Table S1: Information on primers used for algae and viruses in this study											
Target	Forward primer sequence $(5' - 3')$	Reverse primer sequence $(5' - 3')$	Product	Reference							
organism			size								
			(bp)								
Emiliania	TCAAGCAGGCAGTCG	CACCAGAGTCCTATTTCA	58	Nejstgaard							
huxleyi				et al.,							
				2008							
Micromonas	CCGCGGTAATTCCAGCTC	CGCGTCCTCTACAGGAAGTTG	135	Zhu et al.,							
sp.				2003							
Emiliania	ACGCACCCTCAATGTATGGAAGG	RTSCRGCCAACTCAGCAGTCGT	90	Pagarete							
huxleyi				et al.,							
virus				2009;							
				Mayers et							
				al., 2021							
Micromonas	GACGAGTCCAAGAAGGC	CGGACCTCGTGGTACTG	134	This study							
<i>pusilla</i> virus											

Text S1. Supplementary information regarding *Micromonas pusilla virus* PCR assay design and optimisation.

To design an assay specific to *Micromonas pusilla* virus (MpV), we obtained two virus strains (MpV-02T and MpV-08T) and cloned, and sanger sequenced their major capsid proteins using primers from Larsen et al., 2008. The obtained sequences were aligned using Clustal Omega (Sievers et al., 2011) as implemented in the EMBL-EBI web portal (https://www.ebi.ac.uk/Tools/msa/clustalo/). From these aligned sequences, we designed a ddPCR assay using the forward primer (5'-GACGAGTCCAAGAAGGC-3') and reverse primer (5'-CGGACCTCGTGGTACTG-3') (Table S1). These primers were tested against the two MpV strains, a water sample taken from day 18 of the mesocosm experiment and filtered sequentially through 3µm and GF/F (Whatman) filters to remove cells (see Mayers et al., 2021). To confirm correct amplification, the products were cloned and Sanger sequenced. Nucleotide blast searches of the NCBI nt/nr database revealed all cloned sequences gave best blastn hit to cultured MpV sequences, or uncultured Phycodnaviridae from Raunefjorden which we believe to be MpV. The primers were also tested for specificity against 3 other common algae viruses (Figure S1) and showed specificity only to MpV and no other algae viruses tested.

References:

Larsen JB, Larsen A, Bratbak G, Sandaa RA (2008) Phylogenetic Analysis of Members of the Phycodnaviridae Virus Family, Using Amplified Fragments of the Major Capsid Protein Gene. Applied and Environmental Microbiology, 74, 10 <u>https://doi.org/10.1128/AEM.02548-07</u>

Mayers KMJ, Lawrence J, Sandnes Skaar K, Töpper JP, Petelenz E, Rydningen Saltvedt M, Sandaa RA, Larsen A, Bratbak G, Ray JL (2021) Removal of large viruses and their dispersal through fecal pellets of the appendicularian Oikopleura dioica during Emiliania huxleyi bloom conditions. Limnol Oceanogr 66:3963–3975 https://doi.org/10.1002/lno.11935

Sievers F, Wilm A, Dineen D, Gibson TJ, Karplus K, Li W, Lopez R, McWilliam H, Remmert M, Söding J, Thompson JD, Higgings DG (2011) Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. Mol. Syst. Biol. 7: 1-6 <u>https://doi.org/10.1038/msb.2011.75</u>



Figure S1. Specificity of the droplet digital PCR detection for *Micromonas pusilla* virus major capsid protein (*mcp*) gene. Scatterplots show individual fluorescence measurements for all droplets during ddPCR reaction, the y-axis show the relative EvaGreen fluorescence (Ch1 amplitude) while individual samples are shown along the x-axis. Horizontal magenta line displays manually set cut-off between positive (blue) and negative (grey) droplets. Viruses used to test specificity included MpV-02T and MpV08-T (left are using 250 nM primer concentration which was used in our study, and right two are with 150 nM primer concentration), and *Chrysochromulina ericina* virus (CeV), *Phaeocystis pouchetii* virus (PpV) and *Emiliania huxleyi* virus (EhV) and non-template control (negative, NTC).



