

Bartonella species detected in rodents and hedgehogs from Algeria

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INTRODUCTION

Bartonella spp. are fastidious, gram-negative and oxidase-negative bacteria [1]. Since the last decade of the 20th century, more than 22 species of genus *Bartonella* have been recognised. According to previous studies of *Bartonella* spp., five species are associated with rodents, including *B. tribocorum*, *B. elizabethae*, *B. taylorii* and *B. birtlesii*, which were detected in *Apodemus mouse*, and *B. vinsonii* subsp. *arupensis* detected in mice. To date 11 species have been implicated in human diseases. The objective of this study was to detect and to identify *Bartonella* species in rodents and hedgehogs from Algeria.

MATERIALS AND METHODS

Rodents and hedgehogs were captured between 2005 and 2007 in four different regions of Algeria: Algiers (36°46'N, 3°02'E), Benaouali (35°33'N, 0°21'E), Biskra (34°51'N, 5°43'E) and Tiaret (35°22'N, 1°18'E). The animals were caught overnight in strategically-placed BTS (Besenson Technique Service) and Sherman traps. Each animal was weighed, sized, sexed and identified. In the laboratory, each animal was dissected and internal organs (liver, kidney and spleen) were collected and stored at -80°C until analysed. DNA extracts were prepared from a small piece of spleen from individual animals using QIAmp DNA Mini Kit (Qiagen, GmbH, Hilden, Germany). Each sample of undiluted extracted DNA was screened using a *Bartonella*-genus real-time quantitative PCR with Taqman* probe targeting the 16S/23S RNA gene intergenic spacer (ITS) gene as previously described [2]. Positive PCR results were confirmed using standard PCR and sequencing of ITS and cell division protein-encoding gene (*ftsZ*) fragments, as previously described [3].

Sequencing of PCR products was carried out using the BigDye Terminator Cycle Sequencing Ready Reaction Kit (ABI PRISM, PE Applied Biosystems, Coignieres, France), and the sequences obtained were compared with those available in GenBank.

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RESULTS

A total of 75 rodents and hedgehogs were trapped, including *Rattus rattus*, *Mus spretus*, *Psamommys obesus*, *Meriones shawii* and *Atelerix algirus*, in four surveyed cities (Table 1).

At screening with LightCycler, 21 out of the 75 samples (28%) were positive. Partial sequencing of ITS and *ftsZ* genes was obtained, leading to the identification of (i) *B. elizabethae* in three hedgehogs, *A. algirus*, (ii) *B. tribocorum* in nine hedgehogs *A. algirus* and (iii) a *Bartonella* spp. previously detected in rodents from China, in two *R. rattus*, two *Mus spretus*, two *Psamommys obesus* and three *Meriones shawii*. The percentage of similarity of all *Bartonella* species detected in rodents and hedgehogs ranged from 99.2 to 100%.

DISCUSSION

We report the first investigation about the distribution and diversity of *Bartonella* spp. in rodents from Algeria. The finding of *Bartonella* species in the mammalian samples from Algeria suggests that these agents might be responsible for human

Table 1. Species of rodents and *Bartonella* species detected. *Similar sequences were obtained from these samples and were found to be identical to those of a *Bartonella* sp. previously detected in China (GenBank accession numbers: AY518551 and EF190333)

Species sample (number)	<i>Bartonella</i> species (ITS and <i>ftsZ</i> genes amplification and sequencing)	Amplification and sequencing	
		Positive	Negative
<i>Rattus rattus</i> (16)	<i>Bartonella</i> sp.*	2	14
<i>Rattus norvegicus</i> (9)		0	7
<i>Mus spretus</i> (7)	<i>Bartonella</i> sp.*	2	7
<i>Mus musculus</i> (8)		0	8
<i>Psamommys obesus</i> (7)	<i>Bartonella</i> sp.*	2	5
<i>Meriones shawii</i> (12)	<i>Bartonella</i> sp.*	3	9
<i>Atelerix algirus</i> (46)	<i>B. elizabethae</i>	3	4
	<i>B. tribocorum</i>	9	0
Total (75)		21	54

infectious disease of unknown aetiology in Algeria. Indeed, the description of either known or unknown *Bartonella* in arthropods, rodents or mammals has been frequently reported prior to their isolation in humans. This was recently demonstrated with *B. alsatica* and *B. rochalimae*, firstly isolated in rabbits from France and in a *Pulex* flea from Peru prior to their isolation in a patient with endocarditis in France and in a patient with fever and splenomegaly in Peru, respectively [2,4].

Because people in Algeria could be in close contact with rodents, it is possible that some unknown diseases in Algeria may be caused by such *Bartonella* species. More investigations are warranted in order to isolate these *Bartonella*

species and to determine if they can cause any clinical disease.

REFERENCES

1. Boulouis HJ, Chang CC, Henn JB, Kasten RW, Chomel BB. Factors associated with the rapid emergence of zoonotic *Bartonella* infections. *Vet Res* 2005; **36** (3): 383–410.
2. Raoult D, Roblot F, Rolain JM *et al.* First isolation of *Bartonella alsatica* from a valve of a patient with endocarditis. *J Clin Microbiol* 2006; **44** (1): 278–279.
3. Zeaiter Z, Liang Z, Raoult D. Genetic classification and differentiation of *Bartonella* species based on comparison of partial *ftsZ* gene sequences. *J Clin Microbiol* 2002; **40** (10): 3641–3647.
4. Ereemeeva ME, Gerns HL, Lydy SL *et al.* Bacteremia, fever, and splenomegaly caused by a newly recognized *Bartonella* species. *N Engl J Med* 2007; **356** (23): 2381–2387.