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PHYLOGENETIC ANALYSIS OF *BARTONELLA* DETECTED IN RODENT FLEAS IN YUNNAN, CHINA

Dong Mei Li,¹ Qi Yong Liu,^{1,3} Dong Zheng Yu,¹ Jian Zhong Zhang,¹ Zheng Da Gong,² and Xiu Ping Song¹

¹ Department of Vector Biology and Control, National Institute for Communicable Disease Control and Prevention, Chinese Center for Disease Control and Prevention P.O. Box 5, Changping, Beijing 102206, China

² Yunnan Institute of Endemic Diseases Control and Prevention, Dali City, Yunnan, China

³ Corresponding author (email: Liuqiyong@icdc.cn)

ABSTRACT: Previous studies have demonstrated a diversity of *Bartonella* spp. in rodent populations in Yunnan Province, China. Although *Bartonella* spp. have been isolated from cat fleas and cattle ticks collected from their animal hosts, little is known about *Bartonella* carried by rodent fleas. In this study, *Bartonella* DNA was detected by polymerase chain reaction (PCR) in two of five species of rodent fleas. These included *Xenopsylla cheopis* and *Ctenophthalmus lushiensis*, which were collected from *Rattus tanezumi flavipectus* and from the nests of voles, respectively, during 1997 from two sites in western Yunnan Province, China. Sequence analysis of the *Bartonella* citrate synthase gene (*gltA*) amplicons obtained from six of 65 grouped flea samples showed that *Bartonella* genetic variants were clustered in four groups. One from *Xenopsylla cheopis* was identical to *Bartonella tribocorum*, whereas the other three genotypes from *Ctenophthalmus lushiensis* were related to the vole-associated *Bartonella* isolates and cat-associated *Bartonella clarridgeiae*. This is the first detection of this *Bartonella* variant from fleas in China. Therefore, further investigations are needed to clarify the distribution of *Bartonella* in rodents and their ectoparasites in China to define the role of these arthropods in the transmission routes of *Bartonella*.

Key words: *Bartonella*, *Ctenophthalmus lushiensis*, genetic diversity, phylogenetic analysis, rodent flea, *Xenopsylla cheopis*.

INTRODUCTION

The genus *Bartonella* is an oxidase-negative, fastidious, gram-negative hemotropic bacillus. These diverse species infect a variety of mammalian hosts and arthropod vectors, causing a broad spectrum of diseases. In addition to animal hosts in close contact with humans such as cats, dogs, and cattle, rodents are one of the most important reservoirs. Many *Bartonella* species have been identified in rodents, and there is an increasing number of human and canine infections reportedly caused by rodent-borne *Bartonella* (Daly et al., 1993; O'Halloran et al., 1998; Kerkhoff et al., 1999; Welch et al., 1999; Kosoy et al., 2003; Serratrice et al., 2003; Fenollar et al., 2005). Bartonellae are transmitted by variety of bloodsucking arthropods; identified vectors include the sand fly (*Lutzomyia verrucarum*) as a vector for *Bartonella bacilliformis* (Alexander, 1995), the body louse (*Pediculus humanus*) for *Bartonella quintana* (Maurin and Raoult, 1996), and the cat

flea (*Ctenocephalides felis*) for *Bartonella henselae* (Chomel et al., 1996). For rodent Bartonellae, two vectors have been suggested: The oriental rat flea (*Xenopsylla cheopis*) has been demonstrated to be a competent vector of an unidentified *Bartonella* species that infects bank voles (*Clethrionomys glareolus*) (Krampitz, 1962), and the vole ear mite (*Trombicula microti*) has been proposed as the vector of *Bartonella vinsonii vinsonii* (Baker, 1946). Several researchers have suggested a role for rodent fleas as the vector of *Bartonella* species based on detection of *Bartonella* DNA from fleas collected worldwide (Parola et al., 2003; Rolain et al., 2003; Stevenson et al., 2003; Reeves et al., 2005; Loftis et al., 2006; Marie et al., 2006). In experimental transmission studies, Bown et al. (2004) demonstrated that the rodent flea *Ctenophthalmus nobilis* is a competent vector of at least two *Bartonella* species: *Bartonella grahamii*, which has previously been associated with human infection (Kerkhoff et al., 1999; Serratrice et al., 2003), and *Bartonella taylorii*.

