CHAPTER VI
SUMMARY
A total of seventeen species of wild silk moths belonging to nine genera and two sub families namely Saturniinae and Salassinae were collected from different parts of Mizoram.

This constitutes 36.17% and 70.83 % of the silk entomofauna of India and North East India respectively. This high record of wild silk moth in the present study seems encouraging enough as previous preliminary survey reported only one species i.e *S. cynthia* from Mizoram (Gupta, 2007).

Of this occurrence was dominated by *S. canningi* represented by eighty five specimens. This could be due to the availability of large number of primary and secondary host plants throughout the study sites.

Maximum numbers of individual as well as species were encountered during the summer/rainy season with highest number of individual recorded during the month of August followed by July.

Significant positive correlation between abundance and elevation was observed in four species out of the seventeen species recorded during the present study. Nine species had an aggregated distribution and the remaining eight species were found to be randomly distributed throughout Mizoram.

The highest number of individual (145 Nos.) was found in the altitudinal range 600-900 m asl and altitudinal range 1200-1500 m, the highest zone of elevation range in the study harbours the highest number of species.

The differences in moth assemblages and distribution are primarily determined by the distribution of host-plant resources than differences in physical vegetation structure.
As far as geographical area of the study region and number of species of wild silk moths recorded during the present study are considered and compared, it reflected the diversity and richness of wild silk moths in Mizoram.

For CO1 analysis, the present study included thirteen species of wild silk moth belonging to two sub families, Saturniinae and Salassiinae. The 16S analysis included fourteen species belonging to two sub families, Saturniinae and Salasiinae.

In comparison with 16S rRNA, CO1 showed less AT bias and possessed lower variability. The transition/transversion bias was higher in CO1 sequences than 16S rRNA sequences indicating lower genetic divergence in CO1 sequences than in 16S rRNA sequences of Saturniidae.

The present study recovered the monophyly of Attacini tribe with one exception. The ML analysis of 16S and CO1 and Bayesian analysis of CO1 recovered the monophyly of Attaciini tribe of sub family Saturniinae.

However, the Bayesian analysis of 16S failed to recover the monophyly of Attaciini tribe where *Attacus atlas* belonging to Attacini tribe nested at the base of Saturniini tribe thus rendering Attacini non monophyletic.

Monophyly of the much uncertain Saturniini tribe of sub family Saturniinae is also resolved for the most part. The ML analysis of both 16S and CO1 gene and Bayesian analysis of CO1 gene recovered the monophyly of Saturniini.

However, the Bayesian analysis of 16S failed to recover the monophyly of Saturniini tribe where *Cricula trifenestrata* occupied basal position to the other thirteen species included for the analysis.

In the present analysis, *S. megastica* and *S. lemaii* belonging to sub family Salasiinae instead of forming separate clade, nested within sub-family Saturniinae.
in both ML and Bayesian tree topology of CO1 and 16S. This may be due to inclusion of fewer representative of sub family Salasiinae.

- Comparison of recovered topologies for both CO1 and 16S rRNA gene in our analysis revealed that CO1 is better than 16S for resolving phylogeny of wild silk moths.

- The present analysis also showed that ML method is better in comparison to parsimony and Bayesian method for both CO1 and 16S in resolving relationships within wild silk moths.

- Being the first scientific research on the molecular phylogeny of wild silk moths in Mizoram, the phylogenetic status of wild silk moths has been established based on 16S rRNA and CO1 marker. This enabled us to have a better insight to their genetic diversity, classification and study of evolutionary relationship.

- For obtaining more complete picture of the phylogenetic relationship of wild silk moth, sequencing of additional mitochondrial and nuclear markers, comparison with morphological characters and evaluation of more number of taxa is required.