Figure S2. Contribution to flow cytometry carbon by the four groups of phytoplankton (EHUX = *E. huxleyi*, NEUK = nanoeukaryotes, PEUK = picoeukaryotes and SYN = *Synechococcus* spp.)

Table S2: Rates calculated from dilution experiments for total chlorophyll-*a*, picoeukaryotes, nanoeukaryotes, *E. huxleyi* and *Synechococcus* sp. Rates are uncorrected due to negative grazing rates. Viral lysis is calculated as viral lysis – grazing rates. * indicates that rates were significantly (p < 0.1) different between undiluted and diluted (20% FSW) seawater and between FSW and TFF for viral lysis rates. ND indicated not determined for that experiment. ± values are standard deviation of the measurements. Flow cytometry measurements for D20 and D21 were pooled so represent 1 experiment.

Date	ate Chlorophyll-a			Picoeukaryotes			Synechococcus sp.			Emiliania huxleyi			Nanoeukaryotes		
	Growt	Grazin	Viral	Growt	Grazin	Viral	Growt	Grazin	Viral	Growt	Grazin	Viral	Growt	Grazin	Viral
	h (d⁻¹)	g (d ⁻¹)	lysis	h (d⁻¹)	g (d⁻¹)	lysis	h (d ⁻¹)	g (d⁻¹)	lysis	h (d⁻¹)	g (d⁻¹)	lysis	h (d⁻¹)	g (d⁻¹)	lysis
			(d ⁻¹)			(d ⁻¹)			(d ⁻¹)			(d ⁻¹)			(d ⁻¹)
D1	0.44	0.35*	-0.11	-0.22	-0.17	-0.29	-0.02	0.04	-0.10	-0.39	-0.01	-0.23	0.74	0.24*	-0.04
	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±
	0.08)	0.08)	0.16)	0.02)	0.02)	0.08)	0.11)	0.11)	0.20)	0.71)	0.71)	1.77)	0.10)	0.10)	0.16)
								-						-	
D3	0.59	0.35*	-0.08	0.51	0.21*	-0.10	-0.03	0.00	0.04	0.08	0.45	0.47	0.26	0.07	0.21*
	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±
	0.05)	0.05)	0.12)	0.02)	0.02)	0.07)	0.07)	0.07)	0.13)	0.30)	0.30)	0.74)	0.19)	0.19)	0.26)
D 0	0.00	0.00*	0.00	0.00	0.00*	0.00	0.04	0.00*	0.40	0.04	1.00	0.00	0.44	0.14	0.00*
D6	0.22	0.29*	0.00	0.23	0.63*	-0.06	-0.01	0.33*	-0.12	0.94	1.29	-0.60	-0.41	-0.14	0.28*
	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±
	0.04)	0.04)	0.20)	0.02)	0.02)	0.11)	0.05)	0.05)	0.17)	0.75)	0.75)	1.71)	0.09)	0.09)	0.11)
D8	-0.03	0.00	0.12	0.30	0.29*	0.02	0.09	0.01	-0.08	-0.30	-0.41	0.65	-0.56	-0.22	0.11
	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±
	0.10)	0.10)	0.20)	0.03)	0.03)	0.06)	0.01)	0.01)	0.10)	0.51)	0.51)	0.70)	0.11)	0.11)	0.17)
								-						-	
D10	-0.43	0.08*	0.18	-0.28	0.13	0.12	0.10	0.05	-0.04	-0.01	0.40	-0.01	-0.38	0.06	-0.13
	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±
	0.09)	0.09)	0.17)	0.09)	0.09)	0.13)	0.05)	0.05)	0.07)	0.11)	0.11)	0.21)	0.11)	0.11)	0.21)
1							1	1	1						

