

Supplementary information

**Zooming on dynamics of marine microbial communities in the phycosphere of *Akashiwo sanguinea*
(Dinophyta) blooms**

Running title: Microbial dynamics in *Akashiwo sanguinea* HABs

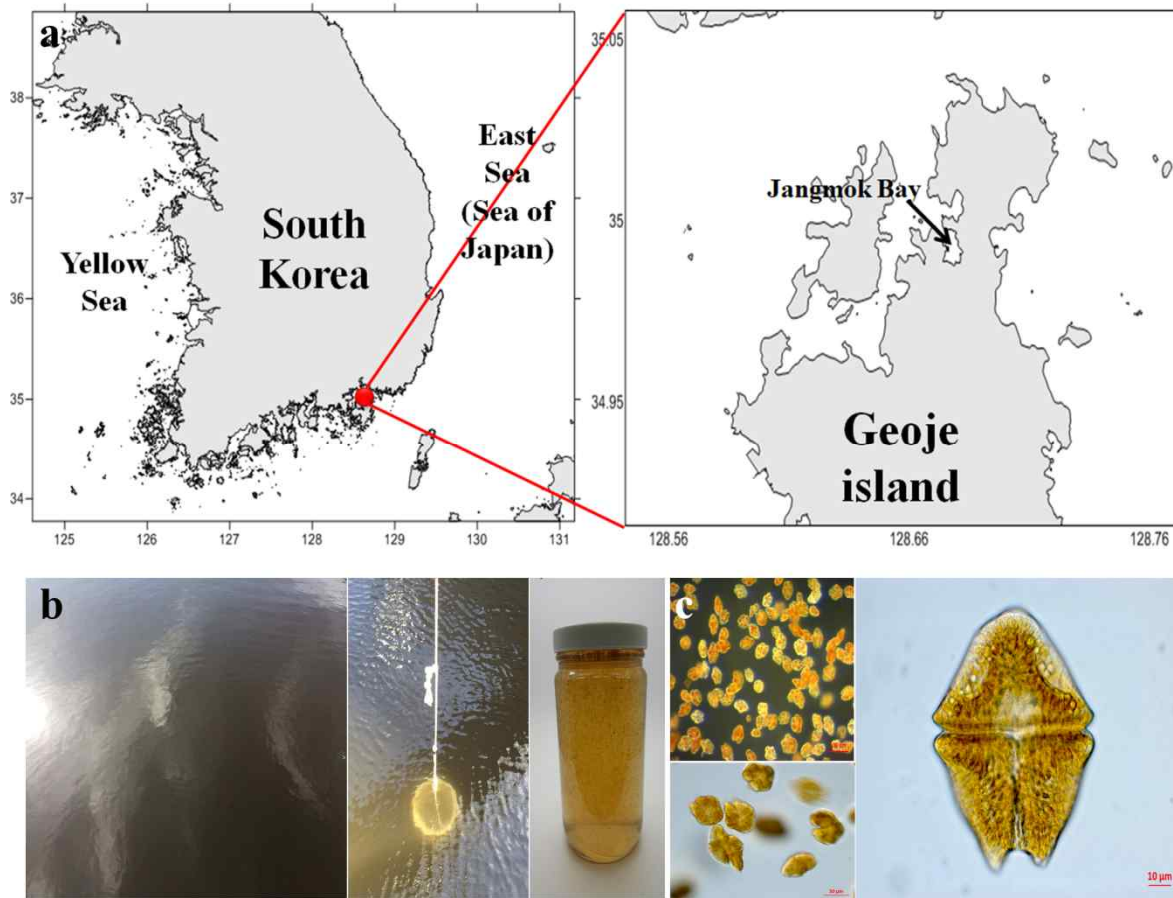
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20 **Supplementary Figures**

