

The background features a central light green cloud-like shape containing the title. Surrounding this are various abstract elements: blue and yellow organic shapes, black and grey hatched circles, and small solid dots in yellow, cyan, and black.

读书报告

牛铭铭

2018.10.14

PNAS

Proceedings of the
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NEW RESEARCH IN

Physical Sciences

Social Sciences

Transitory microbial habitat in the hyperarid Atacama Desert

IF=8.56



Keywords [habitat](#) | [aridity](#) | [microbial activity](#) | [biomarker](#) | [Mars](#)

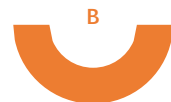


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PART 01

Introduction



Atacama Desert



“

阿塔卡马沙漠 (Atacama Desert)

智利阿塔卡马沙漠是世界上最干燥的地区之一，被称为世界的“干极”，同时也是地球上最接近火星的自然环境，这里土壤荒瘠、高盐，几乎连细菌也不能存活，造成这一切的原因，其中一部分是因为缺水。这里每十年的降雨量，只能用毫米来度量，而在沙漠的某些部分，已经数百年都没有出现过丝毫的降水迹象。美国宇航局选中这里为太空探测车的测试地点。

”



Research Background



在阿塔卡马沙漠核心区域唯一记录的微生物境是由表层盐壳中的微生物群落定殖，其中微生物活动通过潮解实现。
(Wierzchos J, et al. 2011).

尽管在阿塔卡马沙漠的地下存在微生物的痕迹 (Crits-Christoph A, et al. 2013) ，但仍然不清楚这些环境是否支持活跃的微生物生长，或者观察到的细胞是否是通过大气迁移偶尔引入的。





Aim



特殊降雨事件后土壤适宜性的物理化学特征。



确定了指示潜在活跃细胞的生物分子。



从所选样品重建的未培养细菌的基因组的原位复制率的测量。



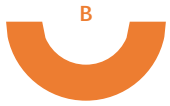
土壤参数和深度特有的微生物群落模式。





PART 02

Materials and Methods



Site description

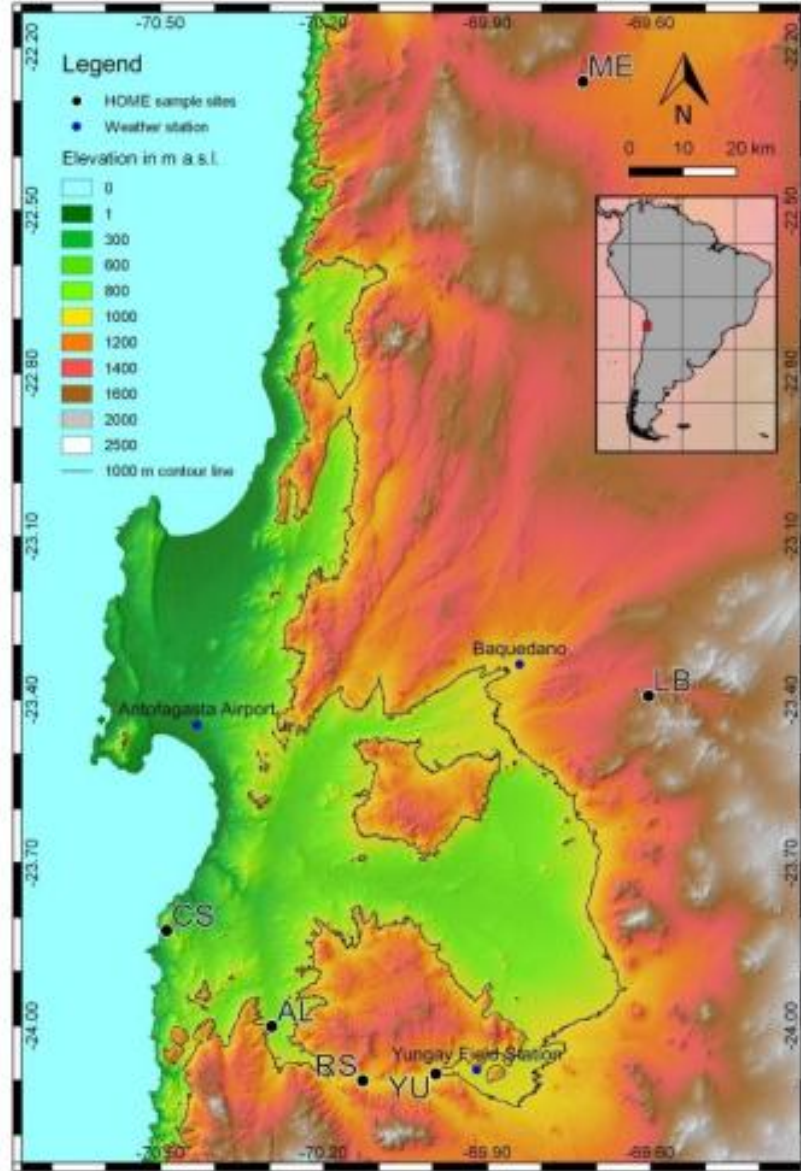
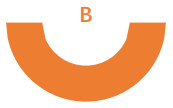


Fig. S1. Map of sampling site locations and rain gauge stations (for site descriptions see Material and Methods Section).



Site description



Coastal Soil(CS)



Alluvial Fan(AL)



Red Sands(RS)



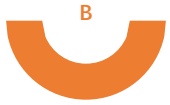
Maria Elena(ME)



Yungay(YU)



Lomas Bayas (LB)



Soil parameters

含水量 { 60°C
105°C

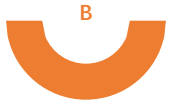
水分吸附等温线和水分活度

地球化学和矿物学分析

无机盐和有机盐测定

矿物学分析

无机同位素地球化学



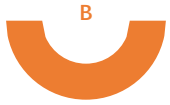
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多环芳烃 (PAHs) 的提取与分析

氯甲烷的稳定氢同位素测量 (GC-IRMS)



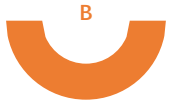
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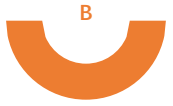
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计算每克沉积物的细胞负荷

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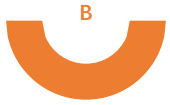
读取宏基因组学，基因组分辨的宏基因组学和原位复制率



