

Biodiversity of Arbuscular Mycorrhizal Fungi in plant roots and rhizosphere soil from different arid land environment of Qatar

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Abstract

Recently more attention or interest has been developed towards the role of Arbuscular Mycorrhizal Fungi (AMF) in plant growth. Qatar as a part of the Arabian Gulf region is mostly arid with hot and dry climatic condition. The current research aims to investigate the Occurrence, species composition and abundance of AMF in Qatar.

Rhizosphere soil samples and roots of 16 plants belonging to 12 families from eight locations were collected. The AMF from different samples were identified based on the sequencing of the PCR product of the amplified conserved ITS region.

The results showed that the AMF infection rate vary with location and plant species. *Tamarix aphylla* recorded the highest AMF infection rate (100%), followed by *Blepharis ciliaris* (98%) and *Sporobolus ioclados* (92%). While all AMF identified at species levels were reported in other regions, this research will be the first to investigate the AMF biodiversity from Qatar. However, new species are still expected since some were identified only at higher taxonomic levels. *Claroideoglossum drummondii* and *Rhizophagus irregularis* were the most widespread species while *Claroideoglossum claroideum* and *Diversispora aurantia* were the less present. This study provides comprehensive biological data about taxonomy, distribution and prevalence of AMF in Qatar soil which opens new research towards developing its future applications for environmental conservation and sustainable agriculture.

Methodology

1- Study site:

Plants and soil samples were collected from different locations in Qatar (Fig. 1) to be used to isolate mycorrhizae species .

