Introduction

Many studies have investigated species compositions in soils of extreme environments (Bontognali et al. 2010, 2012; Farias et al. 2014; Jay et al. 2014); however, most of these have focused on the top layers or subsurface of soils from areas such as hypersaline sediments and Sabkhas (Kjeldsen et al. 2007; Abdeljabbar et al. 2013; Al-Najjar et al. 2014), or saline/soda lakes (Sorokin et al. 2014). In such environments, the biogeochemical cycle of nitrogen and sulphur is very important and shapes the microbial communities (Oren 2008; Al-Thani et al. 2014). Therefore, the abundance and the diversity of species from these sites correlate tightly with the availability of the terminal electron acceptors (oxygen, sulphate, nitrate, ferric ion) that act as source of energy. Recently, novel isolates have been recovered from extreme environments. For example, the extremely halophilic bacterium *Liminonas halophila* was isolated from the mud of hypersaline Lake Aran-Bidgol in Iran (Amoozegar et al. 2013), while *Salinibacter iranicus* and *Salinibacter luteus* were isolated from Aran-Bidgol salt lake in Iran (Makhdoumi-Kakhki et al. 2012). Moreover, volcanic environments (mud, groundwater, aquifers, soil and lakes in craters) have attracted a great deal of attention from many research groups worldwide owing to their microbial diversity and distribution of indigenous species (Herrera & Cockell 2007). This is because the geochemistry of active volcanoes changes frequently, especially in lakes of craters (Mapelli et al. 2015) and their related streams and springs. The typical conditions in these surrounding areas are extreme as they have high temperatures, high concentrations of dissolved metals/minerals and developing patterns of biominerals (Glamoclija et al. 2004), low pH (Löhr et al. 2006). Therefore, screening for new novel species from these volcanic sites has resulted in development of new methods for DNA extraction and isolation (Herrera & Cockell 2007). For example, *Cupriavidus pinatubonensis* and *Cupriavidus laharis* are novel isolates from volcanic mudflow deposits from Mt. Pinatubo, Philippines (Sato et al. 2006). *Methanococcoides* and *Methanosarcina* were isolated and detected in the subsurface of mud volcanoes (Wang et al. 2014). Fluid samples collected from the volcano mud field of Salse di Nirano, Northern Apennines, Italy contained species typical of other saline sediments as well as the sulphate reducers, *Clostridium thiosulfattireducens* and *Desulfovibrio psychrotolerans*, which were involved in cycling of sulphur compounds (Kokoschka et al. 2015). Identifying species in samples collected from volcanic sites is challenging because they include members of the domains Archaea, Bacteria and Eucarya (Mapelli et al. 2015).
Archaea are present in most volcanic environments, including those with very low pH (Löhr et al. 2006). A study of four recent volcanic deposits of different ages (Gomez-Alvarez et al. 2007) showed that Acidobacteria, Alphaproteobacteria, Gammaproteobacteria, Actinobacteria and Cyanobacteria predominated, but the majority of the species were unclassified phylotypes. That study concluded that microorganisms could survive and establish diverse communities in recent volcanic deposits, and the generated consortium shaped their profile according to local deposit parameters. Similarly, many studies have investigated the Atacama Desert (Desierto de Atacama) located as a plateau in South America along the Pacific coast to the west of the Andes mountains. It is the driest, non-polar and oldest desert on Earth (Farias et al. 2014; Rasuk et al. 2014, 2016). Recent findings (Rasuk et al. 2016) have indicated that a large proportion of 16S sequences could not be classified at the phylum level, which may indicate a new phylum is present in this Desert.

The present study was conducted on Wahbah Crater, Saudi Arabia, which is closer in its structure and its morphology to the surface in this Desert. At the phylum level, which may indicate a new phylum is present. Recently, it is considered an ecosystem with a rich palaeo-environmental record that offers its sediments, especially the flat floor, as a potential source to provide a record to serve different sciences and fields. Moreover, flat floor can provide a potential source to disclose the life for the last one million years, where precipitation and evaporation are the most effective factors here.

