

读书报告

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Desiccation- and Saline-Tolerant Bacteria and Archaea in Kalahari Pan Sediments

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Kalahari 沙漠沉积物中耐干旱、耐盐的细菌和古菌

IF=4.9





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Microbial Community Responses to Modern Environmental and Past Climatic Conditions in Omongwa Pan, Western Kalahari: A Paired 16S rRNA Gene Profiling and Lipid Biomarker Approach

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Present and past microbial life in continental pan sediments and its response to climate variability in the southern Kalahari

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Introduction

- Organisms have developed various methods of adapting to the harshest of environments, ranging from hot springs and hydrothermal vents (Kallmeyer, 2017) to permafrost (Mitzscherling et al.,2017) and hypersaline lakes (Ventosa et al., 2011).
- All over the world, hypersaline environments are inhabited by a variety of microorganisms (DasSarma and Arora, 2001), archaea and bacteria.
- Illumina 16S rRNA gene sequencing was using to analyze the microbial diversity and the distribution patterns in Witpan in northwestern South Africa. We compared the microbial communities and geochemical features of Witpan with those of the Omongwa pan.
- This study aims to provide a better understanding of the saline and dry habitats and their diverse microbial ecosystems.



Materials and methods

Kalahari Desert

a large semi-arid sandy savanna



Kalahari in Namibia



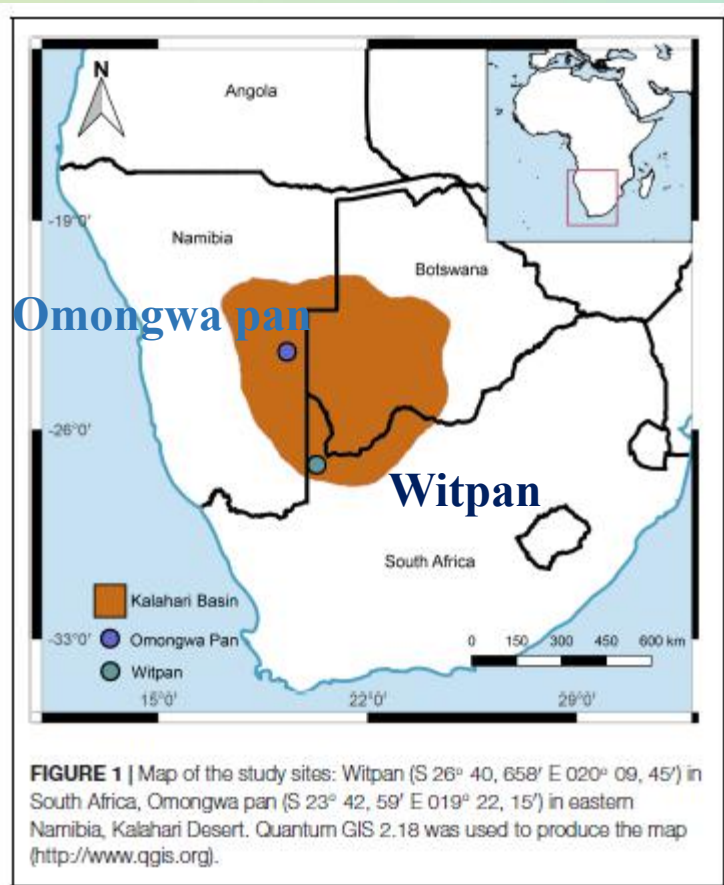
Natural **salt pans** or **salt flats** are flat expanses of ground covered with salt and other minerals, usually shining white under the sun. They are found in deserts, and are natural formations.

