SUPPLEMENTARY INFORMATION of

N₂ fixation in the Mediterranean Sea related to the composition of the diazotrophic community, and impact of dust under present and future environmental conditions

Céline Ridame¹, Julie Dinasquet^{2,3}, Søren Hallstrøm⁴, Estelle Bigeard⁵, Lasse Riemann⁴, France Van Wambeke⁶, Matthieu Bressac⁷, Elvira Pulido-Villena⁶, Vincent Taillandier⁷, Fred Gazeau⁷, Antonio Tovar-Sanchez⁸, Anne-Claire Baudoux⁵, Cécile Guieu⁷

¹ Sorbonne University, CNRS, IRD, LOCEAN: Laboratoire d'Océanographie et du Climat: Expérimentation et Approches Numériques, UMR 7159, 75252 Paris Cedex 05, France

² Scripps Institution of Oceanography, University of California San Diego, USA

³ Sorbonne University, CNRS, Laboratoire d'Océanographie Microbienne, LOMIC, 66650 Banyuls-sur-Mer, France

⁴Marine Biology Section, Department of Biology, University of Copenhagen, 3000 Helsingør, Denmark

⁵ Sorbonne University, CNRS, Station Biologique de Roscoff, UMR 7144 Adaptation et Diversité en Milieu Marin, France

⁶ Aix-Marseille Université, Université de Toulon, CNRS/INSU, IRD, Mediterranean Institute of Oceanography (MIO), UM 110, 13288, Marseille, France

⁷ Sorbonne Université, CNRS, Laboratoire d'Océanographie de Villefranche, LOV, 06230 Villefranche-sur-Mer, France

⁸ Department of Ecology and Coastal Management, Institute of Marine Sciences of Andalusia (CSIC), 11510 Puerto Real, Cádiz, Spain

Correspondence to: Céline Ridame (celine.ridame@locean.ipsl.fr)

Table S1: Nutrients stocks (DIP, DFe, NO_3^{-1}) in the surface mixed layer (SML) and in the euphotic layer (surface to the 1% PAR depth).

* at stations 1 to 4, micromolar NO₃⁻ concentrations were under detection limit (0.05 μ M) in the upper 50 m and samples for the nanomolar level determination (LWCC) were lost. For these stations, maximum NO₃⁻ stocks were calculated considering a concentration of 0.05 μ M when NO₃⁻ concentrations were under this detection limit.

	Lat.	Long.	MLD	1%	DIP Stock	DFe	NO ₃ ⁻	DIP Stock	DFe	NO ₃ ⁻
				PAR	SML	Stock	Stock	euphotic	Stock	Stock
				depth		SML	SML		euphotic	euphotic
	°N	°E	m	m	µmol.m ⁻²	µmol.m ⁻²	µmol.m ⁻²	µmol.m ⁻²	µmol.m ⁻²	mmol.m ⁻²
ST01	41.89	6.33	21	58	160	18.2	<1050*	525	45	<16.4*
ST02	40.51	6.73	21	72	227	24.0	<1050*	1277	63	<27.7*
ST03	39.13	7.68	11	85	53	24.7	<550*	1080	142	<10.3*
ST04	37.98	7.98	15	66	106	30.1	<750*	1284	113	<13.0*
ST05	38.95	11.02	9	78	112	10.9	258	1306	80	16.6
TYR	39.34	12.59	9	68	64	11.7	137	693	71	1.5
ST06	38.81	14.50	18	67	198	35.1	162	708	97	5.0
ST07	36.66	18.15	18	75	104	24.7	162	458	83	2.2
ION	35.49	19.78	14	87	142	23.4	195	982	126	1.6
ST08	36.21	16.63	14	75	169	22.2	911	950	87	5.5
ST09	38.13	5.84	7	87	77	10.0	819	1183	80	15.7
FAST	37.95	2.90	9	83	99	13.8	716	2775	94	13.1
ST10	37.45	1.57	19	87	308	22.3	2016	3187	84	28.3

Table S2: FrameBot annotations of the nearest known references of the 20 most abundant ASVs across all samples.

