

Supplement of Biogeosciences Discuss., 12, 14175–14213, 2015
<http://www.biogeosciences-discuss.net/12/14175/2015/>
doi:10.5194/bgd-12-14175-2015-supplement
© Author(s) 2015. CC Attribution 3.0 License.



Supplement of

Hidden biosphere in an oxygen-deficient Atlantic open ocean eddy: future implications of ocean deoxygenation on primary production in the eastern tropical North Atlantic

C. R. Löscher et al.

Correspondence to: C. R. Löscher (cloescher@geomar.de)

The copyright of individual parts of the supplement might differ from the CC-BY 3.0 licence.

Supplemental material

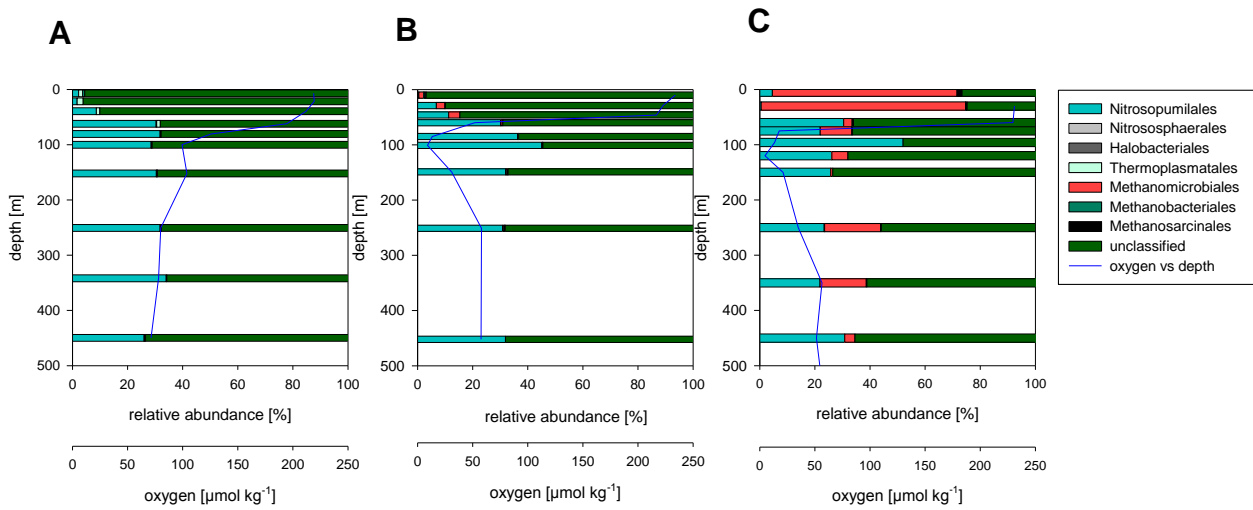


Figure S1: Distribution of archaeal phyla along vertical profiles from (A) CVOO, (B) eddy_1 and (C) eddy_2 based on 16S rDNA amplicon sequencing data. Oxygen profiles are shown in blue.

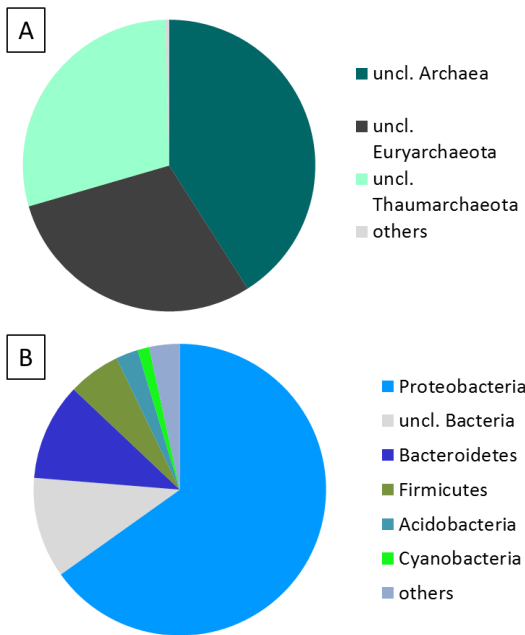


Figure S2: Distribution of archaeal (A) and bacterial (B) phyla from 115 m water depth ($33.9 \mu\text{mol O}_2 \text{L}^{-1}$) at the presumed origin of the eddy on the Mauritanian shelf. Note that data from this shelf station were obtained by a full metagenome sequencing approach.