Sample collection

A pit of approximately 100 cm deep with a diameter of 40 cm was dug using a flat plastic spade in the centre of the Al Wahbah Crater and samples were collected from the following depths: I = 2 cm, II = 20 cm, III = 40 cm, IV = 60 cm, V = 80 cm and VI = 100 cm. The core sediments were solid enough to store and transfer the samples from the field to the laboratory. Each sediment sample was divided into two aliquots, one for geoanalysis parameters and kept at the room temperature while the other for DNA extraction kept in −80°C freezer.

Materials & methods

Site description

Al Wahbah Crater is the deepest and largest crater in Saudi Arabia, being 250 m deep and 2000 m wide. The crater is located in western Saudi Arabia as a part of the Harrat extinct volcanic chain (22°54′5.004″N and 41°8′22.9992″E). Al Wahbah Mountain is 1105 m above sea level. Very few geological studies on Al Wahbah crater have been conducted (Grainger 1996; Moufti et al. 2013; AbdelWahab et al. 2014); however, all of them agreed that the crater was formed by explosive eruptions or volcanic explosions as a result of the interaction between magma and groundwater. Continuous volcanic eruptions resulted in phreatic activities that led to deposition of rocks, lava and debris around the crater and created multiple lava flows, the tuff ring, tephra ring, basement, dolerite plug, scoria cones and wall. Although this unique geotope is considered an ecosystem with a rich palaeo-environmental record that offers its sediments, especially the flat floor, as a potential source to provide a record to serve different sciences and fields.

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Measurements of geoanalysis parameters

Soil samples were dried thoroughly, then sieved through a 2 mm sieve. Next, 0.50 g sieved soil was digested in a mixture of 5 ml of HNO₃, 2 ml of HF and 2 ml of HCl. Trace elements (Na, Mg, K, Ca, Cr, Mn, Fe, Co, Ni, Cu, Zn, As, Se, Sr, Mo, Cd, Ba, Pb, Ti, U) were measured by Inductively Coupled Plasma Mass Spectrometry (ICP-MS), whereas a recovery of 98–100% was achieved using certified reference soil of Internal Atomic Energy Agency soil IAEA-SOIL-7. Sulphate, sulphite, nitrate, nitrite, ammonium and ferric were determined with a DR-3900 spectrophotometer (HACH, Loveland, CO 80 539, USA). Physicochemical parameters (pH, TDS) were measured using an Ultrameter II (Myron L® Company, Carlsbad, CA, USA).

DNA extraction, PCR amplification and pyrosequencing

An amount of 0.25 g of each sediment sample was taken for bacterial identification and analysis. Genomic DNA was extracted using a PowerSoil DNA Isolation Kit (MO BIO Laboratories Inc., Solana Beach, CA, USA) according to the manufacturer procedure. The concentration of the extracted DNA was quantified using Nanodrop 1000 spectrophotometer (Thermo Fisher Scientific, Wilmington, DE, USA). PCR, purification and sequencing of DNA were then carried out in Mr DNA Lab (Molecular Research LP, Shallowater, TX,
DNA samples were adjusted to 100 ng µl$^{-1}$ with PC1 = 46%, PC2 = 19% and PC3 = 13% (three principal coordinates (PCs) were unweighted UniFrac ordinate analysis (PCoA) images were captured to illustrate similarities among each other using Fast UniFrac and principal co-similarity. The overall phylogenetic distance-based, Jackknife, tests with more similar consortium of genera based on matching heatmap for predominant genera and connection lines as cladogram constructed to provide a visual overview of a combined dataset. All analyses. A dual hierarchical dendrogram was used for a single step 30 cycle PCR. The PCR amplification was accomplished using a HotStar Tag plus Master Mix Kit (Qiagen, Valencia, CA, USA) under the following condition: 94°C for 30 min, followed by 28 cycles of 94°C for 30 s, 53°C for 40 s and 72°C for 1 min and then final elongation step at 72°C for 5 min was performed. All amplicon products from different samples were mixed in equal concentrations and purified using Agencourt Ampure beads (Agencourt Bioscience Corporation, Beverly, MA, USA), then subjected to PCR.

