CHAPTER VI

CONCLUSIONS

Now a day, molecular phylogenetics has been proved to be a great tool for systematic study of all organisms. This is because DNA can reveal genetic relationship among organisms more directly than morphology. On the other hand, genetic relationship study considering only morphological data sometimes has given a big error from convergent evolution. In the genus *Aeschynanthus* DNA sequence and phylogenetic analysis of ITS regions (Denduangboripant *et al.*, 2001) have previously shown that we could make a final conclusion based on comparison between both morphological and molecular data, and this conclusion agreed well with prior taxonomic analyses of the genus.

In this MSc thesis, genetic relationship study of some *Aeschynanthus* in Thailand and other countries has given a clearer picture of natural relationship within the genus. These new phylogenetic trees based on ITS regions of nuclear ribosomal DNA support previous studies of Denduangboripant *et al.* (2001) which suggested that members of this genus could be grouped into two major clades. The ITS phylogenetic systematics also fits quite well with the conventionally sectional classification using easily observable characters like seed appendages. An existence of the two major clades in *Aeschynanthus* suggests that the genus may be divided into two natural subgenera.

Unfortunately, lacks of morphological information about testa-cell orientation and geographical distribution of some *Aeschynanthus* species provided by RBGE have limited a deeper discussion on their subgeneric classification. Nevertheless, molecular phylogenetic study has successfully proved to be useful for cultivated and wild *Aeschynanthus* identification.

The molecular identification studies of cultivated and wild *Aeschynanthus* in this thesis have shown that there is a great advantage in using simple molecular techniques, combined with phylogenetic analyses, to identify problematic taxa. This is especially useful when having difficulty in investigating taxonomically significant organs of those organisms. Molecular identification of *Aeschynanthus* cultivars in this MSc study could suggest that *A.* sp. JJ_003 and *A.* sp. JJ_004 were the same species and should be *A. radicans.* This molecular work also identified *A.* sp. JJ_002 to be *A. radicans* but as a cultivated variant. More interestingly, this technique has confirmed that the pink *Aeschynanthus*, *A.* sp. JJ_001, is a true member of the genus and possibly a new species. Such elegant recommendation comes from the position of this strange plant on the ITS phylogenetic tree with a long divergent time. Further study are required to solve this hypothesis. Not only identifying cultivated plants, but this molecular approach has also shown its usefulness on wild sample identification. For seven wild *Aeschynanthus* tested in this experiment, all of them were molecularly identified to be *A. hildebrandii* though having little differences in leaf characteristics possibly caused by different the environment between the two areas.

On the quest to gather evidences to judge whether *A. andersonii*, *A. hildebrandii* (19991628) and *A. humilis* are actually a synonyme of the same species, the phylogenetic analyses and RAPD experiment have been performed. The molecular genetic result suggested that *A. andersonii* was virtually the same taxon as *A. humilis* whereas *A. hildebrandii* was genetically little different from the other two. Furthermore, cytological evidences considering chromosome numbers of these three problematic species also suggested in the same way as molecular result. All three *Aeschynanthus* were found having a chromosome numbers of 2n=28; a rare number within the genus. This rare chromosome number of 2n=28 (and also 2n=30) were suggested to derive through dysploid reduction from a predominantly ancestral chromosome number, 2n=32. This cytogenetic result of *A. andersonii*, *A. humilis* and *A. hildebrandii* is congruent with that from molecular experiments and therefore has given a support of the synonymous hypothesis for *A. andersonii* and *A. humilis*. Moreover, this recommendation could predict that *A. hildebrandii* should be placed into the section *X* following *A. andersonii* and *A. humilis*. More advance techniques such as Fluorescense *in situ* Hybridisation (FISH) or Genomic *in situ* Hybridisation (GISH) could give a clearer picture of chromosomal relationships among these three *Aeschynanthus* taxa. In conclusion, treating *A. andersonii* and *A. humilis* as the same species has been strongly suggested, although more further study either on RAPD analysis or using other genes from different genome to confirm this conclusion is very welcome.