SUMMARY

The social structure and the genome of the Indian false vampire bat *Megaderma lyra* was investigated using specific microsatellites. Genomic library was developed by enrichment method using superSNX linkers. About 320 recombinant clones were obtained, 44 were identified as positive, out of these 17 clones containing repeats were selected and sequenced. Primers were designed for best 10 microsatellite sequences and 8 primers were amplified to test the polymorphism of the loci. The primers were standardized by amplifying the genomic DNA samples from four geographically isolated *M.lyra* populations. All loci amplified well except (MlyraE6 and MlyraE7) and shows high polymorphism alleles ranged from 5 to 24 with an average of 13.1 allele per locus. Observed and expected heterozygosity ranged from 0.876 to 0.982 and 0.986 to 1.000. Two loci deviate from Hardy-Weinberg equilibrium and no significant linkage disequilibrium was observed between any pairs of loci.

The mating system, genetic structure and mother-pup interaction were analyzed during 2008-2010 using microsatellite markers in two different geographically isolated *M.lyra* populations (Tirunelveli: 08°50’N, 77°67’E; Tiruchirappalli: 09°10’N, 78°15’E). The mark and recapture data shows the migration of males to the primary roost and females and few adult males move to the secondary roost during breeding season. The females again returned to their primary roost after the pup becomes volant. The high PIC value determines the polymorphic nature of markers used and increase in heterozygosity value determined the diverse allelic nature of individuals. The negative $F_{IS}$ show the increase in heterozygotes, and positive $F_{ST}$ values show there is no subdivision in the population, occurrence of random mating and absence of genetic divergence. Low relatedness shows that the individuals are distant related genetically.
and hence the genetic diversity in the population was evidenced. Parentage analysis by the most likelihood method determined the communal nursing pattern and the immigration of males into the population, and also the possibility of extra colony copulation.

Infestation of ectoparasite is also a part of the social life in bats, which influences the different behaviour of host. Variations in ectoparasite infestation were studied in the Indian false vampire bat *M. lyra*, by capturing the individuals at their day roost and rate of infestation was recorded continuously for a year. Significantly more severe parasite infestation was recorded in pregnant and lactating females than in either non-reproductive females or males. There is no significant difference in the rate of infestation between the breeding and non-breeding season in males. Relationship between parasite infestation and their reproductive status of bats revealed that pregnant and lactating females with pups were vulnerable hosts to ectoparasites. In addition, the analyzed data suggest the possibility for a well developed coevolutionary strategy for synchronized reproduction within the host-parasite relationship. Moreover, our data suggest that intimacy of parasitism may facilitate horizontal DNA transfer. The DNA fragment obtained at 300 bp by the restriction digestion with *EcoR* I and *Hae* III of positive clones of *M. lyra* and *R. lobulata* shows the presence of SINE copy in host and parasite. The identified mammalian short interspersed nuclear elements (MIR-SINE) in both *M. lyra* and its ectoparasite *R. lobulata*, supporting the possibility of horizontal DNA transfer. The predicted secondary structure and repeats provide additional evidence for the evolutionary origin of mammalian SINE in *R. lobulata* and perhaps suggesting significant shaping of the genome for survival and lesser proneness to stochastic extinction.