By analyzing the DNA of living humans from different locations, geneticists are able to assemble a detailed reconstruction of prehistoric human colonization of the world (Foster & Matsumuze 2005). Our current understanding is that modern humans arose ~1, 50,000 years ago, possibly in East Africa, where human genetic diversity is particularly high. As many anthropologists and now geneticists have opined that there are three waves of migration “Out of Africa”: first into the middle East and Asia and eventually to Europe. By and large our understanding of these ancient travels has been invigorated in the past 10 years as researchers use genes to trace the original homelands of populations.

Earlier investigations based on genetic markers have documented the distinctive features of the genetic differentiation of tribal and non-tribal groups of all regions of India (Balakrishnan 1978; Roy Choudhury 1984a; Majumdar 1998, 1999b, Deepa Edwin et al. 2003; Vishwantahan et al. 2004, 2005). Indian populations examined for various DNA markers showed varying degree of diversity, which is expected from their geographic position and differential inputs of migrants pulsing from Africa and West Asia at different times. The dispersal and subsequent growth of Indian populations since the Neolithic age is one of the most important events to shape the history of South Asia. About 15,000 – 10,000 ybp, when agriculture developed from the Fertile Crescent region that extend from Israel to Mother Syria to Western Iran, there was an eastward wave of human migration (Cavalli-Sforza et al., 1994; Renfrew 1997), a part of which appears to have entered in India. This wave has been postulated to have been brought the Dravidian languages to India (Renfrew 1987) which is now confined to southern India. It is believed that south India was populated by human groups in the early Paleolithic period and it is possible that various tribes of South India are the descendents of the ancient stock (Stephen 1973). It is also evident that large genetic diversity is present not only at the all India level, but even within smaller geographical regions of India (Majumder 1999). Therefore, it is of interest to consider patterns of genetic affinities among endogamous tribal groups inhabiting smaller geographical regions.
It is generally accepted that the tribal populations are the original inhabitants of India (Thaper 1966; Ray 1973). As a result of their long isolation and mating structure, these tribal populations with their distinctive culture and unique features are well differentiated from the non-tribals. The tribal populations of South India today are strongly structured and low heterozygosity along with evidence of genetic drift with nuclear loci in contrast to the culturally recent casts. Indeed, different microevolutionary force may differently shape population structure of two groups within the same proximity. However, both nuclear and mtDNA polymorphisms reported separately with very few milestones. Thus, the scanty state of the availability of the polymorphisms of the both the types, nuclear and mtDNA may lead some insights of their structure, relationships, origins, etc. Thus, by and large, this study is the first extensive analysis of Nuclear and mtDNA polymorphism in four tribal populations (Kurumans, Sholiga, Malayali and Uraly) of Southern India which can help clarify the evolutionary relationships among them with other Indian populations, which will in turn shed better insights into the “Peopling of India”. These autosomal loci were characterized with insertion/deletion polymorphisms, restriction site polymorphisms and haplotyped loci that have proved to be informative in the recent literatures of the genome diversity studies. Mitochondrial DNA polymorphisms are characterized with restriction site polymorphisms, insertion/deletion polymorphisms and Hyper Variable Sequence 1 (HVS1) polymorphisms that have been confirmed as a tool to unravel the past of modern humans through its susceptibility (Stoneking et al.1990), lack of recombination (Merriwhether et al.1991) and high evolutionary rate (Brown et al.1979). The development panels of easily typed population – specific markers have improved our ability to understand the genomic relationships between these endogamous groups that comprise the populations of South India.

