6. SUMMARY

The genetic variation in a total of 497 healthy and unrelated individuals among ten caste populations of Tamil Nadu viz., Kongu Vellala Gounder (n=50), Gavara Naidu (n=33), Reddiyar (n=49), Nadar Christian (n=46), Nadar Hindu (n=50), Kallar (n=54), Agamudayar (n=47), Maravar (n=68), Meenaver (n=50) and Parayan (n=50) have been studied, using 26 biallelic DNA markers. Nine markers are Indels (insertion/deletion) consisting of eight Alu insertion sites (Alu APO, Alu CD4, Alu PV92, Alu TPA25, Alu FXIIIB, Alu ACE, Alu PLAT and Alu D1) and one mitochondrial DNA insertion site (mtNUC), nine unlinked restriction site polymorphisms (RSPs): ESR/PvuII, CYP1A1/MspI, T2/MspI, HOXB4/MspI, NAT/KpnI, LPL/PvuII, PSCR/TaqI, ALB/HaeIII and ADH2 /RsaI and three haplotype loci (DRD2, beta globin cluster and ALAD). These markers are core set of DNA markers selected by the Department of Biotechnology (DBT), Government of India, as part of its Human Genomic Diversity (HGD) initiative in the context of Indian populations.

Kongu Vellalar Gounder, Gavara Naidu and Reddiyar are high rank non-Brahmins and are agriculturists. Gavara Naidu and Reddiyar are Telugu speaking migrants of Andhra Pradesh and are now distributed in various parts of Tamil Nadu. The Nadar religious subgroups (Christian and Hindu), Thevar groups (Kallar, Agamudayar and Maravar) and Meenavers are low rank
non-Brahmins; except Meenavers, others are traditionally agriculturists. Toddy tapping and preparing jaggery out of palm juice were traditional occupations of Nadars. Thevar or Mukkalathor is a community of historical antiquity. Kallars are known to be the oldest immigrants of Neolithic period with Mediterranean racial elements. Meenavers are fishermen on the East coast. Parayan are the lower caste or Harijan. They act as drummers at marriages, funerals, village festivals and also do public announcements. Settled cultivation and labour are their occupation.

The present study is an aim to understand the genomic structure of the contemporary caste populations of Tamil Nadu, South India and also the evolutionary forces that shaped them.

Allele frequencies and their standard errors were computed by the gene counting method. The average heterozygosity, gene diversity and phylogenetic trees by neighbour-joining method were computed using DISPAN (Genetic Distance and Phylogenetic Analysis) software. Haplotype frequencies were computed for the multisite marker loci (DRD2, beta globin cluster and ALAD) using the HAPLOFREQ software. The gene flow experienced by the study populations were calculated using the regression model (Harpending and Ward, 1982).

All loci showed high levels of polymorphism in the study populations. Excess frequency of heterozygous genotypes than expected for biallelic loci was observed in 61 marker-groups.
A total of 240 of the 1170 pair-wise comparisons (20.5%) were statistically significant. Most of the significant differences were between Parayan and other caste groups. Gavara Naidu showed least number of differences with other populations.

The observed genotype frequencies significantly differed with Hardy-Weinberg expectations in six of the 260 chi-square tests (~2.3%).

Of the eight haplotypes of the DRD2 locus, haplotype (A1-D1-B1) was absent in all the populations. The frequency of the ancestral haplotype (A1-D2-B2) varied from 5 percent (Nadar Christian) to 23 percent (Kallar). The frequency observed in Parayan, Meenaver and Thevar groups (Kallar, Agamudayar and Maravar) was within the range observed in African populations. The A2-D1-B2 haplotype (derivative of at least one crossover between the two mutational haplotypes) was absent in Meenaver and the range of 4 to 14 percent observed in other caste populations was within the range observed in Africans. The results are in concordance with the global survey of this locus that India might have been the path of Eastward migration.

Presence of "Arab-India" haplotype (+ + -) of the β-globin gene complex, in all the caste groups and absence of (+ - -) haplotype in all the caste and tribal groups of Tamil Nadu implies that Dravidians were once possibly widespread and have retreated to Southern India to avoid linguistic dominance (Indo-European speakers) after an initial period of admixture and adoption of the caste system.
Of the four possible haplotypes at the ALAD locus, haplotype (+ +) was absent in all caste groups and tribals of Tamil Nadu. The total absence of haplotype (+ +) implies that the Tamil Nadu populations are somewhat closer to Africans than to Caucasoids.

Relatively higher values of average heterozygosity (range: 43-45%) compared to the other Indian and global populations studied with the exception to African populations; and the low population differentiation ($G_{ST} = 0.020$ or 2.0%) probably indicates recent admixture of the populations.

The phylogenetic analysis was carried out along with six other caste groups of Tamil Nadu for which the data was available (Two Brahmin populations: Iyer and Iyengar; a high rank non-Brahmin group (Veerakodi Vellalar); two low rank non-Brahmins: Ambalakarar and Vanniyan; and a Harijan group: Pallan). The analysis showed that the Brahmin populations (Iyer and Iyengar) were more homogenous than the low rank non-Brahmins (Ambalakarar, Vanniyan, Nadar subgroups and Thevar subgroups) and Harijans (Parayan and Pallan). They were closer to one of the high rank non-Brahmin group (Veerakodi Vellalar) than with others (Kongu Vellala Gounder, Gavara Naidu and Reddiyar). Some of the low rank non-Brahmins and Harijans were very close (Meenaver and Parayan; Ambalakarar, Vanniyan and Pallan). The Nadar religious subgroups (low rank non-Brahmins) were closely related, while the Thevar groups formed a separate cluster. In that Kallar and Maravar were more closely related than Agamudayar. The
genetic affinities of the populations broadly corresponded to their known ethno-historical affinities. The Indian populations in general, Tamil Nadu caste populations in particular are genetically in between the Caucasoids and Mongoloids. The Thevar groups were found to be closer to the people of United Arab Emirates and Pakistan, and also intermediate to Africa and Sahul populations (Australians and New Guineans); Thereby confirming the Indian links between Africa and Australia.

- The centroid analysis demonstrated that all studied caste groups have experienced high gene flow than tribes of Tamil Nadu, with the exception of the Nadar subgroups, Parayan and Pallan. The observed and expected heterozygosity were nearly equal for Meenaver. The gene flow probably occurred prior to the subdivision of these groups into distinct endogamous units.

In conclusion, the extensive sharing of the haplotypes and an almost similar allele frequency profiles among the study populations probably indicates a common ancestry or having experienced a high degree of gene flow amongst them during the early period of their coexistence. The present study also provides evidence that the genetic drift and admixture have played a major role in the evolution of the Tamil Nadu caste populations. More comprehensive information on the relationships between these populations will be possible on the availability of the data on mitochondrial and Y chromosomal DNA markers.