

读书报告

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2016-5-21

ORIGINAL PAPER

A snapshot of microbial communities from the Kutch: one of the largest salt deserts in the World

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Japan

[EXTREMOPHILES](#)

IF=2.306

极端微生物

世界上最大的盐碱沙漠中的微生物群落的分类学多样性分析

Kutch（喀奇县）:印度西部古吉拉特邦辖县

宏基因组学

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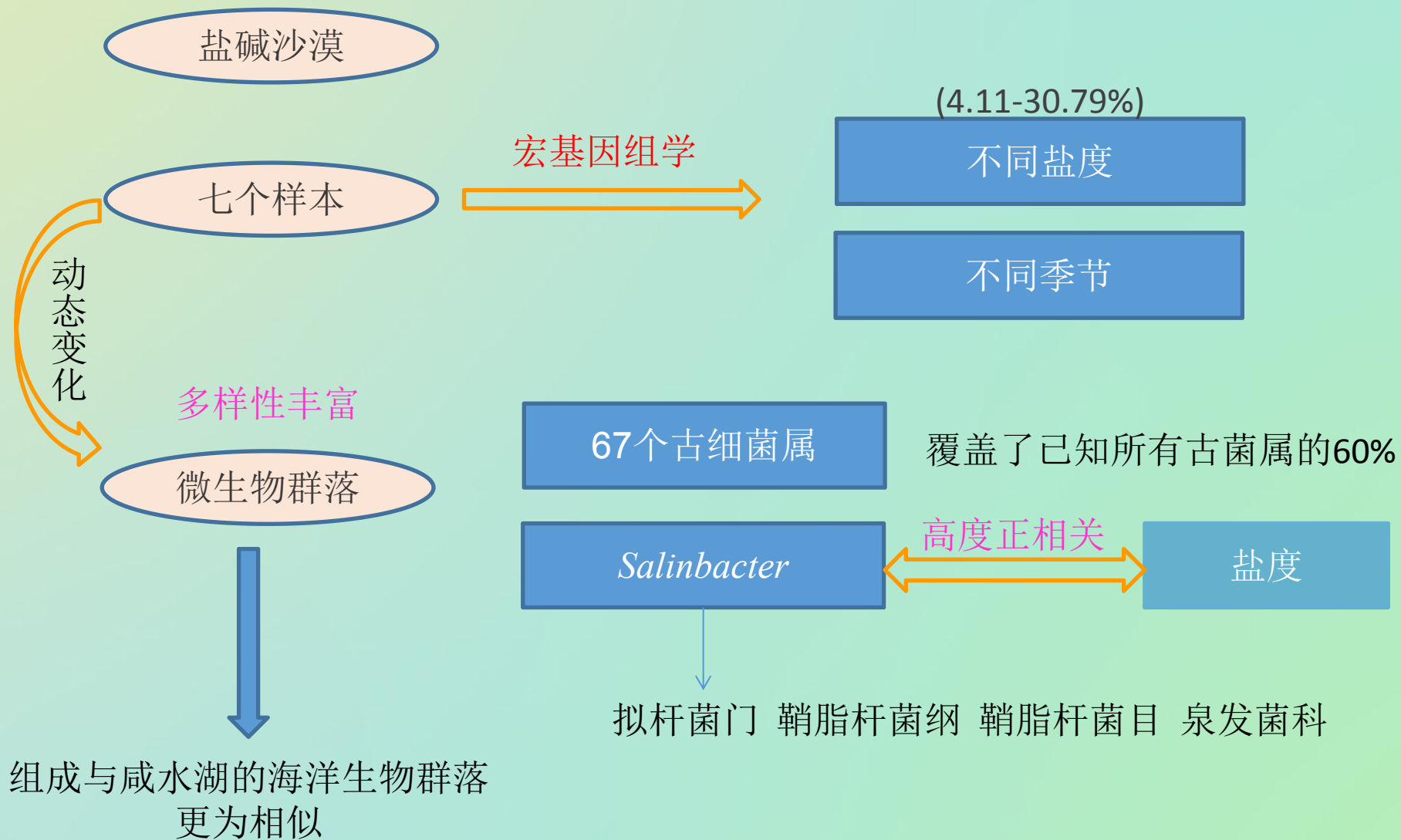
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Abstract



Introduction

极端自然环境-高盐度生态系统

盐湖、苏打水湖泊、咸水泉、
盐沼泽、太阳能盐田

高盐度区域

水生微生物

土壤和沉积物中的
微生物

Kutch

海洋和陆地生态系统的过渡区

占地7505平方公里、干燥、表面覆盖黑色沙土。经历**极端气候条件**（夏季平均气温约44 °C至50°C、冬季最低温度接近或低于零度）和**高盐度**环境使其具有独特的微生物群落多样性。

Introduction

Metagenomics

宏基因组测序

研究对象	特定生境中的微生物群落
研究方法	采用新一代高通量测序技术，获得环境微生物基因信息总和
研究目的	环境微生物的群落结构、物种分类、系统进化、基因功能及代谢网络

综合性分析微生物在极端环境或特殊生态系统中的生存和适应机制

弥补用生物地球化学和细菌培养式的方法的局限性

Materials and methods

1

生境描述、采样

2

样品物理化学分析

3

DNA 提取、测序

4

实时荧光定量PCR

5

生物信息学、统计分析

Materials and methods

- 1、生境：年平均温度45°C，年平均降水量147mm，海侵形成。
- 2、在内陆沙漠，盐度跨度大，无人破坏处采样。

S1 (23° 48' 39" N, 70° 58' 60" E)

S2 (23° 47' 33" N, 71° 0' 29" E)

S3 (23° 54' 29" N, 70° 32' 16" E)

S5 (23° 50' 6" N, 69° 31' 8" E)

S6 (23° 56' 27" N, 70° 11' 18" E)

S4 (23° 56' 29" N, 70° 11' 18" E)

S7 (23° 56' 26" N, 70° 11' 16" E)

取自沙漠150km横断面的各个盐度处

2012.10

2013.4 (最热月份)

2013.7 (最潮湿月份)

