

CHAPTER V

CONCLUSIONS

1. The composite haplotypes of the honeybee from Samut Songkram, Bangkok, Chumphon provinces and Samui island were AAA, AAA, BBA and BCC, respectively. Those indicated that the genetic populations were northern, northern, southern and Samui island honeybees, respectively.
2. The 23.6 and 25.4 mg/cup/day of royal jelly were produced by northern and southern honeybees, respectively and the significant difference between those productions was not found ($P = 0.05$).
3. The moisture of northern and southern honeybee royal jelly were 48.8% and 49.6%, respectively and the significant difference between moisture contents of northern and southern honeybee royal jelly was not found ($P = 0.05$).
4. The protein contents of northern and southern honeybee royal jelly were 20.1 and 22.6 %, respectively and the difference between protein contents of northern and southern honeybee royal jelly was significant ($P = 0.05$).
5. The acidity of northern and southern honeybee royal jelly were 47.1 and 45.0 %, respectively and the significant difference between acidity of northern and southern honeybee royal jelly was not found ($P = 0.05$).
6. The ash contents of northern and southern honeybee royal jelly were 1.8 and 1.7 %, respectively and the significant difference between ash content of northern and southern honeybee royal jelly was not found ($P = 0.05$).

7. The lipid contents of northern and southern honeybee royal jelly were 4.6 and 6.9 %, respectively and the significant difference between lipid content of northern and southern honeybee royal jelly was found ($P > 0.05$).
8. The 10-HDA contents of northern and southern honeybee royal jelly were 0.9 and 1.3 %, respectively and the significant difference between their 10-HDA content was not found ($P > 0.05$).
9. The moisture, protein, acidity, ash and 10-HDA contents between *A. mellifera* and *A. cerana* were different, significantly ($P > 0.05$) while the lipid content was not different ($P = 0.05$).
10. Seven thousands, eight hundreds and twenty nine colonies of cDNA clones were obtained from cDNA cloning by modified method of differential expression.
11. The 23 genes and 17 deduced proteins were derived from one hundred and ten recombinant plasmids sequences by analysis of the homology searching against GenBank DNA and protein databases using blastn and blastx.
12. The 11 (20.8%) and 16 (28.1%) genes of known and unknown genes were found with complete open reading frame (ORF), respectively.