

## CHAPTER 5

### CONCLUSION

In this research, proteins from *Bungarus candidus* venom were studied. Firstly, crude proteins were separated by sodium dodecyl sulfate polyacrylamide gel electrophoresis and ion exchange chromatography. The gel electrophoresis results showed protein profiles. There are 17 and 36 spots in silver stained gel and coomassie brilliant blue stained gel, respectively. Then, the spots in gel were tryptic digested and analyzed by MALDI-TOF MS. After that, peptide mass mapping was performed, the results of searched database were not reasonable.

*B. candidus* venom fraction number 6 and 8, the tryptic fragment which obtained from gel were further analyzed by peptide mass mapping technique. The results of searched database also were not reasonable. The N-terminal sequencing result of protein A has found 11 residues which is KTKI\_PEKD\_QKV. In addition, the N-terminal sequencing of protein B was NLINFMEMIRYT which has 12 residues. The result of peptide mass mapping of protein A, which analyzed by MALDI-TOF, was candoxin.

Furthermore, the tryptic fragments of protein A were sequenced by ESI-Q-TOF. The amino acid sequences of three peptides are VCASGEK, YCFKESWR and EARGTR, which same as the eighteenth to thirty eighth amino acids residues from N-terminal of candoxin. In addition, another chymotryptic fragment, CCTTDDCN, was seemed to be the fifty ninth to sixty sixth amino acid residues of candoxin. The percentage of identity was 45.5%. However, the result of N-terminal sequencing was not matched with candoxin. It might be a new protein. Therefore, further analysis of this protein is required to perform a full sequence.