Short Report: Molecular Detection of *Rickettsia felis*, *Bartonella henselae*, and *B. claridgeiae* in Fleas from Domestic Dogs and Cats in Malaysia

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Abstract. The presence of *Rickettsia felis*, *Bartonella henselae* and *B. claridgeiae* in 209 fleas (*Ctenocephalides felis*) obtained from domestic cats and dogs in several locations in Malaysia was investigated in this study. Using a polymerase chain reaction specific for the citrate synthase (*gltA*) and 17-kD antigenic protein (*17kD*) genes of rickettsiae, we detected *R. felis* DNA in 6 (2.9%) fleas. For detection of bartonellae, amplification of the heme-binding protein (*pap31*) and riboflavin synthase (*ribC*) genes identified *B. henselae* and *B. claridgeiae* DNA in 24 (11.5%) and 40 (19.1%) fleas, respectively. The DNA of *B. henselae* and *B. claridgeiae* was detected in 10 (4.8%) fleas. Two *B. henselae* genogroups (Marseille and Houston-1) were detected in this study; genogroup Marseille (genotype Fizz) was found more often in the fleas. The findings in this study suggest fleas as potential vectors of rickettsioses and cat-scratch disease in this country.

Fleas are hematophagous arthropods that serve as vectors of several bacterial pathogens including *Yersinia pestis*, *Rickettsia typhi*, *R. felis*, and *Bartonella henselae*, which are the etiologic agents of plague, murine typhus, flea-borne ricketsioses, and cat-scratch disease, respectively. Murine typhus is primarily maintained by the rat flea *Xenopsylla cheopis.* 1-3 However, the cat flea *Ctenocephalides felis* is also a competent vector. 4 *R. felis* is maintained and biologically transmitted by *C. felis.* 4 The rickettsiae were initially recognized as a member of the spotted fever group (SFG), but have been recently placed in the transitional group, a fourth phylogenetic lineage within the genus *Rickettsia.* 4, 5 The clinical manifestation of *R. felis* infection in human involves an acute systemic infection that is typified by fever, maculopapular rash, and headache, similar to those of murine typhus and other febrile illnesses, such as dengue, in the tropics. 5

In recent years, *B. henselae* and *B. claridgeiae* have been recognized as two emerging pathogens of veterinary and medical interest. *Bartonella* organisms are parasites of mammalian erythrocytes and endothelial cells that are transmitted by ticks, fleas, lice, and flies. 6 Investigation of the population structure of these organisms is essential because of the association of the organisms with a variety of clinical syndromes and a complex host/reservoir system. 7 Based on the polymorphisms of the heme-binding protein (*pap31*) gene, *B. henselae* isolates are clustered into two genogroups: Marseille, which includes genotypes Marseille, Fizz, and CAL-1, and Houston-1, which includes genotypes Houston-1, SA-2, 90-615, and ZF-1. 8

In Malaysia, data on the presence of human pathogens in the fleas are not available. A serosurvey demonstrated a high prevalence of antibody to SFG rickettsiae in Malaysian febrile patients. 9 However, the specific etiologic agent of spotted fever is yet to be determined because it has not been isolated from any human sample.

Briefly, each flea was immersed in 100 μL of 0.7 M ammonium hydroxide and boiled for 20 minutes. The DNA extracted was then resuspended in 10 μL of sterile distilled water prior to amplification.

Polymerase chain reactions (PCRs) specific for the citrate synthase (*gltA*) and 17-kD antigenic protein (*17kD*) genes of rickettsiae were performed for each flea sample. For detection of bartonellae from fleas, amplification of the heme-binding protein (*pap31*) gene of *B. henselae* and riboflavin synthase (*ribC*) gene of *B. claridgeiae* was conducted. All PCRs assays (25 μL) were performed in a My Cycler™ thermal cycler (Bio-Rad Laboratories, Hercules, CA) by adding 2 μL of DNA template to 19.55 μL of sterile distilled water, 2.5 μL of 10× DreamTaq™ buffer, 0.5 μL of dNTPs (100 μM), 0.1 μL of each primer (100 μM), and 0.25 μL of DreamTaq™ DNA Polymerase (5 U/μL). Amplicons were purified by using the LaboPass PCR Purification Kit (Cosmo Genetech, Seoul, South Korea) before sequencing in both directions by using respective PCR primers.