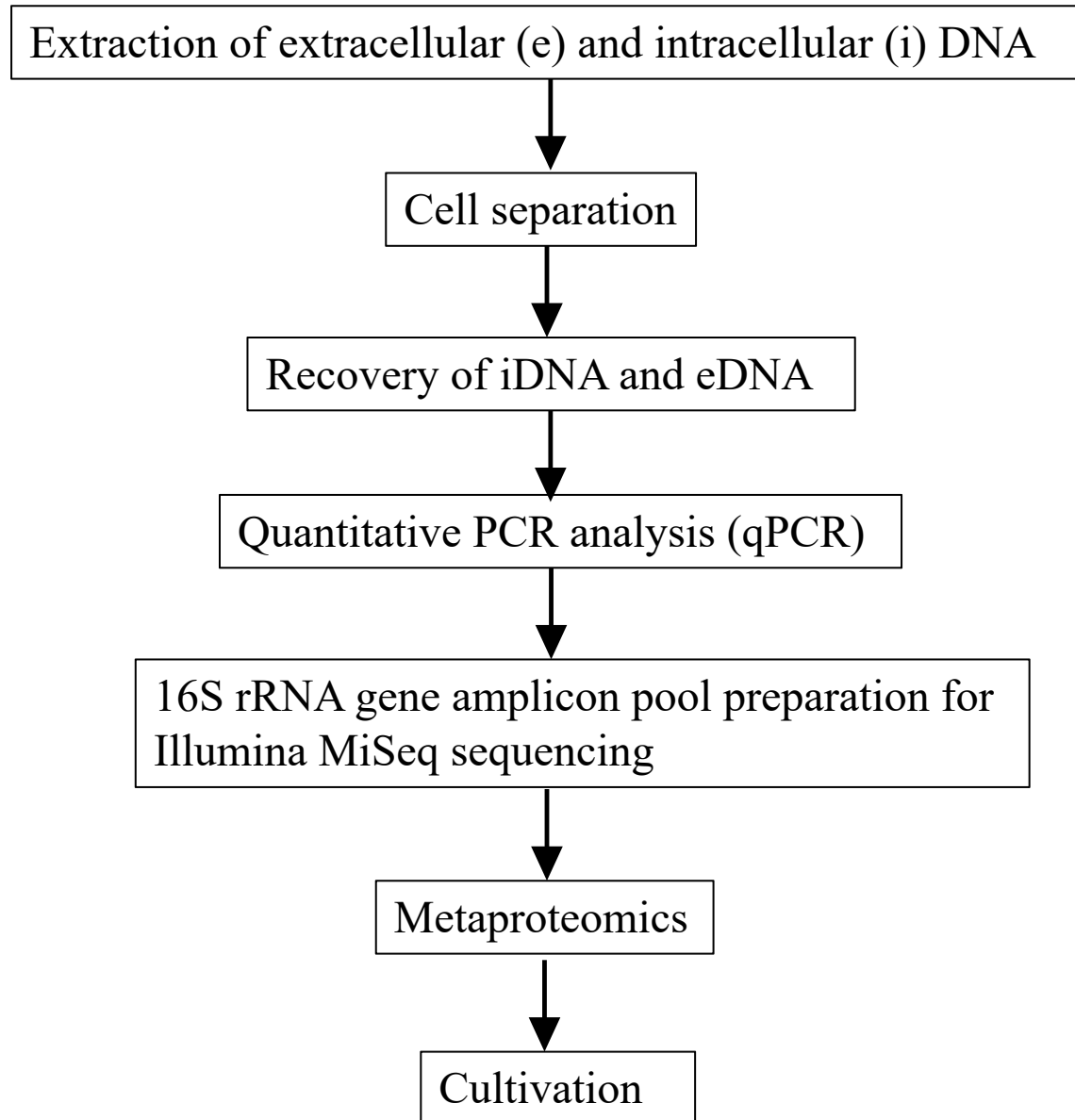
Fungal Analyses

- 真菌生物量
- 真菌多样性
- 内生孢子量化





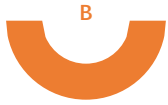
DNA isolation and sequencing





分离方法

- 1、将15g沉淀物样品转移到50mL离心管中并用无菌水润湿。松散地关闭螺旋盖，将管在28°C的水平位置温育3天。在此期间，样品每天润湿一次。
- 2、然后将样品转移至500mL螺旋盖烧瓶中并与4mL NaCl (0.9%, wt / vol) 和1mL TSA培养基 (1/10浓度) 混合，28°C 120rpm震荡温育过夜。用NaCl (0.9%, wt / vol) 稀释涂布在不同的培养基上，28°C培养。



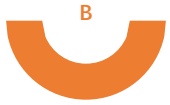
Media

EMH-2 % (1L)

NaCl	20g
MgSO ₄ ×7H ₂ O	10g
Na-citrate	3g
casaminoacids	7.5g
yeast extract	1g
tryptone	5g
Fe(NH ₄) ₂ (SO ₄) ₂ × 6 H ₂ O	0.05g
K ₂ HPO ₄	0.5g
pH 7.8	

EH-5 %, EH-12.5 %, EH-25 % (1L)

NaCl	50/125/250 g
KCl	2g
MgSO ₄ ×7H ₂ O	20g
FeCl ₃	0.023g
Na-citrate	3g
casaminoacids	5g
yeast extract	5g
pH 7.8	



Media

AL 0-5 cm (AL-Na/Ca)

NaCl	15g
CaSO ₄ × 2H ₂ O	3.764g
KNO ₃	0.75g
MgCl ₂ × 6H ₂ O	2g
FeSO ₄ × 7H ₂ O	0.05g
TSA	1g
pH 6.9	

YU 0-5/20-30 cm (YU-Ca)

CaSO ₄ × 2H ₂ O	26g
KNO ₃	0.112g
KCl	2g
MgCl ₂ × 6H ₂ O	0.25g
FeSO ₄ × 7H ₂ O	0.05g
TSA	1g
pH 7.6	

YU 50/100 cm (YU-Na)

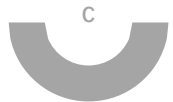
Na ₂ SO ₄	90g
Ca(NO ₃) ₄	8.2g
CaSO ₄ × 2H ₂ O	13.3g
MgCl ₂ × 6H ₂ O	9g
KNO ₃	2.16g
FeSO ₄ × 7H ₂ O	0.05g
TSA	1g
pH 8.0	