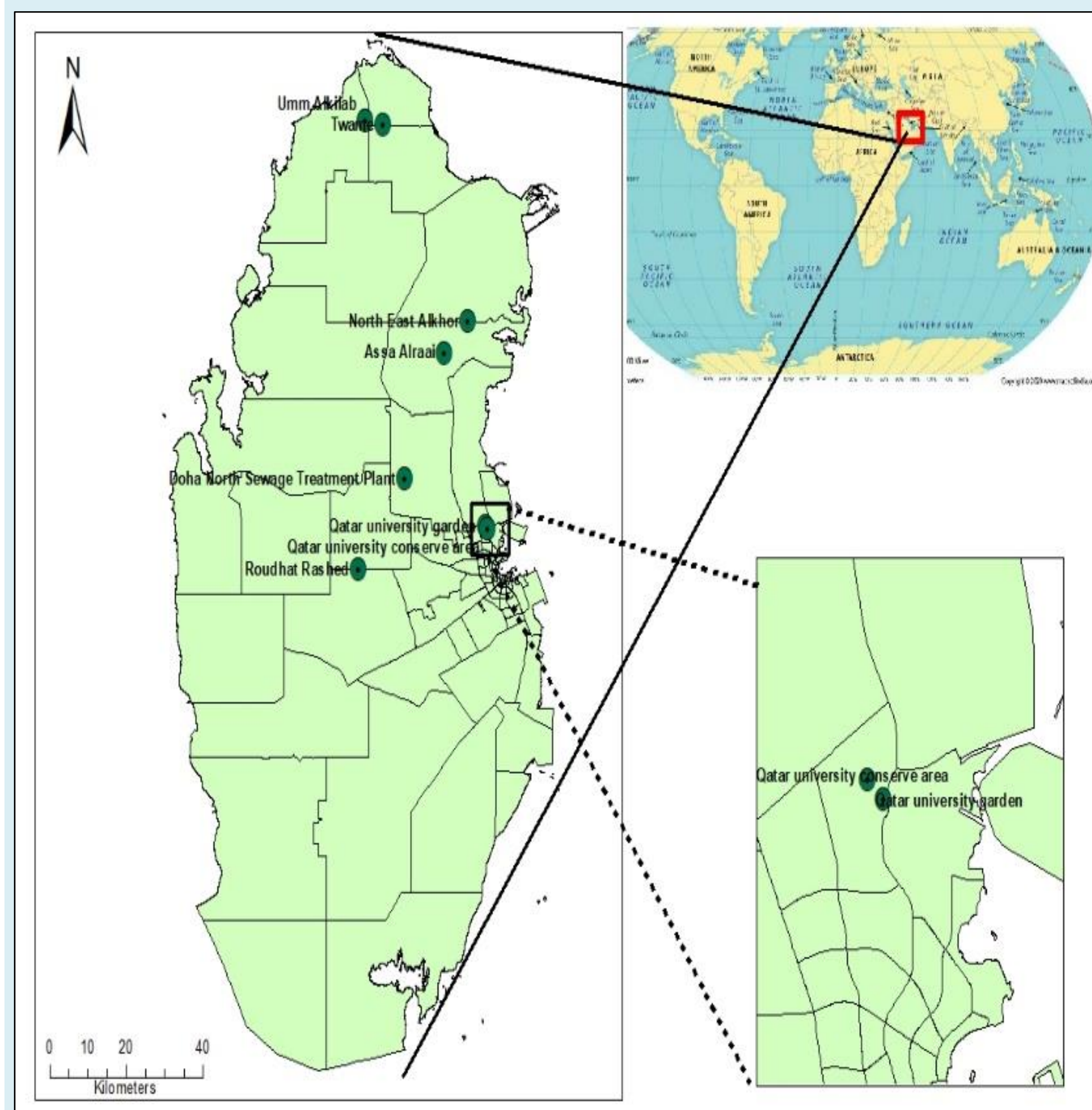


Fig. 1 A map of State of Qatar showing the samples collection sites

2- Isolation of AMF from plant rhizosphere

Using a core borer of 10 x 20 cm soil and roots sample were collected from each location.

Spores were isolated using wet sieving method by take 100 gram of rhizosphere soil and observe the spores under the stereomicroscope.

3- Assessment of AMF root colonization

The roots were cleaned with 10% KOH, then stained with 0.05% trypan blue. Roots were then examined using a compound light microscope at different magnifications. Percent root colonization were counted.

4- DNA Extraction of Rhizosphere Soil Samples

Soil samples (2g/sample) were properly prepared by drying them at room temperature for a week and sifting them with a 500µm sieve. DNA used in the metagenomic analysis was extracted from the 16 soil samples using a modified protocol of the FastDNA Spin Kit for soil and an MP FastPrep-24 5G machine. For each sample, 500mg of fine homogenous soil was transferred and repeated bead-beating was performed using ¼ inch ceramic beads in lysing matrix A to insure a better DNA yield. Samples were then treated as per the manufacturer instruction.

Objectives

- 1- Screening and isolation of AMF from plant rhizosphere.
- 2- Verification of AMF in plant roots.
- 3- Identification of isolated AMF.