TABLE 1. The geographic information of the sampling sites.

County	Latitude (°N)	Longitude (°E)	Mean altitude (m)	Mean annual air temperature (C)	Climate type
Longling	24.36	98.41	1,527	14.9	Subtropical plateau with monsoon climate
Longchuan	24.22	97.58	1,600	18.9	Subtropical monsoon climate
Yingjiang	24.43	97.56	827	19.9	Subtropical monsoon climate
Lincang	23.53	100.05	1,464	17.2	Subtropical monsoon climate
Gengma	23.33	99.24	1,104	19.0	Subtropical monsoon climate

Areas with a high prevalence of *Bartonella* infections in rodents are often characterized by the presence of a diversity of *Bartonella* species and strains (Birtles et al., 1994, 2001; Kosoy et al., 1997). During the period 2001–2005, a high prevalence of *Bartonella* was demonstrated through isolation from rodents (*Apodemus* species, *Eothenomys* species, and *Rattus* species) from the west, northwest, southwest, south, and middle of Yunnan Province, China; isolates typically clustered according to the genus of rodent hosts (Ying et al., 2002; Li et al., 2004a; Bai et al., 2005). Although no evidence of vector involvement was provided in these studies, we have isolated *Bartonella* from cat fleas (*Ctenocephalides felis*) collected from dogs, and ticks (*Boophilus microplus*) collected from cattle in northwestern Yunnan Province (Li et al., 2005). Based on the host range of fleas and the high prevalence of *Bartonella* spp. in rodents in Yunnan Province, we hypothesized that rodent fleas may represent an important vector of *Bartonella* in rodent populations. In this study, we report molecular evidence for the presence of a diversity of *Bartonella* genotypes from the rodent fleas collected in Yunnan Province, China, during 1997.

MATERIALS AND METHODS

Flea samples

Fleas were collected from rodents and burrows at five sites (Table 1) in Longling, Longchuan, Yingjiang, Lincang, and Gengma counties of southwestern Yunnan Province, China, during March to November of 1997. Sites were located in residential and farmland mountainous areas around the towns. All fleas were classified to species level by an entomol-

ogist, and species pools were stored in 70% ethanol.

Preparation of DNA extracts from fleas

Eight to 11 fleas of the same species from the same sites were grouped and washed three times with sterile deionized water for surface decontamination. Each group of fleas was placed in a sterilized mortar and crushed using a sterile pestle in liquid nitrogen. DNA was prepared from the crushed fleas using a QIAamp Tissue Kit (Qiagen, Hilden, Germany) according to the manufacturer's instructions.

PCR amplification

Polymerase chain reaction (PCR) amplification was performed using a MyCycler™ Thermal Cycler (Bio-Rad, Hercules, CA, USA). Three pairs of primers were used for the amplification of *Bartonella* DNA. The previously described PCR primers: BhCS.781p-BhCS.1137n (5'-GGGGACCAGCTC ATGGT GG-3', 5'-AATGCAAA AAGAACAGTAAACA-3') described by Norman et al. (1995) targets a 379 base-pair (bp) fragment of the citrate synthase gene (*gltA*); Bh.311p-Bh.452n (5'-CTCTTTCTTCAGATGATGATCC-3', 5'-AA CCAACTGAGCT ACAAGCCCT-3') described by Jensen et al. (2000) targets the 5'-terminal 200 bp partial sequence of the 16S-23S rRNA intergenic spacer region (ITS); and T1le.455p-T1la.885n (5'-GCTTGTA GCTCAGTTGGT-TAG-3', 5'-TGCTTGCAAAGCAGGTGC TCT-3') described by Li et al. (2004b) amplifies about 200–400 bp of tRNA^{leu}-tRNA^{Ala} ITS in the 16S-23S rRNA ITS. DNA amplification was performed using a 25 µl reaction volume. Each reaction mixture contained 1 µl of 10 pmol/µl of each primer, 1.5 U *Taq* DNA polymerase (Sino-American Biotechnology Co., Beijing, China), 2 µl of 2.5 mM deoxynucleosides triphosphate mixture, 2.5 µl of 10× PCR buffer, 1.5 µl of 20 mM MgCl₂, and 5 µl of DNA template. Each PCR analysis was performed using

