Supplementary Material

An update of knowledge of the bacterial assemblages associated with the Mexican Caribbean corals *Acropora palmata, Orbicella faveolata,* and *Porites porites*

Joicye Hernández-Zulueta [1,2], Leopoldo Díaz-Pérez [1], Alex Echeverría-Vega [2], Gabriela Georgina Nava-Martínez [4], Miguel Ángel García-Salgado [4], Fabián A. Rodríguez-Zaragoza [1]*

1. Laboratorio de Ecología Molecular, Microbiología y Taxonomía, Departamento de Ecología, Centro Universitario de Ciencias Biológicas y Agropecuarias, Universidad de Guadalajara, Av. Ing. Ramón Padilla Sánchez, Zapopan, Jalisco, México; joicye.hernandez@academicos.udg.mx: https://orcid.org/0000-0002-3147-7069; leopoldo.diaz@academicos.udg.mx: https://orcid.org/0000-0003-0271-9257; fabian.rzaragoza@academicos.udg.mx: https://orcid.org/0000-0002-0066-4275

2. Departamento de Biología Celular y Molecular, Centro Universitario de Ciencias Biológicas y Agropecuarias, Universidad de Guadalajara, Av. Ing. Ramón Padilla Sánchez, Zapopan, Jalisco, México; joicye.hernandez@academicos.udg.mx: https://orcid.org/0000-0002-3147-7069;

3. Centro de Investigación de Estudios Avanzados del Maule (CIEAM), Universidad Católica del Maule, Talca, Chile; aecheverria@ucm.cl: https://orcid.org/0000-0002-0110-1079

4.OCEANUS A.C. Calle Río verde Lote 7 Mza. 235. Col. Proterritorio, Chetumal, Quintana Roo, CP 77086, México; gnavam01@gmail.com: https://orcid.org/0000-0001-8342-6389; info@oceanus.org.mx: https://orcid.org/0000-0001-5247-4695

*Corresponding author: Fabián A. Rodríguez-Zaragoza (fabian.rzaragoza@academicos.udg.mx)

Table S1. Average environmental variables at three sampling sites of the Mexican Caribbean. Codes: SST is sea surface temperature; SAL is salinity; pH is potential of hydrogen; NO_{3-} is nitrate; NO_{2-} is nitrite; PO_4 is phosphate; NH_4 is ammonium and Depth; CHK is Chankanaab; PTM is Puerto Morelos and PUM is Punta Maroma.

Sites	**Variables**							
	SST	SAL	pH	NO_{3-}	NO_{2-}	PO_4	NH_4	Depth
	(° C)	ppt		(μM)	(μM)	(μM)	(μM)	(m)
CHK	29.6	35.3	8.04	0.53	0.005	1.143	0.05	3.93
PTM	30.6	37.6	8.09	0.01	0.005	1.603	0.01	2.33
PUM	29.3	38.0	8.21	0.01	0.003	1.146	0.06	2.77