所有培养基用20g琼脂固化并补充环己酰亚胺
(10μg/ mL) 以避免真菌生长。

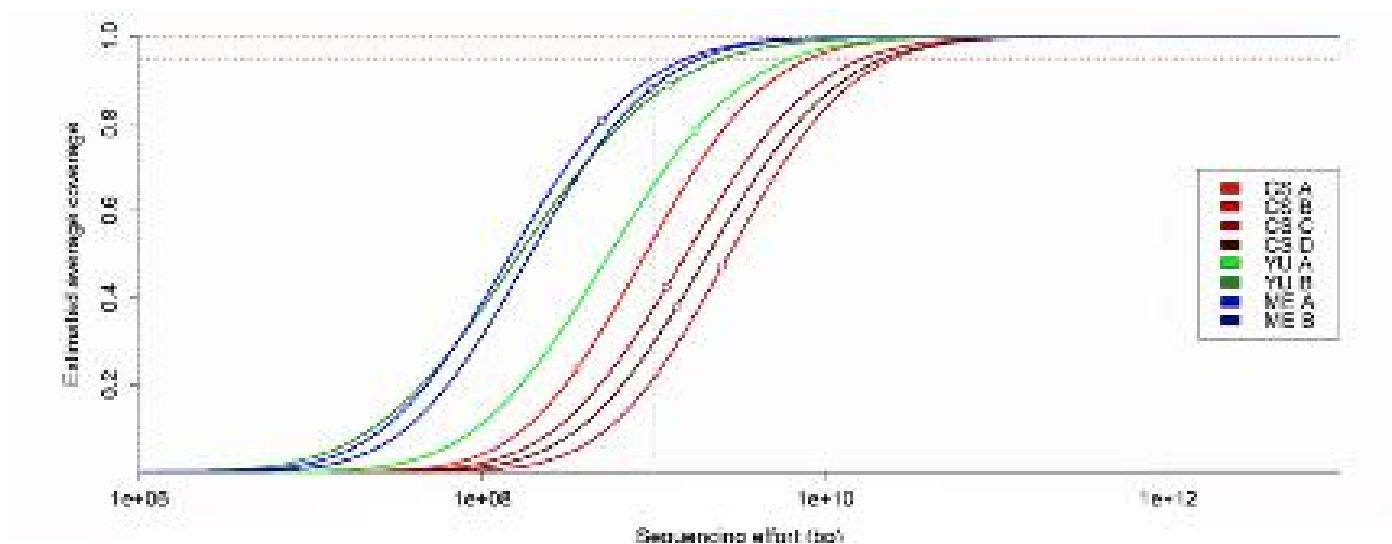


PART 03

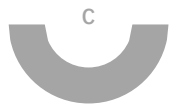
Results



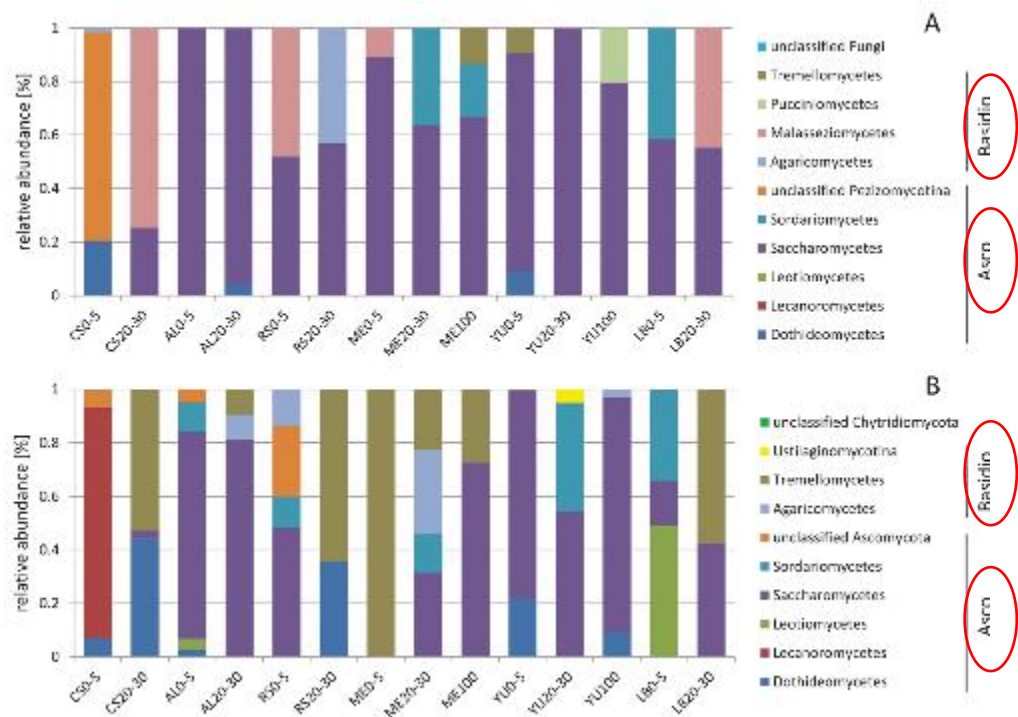
Microbial Diversity



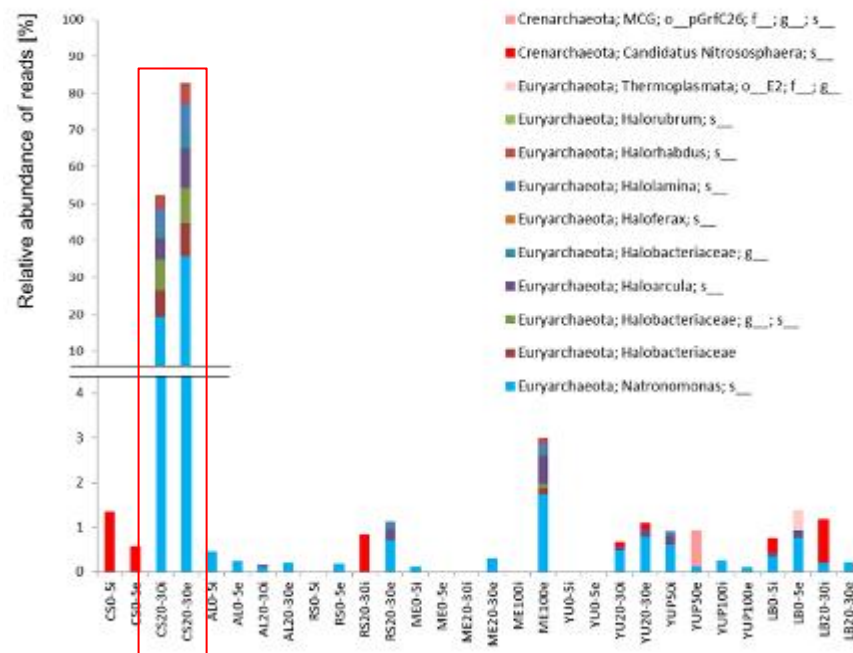
DNA库的宏基因组分析揭示了CS的高细菌多样性，与沙质土壤类似，但与YU和ME的干燥区域相比要高得多。



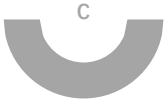
Microbial Diversity



真菌



细菌



Abundance and Identification of Dead and Living Microorganisms

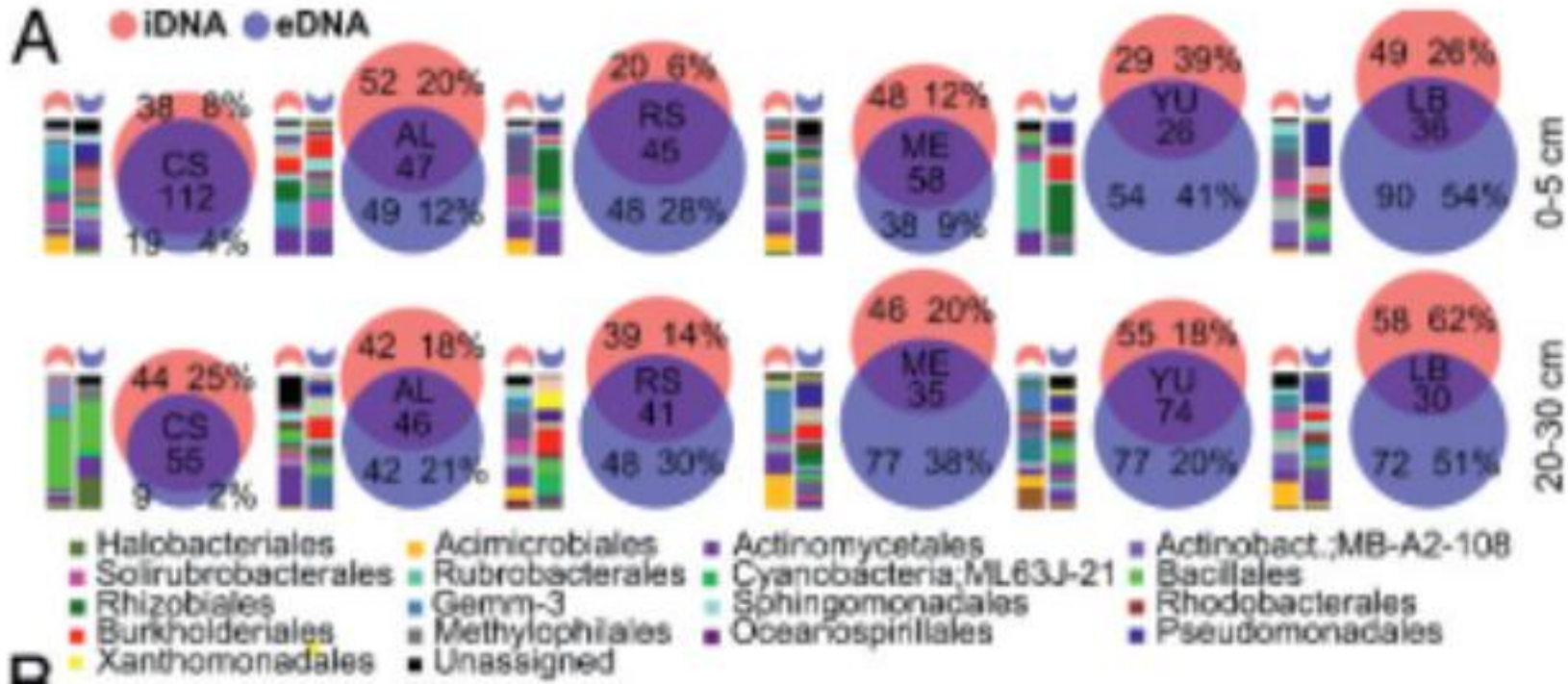
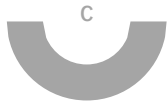
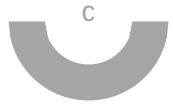


