

**Response of bacterioplankton community structure to an artificial
gradient of $p\text{CO}_2$ in the Arctic Ocean**

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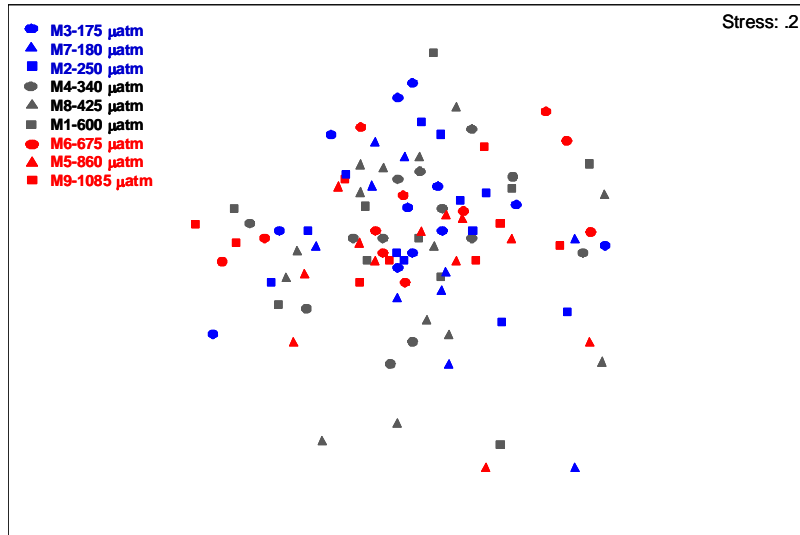
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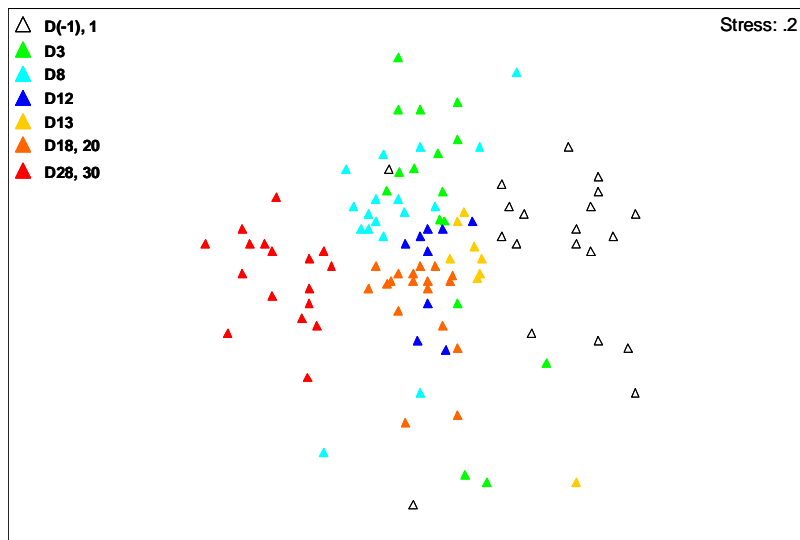
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1 Fig. S1. MDS plots, based on single enzyme digested T-RFLP analysis, showing
2 bacterial community dynamics during mesocosm experiment. A: displaying
3 with mesocosm; B: displaying with incubation time.



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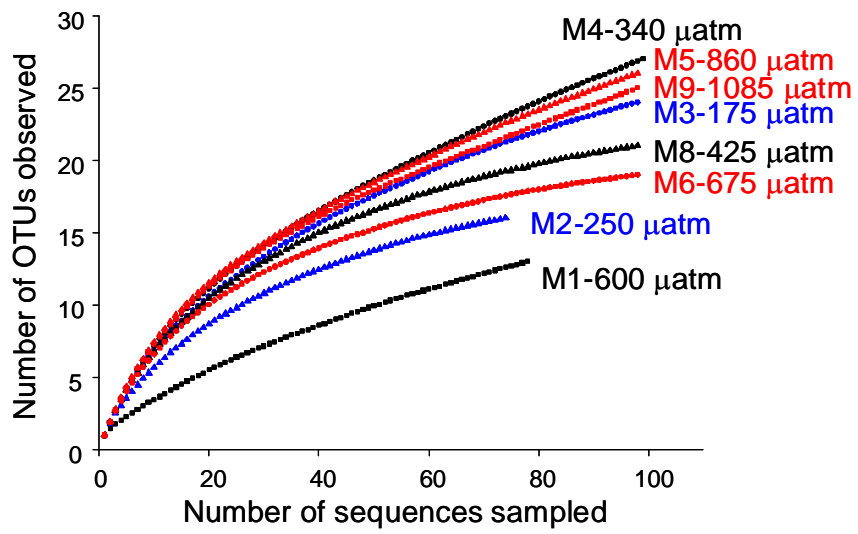
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1 Fig. S2. Rare fraction analysis of eight clone libraries constructed for Day30 samples.

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Table S1. ANOSIM analysis based on the matrix of T-RF position and peak area showing similarity among nine mesocoms. R statistic and significance level (%) are shown for each pair comparison.

