

Phylogenetic analyses of *Bartonella* sp. (Bacteria) of rodents from four separated valleys in Sinai Mountains (Egypt)

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Bartonella sp. is a parasite of mammalian erythrocytes and endothelial cells transmitted by blood-feeding arthropod ectoparasites. Different species of rodents constitute the main hosts of *Bartonella*, including several zoonotic species. The aim of this study was to identify and compare the *Bartonella* species/subspecies in two rodent hosts in four isolated populations. Rodents were trapped and sampled in 2000, 2004, 2008, and 2012 in four dry montane wadis around St. Katherine town in South Sinai. At each site, rodents were caught live in Sherman traps. 40% of captured rodents had undergone necropsy and the other were released close to the point of capture. From the culled animals, 200 µl of the whole blood were also collected into 0.001M EDTA and frozen at -20°C. Genomic DNA was extracted from the whole blood. The DNA isolates were genotyped by the amplification and sequencing of *Bartonella*-specific 860-bp gene fragment of *rpoB* and 810-bp gene fragment of *gltA*. We analysed the prevalence and diversity of *Bartonella* in 111 *Dipodillus dasyurus* and 65 *Sekeetamys calurus*. Overall prevalence of *Bartonella* was 30.63% in *D. dipodillus* and 10.65% in *S. calurus*. The phylogenetic analyses of five isolates of *Bartonella*, four of them were from *D. dasyurus* and one from *S. calurus* clustered in paraphyletic group/clade with three African isolates of *Bartonella* sp. from Egypt, also this clad/group was separated from all others sequences. Based on *gltA* marker, all our sequences grouped together in one monophyletic group/clad separated from the others sequences. The analyses of *rpoB* and *gltA* markers justify the description of two new species of *Bartonella*, with some genetic variation among isolates.

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