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Supplement of

Impact of dust addition on the microbial food web under present and future conditions of pH and temperature

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Supplementary material

Table S1: Values at T24h for bacterial production (BP), Bacterial biomass specific growth rates (BBGR), prokaryotes abundance (HB), mortality, % of lytic (FLIC) and lysogenic (FLC) cells, viral production (VP), virus and heterotrophic nanoflagellates (HNF) abundance.

	TYR					
	C1	**C2**	**D1**	**D2**	**G1**	**G2**
BP (ngC/L/h)	101.0	66.1	741.0	619.2	1027.8	847.8
BBGR (/d)	0.2	0.1	1.2	0.9	1.6	1.2
HB (cells/mL)	5.8E+05	6.0E+05	7.4E+05	7.9E+05	7.9E+05	8.6E+05
Mortality (/d)	0.2	0.1	0.5	0.5	0.6	0.5
FLIC (%)	10.8	17.2	4.8	16.8	31.4	9.2
FLC (%)	6.9	0.0	0.0	0.0	0.0	0.0
VP (VLP/L/h)	2.6E+07	2.2E+07	1.2E+08	7.8E+07	4.7E+07	2.0E+08
virus (/mL)	2.4E+06	2.6E+06	2.6E+06	2.6E+06	2.4E+06	
HNF (cells/mL)	97.0	97.0	143.4	73.9	427.3	
	ION					
	C1	**C2**	**D1**	**D2**	**G1**	**G2**
BP (ngC/L/h)	65.5	59.8	231.8	419.8	798.6	645.2
BBGR (/d)	0.0	0.3	0.8	1.2	1.8	1.6
HB (cells/mL)		2.8E+05	3.5E+05	4.2E+05	5.3E+05	4.9E+05
Mortality (/d)		0.2	0.4	0.5	0.6	0.6
FLIC (%)	23.1	39.1	28.9	2.9	10.7	12.6
FLC (%)	0.0	0.0	0.4	6.1	2.1	0.0
VP (VLP/L/h)	1.7E+07	5.1E+07	6.4E+07	9.7E+06	7.0E+07	1.6E+08
virus (/mL)	1.4E+06	1.6E+06	1.4E+06	1.5E+06	1.4E+06	1.5E+06
HNF (cells/mL)	56.9	58.4	59.1	65.6	64.9	96.6
	FAST					
	C1	**C2**	**D1**	**D2**	**G1**	**G2**
BP (ngC/L/h)	69.4	102.4	201.7	306.4	1073.1	1966.7
BBGR (/d)	0.1	0.2	0.4	0.5	1.6	2.9
HB (cells/mL)	6.0E+05	6.3E+05	6.6E+05	7.1E+05	8.2E+05	8.2E+05
Mortality (/d)	0.1	0.2	0.3	0.3	0.6	0.7
FLIC (%)	17.3	1.1	12.4	1.1	6.6	14.0
FLC (%)	0.0	4.8	0.5	9.7	0.0	0.0
VP (VLP/L/h)	2.9E+07	2.6E+07	2.2E+08	1.4E+07	3.1E+07	8.5E+07
virus (/mL)	3.1E+06	3.0E+06	2.6E+06	3.1E+06	3.0E+06	3.5E+06
HNF (cells/mL)	181.4	177.2	202.6	206.8	614.8	312.7

Table S2. Similarity percentage analysis (SIMPER) of the bacterioplankton community (based on Bray Curtis similarities). The table shows the contribution of the ASVs responsible for more than 50% of the cumulative dissimilarities between the clusters (based on Bray Curtis similarity in Fig. 3). a) Comparison between the clusters control (*in situ*, all t0 and C t24h, t72h) and the cluster DG (DUST and GREENHOUSE t24h and t72h) during the experiment at TYR between. b) Comparison between the cluster control (*in situ*, all t0 and C t24h, t72h) and the cluster D (t24h and t72h) and between the cluster D and the cluster G (t24h and t72h) during the experiment at ION. c) Comparison between the cluster Control (*in situ*, all t0 and C, D t24h) and the cluster G24h (t24h) and between the cluster control t96h and the cluster DG at t96h during the experiment at FAST. Grey gradient shows in which cluster the relative abundance of an ASV is the highest.

(-) no significant contribution to the difference between clusters

a)

		Relative abundance (%)		
ASV	**Taxonomic affiliation**	**Control**	**DG**	**SIMPER**
16S-ASV8	*Alteromonas marina*	0.3	8.2	6.83
16S-ASV3	Verrucomicrobia Opitulales	6.0	5.5	4.79
16S-ASV16	*Alteromonas* sp.	0.2	5.3	4.45
16S-ASV1	SAR11 clade Ia	11.4	6.6	4.36
16S-ASV10	*Alteromonas* sp.	0.2	4.8	4.02
16S-ASV2	*Synechococcus* C9902	3.3	3.1	3.07
16S-ASV18	*Alteromonas mediterranea*	0.0	3.4	2.89
16S-ASV7	Rhodospirillales AEGEAN169	3.8	0.9	2.58
16S-ASV41	*Pseudophaeobacter* sp.	0.3	2.7	2.1
16S-ASV27	*Alteromonas mediterranea*	0.1	2.3	1.95
16S-ASV19	*Alteromonas* sp.	0.1	2.3	1.92
16S-ASV14	Flavobacteriaceaea	1.7	1.9	1.89
16S-ASV28	*Aestuariibacter* sp.	0.0	2.2	1.85
16S-ASV4	*Alteromonas* sp.	3.4	1.7	1.83
16S-ASV45	*Alteromonas* sp.	0.1	2.1	1.78
16S-ASV13	OM60	1.9	3.1	1.66
16S-ASV5	SAR11 clade Ia	4.5	2.8	1.64
16S-ASV6	*Erythrobacter* sp.	0.1	1.9	1.62

b)