Salt pans



Materials and methods

Study Site and Sampling



Sample material was collected from the pan sediments of Witpan in northwestern South Africa and from the Omongwa pan in Namibia in the western Kalahari

0-15cm, at 3-cm intervals

15-50cm, at 5-cm intervals

50–180 cm, at 15-cm intervals



Materials and methods

Quantification of Phospholipid-Derived Fatty Acids

Sediment Properties

DNA Extraction and Preparation of Next-Generation Sequencing

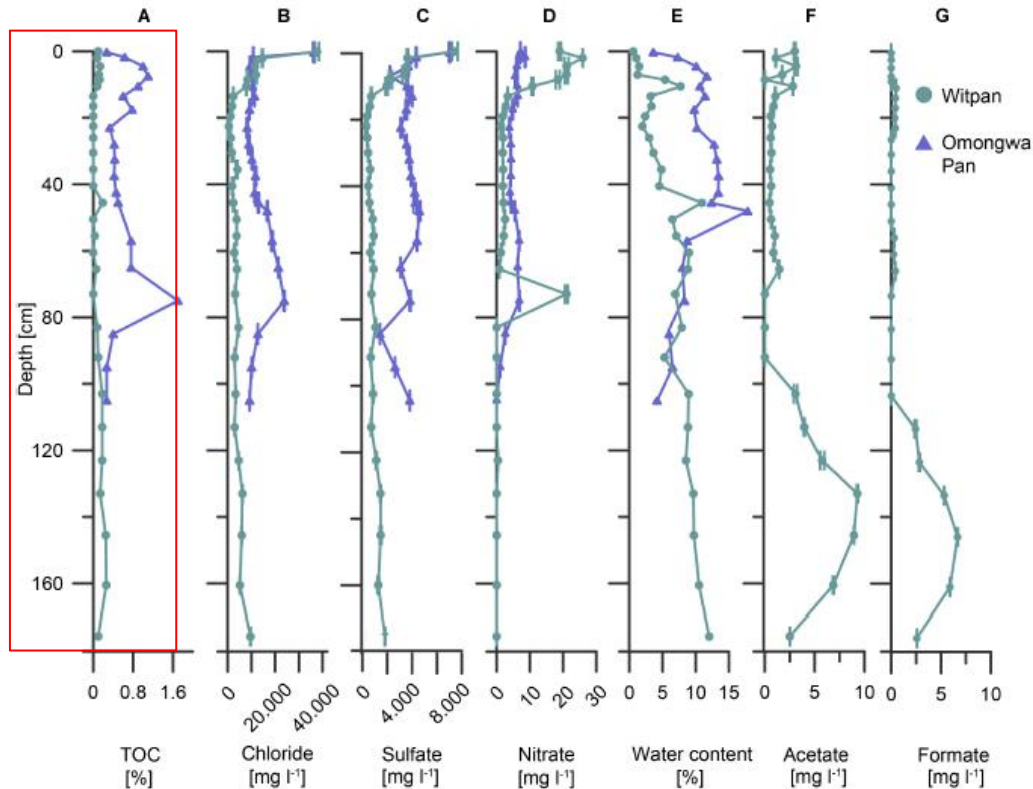
Quantitative Polymerase Chain Reaction Analysis of Archaeal and Bacterial