**Microbial analysis**

The sequence data were processed using a proprietary analysis pipeline owned by Molecular Research Lab (http://www.mrdnalab.com, MR DNA, Shallowater, TX, USA). Briefly, the following sequences were removed; sequences are encoded with barcodes and primers that shorter than 200 bp, sequences with ambiguous base calls and sequences with homopolymer runs exceeding 6 bp. Finally, chimeras were removed after de-noising sequences. After removal of singleton sequences, operational taxonomic units (OTUs) were defined and clustered at 3% divergence. Taxonomic classification of OTUs obtained was conducted by BLASTn searches against a curated Greengenes/RDP/NCBI-derived database (DeSantis et al. 2006) and compiled into each taxonomic level. A compact package of different statistical analyses including XLStat, NCSS 2007, ‘R’ and NCSS 2010 was used. Alpha and beta diversity analysis was conducted (Swanson et al. 2011) using Qima (http://www.qima.org). A p < 0.05 was considered to indicate significance for all analyses. A dual hierarchical dendrogram constructed to provide a visual overview of a combined heatmap for predominant genera and connection lines as clusters with more similar consortium of genera based on matching similarity. The overall phylogenetic distance-based, Jackknife, on the OTU data showing the biodiversity of bacterial communities among each other using Fast UniFrac and principal coordinate analysis (PCoA) images were captured to illustrate differences in the microbiota. UniFrac PCoA analyses for the three principal coordinates (PCs) were unweighted UniFrac with PC1 = 46%, PC2 = 19% and PC3 = 13% (p = 0.001).

**Results**

**Geoanalysis results**

All six soil samples (different depths) were saline ( ~ 23 000–29 000 ppt; Table 1), which is very close from TDS value of the seawater (~ 33 000 ppm). The pH in the different depth layers is slightly alkaline (average pH = 8.69; Table 1). Generally, Al Wahbah soil contained higher concentrations of trace elements than those of the reference soil (IAEA 1984) especially Na, Sr and Cu, which were present at 19, 7 and 4%, respectively (Table 2). However, the concentration of elements such as Ca, Se and Pb were less in Al Wahbah soil than that of the reference soil.

In the upper 60 cm of Al Wahbah studied soil, sulphate and sulphite concentrations did not considerably vary (from 26.5 to 27.5 mM for sulphate and it was around 37 mM for sulphite; Fig. 1). The concentrations for both sulphate and sulphide decreased ~ 18 and 13%, respectively, which suggest consumption of sulphate through probably sulphate reducing bacteria. The concentration of other nutrients such as nitrate, nitrite, ammonium and iron containing nutrients were below detection limits. The concentration of sulphates and sulphites exceeded 25 mM and they showed similar depletion profiles.

**Microbial community structure**

After stringent quality sequence curation, 41 524 sequences were parsed and 33 081 were then clustered. A total of 33 063 sequences identified as bacteria or archaea were used for the final analyses. The average number of reads per sample was 2755. For alpha and beta diversity analysis, samples were rarified to 1000 sequences and bootstrapped at 800 sequences. Table 3 summarizes the number of sequences and OTUs at 97% similarity, as well as the diversity indices for bacteria.

The Shannon–Wiener Index curve plot (Fig. 2) reached a plateau at just over 100 sequences, indicating that sequencing depth was sufficient to capture the full scope of microbial diversity and the rarefaction curve was sufficient to reflect the full coverage of bacterial and archaeal richness. The biodiversity was very high among samples, with that of sample I being highest (7.18) and sample IV (i.e., 60 cm) lowest (5.88). Interestingly, the deepest layer (i.e., 100 cm) showed the second highest biodiversity, based on Shannon–Wiener index, after the uppermost layer (Table 2). Additionally, the greatest microbial richness (bacteria and archaea) was observed in sample I (i.e., 2 cm).

Archaea genera dominated the uppermost layer and the deepest two layers (at 2.0, 80.0 and 100.0 cm), while bacteria genera comprised ~ 50% of the microbial community in the middle section of the pit (20.0–60.0 cm), Fig. 3. The most predominant phylum identified from Al Wahbah Crater soil was Euryarchaeota, which comprised ~ 91% of the total microbial population for sample I (Fig. 4). As depth increased, the relative abundance of Euryarchaeota decreased to ~ 50% for samples II, III and IV. However, the abundance of Euryarchaeota increased again to ~ 70 and ~ 80% for samples V and VI, respectively (Fig. 4). Moreover, when considering genera accounting for >5% of the relative abundances, the archaeal halophilic genera Halorhabdus and Halorubrum showed the greatest abundance across samples, with average values of 30 and 14%, respectively. Conversely, Bacillus accounted for an average of 17% of the community in the middle section (Fig. 5).
Majed Albokari et al.