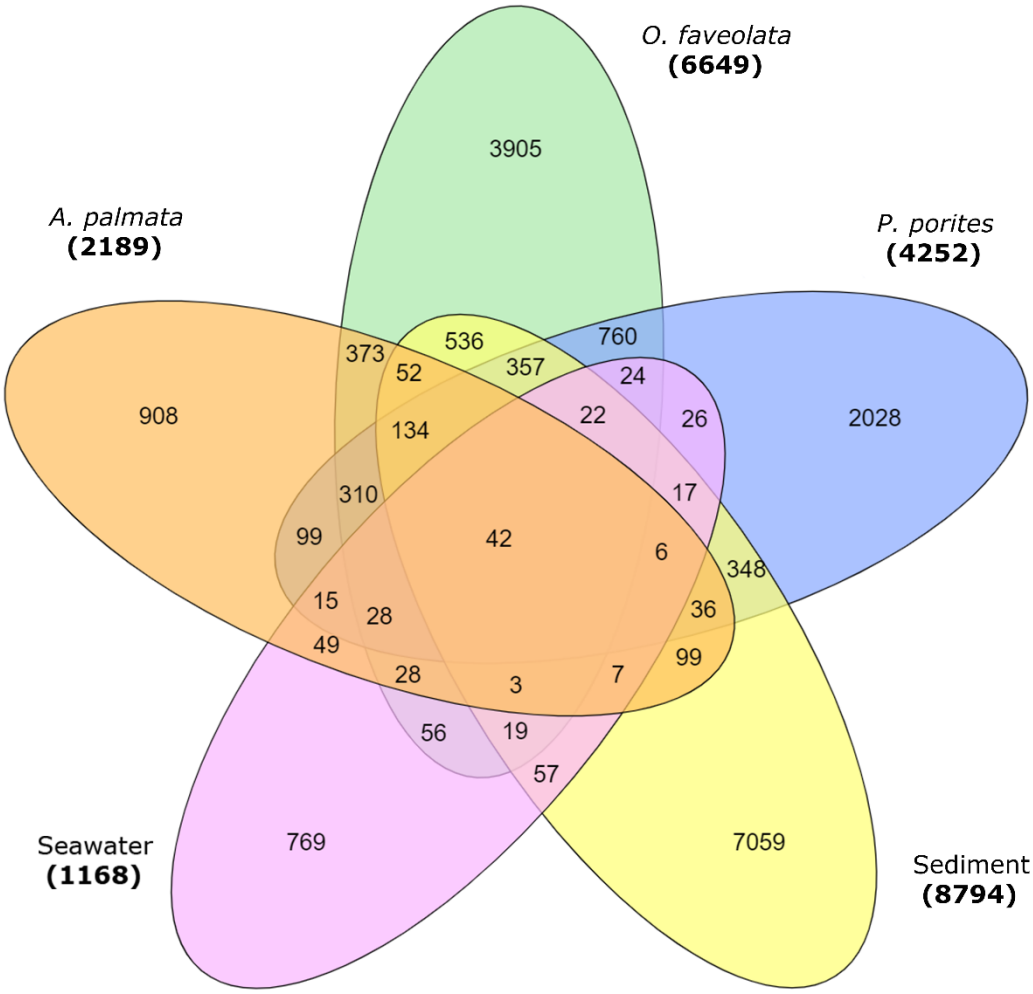

Figure S1. Venn's diagram showing number of amplicon sequence variants (ASVs) in each substrate.

Table S2. Results of the two-way crossed PERMANOVA with replication of the community attributes (ASV richness [*AR*], Shannon diversity [*H'*, nats]), and the bacterial ASV composition and abundance among substrates and sampling sites. Codes: C.V.(%) is the component of variation; P is the P-value. The P-values ≤ 0.05 are shown in bold.

	Community attributes			**Bacterial ASVs' composition and abundance**		
Source of variation	**Pseudo-F**	**P**	**C.V.(%)**	**Pseudo-F**	**P**	**C.V.(%)**
Substrate	21.593	**0.0001**	42.6	6.423	**0.0001**	30.6
Site	4.236	**0.0091**	13.1	2.012	**0.0001**	10.3
Substrate x Site	1.976	**0.0412**	16.1	1.751	**0.0001**	19.7
Residuals			28.2			39.4

Table S3. Results of the Post hoc tests of the two-way crossed PERMANOVA of the community attributes (ASV richness [AR] and Shannon diversity [H', nats]) of the interaction Substrate x Site, considering the substrate within and among sites. Codes: P is the P-value; Ap is *A. palmata*; Of is *O. faveolata*; Pp is *P. porites*; Sw is seawater and Sd is sediment; CHK is Chankanaab; PTM is Puerto Morelos and PUM is Punta Maroma. The P-values ≤ 0.05 are shown in bold. Statistical significance was tested with a Monte-Carlo (MC) procedure because the number of permutations in the *Post hoc* tests was ≤ 100.