每个样点5-10个样本随后混合用于宏基因组测序

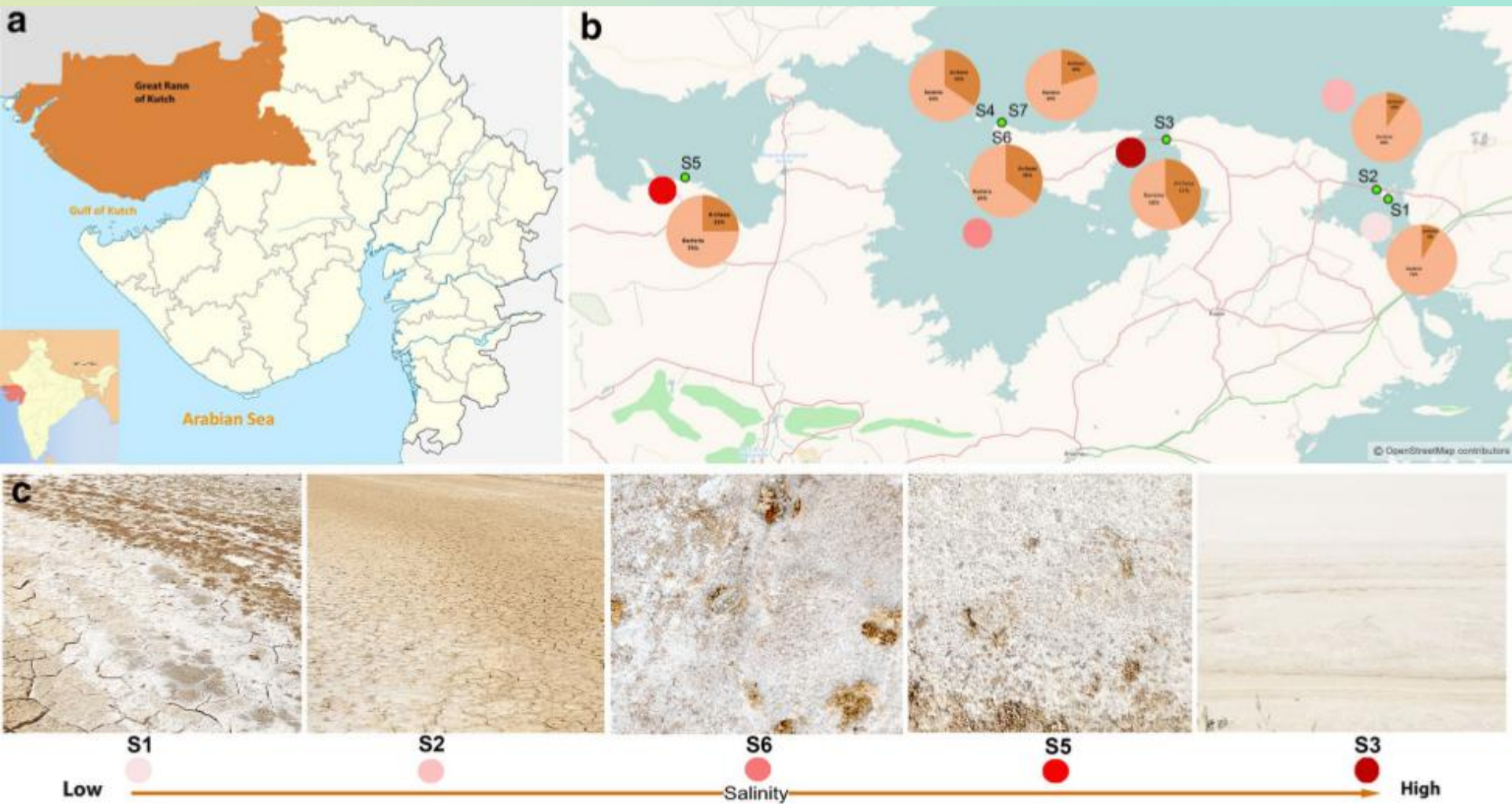


Fig. 1 Map showing Great Rann of Kutch, Gujarat, INDIA and Images of sample collection sites (S1, S2, S3, S4, S5, S6, S7). a Map of Gujarat showing Great Rann of Kutch in the inset of India. b Geographical location of sample collection sites of Great Rann of Kutch.

Results

1. 样品物理化学性质

Table 1 Details of the metagenomes of saline desert of Kutch

Sample ID	GPS coordinates	pH	Electrical conductivity mS/cm	Salinity (%)	Organic carbon mg/kg	Total nitrogen mg/kg
S1	23° 48' 39" N, 70° 58' 60" E	8	83.8	5.02	15,900	1200
S2	23° 47' 33" N, 71° 0' 29" E	7.99	68.5	4.11	165,400	4800
S3	23° 54' 29" N, 70° 32' 16" E	7.84	513.3	30.79	11,800	1200
S4	23° 56' 29" N, 70° 11' 18" E	8.23	97.5	5.85	12,600	1500
S5	23° 50' 6" N, 69° 31' 8" E	7.33	328	19.68	11,200	990
S6	23° 56' 27" N, 70° 11' 18" E	8.6	98	5.88	14,000	1200
S7	23° 56' 26" N, 70° 11' 16" E	7.18	71.8	4.3	15,200	900

PH:7.18-8.6 → 微碱性

导电率: 68.5MS/cm-513.3MS/cm

7倍以上的盐度差别

总有机碳: 1.1-1.6%

总有机氮: 0.09-0.48%

Table S2: Statistics of the saline desert datasets

Samples	Total no. of sequences	Total sequence size (bp)	Avg sequence length (bp)	No. of sequences that passed QC	GC content (%)
S1	24,23,783	38,77,83,372 bp	159	2111150(87.1%)	54
S2	24,20,832	322,114,449 bp	133	1803845 (74.5%)	54
S3	20,16,127	282,578,916 bp	140	1219000 (60.5%)	51
S4	31,00,617	467,782,469 bp	150	1952498(62.9%)	59
S5	23,49,820	235,993,491 bp	100	847464(35.5%)	57
S6	30,41,048	343,077,214 bp	112	2039121(67%)	60
S7	20,48,827	308,124,473 bp	150	1625955(79.4%)	60

235993491–387783372 bp 序列

M5nr IMG/M NCBI 数据库

细菌: 56-87%

古菌: 8-40%

病毒: 0.02-1%

真核生物: 0.1-2%

不可读取序列: 9-14%

主要原核生物: 变形菌门 (18.6-47.7%)、广古菌门 (7.9-40.1%)、拟杆菌门 (9.1-18.7%)、厚壁菌门 (5.8-8.4%)、放线菌门 (2.1-5.8%)、蓝藻细菌 (2-4.2%)。

含量较少的门: 绿弯菌门 (1-5.3%)、异常球菌-栖热菌门 (0.5-1.4%)、浮霉菌门 (1.3-3.9%)、芽单胞菌门 (1-1.9%)。

Results

2. 微生物多样性 – 细菌

变形菌门 —— 相对丰度

门水平:

α -变形菌 (5.7-19.4%)、 γ -变形菌 (5.4-17.6%)、 δ -变形菌 (5.4-11.6%)

β -变形菌 (1.7-5.1%)、 ϵ -变形菌 (0.2-0.5%)、 ζ -变形菌

属水平:

α -变形菌 (135个)、 γ -变形菌 (167个)、 δ -变形菌 (60个)、 β -变形菌 (75个)

海杆菌属、地杆菌属、硫杆菌属、伯克氏菌属

Results

2. 微生物多样性 – 细菌

拟杆菌门 (68个属)

Salinibacter (0.7–13.8 %)
Rhodothermus(0.7–1.7 %)

厚壁菌门 (146个属)

芽孢杆菌属 (0.8–1.2 %)

放线菌门

广泛存在于土壤和淡水和盐度较低的生境中

93个属

红色杆菌属 (0.2-0.7%)

丰度最高

蓝藻细菌 (优势种为聚球藻属)、绿弯菌门、浮霉菌门

高盐度生境

Results

2. 微生物多样性 - 古菌

古菌 (8-40%)

广古菌门 (67个属)