		Relative abundance (%)				
ASV	**Taxonomic affiliation**	**Control**	**D**	**G**	**SIMPER C to D**	**SIMPER D to G**
16S-ASV6	*Erythrobacter* sp.	0.81	6.64	8.47	6.05	6.19
16S-ASV49	*Dokdonia* sp.	0.20	4.89	0.45	5.02	6.05
16S-ASV10	*Alteromonas* sp.	0.50	4.62	4.41	4.27	2.23
16S-ASV1	SAR11 clade Ia	9.13	6.82	3.04	3.25	4.95
16S-ASV16	*Alteromonas* sp		1.70	5.08		4.25
16S-ASV28	*Aestuariibacter* sp.	0.02	2.80	0.75	2.89	3.29
16S-ASV48	*Synechococcus* sp.		1.28	3.20		2.99
16S-ASV13	OM60	1.75	4.46	4.40	2.85	1.97

16S-ASV3	Verrucomicrobia Opitulales	5.49	4.32	0.48	2.8	2.07
16S-ASV18	*Alteromonas mediterranea*	0.18	2.69	-	2.6	-
16S-ASV17	OM60	1.43	3.73	-	2.41	-
16S-ASV19	*Alteromonas* sp.	0.13	2.20	1.41	2.15	1.82
16S-ASV33	Flavobacteria NS5	2.55	0.50	-	2.15	-
16S-ASV2	*Synechococcus* C9902	2.61	0.55		2.14	-
16S-ASV7	Rhodospirillales AEGEAN169	3.99	2.05		2.01	-
16S-ASV8	*Alteromonas marina*	0.49	2.27	5.85	1.88	4.5
16S-ASV20	Flavobacteria NS4	2.14	0.45		1.75	-
16S-ASV51	*Alteromonas* sp.	0.12	1.72	1.14	1.7	2.1
16S-ASV27	*Alteromonas mediterranea*	0.18	1.79		1.67	-
16S-ASV4	Flavobacteria NS4	2.51	0.95	3.73	1.63	3.5
16S-ASV5	SAR11 clade Ia	4.56	3.41	1.59	1.62	2.38
16S-ASV40	*Erythrobacter* sp.		1.42	2.44		2.08

c)

		Relative abundance (%)					
ASV	**Taxonomic affiliation**	**Control**	**G24h**	**C96h**	**GD96h**	**SIMPER C to G24h**	**SIMPER C96h to GD96h**
16S-ASV6	*Erythrobacter* sp.	1.40	10.81	0.94	8.42	8.35	8.17
16S-ASV36	*Celeribacter* sp.			10.52	2.46		8.81
16S-ASV12	Verrucomicrobia Opitulales			9.36	1.31		8.8
16S-ASV9	*Prochlorococcus* MIT9313	9.37	0.34			7.52	
16S-ASV2	*Synechococcus* C9902			12.36	19.06		7.33
16S-ASV28	*Aestuariibacter* sp.	0.11	6.85	0.09	2.67	5.62	2.82
16S-ASV10	*Alteromonas* sp.	0.86	6.82	0.73	3.03	5.05	2.52
16S-ASV19	*Alteromonas* sp.	0.63	6.23			4.67	
16S-ASV18	*Alteromonas mediterranea*	0.51	4.59			3.41	
16S-ASV1	SAR11 clade Ia	6.53	2.68	4.98	1.65	3.21	3.63
16S-ASV4	Flavobacteria NS4			1.03	3.89		3.13
16S-ASV27	*Alteromonas mediterranea*	0.45	3.61			2.65	
16S-ASV62	Rhodobacteraceae	0.02	2.61			2.16	
16S-ASV7	Rhodospirillales AEGEAN169	2.99	0.44			2.12	
16S-ASV14	Flavobacteriaceaea	1.42	3.93	5.94	7.44	2.09	3.45
16S-ASV78	*Thalassobius* sp.			3.26	1.35		2.08
16S-ASV8	*Alteromonas marina*	0.71	2.76			2.01	
16S-ASV16	*Alteromonas* sp.	0.47	2.12			1.55	

Table S3. Similarity percentage analysis (SIMPER) of the micro-eukaryotes community (based on Bray Curtis similarities). The table shows the contribution of the ASVs responsible for more than 40% of the cumulative dissimilarities between the clusters (based on Bray Curtis similarity in Fig. 4). a) Comparison between the cluster controls (*in situ*, all t0 and t24h in the controls) and the cluster DG24h (DUST and GREENHOUSE at t24h) during the experiment at TYR. b) Comparison between the cluster control (*in situ*, all minicosms at t0 and t24h as well as controls at t72h) and the cluster D (DUST minicosms at t72h) and between the cluster D and the cluster G (t72h) during experiment at ION. c) Comparison between the cluster control (*in situ*, all minicosms at t0 and controls at t24h and t96h) and cluster DG24 (DUST and GREENHOUSE at t24h) and between DG24 and DG96 (DUST and GREENHOUSE at t96h) during the experiment at FAST. Grey gradient shows in which cluster the relative abundance of an ASV is the highest.

