

Erect macroalgae influence epilithic bacterial assemblages and reduce coral recruitment

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Table S1. PERMANOVA on Bray-Curtis similarity coefficients calculated using untransformed data analyzing the effects of Treatments (3 levels: control = CTRL versus macroalgal canopy removal = MCR versus total macroalgal removal = TMR; fixed) and Bommie (random and nested within the Treatment) on the structure of the bacterial community at the OTU level, after 3.5 mo since the start of the experiment.

Sources of variation	<i>df</i>	MS	Pseudo- <i>F</i>	<i>p</i>
Treatment	2	6436.5	3.37	0.001
Bommie (Treatment)	12	1916.5	1.07	0.211
Residual	22	1793.4		

Pairwise tests	<i>t</i>	<i>P</i>
CTRL – TMR	1.964	0.010
CTRL – MCR	1.962	0.006
TMR – MCR	1.425	0.022

Table S2. PERMANOVA on Bray-Curtis similarity coefficients calculated using presence/absence transformed data analyzing the effects of Treatment (3 levels: control = CTRL versus macroalgal canopy removal = MCR versus total macroalgal removal = TMR; fixed) and Bommie (random and nested within the Treatment) on the structure of the bacterial community (family level), 3.5 mo after the start of the experiment.

Sources of variation	<i>df</i>	MS	Pseudo- <i>F</i>	<i>p</i>
Treatment	2	986.15	3.174	0.001
Bommie (Treatment)	12	312.84	1.108	0.192
Residual	22	282.37		

Pairwise tests	<i>t</i>	<i>P</i>
CTRL – TMR	2.112	0.009
CTRL – MCR	1.867	0.006
TMR – MCR	1.219	0.095

Table S3. SIMPER analysis identifying the bacterial families contributing to percentage dissimilarities between pairs of experimental treatments (control = CTRL, macroalgal canopy removal = MCR and total macroalgal removal = TMR). The average abundance of families within each treatment, the average dissimilarity between treatments and the % contribution of each family to total dissimilarity are reported. Variables which contributed $\geq 2\%$ at least in one of the comparisons are shown.

Comparison: Species	CTRL Av.Abund	MCR Av.Abund	Av. Diss.	Contribution %
Cyanobacteria GpI	441.17	895.00	6.40	15.39
Rhodobacteraceae	866.17	607.77	3.35	8.06
Flavobacteriaceae	460.75	269.69	2.36	5.68
Vibrionaceae	267.75	238.23	2.29	5.51
Cyanobacteria GpIV	248.17	107.92	1.86	4.46
Cyanobacteria GpVIII	182.00	25.15	1.64	3.93
Saprospiraceae	314.75	251.85	1.43	3.42
Cyanobacteria GpIIa	121.75	211.00	1.24	2.98
Phyllobacteriaceae	237.50	231.08	1.12	2.69
Flammeovirgaceae	190.25	194.23	0.97	2.33
Kiloniellaceae	95.67	127.92	0.96	2.30
Verrucomicrobiaceae	149.25	69.46	0.94	2.26
Erythrobacteraceae	152.42	87.08	0.93	2.22
Rubritaleaceae	114.25	53.85	0.88	2.13
Rhizobiaceae	74.42	119.38	0.83	2.00
Comparison: Species	CTRL Av.Abund	TMR Av.Abund	Av. Diss.	Contribution %
Cyanobacteria GpI	441.17	492.00	4.61	9.78
Rhodobacteraceae	866.17	502.08	4.36	9.23
Flavobacteriaceae	460.75	230.25	3.08	6.52
Cyanobacteria GpIV	248.17	51.75	2.41	5.11
Vibrionaceae	267.75	200.67	2.38	5.04
Cyanobacteria GpVIII	182.00	9.17	1.93	4.10
Saprospiraceae	314.75	252.25	1.63	3.45
Kiloniellaceae	95.67	197.17	1.46	3.09
Hyphomonadaceae	175.58	141.92	1.39	2.95
Phyllobacteriaceae	237.50	198.83	1.34	2.85
Cyanobacteria GpIIa	121.75	160.92	1.19	2.53
Erythrobacteraceae	152.42	42.42	1.18	2.51
Flammeovirgaceae	190.25	137.33	1.12	2.37
Rhizobiaceae	74.42	136.75	1.08	2.29
Verrucomicrobiaceae	149.25	61.58	1.01	2.14

Alteromonadaceae	116.08	119.50	1.01	2.14
Rubritaleaceae	114.25	94.50	0.98	2.09
Comparison:	TMR	MCR		
Species	Av.Abund	Av.Abund	Av. Diss.	Contribution %
Cyanobacteria GpI	492.00	895.00	7.03	19.59
Rhodobacteraceae	502.08	607.77	2.63	7.31
Vibrionaceae	200.67	238.23	2.03	5.64
Cyanobacteria GpIIa	160.92	211.00	1.94	5.41
Flavobacteriaceae	230.25	269.69	1.76	4.90
Kiloniellaceae	197.17	127.92	1.62	4.52
Hyphomonadaceae	141.92	147.38	1.37	3.81
Flammeovirgaceae	137.33	194.23	1.34	3.73
Phyllobacteriaceae	198.83	231.08	1.28	3.56
Alteromonadaceae	119.50	141.54	1.27	3.37
Saprospiraceae	252.25	251.85	0.95	2.65
Cyanobacteria GpIV	51.75	107.92	0.88	2.45
Rhizobiaceae	136.75	119.38	0.81	2.27
Rubritaleaceae	94.50	53.85	0.79	2.21
Rhodospirillaceae	104.42	86.08	0.76	2.13

Table S4. Summary of the results of linear mixed-effect models assessing the effects of the treatment on the abundance of bacterial families most contributing to multivariate patterns. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.

Source of variation	<i>Alteromonadaceae</i>		<i>Vibrionaceae</i>		<i>Hyphomonadaceae</i>		<i>Kiloniellaceae</i>		<i>Phyllobacteriaceae</i>	
	MS	<i>F</i>	MS	<i>F</i>	MS	<i>F</i>	MS	<i>F</i>	MS	<i>F</i>
Treatment	0.775	1.411	0.232	0.299	5619.8	0.700	1.873	3.494*	5188.1	0.498
Data transformation	Log		Log		None		Log		None	
	<i>Rhizobiaceae</i>		<i>Rhodobacteraceae</i>		<i>Rhodospirillaceae</i>		<i>Erythrobacteraceae</i>		Family I	
	MS	<i>F</i>	MS	<i>F</i>	MS	<i>F</i>	MS	<i>F</i>	MS	<i>F</i>
Treatment	12459	2.549	0.832	8.346**	0.138	0.296	4.126	9.684***	786100	4.061*
Data transformation	None		Log		Log		Log		None	
	Family IIa		Family IV		Family VIII		<i>Rubritaleaceae</i>		<i>Verrucomicrobiaceae</i>	
	MS	<i>F</i>	MS	<i>F</i>	MS	<i>F</i>	MS	<i>F</i>	MS	<i>F</i>
Treatment	1.075	1.580	6.621	10.863***	19.866	17.604***	10294	2.459	1.729	6.690**
Data transformation	Log		Log		Log		None		Log	
	<i>Flammeovirgaceae</i>		<i>Flavobacteraceae</i>		<i>Saprospiraceae</i>					
	MS	<i>F</i>	MS	<i>F</i>	MS	<i>F</i>				
Treatment	10560	1.424	1.569	5.309*	18507	1.108				
Data transformation	None		Log		None					