图2 在0-5cm和20-30cm深度收集的样品的iDNA和eDNA OTU交叉点的维恩图



Year		2015		2016		2017	
Depth [cm]		0 – 5	20 – 30	0 – 5	20 - 30	0 - 5	20 - 30
CS	iDNA	6.1×10^7 ($\pm 4.9 \times 10^7$)	2.3×10^8 ($\pm 4.3 \times 10^8$)	n.s.	n.s.	9.7×10^1 ($\pm 1.2 \times 10^2$)	0 *
	eDNA	3.9×10^7 ($\pm 1.7 \times 10^7$)	6.5×10^8 ($\pm 3.5 \times 10^8$)	n.s.	n.s.	9.3×10^4 ($\pm 1.1 \times 10^5$)	1.1×10^4 ($\pm 4.0 \times 10^3$)
	iATP	3.1×10^{-12} ($\pm 2.6 \times 10^{-12}$)	9.0×10^{-16} ($\pm 5.0 \times 10^{-15}$)	n.s.	n.s.	1.0×10^{-12} ($\pm 5.1 \times 10^{-13}$)	5.1×10^{-14} ($\pm 3.3 \times 10^{-14}$)
	eATP	3.0×10^{-12} ($\pm 9.5 \times 10^{-13}$)	9.6×10^{-14} ($\pm 1.2 \times 10^{-14}$)	n.s.	n.s.	7.9×10^{-13} ($\pm 1.4 \times 10^{-13}$)	8.4×10^{-15} ($\pm 5.3 \times 10^{-15}$)
AL	iDNA	1.3×10^5 ($\pm 4.9 \times 10^2$)	5.8×10^5 ($\pm 2.9 \times 10^5$)	n.s.	n.s.	0 *	7.0×10^1 ($\pm 5.2 \times 10^1$)
	eDNA	2.8×10^5 ($\pm 3.5 \times 10^5$)	1.2×10^4 ($\pm 1.6 \times 10^4$)	n.s.	n.s.	1.1×10^2 ($\pm 1.5 \times 10^2$)	0 *
	iATP	4.7×10^{-15} ($\pm 4.7 \times 10^{-15}$)	n.s.	n.s.	n.s.	4.8×10^{-15} # ($\pm 7.3 \times 10^{-16}$)	6.5×10^{-15} # ($\pm 9.9 \times 10^{-16}$)
	eATP	9.9×10^{-15} ($\pm 3.7 \times 10^{-15}$)	n.s.	n.s.	n.s.	3.4×10^{-15} # ($\pm 1.4 \times 10^{-16}$)	3.43×10^{-15} # ($\pm 7.4 \times 10^{-16}$)
RS	iDNA	4.6×10^4 ($\pm 7.8 \times 10^4$)	1.1×10^6 ($\pm 2.5 \times 10^6$)	n.s.	n.s.	2.2×10^1 ($\pm 1.7 \times 10^1$)	0 *
	eDNA	7.0×10^4 ($\pm 7.9 \times 10^4$)	7.5×10^2 ($\pm 2.7 \times 10^2$)	n.s.	n.s.	1.3×10^2 ($\pm 7.9 \times 10^1$)	7.4×10^1 ($\pm 1.1 \times 10^2$)
	iATP	8.0×10^{-15} # ($\pm 2.7 \times 10^{-15}$)	1.8×10^{-14} ($\pm 4.4 \times 10^{-15}$)	n.s.	n.s.	2.3×10^{-15} ($\pm 1.4 \times 10^{-15}$)	0 *
	eATP	1.8×10^{-14} ($\pm 3.1 \times 10^{-15}$)	7.1×10^{-14} ($\pm 1.4 \times 10^{-14}$)	n.s.	n.s.	3.0×10^{-15} # ($\pm 1.0 \times 10^{-15}$)	1.8×10^{-14} ($\pm 2.9 \times 10^{-14}$)
ME	iDNA	6.3×10^4 ($\pm 5.3 \times 10^3$)	8.6×10^5 ($\pm 4.1 \times 10^5$)	n.s.	n.s.	1.1×10^2 ($\pm 4.8 \times 10^1$)	5.6×10^1 ($\pm 2.0 \times 10^1$)
	eDNA	1.8×10^4 ($\pm 9.9 \times 10^3$)	8.3×10^1 ($\pm 1.2 \times 10^2$)	n.s.	n.s.	0 *	0 *
	iATP	n.s.	n.s.	n.s.	n.s.	0 *	0 *
	eATP	n.s.	n.s.	n.s.	n.s.	7.9×10^{-16} ($\pm 4.3 \times 10^{-16}$)	0 *
YU	iDNA	1.0×10^4 ($\pm 3.3 \times 10^2$)	6.2×10^5 ($\pm 7.2 \times 10^4$)	3.1×10^2 ($\pm 2.1 \times 10^2$)	9.5×10^2 ($\pm 2.1 \times 10^2$)	4.2×10^1 ($\pm 3.6 \times 10^1$)	0 *
	eDNA	8.6×10^1 ($\pm 1.2 \times 10^2$)	1.9×10^4 ($\pm 3.4 \times 10^3$)	2.4×10^1 ($\pm 6.0 \times 10^1$)	2.2×10^2 ($\pm 5.3 \times 10^1$)	1.5×10^1 ($\pm 2.2 \times 10^1$)	0 *
	iATP	3.9×10^{-14} ($\pm 2.8 \times 10^{-14}$)	1.8×10^{-14} ($\pm 4.2 \times 10^{-15}$)	7.2×10^{-15} # ($\pm 3.3 \times 10^{-15}$)	8.6×10^{-15} # ($\pm 5.1 \times 10^{-15}$)	0 *	1.9×10^{-14} ($\pm 1.1 \times 10^{-14}$)
	eATP	1.9×10^{-13} ($\pm 3.9 \times 10^{-14}$)	4.4×10^{-13} ($\pm 4.1 \times 10^{-14}$)	2.5×10^{-14} ($\pm 1.1 \times 10^{-14}$)	1.5×10^{-14} ($\pm 1.7 \times 10^{-14}$)	1.7×10^{-14} ($\pm 3.3 \times 10^{-15}$)	3.0×10^{-14} ($\pm 3.8 \times 10^{-15}$)
LB	iDNA	1.6×10^5 ($\pm 8.7 \times 10^4$)	7.4×10^4 ($\pm 3.7 \times 10^4$)	n.s.	n.s.	6.2×10^1 ($\pm 4.9 \times 10^1$)	2.0×10^2 ($\pm 1.0 \times 10^2$)
	eDNA	0 *	0 *	n.s.	n.s.	2.4×10^1 ($\pm 3.4 \times 10^1$)	1.2×10^2 ($\pm 9.8 \times 10^1$)
	iATP	n.s.	n.s.	n.s.	n.s.	3.2×10^{-15} # ($\pm 1.1 \times 10^{-15}$)	0 *
	eATP	n.s.	n.s.	n.s.	n.s.	1.7×10^{-13} ($\pm 3.4 \times 10^{-14}$)	0 *

n.s. = no sample; * = below the detection limit (DNA < 80 copies g⁻¹; ATP < 8.6 x 10⁻¹⁸ mol g⁻¹); # = below the qualification limit of ATP (< 2.8 x 10⁻¹⁵ mol g⁻¹).

