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26 **Abstract**

27 *Bartonella* species, intracellular parasite of erythrocytes and endothelial cells, are  
28 zoonotic pathogens of wild and domestic animals including rodents. Many species of rodents  
29 are commensally infected with a few *Bartonella* species in Asia. However, there are only few  
30 reports on detection of *Bartonella* in Thailand. Our objective was to detect the presence of  
31 *Bartonella* species in rodents from Thailand. Among 247 rodents captured in five provinces  
32 from Thailand we identified *Bartonella* species using molecular methods targeting 3 genes i.e  
33 citrate synthase (*gltA*),  $\beta$ -subunit of the RNA polymerase (*rpoB*) and cell division protein  
34 gene (*ftsZ*) and the 16-23S rRNA intergenic spacer (ITS). Overall, we found 21 rodents being  
35 infected with a *Bartonella* species including 7 *B. coopersplainsensis*, 4 *B. phoceensis*, 6 *B.*  
36 *queenslandensis*, 1 *B. rochalimae*, 1 *Bartonella* sp. RN24BJ and 2 genotypes of a new  
37 *Bartonella* that we propose to give the provisional status “*Candidatus* *Bartonella*  
38 *thailandensis*”. To the best of our knowledge, these *Bartonella* species have been detected for  
39 the first time in Thailand.

40 **Keywords:** *Candidatus* *Bartonella* thailandensis, rodent

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## 51 1. Introduction

52 *Bartonella* species are intracellular parasites of erythrocytes and endothelial cells of  
53 several animals including rodents, ruminants, cats and dogs. *Bartonella* species are considered  
54 emerging pathogens in humans. A wide range of mammalian reservoir hosts including rodent  
55 and arthropod vectors have been involved in the natural cycle of various *Bartonella* spp. The  
56 persistent bacteremia is more readily documented in the primary reservoir species and may  
57 occur less frequently or to a much lower level in accidental hosts. In the natural host, clinical  
58 manifestation of the infection may be minimal or unrecognized (Chomel et al., 2003). Some  
59 *Bartonella* species such as *B. elizabethae*, *B. grahamii*, *B. vinsonii* subsp. *arupensis* and *B.*  
60 *washoensis* have been isolated from humans and linked to a rodent reservoir (Ellis et al.,  
61 1999; Kosoy et al., 2003). The close relation between rodents and humans throughout the  
62 world makes the study of rodent-borne *Bartonella* essential to determine the extent to which  
63 rodents may serve as a source of human infections (Castle et al., 2004).

64 *Bartonella* species associated with animals and fleas have been recovered in Asia  
65 (Ying et al., 2002; Parola et al., 2003; Castle et al., 2004), Australia (Fournier et al., 2007;  
66 Gundi et al. in press) and Europe (Gundi et al., 2004). Different species of mice (*Apodemus*  
67 spp., *Mus* spp.), rodents (*Bandicota* spp., *Eothenomys* spp., *Rattus* spp.), shrews (*Crocidura*  
68 spp., *Sorex* spp) and voles (*Microtus* spp., *Clethrionomys* spp.) also act as a primary  
69 vertebrate reservoir of *Bartonella* species that were reported in Asia (Table 1). There are only  
70 a few reports on detection of *Bartonella* in Thailand. Castle et al. (2004) reported a prevalence  
71 of 9% in *Bandicota indica* and *Rattus* spp. in Chiangrai, Thailand and Parola et al. (2003)  
72 identified *Bartonella* BNFs in flea (*Nosopsyllus fasciatus*) collected from *Rattus surifer* in  
73 Kanchanaburi province, on the Thai-Myanmar border. The newly described *B. tamiae*  
74 pathogen was isolated from human patients in Thailand (Kosoy et al., 2008) while *B. henselae*  
75 was recently isolated from biopsy skin lesions of bacillary angiomatosis (Paitoonpong et al.,

76 2008). The objective of our study was to detect the presence of *Bartonella* species from  
77 rodents captured in Thailand by using molecular tools to identify the species.