	M3-175 μatm	M7-180 μatm	M2-250 μatm	M4-340 μatm	M8-425 μatm	M1-600 μatm	M6-675 μatm	M5-860 μatm	M9-1085 μatm
M3-175 μatm									
M7-180 μatm	-0.041 (89.2)								
M2-250 μatm	-0.063 (98.3)	-0.022 (70.3)							
M4-340 μatm	-0.059 (97.1)	-0.021 (69.8)	-0.058 (99.0)						
M8-425 μatm	-0.053 (94.8)	-0.026 (73.5)	-0.055 (96.9)	-0.036 (88.7)					
M1-600 μatm	-0.030 (79.0)	-0.014 (62.0)	0.007 (34.4)	-0.033 (82.5)	-0.020 (66.1)				
M6-675 μatm	-0.008 (50.7)	0.035 (14.9)	-0.003 (43.6)	-0.019 (71.5)	-0.015 (63.8)	-0.017 (63.8)			
M5-860 μatm	-0.050 (96.5)	-0.036 (89.9)	-0.030 (83.8)	-0.030 (84.5)	-0.049 (97.0)	-0.030 (80.5)	-0.005 (50.5)		
M9-1085 μatm	-0.024 (71.5)	0.011 (32.0)	-0.020 (70.7)	-0.013 (62.3)	-0.053 (98.6)	-0.018 (63.7)	-0.017 (68.1)	-0.024 (76.2)	

4	0.1)	0.1)	.1)	0.1)	0.1)	0.1)	0.1)	0.1)	0.4)	18.3)								
D1	0.614(0.573(0.721(0	0.626(0.828(0.482(0.744(0.192(0.182(0.132(0.057(
6	0.1)	0.1)	.1)	0.1)	0.1)	0.1)	0.1)	5.3)	5.3)	5.3)	22.3)							
D1	0.725(0.597(0.611(0	0.538(0.685(0.421(0.505(0.193(0.226(0.152(0.221(0.003(
8	0.2)	0.1)	.1)	0.1)	0.1)	0.1)	0.1)	1.3)	0.3)	1.4)	0.2)	40.8)						
D2	0.909(0.752(0.771(0	0.657(0.798(0.621(0.606(0.342(0.301(0.418(0.450(0.113(0.035(
0	0.1)	0.1)	.1)	0.1)	0.1)	0.1)	0.1)	0.2)	0.1)	0.1)	0.1)	10.8)	22.8)					
D2	0.824(0.626(0.650(0	0.592(0.754(0.545(0.619(0.284(0.390(0.417(0.478(0.224(0.066(0.052(
2	0.1)	0.1)	.1)	0.1)	0.1)	0.1)	0.1)	0.1)	0.1)	0.1)	0.1)	1.6)	12.2)	18.6)				
D2	0.911(0.659(0.684(0	0.635(0.836(0.636(0.612(0.365(0.459(0.547(0.609(0.299(0.164(0.034(0.051(
4	0.1)	0.1)	.1)	0.1)	0.1)	0.1)	0.1)	0.9)	0.2)	0.2)	0.1)	0.6)	2.9)	27.6)	24.0)			
D2	0.943(0.653(0.818(0	0.684(0.934(0.712(0.761(0.540(0.641(0.824(0.854(0.673(0.528(0.542(0.268(0.209(
6	0.1)	0.1)	.2)	0.1)	0.1)	0.1)	0.1)	0.1)	0.2)	0.1)	0.1)	0.2)	0.2)	0.1)	1.8)	3.9)		
D2	0.951(0.794(0.838(0	0.750(0.891(0.848(0.759(0.519(0.484(0.780(0.679(0.464(0.474(0.522(0.312(0.405(0.106(
8	0.1)	0.1)	.1)	0.1)	0.1)	0.1)	0.1)	0.1)	0.1)	0.1)	0.1)	0.2)	0.1)	0.1)	0.3)	0.1)	11.0)	
D3	0.939(0.810(0.901(0	0.750(0.967(0.866(0.948(0.719(0.875(0.863(0.943(0.828(0.650(0.825(0.517(0.574(0.222(0.351(
0	0.1)	0.1)	.1)	0.1)	0.1)	0.1)	0.2)	0.1)	0.1)	0.1)	0.1)	0.1)	0.2)	0.1)	0.1)	0.1)	1.5)	0.1)

Table S3. Pair comparisons of clone library using Libshuff analysis. $C_{\text{column, row}}$ and $C_{\text{row, column}}$ are given above and below the diagonal, respectively. P values of less than 0.05 are in bold. Underlining indicates that both $C_{\text{column, row}}$ and $C_{\text{row, column}}$ are significant.

	M3	M2	M4	M8	M1	M6	M5	M9
M3		<0.0001	0.2613	0.083	<0.0001	0.0018	0.0167	0.0309
M2	0.0166		0.3881	0.9202	0.012	0.0719	0.7214	0.2917
M4	0.0241	0.5284		0.7007	0.0243	0.2199	0.5103	0.15
M8	0.0214	<0.0001	0.0191		0.0012	0.0057	0.0468	0.1291
M1	0.5041	0.4231	0.3848	0.388		0.2846	0.6417	0.0837
M6	<0.0001	0.0002	0.1391	0.0491	0.001		0.616	0.0098
M5	0.002	0.0002	0.602	0.0309	0.0009	0.2673		0.0073
M9	0.0295	0.0016	0.1932	0.6272	0.0148	0.0974	0.5661	