The present study populations live in relatively restricted areas among the Tamil/Kannada populations, who are predominant in South India. In the process of sampling the individual populations efforts were made to sample only individuals, whose ancestors, so far as could be determined, were all from the same area and ethnic group. Thus, while recognizing that there is no such thing as ‘pure’ human population, these samples are the representatives of the corresponding tribal groups in the particular geographical region.
Alu elements appear to be stable integrations in the genome, which rarely delete from a location (Sawada et al. 1985; Sawada and Schmid, 1986; Baily and Shen, 1983); even when a rare deletion occurs, a signature of the original insertion event is left behind (Edward and Gibbs, 1992), as an exact excision would be extremely low-probability event. In addition Alu elements are subject to very limited amount of gene conversion (Kass et al. 1995; Batzer et al. 1995). Furthermore, the direction of the mutation that results in Alu polymorphisms is known to be forward (i.e. the insertion of the element), facilitating an accurate estimation of the root in trees of population relationships (Batzer et al., 1994). Since new alleles at these loci are unlikely under any selection pressure, the effects of genetic drift and migration must necessarily have generated allele frequency variation among populations in respect of these loci. As it has been reported in ethnic populations from various parts of the world (Batzer et al. 1994, 1996; Stoneking et al. 1997; Novick et al. 1998) including India (Majumder et al. 1999b; Mukherjee et al. 2000, Veerraju et al. 2001; Vishwanathan et al. 2003, 2004), these loci showed high levels of polymorphisms in the tribal populations of South India. Similarly the most exclusively studied RSPs and haplotyped loci also showed high levels of polymorphisms in the study groups, which were in good agreement with the earlier reports on global populations (Jorde et al. 1995; Kidd et al. 1998). It is also reasonable to speculate that the bottlenecks and genetic drifts have been important factors in generating dramatic allele frequency differences in these populations and in extreme case while frequencies are driven towards fixation (frequency of 1) in the Uraly and Sholiga for Alu TPA 25.

Twenty-five chi-square tests for goodness of fit test to Hardy-Weinberg equilibrium were significant. This is higher than the 5% (12.2 significant chi-square tests) expected from chance alone (Table 6 and 7). All the values that were significant probably due to deficiency in the observed heterozygotes where, if they were normal statistical fluctuation, a similar number of departures from the expected heterozygotes for excess and deficiency would be expected. Occasionally preferential amplification of the shorter fragments, which could lead to misclassification, was observed. However, increasing the amount of primer compensates for this problem, and all samples in which this might have occurred were reanalyzed with higher primer concentrations. Another explanation is that the tribal groups reflect a true heterozygote deficiency, possibly because inbreeding. Although all the samples came
from a closer geographical proximity, the Eastern Ghats is relatively accessible and there is mate exchange within the populations. Therefore, it may be concluded that the deficiency in heterozygotes is probably real, which may be due to reflection of a variable degree of inbreeding within the populations or a lack of gene flow.

In the present study, the estimated levels of average heterozygosities are consistently high in all the populations. The heterozygosity levels ranged from 0.426 in Sholiga to a maximum of 0.474 in Kurumans (Fig 7), which were substantially higher than the average heterozygosity levels of other Indian populations (Majumder et al. 1999b; Mukherjee et al. 2000; Veerraju et al. 2001), but slightly low than Nilgiri hill tribes (Vishwanathan et al. 2004) using nuclear DNA markers. Interestingly, the average heterozygosity levels are higher than the other global populations studied with exception to African populations (Stoneking et al. 1997; Novick et al. 1998). Thus, the DNA markers demonstrate that the study groups exhibit high levels of genomic diversity.

Investigating the haplotypes of multiple genetic markers distributed through and around the gene is a powerful tool for resolving the controversial issues and association based on individual polymorphisms. Haplotypes provide information on evolutionary histories, beyond what can be learned from individual markers. There is a need to understand the evolutionary histories of normal allelic variants of the locus because, if the locus really has genetic variation affecting to complex trait, that variation also an evolutionary history that is tied to the history of the entire region, as revealed by the adjacent normal genetic variation (Kidd et al. 1996b). As an aid in the interpretation of haplotype data, known polymorphisms in the DRD2, β-globin and ALAD regions were precisely mapped (Kidd et al. 1998; Majumder et al. 1999a) to facilitate obtaining haplotype frequencies in the four tribal populations of Southern India.

