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Master Thesis Defense

Entitled

ANALYSIS OF THE 16S RRNA FOR THE IDENTIFICATION OF MICROBIAL COMMUNITIES IN THE RHIZOSPHERE OF CULTIVATED DATE PALMS TREES UNDER SALT STRESS CONDITION IN THE UAE ECOSYSTEM

by

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Date & Venue

10.00 am

Sunday, 14 November 2021

Room: F3-040

Abstract

Increasing soil salinity is an emerging global issue, generating land degradation, affecting agricultural production and further affecting quality of ground water. In arid environment with water scarcity, saline ground water has been regularly used for irrigation purpose in date palm (*Phoenix dactylifera*) plantation, without knowing its impact on their root-associated bacterial communities. The aim of this study is to investigate the impact of saline water irrigation on date palm root-associated bacterial community compositional structure and their diversity. Plant root samples were collected from date palm farms located in Abu Dhabi Emirate, irrigated with either saline, or non-saline water. Overall, we observed that bacterial richness was influenced by the soil pH, EC, and organic matter. Source of irrigation water did not significantly affect the bacterial richness, but affected community structure and patterns, driven by soil EC and irrigation water pH. Out of the total, 40.5% bacterial OTUs were uniquely observed in samples where irrigation source was non-saline water, whereas 26% were unique to sites with saline water as an irrigation source. Bacterial phyla Proteobacteria, Actinobacteria, Acetobacter and Chloroflexi dominated both types of samples with similar abundance. However, phylum Chloroflexi was highly abundant in the non-saline samples than in the saline irrigated samples. In contrast, phylum Firmicutes showed relatively higher abundance in saline than in non-saline samples. Rhizobium, one of the most significant micro-symbiotic genera was abundant at the non-saline site but significantly low in saline site. Our study indicates a possible role of the identified microbial communities in the adaptation of the date palm to salinity stress. The current findings from the date palm saline and non-saline soil microbiomes expands the inventory of soil bacteria for saline environments that can help in the discovery of potential inoculants for crops growing on salt-affected land. A detailed investigation is necessary in this area, and the use of PGPR and other symbiotic microorganisms may lead to a new method of developing sustainable agriculture in saline soils.

Keywords: 16S rRNA; Arid agroecosystem; Bacterial communities; Date palm (*Phoenix dactylifera*); Root-associated bacteria; Salinity