

Sato S.,Kabeya H.,Fujinaga Y.,Inoue K., Uneyama Y.,Yoshikawa Y. and Maruyama S. *Bartonella jaculi* sp.nov.,*Bartonella callosciuri* sp.nov.,*Bartonella pachyuromydis* sp.nov.,and *Bartonella acomydis* sp.nov. isolated from wild Rodentia. Int J Syst Evol Micr. in press (2013)

SUMMARY

Four novel *Bartonella* strains, OY2-1T, BR11-1T, FN15-2T, and KS2-1T, were isolated from the blood of wild-captive greater Egyptian jerboa (*Jaculus orientalis*), plantain squirrel (*Callosciurus notatus*), fat-tailed gerbil (*Pachyuromys duprasi*), and golden spiny mouse (*Acomys russatus*). All the animals were imported to Japan as pets from Egypt, Thailand, and the Netherlands. The phenotypic characterization (growth conditions, incubation periods, biochemical properties and cell morphologies), DNA G + C contents (37.4 mol% for strain OY2-1T, 35.5 mol% for strain BR11-1T, 35.7 mol% for strain FN15-2T, and 37.2 mol% for strain KS2-1T), and sequence analyses of the 16S rRNA genes indicated that those strains belong to the genus *Bartonella*. Sequence comparisons of *gltA* and *rpoB* genes suggested that all of the strains should be classified as novel *Bartonella* species. In phylogenetic trees based on the concatenated sequences of 5 loci including the 16S rRNA, *ftsZ*, *gltA*, *rpoB* genes, and the ITS region and on the concatenated deduced amino acid sequences of 3 housekeeping genes (*ftsZ*, *gltA*, and *rpoB*), all strains formed distinct clades and showed unique mammalian hosts that could be discriminated from other known species of the genus *Bartonella*. These data strongly support that strains OY2-1T, BR11-1T, FN15-2T, and KS2-1T should be classified as novel species of the genus *Bartonella*. The names *Bartonella jaculi* sp. nov., *Bartonella callosciuri* sp. nov., *Bartonella pachyuromydis* sp. nov., and *Bartonella acomydis* sp. nov. are proposed for these novel species. Type strains of *Bartonella jaculi* sp. nov., *Bartonella callosciuri* sp. nov., *Bartonella pachyuromydis* sp. nov., and *Bartonella acomydis* sp. nov. are OY2-1T (=JCM17712=KCTC 23655), BR11-1T (=JCM 17709=KCTC 23909), FN15-2T (=JCM 17714=KCTC 23657), and KS2-1T (=JCM17706=KCTC 23907), respectively.

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Mongoose and masked palm civets as new reservoirs of *Bartonella henselae* and potential sources of infection for humans. Clin. Microbiol. Infect. In press (2013)

SUMMARY

In the present study, the prevalence and genetic properties of *Bartonella* species were investigated in mongooses and masked palm civets in Japan. *Bartonella henselae*, the causative agent of cat-scratch disease (CSD) was isolated from 15.9% (10/63) of the mongooses and 2.0% (1/50) of the masked palm civets, respectively. The bacteremic levels in the animals ranged from 30 to 8,015 CFU/ml in mongooses and 7,000 CFU/ml in a masked palm civet. Multispacer typing (MST) analysis based on 9 intergenic spacers resulted in the detection of 5 MST genotypes (MSTs 8, 14, 37, 58 and 59) for the isolates, which grouped in lineage 1 with MST genotypes of isolates from all CSD patients and most of the cats in Japan. This is the first report suggesting that mongooses and masked palm civets serve as new reservoirs for *B. henselae* and may play a role as potential sources of human infection.