产甲烷古菌、嗜盐古菌、嗜热古菌

4-11%

存在于炎热的高盐度生境

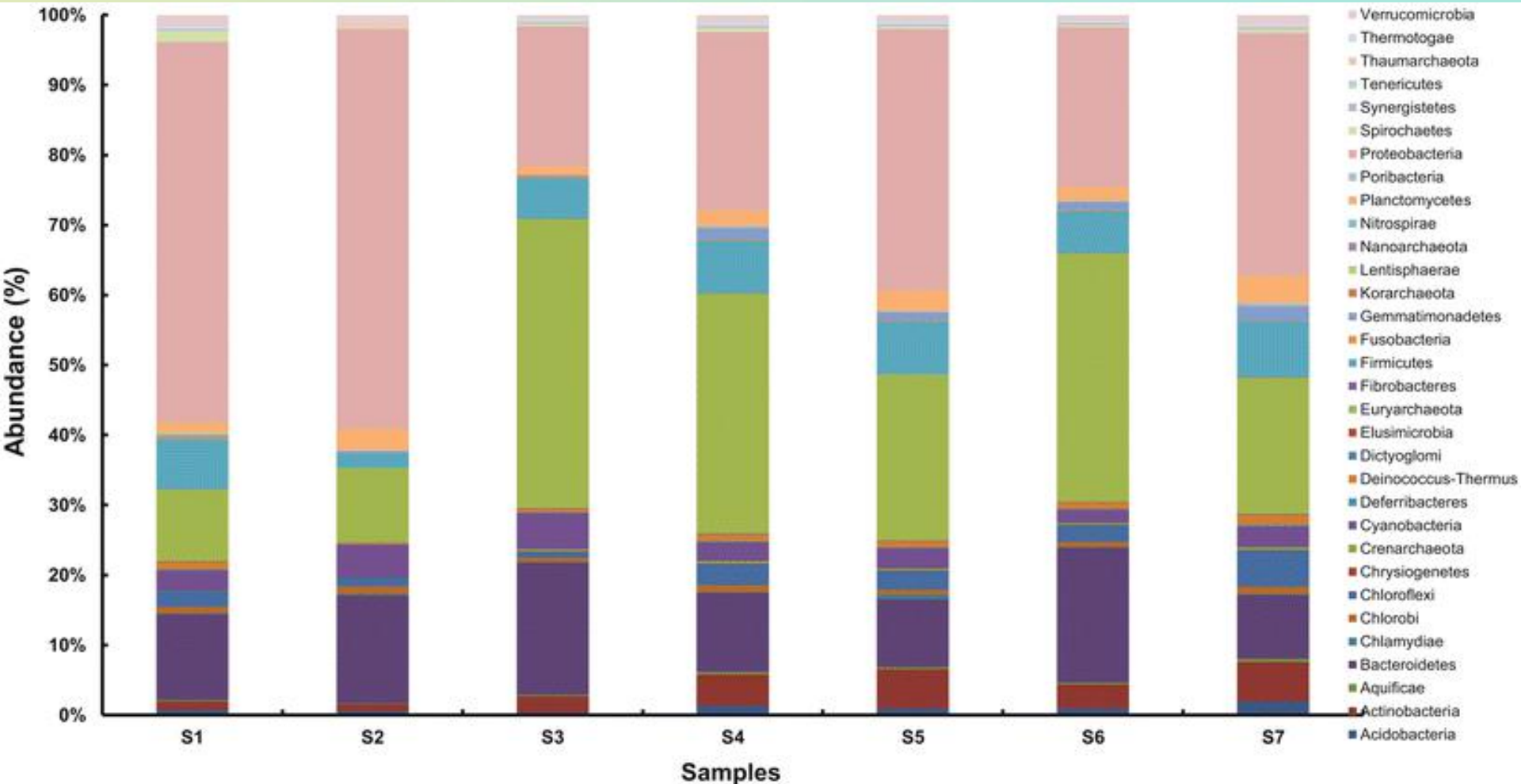
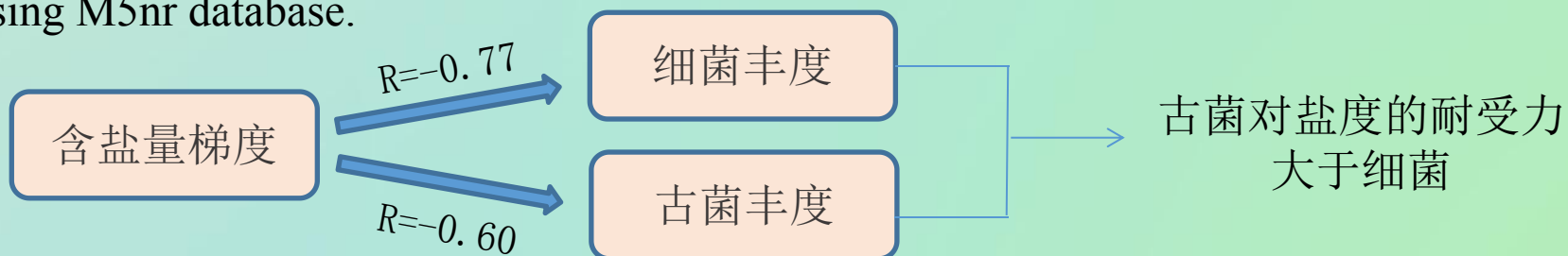


Fig. 2 Taxonomic distribution of bacterial and archaeal phyla of saline desert of Kutch. Relative abundance of reads assigned to bacterial and archaeal phyla in the 7 metagenomes using M5nr database.



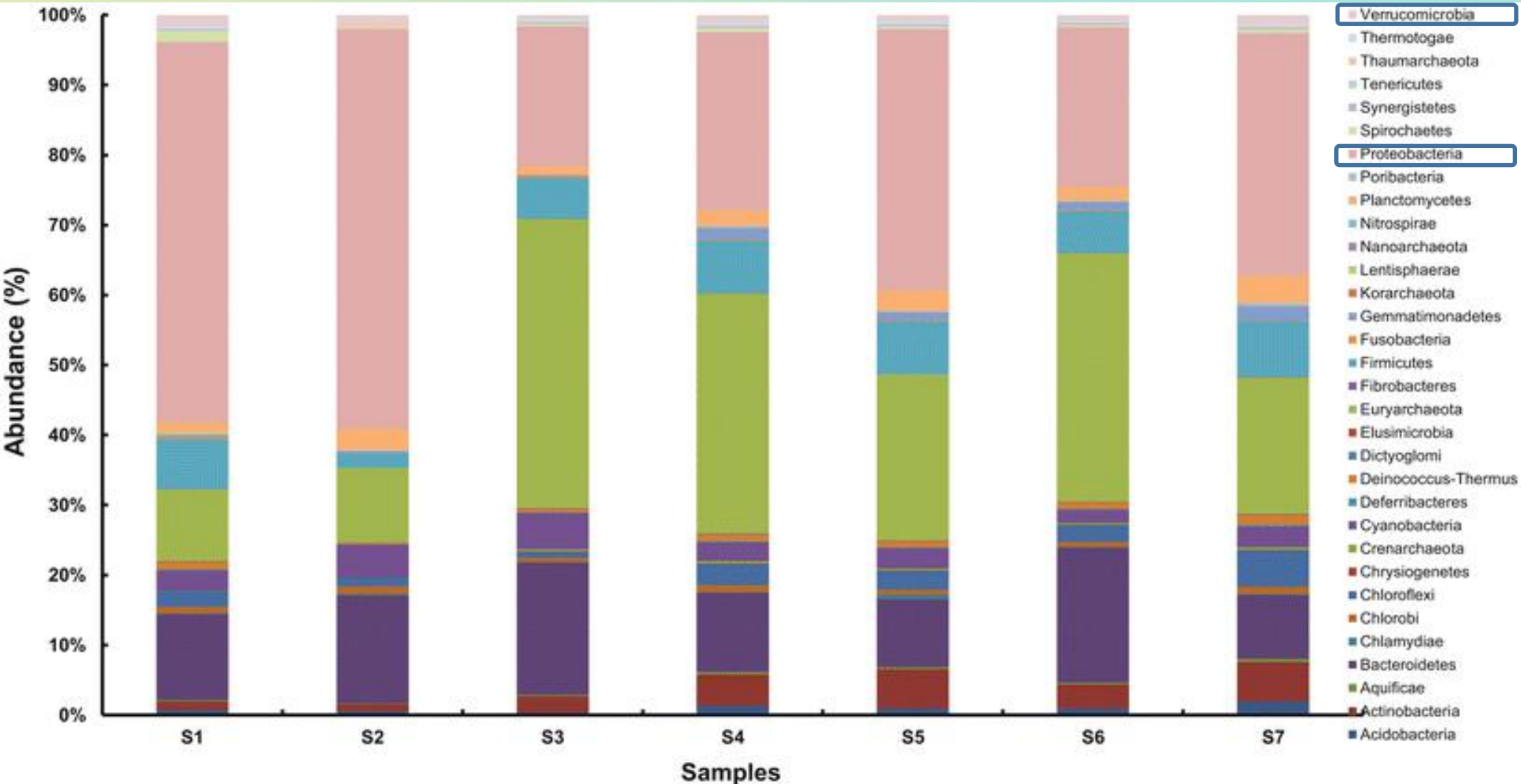
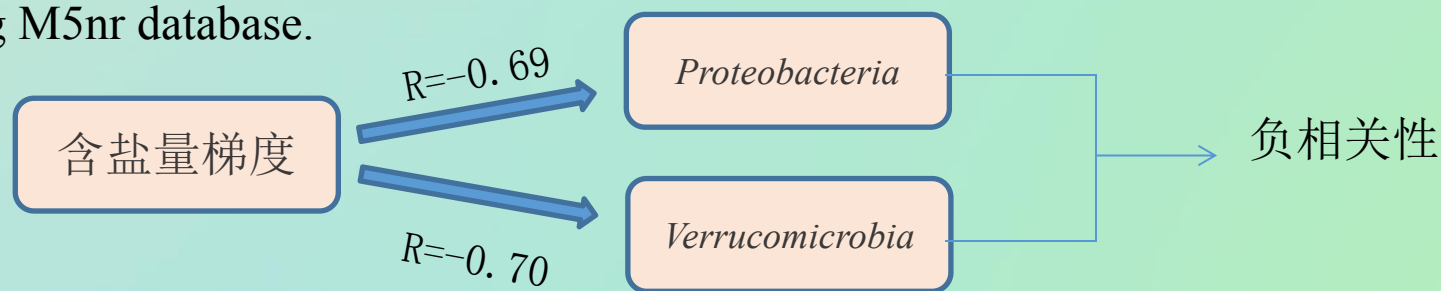


Fig. 2 Taxonomic distribution of bacterial and archaeal phyla of saline desert of Kutch. Relative abundance of reads assigned to bacterial and archaeal phyla in the 7 metagenomes using M5nr database.



