

CHAPTER 5

CONCLUSIONS

1. Digestion of amplified ATPase6-ATPase8 with *TaqI*, *SspI* and *VspI* revealed 2, 5 and 6 different restriction patterns, respectively. A total of ten composite haplotypes were generated in this study.
2. Length heteroplasmy of ATPase6-ATPase8 mtDNA were found only in the Southern (South and the Samui Island) *A. cerana*. This strong evidence that the Northern and the Southern *A. cerana* are evolutionary different lineages.
3. Haplotype C of *VspI* digest was a population specific for the Samui Island *A. cerana* which can be used as molecular markers for conservative program of *A. cerana* in Thailand.
4. The UPGMA phenogram of populations derived from PCR-RFLP data can allocated five geographic locations of *A. cerana* in Thailand into 2 evolution lineage : 1) the Northern and 2) the Southern *A. cerana*.
5. Based on Monte Carlo simulation, five geographic locations of *A. cerana* in Thailand could be genetically divided into 3 groups included of the Northern, the South and the Samui Island *A. cerana*.
6. The Southern *A. cerana* is most likely to be the ancestor of *A. cerana* in Thailand.