Results

1- AMF spores in rhizosphere and root colonization

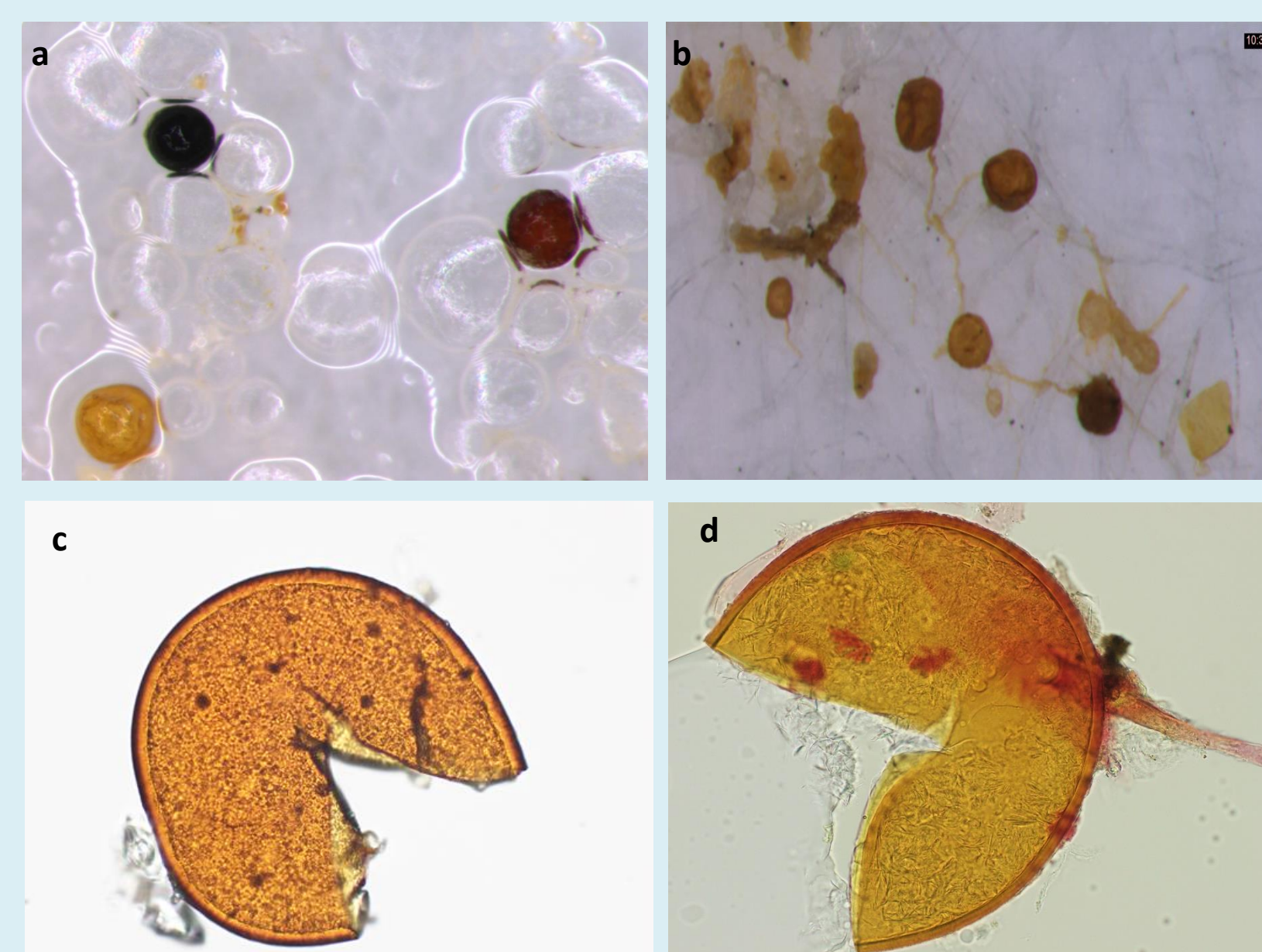


Fig2. Different AMF species: a-b stereoscopic at 10x, c-d compound microscope 10x.

