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Supplement of

Mechanisms of *Trichodesmium* demise within the New Caledonian lagoon during the VAHINE mesocosm experiment

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Supplement

Figure S1: Time line of sampling during pre-bloom days (yellow circles, days 1-23), and during experiment 1 (blue circles, days 23-24) and experiment 2 (green circles, days 23-26). For experiment 1, *Trichodesmium* filaments and colonies were collected from the dense surface bloom using a plankton net (mesh size, 80 μm) from surface water (day 23, 12:00 h; designated T_0). *Trichodesmium* was resuspended in filtered seawater (FSW) that was split to six 4.5 L bottles that were incubate (see below) and sampled every 2-4 h until the biomass crashed. For experiment 2, seawater from the surface bloom was collected 5 h after the initial surface bloom was sighted (day 23, 17:00) by directly filling 20 L polyethylene carboys using a Teflon® PFA pump. Carboys were sampled every 4 h during the first 23 hours and then after 42 h and 72 h since the beginning of the experiment. Bottles and carboys from both experiments were placed in on-deck incubators filled with running seawater to maintain ambient surface temperature (~ 26 °C) and covered with neutral screening at 50 % surface irradiance levels.

Figure S1

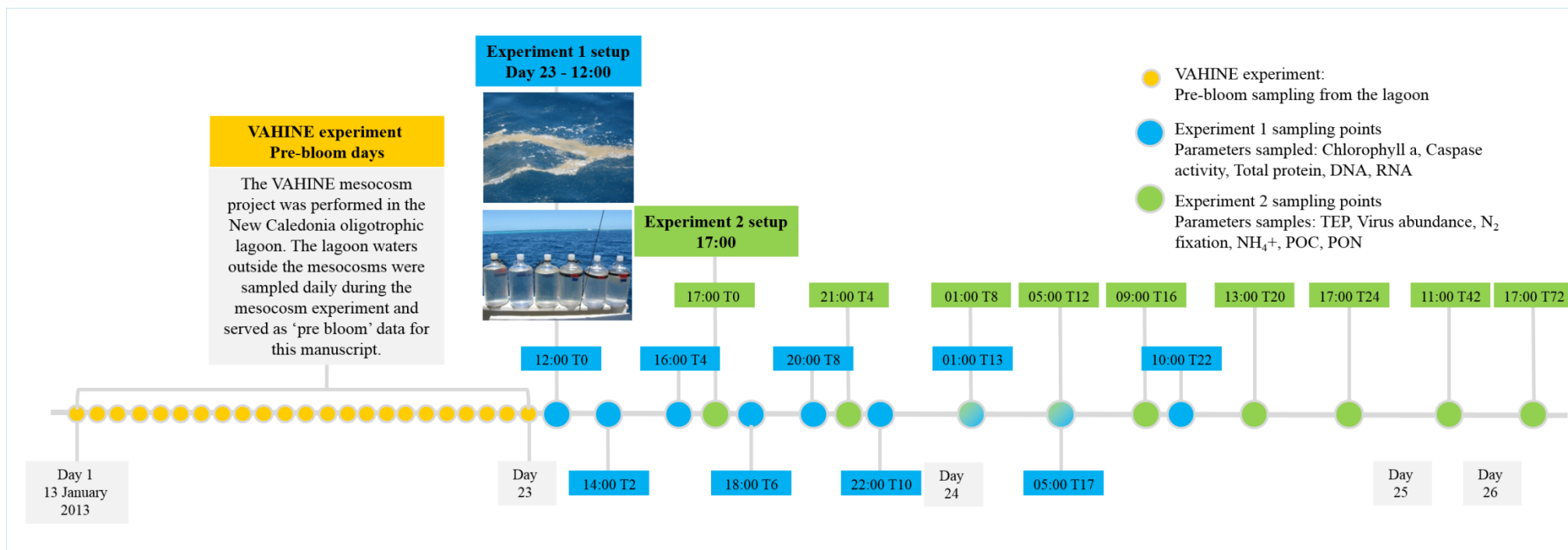


Table S1. Metatranscriptomic changes of selected marker genes in samples from *Trichodesmium* bloom and crash. Metatranscriptomic samples were obtained from the *Trichodesmium* bloom on day 23 at three successive time points [(T₀, T₈ and T₂₂, representing 0, 8, and 22 h from surface bloom]. Table data provides the respective locus_tag in the *T. erythraeum* genome, gene name and annotation, expected fold-change calculated from the results of ASC (see methods section), log₂ fold change, posterior probabilities for these fold-changes as calculated by ASC (significant if P > 0.98, in bold), and the reads per million reads (RPM) for each time point.