Table 1. Physicochemical proprieties of Al Wahbah soil samples

| Elements          | I, 2.0   | II, 20  | III, 40 | IV, 60  | V, 80   | VI, 100 | AV  |
|-------------------|----------|---------|---------|---------|---------|---------|-----|
| Moisture content (%) | 21.4     | 19.5    | 18.7    | 18.7    | 21.1    | 22.8    | 20.4|
| pH                | 9.31     | 8.31    | 8.39    | 8.62    | 8.37    | 8.83    | 8.64|
| TDS (ppt)         | 28 960   | 23 700  | 23 060  | 26 840  | 25 470  | 26 830  | 25 810|

Discussion

Extreme habitats comprise one of the few ecological systems that can benefit several other fields such as biotechnology and site remediation. Additionally, extreme habitats provide valuable historical information that help scientists to recover and to draw vital findings about past life and about the adaptations for survival. For example, the theory of life possibility on Mars might be supported by the presence of active microbial life in Earth’s extreme habitats, which are similar to that on Mars. In this study, the bacterial and archaeal communities associated with soil in an ancient, inactive and remote crater in Saudi Arabia, Al Wahbah, were investigated in the upper 100 cm. The geochemical parameters and the physicochemical parameters were measured and were linked to the microbial community structure of the Al Wahbah Crater to evaluate vibrant performance. Rare rainfall on the studied site, together with high evaporation rate will evaporate the water shortly leaving dry surface. This will select against the microorganisms that cannot tolerate these conditions, which are most likely the ones introduced to the system by the rain and will keep those who can survive the extreme conditions.

The level of trace elements in the soil samples did not show any metal contamination or radioactivity, although extreme salinity was observed, with an average total dissolved salts of approximately 25 810 ppt. The absolute pH values (I = 9.3, II = 8.3, III = 8.4, IV = 8.6, V = 8.4, VI = 8.8) were slightly alkaline while the moisture content ranged from 18 to 23%. Electron donors and acceptors used usually by the microbial community, such as nitrate, nitrite, sulphate, ferric ions and manganese, were almost negligible at along the depth. Specifically, nitrate, nitrite, ammonium and ferric ions were present at less than 2, 0.05, 1.5 and 0.2 mg l⁻¹, respectively, indicating poor conditions for most microorganisms. Sulphates and sulphites showed similar behaviour throughout the depth profile (Fig. 1), where the substances slowly depleted from approximately 27.2 and 0.090 mM down to 22.5 and 0.070 mM for sulphates and sulphites, respectively. This depletion of sulphate and sulphite coincided with increase in the relative abundance of members belonging to the family Thermodesulfobacteriaceae that are well known by their sulphate reduction activities. The relative abundances of this order increased gradually with the depth reaching to the highest at 60 cm (Fig. S1), where sulphate concentrations started to decrease steeply (Fig. 1). These conditions have resulted in formation of obvious stratification in the bacterial and archaeal communities (Löhr et al. 2006; Al-Thani et al. 2014; Mapelli et al. 2015). Although the changes in the measured sulphur species content were small, they may contribute to the proliferation of sulphates/sulphites reducers (Kokoschka et al. 2015). Higher relative abundances of archaeal OTUs were observed than bacterial OTUs throughout the depth profile, which suggests that the available conditions are more suitable for archaeal growth than those for bacteria. Additionally, there were higher Shannon and Chao1 values (Fig. 2 and Table 3) for sample I than the other samples suggesting much more biodiversity in that layer. Indeed, this increased biodiversity can be seen from the presence of different groups of microorganisms including sulphate reducers (Fig. S1) and photosynthetic cyanobacteria (Fig. S2). This microbial composition is very similar to that for hypersaline microbial mat ecosystems (Frank & Stolz 2009; Al-Najjar et al. 2014). Typically, in a microbial mat, the upper most layer is characterized by having photosynthetic microorganisms such as cyanobacteria, which are efficient light utilizing microorganisms. They use light energy to reduce CO₂ and subsequently produce organic material that acts, normally, as C and energy source for the subsequent layers in the mat. The deeper layers of a microbial mat, where O₂ is depleted, are typically dominated by anaerobic microorganisms such as sulphate reducers, methane producers and other fermenting bacteria. The microbial community structure in Al Wahbah crater showed the presence of cyanobacteria in the upper most layer (Fig. S2); however, the presence of the cyanobacteria in the deeper layers suggests burial events. It is well documented that cyanobacteria in the deeper layers shift their metabolism to heterotrophy or to fermentation (Jørgensen et al. 1988). The deep layers of Al Wahbah Crater were dominated by other groups of microorganisms (Figs. 3 and 4). Moreover, heatmap analysis and RDP classifiers revealed that five diverse genera were commonly present among samples, Halorhabdus, Halorubrum, Bacillus, Salinibacter and Halorhodospira (Fig. 6). Among these, Halorhabdus was dominant and consistent, followed by Halorubrum and Bacillus, which comprised 19% of the