All the populations of the present study share the same set of common haplotypes, with seven haplotypes (B2D2A2, B2D1A2, B1D2A2, B1D1A2, B2D2A1, B2D1A1 and B1D1A1) accounting for at least half of the chromosomes in all the populations (Fig. 8). The ancestral B2D2A1 haplotype background in the human DRD2 loci accounts for 0.028 to 0.166 frequency, which is consistently present in all
the studied groups but it is found to be lower than the sub-Saharan Africa (0.158 to 0.249) (Kidd et al. (1996b). Kidd et al. (1996b) state that this ancestral haplotype is common in the Africans, but rare or absent elsewhere. The present study is in accordance with this but it is higher in the neighboring region the Nilgiris (Vishwanathan et al. 2003a). The three background haplotypes that differ from the ancestral haplotype by one mutation are B1D2A1, B2D2A2 and B2D1A1 (Fig. 9). The B1D2A1 and B2D1A1 haplotypes, which are uncommon in Africa but common in all the other parts of the world are seen in lower frequency and the B1D2A1 haplotype is completely absent in the Malayalis. The B2D2A2 haplotype background is common, with a frequency range of 0.225 in Malayalis to 0.461 in Sholiga population. The three doubly-derived background haplotypes are B1D1A1, B1D2A2 and B2D1A2 and are present at low frequencies in all the study populations. In contrast, except B1D2A1, all the haplotype are present in all the study populations at ~5 - 46%, while it is seen with modest frequencies (8-15%) in Africans (Kidd et al. 1998).

Much of the variation observed today arose some time ago and was present in the ancestral African population from which modern populations descended, and that all of these populations have had large effective population size, allowing them to maintain all the different haplotypes (Kidd et al. 1996b). This is consistent with the single migration of modern Homo sapiens out of Africa, and additional loss of variation as that initial non-African founder populations grew and expanded to the east and later into the Americas. Using nuclear DNA markers, Majumder et al. (1999b) Vishwanthan et al. (2003) and also the recent DRD2 locus study (Vishwanthan et al. 2003) found that a major population expansion has taken place in India. It is also clear from the recent reports on Indian populations that India has played a vital role of being a major corridor in the out-of-Africa migration (Vishwanthan et al. 2003, 2004; Roychoudhury et al. 2000, 2001). By and large, the present study using the same set of markers is concordant with the global survey (Kidd et al. 1998) and South Indian (Vishwanthan et al. 2003) study of DRD2 locus, affirming that India might have been in the path of this eastward migration and also once again strongly supports the ‘Out-of-Africa’ model of Human Evolution. In contrast with the regional consideration with the comparison of the same study (Vishwanthan et al. 2003) of the neighboring region, the Nilgiris of
Western ghats, one of the global hot spot in India possessing the low significant results (including average heterozygosity, haplotype frequencies, LD values) indicates the possibility of gene flow from the present study area, Eastern Ghats to Western Ghats. So with this new finding of the present study, we claim that these ancestral populations of India might have settled in Eastern Ghats and later moved to Western Ghats because of so many social forces like temperature, natural livelihood resources, etc. The human evolution has been heavily affected by cultural and technological developments, which cause major episodes of population expansions followed by migration because of pressure on natural resources stemming from demographic growth (Cavalli-Sforza et al. 1994; Seielstad et al. 1998). More recent migrations have entangled, but not completely erased by this footprints of modern human expansions. Since the gene investigated in the present study is expressed in the brain and has been associated with the risk for psychiatric illness and so many others, our findings may also provide some insight into complex issues of behavior adaptations and other significant importance and also may give the accurate insights in the peopling of India.