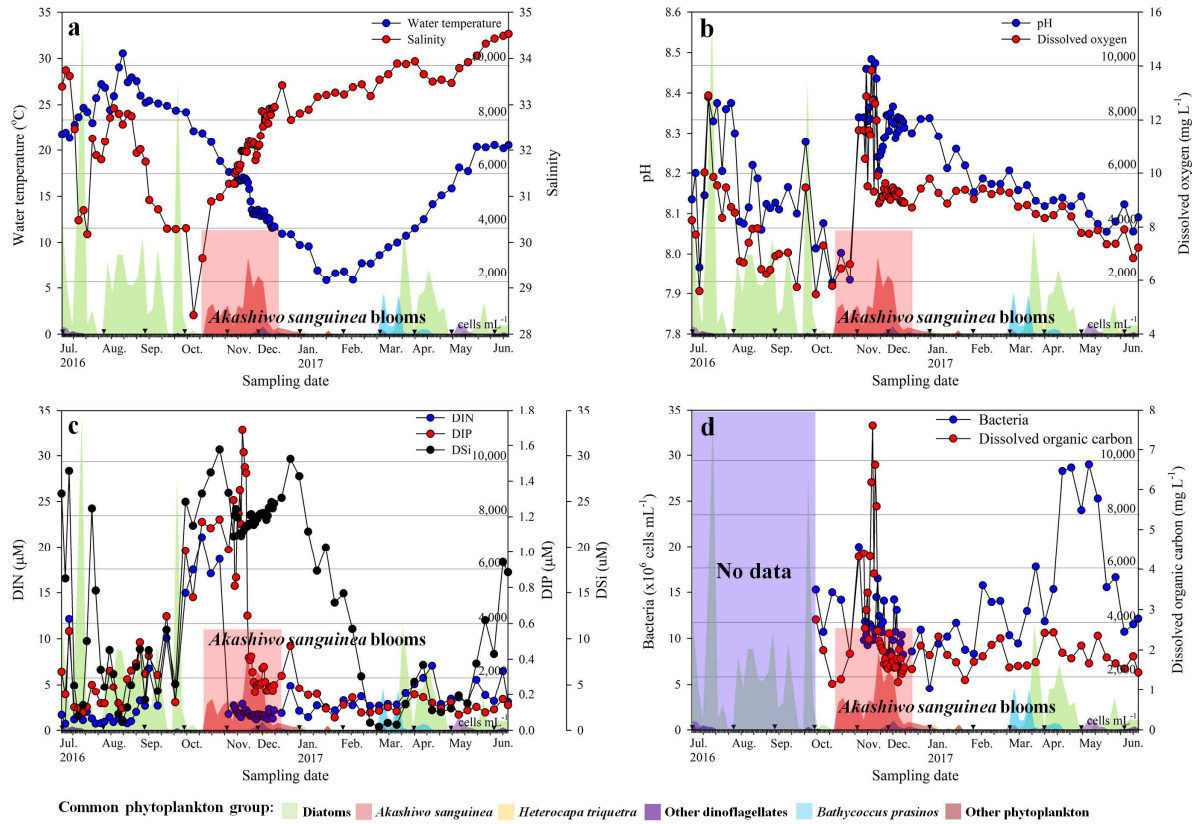


21

22 **Supplementary Figure 1.** Sampling site located in Jangmök Bay Time-series Monitoring Site (JBTMS: 34° 59'