SSU rRNA Genes



Results

Abiotic and Biotic Parameters of Witpan and Omongwa Pan



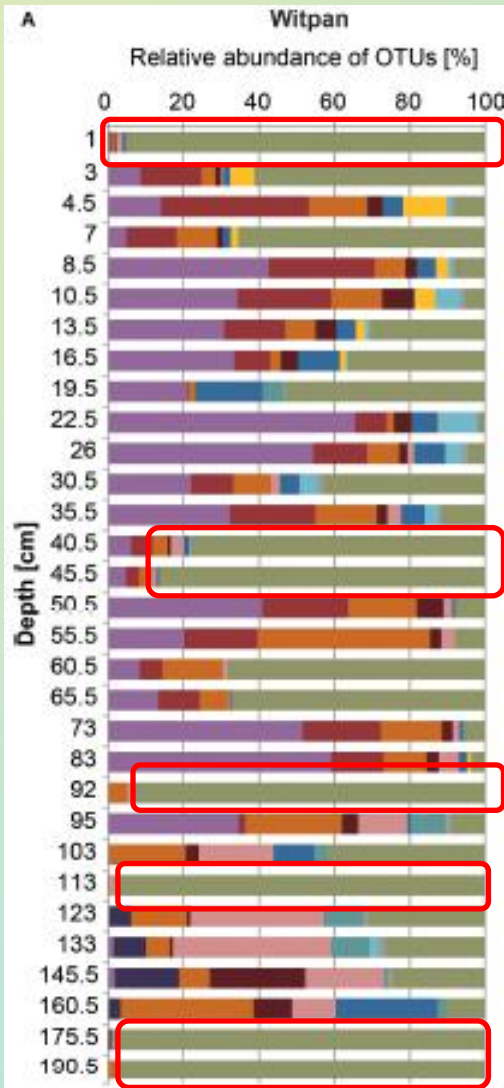
Witpan: TOC 0.03-0.26wt%

Omongwa pan: 0.3-1.7wt%

FIGURE 2 | Abiotic and biotic parameters of Witpan (turquoise) and the Omongwa pan (purple) with depth. **(A)** Total organic carbon (TOC), **(B)** chloride, **(C)** sulfate, **(D)** nitrate, **(E)** water content, **(F)** acetate, and **(G)** formate [(B-D,F,G) were obtained from sample leaching]. Note different x-scales.



Microbial Community Composition of Witpan and Omongwa Pan



All sequence were detected as 407 OUTs

Witpan: majority of archaeal sequences:17 OTUs,

Euryarchaeota(depth 0-150cm);

Class *Halobacteria*:14 OTUs, genera *Halobiforma*,

Natronococcus, *Halococcus*, *Halomicrobium*, uncultured genera.

Sequences of Firmicutes were detected throughout the entire depth profile. Several layers are dominated by Firmicutes at top layer,40-45.5cm,92cm,113cm,175cm.

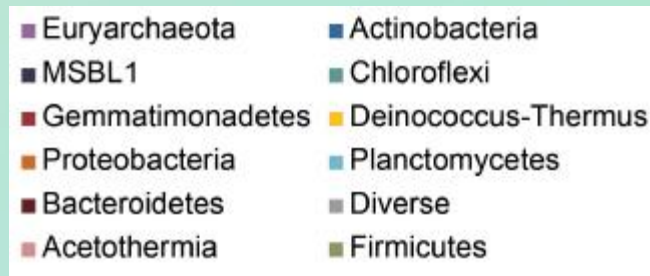
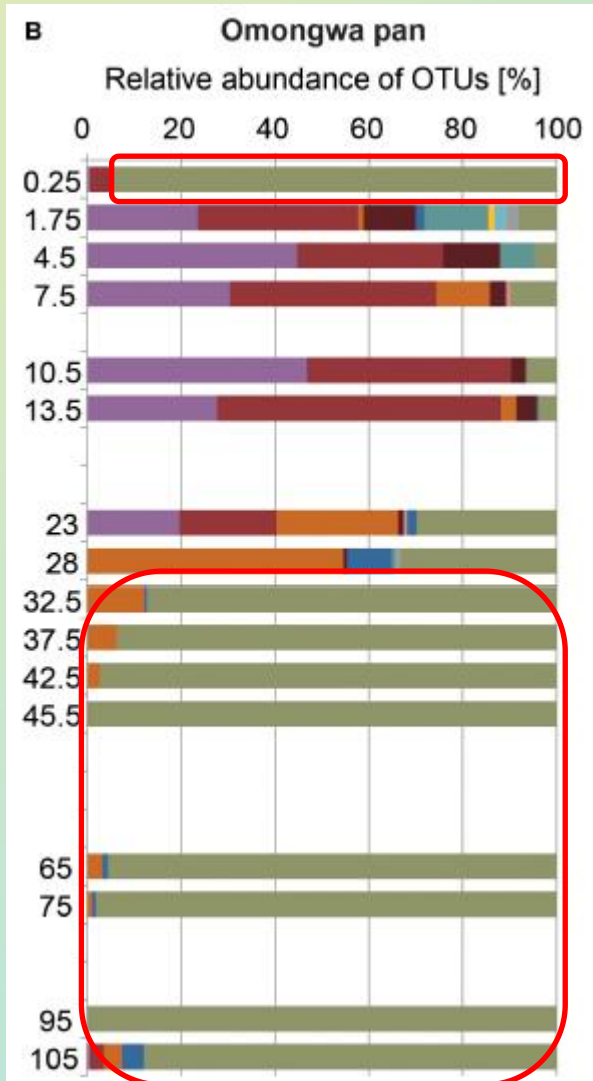


