

ARTHROPOD VECTORS FOR GENUS *RICKETTSIA* AND *BORRELIA* IN EASTERN REGION OF THAILAND BY MOLECULAR TECHNIQUES**KAMONWAN SIRIWATTHANAKUL 5536618 PPHP/M****M.Sc. (PUBLIC HEALTH) PROGRAM IN INFECTIOUS DISEASES AND EPIDEMIOLOGY****THESIS ADVISORY COMMITTEE: CHAKRIT HIRUNPETCHARAT, Ph.D. (TROPICAL HEALTH), CHARNCHUDHI CHANYASANHA, Ph.D. (MEDICAL SCIENCE), JARIYANART GAYWEE, Ph.D. (MOLECULAR MICROBIOLOGY).****ABSTRACT**

Arthropod-borne diseases are difficult to prevent and control due to variety factors involving disease transmission. Gaining insight of specific arthropod vector species harboring specific strains of pathogens in particular area will allow public health stakeholders to adopt effective measures for disease prevention and control. In recent years, several outbreaks of mite borne Scrub Typhus emerged in the eastern Thailand. This region is extraordinary since it is the closest border area to the capital city with diverse important land uses. To establish an effective disease prevention and control, it is necessary to investigate for the vectors of arthropod borne diseases in this area. This study aims to survey for the presence of *Rickettsia* and *Borrelia* pathogens in blood sucking arthropods in the eastern region of Thailand and to subsequently generate risk area maps. A survey of 180 locations in 7 provinces in eastern Thailand resulted in a collection of 421 blood sucking arthropod obtained from pets, poultry, livestock and rodents in 167 locations. Six species of ticks (*Rhipicephalus sanguineus*, *R. haemaphysaloides*, *Dermacentor* sp., *Haemaphysalis* sp., *Boophilus microplus* and *Ixodes* sp.), 3 species of fleas (*Ctenocephalides felis orientis*, *C. felis felis* and *Echidnophaga gallinacean*) and 6 species of lice (*Chelopistes meleagridis*, *Haematopinus eurysternus*, *Heterodoxus spinigerum*, *Liperus caponis*, *Menopon gallinae* and *Trichodectes canis*) were identified. Using real-time PCR, *Rickettsia* 17 kDa and *Borrelia* 23S rRNA were detected in 187 (44.4%) and 1 (0.2%) of total 421 pools, respectively. Of 217 tick pools, 44 (20.3%) were positive for *Rickettsia* and 1 (0.5%) was positive for *Borrelia*. Only rickettsial DNA was detected in 128/158 (81.0%) flea pools and 14/46 (30.4%) louse pools. Sequence analysis of one *Borrelia* detected in *Ixodes* ticks collected from a rat in Chanthaburi province was pathogenic *Borrelia valaisiana* strain QX-S13. Furthermore, sequencing results of 24 detected rickettsiae demonstrated pathogenic *Rickettsia marmionii* in 4 *R. sanguineus* ticks collected from dogs in Chanthaburi and Chonburi provinces and 20 *Rickettsia felis*, *Cf1* and *Cf5* infected *R. sanguineus* and *C. felis orientis* collected from dogs in 7 provinces of eastern Thailand. The survey results clearly demonstrated the presence of *Rickettsia* and *Borrelia* vectors. The geographical risk maps were subsequently generated to conveniently use as tool for epidemiological warning of arthropod borne disease threatening in those areas.

KEY WORDS: *RICKETTSIA*/ *BORRELIA*/ARTHROPOD-BORNE DISEASES

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