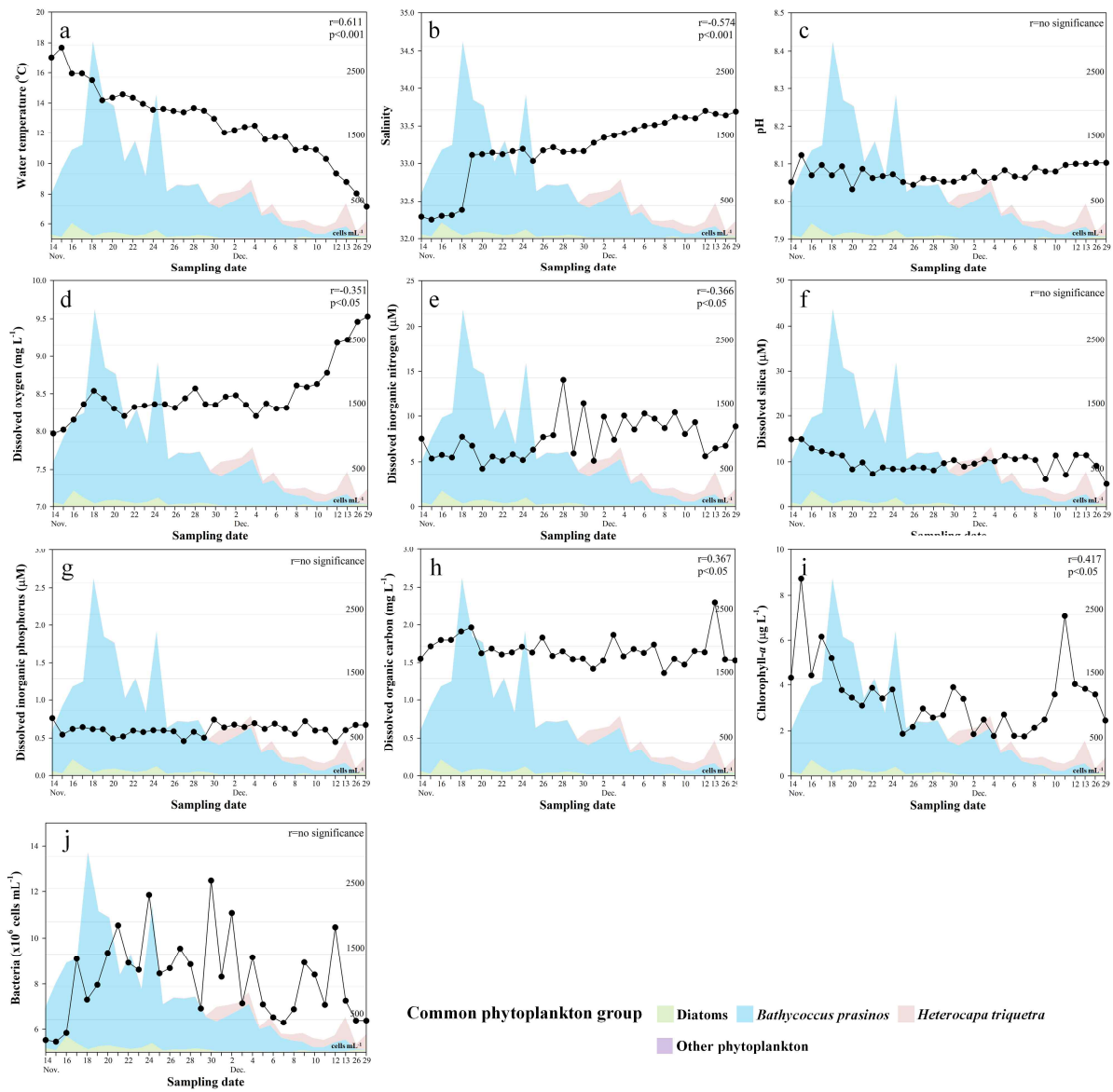
23 37'' N and 128° 40' 27'' E), a semi-closed bay on the southern coast of South Korea, a, b, sea water colour in

24 *Akashiwo sanguinea* bloom; c, light microscopic observation of *Akashiwo sanguinea* cells.