Omongwa Pan

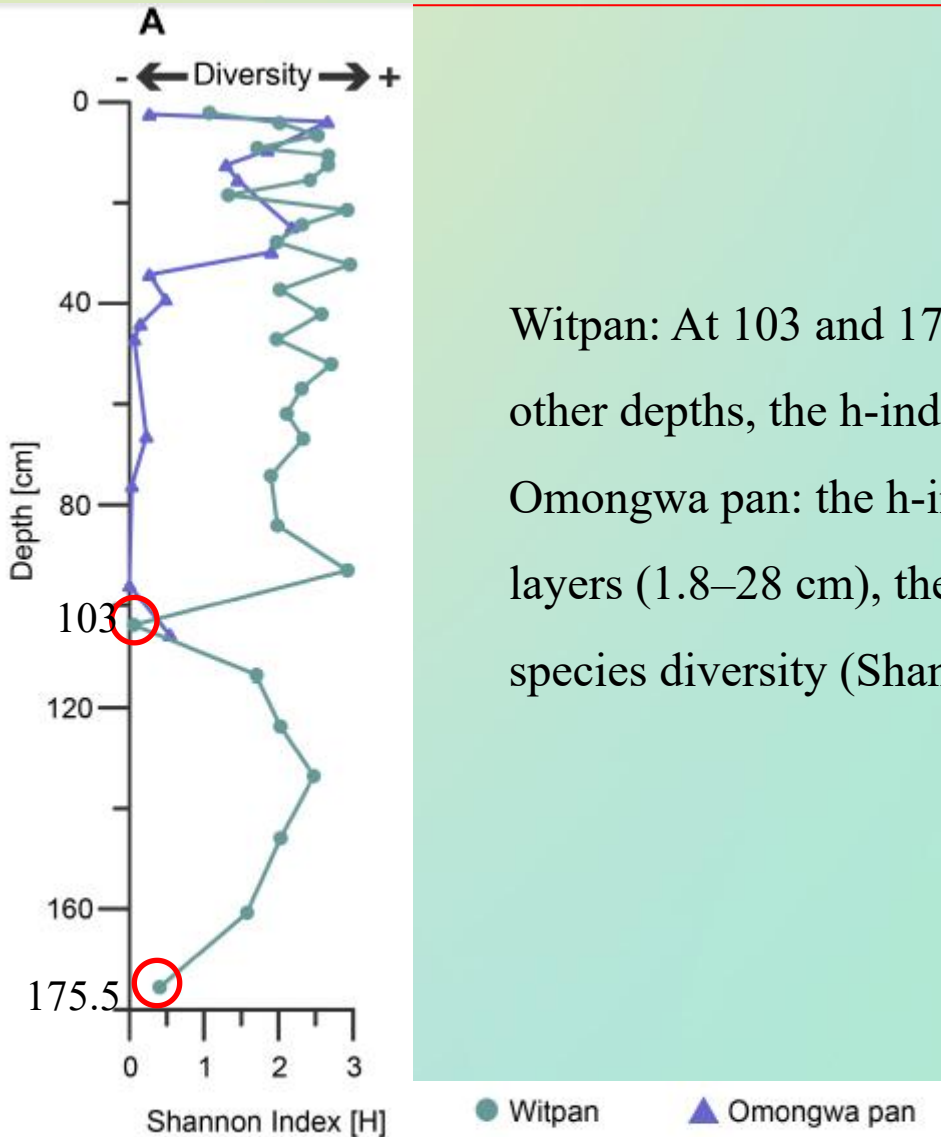
121 OTUs, 13 phyla

Firmicutes dominate the depth profile from 32.5–105 cm as well as the surface layer. At 1.75-23cm layer, a high proportion of *Euryarchaeota* (20–47%) and *Gemmatimonadetes* (21–61%), were detected.

25 OTUs of *Euryarchaeota* can be assigned to *Halobacteria*



Statistical Analyses and Description of Core Taxa Among Two Different Continental Pans



Witpan: At 103 and 175.5 cm, the h-index is below 0.4. for all other depths, the h-index varies between 1 and 3.

Omongwa pan: the h-index varies from 0 to 2.2, Within the top layers (1.8–28 cm), the community is characterized by higher species diversity (Shannon index \bar{O} 1.8)