TABLE 2. Numbers and geographic distribution of five species of fleas from Yunnan, China.

Flea species	Location					Total
	Longling	Longchuan	Yingjiang	Lincang	Gengma	
<i>Xenopsylla cheopis</i>	50	19	50	99	99	317
<i>Leptopsylla segnis</i>	58	50	48	18	0	174
<i>Ctenophthalmus lushuiensis</i>	49	0	0	0	0	49
<i>Nosopsyllus elongatus</i>	0	50	0	0	0	50
<i>Palaeopsylla remota</i>	0	0	51	0	0	51
Total	157	119	149	117	99	641

a negative control (molecular-grade water) and positive control (DNA from *B. henselae* strain Houston-1 [ATCC49882]). The extraction, creation of the reaction mixture, sample addition, PCR amplification, and product analysis were performed in different rooms to minimize cross contamination.

DNA sequencing and data analyses

The citrate synthase sequence (*gltA*) is acknowledged as the phylogenetic marker for *Bartonella* (Birtles and Raoult, 1996; La Scola et al., 2003). To detect and identify *Bartonella* DNA, we used PCR assays and sequencing of the amplicons derived from the *gltA* gene of *Bartonella* species and compared the *Bartonella* species from the rodent fleas with the available *Bartonella* strains in GenBank. The PCR amplicons from the *gltA* fragments amplified using BhCS.781p-BhCS.1137n primers were purified using the Promega Wizard PCR Preps Kit (Promega, Madison, Wisconsin, USA); the purified amplicons were cloned into pGEM-T Easy vector system (Promega) according to the manufacturer's protocol; and the white-colored recombinant colonies were selected. Sequencing was performed using a Big-Dye® Terminator v3.1 Cycle Sequencing Kit and an ABI PRISM 3730xl DNA analyzer (Applied Biosystems, Foster City, California, USA). New sequences were compared with published sequences using the BLAST program from the National Center for Biotechnology Information Website (available from: <http://www.ncbi.nlm.nih.gov/BLAST/>). Values of similarity between the sample sequences and published *Bartonella* sequences were calculated using the clustalV analysis with the Megalign module of the DNASTar5 Package (DNASTAR, Inc., Madison, Wisconsin, USA). The sequences were aligned using ClustalX version 1.81 (Thompson et al., 1997). Phylogenetic analysis was performed using MEGA3.1 (Kumar et al., 2004) and the PAUP* 4.0 beta version programs (Sinauer Associates, Inc., Sunderland, Massachusetts, USA).

Nucleotide sequence accession numbers

The *gltA* gene partial sequences of the *Bartonella* spp. detected in the different groups of rodent fleas in this study are available in the GenBank database under accession numbers DQ884382 (F12YN), DQ884378 (F13YN), DQ884379 (F14YN), DQ884380 (F15YN), DQ884381 (F16YN), and DQ884377 (F47YN).