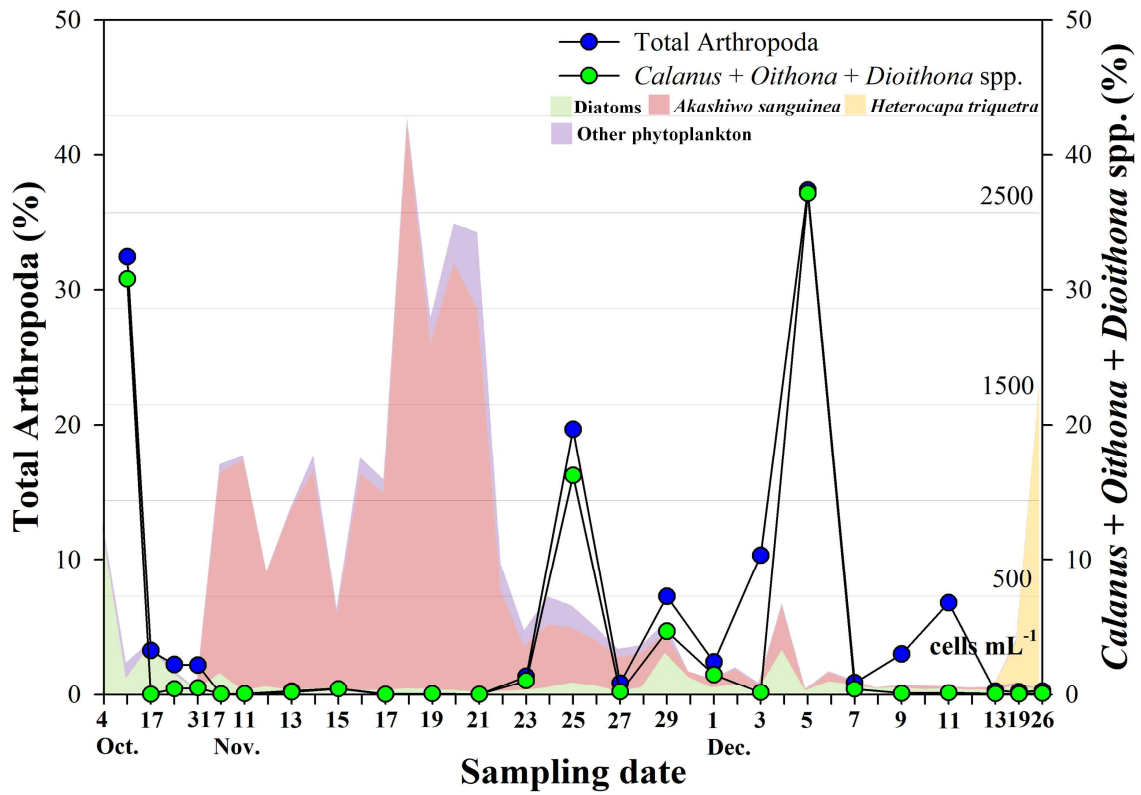
25

26 **Supplementary Figure 2.** Weekly and daily changes in the measured environmental factors and phytoplankton
 27 communities in Jangmok Bay Time-series Monitoring Site (JBTMS) from June 2016 to June 2017. a, water
 28 temperature and salinity; b, pH and dissolved oxygen; c, dissolved inorganic nitrogen (DIN), dissolved
 29 inorganic phosphorus (DIP), and dissolved silica (DSi); d, total bacterial abundance and dissolved organic
 30 carbon concentration.



31

32 **Supplementary Figure 3.** Daily changes in environmental factors under dominant presence of the pico-sized
 33 green alga, *Bathycoccus prasinos* in 2017. a, water temperature; b, salinity; c, pH; d, dissolved oxygen; e,
 34 dissolved inorganic nitrogen; f, dissolved silica; g, dissolved inorganic phosphorus; h, dissolved organic
 35 carbon; i, chlorophyll-*a*; j, total bacteria abundance. Coloured areas in the figure correspond to the common
 36 phytoplankton groups in 2017. *r* value in each figure (upper right) indicates Pearson correlation coefficient
 37 between changes in each environmental factor and *B. prasinos* abundance.



38

39 **Supplementary Figure 4.** Daily changes in relative abundance (%) of the microzooplankton (total Arthropoda)
 40 communities and *Akashiwo sanguinea* feeding herbivores (*Calanus* spp. + *Oithona* spp. + *Dioithona* spp.)
 41 obtained from metagenomic next-generation sequencing during *Akashiwo sanguinea* blooms in 2016, The
 42 coloured areas in the figure correspond to the common phytoplankton groups in 2016.