	Locus_tag	Symbol	Annotation	Fold-change (from ASC)			log2(Fold-change)			Posterior probabilities (P) from ASC						Reads per Million reads		
				(T8/T0)	(T22/T8)	(T22/T0)	(T8/T0)	(T22/T8)	(T22/T0)	P(T0/T8>2)	P(T8/T0>2)	P(T8/T22>2)	P(T22/T8>2)	P(T22/T0>2)	P(T0/T22>2)	T0	T8	T22
Gas Vesicle Protein (Gvp) formation	Tery_2322	gvpA	Gas vesicle synthesis protein- GvpA	0.53	NA	0.27	-0.92	NA	-1.88	0.43	0.00	NA	NA	0.00	0.81	8	0	0
	Tery_2323	gvpA	Gas vesicle synthesis protein- GvpA	0.41	NA	0.20	-1.29	NA	-2.32	0.73	0.00	NA	NA	0.00	0.93	15	0	0
	Tery_2324	gvpA	Gas vesicle synthesis protein- GvpA	0.12	4.09	0.48	-3.07	2.03	-1.06	1.00	0.00	0.00	1.00	0.00	0.97	5042	603	3009
	Tery_2325	gvpA	Gas vesicle synthesis protein- GvpA	0.12	2.12	0.26	-3.01	1.08	-1.94	1.00	0.00	0.00	0.79	0.00	1.00	4022	497	1285
	Tery_2329	gvpN	Gas vesicle protein- GvpN	0.58	0.45	0.26	-0.78	-1.14	-1.93	0.00	0.00	0.91	0.00	0.00	1.00	1964	1198	653
	Tery_2330	gvpA	Gas vesicle synthesis protein- GvpA	0.08	2.54	0.13	-3.65	1.35	-2.90	1.00	0.00	0.00	0.78	0.00	1.00	444	19	71
	Tery_2332	gvpK	Gas vesicle protein- GvpK	0.21	0.70	0.15	-2.22	-0.52	-2.78	1.00	0.00	0.01	0.00	0.00	1.00	1408	306	257
	Tery_2334	gvpN	Gas vesicle protein- GvpN	1.37	0.04	0.05	0.46	-4.57	-4.45	0.00	0.00	1.00	0.00	0.00	1.00	464	674	19
	Tery_2335	gvpA	Gas vesicle synthesis protein- GvpA	0.67	0.41	0.27	-0.58	-1.27	-1.88	0.00	0.00	0.90	0.00	0.00	1.00	479	335	164
	Tery_2338	gvpG	Gas vesicle protein- GvpG	1.11	0.26	0.28	0.15	-1.95	-1.84	0.00	0.00	1.00	0.00	0.00	1.00	431	505	152
Tery_2339	gvpL/gvpF	Gas vesicle synthesis protein- GvpLGvpF	2.05	0.33	0.67	1.04	-1.61	-0.58	0.00	0.85	1.00	0.00	0.00	0.00	1608	3473	1371	
Tery_2340	gvpL/gvpF	Gas vesicle synthesis protein- GvpLGvpF	0.24	2.17	0.39	-2.08	1.12	-1.36	1.00	0.00	0.00	0.59	0.00	0.85	102	15	50	
Phosphite Utlalization genes	Tery_0365	ptxA	Phosphonate transport	3.29	1.18	4.59	1.72	0.24	2.20	0.00	1.00	0.00	0.01	1.00	0.00	16	72	105
	Tery_0366	ptxB	Phosphonate transport	1.99	0.27	0.53	0.99	-1.88	-0.92	0.00	0.48	1.00	0.00	0.00	0.36	193	412	130
	Tery_0367	ptxC	Phosphonate transport	0.62	1.93	1.18	-0.69	0.95	0.24	0.06	0.00	0.00	0.42	0.00	0.00	126	79	192
Phosphonate transporters and metabolism	Tery_4993	phnD	Phosphonate transport	1.44	1.19	1.77	0.53	0.25	0.82	0.00	0.01	0.00	0.00	0.23	0.00	61	97	142
	Tery_4994	phnC	Phosphonate transport	0.87	7.90	7.71	-0.20	2.98	2.95	0.00	0.00	0.00	1.00	1.00	0.00	34	30	344
	Tery_4995	phnE	Phosphonate transport	1.78	4.49	9.34	0.83	2.17	3.22	0.00	0.26	0.00	1.00	1.00	0.00	25	54	319
	Tery_4996	phnE	Phosphonate transport	5.18	0.40	2.19	2.37	-1.31	1.13	0.00	1.00	0.85	0.00	0.67	0.00	26	166	77
