group and speak Tamil with others. Settled cultivation, animal husbandry and pastoralism are their traditional occupations. In Hindu caste structure they belong to low rank non-Brahmins and come under “Sudra” varna. The Yadavas are distributed in Ramanathapuram, Tirunelveli, North Arcot, South Arcot Ambedkar, Thiruchirapalli and Thanjavur (Singh 1998).

Naidu is a title used by many Telugu speaking community like Balija, Bestha, Boya, Gavara, Golla, Kapu, Mutracha and Velama. Tamils call Naidus as Naickers. However, Naidu essentially refers to Balija, Gavara and Kamma. Naidu is a community concentrated in the Vishakapatnam

district of Andhra Pradesh. The traditional and primary occupation of the Gavara Naidu is agriculture, and business is their secondary occupation (Singh 1998).

Reddiyar, a large dominant community in Andhra Pradesh, they are also distributed in Tamil Nadu (migrated during Vijayanagar empire). At present they are distributed in districts of Kanyakumari, Tirunelveli, Chidambaram, Dharmapuri, Salem, Coimbatore, North Arcot, Chenglepet, Tiruchirapalli and Kamaraj. There are fifteen subgroups within this caste. They are agriculturists and wage-labours (Singh 1998).

The present study is an attempt to verify the affinity of the Telugu – speaking Tamil Nadu groups (Reddiyar, Gavara Naidu and Yadavar) by comparing with an Andhra Pradesh caste population, Yadavar and other two Tamil Nadu caste population (Vanniyar and Ambalakarar) for which the data available, using three polymorphic autosomal DNA loci (*Alu* APO, *Alu* PV92 and *Alu* ACE).

MATERIALS AND METHODS

The three endogamous groups have been sampled from their primary regions of habitat with prior informed consent. Information on age, sex, caste and any information concerning their origin, provided by respondents were recorded. Blood samples of healthy and unrelated individuals were collected from Reddiyar (49) distributed in the areas of Tiruchi; Gavara Naidu (33) of Madurai and Tamil Nadu Yadavar (50) of Kanchipuram.

After obtaining prior informed consent from the individuals, blood samples (5 ml by venipuncture) were collected in sterile EDTA vials. DNA was isolated using the method of Miller *et al.* (1988). Each DNA sample was screened with respect to three autosomal insertion/deletion polymorphisms (*Alu* APO, *Alu* PV92, *Alu* ACE). DNA samples were amplified by polymerase chain reaction (PCR) using locus-specific primers (Majumder *et al.* 1999). All the polymorphic loci studied were genotyped by amplifying 50 – 100 ng of genomic DNA in a standard 30 – cycle three step PCR (Eppendorf Mastercycler Gradient, with heating lid). The PCR reaction mixture contained the following components in a total volume of 20 μ l: 10mM Tris HCl (pH 8.4), 50mM KCl, 1.5mM MgCl₂, 200 μ M dNTPs, 0.5 μ M each primers, 0.5U Taq DNA Polymerase. Amplified PCR products were run on agarose gel, stained with ethidium

bromide, and visualized under UV light.

Allele frequencies and their Standard Errors are computed by the gene counting method. The average heterozygosity was calculated using the estimated allele frequencies for each population. To assess the extent of gene differentiation among the population groups, Nei's (1973) measure of gene diversity was calculated separately for each locus and for all loci considered jointly. The genomic relationships among the populations and dendrograms were constructed using DISPAN (Genetic Distance and Phylogenetic Analysis) software (Ota 1993).

RESULTS AND DISCUSSION

The present study populations are compared with three caste populations (Vanniyar and Ambalakarar of Tamil Nadu; Yadavar of Andhra Pradesh) for which data is available (Basu *et al.* 2003; Ravindranath *et al.* 2005). Allelic frequencies for the '+' alleles (presence of *Alu* insertions) for the three DNA markers are given in Table 1. The average heterozygosities of all loci are presented in the Table 2. The values ranged from 38.7% in Reddiyar to a maximum of 49.5% in Andhra Yadavar. The present study population also exhibits high levels of heterozygosity similar to other Indian population studies (Majumder *et al.* 1999). The amount of genetic differentiation among populations, G_{ST} values (a measure of the interpopulations variability) for all polymorphic loci was observed to be 3.9%. The total genomic diversity (H_T) was found to be 0.45. However, most of the genomic diversity is attributable to diversity between individuals within the populations (H_S 0.43).