(A) Shannon index [H] based on OTU sequencing data,

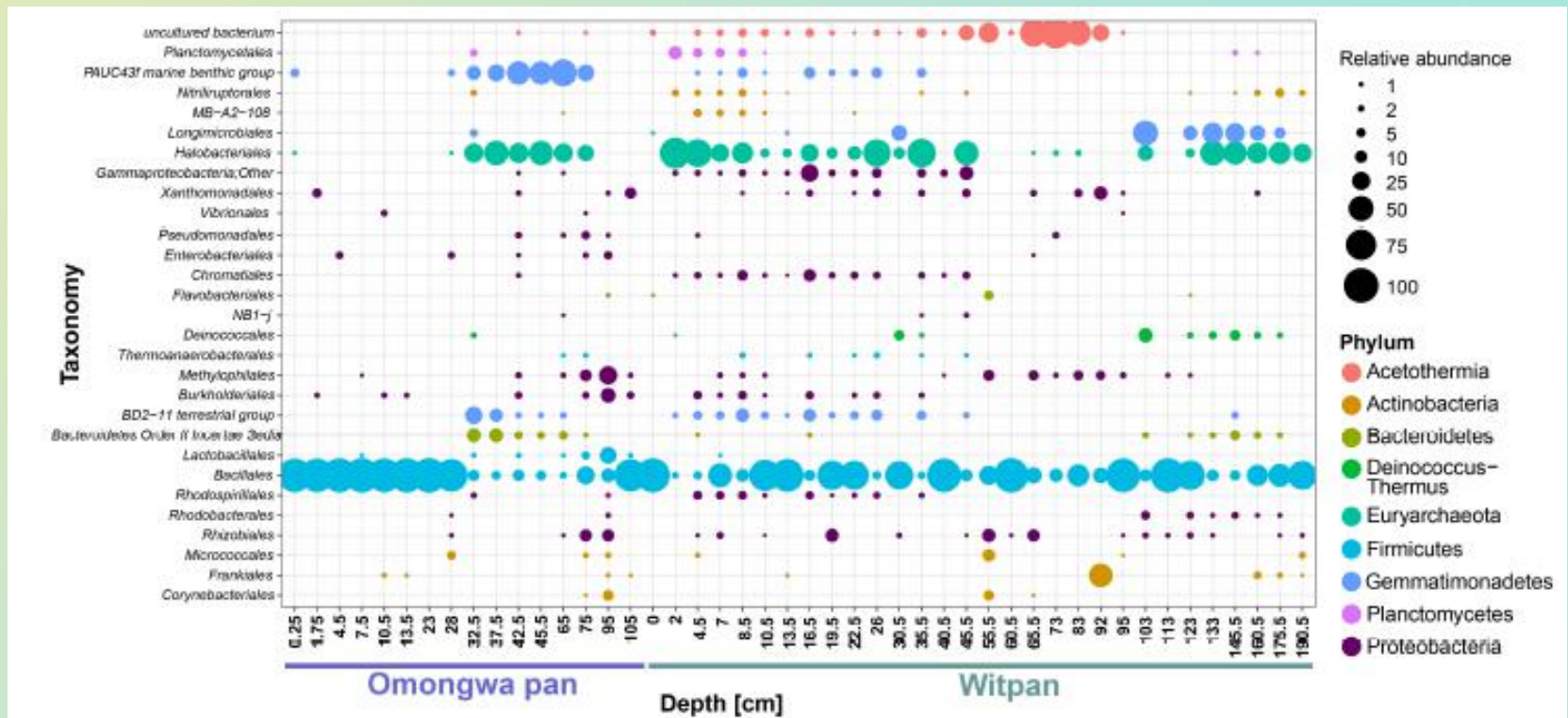
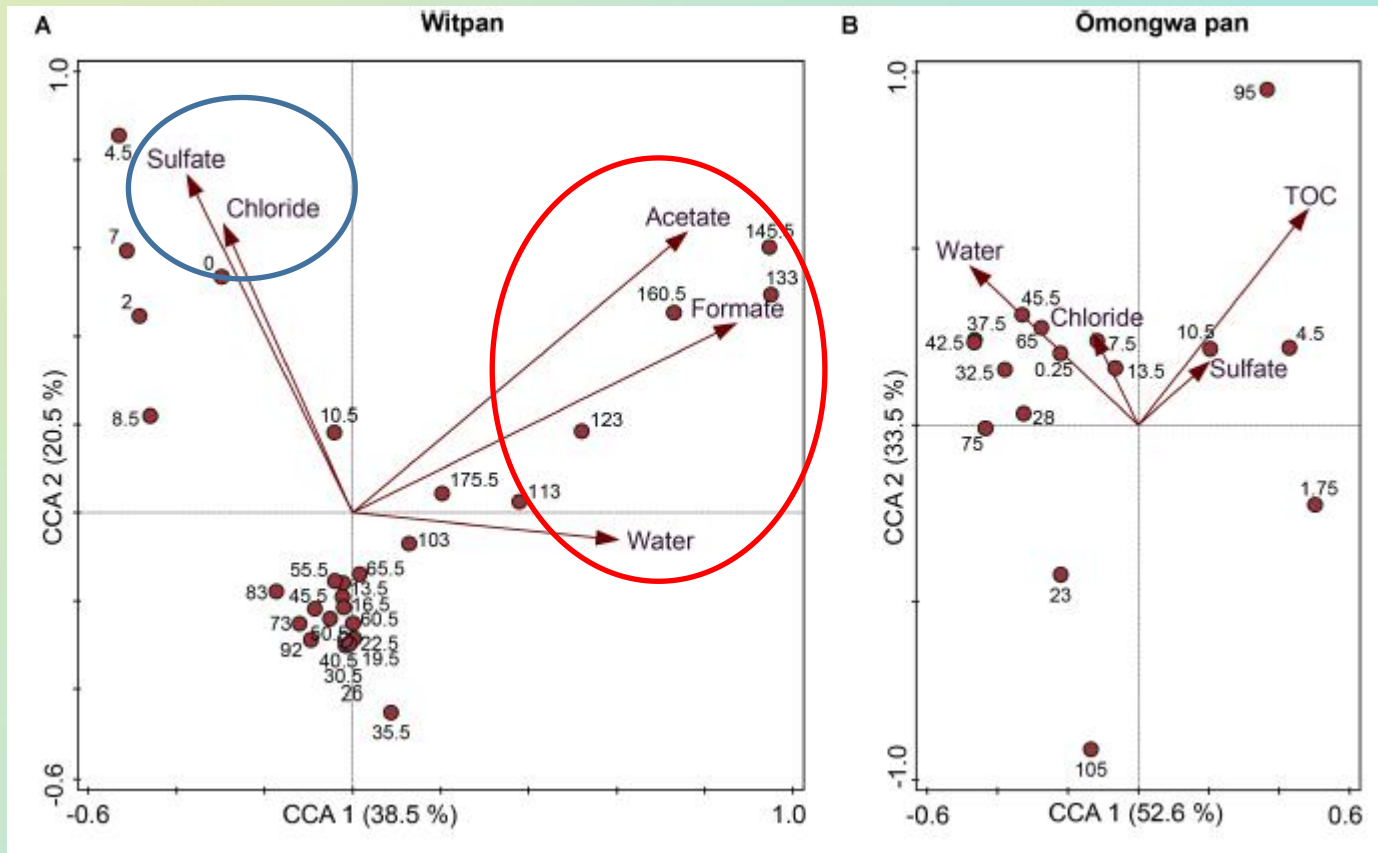