Pairwise comparisons	Groups	t	P (MC)
1. Site x Substrate by substrate	Ap *vs.* Of	3.7989	**0.0161**
Chankanaab	Ap *vs.* Pp	2.7029	**0.0394**
	Ap *vs.* Sd	3.7003	**0.0158**
	Ap *vs.* Sw	0.8076	**0.4874**
	Of *vs.* Pp	1.5521	0.1631
	Of *vs.* Sd	1.8739	0.0887
	Of *vs.* Sw	6.1449	**0.0017**
	Pp *vs.* Sd	0.8382	0.4867
	Pp *vs.* Sw	2.8690	**0.0248**
	Sd *vs.* Sw	5.3474	**0.0029**
Punta Maroma	Ap *vs.* Of	2.9018	**0.0266**
	Ap *vs.* Pp	3.1097	**0.0182**
	Ap *vs.* Sd	12.242	**0.0003**
	Ap *vs.* Sw	2.9772	**0.0415**
	Of *vs.* Pp	0.5870	0.5958
	Of *vs.* Sd	2.3451	0.0763
	Of *vs.* Sw	2.0204	0.1006
	Pp *vs.* Sd	4.0514	**0.0149**
	Pp *vs.* Sw	1.8799	0.1088
	Sd *vs.* Sw	25.751	**0.0001**
Puerto Morelos	Ap *vs.* Of	1.7175	0.1496
	Ap *vs.* Pp	4.0448	**0.0152**
	Ap *vs.* Sd	4.3697	**0.0054**
	Ap *vs.* Sw	4.359	**0.0119**
	Of *vs.* Pp	1.3762	0.2236
	Of *vs.* Sd	1.9915	0.0847
	Of *vs.* Sw	1.1735	0.3035
	Pp *vs.* Sd	1.9947	0.0956
	Pp *vs.* Sw	1.0222	0.3685
	Sd *vs.* Sw	2.6700	**0.0434**
2. Site x Substrate by site	CHK *vs.* PUM	0.3143	0.8617
Acropora palmata	CHK *vs.* PTM	1.8898	0.1203
	PUM *vs.* PTM	2.0275	0.1040
Orbicella faveolata	CHK *vs.* PUM	0.1668	0.9396
	CHK *vs.* PTM	1.8846	0.1274
	PUM *vs.* PTM	1.5384	0.1765
Porites porites	CHK *vs.* PUM	0.1664	0.9548
	CHK *vs.* PTM	1.0030	0.3816
	PUM *vs.* PTM	0.8979	0.4475

Seawater	CHK *vs.* PUM	1.1046	**0.0332**
	CHK *vs.* PTM	1.4141	0.2351
	PUM *vs.* PTM	0.6199	0.5936
Sediment	CHK *vs.* PUM	10.832	**0.0002**
	CHK *vs.* PTM	1.1091	0.3334
	PUM *vs.* PTM	1.3599	0.2408

Table S4. Results of the Post hoc tests of the two-way crossed PERMANOVA of the bacterial ASV composition and abundance of the interaction Substrate x Site, considering the substrate within and among sites. Codes: P is the P-value; Ap is *A. palmata*; Of is *O. faveolata*; Pp is *P. porites*; Sw is seawater and Sd is sediment; CHK is Chankanaab; PTM is Puerto Morelos and PUM is Punta Maroma. The P-values ≤ 0.05 are shown in bold. Statistical significance was tested with a Monte-Carlo (MC) procedure because the number of permutations in the *Post hoc* tests was ≤ 100.