(-) no significant contribution to the difference between clusters

a)

		Relative abundance (%)		
ASV	**Taxonomic affiliation**	**Control**	**DG24h**	**SIMPER**
18S-ASV2754	*Heterocapsa rotundata*	19.8	20.6	9.38
18S-ASV1689	Uncultured Syndiniales	1.6	7.8	6.04
18S-ASV1058	Uncultured Gymnodiniales	5.4	0.3	4.93
18S-ASV621	Uncultured Gymnodiniales	4.5	6.0	3.44
18S-ASV477	Chlorophyta	0.1	2.1	1.97
18S-ASV807	*Gonyaulax* sp.	0.3	2.3	1.94
18S-ASV1197	Uncultured Syndiniales	3.5	4.9	1.84
18S-ASV1917	*Heterocapsa rotundata*	1.5	3.2	1.72
18S-ASV2742	Uncultured Syndiniales	1.6	1.2	1.64
18S-ASV2112	*Gyrodinium* sp.	1.8	0.2	1.6
18S-ASV1155	Uncultured Gymnodiniales	1.0	1.6	1.43
18S-ASV2479	*Tripos Muelleri*	0.8	1.4	1.33
18S-ASV2116	*Tripos Furca*	0.5	1.6	1.31
18S-ASV173	*Amoebophrya* sp. Syndiniales	1.2	2.1	1.09
18S-ASV1770	Uncultured dinophyceae	1.4	0.3	1.06

b)

		Relative abundance (%)				
ASV	**Taxonomic affiliation**	**Control**	**D72h**	**G72h**	**SIMPER C to D72h**	**SIMPER D72h to G72h**
18S-ASV621	Uncultured Gymnodiniales	15.2	3.4		5.92	
18S-ASV2754	*Heterocapsa rotundata*	19.4	8.3	27.0	5.57	13.3
18S-ASV1500	*Karlodinium veneficum*	9.0	3.6	11.5	2.74	5.62
18S-ASV1917	*Heterocapsa rotundata*	4.1	0.6	8.3	1.79	5.49
18S-ASV1086	Peridiniales	5.1	2.2	6.5	1.43	3.07
18S-ASV621	Uncultured Gymnodiniales		3.4	0		2.42
18S-ASV599	Chlorophyta		1.3	4.6		2.39
18S-ASV1344	Uncultured dinophyceae	3.4	0.7		1.38	
18S-ASV9	*Emiliania huxleyi*	0.8	3.3		1.22	
18S-ASV1058	Uncultured Gymnodiniales	0.4	2.8	0	1.17	1.99

18S-ASV2509	*Tripos sp.*	0.2	2.1	0	1.05	1.52
18S-ASV2278	Uncultured syndiniales	2.1	0.4		0.88	
18S-ASV2446	Cryptophyceae	0.4	1.9		0.88	
18S-ASV2696	Choanoflagellata	0.1	1.6		0.79	
18S-ASV1770	Uncultured dinophyceae	1.3	2.2		0.72	

c)

		Relative abundance (%)				
ASV	**Taxonomic affiliation**	**Control**	**DG24h**	**DG96h**	**SIMPER C to DG24h**	**SIMPER DG24h to DG96h**
18S-ASV1500	*Karlodinium veneficum*	17.2	16.4	24.2	7.49	9.91
18S-ASV1155	Uncultured Gymnodiniales	2.3	8.0	0	6.53	9.15
18S-ASV2754	*Heterocapsa rotundata*	12.9	7.7	8.7	5.89	1.93
18S-ASV1227	*Protodinium sp.*		0.7	5.4		5.3
18S-ASV1058	Uncultured Gymnodiniales	1.5	2.8	0.1	3.39	3.17
18S-ASV1689	Uncultured Syndiniales	1.8	4.7		3.3	
18S-ASV2037	*Heterocapsa rotundata*	4.2	1.7	4.9	2.99	3.96
18S-ASV3236	Uncultured Gymnodiniales	0.6	2.9		2.65	
18S-ASV1547	Uncultured Syndiniales	2.2	0.4		2.01	
18S-ASV2346	Uncultured Gymnodiniales	1.6	0.4		1.89	
18S-ASV1917	*Heterocapsa rotundata*	2.0	3.4	4.8	1.74	2.7
18S-ASV2536	Acantharea		1.0	2.1		2.24
18S-ASV1533	Gonyaulacales	0.3	1.6		1.54	
18S-ASV979	*Heterocapsa rotundata*	3.3	2.6		1.5	
18S-ASV9	*Emiliania huxleyi*	1.9	0.6	8	1.48	8.5