## 78 **2. Materials and methods**

### 79 *2.1. Study area*

80 During May and July 2005, rodents were captured in five districts of Thailand near  
81 Myanmar (Sangkhlaburi district, Kanchanaburi province; Pobphra district, Tak province),  
82 near Laos PDR (Ponepisai district, Nongkhai province) and near Cambodia (Pongnamron  
83 district, Chanthaburi province; Sangkha district, Surin province). The localities of study sites  
84 were rice paddies, forests and plantations where populations were mainly made up of farmers.  
85 Everyday, 200 wire mesh traps were put following rodent signs, rodent burrow, feces  
86 footprint or rodent runway from 6 p.m. to 6 a.m. The traps were set up for 5 days in each  
87 province. This study was conducted on the animal welfare by the authority of National  
88 Institute of Health, Thailand.

### 89 *2.2. Samples preparation*

90 Each animal was identified before being euthanased. Blood samples were collected,  
91 separated by centrifugation and total genomic DNA were extracted using NucleoSpin Blood  
92 Kit (Macherey-Nagel GmbH, Germany) and kept at -20°C. Samples were handled under  
93 sterile conditions to avoid the risk of cross-contamination.

### 94 *2.3. Samples analysis*

95 The DNA samples were screened for the presence of *Bartonella* spp. by the use of a  
96 real-time quantitative PCR targeting the 23S rRNA gene with Taqman probe. The primers and  
97 probe using in this study were: Barto23SF, 5'-GAGTAAGTGGTAGCGGAGCG-3';  
98 Barto23SR, 5'-GCCGACTCACCTGCTCAG-3' and Barto23Sprobe, 6-FAM-  
99 GAGAGCTCCTGGAGGTATCGGAAG-TAMRA; size of the PCR product was 172 bp.  
100 Positive samples at screening were further studied by PCR amplification and DNA

101 sequencing of 3 genes including citrate synthase (*gltA*) (Birtles and Raoult. 1996),  $\beta$ -subunit  
102 of the RNA polymerase (*rpoB*) (Renesto et al., 2001) and cell division protein gene (*ftsZ*)  
103 (Zeaiter et al., 2002) and 16S-23S rRNA intergenic spacer (ITS). Sequencing of PCR  
104 products were carried out using the BigDye Terminator Cycle sequencing Ready Reaction  
105 (ABI PRISM, Applied Biosystems) and sequences obtained were compared to those available  
106 in GenBank. Phylogenetic relationships among the studied Bartonellae were inferred from  
107 sequence alignment from concatenated gene sequences using the maximum parsimony and  
108 neighbor-joining methods within the MEGA version 4.1 software package.

### 109 **3. Results**

#### 110 *3.1. Rodent species and prevalence of Bartonella infection*

111 A total of 247 rodent samples representing nine species within three different genera  
112 were collected and identified during the study including 2 species of bandicoot rats  
113 (*Bandicota* spp.), mouse (*Mus* spp.) and 6 species of rats (*Rattus* spp.) (Table 1).

114 Overall, the prevalence of *Bartonella* was 12.7% (17 of 134) in the provinces on the  
115 border of Cambodia, 3.7% (2 of 54) in the provinces on the border of Myanmar and 3.4% (2  
116 of 59) in the province on the border of Laos PDR as determined using our *Bartonella* genus  
117 RT-PCR. *Bartonella* DNA was detected in 6 rodent species: *B. savilei*, *M. cervicolor*, *R.*  
118 *berdmorei*, *R. exulans*, *R. rattus* and *R. surifer* (Table 1).

#### 119 *3.2. Bartonella identification*

120 Using standard PCR and sequencing of all four loci: *gltA*, *rpoB*, *ftsZ* and ITS, we  
121 identified the presence of 7 *B. coopersplainsensis*, 4 *B. phoceensis*, 6 *B. queenslandensis*, 1 *B.*  
122 *rochalimae*, 1 *Bartonella* sp. RN24BJ previously identified from *R. norvegicus* and 2  
123 genotypes of a new *Bartonella* in *R. surifer*. The percentage similarity of DNA sequences  
124 from known *Bartonella* species ranged from 96 to 97% on *gltA*, 96 to 97% on *ftsZ* and 96 to  
125 98% on *rpoB*. Among known validated species, the two new species shared 90.1 to 90.2%

126 homology with *B. phoceensis* for partial *rpoB*, 90.3 to 90.9% homology with *B. washoensis*  
127 for *ftsZ* and 92.0 to 92.6% homology with *B. grahamii* for *gltA* gene. The GenBank accession  
128 numbers for this new species are as follows: FJ411481 (*ftsZ*), FJ411482 (*gltA*), FJ411483  
129 (*rpoB*), FJ411484 (ITS) and FJ411485 (ITS).