Figure 6 shows a dual hierarchal dendrogram constructed to provide a visual overview of a combined heatmap for predominant genera and connection lines as clusters with more similar consortium of genera based on matching similarity. Samples I, V and VI formed a cluster separate from that of samples II, III and IV, indicating a significant difference between the two clusters.

UniFrac significance tests (Table S2) were made based on comparisons with 1000 randomized trees and p values were only listed if they were >0.05. Hence, all other pairwise comparisons indicated a significant difference between samples.

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Table 2. Trace elements concentration of Al Wahbah soil samples relative to reference soil

| Elements | Al Wahbah Samples, ppm | Reference Soil, ppm | Niche for high abundant extremophilic microbial communities in an ancient crater |
|----------|------------------------|---------------------|---------------------------------------------------------------------------------|
| Na       | 46 100                 | rsd 2.21 rsd 36 000 | rsd 1.68 rsd 42 600 rsd 1.59 rsd 28 100 rsd 2.28 rsd 46 700 rsd 1.03 rsd 40 500 rsd 1.95 rsd 40 001 rsd 2080 rsd 1.19 rsd 19.2 |
| Mg       | 22 100                 | rsd 1.48 rsd 29 000 | rsd 1.53 rsd 29 900 rsd 1.38 rsd 17 700 rsd 1.68 rsd 30 600 rsd 0.31 rsd 34 300 rsd 2.28 rsd 27 268 rsd 9570 rsd 0.22 rsd 2.8 |
| K        | 15 200                 | rsd 1.65 rsd 14 700 | rsd 1.5 rsd 15 000 rsd 1.59 rsd 10 800 rsd 1.21 rsd 14 800 rsd 0.96 rsd 14 300 rsd 0.68 rsd 14 134 rsd 12 100 rsd 0.91 rsd 1.2 |
| Ca       | 41 700                 | rsd 2.41 rsd 46 600 | rsd 1.73 rsd 49 700 rsd 1.94 rsd 31 400 rsd 1.25 rsd 53 700 rsd 1.08 rsd 56 500 rsd 0.77 rsd 46 601 rsd 114 000 rsd 5.02 rsd 0.4 |
| Cr       | 104                    | rsd 1.74 rsd 104    | rsd 1.95 rsd 101 rsd 2.23 rsd 73 rsd 2.48 rsd 104 rsd 1.51 rsd 98 rsd 1.17 rsd 99 rsd 61 rsd 1.95 rsd 1.6 |
| Mn       | 927                    | rsd 2.28 rsd 1070   | rsd 0.63 rsd 1080 rsd 1.9 rsd 772 rsd 2.09 rsd 1050 rsd 1.32 rsd 1050 rsd 1.25 rsd 993 rsd 729 rsd 2.66 rsd 1.4 |
| Fe       | 48 900                 | rsd 1.75 rsd 54 200 | rsd 1.9 rsd 54 400 rsd 1.24 rsd 37 700 rsd 1.4 rsd 52 500 rsd 0.58 rsd 52 000 rsd 3.12 rsd 49 951 rsd 25 000 rsd 2.56 rsd 2.0 |
| Co       | 25                     | rsd 2.18 rsd 27     | rsd 2 rsd 30 rsd 14.4 rsd 21 rsd 13.3 rsd 27 rsd 0.831 rsd 26 rsd 1.8 rsd 31 rsd 16 rsd 16.6 rsd 1.9 |
| Ni       | 85                     | rsd 1.28 rsd 81     | rsd 0.28 rsd 83 rsd 1.11 rsd 60 rsd 1.79 rsd 80 rsd 1.01 rsd 82 rsd 2.29 rsd 79 rsd 26 rsd 1.22 rsd 3.1 |