Results

3. 随含盐量梯度变化的分类变化

含盐量梯度

非线性

放线菌门、绿弯菌门、螺旋体门

反向的U型弯曲

在低盐度和高盐度时丰度低

含盐量最高的样品S3

α -变形菌百分比含量最高
 β -变形菌百分比含量最低

变形菌门

含盐量较低的样品S2

结果相逆

蓝藻细菌随着盐度从低到高，微生物群落有种群衰落的迹象。

含盐量梯度

$R=0.85$

Salinibacter

Results

3. 随含盐量梯度变化的分类变化

高盐度

S3 S5

S6

中盐度

富含广古菌门（盐盒菌属、盐方菌属、盐几何菌属、富盐菌属、嗜盐碱单孢菌属）

优势菌属：*Salinibacter* 属

S3		S5		S6	
Species	Abundance	Species	Abundance	Species	Abundance
<i>Salinibacter ruber</i>	36356	<i>Salinibacter ruber</i>	8187	<i>Salinibacter ruber</i>	91590
<i>Haloarcula marismortui</i>	19569	<i>Haloarcula marismortui</i>	5878	<i>Haloarcula marismortui</i>	41861
<i>Haloquadratum walsbyi</i>	10469	<i>Halogeometricum borinquense</i>	3704	<i>Halogeometricum borinquense</i>	22043
<i>Halogeometricum borinquense</i>	9586	<i>Natronomonas pharaonis</i>	3348	<i>Natronomonas pharaonis</i>	20473
<i>Natronomonas pharaonis</i>	9170	<i>Halobacterium salinarum</i>	3038	<i>Halomicrobium mukohataei</i>	18814
<i>Halomicrobium mukohataei</i>	8386	<i>Halomicrobium mukohataei</i>	2733	<i>Halobacterium salinarum</i>	17332
<i>Halobacterium salinarum</i>	7825	<i>Haloquadratum walsbyi</i>	2691	<i>Haloquadratum walsbyi</i>	16254
<i>Halorhabdus utahensis</i>	7711	<i>Halorhabdus utahensis</i>	2471	<i>Halorhabdus utahensis</i>	16201
<i>Halorubrum lacusprofundi</i>	5569	<i>Haloterrigena turkmenica</i>	2119	<i>Haloferax volcanii</i>	12611
<i>Haloferax volcanii</i>	5496	<i>Haloferax volcanii</i>	2080	<i>Haloterrigena turkmenica</i>	12177
<i>Haloterrigena turkmenica</i>	4687	<i>Haladaptatus paucihalophilus</i>	1835	<i>Haladaptatus paucihalophilus</i>	10124
<i>Natrialba magadii</i>	3671	<i>Rhodothermus marinus</i>	1589	<i>Halorubrum lacusprofundi</i>	9816
<i>Haladaptatus paucihalophilus</i>	3569	<i>Halorubrum lacusprofundi</i>	1575	<i>Halalkalicoccus jeotgali</i>	8466
<i>Halalkalicoccus jeotgali</i>	2980	<i>Halalkalicoccus jeotgali</i>	1518	<i>Natrialba magadii</i>	8328
<i>Rhodothermus marinus</i>	2308	<i>Natrialba magadii</i>	1460	<i>Rhodothermus marinus</i>	8323
<i>Desulfohalobium retbaense</i>	1444	<i>Gemmatimonas aurantiaca</i>	1390	<i>Gemmatimonas aurantiaca</i>	6548
<i>Synechococcus sp.</i>	944	<i>Rhodopirellula baltica</i>	978	<i>Candidatus Solibacter usitatus</i>	3079
<i>Desulfovibrio vulgaris</i>	912	<i>Rhodobacter sphaeroides</i>	860	<i>Rubrobacter xylanophilus</i>	2895
<i>Rhodopirellula baltica</i>	835	<i>Bradyrhizobium japonicum</i>	857	<i>Anaerolinea thermophila</i>	2613
<i>Microcoleus chthonoplastes</i>	827	<i>Blastopirellula marina</i>	835	<i>Rhodopirellula baltica</i>	2612

Results

3. 随含盐量梯度变化的分类变化

低盐度

S1 S2

S1		S2	
Species	Abundance	Species	Abundance
<i>Marinobacter hydrocarbonoclasticus</i>	20476	<i>Gramella forsetii</i>	12230
<i>Haloarcula marismortui</i>	18763	<i>Salinibacter ruber</i>	12121
<i>Rhodobacter sphaeroides</i>	16762	<i>Halogeometricum borinquense</i>	12032
<i>Ruegeria pomeroyi</i>	14777	<i>Haloarcula marismortui</i>	11819
<i>Halogeometricum borinquense</i>	13965	<i>Rhodothermus marinus</i>	10587
<i>Desulfobacterium autotrophicum</i>	13383	<i>Microcoleus chthonoplastes</i>	8968
<i>Roseobacter denitrificans</i>	13272	<i>Haladaptatus paucihalophilus</i>	8869
<i>Marinobacter adhaerens</i>	13168	<i>Saccharophagus degradans</i>	7760
<i>Ruegeria sp. TM1040</i>	11577	<i>Hahella chejuensis</i>	7385
<i>Desulfococcus oleovorans</i>	11260	<i>Marinobacter hydrocarbonoclasticus</i>	7175
<i>Dinoroseobacter shibae</i>	10407	<i>Chromohalobacter salexigens</i>	6511
<i>Desulfatibacillum alkenivorans</i>	10181	<i>Zunongwangia profunda</i>	6470
<i>Salinibacter ruber</i>	10112	<i>Cellvibrio japonicus</i>	6216
<i>Rhodothermus marinus</i>	10101	<i>Haloquadratum walsbyi</i>	5927
<i>Halobacterium salinarum</i>	10045	<i>Halobacterium salinarum</i>	5519
<i>Roseovarius sp. 217</i>	9943	<i>Sorangium cellulosum</i>	5449
<i>Roseobacter sp. AzwK-3b</i>	9845	<i>Rhodopseudomonas palustris</i>	5422
<i>Jannaschia sp. CCS1</i>	9839	<i>Haloferax volcanii</i>	5403
<i>Marinobacter algicola</i>	9271	<i>Rhodopirellula baltica</i>	5155
<i>Natronomonas pharaonis</i>	9248	<i>Natronomonas pharaonis</i>	5127

细菌丰度 > 古菌丰度

产色素微生物、
硫酸还原微生物
丰度较高。

Results

4. 微生物群落的季节性变化

S6

10月（2012-10-31）：最高盐度样本

S4

4月（2013-4-28）：最热。平均气温41°C、最高达到49.5°C

S7

7月（2013-7-27）：最潮湿。月平均降水量147mm

	4月	10月	7月
细菌：古菌	1.8:1		4:1
广古菌门	33.7%	34.4%	19.5%
拟杆菌门	11.3%	18%	9.11%
产甲烷古菌	7月相比4月增长了1.6倍		
不产甲烷古菌	7月相比4月下降了1.2倍		