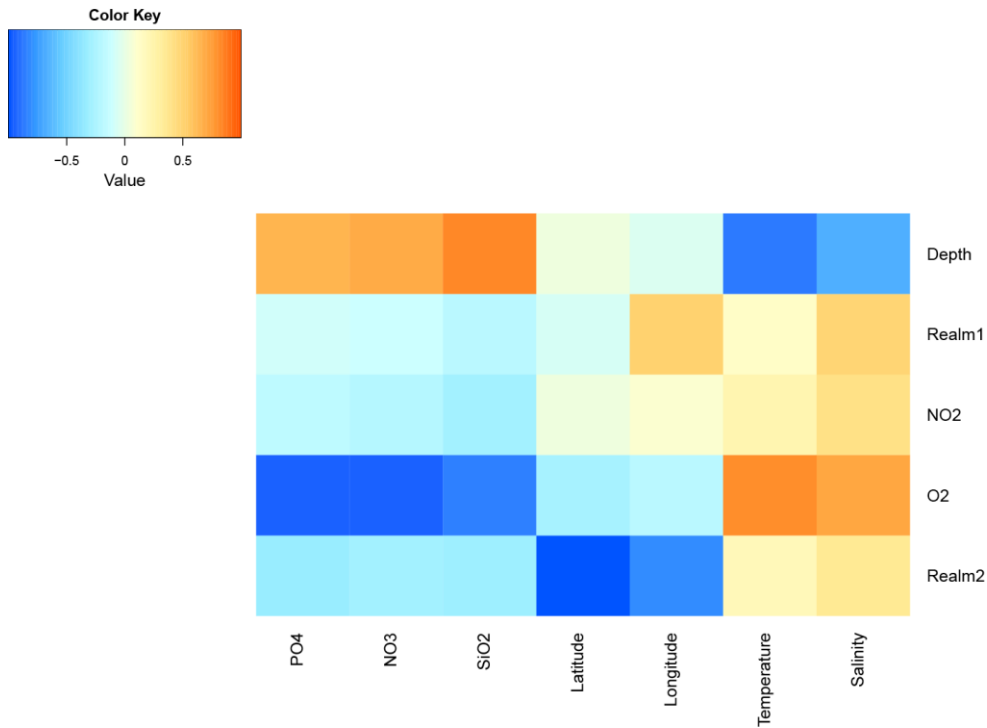


Figure S3: Correlation matrix of environmental variables with low variance inflation factors (rows) and other variables in the meta-dataset (columns). Warm colors denote positive correlations, cold colors denote negative correlations.