43 **Supplementary Tables**44 **Supplementary Table 1.** Experimental information for PCR amplification of V3-V4 regions in 16s rDNA

Target region	Step	Primer		PCR reaction mixtures (total 25- μ L)	PCR condition	Reference
		Forward	Reverse			
16s rDNA (V3-V4 region)	First PCR	Illumina preadapter +Sequencing primer sequence+341F (5'- CCTACGGGN GGCWGCAG-3')	Illumina preadapter +Sequencing primer sequence+800R (5'- TACCAGGGT ATCTAATCC-3')	200 μ mol L ⁻¹ each dNTP, 1.5 mmol L ⁻¹ MgCl ₂ , 0.3 μ mol L ⁻¹ each primer, 2.5 U Taq DNA polymerase (TaKaRa, EX Taq, Kyoto, Japan), and DNA template (20 ng μ L ⁻¹)	initial denaturation step at 95°C for 3 min, followed by 35 cycles of denaturation at 95°C for 10 s, annealing at 52°C for 45 s, and extension at 72°C for 1 min, and a final extension step of 72°C for 5 min.	
	Second PCR	Illumina preadapter +Sequencing primer sequence+341F (5'- CCTACGGGN GGCWGCAG-3')	Illumina preadapter +Sequencing primer sequence+800R (5'- TACCAGGGT ATCTAATCC-3')	200 μ mol L ⁻¹ each dNTP, 1.5 mmol L ⁻¹ MgCl ₂ , 0.3 μ mol L ⁻¹ each primer, 2.5 U Taq DNA polymerase (TaKaRa, EX Taq, Kyoto, Japan), and DNA template (800 ng), and Nextera XT index Kit (Illumina, CA, USA)	initial denaturation step at 95°C for 3 min, followed by 12 cycles of denaturation at 95°C for 10 s, annealing at 52°C for 45 s, and extension at 72°C for 1 min, and a final extension step of 72°C for 5 min.	1, 2
	Pooling	Triplicate reaction products (same amount) were pooled and purified using an Qiaquick PCR purification Kit (No. 28104, Qiagen Inc.). Their DNA concentration was measured in a Bio-analyzer 2100 (Agilent Technologies, Palo Alto, CA, USA).				

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46 **Supplementary Table 2.** Experimental information for PCR amplification of V4-V5 regions in 18s rDNA

Target region	Step	Primer		PCR reaction mixtures (25- μ L)	PCR condition	Reference
		Forward	Reverse			
18s rDNA (V4-V5 region)	First PCR	Illumina preadapter +Sequencing primer TAREuk454FWD1 (5'-CCAGCASCYGCG GTAATTGG-3')	Illumina preadapter +Sequencing primer sequence+TAREuk REV3 (5'-ACTTTC GTTCTTGATYRA-3')	200 μ mol L ⁻¹ each dNTP, 1.5 mmol L ⁻¹ MgCl ₂ , 0.3 μ mol L ⁻¹ each primer, 2.5 U Taq DNA polymerase (TaKaRa, EX Taq, Kyoto, Japan), and DNA template (20 ng μ L ⁻¹)	initial denaturation step at 95°C for 3 min, followed by 35 cycles of denaturation at 95°C for 10 s, annealing at 52°C for 45 s, and extension at 72°C for 1 min, and a final extension step of 72°C for 5 min.	
	Second PCR	Illumina preadapter +Sequencing primer TAREuk454FWD1 (5'-CCAGCASCYGCG GTAATTGG-3')	Illumina preadapter +Sequencing primer sequence+TAREuk REV3 (5'-ACTTTC GTTCTTGATYRA-3')	200 μ mol L ⁻¹ each dNTP, 1.5 mmol L ⁻¹ MgCl ₂ , 0.3 μ mol L ⁻¹ each primer, 2.5 U Taq DNA polymerase (TaKaRa, EX Taq, Kyoto, Japan), DNA template (600 ng), and Nextera XT index Kit (Illumina, CA, USA)	initial denaturation step at 95°C for 3 min, followed by 12 cycles of denaturation at 95°C for 10 s, annealing at 52°C for 45 s, and extension at 72°C for 1 min, and a final extension step of 72°C for 5 min.	3, 4
	Pooling	Triplicate reaction products (same amount) were pooled and purified using a Qiaquick PCR purification Kit (No. 28104, Qiagen Inc.). Their DNA concentration was measured in a Bio-analyzer 2100 (Agilent Technologies, Palo Alto, CA, USA).				

