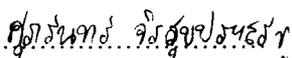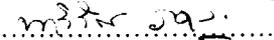172821

SUPPARIN JIRASUKPRASERT: THE ANALYSIS OF GENETIC VARIATIONS OF *Trypanosoma evansi* BY POLYMERASE CHAIN REACTION. THESIS ADVISOR: NAREERAT VISESHAKUL, Ph.D., THESIS COADVISOR: ASSOC. PROF. KOSUM CHANSIRI, Ph.D. 75 pp. ISBN 974-17-6039-6

Surra in animals is a result of infection by the protozoan *Trypanosoma evansi*, a haemoflagellated parasite. The disease shows considerable diversity of clinical signs from a mild chronic infection in dogs or swine to the fatally acute disease in horses. In this study, we genetically characterized four isolates and one cloned *T. evansi* in Thailand by three molecular approaches. Aims are to develop the method of genetic identification of *T. evansi* using VPh03 which was isolated from the infected horse. Firstly, the 511 bp sequences of the ITS1 region have been analyzed phylogenetically compared to the *T. evansi* sequences retrieved from GenBank database. Results showed that the Thai isolates were clustered into a group of at least five genotypes. Secondly, the method of Amplification Fragment Length Polymorphisms (AFLP) was developed. Using primer 122-2/122 in the AFLP reaction was able to detect the genetic variations showing a banding pattern on the agarose gel electrophoresis. Lastly,
*T. evansi* parasites from VPh03 was cloned and subsequently passed onto mice up to three passages. By all means, cloned VPh03 comprised at least four genotypes, f, g, j and k, analyzed by the ITS1 region. However, there are only two AFLP fingerprint patterns detected. By using all methods and although there were no correlations between ITS1 sequences and the AFLP pattern, our conclusion is that VPh03 is a mixture of at least four *T. evansi* populations. Moreover, genotype f is the major population among Thai isolates.

| | |
|---|---|
| Department Veterinary Pathology | Student's signature......................... |
| Field of study Veterinary Pathobiology | Advisor's signature......................... |
| Academic Year 2005 | Co-advisor's signature..................... |