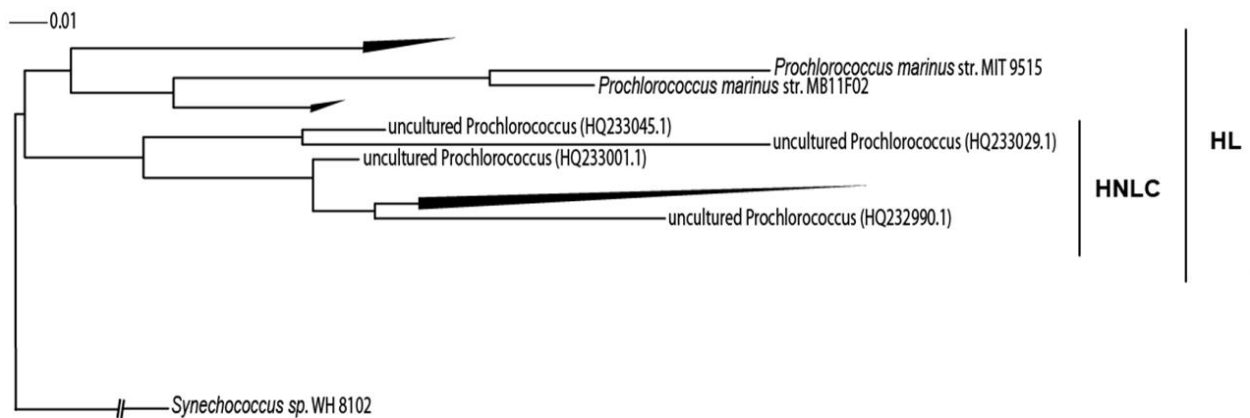


Figure S4: Phylogenetic relationships of detected cyanobacteria (black triangles). The tree was constructed using a MUSCLE alignment on a 16S rDNA fragment, followed by neighbor joining analysis and tree visualization via iTOL. Black triangles represent identified clusters from our samples. HL denotes high-light strains; HNLC denotes high-nutrient-low-chlorophyll strains.

Table S1: Sequencing depths of 16S rDNA amplicon sequencing of the bacterial hypervariable regions V1-V2, “seqDepth” denotes the number of OTUs after quality filtration, “seqDepth filtered” denotes the number of reads after removing low-abundant OTUs. The relative quantity of remaining sequences is given as percentage.

Cruise	Station	Water Depth [m]	seqDepth	seqDepth filtered	Percentage
	CVOO	449.7	49419	48623	98.39
	CVOO	341.8	47129	46249	98.13
	CVOO	250.6	42955	41752	97.2
	CVOO	152.1	14880	14598	98.1
	CVOO	100.1	79994	78791	98.5
	CVOO	80.6	72576	71610	98.67
	CVOO	62.1	83625	82620	98.8
	CVOO	39.4	76540	75756	98.98
	CVOO	21.5	41141	40410	98.22
	CVOO	10.9	29032	28558	98.37
Islandia	Eddy_1	452	42139	41276	97.95
Islandia	Eddy_1	251	31277	30718	98.21
Islandia	Eddy_1	149	61299	60751	99.11
Islandia	Eddy_1	101	296854	294485	99.2
Islandia	Eddy_1	85	87598	86466	98.71
Islandia	Eddy_1	57	80614	79661	98.82
Islandia	Eddy_1	46	78950	78584	99.54
Islandia	Eddy_1	29	95456	95137	99.67
Islandia	Eddy_1	10	97518	96966	99.43
Meteor_M105	Eddy_2	5	36924	36637	99.22
Meteor_M105	Eddy_2	10	10198	10198	100
Meteor_M105	Eddy_2	30	25047	24839	99.17
Meteor_M105	Eddy_2	65	18262	18171	99.5
Meteor_M105	Eddy_2	75	21094	21003	99.57
Meteor_M105	Eddy_2	96	30716	30590	99.59
Meteor_M105	Eddy_2	120	33827	33759	99.8
Meteor_M105	Eddy_2	150	18071	17944	99.3
Meteor_M105	Eddy_2	250	12998	12938	99.54
Meteor_M105	Eddy_2	350	37833	37747	99.77
Meteor_M105	Eddy_2	450	54185	54081	99.81
Meteor_M105	Eddy_2	600	19447	19398	99.75