In order to assess the relationship between the populations, genetic distance (DA) was calculated and depicted in a neighbour-joining (NJ) tree. Tree shows population relationships as a series of bifurcations, which are commonly interpreted as population splits. But, they could also arise from migration instead of shared ancestry. The neighbour-joining tree depicting the study population relationships is presented in Figure 1. The six populations grouped themselves in 4 clusters: (Reddiyar and Tamil Nadu Yadavar), (Gavara Naidu and Ambalakarar), (Vanniyar) and (Andhra Yadavar). The genetic relationship of these six caste groups along with two tribal populations of Andhra Pradesh (Koya Dora and Konda Reddi) and five-tribal population

Table 1: Allele frequencies at three polymorphic loci in 6 caste populations of Tamil Nadu

| Populations | N | Alu ACE | N | Alu APO | N | Alu PV 92 |
|-----------------|----|---------|----|---------|----|-----------|
| Reddiyar | 49 | 0.459 | 49 | 0.787 | 49 | 0.192 |
| Gavara Naidu | 33 | 0.379 | 33 | 0.773 | 33 | 0.485 |
| Vanniyar* | 50 | 0.620 | 50 | 0.860 | 50 | 0.490 |
| Ambalakarar* | 50 | 0.480 | 50 | 0.800 | 50 | 0.390 |
| Andhra Yadavar* | 48 | 0.531 | 48 | 0.609 | 37 | 0.550 |
| Tamil Yadavar | 50 | 0.460 | 50 | 0.760 | 49 | 0.286 |

* Data Available (Basu et al. 2003; Ravindranath et al. 2005)

N = Sample size

Table 2: Average Heterozygosity with standard error based on three loci in six caste populations

| Populations | Average Heterozygosity |
|-----------------|------------------------|
| Reddiyar | 0.387±0.057 |
| Gavara Naidu | 0.447±0.046 |
| Vanniyar* | 0.408±0.082 |
| Ambalakarar* | 0.436±0.057 |
| Andhra Yadavar* | 0.495±0.007 |
| Tamil Yadavar | 0.427±0.039 |

of Tamil Nadu (Kurumba, Toda, Irula, Kota and Badaga) were also analysed (given in the Figure 2). Except Koya Dora, Tribals and castes formed separate clusters. Although, Telugu-speaking Yadavar, Reddiyar and Gavara Naidu of Tamil Nadu are known to be immigrants from Andhra Pradesh, they did not show any affinity with the Andhra Yadavar. But, they showed closeness

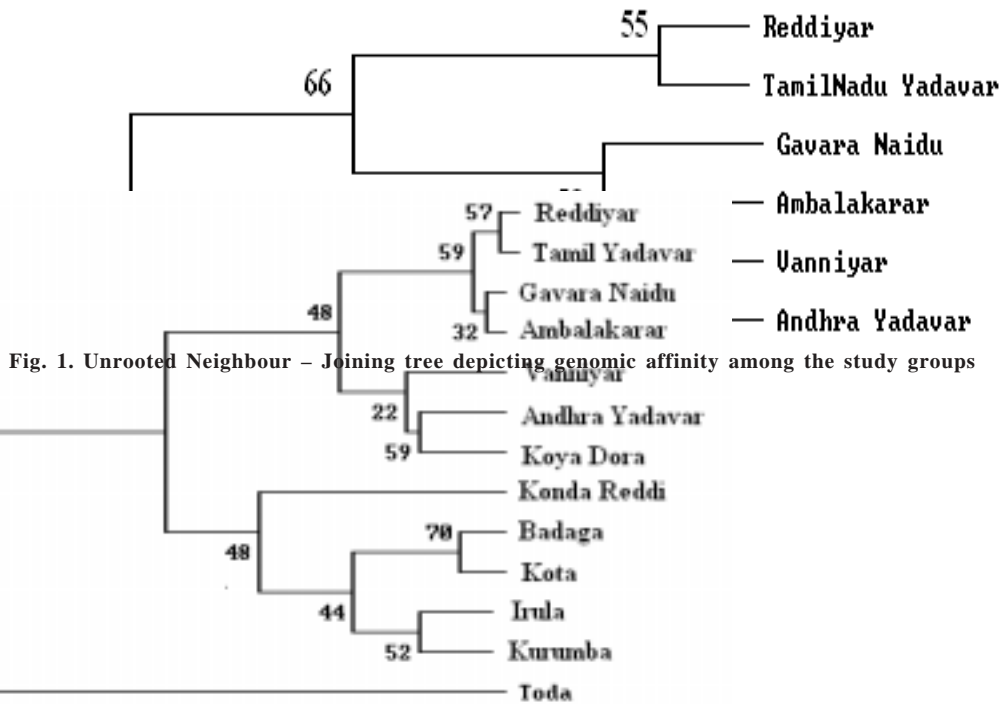


Fig. 1. Unrooted Neighbour - Joining tree depicting genomic affinity among the study groups

Fig. 2. Unrooted Neighbour - Joining tree depicting genomic affinity among the Caste and Tribal populations of Tamil Nadu and Andhra Pradesh

with among themselves. This probably indicates that these immigrant populations may have received high levels of gene flow from other Tamil Nadu populations.

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