V. Summary and Conclusions
1. *Dalbergia*, a fabaceous genus of tribe Dalbergiae with over 100 species of trees, shrubs and woody climbers are widely distributed throughout the tropics of the world. Ten species out of 35 Indian species found in western ghat area of Karnataka constitute the present study.

2. This investigation presents the first comprehensive report on nuclear DNA amount variation in 20 *Dalbergia latifolia* populations and its nine related species.

3. In *Dalbergia latifolia*, 4C DNA amounts ranges from 6.85 pg. to 6.90 pg. at the constant chromosome number of 2n=20. A difference of 0.72% genome size variation is apparent. Analysis of variance (ANOVA) shows that, DNA content variation in different populations of rosewood is non-significant. This study reveals that *D.latifolia* has stable genome over a wide range of distribution in western ghat region. Present investigation supports the idea that, genome size of an organism is more or less constant among various populations of a species.

4. The 4C nuclear DNA contents were determined for 10 species of *Dalbergia* involving 48 collections. The 4C DNA values ranges from 5.85 pg. in *D.lanceolaria* to 7.88 pg. in *D.horrida*. 
Approximately, 1.3-fold variation is evident in the genus *Dalbergia* at a constant chromosome number. ANOVA test reveals the significant variation between the species. Like most woody genera, *Dalbergia* also exhibits a small genome with narrow range of genome size variation.

5. The tree species of *Dalbergia* exhibit small genome size ranging from 5.85 pg. in *D.lanceolaria* to 7.22 pg. in *D.sissooides*. While, the shrubs and climbers of this genus reveal a narrow range of genome size variation ranging from 7.36 pg. in *D.rubiginosa* to 7.88 pg. in *D.horrida*. Apparently, climbers exhibit higher amount of DNA than their ancestral tree species.

6. The lianas or climber species of *Dalbergia* occupying evergreen/semi-evergreen forests have evolved from tree species of *Dalbergia* through evolutionary increase in genome size. Thus, diversification of climber species in *Dalbergia* from their ancestral tree taxon is accompanied by increase in genome size.

7. Economically important timber tree species Shisham (*D.sissoo*), Indian rosewood (*D.latifolia*) and Malabar blackwood (*D.sissooides*) exhibit 6.46 pg., 6.86 pg. and 7.22 pg. of DNA respectively. These three species are closely related and form one genetic assemblage.
8. From distributional point of view, the *D.sissoo* is primitive species with a wider distribution than *D.latifolia*. It appears that *D.latifolia* is evolved from *D.sissoo*. The south Indian endemic species *D.sissoides*, restricted to patches of semi evergreen / evergreen forest appears to be evolved from *D.latifolia*. In general, it appears that the species differentiation in these closely related tree species, have occurred through small increase in genome size.

9. *D.lanceolaria* and *D.paniculata* are morphologically similar with DNA content of 5.85 pg. and 6.33 pg. respectively. The latter species have 7.6% more DNA than the former taxon. *D.paniculata* appears to have evolved from *D.lanceolaria* through an evolutionary increase in genome size. Thus, *D.paniculata* may be merged with a primitive taxon *D.lanceolaria* with a subspecies status as suggested by some botanists.

10. Lianas or climbers, *D.volubilis*, *D.horrida*, *D.rubiginosa* and *D.malabarica* have evolved from primitive tree species through evolutionary increase in genome size. While, species differentiation among tree species *D.sissoo*, *D.latifolia*, *D.sissoides* and also in *D.paniculata* has occurred through small increase in genome size.
Thus, an increase in DNA amount is the predominant evolutionary trend during species differentiation in Dalbergias.

11. Chromosome size and the DNA content of ten *Dalbergia* species was compared to determine the correlation between these two parameters. Total chromatin length (TCL) varies from 18\(\mu\)m in *D.sissoo* to 29\(\mu\)m in *D.melanoxyylon*, whereas, 4C DNA amount ranges from 5.85 pg in *D.lanceolaria* to 7.88 pg in *D.horrida*. A close examination of the data reveals that there is no significant correlation (r=0.283) between DNA amount and chromosome size.

12. Genetic diversity has been analyzed in fifteen populations of *Dalbergia latifolia* by SDS-PAGE. The study demonstrates the greater genetic variability at the interpopulation level. Thus, the greater amount of genetic variability in seed protein profiles observed among different populations of *D.latifolia* agrees with the behavior of an out crossing or allogamous species.

