

Supplementary material

Table S1. 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 (%)		SIMPER
		Control	DG	
ASV	Taxonomic affiliation			
16S-ASV8	<i>Alteromonas marina</i>	0.3	8.2	6.83
16S-ASV3	Verrucomicrobia Opitulales	6.0	5.5	4.79
16S-ASV16	<i>Alteromonas</i> sp.	0.2	5.3	4.45
16S-ASV1	SAR11 clade Ia	11.4	6.6	4.36
16S-ASV10	<i>Alteromonas</i> sp.	0.2	4.8	4.02
16S-ASV2	<i>Synechococcus</i> C9902	3.3	3.1	3.07
16S-ASV18	<i>Alteromonas mediterranea</i>	0.0	3.4	2.89
16S-ASV7	Rhodospirillales AEGEAN169	3.8	0.9	2.58
16S-ASV41	<i>Pseudophaeobacter</i> sp.	0.3	2.7	2.1
16S-ASV27	<i>Alteromonas mediterranea</i>	0.1	2.3	1.95
16S-ASV19	<i>Alteromonas</i> sp.	0.1	2.3	1.92
16S-ASV14	Flavobacteriaceaea	1.7	1.9	1.89
16S-ASV28	<i>Aestuariibacter</i> sp.	0.0	2.2	1.85
16S-ASV4	<i>Alteromonas</i> sp.	3.4	1.7	1.83
16S-ASV45	<i>Alteromonas</i> 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	<i>Erythrobacter</i> sp.	0.1	1.9	1.62

b)		Relative abundance (%)			SIMPER C to D	SIMPER D to G
		Control	D	G		
ASV	Taxonomic affiliation					
16S-ASV6	<i>Erythrobacter</i> sp.	0.81	6.64	8.47	6.05	6.19
16S-ASV49	<i>Dokdonia</i> sp.	0.20	4.89	0.45	5.02	6.05
16S-ASV10	<i>Alteromonas</i> 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	<i>Alteromonas</i> sp.		1.70	5.08		4.25
16S-ASV28	<i>Aestuariibacter</i> sp.	0.02	2.80	0.75	2.89	3.29

16S-ASV48	<i>Synechococcus</i> 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	<i>Alteromonas mediterranea</i>	0.18	2.69	-	2.6	-
16S-ASV17	OM60	1.43	3.73	-	2.41	-
16S-ASV19	<i>Alteromonas</i> sp.	0.13	2.20	1.41	2.15	1.82
16S-ASV33	Flavobacteria NS5	2.55	0.50	-	2.15	-
16S-ASV2	<i>Synechococcus</i> C9902	2.61	0.55		2.14	-
16S-ASV7	Rhodospirillales AEGEAN169	3.99	2.05		2.01	-
16S-ASV8	<i>Alteromonas marina</i>	0.49	2.27	5.85	1.88	4.5
16S-ASV20	Flavobacteria NS4	2.14	0.45		1.75	-
16S-ASV51	<i>Alteromonas</i> sp.	0.12	1.72	1.14	1.7	2.1
16S-ASV27	<i>Alteromonas mediterranea</i>	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	<i>Erythrobacter</i> sp.		1.42	2.44		2.08

c)

ASV	Taxonomic affiliation	Relative abundance (%)				SIMPER C to G24h	SIMPER C96h to GD96h
		Control	G24h	C96h	GD96h		
16S-ASV6	<i>Erythrobacter</i> sp.	1.40	10.81	0.94	8.42	8.35	8.17
16S-ASV36	<i>Celeribacter</i> sp.			10.52	2.46		8.81
16S-ASV12	Verrucomicrobia Opitulales			9.36	1.31		8.8
16S-ASV9	<i>Prochlorococcus</i> MIT9313	9.37	0.34			7.52	
16S-ASV2	<i>Synechococcus</i> C9902			12.36	19.06		7.33
16S-ASV28	<i>Aestuariibacter</i> sp.	0.11	6.85	0.09	2.67	5.62	2.82
16S-ASV10	<i>Alteromonas</i> sp.	0.86	6.82	0.73	3.03	5.05	2.52
16S-ASV19	<i>Alteromonas</i> sp.	0.63	6.23			4.67	
16S-ASV18	<i>Alteromonas mediterranea</i>	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	<i>Alteromonas mediterranea</i>	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	Flavobacteriaceae	1.42	3.93	5.94	7.44	2.09	3.45
16S-ASV78	<i>Thalassobius</i> sp.			3.26	1.35		2.08
16S-ASV8	<i>Alteromonas marina</i>	0.71	2.76			2.01	
16S-ASV16	<i>Alteromonas</i> sp.	0.47	2.12			1.55	