The β-globin gene has certainly been much studied for extended haplotypes, initially because of mutant allele involved in thalassemias and opportunity to assess selective force in various human populations. Although, data on restriction gene polymorphisms in the β-globin gene cluster are most extensive from India (Laboe et al. 1989; Sirajuddin et al. 1994; Majumder et al. 1999a; Chakrabarthi et al. 2002; Vishwanathan et al. 2004), the utility of these datas for evolutionary studies were limited. The haplotype most frequently associated with sickle cell allele is -++ background, which is a part of the Arab-India Haplotype. This Haplotype background is present in all the study populations with an average of 3.4 % with a maximum in Kurumans (13.3 %) (Table12). Other haplotypes of Benin and Bantu were also observed in the present study. A more plausible explanation seems to be that this Haplotype have locally arisen from recombination from the most frequent haplotype associated with the Hb-A and Hb-S alleles. Kurumans in South India have high incidence of sickle-cell trait but it is conspicuously absent in the neighboring tribes. The results of the present investigation were concordant with the earlier reports of Majumder et al. 1999a; Roychodhudry, 1982 and Vishwanthan et al. 2004.
Out of the four possible ALAD haplotypes, all the haplotypes were shared by all the four populations studied. Earlier reports (Battistuzzi et al., 1981; Benkamm et al., 1983) have determined this allele in American and European populations. Benkman et al., (1983) states that this Haplotype was not detected in the African populations and argue that this allele may have become established in the Caucasian population by selection. Thus it implies that the present study population might be closer to Caucasian population than African population by selection. However, Vishwanathan et al., (2004) proposed that the some of the South Indian populations (Irula, Kurumba, Kota, Badaga and Toda) are somewhat closer to African populations. Hence, interestingly it is not consistent with their report that the present study populations are somewhat distant from Africans.

In all the populations sampled, the disequilibrium at the DRD2 locus is highly significant (Table 11). Among the SNPs the Taq1 ‘B’ and ‘A’ sites show low pairwise disequilibrium values when compared to Taq1 ‘A’ and ‘D’ sites. The Taq1 ‘B’ and ‘A’ sites with high LD values was clearly observed in the Asian and American populations, but is also exists in Africans (Kidd et al. 1998). The pattern of linkage disequilibrium observed among the β-globin loci is somewhat interesting. The LD between 3'pβHincII and pβHincII and pβHincII and 5'βHinf and I loci is unclear and raising that why it happens. It is difficult to offer any explanation for the observed pattern of linkage disequilibrium on the basis of known histories of the tribal populations. The Msp and Rsa I sites of the ALAD locus showed linkage disequilibrium in all the loci that are located on eight nucleotide pairs. This is because it has low heterozygosity in all the populations and there is no sufficient power in those cases to detect weaker disequilibrium. However if it is more heterozygous, in the populations, disequilibrium is strong and significant. Thus, the distribution of haplotype frequency and linkage disequilibrium in extant populations is the results of the several processes, such as mutation at the SNPs, recombination between the two sites, random genetic drift and gene flow among populations.

The extent of genomic differentiation, \( G_{ST} \) estimates based on the twenty five polymorphic markers for the four tribal populations (Table 15) are higher than those observed in all other parts of India (Majumder et al. 1999b; Mukerjee et al. 2000; Veerraju et al. 2001: Chakrabarthi et al. 2002) but slightly lower than the latest study.
(Vishwanathan et al, 2004). The $G_{ST}$ values are smaller when the continental-level estimates were made on the basis of autosomal RSPs and STRPs (Bowcock et al., 1991; Deka et al. 1995; Barbujini et al. 1997; Novick et al. 1998; Jorde et al. 2000), but when the African populations were removed, the values reduce to 4.8 % which is lower than the present study (5.1 %). Watkins et al. (2001) has reported 2.4 % of $G_{ST}$ estimates in the twelve Indian populations using Alu insertion polymorphisms, which was lower than half of the estimated $G_{ST}$ values of the present study. Thus a significant interpopulation variability was observed in the study population, which indicates heterogeneity in conjugation with the Chi-square analyses. From the present study on genetic diversity, it is also clear that drift effect have emphasized the process of genetic differentiation of the South Indian tribals. This also indicates a rapid population expansion which is concordant with the earlier reports using insertion/deletion markers (Majumder et al. 1999b; Vishwanathan et al. 2003).