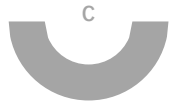


Abundance of Endospores

Sample / depth	0-5 cm	20-30 cm	50 cm	100 cm
CS	7.74×10^5	2.78×10^6	N/A	N/A
AL	4.14×10^5	4.43×10^5	N/A	N/A
RS	1.62×10^4	2.41×10^4	N/A	N/A
ME	1.52×10^4	3.03×10^4	N/A	5.63×10^4
YU	$<7.18 \times 10^3$	$<9.31 \times 10^3$	2.62×10^5	1.66×10^5
LB	$<1.22 \times 10^4$	4.04×10^4	N/A	N/A

N/A = Not analyzed

表2 基于DPA的内生孢子浓度 (g-1)



Abundance of Endospores

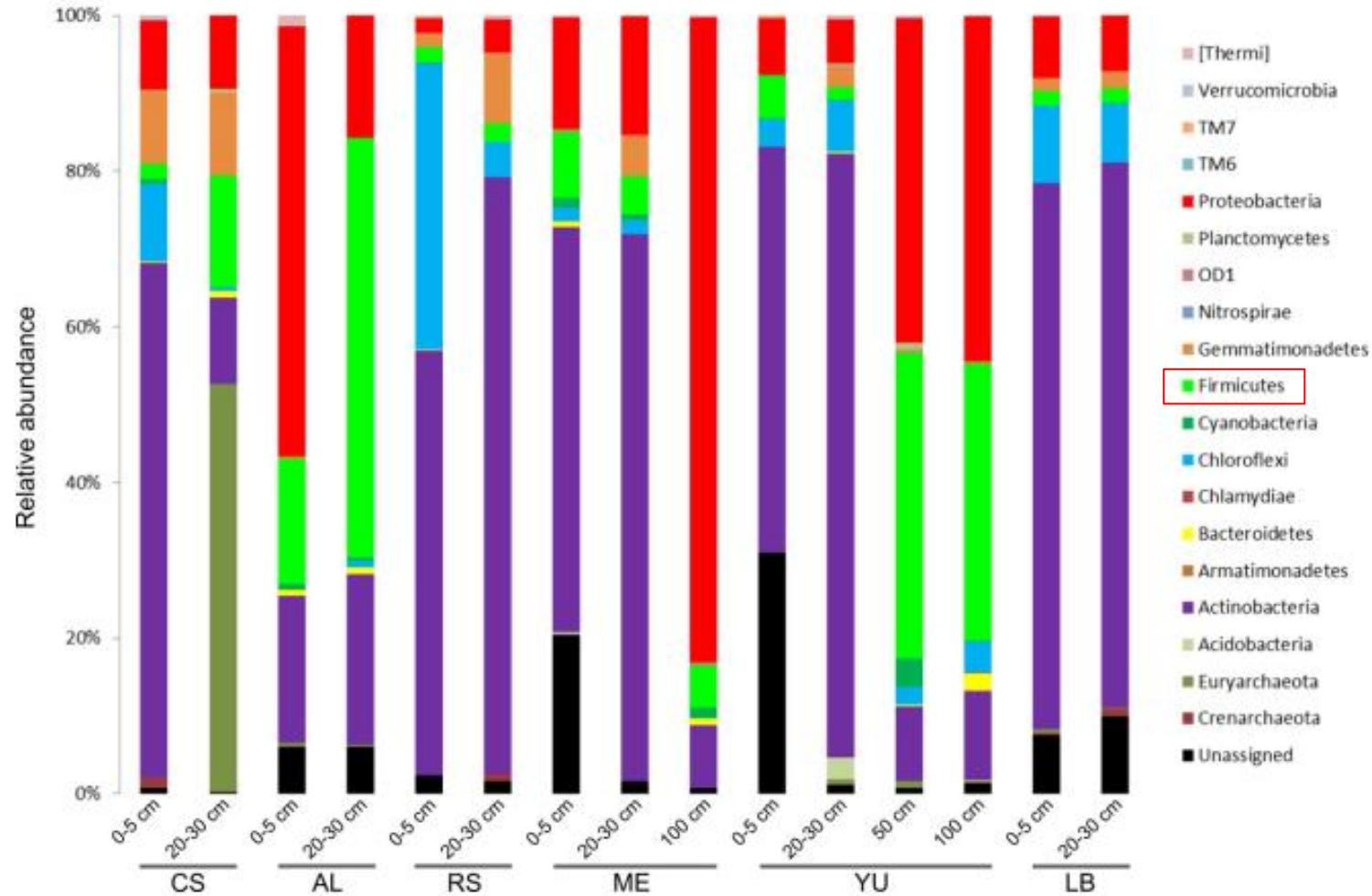
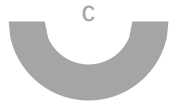


Fig. S7. Relative abundances of microbial phyla in iDNA pools of the six sampling sites Coastal Soil (CS), Alluvial Fan (AL), Red Sands (RS), Maria Elena (ME), Yungay (YU), and Lomas Bayas (LB) for the sampling depths 0-5 cm, 20-30 cm, 50 cm, and 100 cm. Results from merged triplicates.



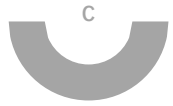
Metabolic Activity

1、通过荧光素二乙酸酯水解测定法获得微生物活性的证据以确定酶活性。

Table S3. Sediment enzymatic activity as released fluorescein from fluorescein diacetate hydrolysatation ($\text{nmol g}^{-1} \text{h}^{-1}$).

Depth (cm)	CS	AL	RS	ME	YU	LB
0–5	0.850	0.130	0.250	0.754	0.228	1.475
20–30	0.124	0.180	0.053	0.410	0.018	b.d.
50	-	-	-	-	b.d.	-
100	-	-	-	b.d.	b.d.	-

Notes: b. d., below detection limit of $0.001 \text{ nmol g}^{-1} \text{h}^{-1}$; for comparison freshly sampled garden soil showed an activity of $0.14 \text{ } \mu\text{mol g}^{-1} \text{h}^{-1}$



