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**Master Thesis Defense**

Entitled

*HONEYBEES IN THE UAE: DISEASES, ASSOCIATED MICROBIAL COMMUNITIES, AND PARASITIC  
VARROA MITES*

by

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Abstract

*Apis mellifera* honeybees are the most important pollinator worldwide. Numerous diseases and parasites are causing the decreasing numbers of the *A. mellifera* honeybee. The main objective of this thesis is to study the *A. mellifera* honeybee diseases along with the *Varroa destructor* mite. First, studying bacterial communities associated with *Apis mellifera* and *Apis florea* in the UAE. Second, conducting a molecular detection of *A. mellifera* honeybee diseases in the UAE. Third, studying *Varroa* mites and *Varroa*-associated diseases in the UAE. DNA and RNA were extracted from *A. mellifera* honeybees and *Varroa destructor* mites. Subsequently, PCR assays were conducted. Sequencing results revealed 23 bacterial operational taxonomic units (OTUs) in both *A. mellifera* and *A. florea* honeybees. Another result, *Nosema ceranae* disease was detected, while *Nosema apis* was not found in any of the *A. mellifera* honeybee samples. In addition, two viral diseases were detected in both *A. mellifera* honeybee and *Varroa destructor* mites. The species of the *Varroa destructor* mite was confirmed using DNA sequencing. This study is the first of its kind in the UAE. Further studies are needed to investigate the effect of these diseases on honey production in the UAE.

**Keywords:** Metagenomics, *Apis mellifera*, *Varroa destructor*, *Nosema ceranae*, *Nosema apis*, DWV, VDV, Bacterial community diversity, Next-generation sequencing.