TITLE: FLEAS (*CTENOCEPHALIDES FELIS*) RAISED IN A LABORATORY COLONY PRESENT A STABLE CORE MICROBIOTA PREDOMINATED BY STAPHYLOCOCCAL SPECIES

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ABSTRACT:

The flea (Ctenocephalides felis) is the principal ectoparasite of domestic dogs and cats worldwide and acts as a vector of emerging zoonotic pathogens including Rickettsia felis and Bartonella spp. The diversity of host associated microbes and their interactions within the microbiota of living beings, including arthropods, are fundamental to the ecological functions within the communities and may contribute to host evolution. Moreover, symbiotic interactions may influence the transmissions of pathogens with zoonotic potential, via effects upon vectoral competence. Knowledge in relation to the microbiota of vectors has been used to develop novel approaches for control based on the concept of microbiota manipulation, as exemplified by the artificial infection of Aedes aegyptiwith Wolbachia to inhibit natural infection of the mosquito by the dengue virus. A key component in this strategy is the presence of a stable/core microbiota. The present study sought to characterize the stability, over seven years, of the cultivable microbiota of a laboratory colony of C. felis maintained at UFRRJ. Bacteria associated with eggs, F1 larvae and adults (males and females) were isolated on nutrient agar and used to produce pure cultures. Isolates were identified, to the species level, by sequencing a hyper-variable region (500 base pairs) of the gene encoding prokaryotic16S ribosomal RNA (rRNA). Cultures were further characterized in terms of their resistance to antibiotics and were screened for the presence of lysogenic phages. Each of the different life stages presented a unique microbiota, however a core component of all samples were members of the genus Staphylococcus including S. cohnii, S. nepalensis, S. saprophyticus and S. xylosus. Analysis, of antimicrobial resistance profiles identified numerous multiple-drug resistant organisms, with resistance to oxytetracycline observed as the most common resistance phenotype. Analysis of phage carriage is on-going. The data recovered to date, provide evidence for a stable core microbiota predominated by Staphylococcus species. The constant presence of the same species, in multiple life stages, suggests that those microbes are essential components of the microbiota and by implication of the biology of the fleas. Future research will examine the effects of manipulating the core bacterium as the first step in the development of novel strategies for infestation control.

Keywords: microbiota, antibiotic resistance, *Staphylococcus*

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