RESULTS

Flea sampling

A total of 641 rodent fleas comprising five species was found: 317 *X. cheopis*, 174 *Leptopsylla segnis*, 49 *Ctenophthalmus lushuiensis*, 50 *Nosopsyllus elongatus*, and 51 *Palaeopsylla remota* (Table 2). *Xenopsylla cheopis*, *L. segnis*, and *N. elongatus* were collected from the bodies of *Rattus tanezumi flavipectus*. *Ctenophthalmus lushuiensis* specimens were collected in three nests of voles (*Eothenomys* spp. based on range and habitat). Because all the *C. lushuiensis* samples were mixed, we have no detailed information to infer about the origin of the four positive samples and if they came from different nests of voles. *Palaeopsylla remota* specimens were collected from the bodies of *Anourosorex squamipes*. Fleas were divided into 65 groups as follows: 33 groups of *X*, 17 groups of *L. segnis*, five groups of *C. lushuiensis*, five groups of *N. elongatus*, five groups of *P. remota*.

PCR detection of *Bartonella* DNA in rodent fleas

Six of the 65 groups were PCR positive (F12YN, F13YN, F14YN, F15YN, F16YN, and F47YN); PCR products were the

TABLE 3. Epidemiological characteristics of the polymerase chain reaction (PCR) positive groups of flea samples.

Group no.	Quantity of fleas	Flea species	Sampling site	Sampling date	Environment	Altitude (m)
F12YN	10	<i>Ctenophthalmus lushuiensis</i>	Longling	10 March 1997	Suburb	1,527
F13YN	10	<i>Ctenophthalmus lushuiensis</i>	Longling	10 March 1997	Suburb	1,527
F14YN	10	<i>Ctenophthalmus lushuiensis</i>	Longling	10 March 1997	Suburb	1,527
F15YN	10	<i>Ctenophthalmus lushuiensis</i>	Longling	10 March 1997	Suburb	1,527
F16YN	9	<i>Ctenophthalmus lushuiensis</i>	Longling	10 March 1997	Suburb	1,527
F47YN	10	<i>Xenopsylla cheopis</i>	Lincang	19–24 November 1997	Residential area in town	1,464

expected size, using all three primer pairs. Among the six groups collected from two sites, five groups were *C. lushuiensis* collected from nests of voles and the other was *X. cheopis* collected from *Rattus tanezumi flavipectus* (Table 3). Negative controls failed to yield detectable PCR products, whereas the positive controls gave consistent expected PCR products.

Comparison of the sequences from the flea samples and the *Bartonella* deposited in GenBank

A pair-wise comparison was performed using *Bartonella* deposited in the GenBank. The *gltA* sequences of F12YN and F14YN were identical and had 100% sequence similarity to a homologous amplicon of the *Bartonella* strain Em1712yn (AF391282) of *Eothenomys miletus* from northwestern Yunnan, China (Ying et al., 2002). There was one nucleotide mutation, G→A, at position 206 among the DNA sequences of F13YN, F12YN, and F14YN; however, the deduced amino acid composition was not affected. These *gltA* amplicon sequences differed from those described for all the known *Bartonella* variants. F15YN had the highest BLAST sequence similarity (97%) to *Bartonella* strains detected from rodents from Greece (Tea et al., 2004) and Sweden (Holmberg et al., 2003) and 95% similarity to *B.*

claridgeiae. Based on the pair-wise divergences of 338 bp *gltA* sequences, F16YN was most similar (98%) to the *Bartonella* strain Em1531yn (AF391281) (Ying et al., 2002) of *E. miletus* from the middle of Yunnan among all available sequences of *Bartonella* deposited in the GenBank at 97.4–97.6% (with nine nucleotide mutations) and similar to F13YN, F12YN, and F14YN, which had no variation in amino acid sequences. DNA similarity values based on the 379 bp of the *gltA* gene from F47YN compared to other *Bartonella* strains show that F47YN was more than 99% similar to *Bartonella* strains from *Rattus norvegicus* from Beijing (GenBank accession numbers DQ 884392, DQ884391, DQ884389, DQ 884388, DQ884387, and DQ884383), *Bartonella* strains from *R. tanezumi flavipectus* and *R. norvegicus*, fleas from *X. cheopis* from Indonesia (GenBank accession numbers AY902189, AY902191, AY902190, and AY902188), and the *Bartonella* strains from *Rattus rattus* from Portugal (GenBank accession no. AF 086636). All of these *Bartonella* are almost identical to *Bartonella tribocorum*, but there are two different amino acids found at two different positions (I→T, I→V) in F47YN compared to *B. tribocorum* and the other *Bartonella* strains, which had the

same amino acid (I) at these two positions based on 109 amino acids.

