

Prevalence and diversity of *Bartonella species* in ectoparasites from wild-caught rodents and domestic animals in the Northern and Northeastern regions of Thailand

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Ectoparasites are thought to be the important vectors of *Bartonella* transmission among animals, including humans. The *Bartonella* prevalence and species diversity in several types of ectoparasites (ticks, fleas, chiggers, and lice) collected from rodents and domestic animals (cats, dogs, cattle, and chickens) were investigated in this study. The surveillance study was conducted in 2 regions, 4 provinces; 2 provinces from the Northern region (Nan and Mae Hong Son) and 2 provinces from the Northeastern region (Loei and Nong Bua Lam Phu) during September 2013 to October 2014. Overall, a total of 539 pooled ectoparasites (102 fleas pools, 80 ticks pools, 6 lice pools, and 351 chiggers pools) were collected from wild-caught rodents and a total of 650 pooled ectoparasites (384 fleas pools, 213 ticks pools and 53 lice pools) were collected from domestic animals. Real-time PCR assay with TaqMan probe targeting *Bartonella*-specific *ssrA* gene was used for *Bartonella* DNA detection. Amplification of *Bartonella gltA* gene was confirmed using published primers, CS443f and CS1210r. Fleas were the major ectoparasites collected from domestic animals (59.0%), followed by ticks (32.8%), and lice (8.2%). Chiggers were the most common ectoparasites collected from rodents (65.1%), followed by fleas (18.9%), ticks (14.9%) and lice (1.1%). *Bartonella* DNA was detected in all ectoparasites types. Among ectoparasites collected from rodents, the

highest prevalence of *Bartonella* DNA was found in fleas pools (24.5%, 25/102), then in lice pools (16.7%, 1/6) and ticks pools (12.5%, 10/80), respectively. However, low prevalence of *Bartonella* DNA was found in chiggers pools (2.8%, 10/351). Likewise, high prevalence of *Bartonella* DNA was also found in fleas pools collected from domestic animals (14.1%, 54/381), while low prevalence was found in lice pools (5.7%, 3/53) and tick pools (6.6%, 14/213). Phylogenetic analysis of *Bartonella gltA* sequences (638 bp) presented the diverse range of *Bartonella* species found in ectoparasites collected from rodents including 4 *Bartonella* species in *B. elizabethae* species complex (*B. elizabethae*, *B. tribocorum*, *B. rattimassiliensis*, and *B. queenslandensis*), *B. rochalimae* and *Candidatus B. thailandensis*. However, only 2 species (*B. clarridgeiae* and *B. tamiae*) was detected in ectoparasites collected from domestic animals. Our data showed an important role of ectoparasites as potential vectors for *Bartonella* transmission among rodents and domestic animals residing in close association with humans.

Speaker Biography

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