48 **Supplementary Table 3.** Summary of numbers of read counts and operational taxonomic units (OTUs) of bacterial community (16s rDNA V3-V4 regions) obtained from
 49 metagenomic next-generation sequencing analysis and the alpha-diversity indices of the Jangmok Bay Time-series Monitoring Site in 2016 (*Akashiwo sanguinea* bloom)
 50 and 2017 (No *A. sanguinea* bloom). Group I–IV in 2016 and Group I and II in 2017 were obtained from nMDS analysis presented in Figs. 2a and 2b.

Group	Date	Total sequence (mean)	Read Count (mean)	OTUs (mean)	Chao1 richness (mean)	Shannon diversity (mean)	Simpson evenness (mean)	Remark
Group I	Oct., 4 - 31, 2016	32,298,622-62,271,417 (46,112,019)	73,321-140,807 (104,034)	261-406 (313)	407-677 (489)	2.804-3.680 (3.316)	0.564-0.773 (0.678)	Before <i>A. sanguinea</i> bloom
Group II	Nov., 7 – 28, 2016	7,696,433-44,490,558 (23,987,481)	17,197-99,823 (53,723)	113-220 (162)	157-343 (242)	2.373-4.791 (3.791)	0.538-0.930 (0.821)	During <i>A. sanguinea</i> bloom
Group III	Nov., 13 – 14, 2016	7,397,953-13,327,844 (10,362,899)	16,499-29,667 (23,083)	104-119 (112)	178-199 (188)	2.988-3.107 (3.047)	0.798-0.807 (0.802)	
Group IV	Nov., 29 – Dec., 26, 2016	23,022,820-82,174,372 (54,400,274)	51,437-183,273 (121,405)	179-296 (241)	245-433 (351)	4.380-4.837 (4.614)	0.893-0.939 (0.917)	After <i>A. sanguinea</i> bloom
Group I	Nov., 14 – Dec., 13, 2017	8,656,023-69,720,710 (31,791,259)	19,470-156,620 (71,464)	135-310 (207)	176-434 (288)	3.539-4.295 (3.935)	0.759-0.889 (0.823)	Dominance of <i>B. prasinus</i>
Group II	Dec., 19 – 26, 2017	6,804,524-7,552,004 (7,178,264)	15,400-17,180 (16,290)	105-109 (107)	167-169 (168)	2.971-3.025 (2.998)	0.662-0.768 (0.715)	After decrease of <i>B. prasinus</i>

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52 **Supplementary Table 4.** Summary of numbers of read counts and operational taxonomic units (OTUs) of Nucleo Cytoplasmic Large DNA Viruses (NCLDV) obtained
53 from metagenomic next-generation sequencing analysis of the Jangmok Bay Time-series Monitoring Site in 2016 (*Akashiwo sanguinea* blooming period) and 2017 (No *A.*
54 *sanguinea* bloom period). Groups I–IV were obtained from nMDS analysis presented in Figs. 4a and 4b.

Group	Date	Total sequence (mean)	Number of Virus contigs (mean)	Number of NCLDVs contigs (mean)	NCLDVs OTUs (mean)	Remark
Group I	Oct.24-31, Nov.15, 2016	1,688,012,192-2,358,455,848 (1,986,633,842)	1,557-1,643 (1,605)	1,080-1,241 (1,139)	92-95 (94)	Before <i>A. sanguinea</i> bloom
Group II	Nov. 7-11, 21, 2016	1,464,097,818-1,948,331,006 (1,770,470,006)	498-505 (463)	229-327 (282)	57-69 (64)	Early <i>A. sanguinea</i> bloom
Group III	Nov. 17, 2016	2,233,117,474	361	179	52	
Group IV	Oct.10-17, Nov.13, 19, Nov.23-Dec.26, 2016	1,171,719,382-2,208,330,660 (1,793,789,254)	674-2,594 (1,407)	443-1,962 (1,072)	72-105 (87)	Before, Peak and decline <i>A. sanguinea</i> bloom
Group I	Nov., 15-Dec.19, 2017	1,541,147,082-2,348,387,360 (1,935,432,940)	3,272-5,260 (4,169)	2,789-4,161 (3388)	98-117 (108)	Dominance of <i>B. prasinus</i>
Group II	Dec.26, 2017	2,382,864,316	5,107	3,570	112	After decrease of <i>B. prasinus</i>