Population relationships are shown by the topology of the neighbor-joining tree (Fig. 12). The structure of the tree consists of two branches: Sholiga / Uraly and Malayali / Kuruman. The comparisons of gene frequencies in the above systems imply that Sholiga and Uraly communities are more similar than to their tribal neighbors. The Sholiga and Uraly populations are similar in physical and cultural features from the Negroid and Australoid groups respectively and are Dravidian speaking people of the area. Though the Uraly and Sholiga have been considered and classified as two different populations (It is notable that Uraly sholigar is different form these two populations) most of the statistical results of the present study including this NJ tree confirm that they are closely related. A genetic distance also reveals that these two communities are closer to each other, in agreement with their traditions. Surprisingly, the Kurumans clustering with Malayali; though they are distinctly different in physical, cultural, social, behavioral, linguistical and economic conditions. The possible explanation might be the recent admixture between these groups because of various social forces (e.g. Intercommunity marriages). Hence it is clear that, on the way genetic drift might have played an important role in shaping the genomic differentiation of the tribes of Eastern Ghats. This random genetic drift operation might have been due to their small population sizes and isolation in the hilly terrains (though Kurumans are now distributed in plains). The fact that significant genetic heterogeneity and clustering of these populations into groups of two in such
a closer geographical proximity attests to the sensitivity of the demographic and genetic approaches in unraveling human history.

Further the relationships between populations comparing the global populations using *Alu* markers are shown in figure 15. This tree is consistent with that reported by Majumder *et al.* (1999b) and Vishwanthan *et al.* (2003) stating that the Indian populations are genetically between the Caucasoids and Mongoloids. Veerraju *et al.* (2001) states that the Dravidian and Austro-Asiatic speaking tribals are genetically similar. In contrast, the present study shows higher gene diversity than Austro-Asiatic speakers and also in the most of studied Indian populations. The study group stands apart genetically and did not form any cluster with any populations. The possible reason for the isolation of the tribes might be the remote mating structure and also the isolated cultural background such as strict community practice in marriages. Another interesting finding to note that though one of the present study population, Kurumans of Eastern Ghats and Kurumbas of the Nilgiris are considered as same these two tribes did not form any cluster or relationships (Fig 13), hence it is strongly hypothesized that both the tribes (Kurumans and Kurumbas) have come from different lineages. The possible justification for the local thought might be the similar cultural and occupational practices and also an echo of their name when sounding pressed others to made as same. In addition, the NJ tree constructed by using RSPs (Fig 15) showed a different picture that the study populations stand apart genetically except Kurumans, who are having a remote genetic relationship with other North and South Indian populations. The present study also confirms the earlier findings with classical markers (Majumder and Mukherjee 1993*).

The relationships of specific tribal and caste populations of South India to the European, Asian and African populations remain controversial (Roychoudhury 1977). African admixture with East Indian had two potential sources: First the aboriginal populations that were of African origin and that migrated into South India from the north or by sea (Chandler 1988) and secondly forced immigrations of Africans into South India by the Portuguese in the sixteenth century (Watson 1979). Morphological features such as fizzy hair and broad nose, fleshly everted lips and skin color (Roychoudhury 1982) found in some Indian encouraged exploration for a connection with African and/or Australian aboriginal populations (Guha 1944; Kirk *et al.* 1962;
Sarkar 1954; Roychoudhury 1977, 1984a). In fact it has been suggested that at one time a “negrito element’ was widespread throughout India and was eventually forced into a more restricted location in South India (Majumder and Mukherjee 1993).

Cavalli-Sforza et al. (1994) stated that the tribal populations of the Indian subcontinent may represent the remnants of early Paleolithic expansions out of Africa. The higher Gst estimates of the present south Indian populations with the analysis of more isolated “negrito” populations of the trophies, indicates signals of the early hominoid expansion in tropical regions between Africa and Australia. The results of the present study also confirm earlier findings based on classical markers (Majumder and Mukherjee 1993) and also the recent molecular analysis (Roychoudhury et al. 2000; Thangaraj et al. 2001; Deepa Edwin et al. 2003; Vishwanathan et al. 2003, 2004) stating that India, geographically located between Europe and Oceania, is relatively easy to reach from Africa to across the sea and thus served as major corridor or lane for the out of Africa origin hypothesis.