FIGURE 5 | Identification of shared OTUs between Omongwa pan and Witpan is based on order level taxonomic distribution in sediment depth profile. Bubble size indicates the relative abundance. Different phyla are indicated via color-coding.

At the order level, 29 shared taxa from Witpan and the Omongwa pan (Figure 5) are distributed among nine different phyla. This core community is dominated by *Bacillus*, *Halobacteria*, and *Gemmatimonadetes*. The remaining sequences can be assigned to *Actinobacteria*, *Bacteroidetes*, and *Proteobacteria*.



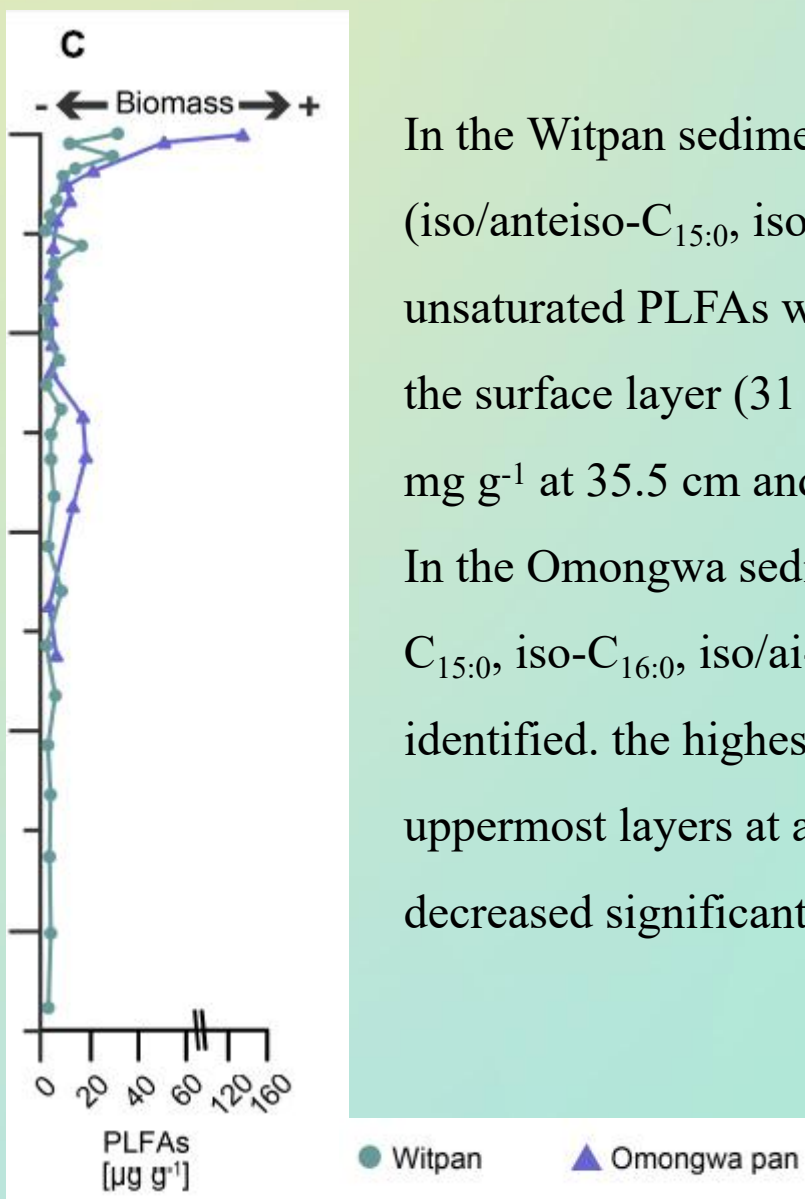


The upper layers (0–19.5 cm) of Witpan are characterized by high chloride and sulfate concentrations.

Chloride and sulfate concentrations are related to the surface layer and to the deeper layers (42.5–105 cm) of the Omongwa pan. In contrast, the layers between 25 and 75 cm can be grouped according to the water content.



Analyses of Phospholipid Fatty Acids (PLFAs) From Witpan and Omongwa Pan



In the Witpan sediments, saturated ($C_{14:0}$ to $C_{20:0}$), branched (iso/anteiso- $C_{15:0}$, iso- $C_{16:0}$, iso/ai- $C_{17:0}$, 10Me-10Me- $C_{16:0}$), unsaturated PLFAs were identified. the highest values were found in the surface layer (31 mg g^{-1}) and decreased with depth down to 0.9 mg g^{-1} at 35.5 cm and 2 mg g^{-1} at 175 cm.

In the Omongwa sediments, saturated ($C_{14:0}$ to $C_{22:0}$), (iso- $C_{14:0}$, iso/ai- $C_{15:0}$, iso- $C_{16:0}$, iso/ai- $C_{17:0}$, 10Me- $C_{16:0}$), unsaturated PLFAs were identified. the highest concentration of PLFAs was identified in the uppermost layers at a sediment depth from 0–3 cm (135 mg g^{-1}) and decreased significantly with depth (down to 3.2 mg g^{-1} at 32.5 cm).



Discussion