从门水平、属水平观察到群落明显的季节性变化

优势种群维持不变

Results

5. 多样性评估

稀疏曲线法

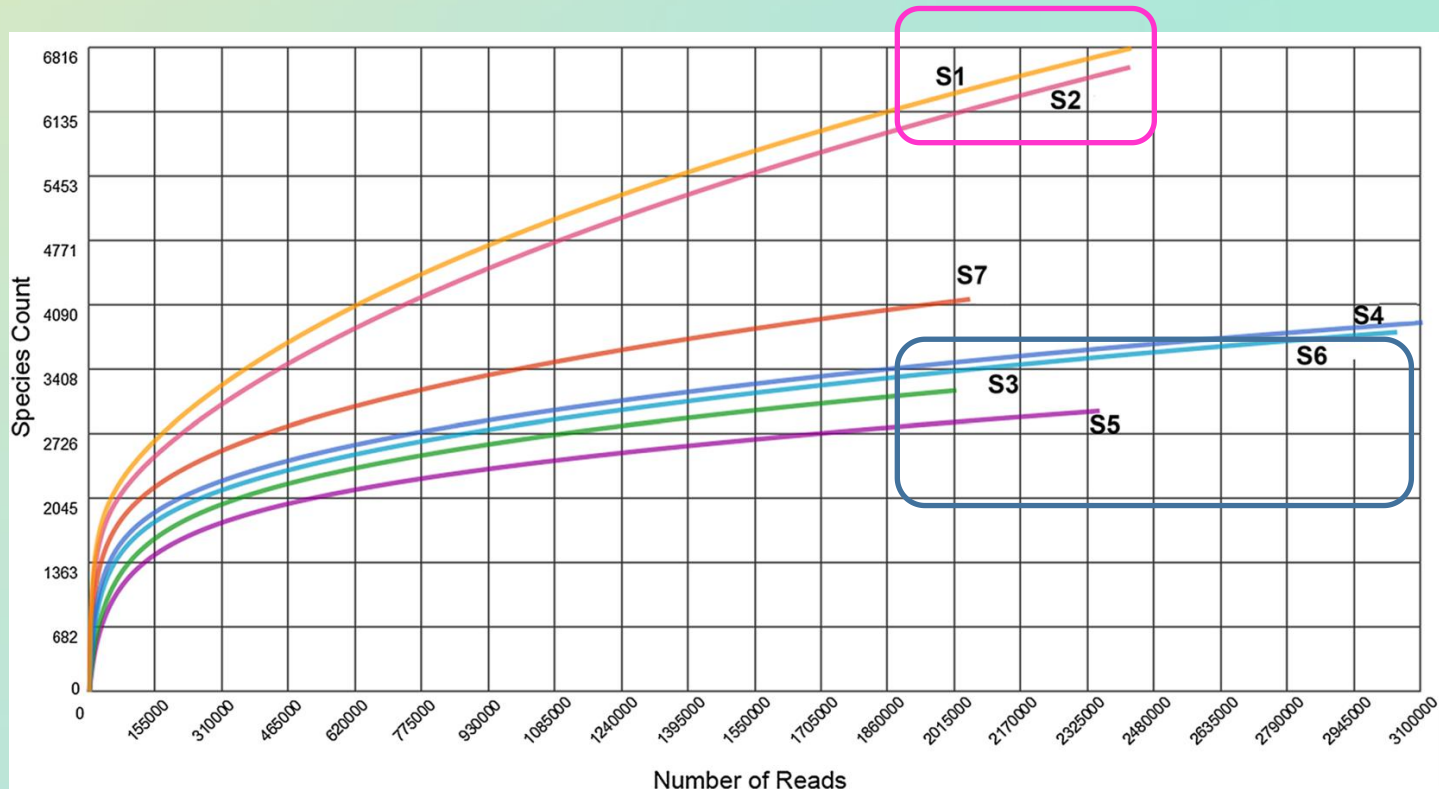


Fig. 3 Rarefaction analysis for the observed species. The rarefaction curves for samples S3, S4, S5, S6 and S7 reached the near-plateau phase representing good sampling depth; however, S1 and S2 did not reach a clear asymptote

Results

5. 多样性评估

香农指数 S3: 细菌多样性最低 S2: 古菌多样性最低 S5: 细菌、古菌多样性最高

Table 2 Alpha diversity indices of the bacterial and archaeal communities of seven saline desert metagenomes

Diversity indices	S1 (bacteria)	S1 (archaea)	S2 (bacteria)	S2 (archaea)	S3 (bacteria)	S3 (archaea)	S4 (bacteria)	S4 (archaea)	S5 (bacteria)	S5 (archaea)	S6 (bacteria)	S6 (archaea)	S7 (bacteria)	S7 (archaea)
Shannon index	6.3	3.073	5.91	2.56	5.05	2.95	6.2	2.991	6.44	3	5.69	2.909	4.97	3.322
Evenness	0.2151	0.0935	0.2225	0.0952	0.1391	0.0673	0.1972	0.5773	0.3142	0.1019	0.1225	0.04958	0.3979	5773
Chao1	3192	252	2386	156	2311	345.9	2990	381.6	2400	258.9	2871	422.4	594.3	61.6

均匀性分析

非参数丰富度估计 { 细菌: S1最高 S3最高
古菌: S6最高 S2最高

季节性变化 { S4: 细菌丰富度和多样性最高
S6: 古菌丰富度和多样性较高

Results

6. 功能基因与代谢

主要功能基因分类



核心代谢功能

蛋白质代谢
(9.5-10.9%)

碳水化合物代谢
(6.4-10.2%)

氨基酸及其衍生物代谢
(5.0-8.8%)

维生素和色素代谢
(3.9-6.8%)

外源性物质的降解与代谢
(4.3%)

Results

适应复杂的
生境所采取
的生存策略

6. 功能基因与代谢

应激响应基因 占有所有功能基因的2.1-4.1%

氧化应激（45.1-58.4%）、渗透压应激（15.4-20.5%）、热休克应激（12.4-28.2%）

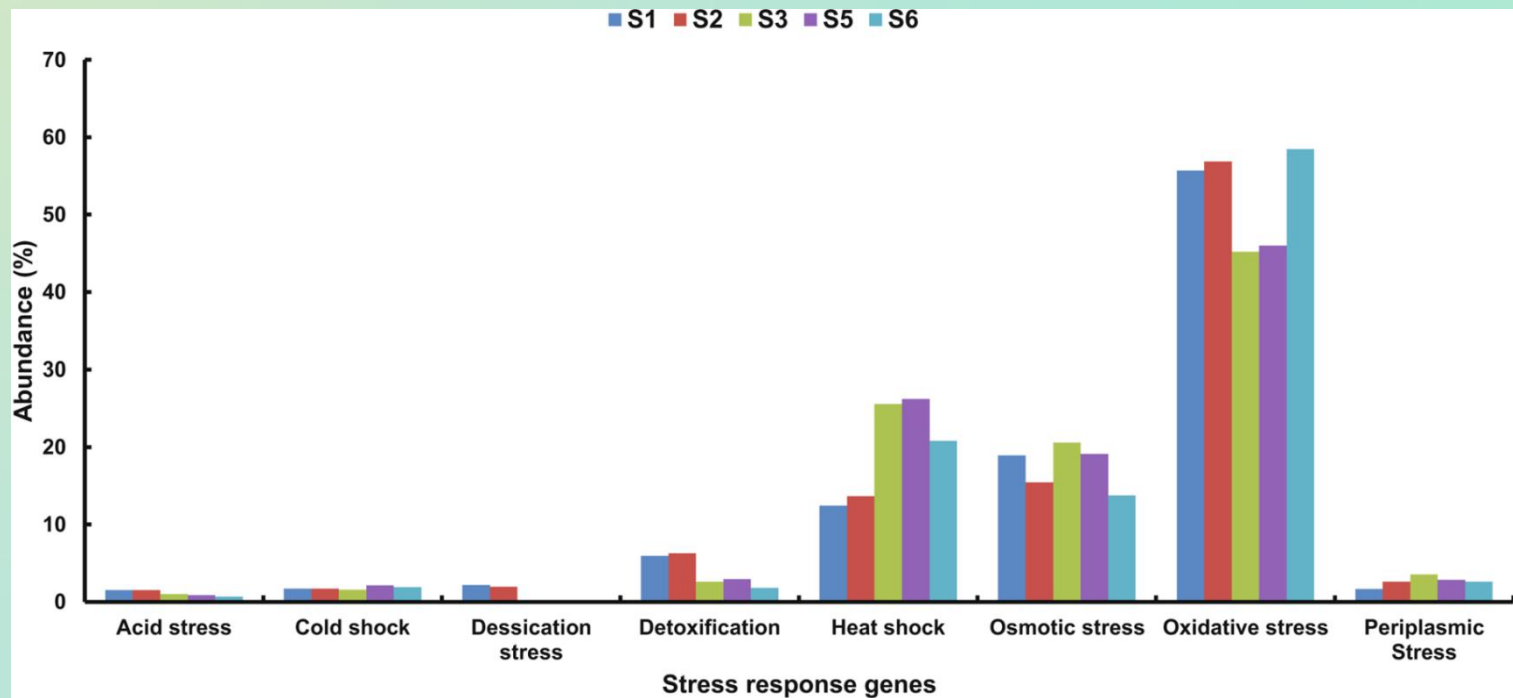


Fig. 5 Relative abundance of stress response gene categories. Relative abundances of genes related to stress response in SEED subsystem obtained from five location-based samples (S1, S2, S3, S5 and S6). *Bar graph* represents percentage of abundance