Findings for detection of *R. felis*, *B. henselae*, and *B. claridgeiae* DNA in fleas obtained in this study are shown in Table 1. Genes encoding citrate synthase and 17-kD antigenic protein of rickettsiae were successfully amplified from six fleas obtained from two dogs and a cat from one of the sampling sites (Ampang). The *gltA* sequences obtained were similar to previously reported sequence of *R. felis* URRWCa2 (GenBank accession no. CP000053), except for three nucleotide changes. However, the sequences were identical with that of *Rickettsia* sp. RF2125 (GenBank accession no. AF516333), a genotype closely related to *R. felis*, which has been reported from different arthropod vectors in various regions: *Echidnophaga gallinacea* in Egypt, 14 *Archeopsylla erinacei* in Algeria, 15 *C. felis* at the Thailand–Myanmar border, 16 and *Pulex irritans* in Hungary. 17 In addition, the *17kD* sequences obtained in this study were identical with *Rickettsia* sp. RF2125, which was detected in fleas obtained from the United States, 9 Peru, 19 and Uruguay. 20 Although existing data suggest a worldwide distribution of *Rickettsia* sp. RF2125, the pathogenic role of this organism has yet to be determined because it has not been isolated from any human sample.

*Bartonella henselae* DNA was detected in 28 (13.4%) fleas in this study. Analysis of *pap31* sequences differentiates the bartonellae into two *B. henselae* genogroups. A total of
10 (35.7%) and 18 (64.3%) \textit{B. henselae} in this study were identified as genogroup Houston-1 (all were genotype Houston-1), and genogroup Marseille (all were genotype Fizz), respectively (Table 1). \textit{Bartonella clarridgeiae} DNA was detected in 40 (19.1%) fleas. Analysis of \textit{ribC} demonstrated matching sequences of the Bartonella with that of \textit{B. clarridgeiae} strain 73 (GeneBank accession no. AJ236916, between positions 434 and 1185). The DNA of \textit{B. henselae} and \textit{B. clarridgeiae} was detected in 10 (4.8%) fleas. In addition, \textit{B. clarridgeiae} was the predominant Bartonella detected in fleas from Ampang compared with \textit{B. henselae}, which was detected more frequently in fleas from two other sampling sites (Table 1). Collectively, the prevalence of bartonellae (11.5%) in fleas was higher than that of \textit{R. felis} (2.9%) in this study.

Our finding provides molecular evidence on the type of rickettsiae and bartonellae in Malaysia. Up to now, no clinical cases attributed to \textit{R. felis} and \textit{Bartonella} species have been reported in Malaysia. These infections may present as under-recognized causes of acute febrile illness because of their lack of clinical suspicions and appropriate laboratory tests. With the detection of \textit{SFG rickettsiae} was assessed by using 

<table>
<thead>
<tr>
<th>Sampling sites</th>
<th>No. (%) fleas examined</th>
<th>No. (%) fleas positive for \textit{R. felis}</th>
<th>Genotype Houston-1</th>
<th>Genotype Fizz</th>
<th>No. (%) fleas positive for \textit{B. clarridgeiae}</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kuala Nerang (6°15′0″N, 100°36′0″E)</td>
<td>57 (27.3)</td>
<td>0 (0)</td>
<td>5 (8.8)</td>
<td>10 (17.5)</td>
<td>12 (21.1)</td>
</tr>
<tr>
<td>Pendang (6°0′0″N, 100°28′0″E)</td>
<td>16 (7.6)</td>
<td>0 (0)</td>
<td>0 (0)</td>
<td>8 (50.0)</td>
<td>5 (31.3)</td>
</tr>
<tr>
<td>Ampang (3°9′0″N, 101°46′12″E)</td>
<td>136 (65.1)</td>
<td>6 (4.4)</td>
<td>0 (0)</td>
<td>1 (0.7)</td>
<td>23 (16.9)</td>
</tr>
<tr>
<td>Total</td>
<td>209 (100)</td>
<td>6 (2.9)</td>
<td>5 (2.4)</td>
<td>19 (9.1)</td>
<td>40 (19.1)</td>
</tr>
</tbody>
</table>

for the surveillance, prevention and control of rickettsioses and bartonelloses in Malaysia.

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