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PhD Dissertation Defense

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LIVESTOCK TICKS IN THE UAE: PREVALENCE, DISTRIBUTION, POPULATION DYNAMICS, AND ASSOCIATED MICROORGANISMS

<u>by</u>

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<u>Abstract</u>

Ticks are important vectors of an array of viral, bacterial and protozoan pathogens resulting in a wide range of animal and human diseases in the Middle East and North Africa (MENA). In this study, I collected ticks from camels, cows, sheep, and goats in Abu Dhabi, Dubai, and Sharjah in the United Arab Emirates (UAE). The objectives of the study are (1) identify tick species of livestock through taxonomic keys and using molecular markers, and determine their prevalence and distribution in the UAE, (2) assess *Hyalomma dromedarii* seasonal population fluctuation over a year under common camel breeding and management practices by evaluating life stage changes and sex ratio during 12 months, and measure parasitological indicators of *H. dromedarii* infestation, (3) determine bacterial communities' composition and diversity in camel tick, *H. dromedarii* using Next Generation Sequencing, and (4) detect tick-borne microbes and their prevalence in *Hyalomma* ticks collected from livestock. In the MENA region, a taxonomic record of 55 tick species infesting livestock was established representing the following eight genera: *Ornithodoros*, *Otobius*, *Amblyomma*, *Dermacentor*, *Haemaphysalis*, *Hyalomma*, *Ixodes*, and *Rhipicephalus*. In addition, 15 tick-borne pathogens were recorded, which cause diseases of humans and veterinary importance including Crimean–Congo hemorrhagic fever (CCHF), theileriosis, babesiosis and anaplasmosis, being widely distributed diseases in the region. In the UAE, information on the ticks on camels and other livestock is limited, which is essential for designing and instigating effective control strategies in the country. So far, few studies have been done on the ticks and tick-borne microorganism and their prevalence in the UAE. In this study, four aspects of ticks and tick-borne diseases of livestock have been investigated in the UAE. First, I identified four tick species, *H. dromedarii*, *Hyalomma anatolicum*, *Amblyomma lepidum* and *Rhipicephalus sanguineus* from livestock including camel, cow, sheep and goat from the UAE. These tick species were morphologically identified by using taxonomic keys and later molecular characterization was done by using different molecular tools. This study provided the first DNA molecular record of *H. anatolicum*, *A. lepidum* and *R. sanguineus* from the UAE. Second, I evaluated the population fluctuation of *H. dromedarii* over one year under common camel breeding and management practices in the study area. Further, I calculated *H. dromedarii* sex ratio during 12 months and measured the parasitological indicators of its infestation. I performed monthly on-site tick visual counts and collected them from camels in Al Ain, UAE, over 12 months (March 2019 to February 2020). My results showed that the infestation prevalence was very high during the whole study period, with a mean of 94.33%. The maximum infestation intensity occurred in June, while the minimum occurred in November. Overall, *H. dromedarii* ticks were found on camels during the entire year in spite of monthly applications of an acaricide. Third, I determined the composition and diversity of bacterial communities associated with H. dromedarii collected from camels in Al Ain, UAE, during a genomic study. A total of 100 partially engorged female ticks were taken from tick samples collected from camels and subjected to DNA extraction and Next Generation Sequencing. The 16S rRNA gene was amplified from genomic DNA and sequenced using Illumina MiSeq platform to reveal the bacterial communities. Principal Coordinates Analysis (PCoA) was conducted to determine patterns of diversity in bacterial communities. Twenty-five bacterial families with high relative abundance were identified and the following were the most common: Moraxellaceae, Enterobacteriaceae, Staphylococcaceae, Bacillaceae, Corynebacteriaceae, Flavobacteriaceae, Francisellaceae, Muribaculaceae, Neisseriaceae, and Pseudomonadaceae. Francisellaceae and Enterobacteriaceae coexisted in *H. dromedarii* and they thrive under similar conditions and microbial interactions inside the host. Fourth, I determined the presence and prevalence of tick-borne *Francisella* sp., *Rickettsia* sp., and piroplasmids in ticks infesting livestock, and estimated their infection rates by using different PCR-based approaches. A total 562 tick samples were collected from camels, cows, sheep, and goats in the Emirates of Abu Dhabi, Dubai, and Sharjah from 24 locations. DNA was extracted from ticks and PCRs were performed. Hyalomma dromedarii ticks collected from camels were infected with *Francisella*-like endosymbionts (FLE) (5.81%) and *Candidatus* Rickettsia andeanae (1.36%). *Hyalomma anatolicum* ticks collected from cows were found positive with *Theileria annulata* (4.55%) whereas *H. anatolicum* collected from goats were positive with *Theileria ovis* (10%). *Theileria ovis* was detected for the first time in the UAE. Therefore, further investigations on tick species and tick-borne microbes are required to understand ticks biology, ecology and microbes' interaction and their role in tick-borne diseases epidemiology in the UAE. In addition, active surveillance of key species is suggested to reduce health hazards in the livestock industry, protect livestock and people, and eliminate the threat to food security.

Keywords: Ticks, tick-borne microorganisms, population dynamics, microbial communities, UAE