The centroid analysis (Fig. 17) also shows that there has been a considerable amount of gene flow between the set of populations under consideration and other populations. Thus, by and large, is in accordance with anthropological findings (Fuchs 1973; Majumder and Mukherjee 1993; Majumder 1998). In spite of considerable gene flow as inferred from the centroid analysis, is extent of gene differentiation among South Indian populations continues to be very high. Since this analysis does not permit timing of the period, which the gene flow might have occurred between these South Indian populations, it is difficult to offer clear interpretation of this finding. A probable explanation is that gene flow occurred prior to the subdivision of these South Indian populations in to distinct endogamous divisions.

The dominant view on the origin and spread of modern humans which is prevailing is that Homo sapiens originated in Africa 1,00,000 – 2,00,000 years ago and that all present human populations outside sub-Saharan Africa are primarily descendants of a population that moved from out of Africa about 100 000 years ago (Nei 1995). Harpending et al. (1993) have suggested that after the migration of modern humans from Africa, there were many rapid population expansions following an initial period of isolation. The high levels of heterozygosity observed in African populations are compatible with a number of hypotheses that do not assume an
African origin (Templeton 1994). The findings that the root (ancestral states) of these 
Alu polymorphisms lies close to the cluster of African population (Stoneking et al.
1997; Batzer et al. 1996) and that heterozygosities observed in African populations
are higher than those predicted (Stoneking et al. 1997; Batzer et al. 1996) and
evidence supporting that out of Africa theory and of a greater effective population
size across Africa. Thus, African populations most probably underwent a large
expansion before they moved from out of continent and were to become the source of
modern humans in other parts of the world.

In the present study, we have presented evidence that, with respect to the
autosomal DNA polymorphisms, the South Indian tribals show high levels of
heterozygosity, although not always significant, than most global populations,
including African populations. Further, it was found that majority of the South Indian
populations show high levels of heterozygosity than predicted by Harpending –Ward
(Harpending and Ward 1982) gene flow model. If these patterns of high
heterozygosities were simply due to higher levels of gene flow, then one would be
genetically differentiated. However, it was found that the coefficient of gene
differentiation among South Indian populations is higher than among
populations inhabiting all other regions of the world, except Africa (Stone king et
al. 1997; Majumder et al. 1999b; Watkins et. 2001; Vishwanathan et al. 2004). Two
explanations for those observations of higher than predicted heterozygosities coupled
with the high levels of genetic differentiation may be due to, first, inflow of gene into
populations under study have been high (resulting in higher than predicted
heterozygosities), but different study populations have had different sources (resulting
in a high levels of genetic differentiation), and secondly, an early inflow of genes in
to a population followed by a rapid expansion of this population (resulting in high
heterozygosities) and subsequent splits of this population into largely isolated
(endogamous) population (resulting in a high levels of genetic differentiation).

The present investigation is unable to provide any strong evidence favoring
either two of these alternative possibilities. In the anthropological literature pertaining
to study populations, there are no observations to support the hypothesis that the
different study populations have had inflow of genes from different external sources.
The present data and analyses also do not permit evaluation of the process and estimate of rate of increase of heterozygosities. However, it is emphasized that since the joint observation of higher than predicted heterozygosities and high level of genetic differentiation have earlier been accepted as hallmarks of population expansion (Stoneking et al. 1997; Batzer et al. 1996; Majumder et al. 1999b), the possibility of an early demographic expansion of modern humans with in South India especially among the Deccan Plateau (Western and Eastern Ghats and central plateau, consisting the states of South India) might be possible one. Support for such a possibility also comes from material culture remains in India that show the evidence that upper Palaeolithic (4,00,000 ybp) cultures flourished in different parts of India (Misra 1989). By and large, the overall results of the highly sensitive and polymorphic DNA markers are good concordant with the known population histories of the Eastern Ghats tribes.

Biological (genetic) and cultural variation does not reveal itself in uniform patterns of the same direction and intensity with the one ecological setting. Indeed, different (micro) evolutionary forces may differently shape population structure of two groups with in the same proximity. The present tribal groups who are in a closer geographical region also evidence a similar terrain and culture. Nevertheless, amid the many apparent similarities in natural and human ecology, one is still faced with great variability of the ongoing and dynamic process of population structuring of different communities.