	Tery_4997	phnG	Membrane associated C-P lyase	0.39	2.97	0.68	-1.37	1.57	-0.55	0.79	0.00	0.00	0.75	0.00	0.22	17	0	15
	Tery_4998	phnH	Phosphonate metabolism	1.16	2.70	4.04	0.21	1.43	2.01	0.00	0.03	0.00	0.82	0.99	0.00	10	14	59
	Tery_4999	phnI	Phosphonate metabolism	2.06	1.77	4.58	1.05	0.82	2.20	0.00	0.56	0.00	0.33	1.00	0.00	12	35	80
	Tery_5000	phnJ	Membrane associated C-P lyase	2.93	0.91	3.24	1.55	-0.13	1.70	0.00	0.96	0.02	0.00	0.95	0.00	11	47	53
	Tery_5001	phnK	C-P lyase system	2.50	0.97	2.92	1.32	-0.05	1.54	0.00	0.83	0.02	0.01	0.89	0.00	11	39	46
	Tery_5002	phnL	C-P lyase system	3.36	2.09	9.25	1.75	1.06	3.21	0.00	0.99	0.00	0.58	1.00	0.00	11	55	149
Tery_5003	phnM	Membrane associated C-P lyase	0.84	3.94	3.87	-0.25	1.98	1.95	0.04	0.00	0.00	0.98	0.99	0.00	13	11	74	
Inorganic P transporters	Tery_3534	sphX	Phosphate bindig protein (regulated by P supply)	2.57	0.57	1.47	1.36	-0.82	0.55	0.00	0.99	0.22	0.00	0.02	0.00	71	202	136
	Tery_3537	pstS	Phosphate bindig protein	0.39	4.97	1.77	-1.34	2.31	0.83	0.87	0.00	0.00	1.00	0.23	0.00	62	19	146
	Tery_3539	pstS	Phosphate transport system permease protein 2	0.68	1.01	0.66	-0.56	0.01	-0.61	0.04	0.00	0.01	0.00	0.00	0.12	69	47	59
	Tery_3540	pstB	Inorganic P transporter	0.57	0.69	0.38	-0.80	-0.54	-1.40	0.12	0.00	0.08	0.00	0.00	0.92	162	94	77
	Tery_3583	pstC	Inorganic P transporter	2.17	1.34	3.25	1.12	0.42	1.70	0.00	0.68	0.00	0.03	0.99	0.00	25	66	111
Degradation of organic P sources	Tery_3467	phoA	Alkaline phosphatase	1.47	2.58	3.86	0.55	1.37	1.95	0.00	0.00	0.00	1.00	1.00	0.00	179	279	885
	Tery_3845	phoX	Alkaline phosphatase	0.79	0.87	0.68	-0.34	-0.20	-0.55	0.00	0.00	0.00	0.00	0.00	0.01	223	184	195
Trichodesmium Fe acquisition, storage, regulation ans quota reduction genes. (Gene list from Chappell and Webb 2009)	Tery_1560	tonB	TonB family protein	2.38	0.37	0.88	1.25	-1.44	-0.19	0.00	1.00	1.00	0.00	0.00	0.00	979	2459	1096
	Tery_1666	fldA	Flavodoxin FldA	0.39	1.02	0.40	-1.34	0.02	-1.33	1.00	0.00	0.00	0.00	0.00	1.00	1535	629	777
	Tery_1667	isiA	iron-stress induced protein A, photosystem antenna protein-like, isiA	1.72	1.15	2.06	0.78	0.20	1.04	0.00	0.13	0.00	0.00	0.57	0.00	55	105	149
	Tery_1953	fur	Ferric uptake regulator	1.81	0.86	1.67	0.86	-0.22	0.74	0.00	0.31	0.03	0.00	0.27	0.00	20	44	46
	Tery_1958	fur	Ferric uptake regulator	0.42	0.26	0.09	-1.26	-1.94	-3.41	0.88	0.00	0.95	0.00	0.00	1.00	127	50	9
	Tery_2559	flavodoxin	Flavodoxin	0.15	2.97	0.38	-2.78	1.57	-1.38	1.00	0.00	0.00	0.99	0.00	0.99	541	69	263
	Tery_2787	dps	Ferritin and Dps	2.12	0.24	0.29	1.09	-2.06	-1.80	0.00	0.60	0.92	0.00	0.00	0.78	7	25	0
	Tery_2878	feoB	ferrous iron transport protein B	1.09	1.121	1.23	0.12	0.17	0.30	0.00	0.00	0.00	0.00	0.00	0.00	81	94	130