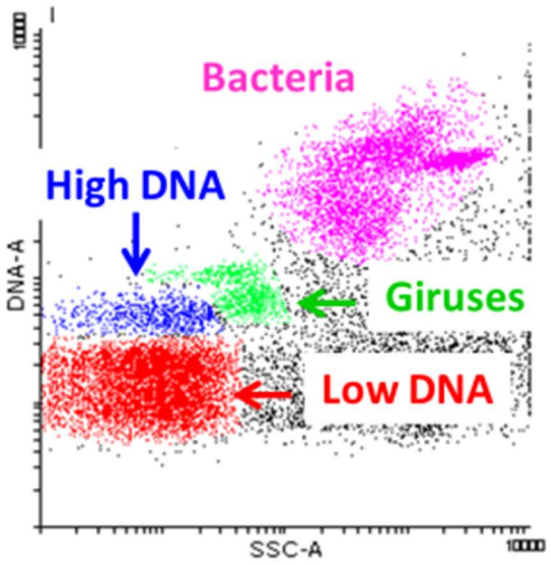

Figure S1: Determination of the viral populations by flow cytometry. Three main viral populations were discriminated based on their DNA fluorescence (DNA axis) and Side Scatter (SSC axis). The population of Low DNA viruses generally comprises viruses of bacteria (phages) with small genome, that of High DNA viruses is made of viruses with larger genome size (generally 200 – 300 kb) such as for some viruses of cyanobacteria or picoeukaryotes) while the Girus (giant virus) population typically comprises viruses of nanoeukaryotes (*e.g.*, microalgae, HNF) with giant genome (generally > 300 kb).

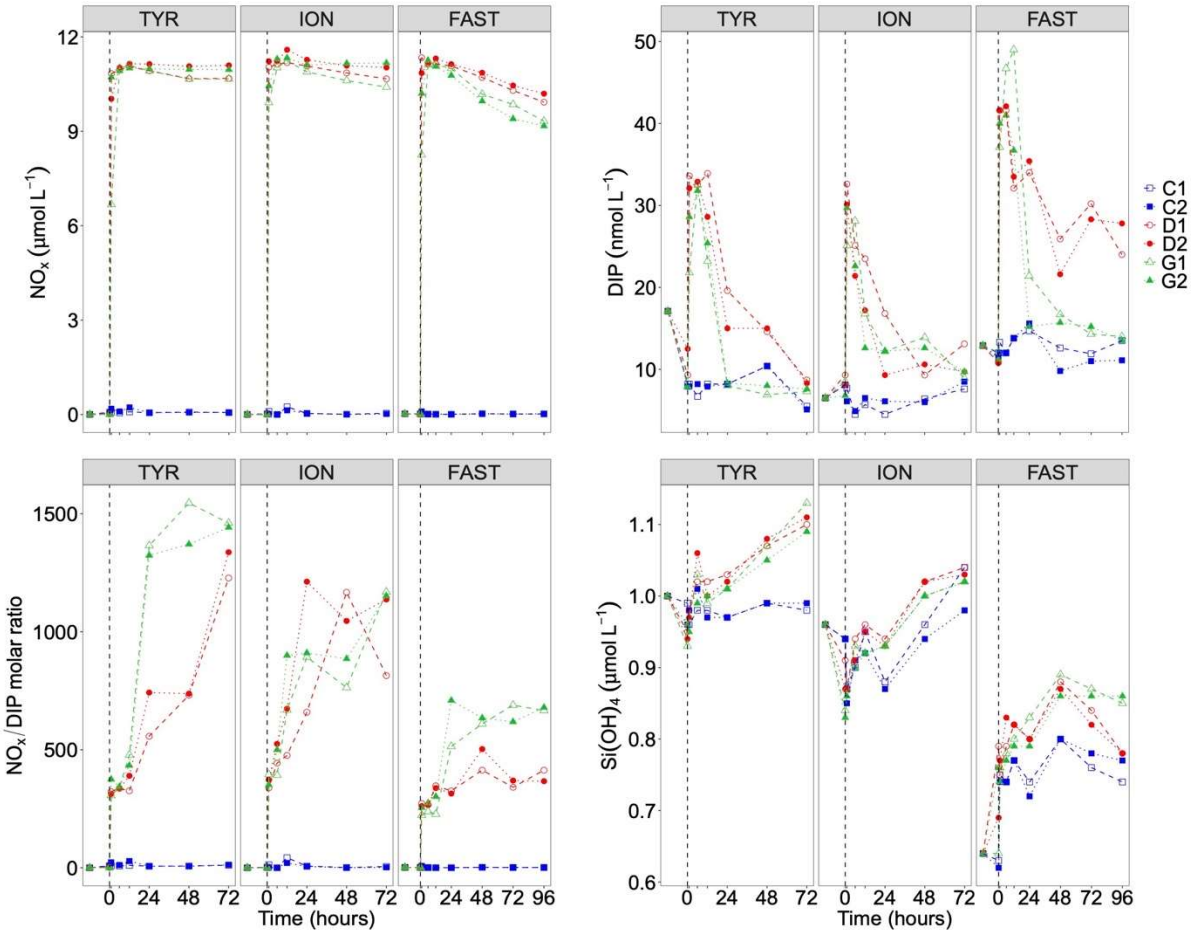

Figure S2. Nutrients (nitrate + nitrite): NO_x, dissolved inorganic phosphorus: DIP, silicate: $Si(OH)_4$ and the molar ratio between NO_x and DIP, measured in each tank during the experiments at TYR, ION and FAST. The dashed vertical line indicates the time of seeding (after t0). Reproduced from Gazeau et al. (2021a).