The *gltA*-based phylogeny of *Bartonella*

The sequence alignment of *gltA* of the *Bartonella* was 338 base pairs. The phylogenetic tree derived from the *gltA* data set using distance methods with MEGA3.1 showed four clusters of *Bartonella* strains identified within the flea samples (Fig. 1). The clusters between the flea sample sequences and published *Bartonella* sequences derived from interpretations of the parsimony analysis with the PAUP* 4.0 beta version were identical (data not shown). The genotype of F15YN formed a clade with the Grecian (strain af102nev, AY435103) and Swedish (strain af82up, AF391788) *Bartonella* isolates and was related to *Bartonella clarridgeiae*. Another two groups were the *E. miletus*-associated *Bartonella* isolates originating from different geographic areas of Yunnan Province. One group consisted of F12YN, F13YN, F14YN, and Em1712yn (AF391282) using supporting significant bootstrap values (99%). This genotype was similar to another *E. miletus*-associated group, which included F16YN and Em1531yn (AF391281). These two vole-associated *Bartonella* spp. represent a genotype that is related to *Bartonella taylorii* (from *Apodemus* spp. or voles). The genotype of F47YN, the five Beijing's *R. norvegicus* isolates (DQ884392, DQ884391, DQ884389, DQ884388, DQ884387, and DQ884383), the four Indonesian isolates (AY902189, AY902191, AY902190, and AY902188), and the one Portuguese *Rattus rattus* isolate (AF086636) formed a well-supported cluster (94% bootstrap support) and were closely related to *B. tribocorum*.

DISCUSSION

Using PCR assay, we found *Bartonella* DNA in two flea species, *C. lushuiensis* from Longling county, and *X. cheopis* from Lincang county of Yunnan Province,

China. The phylogenetic tree of these *gltA* sequences showed that there were divergent *Bartonella* groups from the two flea species. In this study, F47YN represented the genotype *B. tribocorum* based on the phylogenetic analysis; however, there are several mutations in the *gltA* gene among the *Bartonella* (F47YN) from *X. cheopis* from Lincang, the Portuguese *Bartonella* isolate from *R. rattus*, the Indonesian isolates (*R. norvegicus*, *R. tanezumi flavipectus*, and *X. cheopis*), and the Beijing *R. norvegicus* isolates. We infer that these mutations occurred among the different original isolates that are hypothetically attributed to the variants in host and geographic factors. *B. tribocorum* is a rodent-associated species that is distributed widely and that has been isolated from *R. norvegicus* in Europe and North America (Heller et al., 1998; Ellis et al., 1999). Ying et al. (2002) demonstrated a *B. tribocorum* bacteremia in *R. norvegicus* and *R. tanezumi flavipectus* in western Yunnan, China. Li et al. (2004) reported a high prevalence of *Bartonella* (42.0%) from *R. tanezumi flavipectus*, with *X. cheopis* as dominant species (Guo et al., 2000), which inhabits indoor areas and courtyards, usually in south China, and is in close contact with human beings.

