

Supplementary Information

Functional profiling of coastal microbial mats from the Yucatan Peninsula: methane, nitrogen and sulfur metabolism

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Table S1. Quality and assembly statistics of shotgun sequences.

Sample	Number of raw reads	Number of clean reads	Total contigs	N50	L50	Shannon index
PF	94,473,962	92,803,286	177,856	2,445	38,402	5.21
PP	109,116,380	107,772,462	137,721	2,893	24,178	5.12
RLF	141,878,736	140,346,140	224,346	2,822	42,305	5.33
SFI	89,619,544	87,910,192	121,109	2,343	28,124	5.16

PF= Progreso flat, PP= Progreso pustular, RLF= Ría Lagartos flat, SFI= Sisal floating. N50= the contig size at which 50% of the total assembly length is contained. L50= the minimum number of contigs that sum to 50% of the total assembly length.

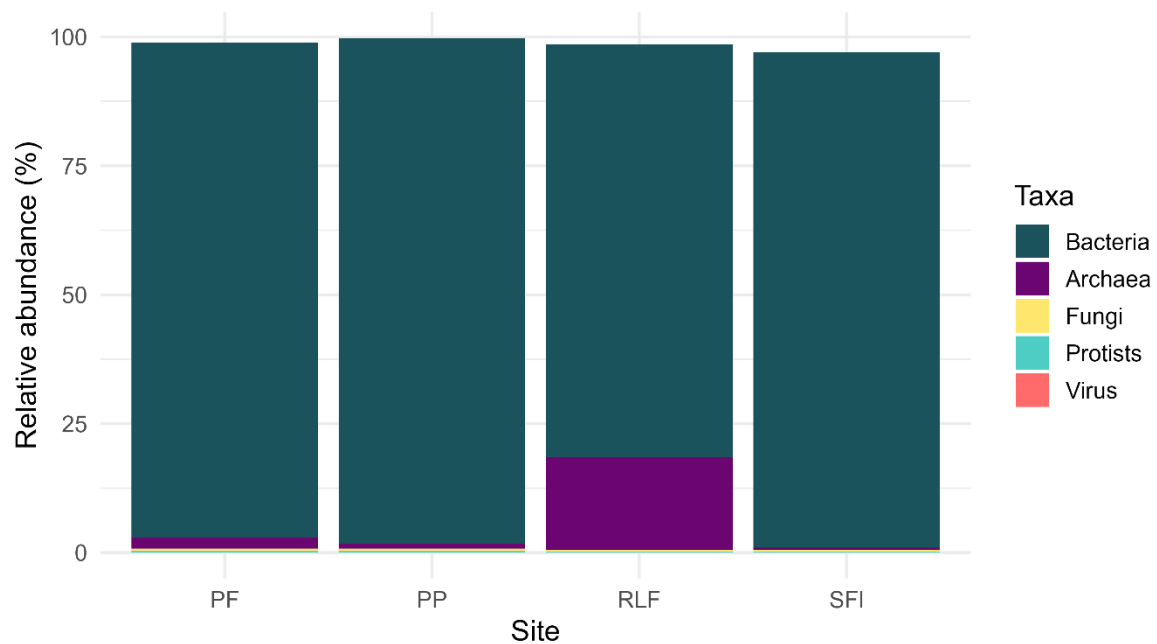


Fig. S1 Relative abundance of microbial taxa in microbial mats from the Yucatan Peninsula. PF= Progreso flat, PP= Progreso pustular, RLF= Ría Lagartos flat, SFI= Sisal floating

23 **Table S2.** Abundance of genes involved in aerobic methane oxidation.

Pathway	Gene	PF	RLF	PP	SFI
Serine cycle	glyA	23730	24588	23422	24457
	hprA	5899	5934	5681	4596
	gck	2592	3117	2511	2106
	eno	11082	12104	10918	10383
	ppc	4800	7024	5269	4304
	mtkA/B	10339	10197	10529	9486
	mcl	4915	5486	4905	4073
	mdh	10781	11520	10873	10540
	serA	15525	17948	15336	11541
	serC	3159	3249	3243	3667
	serB	7250	7300	7262	8351
	thrH	390	345	379	285
	psp	40	18	45	63
	Total abundance	100502	108830	100373	93852
RuMP cycle	fae--hps	461	219	429	181
	hxlB	991	802	893	649
	hxlA	773	519	698	458
	pfk(A/B)	14709	12064	13444	11083
	fbaA/B	11230	9588	10551	9337
	fbp	4585	4643	4291	4165
	Total abundance	32749	27835	30306	25873
Xylulose cycle	fbp	4585	4643	4291	4165
	fbp3	4	4	4	3
	glpX	3835	3802	3858	3563
	Total abundance	8424	8449	8153	7731

24 Numbers represent total counts of the genes found at read level with a random subsampling of 50 million reads.

25 PF= Progreso flat, PP= Progreso pustular, RLF= Ría Lagartos flat, SFI= Sisal floating.

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27 **Table S3.** Abundance of genes involved in methanogenesis.