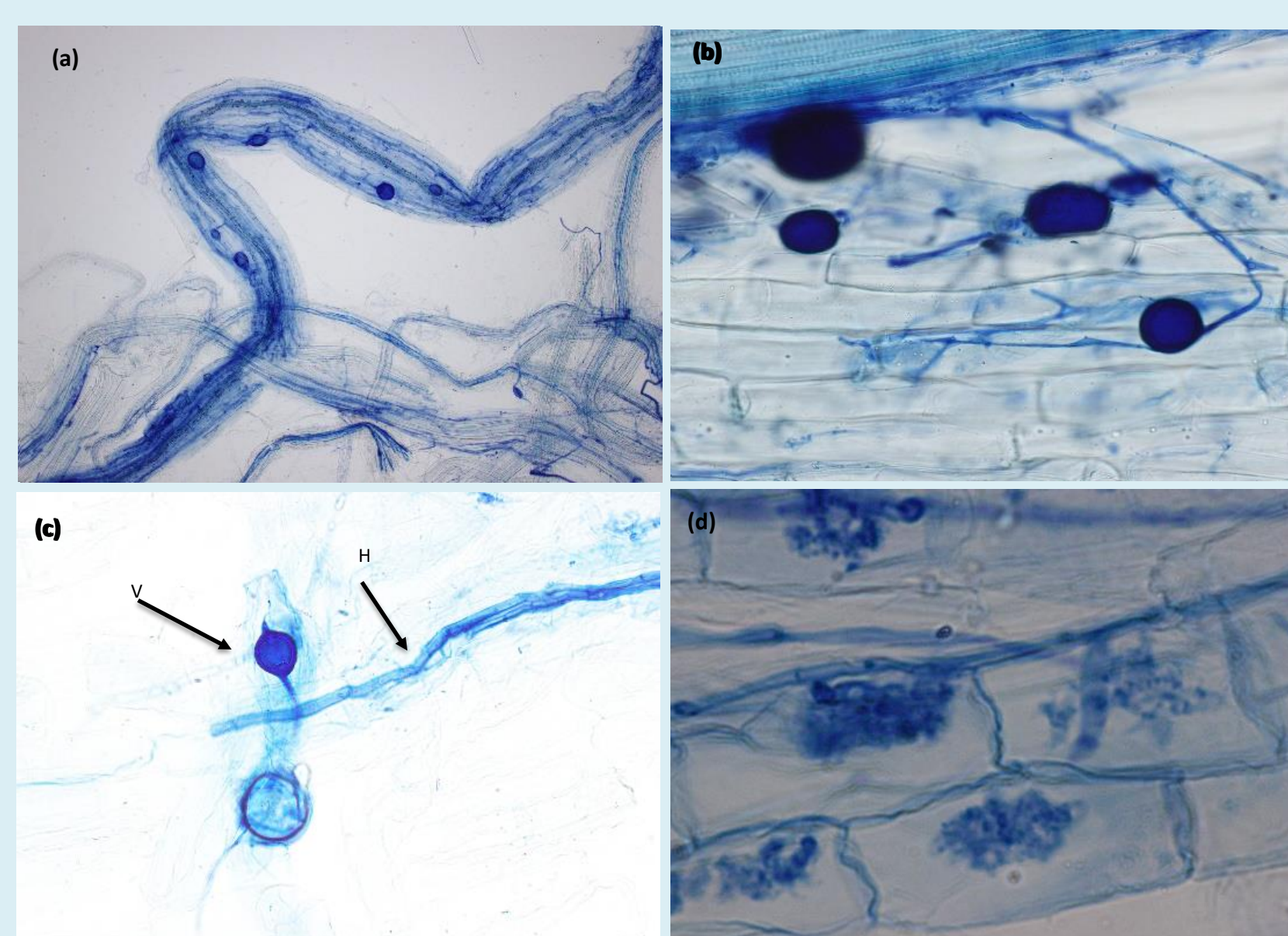


Fig 3. Fungal structures of arbuscular mycorrhizae (AM): (a) Launaea nudicaulis roots (4x). (b) Tamarix aphylla roots (10x). (c) and (d) Pulicaria undulata roots (40x). V: vesicle. H: hypha. A: arbuscular

Table 1. Means of root colonization (±SD, n= 3) (%) of AMF and spore density (number / 100g soil) in different plants at different site locations.

Location	Geographic location Latitude(°N) / Longitude(°E)	() sample No. Host plant	spores/100g soil	AMF root colonization %
Doha North Sewage Treatment Plant	25.454167/51.300564	(2) <i>Zygophyllum qatarense</i>	171.7±6.11	12%
		(3) <i>Tamarix aphylla</i>	150.7±6.11	100%
		(1) <i>Launaea nudicaulis</i>	443±6	63%
Assa Alraai	25.662816/51.393684	(4) <i>Sclerocephalus arabicus</i>	387.3±252.42	32%
		(5) <i>Fagonia indica</i>	643±6.08	32%
Umm Alkhalab	26.049472/51.208722	(11) <i>Spergula fallax</i>	318.3±23.63	10.9%
		(12) <i>Cynodon sp</i>	570.6±88.94	49%
Twame	26.041618/51.249680	(10) <i>Plantago ovata</i>	562.6±76.96	77.8%
North East Alkhor	25.715596/51.449514	(8) <i>Salvia aegyptiaca</i>	581±243.91	78%
		(9) <i>Lycium shawii</i>	407±151.92	50.8%
Roudhat Rashed	25.303106/51.192371	(15) <i>Aizoon canariense</i>	66±6.24	32%
		(16) <i>Pulicaria undulata</i>	39.7±4.93	76.6%
Qatar university Campus	25.374962/51.490011	(13) <i>Malva parviflora</i>	129±36.43	33.9%
		(14) <i>Paronychia arabica</i>	220.3±14.29	22%
Qatar university protected field (Sabkha)	25.370381/51.495726	(6) <i>Blepharis ciliaris</i>	29.3±8.33	98.3%
		(7) <i>Sporobolus ioclados</i>	86.3±8.5	92%

Spore population varied from 29 to 643 spores /100g, the highest spore number was 643 spores /100g dry soil accompanied with *Fagonia indica* at Assa Alraai location followed by *salvia aegyptiaca* 581 at North East Alkhor, while the lowest value was 29 spores /100g accompanied with *Blepharis ciliaris* at Qatar university protected field.

Average number of spores per sample collection was calculated as spore count per 100g soil. The highest spore count was recorded in soil samples of Twame area with 562.7, followed by Assa Alraai 515.2, and Northeast Alkhor 494 spore/ 100g soil (Table 1).