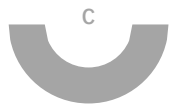
Metabolic Activity

2、ATP分析支持存在活跃的天然微生物群落的假设。

即使在阿塔卡马核心区域最干旱的地方，天然微生物有时也可能具有代谢活性。

Year		2015		2016		2017	
Depth [cm]		0 - 5	20 - 30	0 - 5	20 - 30	0 - 5	20 - 30
CS	iDNA	6.1×10^5 ($\pm 4.9 \times 10^5$)	2.3×10^5 ($\pm 4.3 \times 10^4$)	n.s.	n.s.	9.7×10^1 ($\pm 1.2 \times 10^2$)	0 *
	eDNA	3.9×10^7 ($\pm 1.7 \times 10^7$)	6.5×10^6 ($\pm 3.5 \times 10^6$)	n.s.	n.s.	9.3×10^4 ($\pm 1.1 \times 10^5$)	1.1×10^4 ($\pm 4.0 \times 10^3$)
	iATP	3.1×10^{-12} ($\pm 2.6 \times 10^{-12}$)	9.0×10^{-15} ($\pm 5.0 \times 10^{-15}$)	n.s.	n.s.	1.0×10^{-12} ($\pm 5.1 \times 10^{-13}$)	5.1×10^{-14} ($\pm 3.3 \times 10^{-14}$)
	eATP	3.0×10^{-12} ($\pm 9.5 \times 10^{-13}$)	9.6×10^{-14} ($\pm 1.2 \times 10^{-14}$)	n.s.	n.s.	7.9×10^{-13} ($\pm 1.4 \times 10^{-13}$)	8.4×10^{-15} ($\pm 5.3 \times 10^{-15}$)
AL	iDNA	1.3×10^3 ($\pm 4.9 \times 10^2$)	5.8×10^3 ($\pm 2.9 \times 10^3$)	n.s.	n.s.	0 *	7.0×10^1 ($\pm 5.2 \times 10^1$)
	eDNA	2.8×10^3 ($\pm 3.5 \times 10^3$)	1.2×10^4 ($\pm 1.6 \times 10^4$)	n.s.	n.s.	1.1×10^2 ($\pm 1.5 \times 10^2$)	0 *
	iATP	4.7×10^{-15} ($\pm 4.7 \times 10^{-15}$)	n.s.	n.s.	n.s.	4.8×10^{-15} # ($\pm 7.3 \times 10^{-16}$)	6.5×10^{-15} # ($\pm 9.9 \times 10^{-16}$)
	eATP	9.9×10^{-15} ($\pm 3.7 \times 10^{-15}$)	n.s.	n.s.	n.s.	3.4×10^{-15} # ($\pm 1.4 \times 10^{-16}$)	3.43×10^{-15} # ($\pm 7.4 \times 10^{-16}$)
RS	iDNA	4.6×10^4 ($\pm 7.8 \times 10^4$)	1.1×10^6 ($\pm 2.5 \times 10^5$)	n.s.	n.s.	2.2×10^1 ($\pm 1.7 \times 10^1$)	0 *
	eDNA	7.0×10^4 ($\pm 7.9 \times 10^4$)	7.5×10^2 ($\pm 2.7 \times 10^2$)	n.s.	n.s.	1.3×10^2 ($\pm 7.9 \times 10^1$)	7.4×10^1 ($\pm 1.1 \times 10^2$)
	iATP	8.0×10^{-15} # ($\pm 2.7 \times 10^{-15}$)	1.8×10^{-14} ($\pm 4.4 \times 10^{-15}$)	n.s.	n.s.	2.3×10^{-15} ($\pm 1.4 \times 10^{-15}$)	0 *
	eATP	1.8×10^{-14} ($\pm 3.1 \times 10^{-15}$)	7.1×10^{-14} ($\pm 1.4 \times 10^{-14}$)	n.s.	n.s.	3.0×10^{-15} # ($\pm 1.0 \times 10^{-15}$)	1.8×10^{-14} ($\pm 2.9 \times 10^{-14}$)
ME	iDNA	6.3×10^4 ($\pm 5.3 \times 10^3$)	8.6×10^3 ($\pm 4.1 \times 10^3$)	n.s.	n.s.	1.1×10^2 ($\pm 4.8 \times 10^1$)	5.6×10^1 ($\pm 2.0 \times 10^1$)
	eDNA	1.8×10^4 ($\pm 9.9 \times 10^3$)	8.3×10^1 ($\pm 1.2 \times 10^2$)	n.s.	n.s.	0 *	0 *
	iATP	n.s.	n.s.	n.s.	n.s.	0 *	0 *
	eATP	n.s.	n.s.	n.s.	n.s.	7.9×10^{-16} ($\pm 4.3 \times 10^{-16}$)	0 *
YU	iDNA	1.0×10^4 ($\pm 3.3 \times 10^2$)	6.2×10^5 ($\pm 7.2 \times 10^4$)	3.1×10^2 ($\pm 2.1 \times 10^2$)	9.5×10^2 ($\pm 2.1 \times 10^2$)	4.2×10^1 ($\pm 3.6 \times 10^1$)	0 *
	eDNA	8.6×10^1 ($\pm 1.2 \times 10^2$)	1.9×10^4 ($\pm 3.4 \times 10^3$)	2.4×10^1 ($\pm 6.0 \times 10^1$)	2.2×10^2 ($\pm 5.3 \times 10^1$)	1.5×10^1 ($\pm 2.2 \times 10^1$)	0 *
	iATP	3.9×10^{-14} ($\pm 2.8 \times 10^{-14}$)	1.8×10^{-14} ($\pm 4.2 \times 10^{-15}$)	7.2×10^{-15} # ($\pm 3.3 \times 10^{-15}$)	8.6×10^{-15} # ($\pm 5.1 \times 10^{-15}$)	0 *	1.9×10^{-14} ($\pm 1.1 \times 10^{-14}$)
	eATP	1.9×10^{-13} ($\pm 3.9 \times 10^{-14}$)	4.4×10^{-13} ($\pm 4.1 \times 10^{-14}$)	2.5×10^{-14} ($\pm 1.1 \times 10^{-14}$)	1.5×10^{-14} ($\pm 1.7 \times 10^{-14}$)	1.7×10^{-14} ($\pm 3.3 \times 10^{-15}$)	3.0×10^{-14} ($\pm 3.8 \times 10^{-15}$)
LB	iDNA	1.6×10^5 ($\pm 8.7 \times 10^4$)	7.4×10^4 ($\pm 3.7 \times 10^4$)	n.s.	n.s.	6.2×10^1 ($\pm 4.9 \times 10^1$)	2.0×10^2 ($\pm 1.0 \times 10^2$)
	eDNA	0 *	0 *	n.s.	n.s.	2.4×10^1 ($\pm 3.4 \times 10^1$)	1.2×10^2 ($\pm 9.8 \times 10^1$)
	iATP	n.s.	n.s.	n.s.	n.s.	3.2×10^{-15} # ($\pm 1.1 \times 10^{-15}$)	0 *
	eATP	n.s.	n.s.	n.s.	n.s.	1.7×10^{-13} ($\pm 3.4 \times 10^{-14}$)	0 *

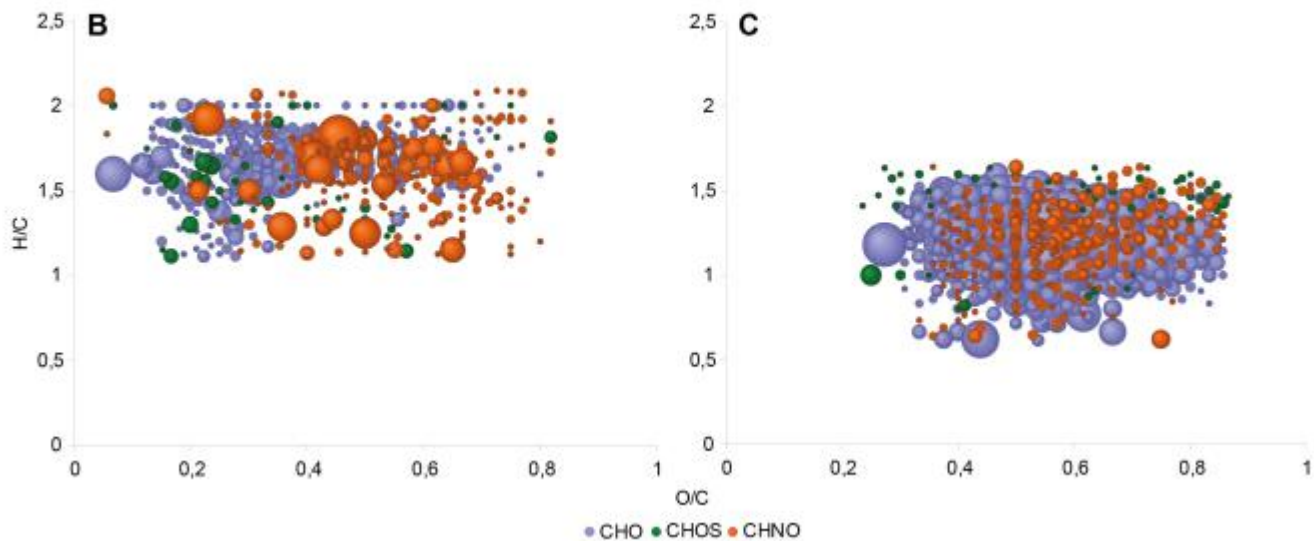
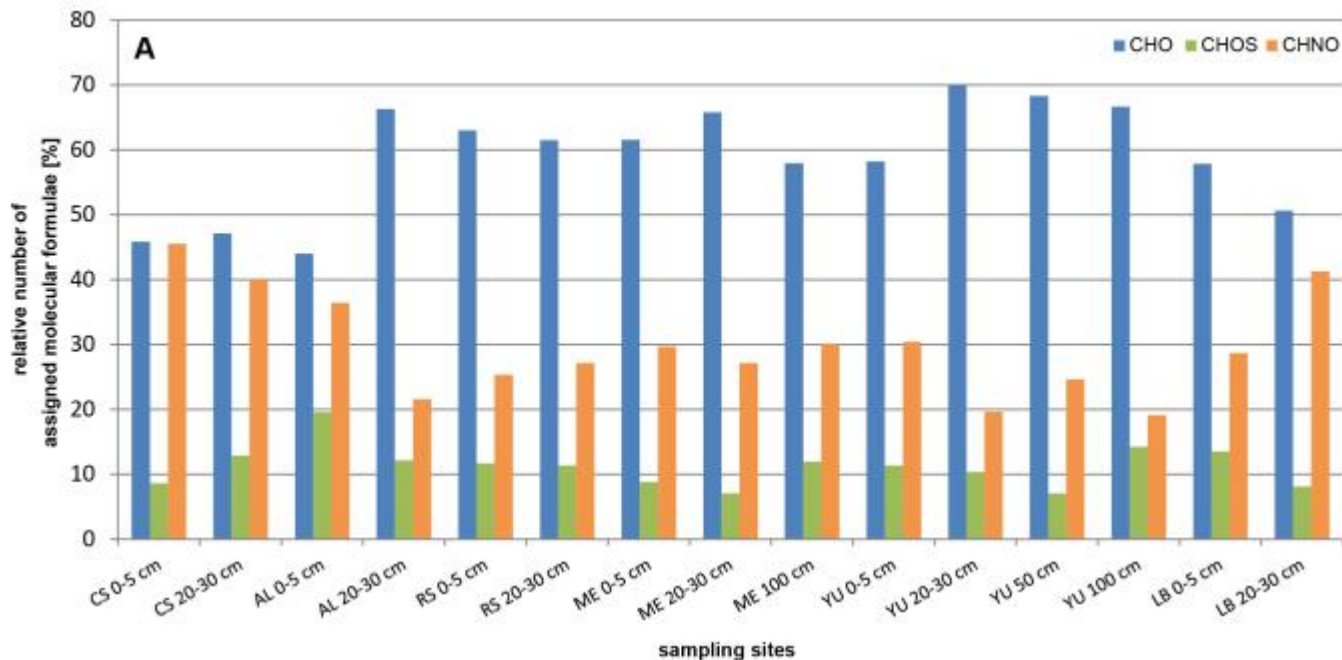
n.s. = no sample; * = below the detection limit (DNA < 80 copies g⁻¹; ATP < 8.6 x 10⁻¹⁸ mol g⁻¹); # = below the qualification limit of ATP (< 2.8 x 10⁻¹⁵ mol g⁻¹).