		% of all		
Feature ID	Reads	reads	FrameBot annotation	% Identity
4f130f7262e949bc20	f7262e949bc20 145569915 1G B 1 1432264_1433145_CP000304		145569915 1G B 1 1432264_1433145_CP000304 Pse	
ae5dcd3eee35db 247955		28,12	udomonas_stutzeri_A1501	98,925
00c85e66b298fa566			213578830 1B B 1 FJ170277_complement_13629_14	
b5587b50e7f3f7f	114420	12,97	492 Uncultured_cyanobacterium_group_A_nif_cluster	100
74fc02da755a36c195			213578830 1B B 1 FJ170277_complement_13629_14	
bbece4dcfb6c3e	69304	7,86	492 Uncultured_cyanobacterium_group_A_nif_cluster	100
3aa5d34aa2ac8a8f75			145569915 1G B 1 1432264_1433145_CP000304 Pse	
06577551a510a0	65812	7,46	udomonas_stutzeri_A1501	98,925
9d2f4ec132745ac31c			145569915 1G B 1 1432264_1433145_CP000304 Pse	
2340a031d726ee	63165	7,16	udomonas_stutzeri_A1501	98,925
ab0ecbee56ec313cd			145569915 1G B 1 1432264_1433145_CP000304 Pse	
a72e61ffdcfb494	56134	6,37	udomonas_stutzeri_A1501	98,925
3474fb451f8b288dcb			145569915 1G B 1 1432264_1433145_CP000304 Pse	
b190ddd9933884	38007	4,31	udomonas_stutzeri_A1501	98,925
e067e3ba7a6570624			213578830 1B B 1 FJ170277_complement_13629_14	
8056188777e1763	27641	3,13	492 Uncultured_cyanobacterium_group_A_nif_cluster	100
66b09bb28a2d6b2c8			213578830 1B B 1 FJ170277_complement_13629_14	
a074c7ef455abcf	25793	2,92	492 Uncultured_cyanobacterium_group_A_nif_cluster	100
f60991866f34f6a2e5			142330 1G B 1 525_1397_M11579 Azotobacter_vinel	
1e132307e5bad4	19615	2,22	andii_DK_cluster_	96,774
106b2b300923c99f0			213578830 1B B 1 FJ170277_complement_13629_14	
a32e68826fb05c3	18111	2,05	492 Uncultured_cyanobacterium_group_A_nif_cluster	100
769ab520efbbb7280f			110168604 1B B 1 6380808_6381698_CP000393 Tric	
93376b03c1c171	/6b03c1c171 18051 2,05 hodesmium_erythraeum_IMS101		98,925	
e48ca7a05e71d1f402	a7a05e71d1f402 145569915 1G B 1 1432264_1433145_CP000304 Pse			
f7f36cc81cb450	8525	0,97	udomonas_stutzeri_A1501	98,925
717a2d9ae33622985			145569915 1G B 1 1432264_1433145_CP000304 Pse	
dde7cb936331c18	8214	0,93	udomonas_stutzeri_A1501	98,925
b5e593c3cbea96f53a			145569915 1G B 1 1432264_1433145_CP000304 Pse	
5e597bd502715d	8117	0,92	udomonas_stutzeri_A1501	98,925
12fa8a7272c36cef11			145569915 1G B 1 1432264_1433145_CP000304 Pse	
6e673efd697ce5	5548	0,63	udomonas_stutzeri_A1501	98,925
90c741ef17c0270782			142330 1G B 1 525_1397_M11579 Azotobacter_vinel	
54972c547ecaaa	4206	0,48	andii_DK_cluster_	96,774
226e7bd030e1242d6			242120818 3E C 2 CP001649_complement_488297_4	
7bffeacc3dfb50a	3984	0,45	89124 Desulfovibrio_salexigens_DSM_2638	98,925
5cd4866faf5030e82d			145569915 1G B 1 1432264_1433145_CP000304 Pse	
079b211a72997b	3410	0,39	udomonas_stutzeri_A1501	98,925
0eabd0c5b6d4ada9c			145569915 1G B 1 1432264_1433145_CP000304 Pse	
3ed3b7458a4d431	3135	0,36	udomonas_stutzeri_A1501	98,925

Table S3: FrameBot annotations of the nearest known references of the 20 most abundant ASVs at station 10

