NOVEL APPROACH TO STUDY THE DIVERSITY OF SOIL MICROBIAL COMMUNITIES IN QATAR

Faculty and PostDoc, Science and Engineering

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INTRODUCTION

A broad diversity of microorganisms can be found in soil, where they are essential for nutrient cycling and energy transfer. Moreover, soil biodiversity is increasingly recognised to provide many benefits for human well-being; clean air, water and food. Recent high-throughput sequencing methods have greatly advanced our knowledge about how soil, climate and vegetation variables structure the composition of microbial communities in many world regions. However, we are lacking information from several regions in the world, e.g. from Middle-East. Only few studies have previously described the diversity of microorganisms but these have been based on culturing methods.

The main aims of this study were the following:

1. To describe the diversity and composition of soil microbial communities (both all fungi and arbuscular mycorrhizal (AM) fungi vs. all bacteria and nitrogen (N) fixing bacteria) in Qatar
2. To determine which edaphic parameters exert the strongest influences on microbial communities in Qatar

Figure 1. Locations of the study sites.

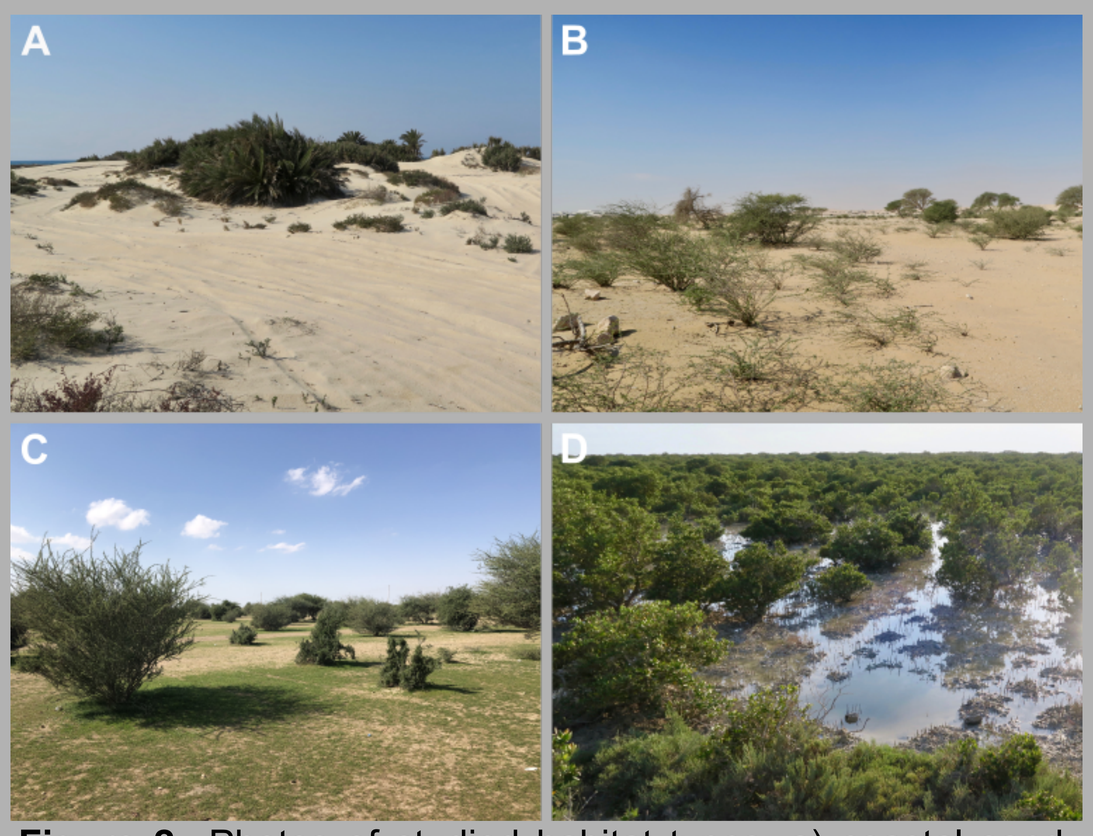

Figure 2. Photos of studied habitat types: a) coastal sand, b) desert, c) rawda and d) mangrove. Photos by J. Oja

MATERIALS AND METHODS

We collected 20 topsoil samples from different habitat types in each of 19 sites across Qatar using standardized protocol (**Figs. 1 and 2**). All 20 soil samples per site were air dried, pooled and grained. For each site, we ran soil chemical analyses (e.g. pH, total N and C, Ca, K, Mg, and P) and extracted DNA from 2 g using DNeasy PowerSoil Kit (Qiagen GmbH, Hilden, Germany).

For amplification of different microbes, we selected four primer sets (**Table 1**).

Table 1. Used primers for each target groups.