Results

6. 功能基因与代谢

Table 3 Taxonomic source of the genes implicated in response to oxidative, osmotic and heat shock stress

Stress type	Protein or subsystem name	Phyla (no. of hits) found in saline desert metagenomes				
		S1	S2	S3	S5	S6
Oxidative stress	Catalase	<i>Deltaproteobacteria</i> (52)	Flavobacteria (5)	Bacteroidetes (92)	Halobacteria (19)	Halobacteria (114)
	Peroxidase	<i>Deltaproteobacteria</i> (32)	<i>Alphaproteobacteria</i> (30)	Halobacteria (25)	Bacteroidetes (13)	Bacteroidetes (98)
	RNA polymerase sigma factor RpoD	<i>Alphaproteobacteria</i> (39)	Flavobacteriia (50)	Bacteroidetes (91)	Bacteroidetes (17)	Bacteroidetes (132)
		<i>Gammaproteobacteria</i> (29)	Bacteroidetes (3)		<i>Gammaproteobacteria</i> (19)	
	NAD-dependent glyceraldehyde-3-phosphate dehydroge		Flavobacteriia (50)	Bacteroidetes (92)	Bacteroidetes (13)	Halobacteria (68)
			Halobacteria (24)	Halobacteria (10)		
Heat shock	Chaperone protein DnaK	Halobacteria (25)	<i>Deltaproteobacteria</i> (18)	Bacteroidetes (29)	Bacteroidetes (5)	Bacteroidetes (56)
		<i>Deltaproteobacteria</i> (15)	<i>Alphaproteobacteria</i> (12)	Halobacteria (20)	Halobacteria (19)	Halobacteria (123)
	Chaperone protein DnaJ	Halobacteria (9)	Bacteroidetes (13)	Bacteroidetes (10)	Bacteroidetes (9)	Bacteroidetes (33)
	<i>Alphaproteobacteria</i> (14)	Halobacteria (5)	Halobacteria (8)	Halobacteria (14)	Halobacteria (28)	
	Translation elongation factor LepA	<i>Deltaproteobacteria</i> (16)	Bacteroidetes	Bacteroidetes (34)	Bacteroidetes (9)	Bacteroidetes (72)
Osmotic stress	Sarcosine Oxidase	<i>Alphaproteobacteria</i> (182)	<i>Alphaproteobacteria</i> (286)		<i>Gammaproteobacteria</i> (9)	-
			Actinobacteria (141)			
	Choline sulphatase	Halobacteria (205)	-	Halobacteria (240)	Actinobacteria (16)	Halobacteria (206)
		<i>Deltaproteobacteria</i> (56)			<i>Alphaproteobacteria</i> (9)	
	High-affinity choline uptake protein BeT	<i>Alphaproteobacteria</i> (68)	<i>Alphaproteobacteria</i> (68)	<i>Deltaproteobacteria</i> (144)	<i>Gammaproteobacteria</i> (16)	<i>Gammaproteobacteria</i> (103)
	<i>Deltaproteobacteria</i> (63)	<i>Deltaproteobacteria</i> (63)	Halobacteria (44)	<i>Alphaproteobacteria</i> (16)	<i>Alphaproteobacteria</i> (103)	
					Actinobacteria (103)	
					Flavobacteriia (103)	
	glucan synthase	<i>Deltaproteobacteria</i> (32)	<i>Gammaproteobacteria</i> (167)		<i>Deltaproteobacteria</i> (4)	<i>Deltaproteobacteria</i> (14)
	ABC transporter	<i>Alphaproteobacteria</i> (182)	<i>Deltaproteobacteria</i> (141)	<i>Gammaproteobacteria</i> (28)	Actinobacteria (6)	Actinobacteria (82)
		Bacteroidetes (141)	<i>Alphaproteobacteria</i> (564)		Bacteroidetes (6)	Bacteroidetes (82)
			<i>Gammaproteobacteria</i> (141)			Bacilli (82)

