CONCLUSION
CHAPTER 5

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From the results and discussions of the present study it can be concluded that-

- The nuclear 18SrRNA and chloroplast rbcL are phylogenetically informative but are much conserved suggesting that they are not rapidly evolving, having a lower percentage of parsimony informative characters.

- The nuclear ITS data set and chloroplast matk had higher percentage of variable sites which suggests that they are rapidly evolving.

- Results suggest that instead of analyzing the individual genes or loci separately it is always better to use multiple data matrix in combination which adds more resolution in phylogenetic interpretation.

- There is no significant difference between the phylogenetic relationship interpreted from nuclear data sets and chloroplast data sets (except for some minor differences of branch positions), which suggests that all the plants studied here originated from single individual ancestor.

- From our study of combined data set obtained from all the four gene sequences in combination, it can be established that the plants (both cultivated and wild) available in Meghalaya can be grouped into three monophyletic clades – Clade I consisting of members of the subgenus *Potatoe*, clade II includes members of the subgenus *Solanum*, and clade III
comprising of members of the subgenus *Leptostemonum*. A very close evolutionary relationship has been noticed between -

1. *Solanum nigrum* and *Solanum clavatum*, 2. *Solanum kurzii* and *Solanum gilo* and 3. *Solanum sisymbriifolium* and *Solanum khasianum* indicating their recent diversifications in the evolutionary pathway. The results also suggest that *Solanum torvum* is sister to the highly supported clade consisting of *Solanum kurzii* and *Solanum gilo*.

- The PCR-RFLP result also suggests the close evolutionary relationship between -
  1. *Solanum nigrum* and *Solanum clavatum*
  2. *Solanum kurzii*, *Solanum gilo* and *Solanum kurzii*

- Total protein profiling revealed phylogenetic tree which is also almost congruent to phylogenetic tree constructed by using molecular data.

- The qualitative screening of secondary metabolites revealed that *S. khasianum* is the richest among all the species studied here with regard to the secondary metabolites screened.

- The fruits of *S. khasianum* contains significantly higher amount of solasodine followed by *S. sisymbriifolium*. Among the species studied here, *S. kurzii* and *S. gilo* contains lowest amount of solasodine.