- Desert environments are ecosystems with limited nutrient availability and high desiccation potential (Pointing and Belnap,2012). Based on our CCA analyses, the microbial community composition is influenced by salinity and the availability of water in Witpan and in the Omongwa pan.
- Archaea comprise up to 65% of the entire microbial community. The majority of the archaeal sequences are related to halophilic archaea, namely *Halobacteria*. These findings are consistent with several other studies on the archaeal community composition in hypersaline environments (Maturrano et al.,2006; Youssef et al., 2012; Weigold et al., 2016).



Discussion

- The members of thermophilic *Chloroflexi* have been assigned to *Dehalococcoidetes*, which uses organohalide respiration for energy conservation (Kaster et al., 2014).
- High-throughput sequencing allows for deep insights to be made into the microbial community structure of Kacing lahari pans. When comparing two different study sites, saline and desiccation-tolerant microorganisms were emphasized and described as dominating taxa. Their present existence in pan sediments is closely related to the surface processes that control water, substrate-, and nutrient availability.



Conclusion

1. Our study provides new insights into the archaeal and bacterial diversity of desert ecosystems. In both the continental pans, halophilic and desiccation-tolerant taxa were found. *Firmicutes*, *Gemmatimonadetes*, and *Halobacteria* were the core community in two different pan sediments.
2. The high abundance of halophilic archaea and their influence on biogeochemical cycles remain largely unexplored yet represent a major aspect of the desert ecosystem.
3. *Dehalococcoides* are also present in the deeper layers of Witpan, this new knowledge might be useful for the treatment of wastewater.
4. An investigation of novel niches that harbor dehalorespiring microorganisms could broaden our knowledge of organohalide biodegradation applications.



THANKS FOR LISTENING!