Table S2: Metadata for statistical analysis of metagenomic samples

Station	Latitude	Longitude	Depth	O2	Temperature	Salinity	NO3	NO2	PO4	SiO2
CVOO	16.74	-25.14	450	71.25	10.54	35.25	31.49	0	1.9	12.29
CVOO	16.74	-25.14	342	78.14	12.21	35.49	27.47	0	1.63	8.94
CVOO	16.74	-25.14	251	80.12	12.87	35.56	24.38	0	1.47	7.46
CVOO	16.74	-25.14	152	103.82	15.31	35.98	19.57	0.02	1.17	4.62
CVOO	16.74	-25.14	100	99.40	16.32	35.95	14.03	0.05	0.86	2.63
CVOO	16.74	-25.14	81	125.57	18.30	36.08	5.37	0.28	0.42	0.74
CVOO	16.74	-25.14	62	194.49	21.08	36.12	0.12	0.05	0.07	0.00
CVOO	16.74	-25.14	39	211.96	21.68	36.01	0.00	0.01	0.06	0.02
CVOO	16.74	-25.14	22	219.38	22.29	35.94	0.00	0.01	0.07	0.08
CVOO	16.74	-25.14	11	218.92	22.49	35.91	0.01	0.01	0.06	0.24
Eddy_1	19.05	-24.30	452	57.59	11.23	35.32	31.31	0.00	1.87	12.49
Eddy_1	19.05	-24.30	251	57.95	13.38	35.46	26.96	0.00	1.65	8.97
Eddy_1	19.05	-24.30	149	30.93	14.75	35.48	27.40	0.00	1.75	8.79
Eddy_1	19.05	-24.30	101	8.99	15.20	35.52	29.09	0.01	1.88	8.41
Eddy_1	19.05	-24.30	85	13.36	15.416	35.538	27.82	0.01	1.8	8.42
Eddy_1	19.05	-24.30	57	51.88	17.014	36.027	17.13	0.25	1.16	4.4
Eddy_1	19.05	-24.30	46	216.81	20.154	36.284	3.24	0.08	0.32	0.51
Eddy_1	19.05	-24.30	29	222.65	20.18	36.29	2.92	0.08	0.29	0.26
Eddy_1	19.05	-24.30	10	233.89	20.23	36.28	2.64	0.08	0.27	0.21
Eddy_2	19.03	-24.77	5	231.03	20.78	35.65	0.06	0.02	0.09	0.20
Eddy_2	19.03	-24.77	10	231.10	20.79	35.65	0.11	0.02	0.09	0.33
Eddy_2	19.03	-24.77	30	229.66	20.78	35.67	0.67	0.03	0.14	0.39
Eddy_2	19.03	-24.77	65	17.66	15.92	35.43	27.00	0.16	1.71	7.70
Eddy_2	19.03	-24.77	75	13.39	15.61	35.42	28.24	0.12	1.80	8.63
Eddy_2	19.03	-24.77	96	4.71	15.14	35.40	30.12	0.07	1.90	8.99
Eddy_2	19.03	-24.77	120	21.08	14.87	35.39	28.90	0.02	1.78	9.19
Eddy_2	19.03	-24.77	150	34.94	14.63	35.39	28.01	0.01	1.70	9.16
Eddy_2	19.03	-24.77	250	56.45	13.24	35.34	27.51	0.01	1.62	9.24
Eddy_2	19.03	-24.77	350	51.40	12.11	35.29	27.07	0.01	1.63	9.80
Eddy_2	19.03	-24.77	450	60.51	10.91	35.23	30.91	0.00	1.80	12.70
Eddy_2	19.03	-24.77	600	69.64	9.43	35.15	31.95	0.02	1.93	15.34

Table S3: Distribution of indicator species in A) low-O₂ and B) high-O₂ realms

A

OTU	Eddy_2	Eddy_1	CVOO	stat	p.value	q.value	Kingdom	Phylum	Class	Order	Family	Genus	Species
43	1	0	0	0.732904404	0.0226	0.086	Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cyclobacteriaceae	unclassified	unclassified
105	1	0	0	0.907024601	0.0005	0.023	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Gramella	unclassified
87	1	0	0	0.915910402	0.0062	0.033	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Leeuwenhoekella	Leeuwenhoekella marinoflava
96	1	0	0	0.771499066	0.0153	0.068	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Bacillus selenatarsenatis
290	1	0	0	0.771708426	0.0063	0.033	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	unclassified	unclassified
6	0	1	0	0.763789162	0.0176	0.072	Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Pelagibacteraceae	unclassified	unclassified
10	0	1	0	0.815643694	0.0036	0.027	Bacteria	Proteobacteria	Deltaproteobacteria	Sva0853	SAR324	unclassified	unclassified
83	0	1	0	0.80300367	0.0029	0.026	Bacteria	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified	unclassified
133	0	1	0	0.784489246	0.0021	0.026	Bacteria	Proteobacteria	Gammaproteobacteria	Thiotrichales	Piscirickettsiaceae	unclassified	unclassified
165	0	1	0	0.784156503	0.0026	0.026	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	NS9	unclassified	unclassified
7	0	0	1	0.730374646	0.0293	0.097	Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Pelagibacteraceae	unclassified	unclassified
17	0	0	1	0.802860647	0.0013	0.023	Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Pelagibacteraceae	unclassified	unclassified
19	0	0	1	0.750603871	0.0097	0.047	Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Pelagibacteraceae	unclassified	unclassified
80	0	0	1	0.753692627	0.0059	0.033	Bacteria	Chloroflexi	SAR202	unclassified	unclassified	unclassified	unclassified
31	0	0	1	0.766712579	0.0293	0.097	Bacteria	Cyanobacteria	Synechococcophycideae	Synechococcales	Synechococcaceae	Prochlorococcus	unclassified