Results Con

2- Molecular Identification of isolated AMF

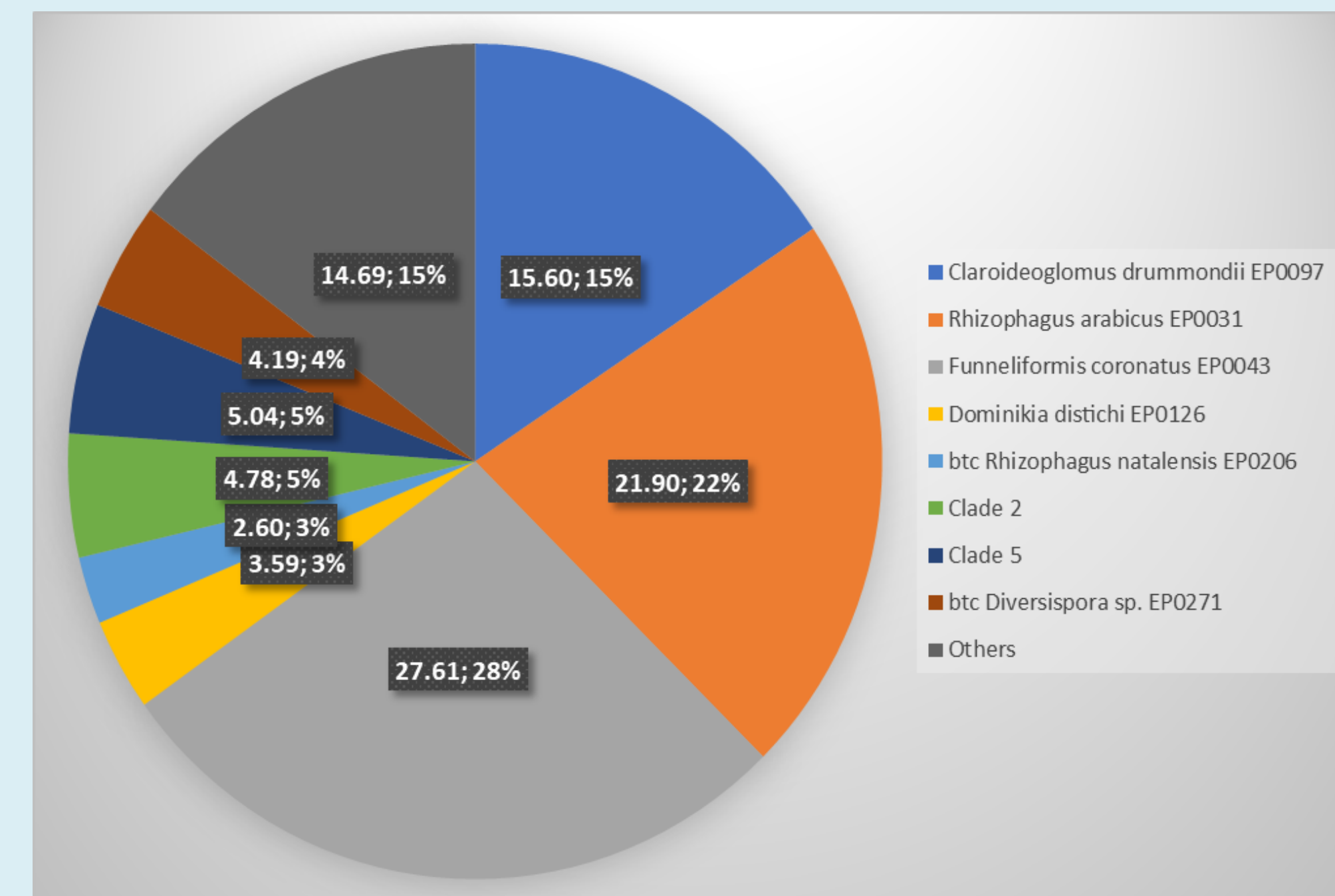


Fig. 4 Identified AMF species abundance (percentage) in respect to overall results

Claroideoglossum drummondii is the most widespread (the only species detected in all samples) and the second most abundant after *Funneliformis coronatus* in terms of read numbers. Sample 16 showed the highest number of identified representative sequences with 26 AMF species detected, followed by samples 13 and 14 with 23 AMF species and samples 8 and 10 with 22 and 21 AMF species respectively. According to Shannon diversity index, samples 8 and 10 are the most diverse (Table 8). *Corymbiglossum pacificum* or a sister species is found with seven reads only in only one sample (sample 7), this is extremely low, but cannot be explained with any artifact, thus is interpreted as a real, but low abundance occurrence. Sample 6 shows the lowest diversity, with three species, all in significant abundance (*Claroideoglossum drummondii* EP0097 66%, *btc Rhizophagus natalensis* EP0206 10%, *btc Rhizophagus silesianum* EP0318 24%).

Conclusion

Rhizosphere soil samples and roots of 16 plant species from eight locations were investigated. 12 representative sequences have been identified at the species levels based on DNA molecular markers. While 2 representative sequences identified at the family level which means these two sequences are either new discovered species or just previously described species which have their DNA not sequenced yet. However, strains that have been discovered to be effective in one environment might be with no effect in another environment, particularly in arid lands so relying on native AMF species is a better choice. Results from such study, will open research for agricultural applications in greenhouse and field crops.

For the selected plant species growing in Qatar, the mycorrhizal colonization with AMF was not studied before. Because all our isolates come from arid environments, these AMF could help in conserving biodiversity of desert ecosystems via biological mechanisms to mitigate the negative effects of abiotic stress. In addition, it might have beneficial applications, mainly in agriculture and food security.

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