

### ***Abstract***

Silk is the one most important raw material in India, which plays a significant role in Indian sericulture Industry. The diverse agro-ecological conditions, and social cultural traditions of the farming communities have contributed to the evolution of an immense range of silkworm diversity as farmers' indigenous races, wild and semi domesticated species. The molecular phylogenetic relationships between different silk producing insects of Saturniidae, Bombycidae, and Lasiocampidae family were examined using the 307 bp partial sequences of 16S ribosomal RNA (16S rRNA), 542bp of mitochondrial cytochrome oxidase gene (COI) and full length sequence of Internal transcribed spacer DNA1 (ITS1) by Maximum parsimony and Maximum likelihood methods. The phylogenetic relationships support the monophyly of the Antheraea, and Attacini tribes of Saturniidae family and Bombycidae family. Attempts were made to characterize the genetic diversity of *Antheraea mylitta* at ecorace level using repetitive DNA. We have cloned and sequenced 289bp and 595bp of *MboI* and *TaqI* digested DNA fragments of Indian tropical tasar silkworm *A. mylitta*. The sequence analysis followed by Southern hybridization showed that the isolated DNA fragment of *MboI* and *TaqI* belong to repeat and is found to be retrotransposon and Satellite DNA families respectively. The sequence analysis of *MboI* and *TaqI* repeats between ecoraces of *A. mylitta* as well as species showed significant homology at nucleotide level. The RFLP pattern between different ecoraces of *A. mylitta* using retrotransposable element as probe enlighten the utility of mobile element as genetic marker in the genome of silkworm. The satellite DNA is evenly distributed in all 31 chromosomes as shown by fluorescent *in situ* hybridization. The phylogenetic relationships between ecoraces on the basis of retrotransposable element are in agreement with geographical and morphological similarities but it is not hold true in case of satellite DNA.