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A Prospective Implementation of Plant-Associated Microbes for a Sustainable Agriculture in Qatar

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Background

The plant growth and production rely on the supporting favorable environmental conditions throughout its growing stages. In harsh environmental conditions such as in Qatar, agricultural growth is limited by water availability, salinity and drought, leading to low yield. In soil, there are different kinds of microbiota including fungi, bacteria, actinomycetes, algae as well as various types of plant species. Fungi are important components of the soil microbiota. For example, soil-borne fungi cause a significant yield loss for many vegetable and fruit crops in Qatar including tomatoes, cucumbers, legumes, limes, strawberries and others. Several recent studies have demonstrated that the adaptation of plants to severe environmental conditions is attributed to genetic abilities of their associated microbes. For example, all plants in natural ecosystems are thought to be symbiotic with mycorrhizal and/or endophytic fungi reflecting fitness benefits conferred by fungi that contribute to or are responsible for plant adaptation to stress. In Qatar, there are many plant species that can survive under adverse abiotic conditions of salinity and drought rendering them as rich resources for structuring their associated microbes.

Objectives

The aims of this study were to: (i) investigate the effect of different ecosystems on the structure and distribution of soil-borne fungi; (ii) inspect the ability of plant-associated microbes to tolerate harsh environmental conditions; and (iii) examine the effectiveness of isolated fungi as potential biological control agents. The ultimate goal of this study is to improve the sustainable agriculture in Qatar through the implementation of plant-associated microbes for biological control of important diseases and enhance plant tolerance to abiotic stress.

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Materials and Methods-Isolation of plant associated microbes

Samples from plant rhizosphere and soil were collected from four different plant species grown under different ecosystems in Qatar. Qatar University Farm (Al-Zubara Area, Qatar) exemplifies the agricultural ecosystem; in addition to six private farms represent different ecosystems. Four plant species were considered in this study namely *Launaea capitata*, *Lycium shawii*, *Ziziphus lotus* and *Zygophyllum qatarense* (*Tetraena qatarense*). Samples from plant rhizosphere and soil were collected in January. Soil-borne fungi were isolated from the rhizosphere and soil using direct plate method. About 0.5 g of homogenized soil sample was plated on melted potato dextrose agar supplemented with Rose Bengal. Plates were incubated at 25°C for 3–7 days and colonies with different morphological characters were isolated and purified. Fungal isolates were identified morphologically using light microscopy. DNA was extracted using QIAGEN kit for molecular analysis. Effect of abiotic stress on the growth of *Trichoderma* spp.: different concentrations of sodium chloride (NaCl) were used to induce salinity stress. NaCl concentrations include 0 (control), 10 mM, 50 mM, 100 mM, 250 mM, 500 mM, 1 M, 1.25 M, 1.5 M, 1.75 M, 2 M, 2.25 M, 2.5 M, 2.75 M and 3 M. Fifty ml of potato dextrose broth medium, with different salt level, was inoculated with five mm disc of *Trichoderma* spp. Poly Ethylene Glycol (PEG) was used to induce drought effect on *Trichoderma* spp. Different percentages of PEG were performed including 0% (control), 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% and 100%. In 100 ml conical flask; 50 ml of PDB medium with different percentages of PEG was inoculated with five mm disc of *Trichoderma* spp. The antagonistic effect of the fungal isolates was tested using the direct opposition method. Antagonistic test was performed between *Trichoderma* spp. which has an effective biocontrol activity towards many soil-borne pathogenic fungi and *Ceratocystis radicola* (*Thielaviopsis paradoxa*), which causes many diseases in date palm trees. The test was performed in dual culture on PDA medium. Five mm disc of each fungus was placed at peripheral end (five cm between each other) of Petri plate. The plates were incubated at 25°C for 7 days. Three replicates were considered.

Results

Thirty-nine of fungal genera were isolated from the plant rhizosphere and soil. Results showed that the most dominant genus was *Aspergillus niger* (48.5%) followed by *Rhizopus* spp. (26.8%). Other fungal communities were also detected such as *Aspergillus vesicology*, *Aspergillus sydowii*, *Aspergillus wentii*, *Fusarium oxysporum*, *Penicillia oxalicum*, and *Rhizoctonia solani*. Results also showed that *Aspergillus terreus* is associated with rhizosphere of plant species growing in harsh conditions. However, plants grown under agricultural conditions showed a biodiversity in their associated-fungal species, the most common fungi are *Fusarium* sp. and *Trichoderma* sp., which were isolated from rhizosphere of *Launaea capitata* and *Ziziphus lotus* grown in harsh conditions. In vitro, *Trichoderma* spp. was able to grow in high concentrations of salt (2 M) and PEG (80%) reflecting a high adaptation of plant associated microbes to both salinity and drought stresses. Results from the antagonistic test showed that *Trichoderma* spp. caused a remarkable growth inhibition of *C. radicola* the causal agent of many diseases in date palm trees.

Conclusion

Data obtained from the current study will lead to the initiation of a Qatari fungal culture collection, which will help conserve the biodiversity and could be essential for future studies. Additionally, plant-associated microbes isolated from different ecosystems can further be used for biological control of important plant diseases and enhancing plant tolerance to abiotic stress. Altogether, results from the current study suggest a prospective implementation of plant-associated microbes for a sustainable agriculture in Qatar.