Assessment of Indigenous Arbuscular Mycorrhizal Fungal Colonization Status in Selected Plants in Kuwait Desert

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Background and Introduction

An examination of arbuscular mycorrhizal (AM) fungal community associated with the roots of selected native plants from Kuwait desert areas has been conducted in this pioneer study. In arid environments, mycorrhizal associations are common and considered a crucial factor for the survival of plants and play an essential role in ecosystem dynamics and productivity (Requena et al., 1996). However, very little attention has been devoted in Kuwait to investigate a comprehensive determination of soil microbial communities, particularly mycorrhizal fungal associations to link biodiversity, ecological processes and structure, and functions. There is no report currently available on the Kuwait Desert areas concerning native plants and the status of AM fungal association.

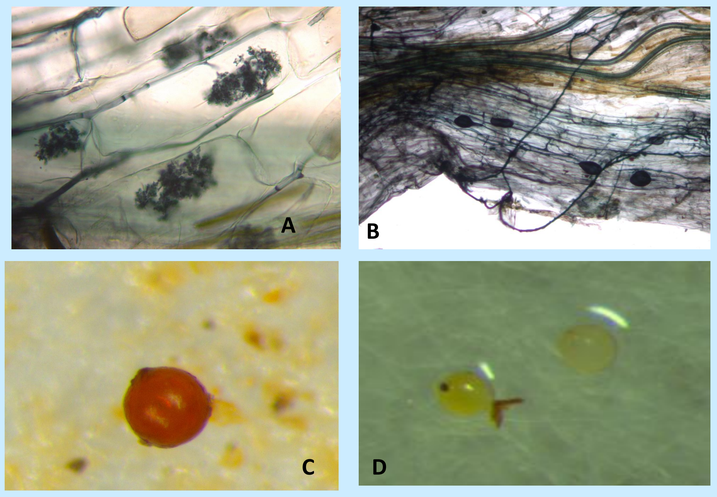
In this research, an attempt was made to characterize AM fungal community associated with common keystone native vegetation growing in the selected study sites in Kuwait desert using both traditional and modern molecular approaches.

Objective

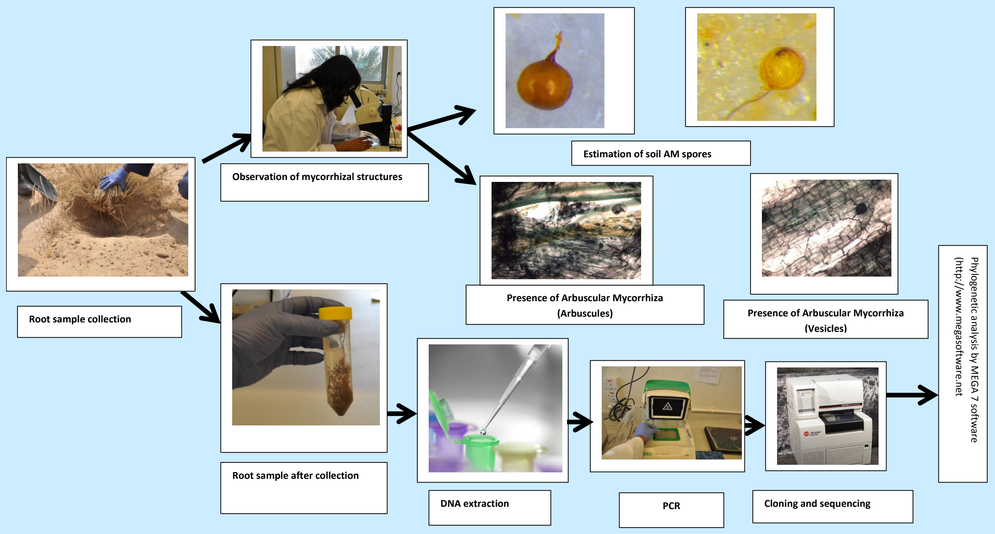
The specific objective is to obtain baseline data and to identify AM fungal association with keystone plant species growing in Kuwait desert areas.

Methodology and Work Plan

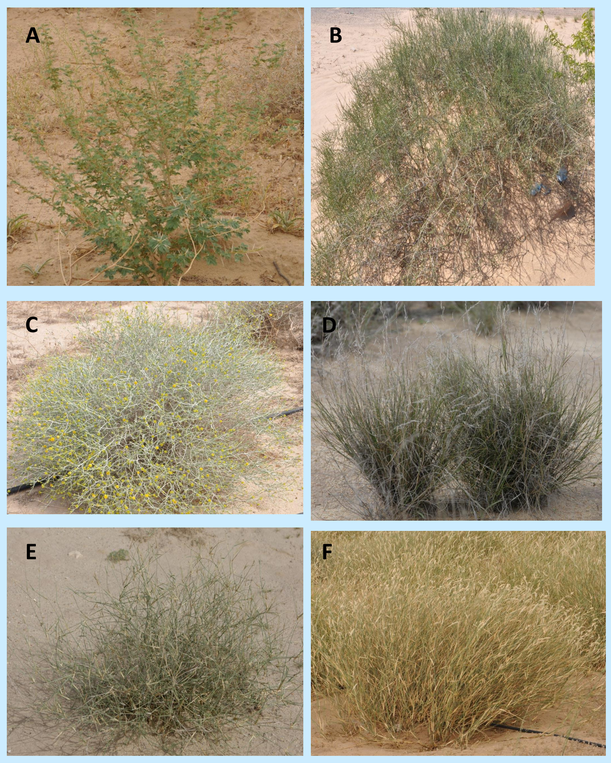
- Key native plant species of Kuwait were selected for this study.
- A total of 20 root samples for winter and 29 root samples for summer were collected from various sites depending upon the availability of plants.
- Chlorazol black E is used to stain the plant roots to detect the presence and rate of infection with AM fungi.
- The mycorrhizal colonization rates in plant roots was determined according to Phillips and Hayman (1970) and Giovannetti and Mosse (1980).
- AM fungal spores in the test soils were evaluated by the wet-sieving and decanting method adopted from Sieverding (1991) and Brundrett et al. (1996).
- DNeasy Plant Mini Kit (Qiagen, Mississauga, Ontario) was used to extract DNA from roots.
- PCR was performed using the fungal universal primers LR1 and NDL22 (van Tuinen et al, 1998, Brito et al. 2012). Cloning and sequencing was adopted for molecular analysis of microbial community.



