

Supplement of Biogeosciences, 12, 4483–4496, 2015
<http://www.biogeosciences.net/12/4483/2015/>
doi:10.5194/bg-12-4483-2015-supplement
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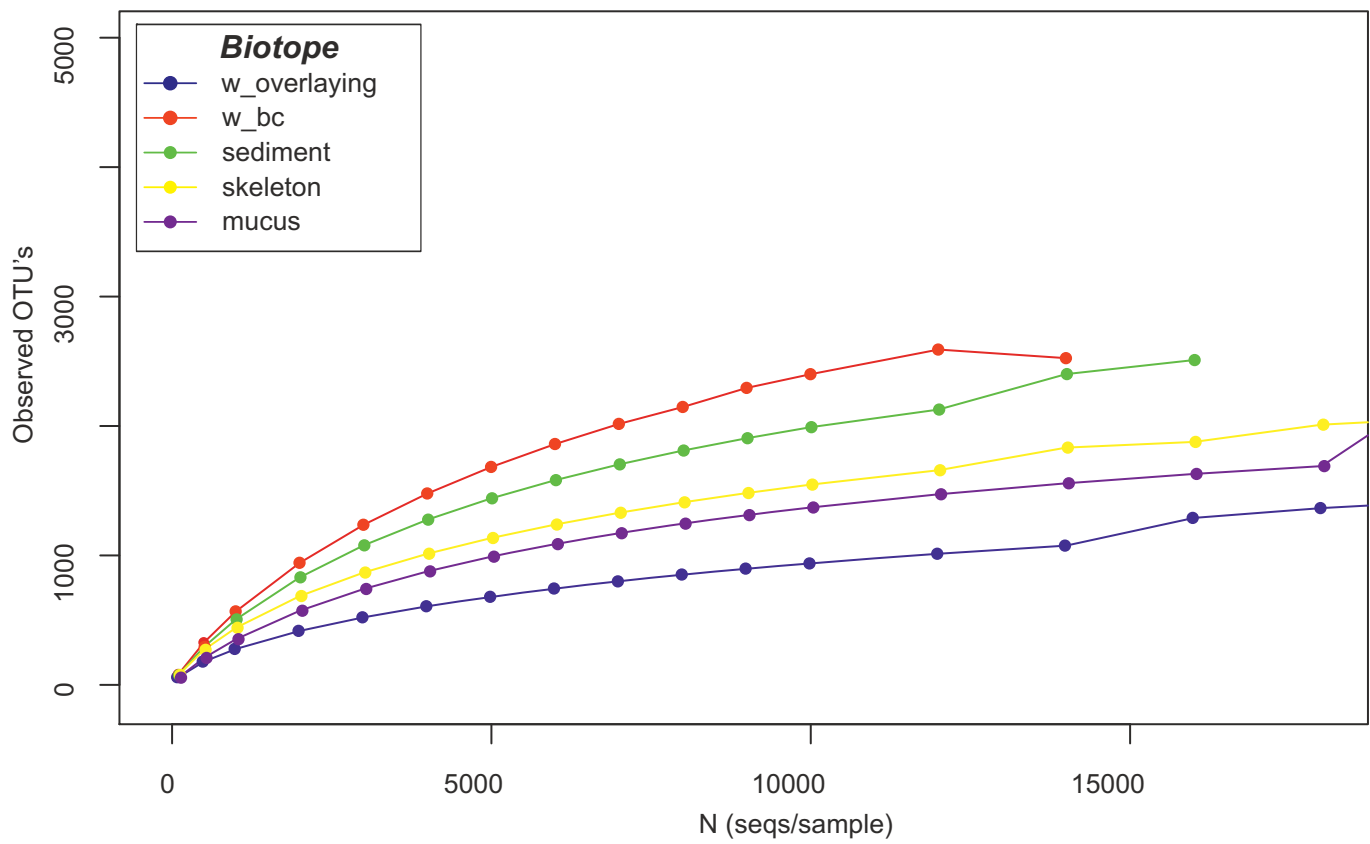
Supplement of

Microbial assemblages on a cold-water coral mound at the SE Rockall Bank (NE Atlantic): interactions with hydrography and topography