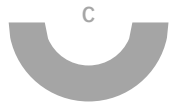


Metabolic Activity

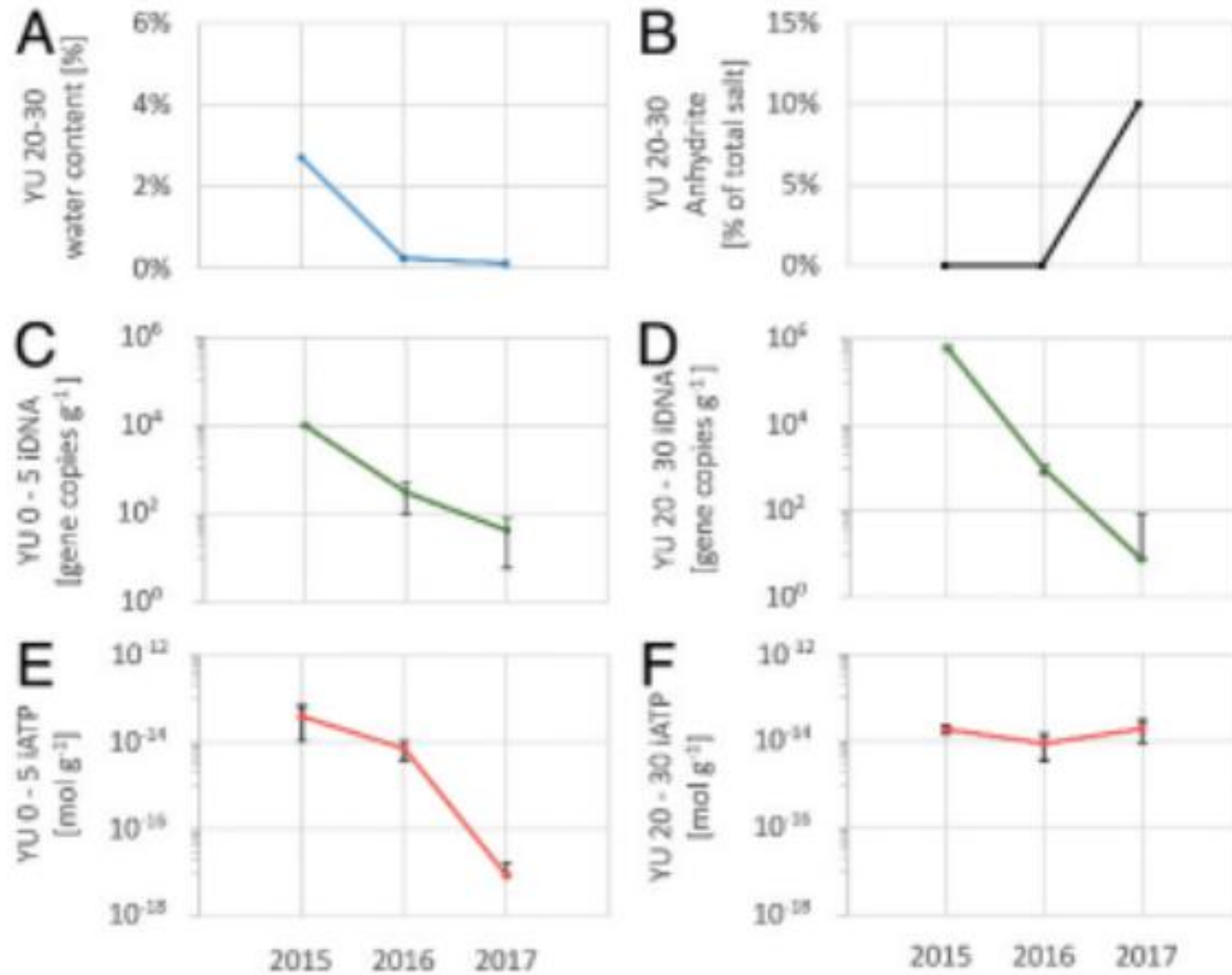
3、通过直接注射电喷雾电离傅里叶变换离子回旋共振质谱[ESI (-) FT-ICR-MS]分析水可提取代谢物，支持具有代谢活性微生物的存在。

结果表明，水溶性有机化合物主要由脂肪族碳水化合物和脂肪酸 (CHO) 组成，而含氮和硫的化合物 (CHNO和CHOS) 则较少。





A Transitory Habitat?