低盐度、中盐度样品
(S1、S2、S6)：氧化应激基因高表达

高盐度样品 (S3、S5)：
氧化应激基因低表达

高盐度样品 (S3、S5)：
渗透压应激基因高表达，
主要为拟杆菌门和嗜盐细菌。

Results

7. 与其他微生物群落组成进行比较

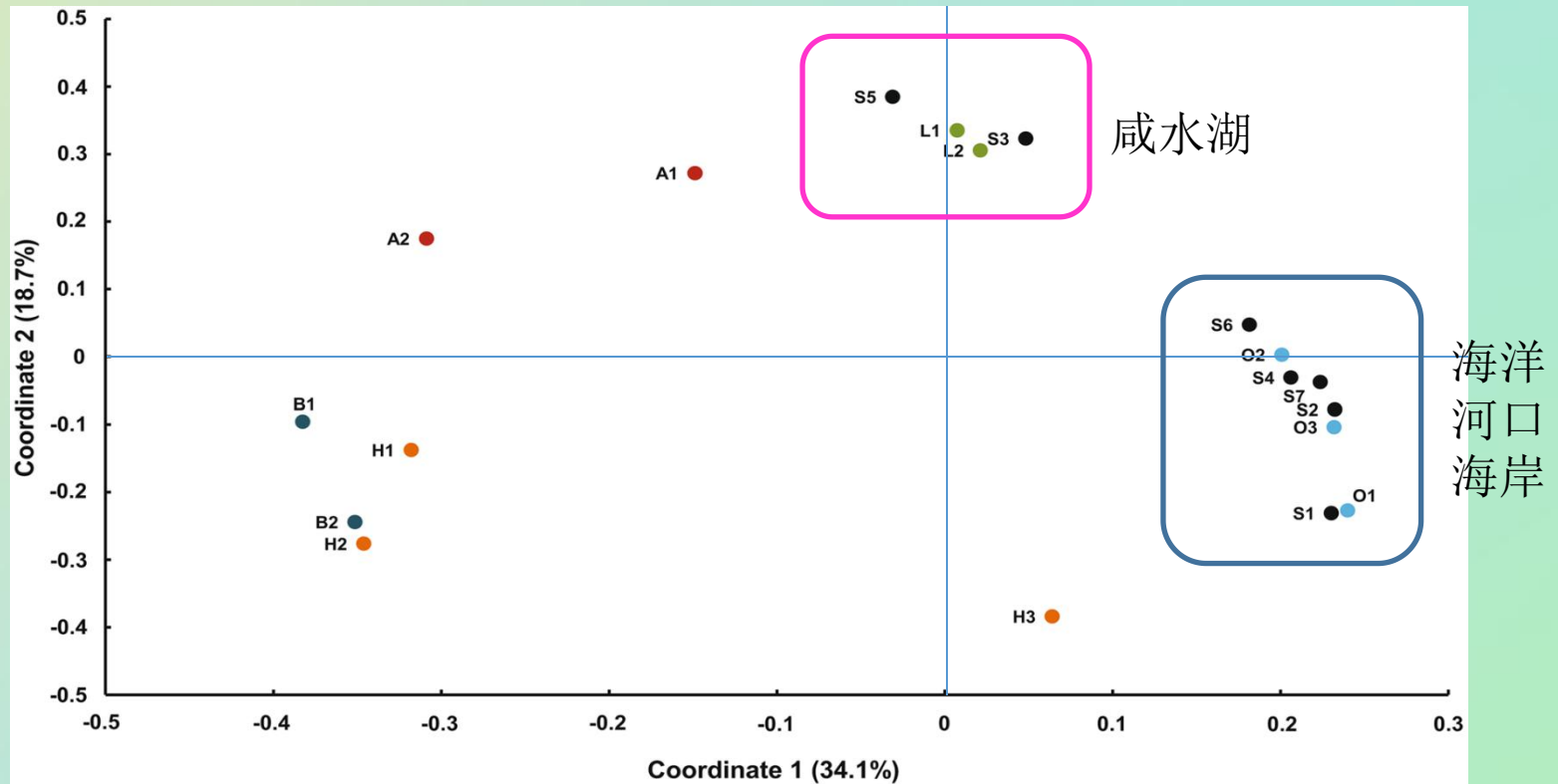
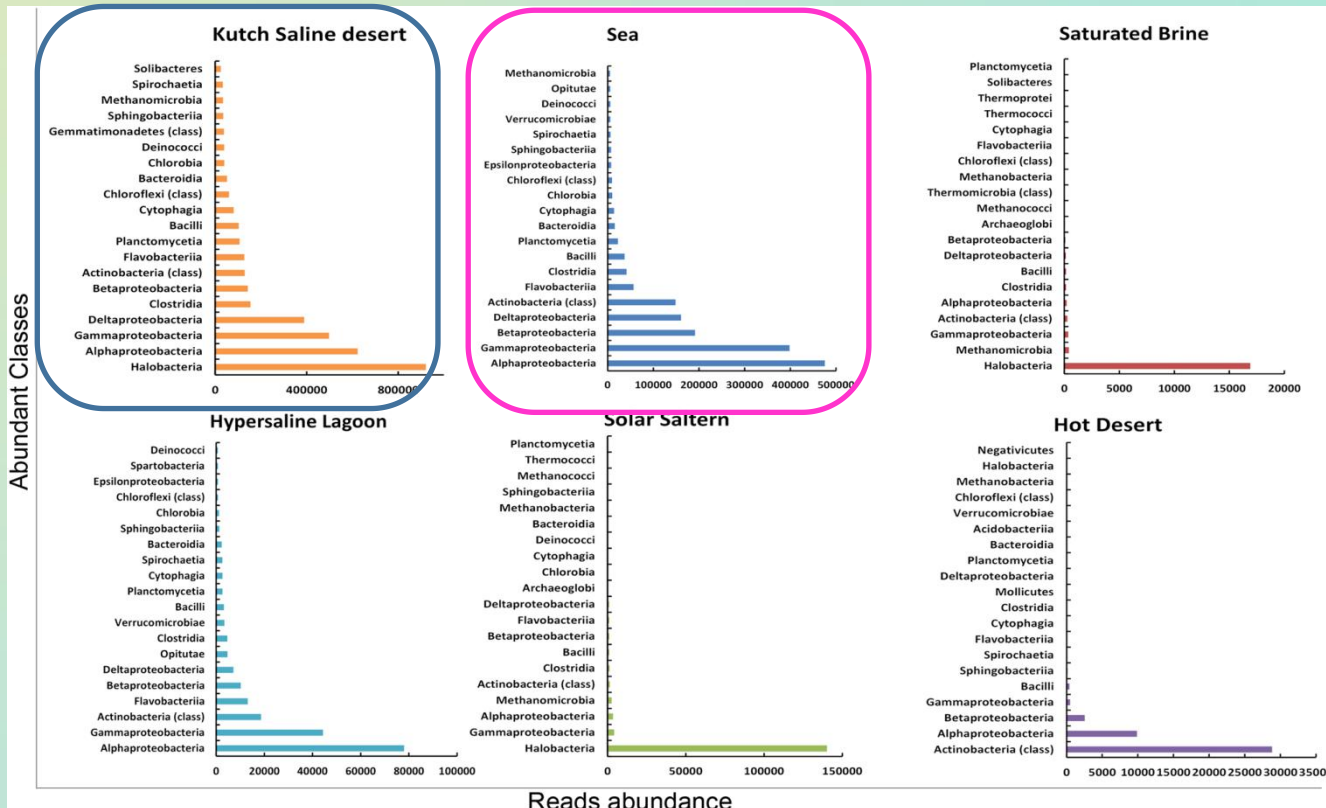


Fig. 6 PCoA plot of the relative abundance of taxonomic (Phylum) profiles of the selected biomes. Principal coordinate analysis using Bray-Curtis distance of the selected biomes. Comparative sites include hot desert *H1*, *H2* (Chihuahuan desert, New Mexico), *H3* (Mojave desert, California); sea *O1* (Puget Sound estuary) *O2* (Elba/Sant Andrea coast) *O3* (Sargasso sea); saturated brine *B1*, *B2* (Spain); solar saltern *A1*, *A2* (Chula Vista, CA); hypersaline lagoon *L1*, *L2* (Marmenor, Murcia) datasets. *S1*, *S2*, *S4*, *S6* and *S7* cluster with *O1*, *O2* and *O3* whereas *S3* and *S5* cluster with hypersaline lagoon *L1*, *L2* metagenomes

Results

7. 与其他微生物群落组成进行比较

嗜盐细菌多



相似度高:
 α -变形菌
 β -变形菌
 Γ -变形菌
 产甲烷菌
 嗜盐细菌

Fig. 7 Stacked bar representing distribution of various classes in saline desert and other saline and desert biomes. Stacked bar showing taxonomic distribution for all retrieved sequences