Table S2. 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) ASV	Taxonomic affiliation	Relative abundance (%)		SIMPER
		Control	DG24h	
18S-ASV2754	<i>Heterocapsa rotundata</i>	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	<i>Gonyaulax</i> sp.	0.3	2.3	1.94
18S-ASV1197	Uncultured Syndiniales	3.5	4.9	1.84
18S-ASV1917	<i>Heterocapsa rotundata</i>	1.5	3.2	1.72
18S-ASV2742	Uncultured Syndiniales	1.6	1.2	1.64
18S-ASV2112	<i>Gyrodinium</i> sp.	1.8	0.2	1.6
18S-ASV1155	Uncultured Gymnodiniales	1.0	1.6	1.43
18S-ASV2479	<i>Tripos Muelleri</i>	0.8	1.4	1.33
18S-ASV2116	<i>Tripos Furca</i>	0.5	1.6	1.31
18S-ASV173	<i>Amoebophrya</i> sp. Syndiniales	1.2	2.1	1.09
18S-ASV1770	Uncultured dinophyceae	1.4	0.3	1.06

b) ASV	Taxonomic affiliation	Relative abundance (%)			SIMPER C to D72h	SIMPER D72h to G72h
		Control	D72h	G72h		
18S-ASV621	Uncultured Gymnodiniales	15.2	3.4		5.92	
18S-ASV2754	<i>Heterocapsa rotundata</i>	19.4	8.3	27.0	5.57	13.3
18S-ASV1500	<i>Karlodinium veneficum</i>	9.0	3.6	11.5	2.74	5.62
18S-ASV1917	<i>Heterocapsa rotundata</i>	4.1	0.6	8.3	1.79	5.49
18S-ASV1086	Peridinales	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	<i>Emiliana huxleyi</i>	0.8	3.3		1.22	
18S-ASV1058	Uncultured Gymnodiniales	0.4	2.8	0	1.17	1.99

18S-ASV2509	<i>Tripos sp.</i>	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)

ASV	Taxonomic affiliation	Relative abundance (%)			SIMPER C to DG24h	SIMPER DG24h to DG96h
		Control	DG24h	DG96h		
18S-ASV1500	<i>Karlodinium veneficum</i>	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	<i>Heterocapsa rotundata</i>	12.9	7.7	8.7	5.89	1.93
18S-ASV1227	<i>Protodinium sp.</i>		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	<i>Heterocapsa rotundata</i>	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	<i>Heterocapsa rotundata</i>	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	<i>Heterocapsa rotundata</i>	3.3	2.6		1.5	
18S-ASV9	<i>Emiliania huxleyi</i>	1.9	0.6	8	1.48	8.5