The *Bartonella* DNA detected in pools of *C. lushuiensis* from three nests of voles showed genotypic diversity into three clusters according to the *gltA* gene phylogenetic analysis: F12YN, F14YN, F13YN, and *E. miletus Bartonella* strain Em1712yn (AF391282) from the west of Yunnan were the same genotype and were different from the F16YN genotype and another *E. miletus Bartonella* strain Em1531yn (AF391281) from the middle of Yunnan. Even though they are branched together, there was no solid evidence to indicate that these *Bartonella* spp. are *B. taylorii* based on the similarity value (86.5%) of the *gltA* gene. Based on La Scola et al. (2003), who proposed that newly encountered *Bartonella* isolates

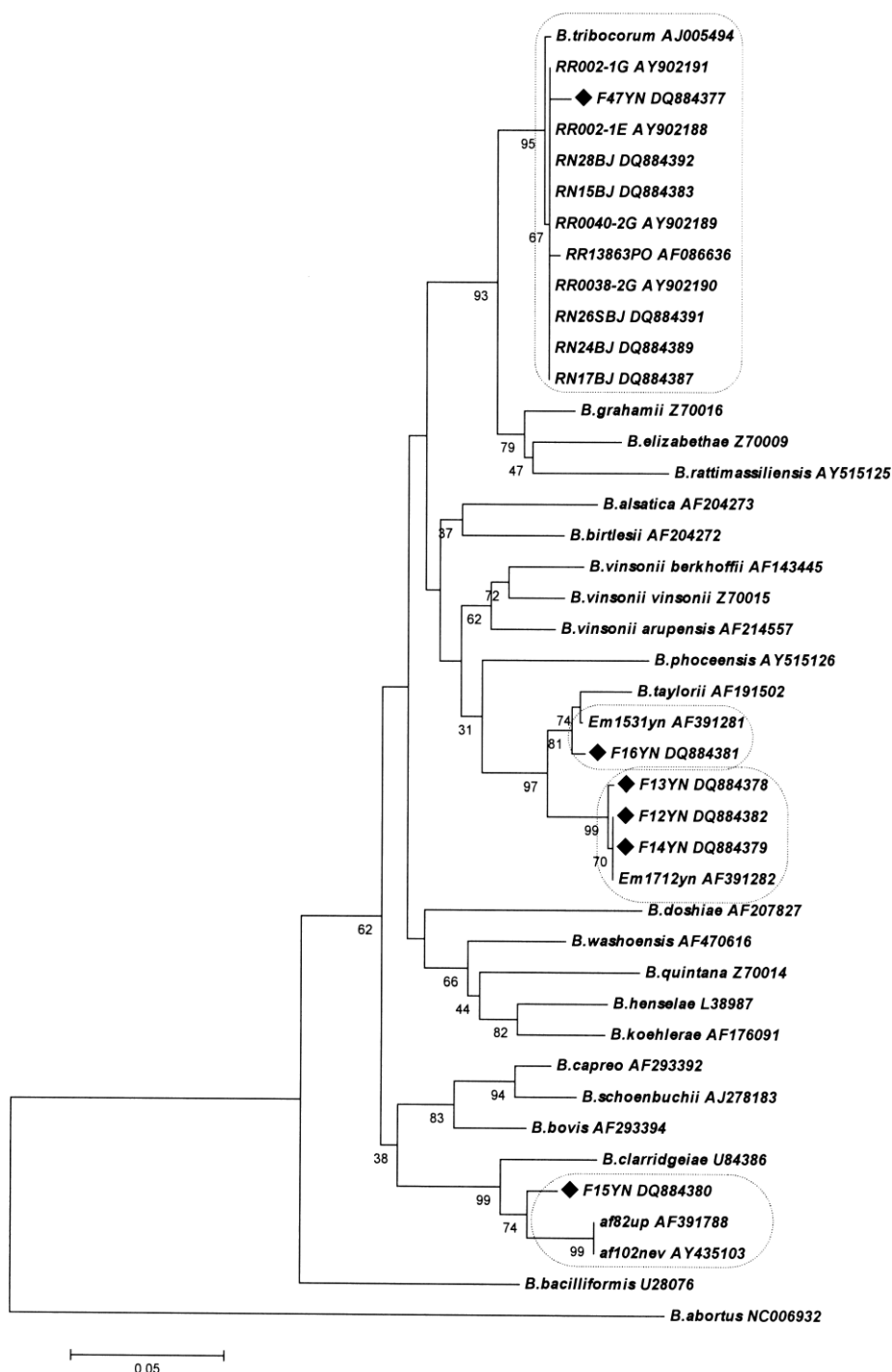


FIGURE 1. The phylogenetic tree based on 338 base pairs (bp) of *gltA* for *Bartonella* strains drawn using the MEGA3.1 software (Sinauer Associates, Inc., Sunderland, Massachusetts, USA). The distance matrix was calculated using the Kimura-2 parameter. The tree was obtained using the neighbor-joining method. The scale bar represents 5% divergence. The support of each branch was determined using 500 bootstrap samples and is indicated by the value at the node. The sequence of *Brucella abortus* was chosen as the out-group in the tree. The position of new sequences generated in this study is indicated with a black diamond.

should be considered new species if a 327 bp *gltA* fragment shares <96.0% sequence similarity with validated species, we suspect that these flea-associated *Bartonella* spp. are new genotypes. Further experiments are needed in order to prove it they are two separate new species or subspecies.

Interestingly, the F15YN genotype is more closely related to cat-associated *B. clarridgeiae* (Kordick et al., 1997) than the other recognized *Bartonella* strains. A similar report by Loftis et al. (2006) showed that the new *Bartonella* genotype from *X. cheopis* in Egypt was related to *B. clarridgeiae* based on the *groEL* gene. Within the *B. clarridgeiae* clade, there are two *Bartonella* isolates from *Apodemus flavicollis* from Greece that are 97.0% similar to the genotype of F15YN. Because *B. clarridgeiae* is a human pathogen, further studies may be warranted related to pathogenesis, range of host species (including rodents), modes of transmission, and epidemiology of human exposure to this *Bartonella* variant.

