

CHAPTER VI

CONCLUSIONS

The study of species diversity at *Khun Mae Kuong* Forest in Chiang Mai province based on morphological characters revealed 30 Fagaceae species: 12 in *Castanopsis*, 11 in *Quercus* and 7 in *Lithocarpus*. *Castanopsis* was found most frequently in Hill evergreen forests, *Quercus* was most common in Dry deciduous forests at low altitudes, whereas *Lithocarpus* was found scattering in a wide variety of forest types. The study has confirmed high species diversity in northern Thailand as expected of a region which is part of the diversity centre of this group of Fagaceae.

The results from rDNA-RFLP and ISSR genetic distance studies show clear separation of the genera and of most species, supporting the taxonomic classification. Furthermore, both types of molecular markers show that the genus *Castanopsis* in this region is genetically diverse, the *Quercus* genus is relatively homogeneous, but the genus *Lithocarpus* has a split diversity. Gene flow is likely to have occurred between species, especially between species of *Castanopsis* and *Lithocarpus* as well as between *Lithocarpus* and *Quercus*, and this may be the reason behind such diversity pattern of Fagaceae in this region. Significant part of the molecular diversity detected in this study is clearly due to taxonomic discrepancies, especially where morphological characters are ambiguous. Further work will include taxonomic revision of certain species.

The results from karyotype analysis show that most of the species had diploid ($2n = 2x = 24$) chromosome number, with the basic number being 12. However, significant variation in the chromosome number was detected - one sample belonging to *Q. lenticellatus* had diploid ($2n = 14$) chromosome number, with the basic number being only seven. This is the first report of $2x = 7$ basic number in Fagaceae, and is

among the very few reports of this basic number among tree species worldwide. This basic number is believed to be ancient and common characteristics of all angiosperms.

The ribosomal gene maps, based on both 18S-25S rRNA and 5S rRNA genes, were significantly species-specific. Almost all of these species showed four sites (two pairs) of 18S-25S rRNA gene and two sites (one pair) of 5S rRNA gene. A few samples of *Castanopsis* and *Lithocarpus* showed an odd number of (unpaired) sites, indicating hybrid origin of species or individual trees. In most *Castanopsis* species, the 18S-25S and the 5S genes were localized on different chromosome pairs, but in most species of *Lithocarpus* these 18S-25S and 5S genes were localized next to each other on the same chromosome arms. The ribosomal gene maps in *Quercus* were variable, including both rRNA genes on different chromosomes, and on the same chromosome arms with subterminal 18S-25S rDNA loci and paracentromeric 5S rDNA loci. The molecular cytogenetic studies not only support the molecular analysis and the taxonomic classification by enlarge, but also reveal possible mechanisms that drive the species diversity in this family in this region.

Studies of genetic diversity, especially intraspecific and interspecific variation, can contribute to the development of conservation strategies. The neutral molecular markers can provide useful information on co-ancestry, gene flow and ecology over species and populations, while molecular cytogenetics can screen cryptic, cytotypic and/or ploidy variation that influence genetic architecture and reproductive potential. Both techniques can contribute to complete conservation in plants.