| Cu       | 46                     | rsd 2.94 rsd 53     | rsd 1.87 rsd 52 rsd 1.39 rsd 38 rsd 1.59 rsd 51 rsd 0.88 rsd 52 rsd 1.23 rsd 50 rsd 13 rsd 1.52 rsd 4.0 |
| Zn       | 108                    | rsd 0.95 rsd 113    | rsd 1.2 rsd 114 rsd 1.55 rsd 79 rsd 2.45 rsd 110 rsd 2.12 rsd 110 rsd 0.71 rsd 107 rsd 113 rsd 1.85 rsd 0.9 |
| As       | 5                      | rsd 10.9 rsd 3      | rsd 8 rsd 3 rsd 9.76 rsd 2 rsd 17.8 rsd 4 rsd 8.55 rsd 2 rsd 8.72 rsd 12 rsd 21 rsd 10.6 rsd 0.6 |
| Se       | 4                      | rsd 10.2 rsd 4      | rsd 15.8 rsd 4 rsd 12.1 rsd 2 rsd 20.8 rsd 4 rsd 10.5 rsd 3 rsd 9.16 rsd 15 rsd 4 rsd 11.6 rsd 3.5 |
| Sr       | 488                    | rsd 0.66 rsd 696    | rsd 1.04 rsd 748 rsd 0.92 rsd 551 rsd 2.12 rsd 798 rsd 1.44 rsd 942 rsd 1.01 rsd 705 rsd 104 rsd 2.27 rsd 6.8 |
| Mo       | 3                      | rsd 2.42 rsd 3      | rsd 2.12 rsd 2 rsd 2.77 rsd 2 rsd 2.32 rsd 2 rsd 1.98 rsd 2 rsd 3.18 rsd 4 rsd 2 rsd 1.59 rsd 2.8 |
| Cd       | 0                      | rsd 3.67 rsd 0      | rsd 4.79 rsd 0 rsd 2.61 rsd 0 rsd 3.42 rsd 0 rsd 11.5 rsd 0 rsd 10.7 rsd 5 rsd 1 rsd 3.87 rsd 3.5 |
| Ba       | 249                    | rsd 2.73 rsd 253    | rsd 2.76 rsd 264 rsd 1.65 rsd 187 rsd 1.62 rsd 273 rsd 5.85 rsd 260 rsd 1.08 rsd 250 rsd 132 rsd 1.36 rsd 1.9 |
| Pb       | 9                      | rsd 2.53 rsd 8      | rsd 2.77 rsd 9 rsd 0.71 rsd 5 rsd 1.81 rsd 7 rsd 0.41 rsd 8 rsd 0.54 rsd 9 rsd 54 rsd 1.85 rsd 0.2 |
| Ti       | 5840                   | rsd 0.82 rsd 6650   | rsd 2.27 rsd 6500 rsd 1.41 rsd 4840 rsd 1.64 rsd 6710 rsd 1.91 rsd 6440 rsd 1.01 rsd 6165 rsd 3110 rsd 0.85 rsd 2.0 |
| U        | 1                      | rsd 0.99 rsd 2      | rsd 2.17 rsd 2 rsd 1.57 rsd 1 rsd 1.7 rsd 1 rsd 0.741 rsd 1 rsd 1.06 rsd 3 rsd 2 rsd 1.17 rsd 1.3 |
population (at upper and lower depth) and 17% (at the middle section), respectively. The variability of this diversity and distribution among the halophilic genera (Fig. 6) are controlled by adaptation to the saline ecosystem (Wainø et al. 2000; Antunes et al. 2008). H. tiamatea, which was isolated from the hypersaline anoxic basin of the Red Sea, might have a common origin with the organisms identified in this study as the Red Sea is about a 100 km to the west from Al Wahbah crater. H. tibetense, which is known as an aloalkaliphilic organism, accounted for 19% of the archaeal community in all samples (Fan et al. 2004), while several other Halorubrum species were detected at very low levels (≤2.0%) by 454 pyrosequencing. Similarly, Bacillus and Salinibacter comprised an average of 27 and 20%, respectively, of the bacterial