Balinger et al. (1992) proposed that the 9-bp deletion (occurring between the np 8272 and 8279) originated in Central China and spread to South East Asian populations and to coastal and island populations of the pacific. It is present in high frequencies among Tharus (Passarino et al. 1993) and Japanese (Cann et al. 1987; Horai and Matsunaga 1986) populations that are postulated to have arisen from human migrations originating from Southern China. In our study only the Uraly populations harbored the 9bp deletions at higher frequency (14.6 %). Among the South East Asian populations, several haplotypes possessed 9bp deletion, most of which were on Ddel (10394) and Alul (10397) -/- background, whereas in our study 9bp deletion occurred in +/+, +/- and also -/- backgrounds. Previous studies have also shown that 9-bp deletion is rare in India (Watkins et al. 1999; Roychoudhury et al.)
Thus, the possibility of modern human migrations from Central and Southern China into India seems to be high. The presence of 9-bp deletion in the present study may, therefore, have been due to an independent origin of deletion in India. However recent reports (Deepa Edwin et al. 2003; Thangaraj et al. 2005) have demonstrated the presence of 9-bp deletion in other tribes of India.

Figure 20 represents the frequencies of +/-, +/- and -/- mtDNA molecules when the Ddel (10394) and AluI (10397) sites are jointly considered. The +/- haplotype that is very common in Africa is also observed in the study populations in a very high frequency as 45% in Kurumans, 40 % in Sholiga and 65 % in Uraly 65 % and completely absent in Malayalis. This higher frequency of this haplotype indicates that the clear presence of the African signatures on the study groups and also South Indian populations. However recent reports (Deepa et al. 2003) have shown that the +/- haplotype is completely absent in South Indian tribes. The -/- haplotype, which has been classified under macrohaplogroup N, which is very prevalent in European populations (Lell and Wallace 2000). The higher frequency of this haplotype in the Malayalis indicates that their admixture with individuals of Caucasian background through multiple invasions India in historical times. Since this haplotype is also found to be more frequent among the North Indian populations (Roychoudhury et al. 2000), it is also plausible that the Malayalis might have a North Indian origin and later pushed to present habitat in the extreme south.

The presence of mtDNA restriction sites Ddel (10394) and AluI (10397) defines the haplogroup M. This haplogroup was recognized an ancient East Asian and subsequently hypothesized (Passarino et al. 1996b) to have arisen before the split between proto-Indians and proto-Orientals and almost certainly predated the invasion of India by Indo-Aryan speakers. In the present investigation, the frequency of this haplogroup in the pooled sample was 70 %. Previous studies have also reported higher frequency of haplogroup M in other tribal populations of India (Roychoudhury et al. 2000; Deepa et al. 2003). One interesting feature is that the Kuruman, Sholiga and Malayali harboured 70.6 %, 80 % and 76.5 % respectively of this haplogroup, while the Uralys harbored only 46.7 (Table 21) which was more or less equal to that reported for other Indian populations (Roychoudhury et al. 2000). This shows that the Uraly are unique and completely different from other South Indian tribal groups.
Quintana-Murci et al. (1999) reported the presence of haplogroup M in Africa (Ethiopia) with a fairly high frequency (18%) and proposed that this haplogroup originated in Africa. A comparison of East African haplogroup M haplotypes from East Africa and India has suggested a southern exit route for the original dispersion of anatomically modern humans out of Africa (Quintana-Murci et al. 1999), which is also consistent with the hypothesis of Lahr and Foley (1994). It is also adds to growing evidence that India has been a major corridor for the migration of people between Africa, Western Asia and South East Asia (Cavalli-Sforza et al. 1994). Different mtDNA HVS1 sequence motifs have been identified on the haplogroup M background. The most frequent subhaplogroup was M2 and M18 followed by M2b and M25 (Table 23). The other subhaplogroups M4a, M6, M6b and M8 occurred at lower frequencies. The HVS1 motif 16066, 16126, 16302, and 16348 is exclusively found in Kurumans at moderate frequency. The HVS1 motif 16223, 16304, 16311 and 16362 is exclusively found in all the study populations. The East Asian haplogroup M (clade M1) characterized by four transitions 16129, 16189, 16249 and 16311 (Quintana-Murci et al. 1999) is also not found in the present study, and other Indian tribal groups (Deepa Edwin unpublished and Roychoudhury et al. 2001), though it is present in various combinations. Although it has not yet found in India, the clade may be present in small frequency in India and may have risen to high frequency in eastern Africa by genetic drift. In fact M1 could be a branch of the Indian cluster as ancestral motifs of the African M1 are found in M3, M4a, M6, M6b, M8, M18 and M25 Indian subclusters (Table 24). Thus the possibility that haplogroup M might have arisen in India and was carried towards eastern Africa by back migration is strongly revealed. However, recent study (Deepa Edwin et al. 2003) hypothesized the same suggestion on haplogroup M and this is also supported by the fact that genetic diversity of M is much greater in India (Kivisild et al. 1999) than in Ethiopia (Quintana-Murci et al. 1999). Passarino et al. (1996a, b) also indicate this haplogroup is very infrequent in sub-Saharan Africa and the Fertile Crescent region, which was the main exit corridor of modern humans, including India.