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56 **Supplementary Table 5.** Summary of number of read counts and operational taxonomic units (OTUs) of eukaryotic plankton community (18s rDNA V4-V5 regions) at
57 size-fractions of >10 μm (focused on eukaryotic plankton and dinospores of *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2 μm (focused on free-living *Amoebophrya*
58 spp. and nano-sized phytoplankton) obtained from metagenomic next-generation sequencing analysis, and alpha-diversity indices of the Jangmok Bay Time-series
59 Monitoring Site in 2016 (*Akashiwo sanguinea* blooming period). Groups I–III (>10 μm) and Groups I–III (2-0.2 μm) were obtained from nMDS analysis .

Filter size	Group	Sampling date	Total sequence (mean)	Read Count (mean)	OTUs (mean)	Chao1 richness (mean)	Shannon diversity (mean)	Simpson evenness (mean)	Remark
> 10 μm	Group I	Oct. 10-31, 2016	12,478,827-47,051,009 (26,192,373)	30,295-113,485 (63,407)	208-289 (256)	273-353 (328)	3.373-4.983 (4.216)	0.715-0.919 (0.849)	Before <i>A. sanguinea</i> bloom
	Group II	Nov.-7-23, 2016	11,388,538-69,954,522 (48,129,687)	27,244-167,974 (115,268)	59-160 (112)	101-243 (195)	0.108-0.805 (0.313)	0.018-0.275 (0.076)	During <i>A. sanguinea</i> bloom
	Group III	Nov.25-Dec.26	6,547,198-107,637,393 (49,803,387)	15,642-257,281 (118,832)	114-307 (208)	193-403 (300)	0.758-2.437 (1.868)	0.191-0.693 (0.521)	After <i>A. sanguinea</i> bloom
2-0.2 μm	Group I	Nov. 11-21, 2016	20,334,734-33,137,157 (27,951,474)	48,658-78,547 (66,663)	144-234 (185)	156-286 (240)	0.656-2.674 (1.842)	0.119-0.716 (0.455)	During <i>A. sanguinea</i> bloom
	Group II	Nov. 23-Dec.26, 2016	20,987,838-49,915,365 (30,248,955)	50,178-118,849 (72,405)	216-329 (282)	229-389 (327)	2.084-5.916 (4.560)	0.464-0.964 (0.845)	After <i>A. sanguinea</i> bloom
	Group III	Dec. 13, 2016	9,663,458	23,109	201	214	5.940	0.960	
	Group I	Nov. 15 - Dec. 26, 2017	28,278,227-61,578,514 (45,329,554)	68,221-147,961 (108,980)	176-392 (306)	257-454 (367)	2.065-5.285 (3.970)	0.517-0.942 (0.820)	No <i>A. sanguinea</i> bloom
	Group II	Nov. 17, 2017	17,867,369	42,759	207	224	5.698	0.951	

60 **Supplementary Table 6.** Abbreviations and node sizes of significant factors ($P < 0.01$ and $Q < 0.05$) in the
 61 Network analysis displayed in Fig. 7.

