

The College of Graduate Studies and the College of Science Cordially Invite  
You to a

**Master Thesis Defense**

Entitled

METAGENOMIC PROFILE OF THE BACTERIAL COMMUNITIES ASSOCIATED WITH  
*ORNITHODOROS MUESEBECKI* (ACARI: ARGASIDAE) TICKS ON SOCOTRA CORMORANT  
COLONY IN THE UNITED ARAB EMIRATES

by

Raheel Nasser Mohammed Alkayoumi

Faculty Advisor

Dr. Mohammad Ali Al-Deeb, Department of Biology

College of Science

Date & Venue

10:00 AM

Thursday, 19 April 2018

Room 0008, H1 Building

Abstract

Ticks are well known to transmit various pathogens including bacteria, viruses and protozoa to humans and animals. A wide spread of the soft tick (*Ornithodoros muesebecki*) was observed on Socotra Cormorant (*Phalacrocorax nigrogularis*) breeding colony in Siniya Island, United Arab Emirates. The aims of the study were (1) to investigate prevalence and conducting genetic characterization of relapsing fever group *Borrelia* spp., spotted fever group *Rickettsia* spp. and *Coxiella burnetii*, (2) understand the overall bacterial community associated with *O. muesebecki* by using Illumina-based metagenomic approach, and (3) establishing a molecular record of *O. muesebecki* based on molecular markers. Ticks were collected from the largest breeding colony of Socotra Cormorant in 2013 and 2016. Subsequently, genomic DNA was extracted from each tick and conventional PCR assays were used to detect certain pathogens. *Borrelia* spp. and *Rickettsia* spp. were not detected, however PCR assay and metagenomic analysis indicated the presence of the *Coxiella* genus. Sequencing results revealed 809 bacterial operational taxonomic units (OTUs) within the 5 samples from 2013 and 2686 OTUs within the 5 samples from 2016. Metagenomic analysis showed that *Firmicutes*, *Proteobacteria*, and *Bacteroidetes* are the most dominant phyla. *Coxiella burnetii* was the highly prevalent species in all samples in 2013 and 2016. This data provide the most complete picture to date of the bacterial communities present within *O. muesebecki* under natural conditions in the UAE using high-throughput sequencing technologies. In addition, this study provided the first DNA molecular record on *O. muesebecki* in GenBank. A further investigation regarding the functional role of *Coxiella* on seabird colonies is needed to study.

**Keywords:** Metagenomic, *Ornithodoros muesebecki*, Socotra Cormorant, *Coxiella*, Bacterial community diversity, Next-generation sequencing, Illumina