Pairwise tests	Groups	t	P (MC)
1. Site x Substrate by substrate			
Chankanaab	Ap *vs.* Of	1.2666	0.2081
	Ap *vs.* Pp	1.3607	0.1572
	Ap *vs.* Sd	1.5101	0.0975
	Ap *vs.* Sw	2.1128	**0.0286**
	Of *vs.* Pp	1.3535	0.1661
	Of *vs.* Sd	1.7048	0.0581
	Of *vs.* Sw	2.6953	**0.0130**
	Pp *vs.* Sd	1.6503	0.0700
	Pp *vs.* Sw	2.5874	**0.0129**
	Sd *vs.* Sw	2.6263	**0.0124**
Punta Maroma	Ap *vs.* Of	1.2085	0.2461
	Ap *vs.* Pp	1.3699	0.1512
	Ap *vs.* Sd	1.9483	**0.0304**
	Ap *vs.* Sw	2.4327	**0.0139**
	Of *vs.* Pp	1.1242	0.3211
	Of *vs.* Sd	1.6036	0.0716
	Of *vs.* Sw	2.1717	**0.0248**
	Pp *vs.* Sd	1.6207	0.0762
	Pp *vs.* Sw	2.1972	**0.0227**
	Sd *vs.* Sw	3.345	**0.0057**
Puerto Morelos	Ap *vs.* Of	1.5633	0.0822
	Ap *vs.* Pp	1.6190	0.0701
	Ap *vs.* Sd	1.7088	0.0547
	Ap *vs.* Sw	2.3703	**0.0198**
	Of *vs.* Pp	1.4441	0.1157
	Of *vs.* Sd	1.4894	0.1051
	Of *vs.* Sw	2.2744	**0.0225**
	Pp *vs.* Sd	1.6343	0.0624
	Pp *vs.* Sw	2.5529	**0.0140**
	Sd *vs.* Sw	2.5493	**0.0129**
2. Site x Substrate by site			
Acropora palmata	CHK *vs.* PUM	1.2065	0.2588
	CHK *vs.* PTM	1.2787	0.2014
	PUM *vs.* PTM	1.3421	0.1631
Orbicella faveolata	CHK *vs.* PUM	1.0555	0.3790
	CHK *vs.* PTM	1.1726	0.2865
	PUM *vs.* PTM	1.1052	0.1631
Porites porites	CHK *vs.* PUM	1.3117	0.1825
	CHK *vs.* PTM	1.5919	0.0814
	PUM *vs.* PTM	1.1304	0.3159
Seawater	CHK *vs.* PUM	2.1230	**0.0222**
	CHK *vs.* PTM	2.9256	**0.0078**

	PUM *vs.* PTM	2.0200	**0.0267**
Sediment	CHK *vs.* PUM	1.7394	0.0521
	CHK *vs.* PTM	1.4674	0.1137
	PUM *vs.* PTM	1.1217	0.3191

Table S5. Dominant bacteria families of each substrate within each site. Codes: Ap is *A. palmata*; Of is *O. faveolata*; Pp is *P. porites*; Sw is seawater and Sd is sediment.

Sites		**Chankanaab**					**Puerto Morelos**					**Punta Maroma**				
Family	**Substrate**	Ap	Of	Pp	Sw	Sd	Ap	Of	Pp	Sw	Sd	Ap	Of	Pp	Sw	Sd
Rhodobacteraceae		999	1842	1177	6037	1815	177	21744	2657	5250	998	418	1397	1977	6756	888
Amoebophilaceae		3357	1797	3503	6	370	2716	371	933	6	74	11149	1228	411	6	44
Cryomorphaceae		139	55	22	9285	0	66	142	132	4819	38	34	54	112	5499	46
Kiloniellaceae		543	2668	2461	0	50	2802	1459	2221	4	1833	505	2283	2231	4	1274
Spirochaetaceae		10097	271	428	0	9	430	150	47	0	14	3300	550	84	0	76
Myxococcaceae		870	220	52	14	76	11205	103	99	7	85	2114	91	234	11	107
Cyanobiaceae		36	0	5	3975	610	17	67	9	3861	46	42	25	60	5713	30
Rhizobiaceae		1197	1130	701	1	960	323	213	5468	0	555	596	878	473	3	430
Pirellulaceae		115	339	355	21	4490	7	280	378	2	3300	106	422	425	12	2796
Cyclobacteriaceae		6537	610	547	72	41	1837	336	752	37	457	710	352	385	44	389
Woeseiaceae		333	1581	623	0	195	14	874	860	4	2429	133	1043	984	5	2223
Nitrosopumilaceae		160	2228	1348	5	6	5	776	106	10	607	43	1816	1378	6	1078
Flavobacteriaceae		197	369	198	1038	35	33	256	346	3380	180	102	157	367	2646	156
Nitrosococcaceae		94	543	1435	2	194	16	98	154	0	2214	85	1091	701	2	1955
Terasakiellaceae		2291	693	66	2	0	1395	91	319	11	19	1756	419	58	6	13
Thermoanaerobaculaceae		144	784	436	0	705	9	121	663	0	841	90	390	777	0	1376
Halieaceae		140	138	48	780	286	1	81	105	792	972	26	42	549	731	1018
Stappiaceae		491	235	276	417	380	5	116	1072	90	42	94	755	915	82	51
Microtrichaceae		135	583	650	21	264	12	199	393	12	894	179	656	392	25	731
Saprospiraceae		92	598	192	4	21	65	176	992	74	662	21	233	976	60	715