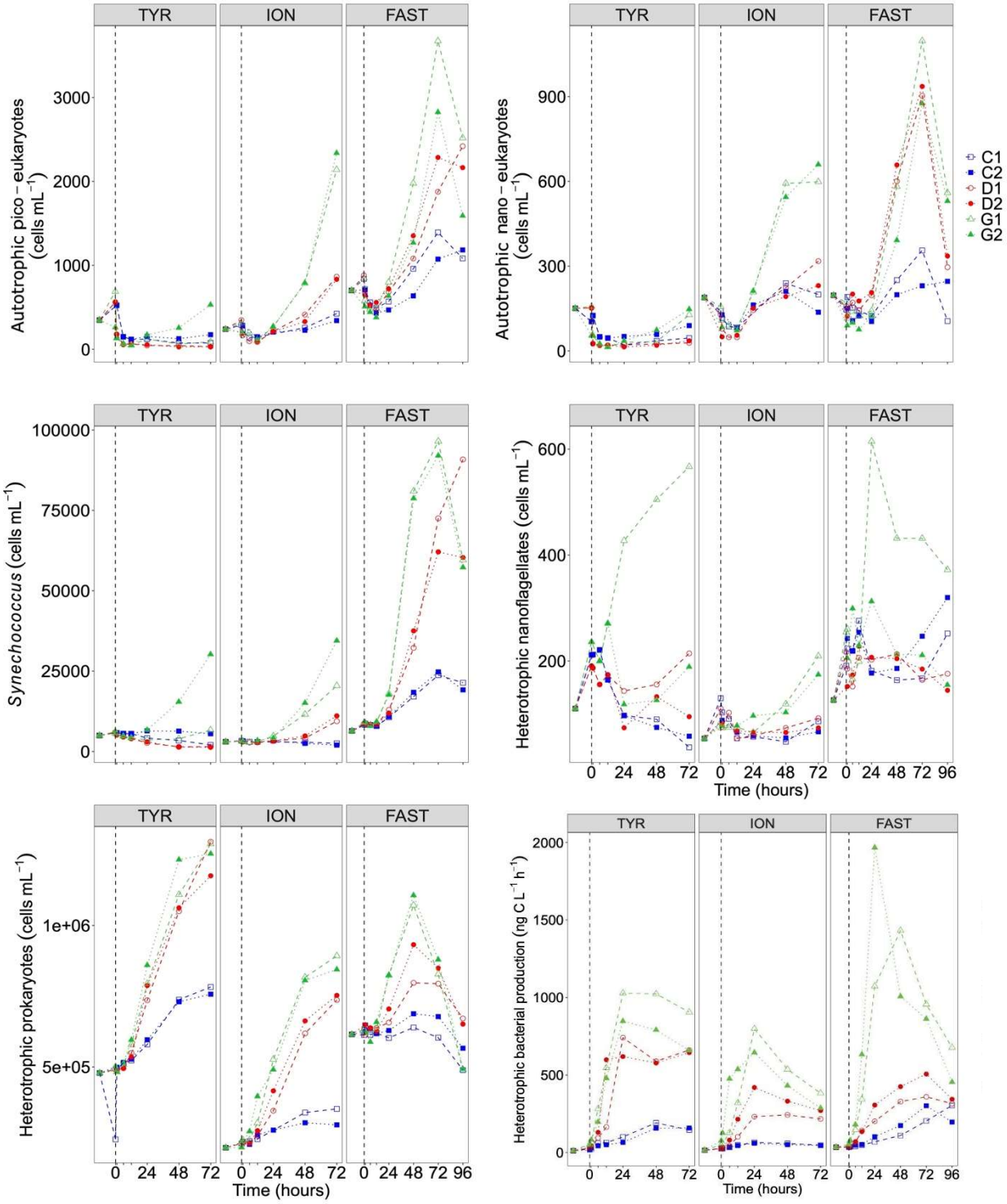

Figure S3. Abundance of autotrophic pico-eukaryotes, autotrophic nano-eukaryotes, *Synechococcus,* heterotrophic prokaryotes (HP), and heterotrophic nano-flagellates (HNF), measured by flow cytometry and heterotrophic bacterial production rates (BP), in each tank during the experiments at TYR, ION and

FAST. The dashed vertical line indicates the time of seeding (after t0). Figures reproduced from Gazeau et al (2021a, b.)