Bartonella organisms cause a persistent, often asymptomatic intra-erythrocytic bacteremia in their mammalian hosts. These arthropod-borne pathogens depend on the ecology of the blood-sucking arthropod vector, and an intra-erythrocytic bacterium can be transmitted among natural reservoir hosts, a cycle that is difficult to interrupt in the natural environment. Various flea vectors play an important role in this infection cycle. *Xenopsylla cheopis*, which uses *R. norvegicus* and *R. tanezumi flavipectus* as its major host, is a notorious vector for transmission of plague (*Yersinia pestis*) and endemic typhus (*Rickettsia typhus*). *Ctenophthalmus lushuiensis* is endemic in Yunnan Province, and it is carried by the common flea of *Eothenomys* spp. (Xie et al., 2000). Our data demonstrate that *Bartonella* spp. detected in fleas associated with voles is similar to *Bartonella* spp. from the voles, and the *Bartonella* spp. detected in the rat fleas is identical to *Bartonella* isolates from rats. This correlation between animal hosts and

arthropod vectors indirectly reflects the characteristics of host specificity of the fleas and partial host specificity of *Bartonella* (Breitschwerdt and Kordick, 2000) and suggests that the two species of fleas presumably play a role as the transmission vectors of rodent-associated *Bartonella* in their natural cycle.

Previous investigations concerning *Bartonella* infections in rodents, cat fleas, and ticks have shown a high genetic diversity in *Bartonella* in Yunnan, China (Ying et al., 2002; Bai et al., 2005; Li et al., 2005). Our findings further confirm that there are different *Bartonella* genotypes in the rodents, and the rodent fleas can carry *Bartonella* in Yunnan Province. Humans are incidental hosts for the numerous rodent-associated *Bartonella* species. An increasing number of bacteria are identical or closely related to *Bartonella* and have been obtained from rodents and are being isolated from human patients. Further studies are needed in China to clarify the characteristics of the new flea-associated *Bartonella* and the potential vectors and the role of the ectoparasites in the route of transmission.

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