Pathway	Gene	PF	RLF	PP	SFI
Hydrogenotrophic methanogenesis	fwdB/C/E/F/G/H	1364	696	1185	682
	ptr	422	109	426	195
	mch	549	913	360	183
	mtd(A/B)	316	101	325	146
	hmd	627	574	597	464
	mer	1344	2032	1669	793
	Total abundance	4622	4425	4562	2463
Acetoclastic methanogenesis	acsA/C/D	24720	29112	25711	23833
	ackA	7113	6590	6830	8009
	pta	14871	16860	13991	15623
	cdhA/B/C/D/E	3066	1424	2872	1797
	cooS/F	6181	4116	6097	4903
	Total abundance	55951	58102	55501	54165
Methylotrophic methanogenesis	mtaA/B/C	1040	540	956	460
	mtbA/B/C	6772	4184	5951	3891
	torACDYZ	2190	2374	2397	4039
	mttA/B/C	6720	2741	6265	3278
	mtmB/C	538	108	569	215
	Total abundance	17260	9947	16138	11883

28 Numbers represent total counts of the genes found at read level with a random subsampling of 50 million reads.

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31 **Table S4.** Abundance of genes involved in sulfur cycling.

Pathway	KEGG	Gene	PF	RLF	PP	SFI
Assimilatory sulfate reduction	K13811	PAPSS	0	0	0	0
	K00955	cysNC	6	4	4	16
	K00956, K00957	cysN/D	20	12	9	28
	K00958	sat	33	16	23	38
	K00860	cysC	4	8	5	9
	K00390	cysH	17	6	14	32
	K00380, K00381	cysJ/I	4	1	2	3
	K00392	sir	4	2	2	1
		Total abundance	88	49	59	127
Dissimilatory sulfate reduction	K00958	sat	33	16	23	38
	K00394, K00395	aprA/B	13	23	15	20
	K11180, K11181	dsrA/B	12	20	12	25
		Total abundance	58	59	50	83
Sulfate oxidation	K17222, K17223, K17224, K17225, K17226, K17227, K22622	soxA/X/B/C/Y/Z/D	3	51	23	25
	K08357	ttrA	0	0	0	0
		Total abundance	3	51	23	25
Thiosulfate reduction	K08352	phsA/psrA	5	9	4	11
		Total abundance	5	9	4	11
Sulfur relay system	K01011	TST/MPST/sseA	23	28	35	77
		Total abundance	23	28	35	77

32 Numbers represent total counts of the genes found at contig level. These abundances were further normalized
 33 for comparison between samples. PF= Progreso flat, PP= Progreso pustular, RLF= Ría Lagartos flat, SFI= Sisal
 34 floating.

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36 **Table S5.** Abundance of genes involved in nitrogen cycling.

Pathway	KEGG	Gene	PF	RLF	PP	SFI
Nitrogen fixation	K00531	anfG	0	0	0	0
	K02586, K02588, K02591	nifD/H/K	28	7	14	26
	K22896, K22897, K22898, K22899	vnfD/K/G/H	0	0	0	0
	Total abundance		28	7	14	26
Denitrification	K00370, K00371, K00374	narG/H/I	10	11	11	39
	K02567, K02568	napA/B	0	11	2	11
	K00368, K15864	nirK/S	3	7	6	24
	K04561, K02305	norB/C	6	6	7	18
	K00376	nosZ	7	5	4	16
	K15877	CYP55	0	0	0	0
	Total abundance		26	40	30	108
Nitrification	K10944, K10945, K10946	amoA/B/C	0	0	0	0
	K10535	hao	16	15	24	23
	K00370, K00371	narG/H	7	9	8	31
	Total abundance		23	24	32	54
Assimilatory nitrate reduction	K10534	NR	0	0	0	0
	K00367	narB	0	0	0	0
	K00360, K00372	nasB/C	0	0	1	1
	K00366	nirA	2	2	0	6
	K17877	NIT-6	0	0	0	0
	K02575	narK/nrtP/nasA	4	8	4	20
	Total abundance		6	10	5	27
Dissimilatory nitrate reduction	K00370, K00371, K00374	narG/H/I	10	11	11	39
	K02567, K02568	napA/B	0	11	2	11
	K00362, K00363	nirB/D	0	0	0	0
	K03385, K15876	nrfA/H	21	15	6	35
	Total abundance		31	37	19	85
Anammox	K20932, K20933, K20934	hzs	0	0	0	0
	K00368, K15864	nirK/S	3	7	6	24
	K20935	hdh	0	0	0	0
	Total abundance		3	7	6	24

37 Numbers represent total counts of the genes found at contig level. These abundances were further normalized
38 for comparison between samples. PF= Progreso flat, PP= Progreso pustular, RLF= Ría Lagartos flat, SFI= Sisal
39 floating.