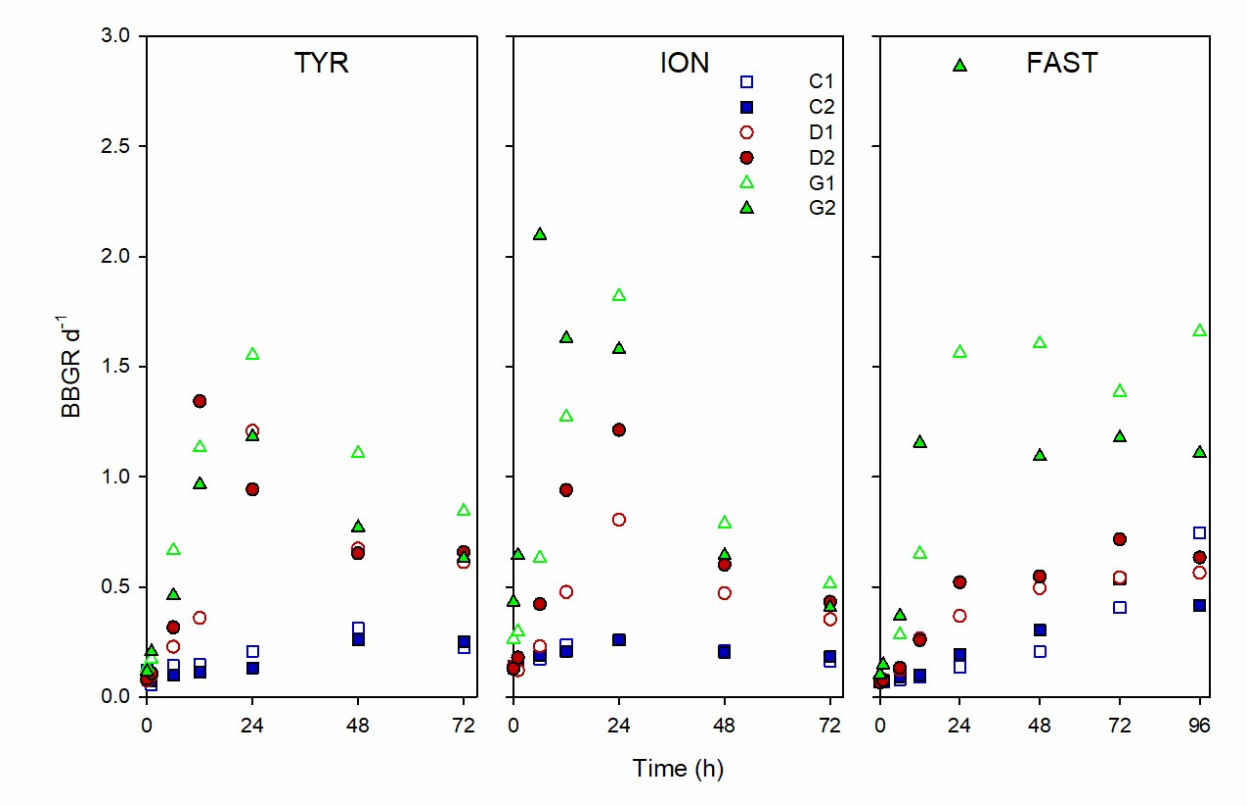

Figure S4: Bacterial biomass specific growth rates (BBGR) in each tank during the experiments at TYR, ION and FAST.

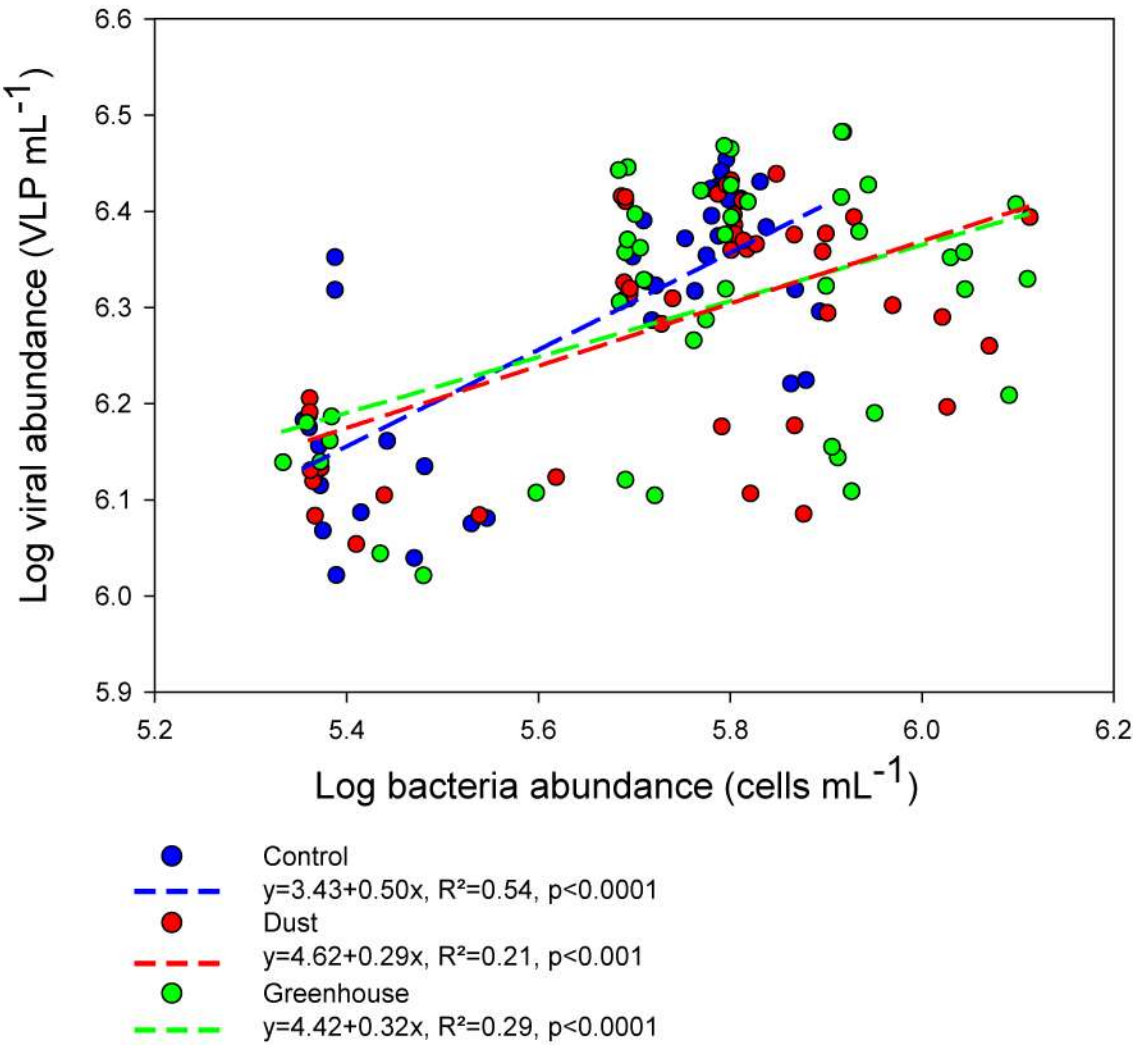

Figure S5. Log transformed relationship between bacterial and viral abundance in the three treatments. Dotted lines represent linear regressions for each treatment.

