

Pacharathon Simking 2014: Molecular Epidemiology of *B.bovis* and *B.bigemina* Infections of Cattle and Buffaloes in Thailand. Doctor of Philosophy (Agricultural Biotechnology), Major Field: Agricultural Biotechnology, Interdisciplinary Graduate Program. Thesis Advisor: Associate Professor Sathaporn Jittapalapong, Ph.D. 100 pages.

Bovine babesiosis is an important tick – borne disease that has an impact on economic losses and animal health due to increase mortality and production losses. This disease in cattle is caused by *Babesia bovis* and *B.bigemina* and transmitted by tropical cattle tick, *Rhipicephalus microplus*. The objectives of this study were to investigate the prevalence and factors associated with *B.bovis* and *B.bigemina* infection of cattle and buffaloes, and to analyze genetic diversity and phylogenetic of *B.bovis* and *B.bigemina* distributed in all areas of Thailand. A total of 2,685 blood samples were collected from dairy and beef cattle, and water buffaloes in the high populated areas, and screened by nested PCR (nPCR) using *B.bovis* SBP 2 gene and *B. bigemina rap1 -  $\alpha$*  gene. The risk factors associated with *Babesia* infection including provinces, regions, herd and age were statistical analyzed. The overall infection of *B.bovis* and *B.bigemina* infection were 7.6% (204/2,685) and 11.2% (300/2,685) respectively. Beef cattle had the highest infection for both organisms and the host speciation showed significant relationship in both *Babesia* spp. ( $p < 0.01$ ). In addition, the high prevalence of *Babesia* spp infection was found in animals under 1 year (31%, 35/113) and this factor characterized as one of the risk factor of *Babesia* infection in the animals. The phylogenetic analysis of *B.bigemina* using *rap - 1  $\alpha$*  gene and *B.bovis* using SBP2 gene showed the cluster of *Babesia* isolation in Thailand were grouped within the host species. Additional analysis of B cell epitope prediction of MSA – 2b gene of *B.bovis* indicated that the polymorphism of this major surface antigen might influence the *Babesia* infection.

---

Student's signature

---

Thesis Advisor's signature