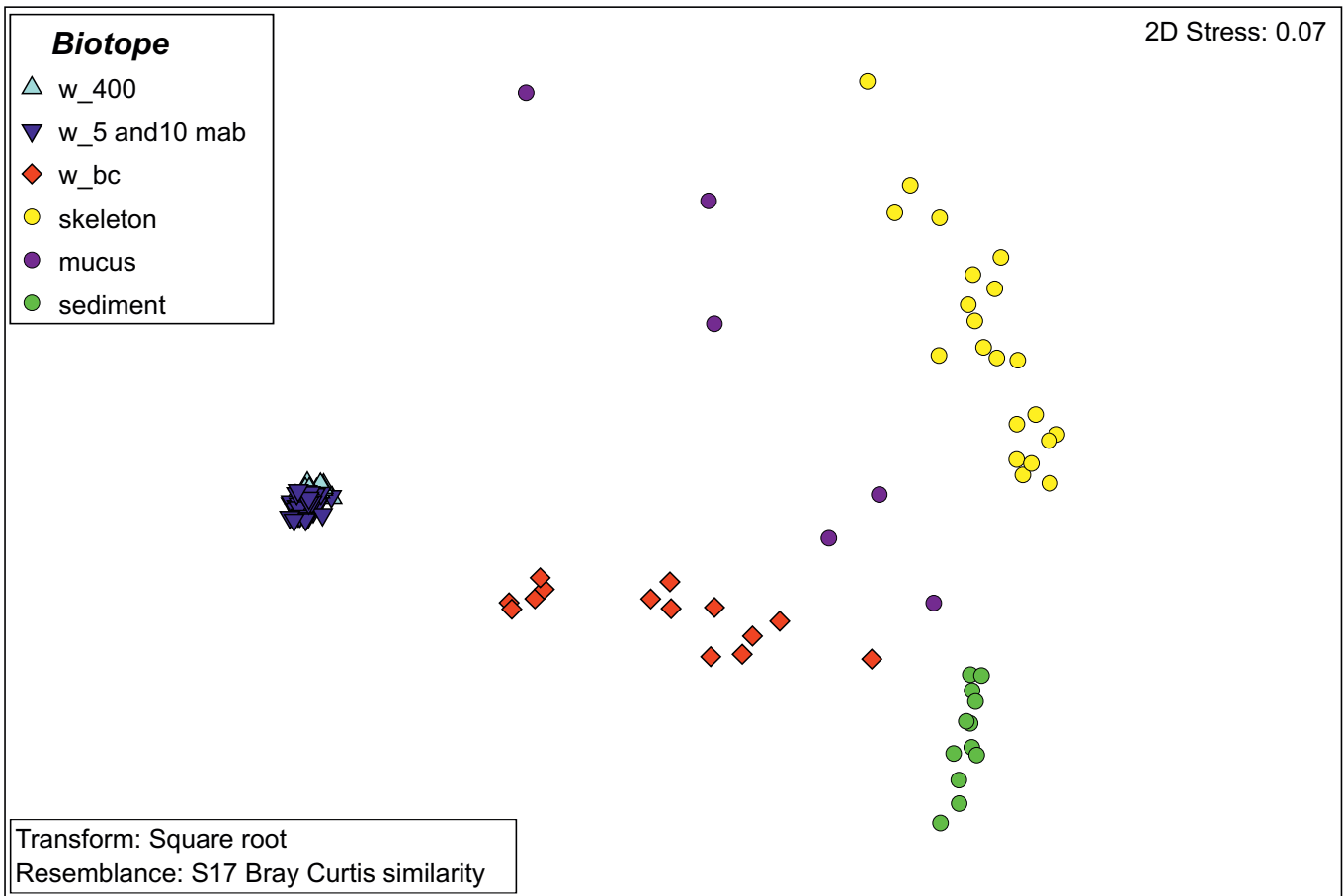
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S1



S2

S1. Sequence output and microbial diversity indices (average \pm standard error) of five biotopes sampled at Haas Mound. Singletons were not excluded in this analysis.