The presence of Eurasian specific haplogroup U in the study populations is rather interesting, though it is present at lower frequency only in Malayali and Sholiga. Haplogroup U has also been reported at higher frequency in the North Indian populations (Roychoudhury et al. 2000). The presence of this haplogroup in these
Dravidian tribal populations in the present study and earlier report (Deepa et al. 2003) is consistent with the theory that Dravidian speaking populations are more widespread in India and that the Aryan speakers pushed them to their present habitat in southern India. This haplogroup may have been present among the Dravidians even when they arrived in India with agriculture from the Fertile Crescent region. With regard to the HVS1 nucleotide diversity (Table 25) the Uraly exhibited the highest values of both nucleotide diversity (0.11) and mean number of mismatches (6.77), which indicates their antiquity. Thus, with regard to the overall mtDNA data in the four tribal populations, the Sholiga and Uraly seems to be genetically closer, while on the other side Malayali and Kurumans are confirming their genetic relations possibly because of remote mating structure and isolation of their geographical habitats. In addition Uralys are most diversified population probably, the African admixture than the neighbors of the study.

To conclude, based on the nDNA and mtDNA analysis, the following findings have been proposed:

1) The DNA markers demonstrate that the study groups exhibit high levels of genomic diversity.

2) India might have been in the path of this eastward migration and also once again strongly supports the ‘Out-of-Africa’ model of Human Evolution.

3) The possibility of gene flow from the present study area, Eastern Ghats to Western Ghats.

4) The present study populations may be considered as an ancient ethnic stock of India and might have settled during the dispersal of anatomically modern humans in Eastern Ghats and later moved to Western Ghats because of many social forces like temperature, natural livelihood resources, etc.

5) Interestingly the present study populations are somewhat distant from Africans and Europeans but when compared they are closer to Africans than East Asians.

6) Indian populations are genetically between the Caucasoids and Mongoloids.

7) The present study populations are engaged with remote mating structure and also the isolated cultural background such as strict community practice in marriages.
8) It is strongly hypothesized that two tribes (Kurumans and Kurumbas) have come from different lineages. The possible justification for the local thought might may due to similar cultural and occupational practices and also an echo of their name.

9) The coefficient of gene differentiation among south Indian populations is higher than among populations inhabiting all other regions of the world, except Africa.

10) The possibility of an early demographic expansion of modern humans with in South India especially among the Deccan Plateau (Western and Eastern Ghats and central plateau, consisting the states of South India) might be possible one.

11) The clear presence of the African signatures on the study groups and also on the South Indian populations.

12) Uralys are most diversified population probably, the African admixture than the neighbors of the study.

13) The possibility that haplogroup M might have arisen in India and was carried towards Eastern Africa by back migration is strongly revealed.