13. UPGMA cluster analysis grouped most of the populations in the same cluster. Four pairs of populations showed highest similarity and grouped according to their geographical origin. Thus, the similarity in these pairs of populations can be attributed to considerable gene flow between them. However, some populations
could not cluster according to their geographical origin, suggesting that there is no correlation between the genetic distance and the geographical distance. The present study shows that, the protein profiles provide a useful tool in detecting the genetic variability in populations of *D.latifolia*, which can be used for the genetic improvement of this species.

14. Genetic relationships among nine *Dalbergia* species have been analyzed using seed protein profiles by SDS-PAGE. The nine species of *Dalbergia* showed species specific seed protein profiles. The species included in the present study were grouped into two clusters, corresponds to section: Dalbergia with *D.paniculata*, *D.lanceolaria*, *D.melanoxyylon*, *D.volubilis* and *D.sissoo*, and section: Sissoa with *D.latifolia*, *D.sissoides* and *D.horrida*. Even though, the *D.sissoo* and *D.melanoxyylon* belongs to section: Sissoa, these two species are grouped into section: Dalbergia. Thus, the results of the present investigation suggests that the sectional classification of *Dalbergia* species requires the evidences form other molecular studies.

15. The principle coordinate analysis and UPGMA dendrogram reveals that *D.paniculata* is closely related to *D.lanceolaria* with 0.61 similarity index. These two species shares most of the polypeptide
bands in common. Thus, the present studies supports the idea that the *D.paniculata* can best be considered as a subspecies of *D.lanceolaria*.

16. *D.sissooides* is genetically closer to *D.latifolia* with 0.32 similarity index. Even though, these two species share some of the polypeptide bands, the protein profiles of these two species are considerably different. Hence, the present studies suggested that *D.sissooides* be considered as a distinct species, rather than a variety of *D.latifolia*, as suggested by some botanists. The present study clearly showed that seed protein profiles provide a sound basis for establishing genetic relationships among *Dalbergia* species.

17. The genetic diversity and the relationships among 15 natural populations of Indian rosewood (*D.latifolia*) were evaluated using random amplified polymorphic DNA (RAPD) markers. A total of 96 different RAPD bands were generated by the 10 primers analyzed and pair wise distances were calculated between populations according to Jaccard, then used to construct UPGMA dendrogram.
18. Cluster analysis based on the genetic similarities placed 15 populations in two clusters, with 11 populations in cluster A and 4 northern populations in cluster B. High genetic variability was detected within each population with an average diversity of 0.221. Northern to southern gradient of genetic diversity was observed in populations analyzed. Partitioning of the genetic diversity indicated that 65% of the variation occurred within populations and 35% between populations. This finding agrees with the behavior of an out crossing species.

19. The reduction in diversity index in northern populations of Indian rosewood can be attributed to overexploitation of this commercial timber-yielding tree in northern parts of Western Ghats. Because of the high value of the timber, the Indian rosewood is under considerable pressure of overexploitation.

20. PCR based DNA fingerprinting was used to study genetic relationships among ten species belonging to two sections of the genus *Dalbergia*. Of the twenty primers initially screened for polymorphism, only 10 amplified genomic DNA across all the ten species. A total of 224 RAPD bands were observed with an average of 22.4 bands per primer, of which 99% were polymorphic. Pair
wise genetic distances were calculated between species according to Jaccard, then used to construct UPGMA dendrogram.

21. Cluster analysis based on the genetic similarities placed ten species of *Dalbergia* in two clusters, with *D.latifolia*, *D.sissoides*, *D.horrida* and *D.melanoxylon* in cluster A and *D.lanceolaria*, *D.paniculata*, *D.volubilis*, *D.rubiginosa* and *D.malabarica* in cluster B. These two clusters correspond to section: Sissoa and Dalbergia respectively.

22. The results of the present investigation showed that *D.paniculata* is closely related to *D.lanceolaria* and it is suggested that *D.paniculata* be considered as a subspecies of *D.lanceolaria*.

23. The RAPD results easily distinguish the *D.sissoides* from *D.latifolia*, and supports the independent species status of *D.sissoides*.

24. As many of the species of *Dalbergia* are used as potential forage and timber legumes, the presence of unique RAPD markers among the various *Dalbergia* species indicate, the utility of the approach for fingerprinting purposes. Present investigation represents the
utility of RAPD markers as a tool to study the genetic relationships
and molecular systematics in *Dalbergia*.