biotope	reads/sample	observed OTUs	Chao1	Shannon
overlying water (n=23)	17651 \pm 1599	1712 \pm 119	2684 \pm 306	5.04 \pm 0.06
near-bottom water (n=5)	11456 \pm 798	3858 \pm 567	7876 \pm 618	6.95 \pm 0.09
sediment (n=4)	14070 \pm 941	3245 \pm 104	5357 \pm 688	6.40 \pm 0.16
skeleton (n=6)	17713 \pm 1952	2856 \pm 300	4637 \pm 709	6.19 \pm 0.07
mucus (n=2)	20140 \pm 2229	2663 \pm 665	2828 \pm 1123	4.93 \pm 0.87

S2. Indicator taxa given for five biotopes sampled at Haas Mound. Only those with the highest statistics values are listed. Numbers between brackets are number of strong indicators ($A > 0.85$) over the total number of significant indicators ($p < 0.0001$) found. w_CTD = water sampled at 400 m and 5 and 10 mab; Near-bottom water (w_bc). A = given the indicator is present, the probability that the sample belongs to the sample group. B = taking one sample from the group, the probability that it contains the indicator.

Sample group (#strong indicators)	Indicator	A	B	stat	p.value	Reads avg % in sample group
w_CTD (4/38)	uncl. SAR11 clade Deep 1	0.8833	1.0000	0.940	0.0001	2.61
	Rhodospirillaceae AEGEAN-169 marine group	0.8796	1.0000	0.938	0.0001	2.20
	uncl. Verrucomicrobia Arctic97B-4 marine group	0.8751	1.0000	0.935	0.0001	0.45
	uncl. Thermoplasmatales Marine Group III	0.8721	1.0000	0.934	0.0001	1.00
	uncl. Oceanospirillales ZD0405	0.8361	1.0000	0.914	0.0001	2.85
w_bc (8/13)	uncl. Dehalococcoidia vadinBA26	0.9437	1.0000	0.971	0.0001	0.36
	uncultured Oceanospirillaceae	0.9460	0.8571	0.900	0.0001	0.05
	uncl. Dehalococcoidia GIF3	1.0000	0.7143	0.845	0.0001	0.27
	uncl. BHI80-139	0.8931	0.7857	0.838	0.0001	0.07
	uncl. Dehalococcoidia Sh765B-AG-111	1.0000	0.6429	0.802	0.0001	0.09
	Sphingobacteriales KD1- 131	0.8881	0.7143	0.796	0.0001	0.09
	Thaumarchaeota Group C3	1.0000	0.5714	0.756	0.0001	0.03
	Brocadiaceae W4	0.9982	0.5000	0.706	0.0001	0.83

sediment (0/3)	Phycisphaerae C86	0.6982	1.0000	0.836	0.0001	0.25
	uncl. Chloroflexi JG30-KF-CM66	0.5118	1.0000	0.715	0.0001	0.56
	uncl. Rhodospirillales AT-s3-44	0.3669	1.0000	0.606	0.0001	0.32
skeleton (0/12)	uncul. Caldilineaceae	0.7979	1.0000	0.893	0.0001	0.71
	<i>Granulosicoccus</i>	0.7513	1.0000	0.867	0.0001	1.87
	<i>Profundibacterium</i>	0.7602	0.9524	0.851	0.0001	0.22
mucus (12/12)	uncl. Oceanospirillales G02-CR02-full	0.9982	1.0000	0.999	0.0001	0.36
	<i>Acinetobacter</i>	0.9872	1.0000	0.994	0.0001	9.11
	uncult. Helicobacteraceae	0.9699	1.0000	0.985	0.0001	0.48
	uncl. Oceanospirillales BPS-CK174	0.9651	1.0000	0.982	0.0001	0.29
	Alteromonadaceae BD1-7 clade	0.9636	1.0000	0.982	0.0001	22.00
	<i>Corynebacterium</i>	0.9259	1.0000	0.962	0.0001	0.11
	<i>Staphylococcus</i>	0.9169	1.0000	0.958	0.0001	0.06
	<i>Sphingomonas</i>	0.9000	1.0000	0.949	0.0001	0.15
	<i>Enhydrobacter</i>	0.9963	0.8333	0.911	0.0001	0.17
	<i>Methylobacterium</i>	0.9705	0.8333	0.899	0.0001	0.24
	<i>Tumebacillus</i>	0.9106	0.8333	0.871	0.0001	0.13
	<i>Micrococcus</i>	0.9773	0.5000	0.699	0.0001	0.06