

CHAPTER 5

CONCLUSIONS

1. PCR-amplified control region of *A. mellifera* and all *A. cerana* using primer AM8-AM11 was 2560 and 2750 bp, respectively.
2. Digestion of the amplification product of *A. cerana* with *TaqI*, *RsaI* and *HinfI* generated 2, 3 and 10 restriction profile, respectively. A total of 11 composite haplotypes were observed.
3. UPGMA phenograms of composite haplotype and geographic samples indicated 2 genetically different lineages composed of Northern latitude (North, North/East, Central) and Southern latitude (South, Samui Island and Phuket Island) of *A. cerana* in Thailand.
4. Geographic heterogeneity and population differentiation analyzes could allocate six geographic location of *A. cerana* in Thailand to 3 groups composed of 1) North, Central and North/East 2) South and Phuket Island and 3) Samui Island.

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