![Figure 1](image1.png)

**Fig. 1.** Vertical depth profile of sulphate and sulphite behaviour in the collected samples of Al Wahbah soil.

| Table 3. Number of sequences and OTUs at 97% similarity diversity indices for bacteria |
|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|
| Index           | I               | II              | III             | IV              | V               | VI              |
| No. of sequences| 18,836          | 4,132           | 1,090           | 3,391           | 1,641           | 3,973           |
| Total OTUs      | 701             | 911             | 915             | 894             | 875             | 836             |
| No. Archaea OTUs| 640             | 459             | 475             | 429             | 624             | 668             |
| No. bacteria OTUs| 61              | 452             | 440             | 465             | 251             | 168             |
| Chao1           | 656.23          | 216.04          | 248.65          | 216.52          | 255.18          | 370.74          |
| Shannon         | 7.18            | 5.99            | 6.19            | 5.88            | 6.64            | 6.89            |
Fig. 2. Shannon–Wiener curve of the samples at different depths.

Fig. 3. Relative percentage of bacteria and archaea per sample.
Fig. 4. Relative abundance of the predominant phyla >5% across samples.

Fig. 5. Relative abundance of the predominant genera >5% across samples.
Fig. 6. Dual hierarchical dendrogram evaluation of the taxonomic classification data.

Fig. 7. UniFrac PCoA image (left) and UniFrac distance-based Jackknife clustering (right) showing differences among the six soil samples based on the OTU data.
community. However, *B. cellosolyticus* and *S. iranicus* were the major identified species among *Bacillus* and *Salinibacter*, respectively and they are known for extremely halophilic (Makhdoumi-Kakhki et al. 2012).

Another pattern of diversity was constructed among phyla to measure the consistency among the six soil samples. The defined archaeal phylum was identified as *Euryarchaeota*, which probably reflected the marked functional diversity (Suh et al. 2015) of halophiles. Three other observed phyla, *Firmicutes*, *Proteobacteria* and *Bacteroidetes*, showed the same pattern and consistency throughout sequencing data, with *Firmicutes* showing slightly more abundance (~4%) (composed mostly of *Bacillus* as soil consortium) than the other two. Overall, 13% of the phyla consisted of *Proteobacteria* (8%) and *Bacteroidetes* (7%). Moreover, the UniFrac PCoA image and UniFrac distance-based Jackknife clustering (Fig. 7) of the whole microbial community (bacterial and archaeal) associated with the six soil samples revealed three clusters, sample I alone, samples II, III and IV, and samples V and VI.

This comparison of the whole microbial community structure for 16S rRNA gene sequences clearly differentiates the whole community (bacterial and archaeal) associated with the six soil samples revealed three clusters, sample I alone, samples II, III and IV, and samples V and VI.

**Conclusion**

Overall, the microbial diversity and structure observed for the six samples in the Al Wahbah Crater site clearly responded to the soil constituents and surrounding environmental conditions. Soil texture, salinity and nutrient levels were found to be the main geochemical parameters influencing variations in the microbial community. Additionally, *Euryarchaeota* was the major phyla and *Halorhabdus* was the dominant genus. This study with the geoanalysis has provided close insights of what the flat floored of Al Wahbah Crater site made of to facilitate the survival of microbial community, which turned to be halophiles. The community observed at 100.0 cm likely reflects the profile of biological activity for a historical era and the isolates can be considered extreme species.

**Supplementary material**

The supplementary material for this article can be found at https://doi.org/10.1017/S1473550417000295.

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