	Tery_2879	feoA	ferrous iron transport protein A	0.38	NA	0.19	-1.38	NA	-2.43	0.79	0.00	NA	NA	0.00	0.95	17	0	0
	Tery_3222	futC	iron(III) ABC transporter, ATP-binding protein	1.08	1.79	1.96	0.11	0.84	0.97	0.00	0.00	0.00	0.18	0.41	0.00	152	174	384
	Tery_3223	futB	iron(III) ABC transporter, permease protein	2.70	1.70	5.02	1.43	0.77	2.33	0.00	0.99	0.00	0.15	1.00	0.00	38	120	254
	Tery_3377	idiA	idiA	3.27	0.37	1.23	1.71	-1.42	0.29	0.00	1.00	1.00	0.00	0.00	0.00	413	1434	647
	Tery_3404	fur	Ferric uptake regulator	0.28	1.01	0.26	-1.82	0.02	-1.94	1.00	0.00	0.00	0.00	0.00	1.00	221	57	71
	Tery_3943	Periplasmic binding protein	Periplasmic binding protein	0.82	0.88	0.71	-0.29	-0.18	-0.50	0.00	0.00	0.01	0.00	0.00	0.04	88	75	80
	Tery_4282	dpsA	Ferritin and Dps	1.21	0.22	0.26	0.27	-2.20	-1.96	0.00	0.00	1.00	0.00	0.00	1.00	491	625	158
Tery_4448	motA/exbB	MotA/TolQ/ExbB proton channel	0.70	1.89	1.31	-0.51	0.92	0.39	0.03	0.00	0.00	0.40	0.01	0.00	57	40	99	
Tery_4449	exbD	Biopolymer transport protein ExbD/TolR	2.02	1.37	3.39	1.02	0.45	1.76	0.00	0.52	0.00	0.09	0.97	0.00	12	33	59	
Metacaspases genes	Tery_0382	TeMC8	Putative Chase2 sensor protein, metacaspase	3.25	1.04	3.49	1.70	0.06	1.81	0.00	1.00	0.00	0.00	1.00	0.00	90	322	409
	Tery_1841	TeMC7	Peptidase C14,C caspase catalytic subunit p20, metacaspase	2.60	1.11	2.92	1.38	0.16	1.54	0.00	1.00	0.00	0.00	1.00	0.00	442	1219	1647
	Tery_2963	TeMC12	Hypothetical protein	0.64	NA	0.41	-0.63	NA	-1.30	0.25	0.00	NA	NA	0.01	0.63	5	0	0
	Tery_2058	TeMC6	Peptidase C14,C caspase catalytic subunit p20, metacaspase	2.91	0.44	1.28	1.54	-1.19	0.35	0.00	1.00	0.76	0.00	0.01	0.00	61	199	102
	Tery_2077	TeMC1	Hypothetical protein, metacaspase	5.31	1.08	5.91	2.41	0.11	2.56	0.00	1.00	0.00	0.00	1.00	0.00	129	747	981
	Tery_2158	TeMC11	Hypothetical+protein	2.60	1.39	3.89	1.38	0.47	1.96	0.00	0.98	0.00	0.01	1.00	0.00	41	124	214
	Tery_2471	TeMC4	Peptidase C14,C caspase catalytic subunit p20, metacaspase	2.38	1.78	4.30	1.25	0.83	2.10	0.00	1.00	0.00	0.04	1.00	0.00	266	675	1461
	Tery_2624	TeMC10	Peptidase C14,C caspase catalytic subunit p20, metacaspase	1.46	2.07	3.19	0.55	1.05	1.67	0.00	0.01	0.00	0.58	1.00	0.00	58	94	245
	Tery_2689	TeMC2	Hypothetical protein, metacaspase	1.98	1.12	2.27	0.99	0.17	1.18	0.00	0.46	0.00	0.00	0.88	0.00	118	253	347
	Tery_2760	TeMC5	Peptidase C14,C caspase catalytic subunit p20, metacaspase	1.84	1.49	2.90	0.88	0.57	1.54	0.00	0.27	0.00	0.04	0.99	0.00	49	102	189
	Tery_3869	TeMC3	WD-40 repeat containing protein, metacaspase	2.79	2.21	6.24	1.48	1.14	2.64	0.00	1.00	0.00	0.97	1.00	0.00	300	889	2390
	Tery_4625	TeMC9	WD-40 repeat-containing protein, metacaspase	2.82	1.54	4.36	1.50	0.62	2.13	0.00	1.00	0.00	0.00	1.00	0.00	507	1516	2826