

Investigation Of Rickettsial Vectors And Reservoir Hosts In Military Areas Of Operation (Aos) Along Thai Borders

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Rickettsioses, febrile diseases caused by rickettsiae, are reported in troops deployed to military areas of operation (AOs) along Thai borders. These pathogens are intracellular bacteria maintained in nature via mammalian hosts and blood sucking arthropod vectors. To understand how these pathogens transmit to human, we investigated reservoir hosts and vectors of rickettsiae in those AOs. Arthropods were collected from wild captured rodents, pet animals and human in AOs along Thai-North Cambodia border and Northern Thai-Myanmar border. Molecular methods were utilized to detect and identify rickettsial agents in arthropod specimens. During April to September 2008, total 96 arthropod clones were collected. Twelve species of fleas, lice, and ticks were identified. Rickettsial gene was detected in 80.7% and 71.8% of arthropods from Northern Thai-Myanmar border and from Thai-North Cambodia border, respectively. *Orientia tsutsugamushi* DNA was not detected. Species of pathogenic rickettsiae identified by sequence analysis were *Rickettsia japonica*, *R. rickettsii* and *R. massiliae*. Those rickettsiae were detected in ticks (*Dermacentor* sp., *Rhipicephalus* sp. and *Haemaphysalis* sp.) collected from human and dogs. *R. marmionii* KB was detected in flea, *Echidnophaga gallinacean*. Spotted fever group rickettsia sp. similar to *Rickettsia* sp. cf1, cf5 and *Rickettsia* sp. SE313 were also detected in fleas (*Ctenocephalides canis*, *C. felis* and *E. gallinacea*), and lice (*Liperus caponis*, *Menopon gallinae* and *Haematopinus asini*) collected from dogs, cats, cattle and chickens. Our finding indicated these AOs are endemic foci for rickettsioses. This information is crucial to establish an effective disease prevention and control strategy specific to such areas.

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