130 According to the current knowledge, newly encountered *Bartonella* strains should be  
131 considered a new species if a 327-bp *gltA* fragment and a 825-bp *rpoB* fragment share  
132 <96.0% and <95.4% sequences similarity with those of the validated species as in the current  
133 case. We propose for this new *Bartonella* species the provisional name “*Candidatus B.*  
134 *thailandensis*” since it was first detected in rodents from Thailand. Figure 2 shows the  
135 phylogenetic position of this new species among members of the genus *Bartonella* based on  
136 comparisons of concatenated sequences of 4 genes.

#### 137 4. Discussion

138 We present in this study the molecular detection of *Bartonella* species detected in  
139 rodents from Thailand. Although blood culture is more sensitive and warranted in order to  
140 obtain isolates, this was not possible in this study and should be done in the future. We have  
141 used the current molecular criteria previously published for detection, identification and  
142 discrimination of bacteria of the genus *Bartonella* (La Scola et al., 2003). These are only few  
143 reports on detection of *Bartonellae* in animals from Thailand (Parola et al., 2003; Castle et al.,  
144 2004). The overall percentages of infected rodents in our study (8.5%) was similar to that of  
145 Castle et al. (2004) who found a prevalence of 9% in rodents (*B. indica*, *R. rattus* and *R.*  
146 *losea*) trapped from Chiangrai province in northern part of Thailand (Castle et al., 2004).  
147 However, the *Bartonella* species detected in the present study were clearly different from  
148 Castle et al. (2004) since these species have never been reported in Thailand before. In this  
149 previous report, phylogenetic analysis of *Bartonella* species isolated in rodents indicates that  
150 isolates from *B. indica* represent a new *Bartonella* species and those from *Rattus* spp. were



151 closely related to *B. elizabethae* and *B. grahamii* (Castle et al., 2004). However, we have  
152 detected in the present study for the first time other *Bartonella* species previously detected in  
153 other studies including *B. phoceensis* (previously isolated from *R. norvegicus* in the city of  
154 Marseille, France) (Gundi et al., 2004), *B. rochalimae* (previously isolated in a woman with  
155 fever, bacteremia and splenomegaly in Peru) (Eremeeva et al., 2007), *B. cooperplainsensis*  
156 and *B. queenslandensis* (previously isolated in Australian rats, Gundi et al., in press) and  
157 *Bartonella* sp. RN24BJ (previously detected in *R. norvegicus* in China, Li et al, unpublished  
158 data). In this study, we have found *B. phoceensis* from 4 rodents (2 samples *R. rattus* of which  
159 1 from Kanchanaburi and 1 from Nongkhai provinces; 2 samples *R. surifer* from Surin  
160 provinces) as previously reported in Asia (Ying et al., 2002; Inoue et al., 2008; Lin et al.,  
161 2008). However we have not detected in our study either the newly described *B. tamiae*  
162 pathogen isolated from human patients from Khon Kaen province, Thailand (Kosoy et al.,  
163 2008) or *B. henselae* isolated from a case of bacillary angiomatosis (Paitoonpong et al., 2008).  
164 On the other hands, Parola et al. (2003) identified a new genotype of *Bartonella* spp.  
165 (*Bartonella* BNfRs) from a *Nosopsyllus fasciatus* specimen collected on a rat (*R. surifer*) from  
166 the Thai-Myanmar border that was not detected in our study. Conversely, phylogenetic  
167 analysis in of concatenated sequences this study indicates that two rodents (*R. surifer*<sub>6</sub> and *R.*  
168 *surifer*<sub>12</sub>) were likely infected with a new genotype of *Bartonella* that we propose to give the  
169 provisional status “*Candidatus B. thailandensis*” according to Murray and Stackerbrandt  
170 (1995) guidelines. According to the current molecular criteria from La Scola et al. (2003), our  
171 sequences obtained from these 2 rodents fulfilled the criteria for a new *Bartonella* species (La  
172 Scola et al., 2003).