Target group (DNA region)	Primer sets
All fungi (ITS)	ITS9MUN (Egger 1995) and ITS4ngsUni (Tedersoo and Lindahl 2016)
AM fungi (SSU rRNA gene)	WANDA (Dumbrell et al. 2011) and AML2 (Lee et al. 2008)
Bacteria (16S rRNA gene (V4-5))	515F (Caporaso et al. 2012) and 926R (Parada et al. 2016)
N-fixing bacteria (NifH gene)	19F and 407R (Ueda et al. 1995)

The presence of PCR products were checked on agarose gels. Later PCR products will be pooled by targeted organism group and sent for sequencing on the Illumina platform. Logistic regression analyses were carried out to assess the effect soil chemical parameters on the presence/absence of different groups based on PCR products on the agarose gel.

RESULTS AND DISCUSSION

Soil chemical analyses showed slightly alkaline to alkaline pH values (7.7-9.1). Preliminary results indicate that in overall bacteria are more abundant in soil than fungi (**Fig. 3**). In few sites we can observe a higher abundance of different targeted microorganisms. For example, there tends to be somewhat greater N-fixing bacterial colonization in mangrove (site 2) than in any other studied site (**Fig. 3d**). This is expected result as previous studies have reported high rate of biological nitrogen-fixing activity in the sediments of mangroves. However, the logistic regression indicates that the presence of all fungi is related with NO2 concentration, whereas AM fungi depend more on Mg and P concentration and N fixing bacteria on the % of total C (**Fig 4**). Our data shows that the higher concentration of NO2 reduces fungal abundance, whereas higher concentrations of Mg and P promote the presence of AM fungi, and similarly higher % of total C enhance the presence of N fixing bacteria. More detailed information on the diversity and composition of soil microbial communities is expected from the high-throughput sequenced data.

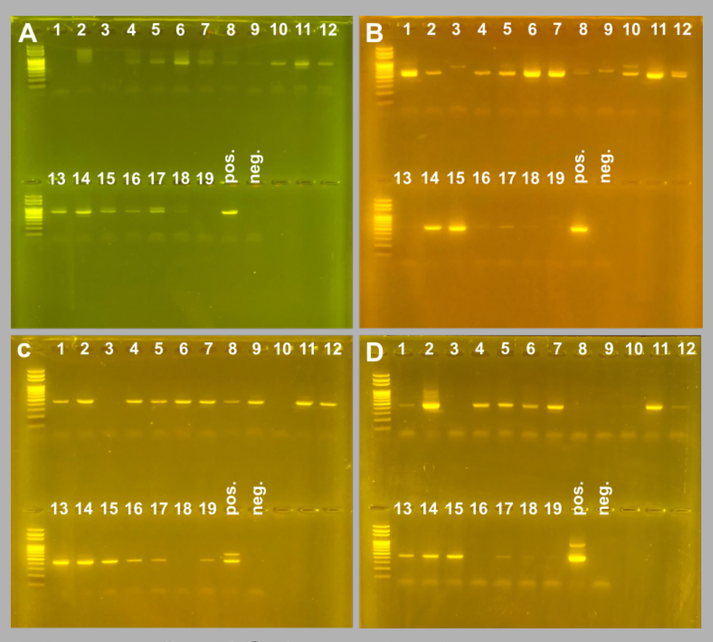

Figure 3. PCR products on agarose gel for a) all fungi, b) AM fungi, c) all bacteria and d) N-fixing bacteria.

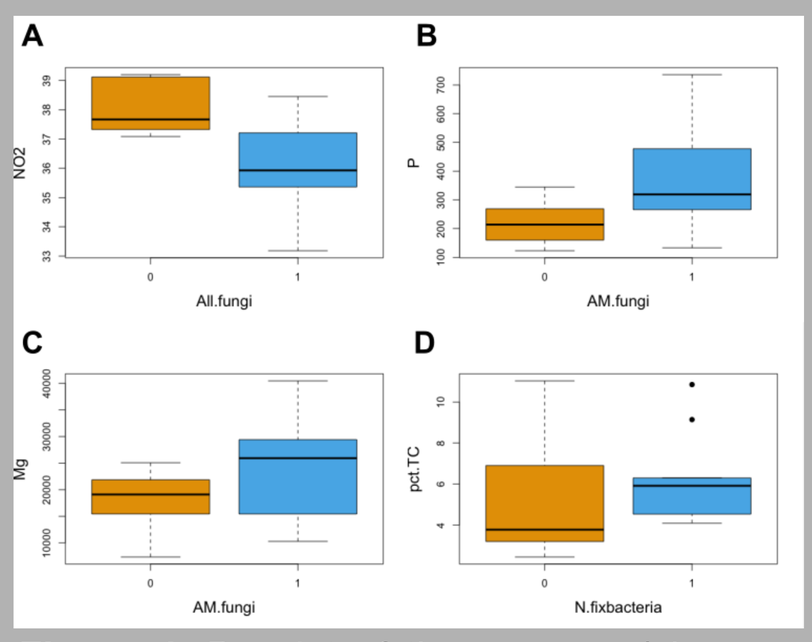

Figure 4. Boxplot of the presence/absence of a) all fungi, b) -c) AM fungi and d) N-fixing bacteria corresponding to NO2, Mg. P concentration and % of total C, respectively.

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