Table S6. BIO-ENV outputs with the best subsets of environmental variables correlated with the bacterial assemblage per substrate. Codes: P is the P-value; ρ correspond to Spearman correlación; SST is sea surface temperature; SAL is salinity; NO_{2}^{-} is Nitrite; NO_{3}^{-} is Nitrate; NH_4 is ammonium; PO_4 is phosphate; pH is the potential of hydrogen . The P-values ≤ 0.05 are shown in bold.

Substrate	*ρ*	P	Best subset
A. palmata			
	0.396	**0.042**	SST, SAL, DEPHT
O. faveolata			
	0.060	0.348	SST, SAL
	0.061	0.340	SST, SAL, pH
P. porites			
	0.403	**0.008**	SST, SAL, NO_{3}^{-}, NH_4
	0.396	**0.011**	SST, NH_4
	0.389	**0.005**	SST, NH_4, PO_4
	0.376	**0.009**	SST, SAL, NH_4
	0.369	**0.022**	SST, NO_{3}^{-}, NH_4
	0.367	**0.024**	SST, DEPHT, NO_{3}^{-}, NH_4
	0.365	**0.017**	SST, DEPHT, NO_{3}^{-}, NH_4, PO_4
	0.363	**0.015**	SST, DEPHT, NO_{3}^{-}, NH_4
	0.360	**0.018**	SST, SAL, DEPHT, NO_{3}^{-}, NH_4
	0.358	**0.011**	SST, SAL, NO_{3}^{-}, NH_4, PO_4
Seawater			
	0.769	**0.005**	SAL, NO_{2}^{-}
	0.757	**0.008**	SAL
	0.754	**0.0001**	SAL, DEPTH, NO_{2}^{-}, NH_4
	0.753	**0.003**	SAL, NO_{2}^{-}, NO_{3}^{-}
	0.744	**0.003**	SAL, DEPTH, NO_{2}^{-}
	0.731	**0.0008**	SAL, DEPTH, NO_{2}^{-}, NO_{3}^{-}, NH_4
	0.723	**0.0007**	SAL, NO_{2}^{-}, NH_4
	0.715	**0.003**	SAL, DEPTH, NO_{2}^{-}, NO_{3}^{-}
	0.714	**0.002**	SAL, pH, DEPTH, NO_{2}^{-}
	0.707	**0.0004**	SAL, DEPTH, NO_{2}^{-}, NH_4, PO_4
Sediments			
	0.567	**0.033**	SAL, NO_{2}^{-}, NO_{3}^{-}
	0.551	**0.006**	NO_{2}^{-}
	0.549	**0.006**	NO_{2}^{-}, NO_3
	0.503	**0.015**	SAL, NO_{2}^{-}
	0.494	**0.011**	SAL, pH, NO_{2}^{-}, NO_{3}^{-}
	0.491	**0.011**	SST, SAL, NO_{2}^{-}, NO_{3}^{-}
	0.484	**0.01**	SAL, NO_{2}^{-}, NO_{3}^{-}, NH_4
	0.467	**0.015**	SST, NO_{2}^{-}, NO_{3}^{-}
	0.451	**0.019**	SAL, NO_{2}^{-}, NO_{3}^{-}, PO_4
	0.450	**0.025**	SAL