173 The epidemiological importance of rodent-borne *Bartonella* spp. as a cause of disease  
174 in animals and humans is emerging, as suggested for a novel rodent *Bartonella*-associated  
175 febrile illness in the rural southwestern USA, based on serological evidence (Boulouis et al.,

176 2005; Iralu et al., 2006). At present, only a limited number of human infections caused by  
177 rodent-borne *Bartonella* species have been reported such as *B. elizabethae*, *B. grahamii*, *B.*  
178 *vinsonii* subsp. *arupensis*, *B. washoensis*. Further studies are required to determine if rodents  
179 could be another natural reservoir of *Bartonella* species i.e *B. rochalimae* identified from *R.*  
180 *norvegicus* in Taiwan (Lin et al., 2008). Further investigations are warranted in order to  
181 isolate these new *Bartonella* species and to determine if they can cause any clinical  
182 manifestations related to unknown diseases in Thailand. However, previous experience has  
183 shown that *Bartonella* species firstly detected or isolated in animals or arthropods could be  
184 later involved in humans. This was the case for example with *B. alsatica* firstly isolated from  
185 wild rabbits (Heller et al., 1999) and later identified as human pathogens in a heart valve of a  
186 patient with endocarditis (Raoult et al., 2006) and in a patient with cat scratch disease  
187 (Angelakis et al., 2008).

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#### 195 **References**

- 196 Angelakis, E., Lepidi, H., Canel-Atbir, M.A., Rispal, R., Perraudeau, F., Barre, I., Rolain,  
197 J.M., Raoult, D., 2008. Human case of *Bartonella alsatica* lymphadenitis. *Emerg. Infect.*  
198 *Dis.* 14, 1951-1952.
- 199 Birtles, R.J., Raoult, D., 1996. Comparison of partial citrate synthase gene (*gltA*) sequences  
200 for phylogenetic analysis of *Bartonella* species. *Int. J. Syst. Bacteriol.* 46, 891-897.