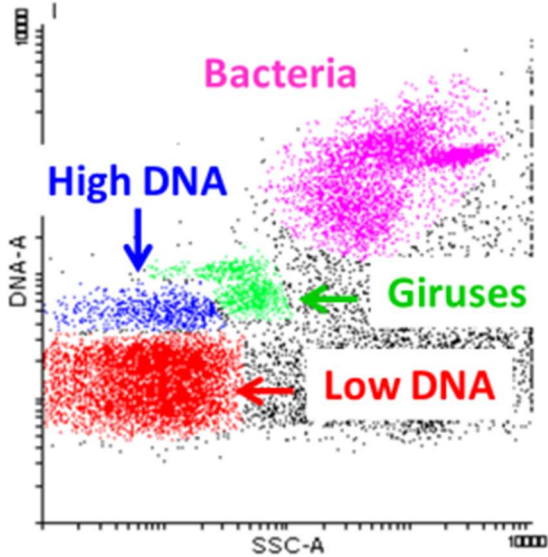


Figure S1: Determination of the viral populations by flow cytometry

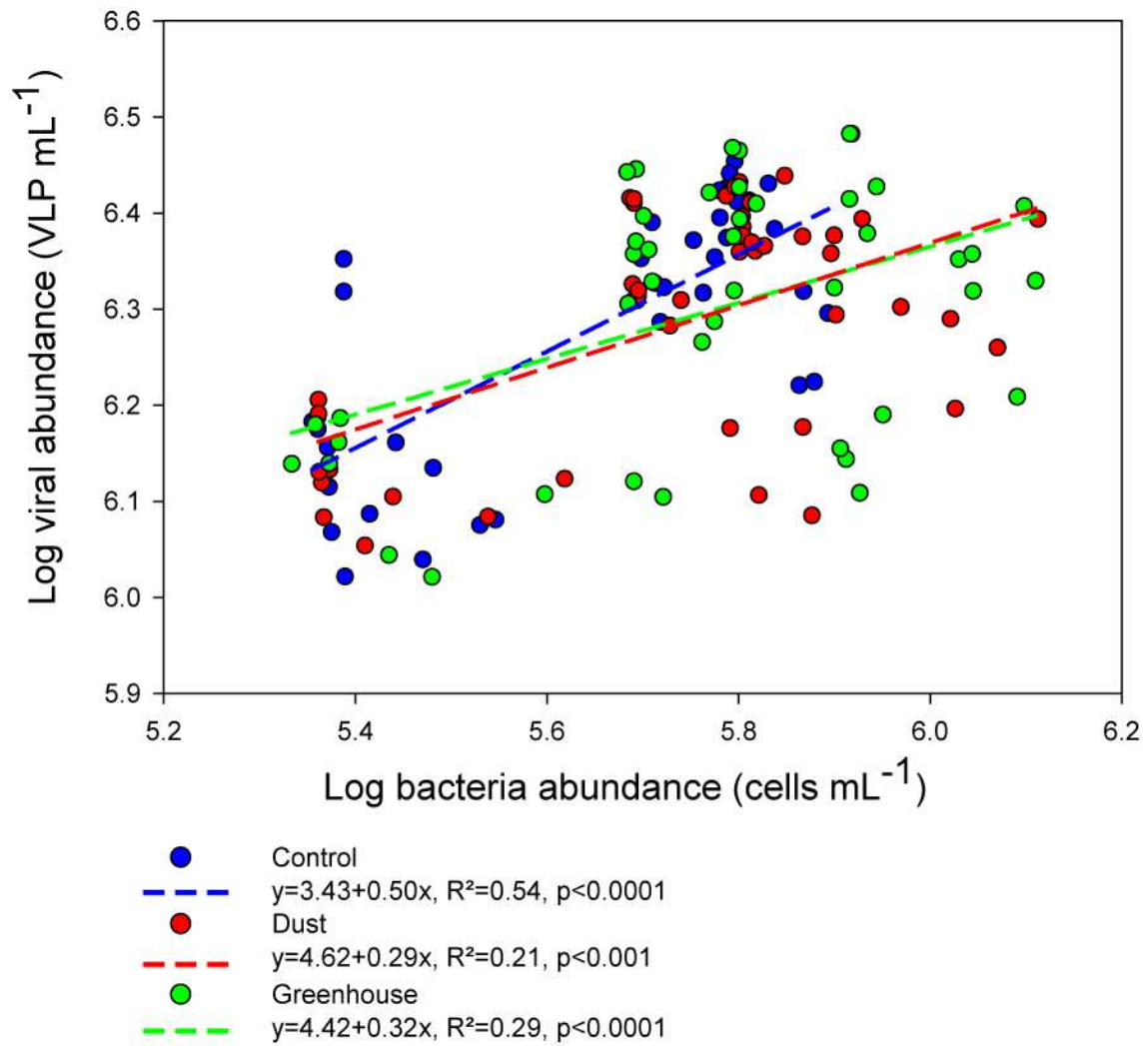


Figure S2. Log transformed relationship between bacterial and viral abundance in the three treatments. Dotted lines represent linear regressions for each treatment.

