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Project Title: Epidemiology and phylogenetic analysis of *Bartonella* spp. in small mammals in Taiwan

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Executing Institute: National Chung Hsing University

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Abstract:

Most of *Bartonella* spp. have been identified as zoonotic pathogens. Previous studies showed that small mammals are important reservoirs for *Bartonella*. In this study, a total of 310 blood specimens were collected, including 169 from *Rattus norvegicus*, 126 from *Suncus murinus*, ten from *Rattus rattus*, three from *Rattus losea* and two from *Mus musculus*. It was identified that 41.3% (128/310) of the animals were *Bartonella* bacteremic. The isolates were characterized by the combination of PCR of the 16S-23S ITS gene, and PCR/RFLP analysis of the *gltA* gene with three different endonucleases. According to the PCR/RFLP analysis, various known species of *Bartonella* were identified in small mammals in Taiwan, including *B. elizabethae* (25.0%, 32/128), *B. grahamii* (7.0%, 9/128), *B. phoceensis* (2.3%, 3/128), *B. tribocorum* (42.2%, 54/128) and *B. rattimassiliensis* (1.6%, 2/128). It was also found that 3.5% (11/310) of the animals were co-infected with different *Bartonella* species. Of major importance, *Bartonella* organisms were first isolated from *Suncus murinus*, an insectivore in Taiwan, with bacteremia prevalence of 28.6%. Moreover, 91.7% of the *Bartonella* isolates from *S. murinus* were with a unique molecular pattern, separated from other *Bartonella* species. Seroprevalences were 0%, 3.2%, 3.2% and 5.6%, by IFA test using the antigens of *B. elizabethae*, *Bartonella* sp. Taiwan-1, *B. grahamii* and *B. tribocorum*, respectively. The phylogenetic analysis showed that species tree constructed by the sequences of *gltA* gene and *ftsZ* gene yielded consistent results. However, using the sequences of *rpoB* and *ribC* genes, some strains were determined to be *B. tribocorum*; these isolates were determined to be *B. grahamii* by analysis of *gltA* and *ftsZ* genes. Unfortunately, sequences of 16S-23S interspacer region and *pap31* gene were not useful for conducting phylogenetic analysis of rodent *Bartonella* isolates, as limited to the available sequence information of *Bartonella* type strains. The results of this study provided valuable information regarding the epidemiology of *Bartonella* infections in small mammals in Taiwan.

Keyword: *Bartonellaceae*, small mammals, epidemiology