Results

8. 与其他微生物群落功能进行比较

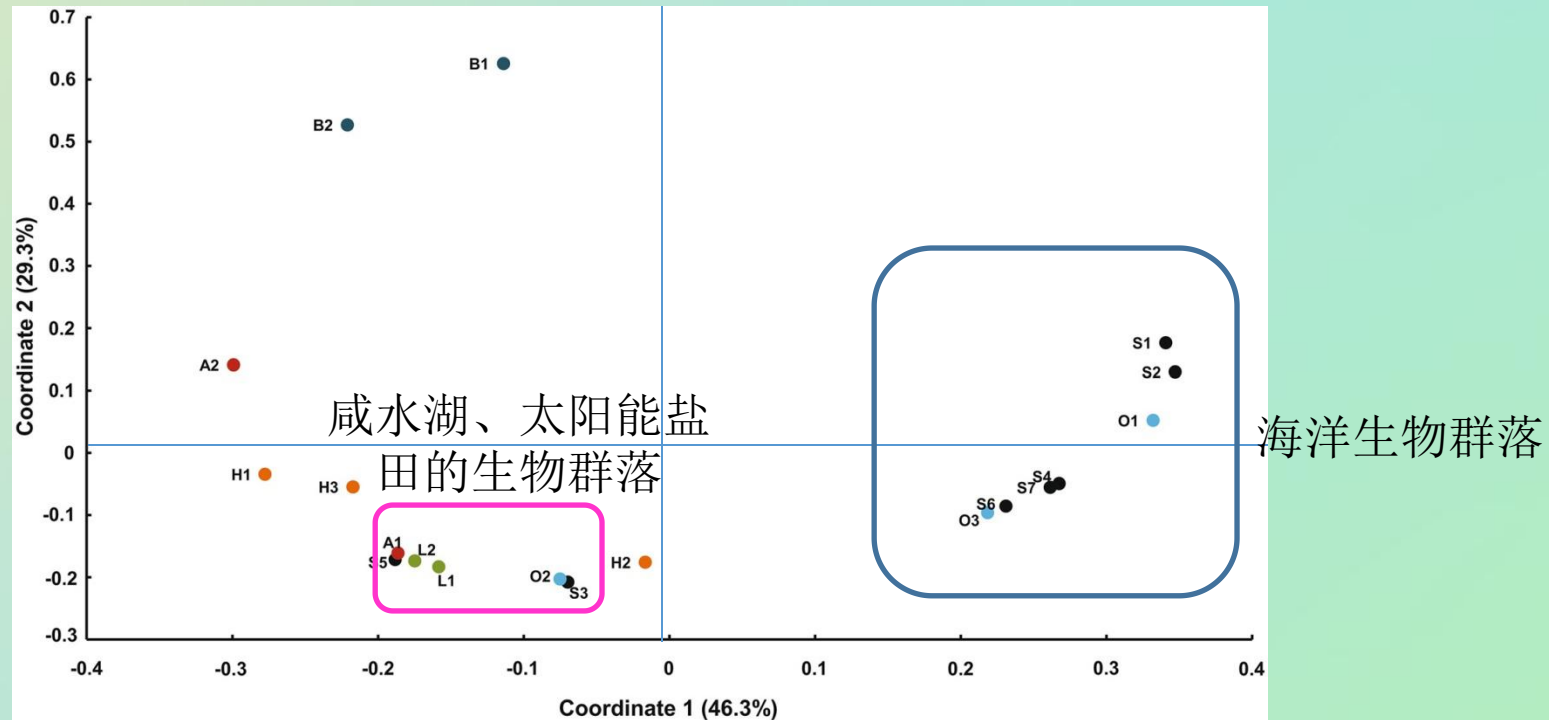


Fig. 8 PCoA plot of functional SEED Subsystem level 1 of the selected biomes. Functional community composition of the saline desert metagenomes (*S1*, *S2*, *S3*, *S4*, *S5*, *S6*, *S7*) and other saline, hypersaline and desert environments, based on principal coordinate analysis of the relative abundances of all MG-RAST subsystems. Principal coordinate analysis using Bray-Curtis distance of the selected biomes. Comparative sites include hot desert *H1*, *H2* (Chihuahuan desert, New Mexico), *H3* (Mojave desert, California); sea *O1* (Puget Sound estuary) *O2* (Elba Sant Andrea coast) *O3* (Sargasso sea); saturated brine *B1*, *B2* (Spain); solar saltern *A1*, *A2* (Chula vista, CA); hypersaline lagoon *L1*, *L2* (Marmenor, Murcia) datasets. Functional diversity patterns amongst biomes shows *S1*, *S2*, *S4*, *S6* and *S7* cluster with *O1* and *O2* whereas *S3* and *S5* cluster with *O2*, *L1* and *L2*

Results

9.qPCR量化细菌和古菌

Table 4 Enumeration of bacterial and archaeal population using qPCR

Sample ID	Bacterial load	Archaeal load
S1	2.56×10^6	1.25×10^4
S2	2.88×10^5	2.55×10^4
S3	9.58×10^5	1.61×10^5
S4	3.67×10^5	8.73×10^4
S5	2.19×10^5	5.45×10^4
S6	5.68×10^5	1.45×10^5
S7	5.09×10^4	2.93×10^4

细菌 > 古菌

低盐度样本

高盐度样本

季节性影响 (S4、S6、S7)：古菌负荷较高

Discussion

季节性盐沼和世界上最大的盐沙漠-喀奇县沙漠

高温、降水、高盐度



宏基因组学

未知微生物群落在极端环境中的生存与适应机制，功能属性

高盐土壤、沉积物：变形菌门、拟杆菌门、厚壁菌门

优势种群

本文研究盐碱沙漠显示了广古菌门的优势地位

Discussion

高盐度主导

Salinibacter

低盐度主导

Marinobacter, Rhodothermus and Rhodobacter

盐盒菌属、盐方菌属、盐几何菌属、富盐菌属、嗜盐碱单孢菌属

盐度是关键影响因素

Salinibacter

关键的环境影响因子

Discussion

qPCR列举分析

→ 验证复杂的微生物组成中的微生物负荷
捕捉季节性变化时细菌和古菌的数量上的变化

功能水平

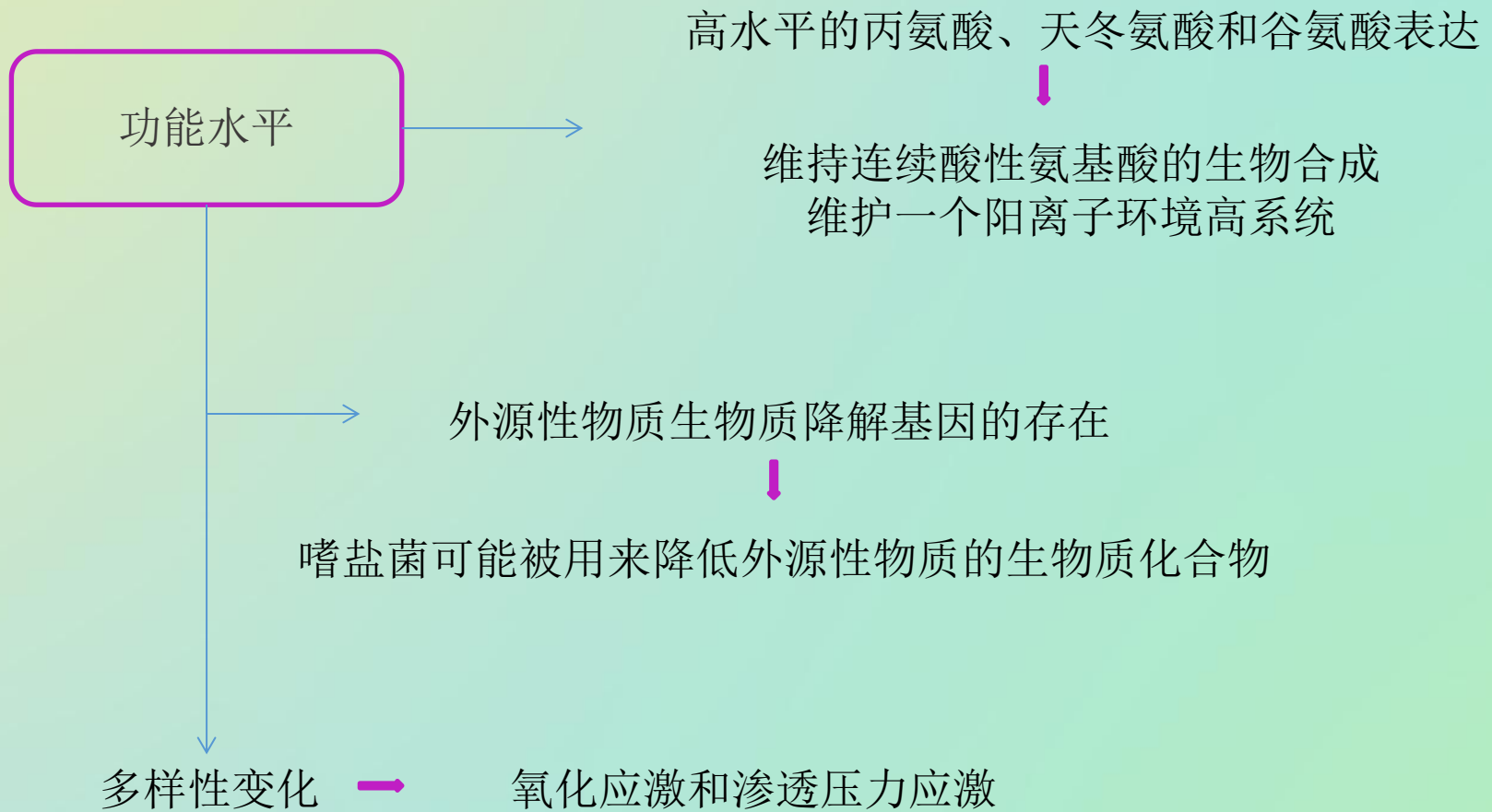
→ 大量的碳水化合物代谢基因和DNA代谢基因

↓
在极端环境下，生物的核心基因对维持细胞的生存与繁殖进行了唯一响应

→ 大量的氨基酸代谢基因表达

↓
用于维持机体渗透压的基于氨基酸的一些溶质

Discussion



低盐度的氧化应激反应大于高盐度可能是相关微生物在更广泛领域的一个可利用性。

Discussion

季节性变化

7月：绿弯菌门、蓝藻细菌、浮霉菌门

气候：干燥、极热

4、10月：广古菌门 → 对潮湿季节时沙漠转换为一个浅的含盐湿地环境的适应

物种进化

Discussion

海洋生态系统

陆地生态系统

盐碱沙漠

微生物生态学、分类学及其功能属性

THANKS FOR LISTENING!