

CHAPTER V

CONCLUSIONS

1. The full length of MRJP4, MRJP5 and MRJP6 cDNAs were newly identified in *Apis cerana*.
2. Complete nucleotide sequence of AcMRJP4, AcMRJP5 and AcMRJP6 cDNA were obtained from the RT-PCR cloning of hypopharyngeal glands mRNA. The complete nucleotide sequence of AcMRJP4, AcMRJP5 and AcMRJP6 cDNA were 1608, 1881 and 1450 bp encoding for 485, 579 and 435 amino acids, respectively.
3. Deduced amino acid sequence after eliminate the signal peptide of AcMRJP 4, AcMRJP 5 and AcMRJP 6 cDNA were used to predict the putative N-glycosylation site, MW and theoretical pI . In AcMRJP4, AcMRJP 5 and AcMRJP 6; the number of N-glycosylation site was 7, 5 and 2 times respectively; the predict MW was 52.8, 66.2 and 47.4 kDa, respectively; the theoretical pI was 5.84, 8.75 and 6.44, respectively.
4. Nucleotide sequence of AcMRJP 4, AcMRJP 5 and AcMRJP 6 cDNA show high homology with those of AmMRJP 4 (89%), AmMRJP 5 (91%) and AmMRJP 6 (92%), respectively.
5. The repetitive region that contained a tripeptide repeat unit (DRM) was observed in AcMRJP5. This region located at the same position in other bee species (*A. dorsata* and *A. mellifera*) but differ in number of repeat unit.

6. The conserved position of 4 cysteines, the presence of several blocks of conserved amino acid and highly hydrophilic character mainly their C-termini was observed in AcMRJPs family like those in *A. mellifera*. This indicates similarity in tertiary structures of these proteins.



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