2097	0	0	1	0.808047895	0.0011	0.023	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	unclassified	unclassified
------	---	---	---	-------------	--------	-------	----------	---------------	----------------	------------------	-------------------	--------------	--------------

B

OTU	Eddy_2	Eddy_1	CVOO	stat	p.value	q.value	Kingdom	Phylum	Class	Order	Family	Genus	Species
13	1	0	0	0.868619385	0.0423	0.098	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	unclassified	unclassified
89	1	0	0	0.854705113	0.0235	0.062	Bacteria	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	Photobacterium	Photobacterium angustum
15	1	0	0	0.823575274	0.0048	0.016	Bacteria	Cyanobacteria	Synechococcophycideae	Synechococcales	Synechococcaceae	unclassified	unclassified
42	1	0	0	0.709224831	0.0136	0.038	Bacteria	Cyanobacteria	Synechococcophycideae	Synechococcales	Synechococcaceae	Synechococcus	unclassified
26	0	1	0	0.902522986	0.0002	0.004	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	unclassified	unclassified
34	0	1	0	0.88676295	0.0002	0.004	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	unclassified	unclassified
16	0	1	0	0.794080841	0.0092	0.027	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	unclassified	unclassified
29	0	1	0	0.820119092	0.0043	0.016	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Thalassobius	unclassified
75	0	1	0	0.833984519	0.0045	0.016	Bacteria	Proteobacteria	unclassified	unclassified	unclassified	unclassified	unclassified
32	0	1	0	0.833356768	0.0019	0.01	Bacteria	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	Candidatus Portiera	unclassified
35	0	1	0	0.859428806	0.0003	0.004	Bacteria	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	Candidatus Portiera	unclassified
170	0	1	0	0.895603782	0.0023	0.01	Bacteria	Actinobacteria	Acidimicrobiia	Acidimicrobiales	OCS155	unclassified	unclassified
72	0	1	0	0.873638666	0.0022	0.01	Bacteria	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	Candidatus Portiera	unclassified
133	0	1	0	0.887405971	0.0002	0.004	Bacteria	Proteobacteria	Gammaproteobacteria	Thiotrichales	Piscirickettsiaceae	unclassified	unclassified
163	0	1	0	0.863554923	0.0005	0.005	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	unclassified	unclassified
192	0	1	0	0.909453277	0.0008	0.007	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Ulvibacter	unclassified
229	0	1	0	0.90346477	0.0028	0.011	Bacteria	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	Candidatus Portiera	unclassified
226	0	1	0	0.895653722	0.0017	0.01	Bacteria	SAR406	AB16	Arctic96B-7	A714017	ZA3312c	unclassified
165	0	1	0	0.90456066	0.0015	0.01	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	NS9	unclassified	unclassified
433	0	1	0	0.918578051	0.0012	0.009	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Cryomorpaceae	Fluviicola	unclassified
2	0	0	1	0.768564656	0.0052	0.016	Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Pelagibacteraceae	unclassified	unclassified
7	0	0	1	0.832273766	0.0443	0.098	Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Pelagibacteraceae	unclassified	unclassified

10	0	0	1	0.877860029	0.0359	0.091	Bacteria	Proteobacteria	Deltaproteobacteria	Sva0853	SAR324	unclassified	unclassified
12	0	0	1	0.835234067	0.043	0.098	Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Pelagibacteraceae	unclassified	unclassified