

Flea-borne pathogens in the cat flea *Ctenocephalides felis* and their association with the mtDNA diversity of the flea hosts

ABSTRACT

Flea-borne pathogens were screened from 100 individual cat fleas using a PCR approach, of which 38 % were infected with at least one bacterium. Overall, 28 % of the flea samples were positive for *Bartonella* as inferred from ITS DNA region. Of these, 25 % (7/28) were identified as *Bartonella clarridgeiae*, 42.9 % (12/28) as *Bartonella henselae* consisted of two different strains, and 32.1 % (9/28) as *Bartonella koehlerae*, which was detected for the first time in Malaysia. Sequencing of *gltA* amplicons detected *Rickettsia* DNA in 14 % of cat flea samples, all of them identified as *Rickettsia asembonensis* (100 %). None of the flea samples were positive for *Mycoplasma* DNA in 16S rRNA gene detection. Four fleas were co-infected with *Bartonella* and *Rickettsia* DNAs. Statistical analyses reveal no significant association between bacterial infection and mtDNA diversity of the cat flea. Nevertheless, in all types of pathogen infections, infected populations demonstrated lower nucleotide and haplotype diversities compared to uninfected populations. Moreover, lower haplotype numbers were observed in infected populations.

Keyword: Association; *Ctenocephalides felis*; Flea; Genetic diversity; Pathogens