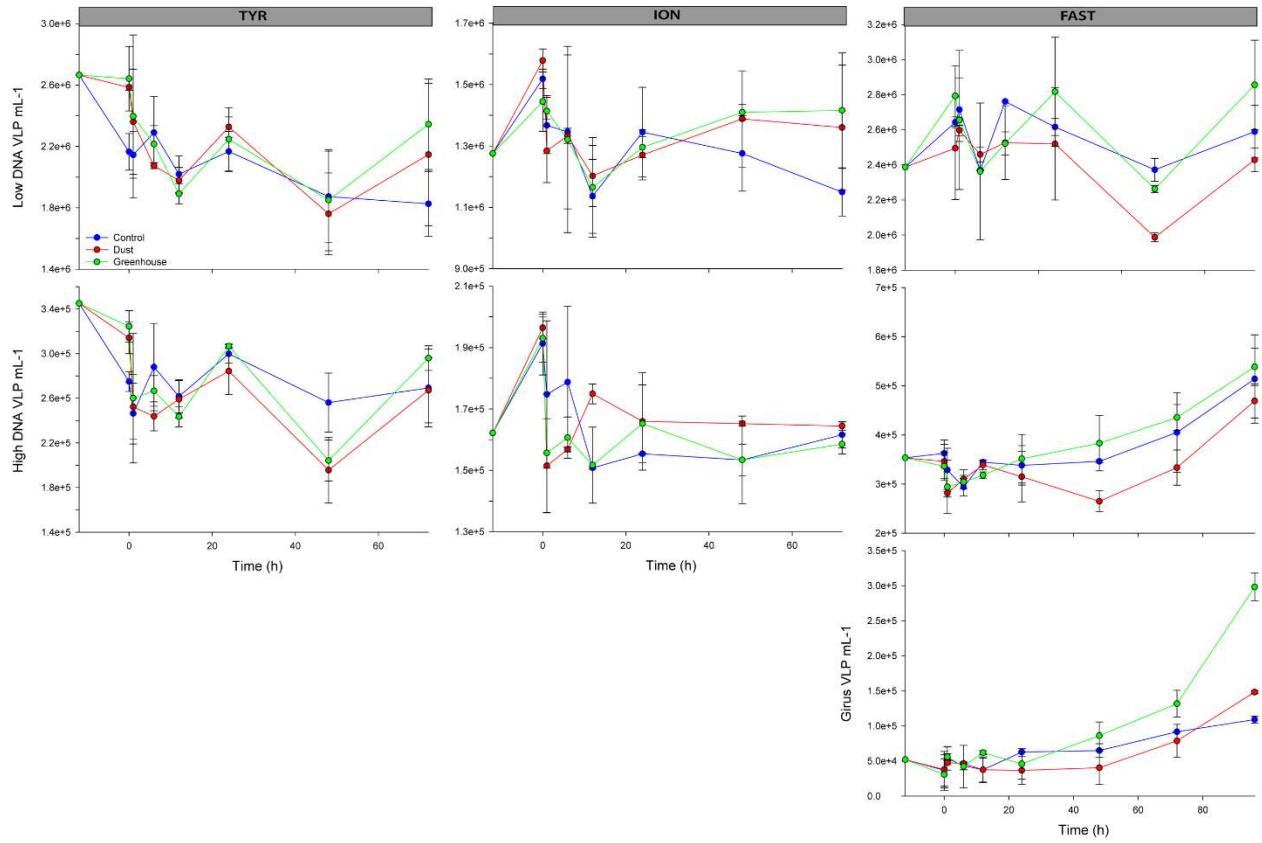


Figure S3. Evolution of Virus like particles abundances (VLP) of three different viral populations over the course of the three experiments (TYR, ION and FAST). The first row represents low DNA viruses or phages, the second row represents high DNA viruses, and the third row represents giant viruses (Giruses).