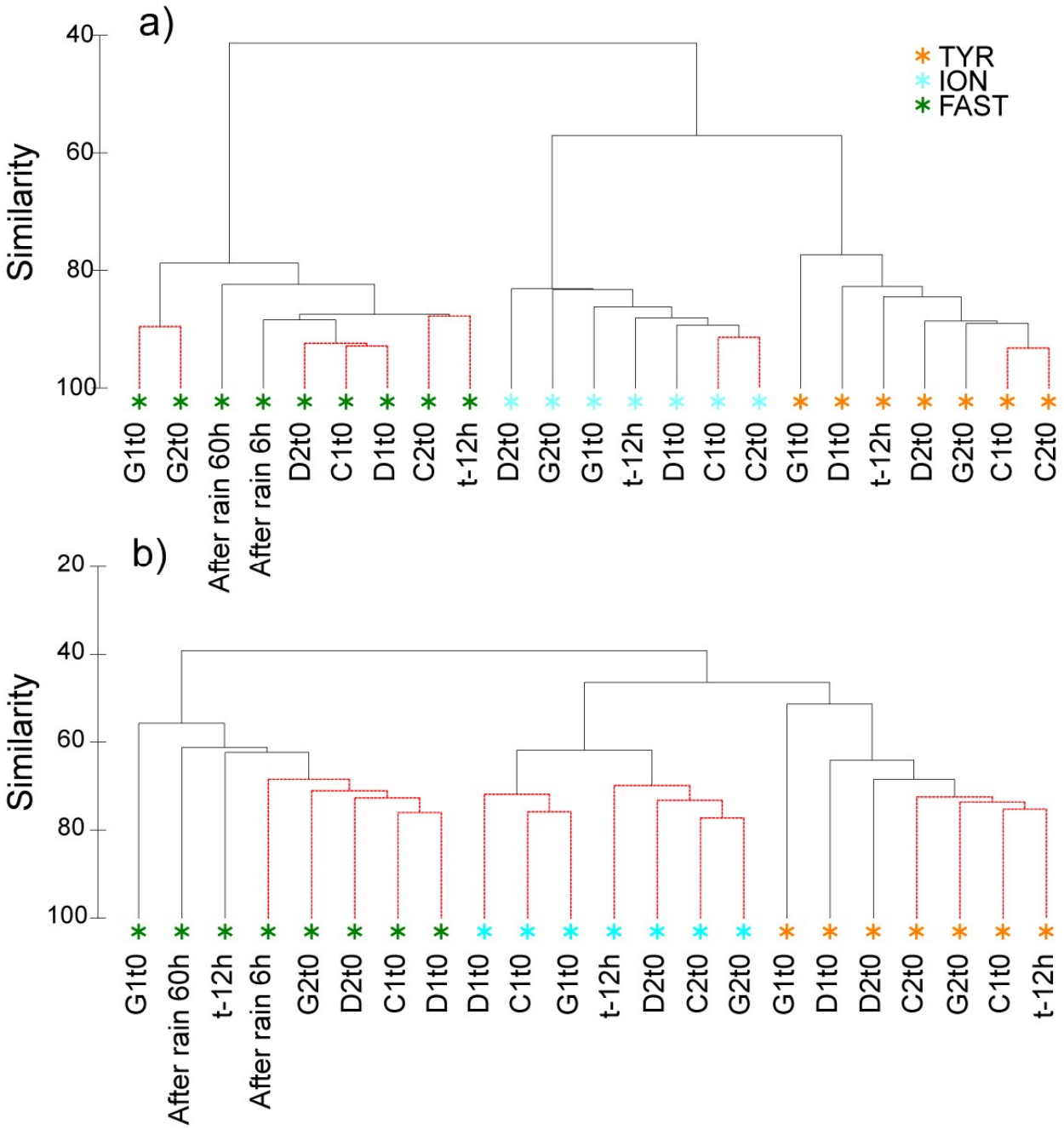

Figure S6. Bray-Curtis clustering showing the difference in microbial community in the initial waters of the 3 experiments, a) bacterial community composition (16S rDNA) and b) micro-eukaryotes community composition (18S rDNA) at the start of the three experiments in the initial water (t-12h) and when the dust was added (t0). Red cluster show samples with no significant differences (based on SIMPROF test).