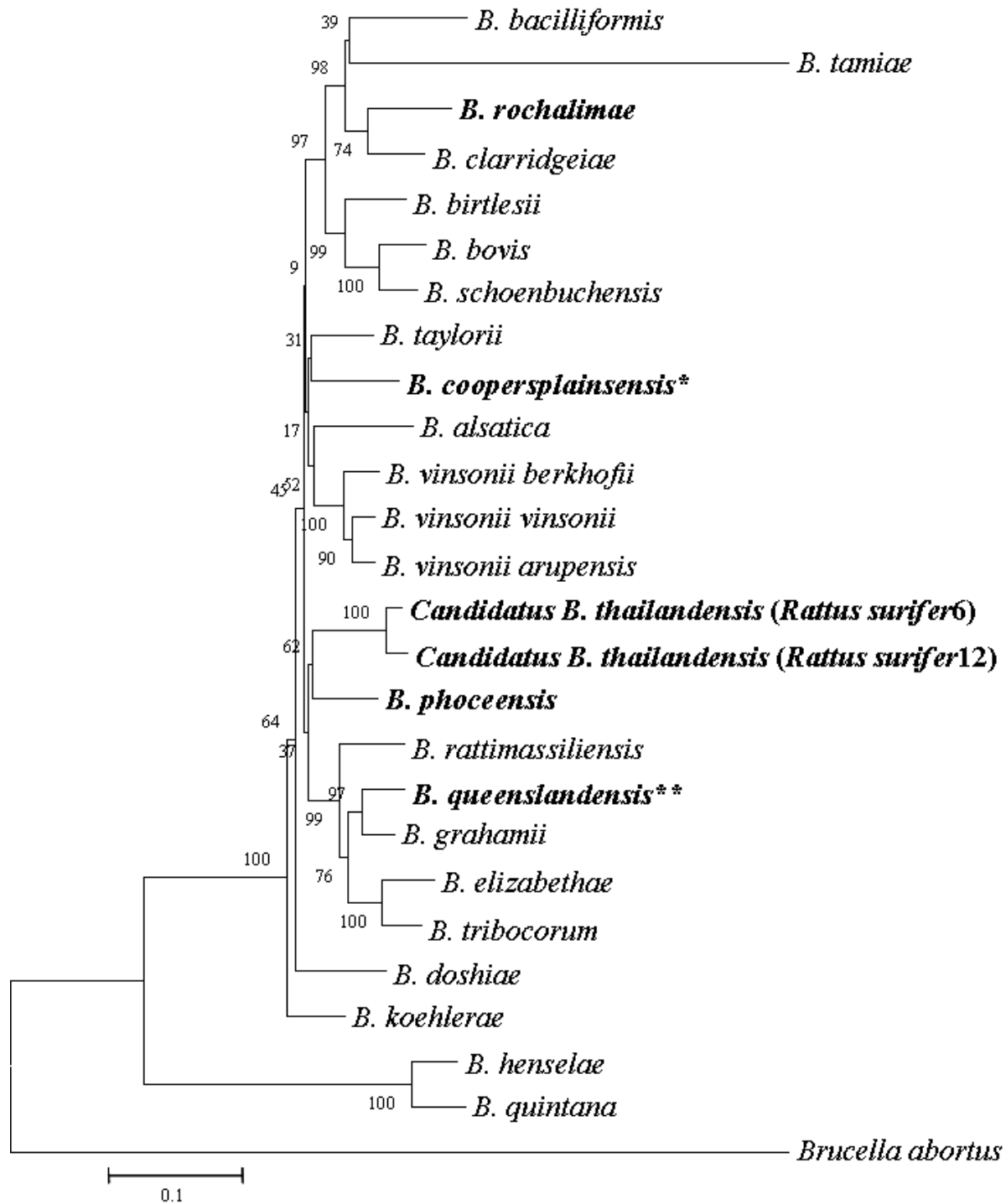
- 201 Boulouis, H.J., Chang, C.C., Henn, J.B., Kasten, R.W., Chomel, B.B. 2005. Factors  
202 associated with the rapid emergence of zoonotic *Bartonella* infections. *Vet. Res.* 36, 383-  
203 410.
- 204 Castle, K.T., Kosoy, M., Lerdthusnee, K., Phelan, L., Ying, B., Gage, K.L., Leepitakrat, W.,  
205 Monkanna, T., Khlaimanee, N., Chandranoi, K., Jones, J.W., Coleman, R.E., 2004.  
206 Prevalence and diversity of *Bartonella* in rodents of northern Thailand: a comparison with  
207 *Bartonella* in rodents from southern China. *Am. J. Trop. Med. Hyg.* 70, 429-433.
- 208 Chomel, B.B., Kasten, R.W., Sykes, J.E., Boulouis, H.J., Breitschwerdt, E.B. 2003. Clinical  
209 impact of persistent *Bartonella* bacteremia in humans and animals. *Ann. N.Y. Acad. Sci.*  
210 990, 267-278.
- 211 Ellis, B.A., Regnery, R.L., Beati, L., Bacellar, F., Rood, M., Glass, G.G., Marston, E.,  
212 Ksiazek, T.G., Jones, D., Childs, E., 1999. Rats of the genus *Rattus* are reservoir hosts for  
213 pathogenic *Bartonella* species: an Old World origin for a New World disease?. *J. Infect.*  
214 *Dis.* 180, 220-224.
- 215 Eremeeva, M.E., Gerns, H.L., Lydy, S.L., Goo, J.S., Ryan, E.T., Mathew, S.S., Ferraro, M.J.,  
216 Holden, J.M., Nicholson, W.L., Dash, G.A., Koehler, J.E., 2007. Bacteremia, fever, and  
217 splenomegaly caused by a newly recognized *Bartonella* species. *N. Engl. J. Med.* 356,  
218 2381-2387.
- 219 Fournier, P.E., Taylor, C., Rolain, J.M., Barrassi, L., Smith, G., Raoult, D., 2007. *Bartonella*  
220 *australis* sp. nov. from Kangaroos, Australia. *Emerg. Infect. Dis.* 13, 1961-1962.
- 221 Gundi, V.A., Davoust, B., Khamis, A., Boni, M., Raoult, D., La Scola, B., 2004. Isolation of  
222 *Bartonella rattimassiliensis* sp. nov. and *Bartonella phoceensis* sp. nov. from European  
223 *Rattus norvegicus*. *J. Clin. Microbiol.* 42, 3816-3818.
- 224 Gundi, V.A., Taylor, C., Raoult, D., La Scola, B., 2009. Identification of new *Bartonella*  
225 species in Australian rats: Description of *Bartonella rattaaustraliani* sp. nov., *Bartonella*