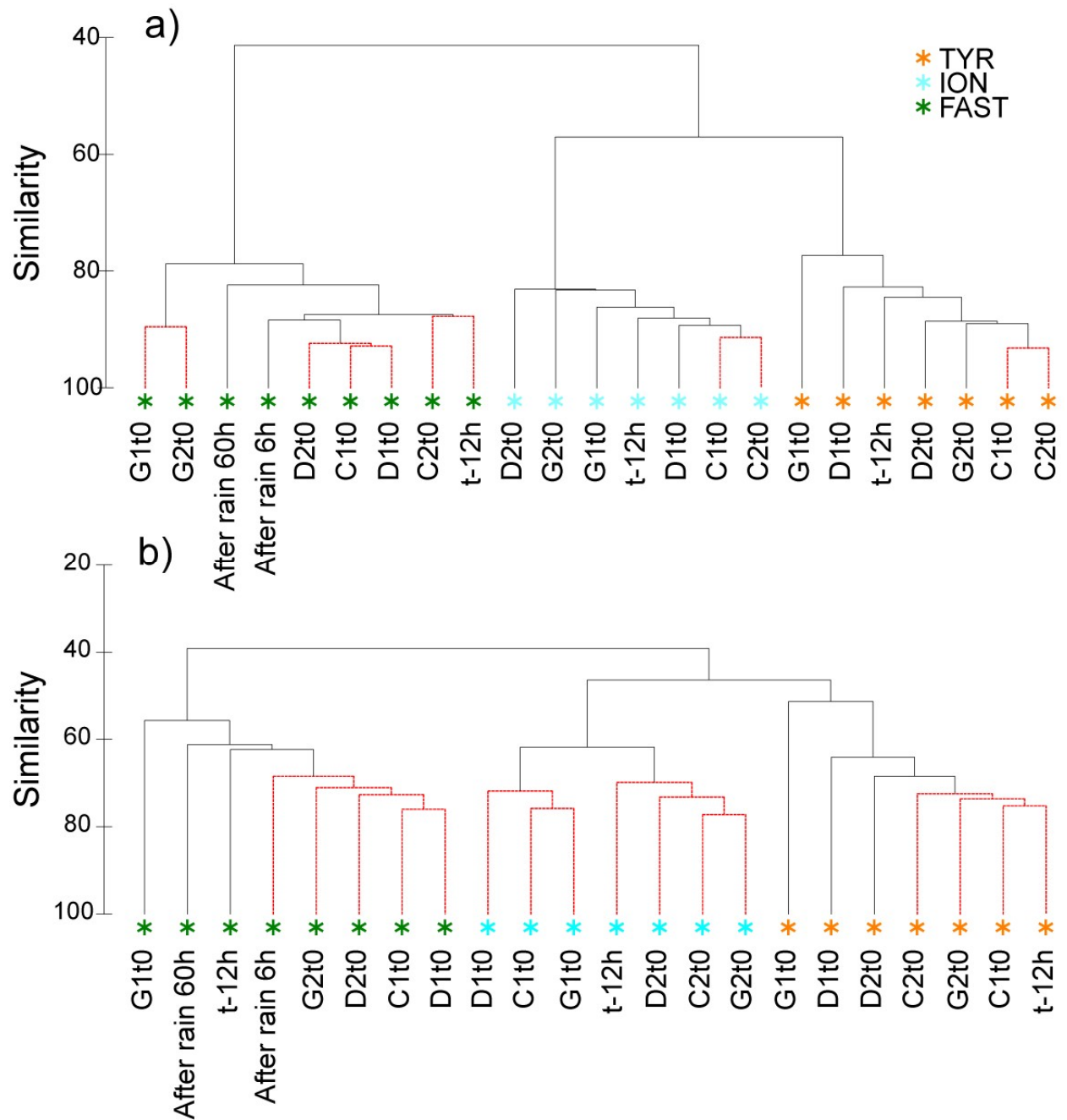


Figure S4. Bray-Curtis clustering showing the difference in microbial community in the initial waters of the 3 experiments, a) bacterial community composition (16S rDNA) and b) micro-eukaryotes community composition (18S rDNA) at the start of the three experiments in the initial water (t-12h) and when the dust was added (t0). Red cluster show samples with no significant differences (based on SIMPROF test).