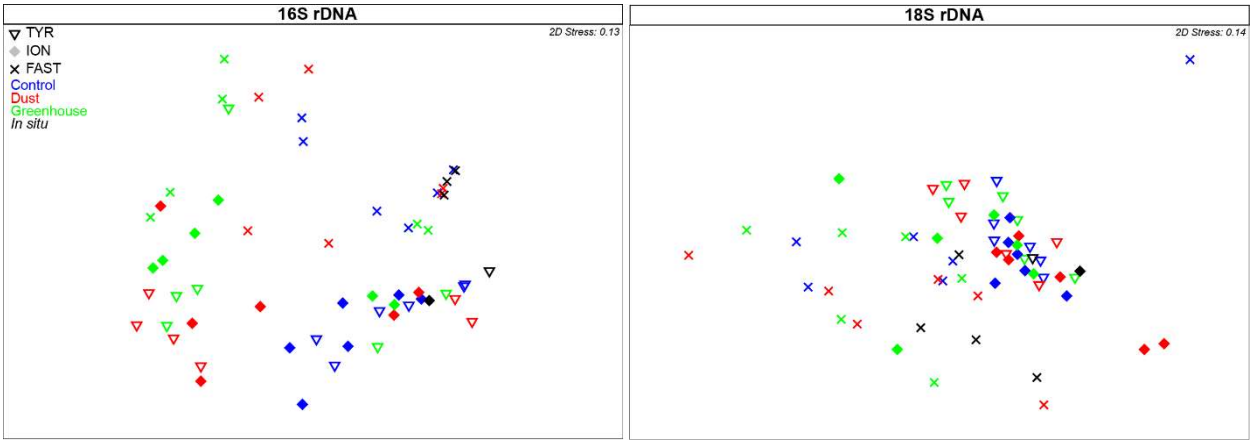

Figure S7: nMDS plots of bacterial (16S rDNA) and micro-eukaryotes (18S rDNA) community composition during the three experiments, based on Bray-Curtis dissimilarity.

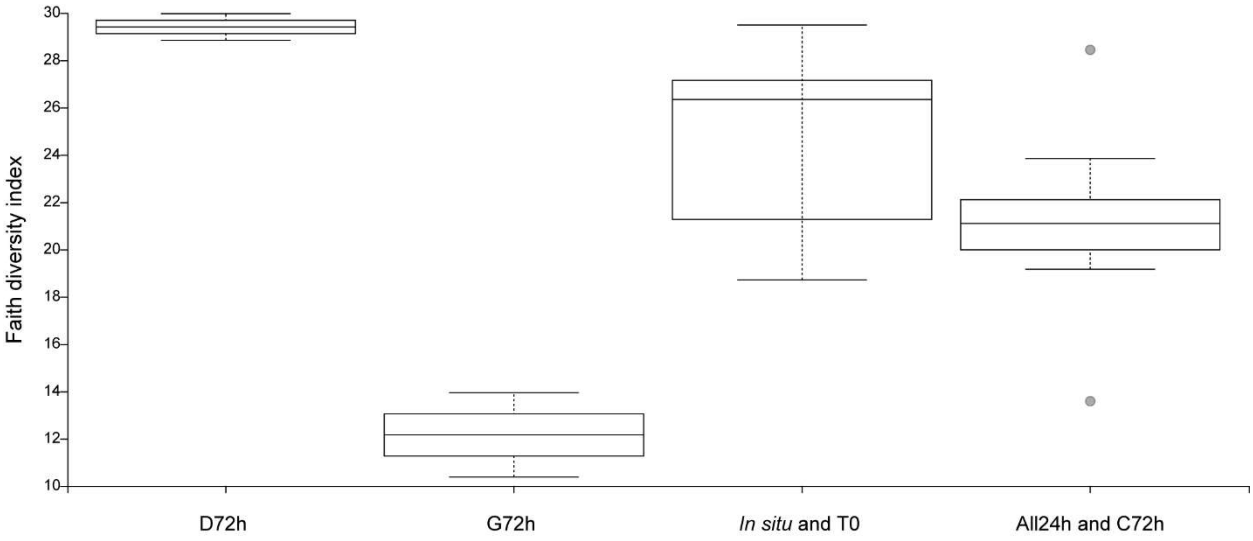

Figure S8. Diversity index (Faith index) between 18S rDNA community of the clusters from Fig. 4 during experiment ION.

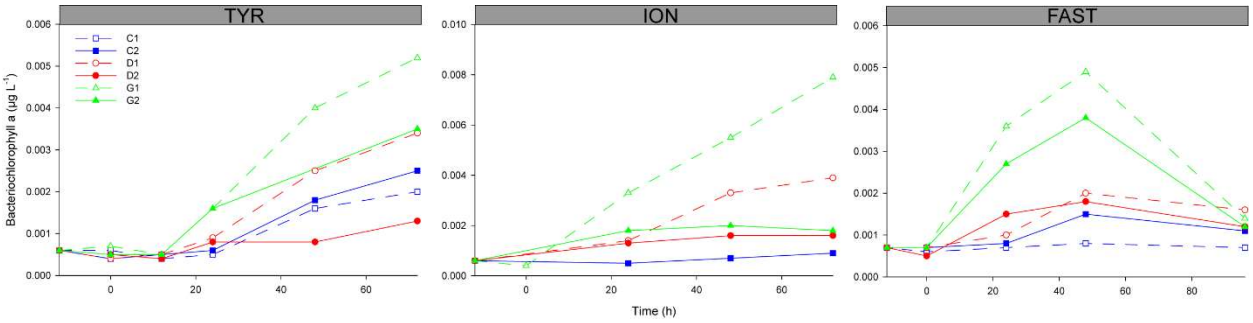

Figure S9: Bacteriochlorophyll a concentration measured by HPLC (see Gazeau et al. (2021a) for pigments measurements) over the course of the three experiments (TYR, ION and FAST).