Feature ID	Reads	% of all	FrameBot annotation	%Identity	Taxonomic group
bbc2563311419e7	58485	39,55	213578830 1B B 1 FJ170277_complement_13629_14492	100	UCYN-A4
3e0612506d81539			Uncultured_cyanobacterium_group_A_nif_cluster		
35	20000	26.20	2125700201101011151170277 annulation 12620 14402	100	
195bbece/dcfb6c	28889	26,30	213578830[18]8]1]FJ170277_complement_13629_14492	100	UCYN-AI
3e			Toucarcarea_cyanobacteriam_group_A_im_claster		
a5ee5acf641bc08	13007	8,80	213578830 1B B 1 FJ170277_complement_13629_14492	100	UCYN-A4
5da0aa23b0637b4			Uncultured_cyanobacterium_group_A_nif_cluster		
e4					
66b09bb28a2d6b	10132	6,85	213578830 1B B 1 FJ170277_complement_13629_14492	100	UCYN-A2
2c8a074c7ef455a			Uncultured_cyanobacterium_group_A_nif_cluster		
106b2b200022c00	0164	6.20	212578820 18 8 1 5 170277 complement 12620 14402	100	
f0a32e68826fb05c	5104	0,20	Uncultured cvanobacterium group A nif cluster	100	UCINIAI
3			loucarda caTchaugaccu aurTbioab7 (TuuTciascu		
00c85e66b298fa5	5970	4,04	213578830 1B B 1 FJ170277_complement_13629_14492	100	UCYN-A3
66b5587b50e7f3f			Uncultured_cyanobacterium_group_A_nif_cluster		
7f					
e067e3ba7a65706	1347	0,91	213578830 1B B 1 FJ170277_complement_13629_14492	100	UCYN-A3
248056188///e1/			Uncultured_cyanobacterium_group_A_nit_cluster		
0d074fa0254f304	1106	0.75	213578830 18 8 1 E 170277_complement_13629_14492	100	UCYN-A4
4df289a87f37c42e	1100	0,75	Uncultured_cyanobacterium_group_A_nif_cluster	100	
6					
f4a69bcdaea0443	1095	0,74	213578830 1B B 1 FJ170277_complement_13629_14492	100	UCYN-A1
67c837f016e3ffae			Uncultured_cyanobacterium_group_A_nif_cluster		
C	1064	0.72	14556001511C18111422364 1422145 CD00020418	08.025	Camma
abuecbee56ec313	1064	0,72	145569915 16 8 1 1432264_1433145_CP000304 Pseud	98,925	Gamma
4			omonas_statzen_Arsor		proteobacteria
d2675af859c82c0	1024	0,69	213578830 1B B 1 FJ170277 complement 13629 14492	100	UCYN-A1
d4bb46f8c3d9131			Uncultured_cyanobacterium_group_A_nif_cluster		
1d					
4f130f7262e949bc	948	0,64	145569915 1G B 1 1432264_1433145_CP000304 Pseud	98,925	Gamma
20ae5dcd3eee35d			omonas_stutzeri_A1501		proteobacteria
17d5b4757a75ad4	727	0.49	213578830 18 8 1 E 170277_complement_13629_14492	100	LICYN-A1
a6a6a8714e6724a	1 121	0,45	Uncultured cvanobacterium group A nif cluster	100	UCIN AI
eb					
e8681f8ab1563b2	581	0,39	213578830 1B B 1 FJ170277_complement_13629_14492	98,925	UCYN-A4
921531f4d68020e			Uncultured_cyanobacterium_group_A_nif_cluster		
b0	444	0.00	2425702201401014151470277 as welcovert 42520, 44402	100	
3760ca017/3205b	411	0,28	213578830[18]8]1]FJ170277_complement_13629_14492	100	UCYN-A4
55			Toucarca chanopacteriam Broah 2011 Claster		
806cee9c1b2488b	409	0,28	213578830 1B B 1 FJ170277_complement_13629_14492	100	UCYN-A1
acb2a595080138b			Uncultured_cyanobacterium_group_A_nif_cluster		
42					
t66f288c4a3ce20f	311	0,21	213578830 1B B 1 FJ170277_complement_13629_14492	100	UCYN-A4
eb425c205abtt58/			Uncultured_cyanobacterium_group_A_hit_cluster		
3aa5d34aa2ac8a8f	293	0,20	145569915 1G B 1 1432264_1433145_CP000304 Pseud	98,925	Gamma
7506577551a510a			omonas_stutzeri_A1501		proteobacteria
0	224	0.10	112570020 18 8 1 5 170377 complement 12500 11400	100	
h929140300-7f7=	234	0,16	Uncultured ovanobacterium group A nif cluster	100	UCTN-A2
4a			Temeananea_cyanosacternam_group_A_im_cluster		
15464fc769f26e7e	225	0,15	237685316 1G B 1 1597309_1598187_CP001614 Teredi	94,624	Gamma
a2e0d3ee53e52a5			nibacter_turnerae_T7901	-	proteobacteria
7					

Figure S1 Integrated primary production (PP) (a) and heterotrophic bacterial production (BP) (b) from surface to euphotic layer depth along the longitudinal PEACETIME transect



Figure S2 : Slope (and standard deviation) of N_2 fixation (a-c) versus time in the controls (C, black), dust treatments under present climate conditions (D, red) and dust treatments under future climate conditions (G, green) during the dust seeding experiments at TYR, ION and FAST. Only data presenting a significant linear relationship with time (Pearson's correlation coefficient, p < 0.05) were included. Slopes that were significantly different within one experiment are labelled with different letters (A, B, C).



Figure S3: Box plots of the relative changes (in %) in ¹³C-primary production (PP) over the duration of the dust seeding experiments at TYR, ION, and FAST stations. D means dust treatments under present climate conditions and G dust treatments under future climate conditions.



Figure S4: Principal coordinate analysis of diazotroph communities. Distances between samples were calculated as Bray-Curtis dissimilarity. Only ASVs above 1% relative abundance were included in this analysis





Figure S5: General diversity trends visualized by Shannon H index, at TYR, ION and FAST. Shows that for TYR and ION the diversity decrease from T0 to Tend whereas the opposite is true for FAST.