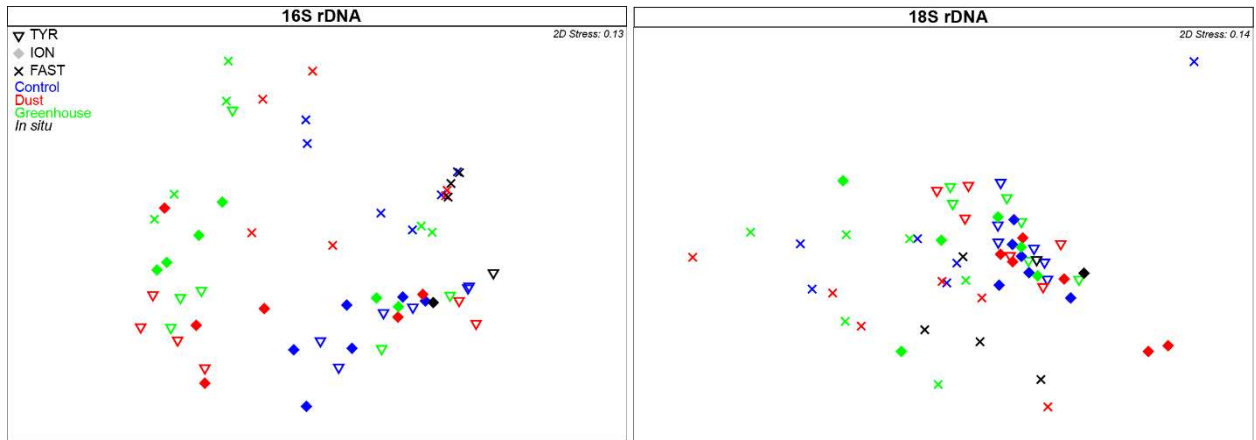


Figure S5: nMDS plots of bacterial (16S rDNA) and micro-eukaryotes (18S rDNA) community composition during the three experiments, based on Bray-Curtis dissimilarity.

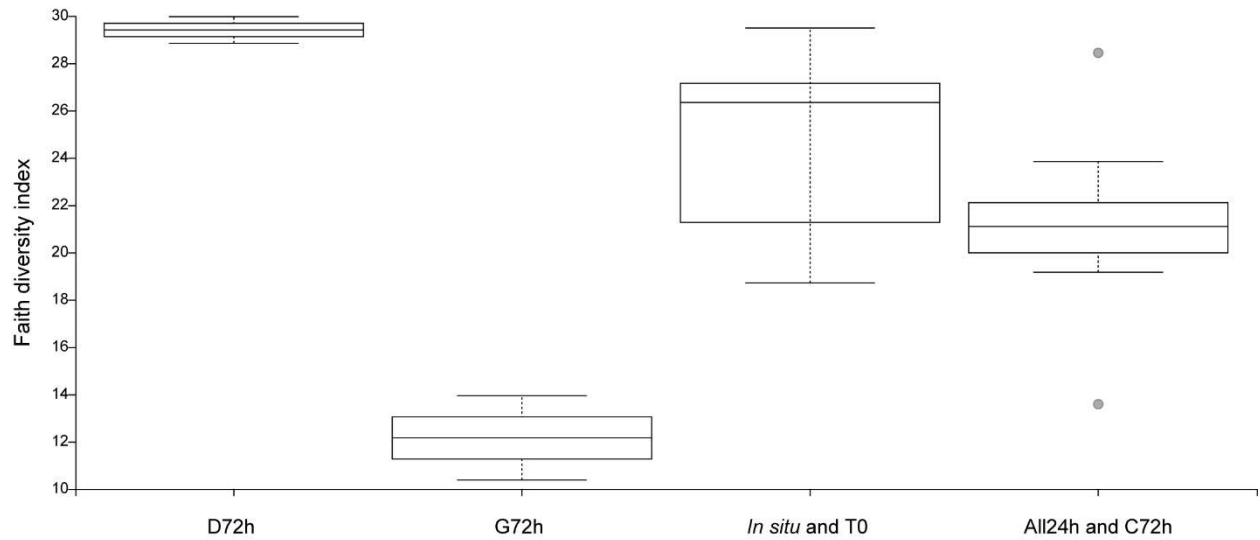


Figure S6. Diversity index (Faith index) between 18S rDNA community of the clusters from Fig. 4 during experiment ION.