

## CHAPTER V

### Conclusions

1. Restriction of amplified sRNA gene, lrRNA gene and inter CO I-CO II region of mtDNA *A. cerana* with *Dra* I revealed 3, 5 and 8 different digestion patterns, respectively. A total of thirteen composite haplotypes was found in this study.
2. Using PCR-RFLP approach, five geographic locations of *A. cerana* could be genetically allocated into 3 groups composed of the Northern, the South and the Samui Island *A. cerana*.
3. The UPGMA dendrogram of populations derived from PCR-RFLP data can divide five geographic locations of *A. cerana* into 2 distinct evolutionary lineages : 1) the Northern and 2) The Southern honey bee in Thailand.
4. Sequencing of lrRNA gene portion provide comparable results to those of PCR-RFLP. Five lrRNA gene haplotypes can be classified into 3 groups composing of haplotype B and C (group A), A and D (group B) and E (group C).
5. Population specific haplotype found in the present study can be used as molecular markers for conservation programmes of *A. cerana* in Thailand.
6. The basic knowledge in this study indicated strong North-South genetic population structure of *A. cerana* in Thailand. Subsequently, mtDNA markers and others (e.g. mini and microsatellite loci, single copy nuclear DNA-RFLP, RAPD and AFLP) can be further developed and utilised in selective breeding programmes of *A. cerana* as marker assisted selection.