D12	-0.14	-0.11	-0.03	0.07	0.14*	-0.27	-0.07	0.24*	-0.04	0.03	0.42	0.21	0.09	0.20*	-0.37
	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±
	0.11)	0.11)	0.23)	0.04)	0.04)	0.10)	0.05)	0.05)	0.08)	0.06)	0.06)	0.30)	0.06)	0.06)	0.14)
D13	0.42	0.34*	-0.02	-0.15	0.10*	0.08	-0.14	0.21*	-0.02	0.02	0.35	0.44	-0.09	0.02	0.05
	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±
	0.04)	0.04)	0.09)	0.10)	0.10)	0.14)	0.01)	0.01)	0.06)	0.13)	0.13)	0.39)	0.08)	0.08)	0.24)
D14	0.47	0.19*	-0.36	-0.16	-0.17	-0.03	0.04	0.11	-0.24	0.32	-0.31	0.33*	-0.32	-0.18	0.13
	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±
	0.15)	0.15)	0.25)	0.01)	0.01)	0.03)	0.07)	0.07)	0.09)	0.02)	0.02)	0.09)	0.07)	0.07)	0.14)
D15	0.22	0.22*	0.14	0.20	0.27*	-0.42	0.20	0.09	-0.09	0.27	0.25*	0.02	-0.86	-0.33	-0.05
	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±
	0.17)	0.17)	0.25)	0.07)	0.07)	0.10)	0.14)	0.14)	0.19)	0.06)	0.06)	0.08)	0.15)	0.15)	0.34)
D16	0.10	0.14*	0.34*(0.00	0.21*	-0.47	0.29	0.07	0.00	-0.14	-0.06	0.38*	-0.20	0.11	0.24
	(±	(±	±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±
	0.03)	0.03)	0.14)	0.03)	0.03)	0.08)	0.01)	0.01)	0.07)	0.13)	0.13)	0.15)	0.45)	0.45)	0.78)
D17	0.15	0.28	-0.04	0.09	0.29*	-0.72	0.16	-0.05	-0.04	-0.05	-0.19	0.71*	-0.02	1.73*	0.24
	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±
	0.05	0.05)	0.18)	0.02)	0.02)	0.05)	0.02)	0.02)	0.05)	0.01)	0.01)	0.05)	0.17)	0.17)	0.19)
D18	-0.06	0.01	-0.01	0.04	0.20*	-0.04	-0.03	-0.01	-0.09	-0.48	-0.02	-0.24	3.77	2.69*	-0.35
	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±
	0.07)	0.07)	0.13)	0.08)	0.08)	0.13)	0.01)	0.01)	0.03)	0.12)	0.12)	0.26)	0.11)	0.11)	0.26)
D19	0.17	0.35*	0.15	-0.42	0.26	0.04	-0.05	0.06	0.00	-0.06	0.00	-0.33	ND	ND	ND
	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±			
	0.12)	0.12)	0.29)	0.23)	0.23)	0.53)	0.04)	0.04)	0.04)	0.05)	0.05)	0.24)			
1	1													1	1

D20	0.37	0.44*	0.03	0.00	0.21*	-0.47	0.29	0.07	0.00	-0.14	-0.06	0.38*	-0.20	0.11	0.33
	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±
	0.16)	0.16)	0.22)	0.03)	0.03)	0.08)	0.01)	0.01)	0.07)	0.13)	0.13)	0.15)	0.45)	0.45)	0.78)
D21	-0.29	-0.05	-0.12	0.00	0.21*	-0.47	0.29	0.07	0.00	-0.14	-0.06	0.38*	-0.20	0.11	0.33
	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±
	0.01)	0.01)	0.10)	0.03)	0.03)	0.08)	0.01)	0.01)	0.07)	0.13)	0.13)	0.15)	0.45)	0.45)	0.78)
D22	-0.16	0.04*	-0.03	-0.71	0.09*	0.14	0.05	0.00	-0.01	-0.36	-0.08	0.05	ND	ND	ND
	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±	(±			
	0.06)	0.06)	0.08)	0.11)	0.11)	0.22)	0.01)	0.01)	0.05)	0.01)	0.01)	0.17)			



Figure S3. Comparison of ddPCR calculated growth rates from 0.6 μ m filters for *Micromonas* (A, B) and *E. huxleyi* (C, D) against the dilution estimated intrinsic growth rates (μ ; A, C) and net growth rates from 100% WSW incubations (B, D). Dashed line indicates 1:1 line.