- 226 *queenslandensis* sp. nov., and *Bartonella coopersplainsensis* sp. nov. Int. J. Syst. Evol.  
227 Microbiol. (in press).
- 228 Heller, R., Kubina, M., Mariet, P., Riegel, P., Delacour, G., Dehio, C., Lamarque, F., Kasten,  
229 R., Boulouis, H.J., Monteil, H., Chomel, B.B., Piemont, Y., 1999. *Bartonella alsatica* sp.  
230 nov., a new *Bartonella* species isolated from the blood of wild rabbits. Int. J. Syst.  
231 Bacteriol. 49, 283-288.
- 232 Inoue, K., Maruyama, S., Kabeya, H., Yamada, N., Ohashi, N., Sato, Y., Yukawa, M.,  
233 Masuzawa, T., Kamori, F., Kadosaka, T., Takada, N., Fujita, H., Kawabata, H., 2008.  
234 Prevalence and genetic diversity of *Bartonella* species isolated from wild rodents in  
235 Japan. Appl. Environ. Microbiol. 74, 5086-5092.
- 236 Iralu, J., Bai, Y., Crook, L., Tempest, B., Simpson, G., McKenzie, T., Koster, F., 2006.  
237 Rodent-associated *Bartonella* febrile illness, southwestern United States. Emerg. Inf. Dis.  
238 12, 1081-1086.
- 239 Kosoy, M., Morway, C., Sheff, K.W., Bai, Y., Cloborn, J., Chalcraft, L., Dowell, S.F.,  
240 Peruski, L.F., Maloney, S.A., Baggett, H., Sutthirattana, S., Sidhirat, A., Maruyama, S.,  
241 Kabeya, H., Chomel, B.B., Kasten, R., Popov, V., Robinson, J., Kruglov, A., Petersen,  
242 L.R., 2008. *Bartonella tamiae* sp. nov., a newly recognized pathogen isolated from three  
243 human patients from Thailand. J. Clin. Microbiol. 46, 772-775.
- 244 Kosoy, M., Murray, M., Gilmore, R.D., Jr., Bai, Y., Gage, K.L., 2003. *Bartonella* strains from  
245 ground squirrels are identical to *Bartonella washoensis* isolated from a human patient. J.  
246 Clin. Microbiol. 41, 645-650.
- 247 La Scola, B., Zeaiter, Z., Khamis, A., Raoult, D., 2003. Gene-sequence-based criteria for  
248 species definition in bacteriology: the *Bartonella* paradigm. Trends. Microbiol. 11, 318-  
249 321.