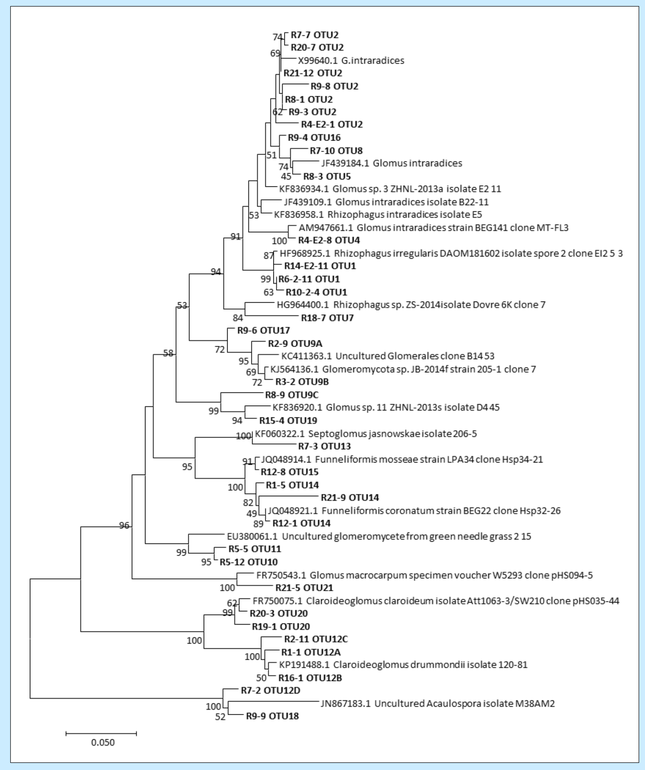
Pic 1. AM fungal infection in selected native plants in Kuwait (A) Arbuscules (B) Vesicles (C) Brown spores (D) Yellow spores.



Pic 2. Flow chart of detailed methodology.



Pic 3. Key native plant species in Kuwait selected for this study; (A) *Acacia pachyceras* (B) *Haloxylon salicornicum* (C) *Rhanterium epapposum* (D) *Stipagrostis plumosa* (E) *Panicum turgidum* (F) *Pennisetum divisum.*



Pic 4. Phylogenetic tree showing the evolutionary relationship of arbuscular fungal taxa.

Results and Discussions

- Typical AM fungal structure were observed with the roots of all the selected test plant species examined from Kuwait desert areas. This observation further supported by the molecular identification of AM communities.
- The degree of AM colonization rates, diversity and soil AM spore count varied widely among the plant species tested, plant communities, between protected and un-protected site, and between winter (2-100%, colonization rates) and summer (0-42%, colonization rates) samples.
- The average spore numbers are much lower in range and smaller in size in our desert soils indicating desertified and anthropogenic nature of soil disturbance in Kuwait desert. Un-protected area had much lower number of spores compared to protected area in each site. Our results are similar to other observations as AM fungal spores are often low in arid soils and zero counts are common (Titus et al. 2002).
- Vesicles of summer samples were found bigger in size with less density, while arbuscules were scanty compared to winter sample.
- A total of 26 clone libraries were produced, on which 3 to 10 clones were successfully sequenced per library. A total of 172 clones were sequenced. However, only 148 clones could be identified in the Glomeromycota group. Other clones belong to Ascomycota with fewer belonging to Basidiomycota and Viridiplantae. Phylogenetic relationships revealed the evolutionary relationship of arbuscular fungal taxa. Most of the identified AM belongs to *Glomus*, *Septoglomus*, *Rhizophagus*, *Funneliformis*, *Claroideoglomus* and a large number of uncultured genus.
- Despite harsh climatic conditions in Kuwait desert, the roots of test plant species exhibited the diverse AM fungal association. Our data demonstrated that AM fungal colonization rates and diversity may differ when collected from different areas with different potential vegetation types, as well as soil conditions, chemical composition, soil inoculum and seasonal effects can also effect the AM colonization (Miller, 2000).

Conclusion

- Despite extreme weather and desertified soil conditions prevailed in Kuwait desert, a considerable level of AM fungal biota present in the Kuwait desert ecosystem.
- Suggesting AM fungi may have adapted to extreme weather condition in Kuwait.
- The most abundant and diversified group identified is in the Glomeromycota group.
- Further investigations using Illumina next-generation sequencing is in progress for further analysis.

Acknowledgement

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