PART 04
Discussion



Discussion

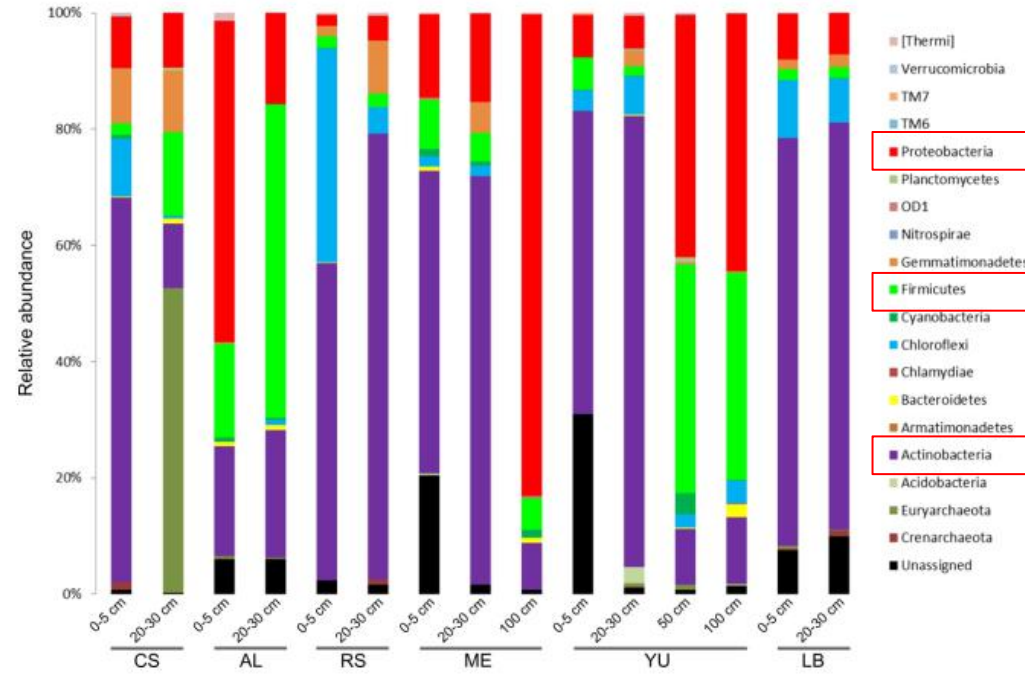


Fig. S7. Relative abundances of microbial phyla in iDNA pools of the six sampling sites Coastal Soil (CS), Alluvial Fan (AL), Red Sands (RS), Maria Elena (ME), Yungay (YU), and Lomas Bayas (LB) for the sampling depths 0-5 cm, 20-30 cm, 50 cm, and 100 cm. Results from merged triplicates.

六个采样点iDNA库的微生物相对丰度



Discussion

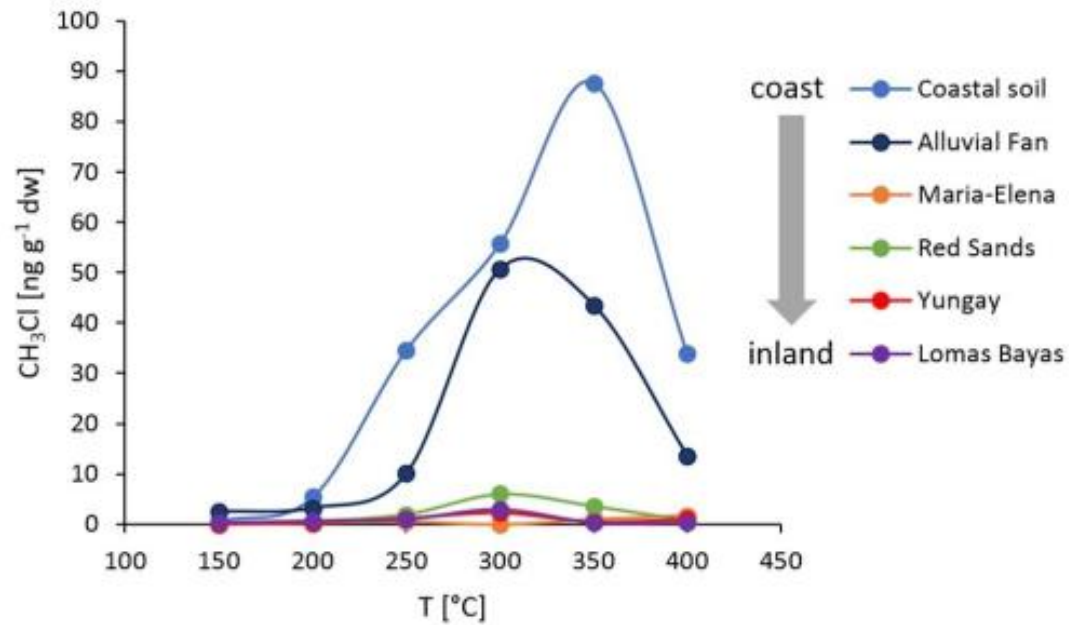
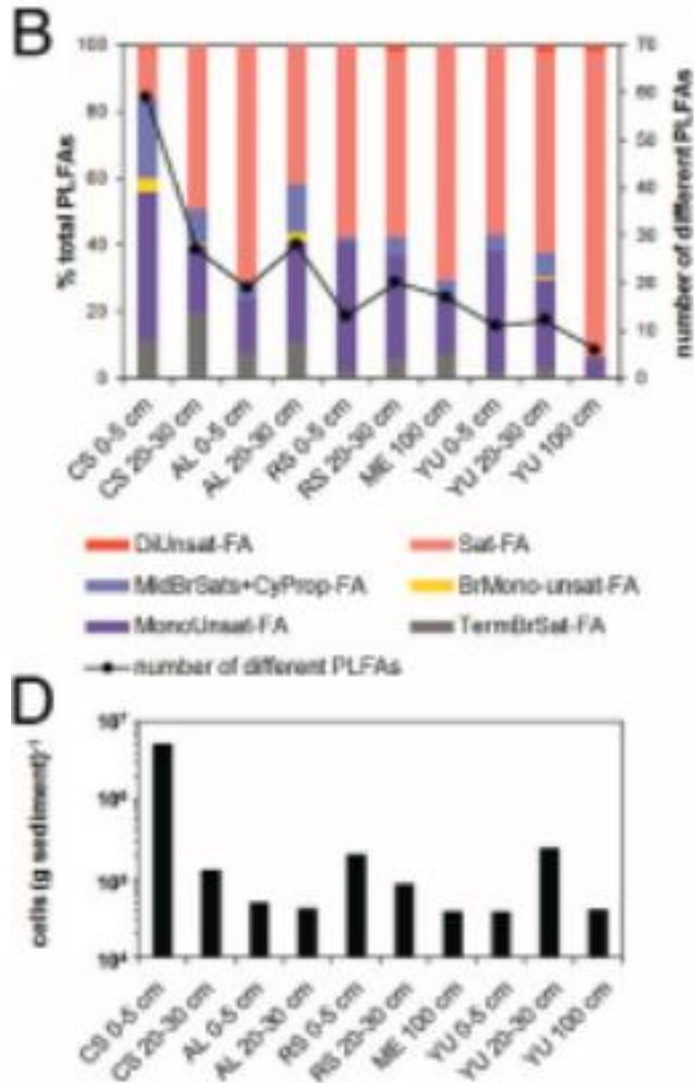


Fig. S10. Low Temperature Pyrolysis (150 to 400 $^{\circ}\text{C}$) of Atacama surface soils shows very distinct chloromethane production profiles for the six regions, with the maximum at CS (Coastal Soil) and the minimum at LB (Lomas Bayas) and Maria Elena (ME).

微生物在表面和地下位置持续存在的另一个挑战是超干旱土壤的低有机质含量特征。较高的TOC和水分含量产生更高的总微生物生物量和多样性。



Discussion



目前火星大气层不会下雨，但是火星表面附近可能存在液态水，其形式为夜间暴风雪/冰微爆，雾，近地表地下水，也可能来自矿物脱水反应。在火星上，具有较高水活度和减少暴露于环境压力（例如，紫外线照射，大的日常温度波动）的较深土层预计更适合于支持生命。因此，在阿塔卡马沙漠的超全境中观察到一个短暂的栖息地，这些微生物在短时间内具有活性，可以作为火星的合理工作模型。



PART 04

Conlusion



Conclusion



“

研究结果强调，即使是超级阿特卡马沙漠也可以为微生物提供一个适宜居住的环境，使它们在水分偶然增加后变得具有代谢活性，一旦它减少，微生物群的活动就会减少。这些结果对火星等其他这些从早期的潮湿环境转变为今天的极端干旱环境星球上的生命前景研究产生了影响。

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Conclusion



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