- 250 Lin, J.W., Chen, C.Y., Chen, W.C., Chomel, B.B., Chang, C.C., 2008. Isolation of *Bartonella*  
251 species from rodents in Taiwan including a strain closely related to '*Bartonella*  
252 *rochalimae*' from *Rattus norvegicus*. J Med Microbiol 57, 1496-501.
- 253 Murray, R.G., Stackebrandt, E., 1995. Taxonomic note: implementation of the provisional  
254 status *Candidatus* for incompletely described prokaryotes. Int. J. Syst. Bacteriol. 45, 186-  
255 187.
- 256 Paitoonpong, L., Chitsomkasem, A., Chantrakooptungool, S., Kanjanahareutai, S.,  
257 Tribuddharat, C., Srifuengfung, S., 2008. *Bartonella henselae*: first reported isolated in a  
258 human in Thailand. Southeast. Asian. J. Trop. Med. Public. Health. 39, 123-129.
- 259 Parola, P., Sanogo, O.Y., Lerdtusnee, K., Zeaiter, Z., Chauvancy, G., Gonzalez, J.P., Miller,  
260 R.S., Telford, S.R.III., Wongsrichanalai, C., Raoult, D., 2003. Identification of *Rickettsia*  
261 spp, and *Bartonella* spp. in fleas from the Thai-Myanmar border. Ann. NY. Acad. Sci.  
262 990, 173-181.
- 263 Raoult, D., Roblot, F., Rolain, J.M., Besnier, J.M., Loulergue, J., Bestides, F., Choutet, P.,  
264 2006. First isolation of *Bartonella alsatica* from a valve of a patient with endocarditis. J.  
265 Clin. Microbiol. 44, 278-279.
- 266 Renesto, P., Gouvernet, J., Drancourt, M., Roux, V., Raoult, D., 2001. Use of *rpoB* gene  
267 analysis for detection and identification of *Bartonella* species. J. Clin. Microbiol. 39, 430-  
268 437.
- 269 Ying, B., Kosoy, M.Y., Maupin, G.O., Tsuchiya, K.R., Gage, K.L., 2002. Genetic and  
270 ecologic characteristics of *Bartonella* communities in rodents in southern China. Am. J.  
271 Trop. Med. Hyg. 66, 622-627.
- 272 Zeaiter, Z., Liang, Z., Raoult, D., 2002. Genetic classification and differentiation of  
273 *Bartonella* species based on comparison of partial *ftsZ* gene sequences. J. Clin. Microbiol.  
274 40, 3641-3647.

1

- 1 Figure 1. Neighbor-Joining concatenated tree of *rpoB*, *gltA*, ITS and *ftsZ* genes on Thai rodent  
 2 samples with known species of *Bartonella*.



- 3 GenBank accession numbers: *rpoB* (EU111792\*, EU111791\*\*); *gltA* (EU111803\*,  
 4 EU111802\*\*); ITS (EU111770\*, EU111769\*\*); *ftsZ* (EU111781\*, EU111780\*\*)

1 Table 1. Percentages of *Bartonella* infections in rodents within three neighboring provinces in Thailand, during May to June, 2005.

Rodent species	Province neighboring Cambodia		Province neighboring Myanmar		Province neighboring Laos	Total (Percentage of rodent infections)
	Chanthaburi	Surin	Kanchanaburi	Tak	PDR	
					Nongkhai	
No. of tested/positive ( <i>Bartonella</i> infection)	No. of tested/positive ( <i>Bartonella</i> infection)	No. of tested/positive ( <i>Bartonella</i> infection)	No. of tested/positive ( <i>Bartonella</i> infection)	No. of tested/positive ( <i>Bartonella</i> infection)		
<i>Bandicota indica</i>	6/0	4/0	8/0	1/0	1/0	20/0 (0)
<i>Bandicota savilei</i>	26/2	3/0	0/0	0/0	4/0	33/2 (6.06)
	(B. queenslandensis {1}, B. rochalimae {1})					
<i>Mus cervicolor</i>	0/0	0/0	0/0	2/1	0/0	2/1 (50)
				(B. queenslandensis {1})		
<i>Rattus berdmorei</i>	16/5	4/0	0/0	0/0	0/0	20/5 (25)
	(B. coopersplainsensis {4}, B. queenslandensis {1})					
<i>Rattus exulans</i>	1/0	1/0	1/0	21/0	45/1	69/1 (1.45)
				(Bartonella sp. RN24BJ {1})		
<i>Rattus fluscens</i>	7/0	0/0	0/0	1/0	0/0	8/0 (0)
<i>Rattus losea</i>	2/0	5/0	4/0	0/0	2/0	13/0 (0)
<i>Rattus rattus</i>	24/2	3/0	12/1	3/0	7/1	49/4 (8.16)
	(B. coopersplainsensis {2})		(B. phoceensis {1})		(B. phoceensis {1})	
<i>Rattus surifer</i>	2/0	30/8	1/0	0/0	0/0	33/8 (24.24)
		(B. coopersplainsensis {1}, B. queenslandensis {3}, B. phoceensis {2}, Candidatus B. thailandensis {2})				
Total (Percentage of infection)	84/9 (10.71)	50/8 (16)	26/1 (3.85)	28/1 (3.57)	59/2 (3.39)	