2016			2017			Classification
Factor	Abbreviation	Node size	Factor	Abbreviation	Node size	
Temperature	Temp.	0.47	Temperature	Temp.	0.47	Environmental factor
Salinity	Sal.	0.63	Salinity	Sal.	0.67	
pH	pH	0.48	pH	pH	0.39	
Dissolved inorganic phosphorus	DIP	0.26	Dissolved inorganic nitrogen	DIN	0.37	
Dissolved organic carbon	DOC	0.23	Dissolved organic carbon	DOC	0.34	
Chlorophyll- <i>a</i>	Chl- <i>a</i>	0.29	Chlorophyll- <i>a</i>	Chl- <i>a</i>	0.29	
Dissolved oxygen	DO	0.25	Dissolved oxygen	DO	0.35	
Dissolved silica	DSi	0.73				
<i>Akashiwo sanguinea</i>	<i>A.san.</i>	0.63	<i>Adenoides eludens</i>	<i>A.elu.</i>	0.08	
<i>Heterocapsa rotundata</i>	<i>H.rot.</i>	0.23	<i>Akashiwo sanguinea</i>	<i>A.san.</i>	0.21	
Uncultured Stramenopile	U.Str.	0.28	<i>Bathycoccus prasinos</i>	<i>B.pra.</i>	0.49	
			<i>Chaetoceros tenuissimus</i>	<i>C.ten.</i>	0.28	
			<i>Chaetoceros</i> sp.	<i>Cha.sp.</i>	0.30	
			<i>Heterocapsa rotundata</i>	<i>H.rot.</i>	0.36	
			<i>Minutocellus</i> sp.	<i>Min.sp.</i>	0.13	
			<i>Teleaulax amphioxeia</i>	<i>T.amp.</i>	0.44	
			<i>Teleaulax</i> sp.	<i>Tel.sp.</i>	0.40	
			<i>Tetraselmis</i> sp.	<i>Tet.sp.</i>	0.13	
			<i>Thalassiosira oceanica</i>	<i>T.oce.</i>	0.43	
			<i>Pyramimonas australis</i>	<i>P.aus.</i>	0.35	
<i>Acartia omorii</i>	<i>A.omo.</i>	0.13	<i>Clytia hemisphaerica</i>	<i>C.hem.</i>	0.07	Heterotroph
<i>Acartia steueri</i>	<i>A.ste.</i>	0.09	<i>Laackmanniella prolongata</i>	<i>L.pro.</i>	0.30	
<i>Calanus sinicus</i>	<i>C.sin.</i>	0.06	<i>Noctiluca scintillans</i>	<i>N.sci.</i>	0.22	
<i>Oithona davisae</i>	<i>O.dav.</i>	0.09	<i>Strombidium capitatum</i>	<i>S.cap.</i>	0.10	
<i>Paracalanus parvus</i>	<i>P.par.</i>	0.22	<i>Strombidium caudispina</i>	<i>S.cau.</i>	0.18	
<i>Acartia steueri</i>	<i>A.ste.</i>	0.09	<i>Strombidium</i> sp.	<i>Sto.sp.</i>	0.18	
<i>Amoebophrya</i> sp1.	<i>Amo.sp1.</i>	0.21	<i>Amoebophrya</i> sp2.	<i>Amo.sp2.</i>	0.17	Endoparasitic dinoflagellate
<i>Amoebophrya</i> sp2.	<i>Amo.sp2.</i>	0.07	Other Syndiniales	Oth.Syn.	0.11	
Other Syndiniales	Oth.Syn.	0.29				
<i>Ahrensia kielensis</i>	<i>A.kie.</i>	0.44	<i>Amylibacter ulvae</i>	<i>A.ulv.</i>	0.31	Bacteria
<i>Amylibacter ulvae</i>	<i>A.ulv.</i>	0.32	<i>Bizionia arctica</i>	<i>B.arc.</i>	0.46	
<i>Asciadiaceihabitans donghaensis</i>	<i>A.don.</i>	0.25	<i>Cribrihabitans marinus</i>	<i>C.mar.</i>	0.36	
<i>Bizionia arctica</i>	<i>B.arc.</i>	0.29	<i>Euzebya tangerina</i>	<i>E.tan.</i>	0.53	
<i>Botrylloides leachi</i>	<i>B.lea.</i>	0.06	<i>Flaviramulus ichthyoenteri</i>	<i>F.ich.</i>	0.23	
<i>Cribrihabitans marinus</i>	<i>C.mar.</i>	0.34	<i>Fluviicola taffensis</i>	<i>F.taf.</i>	0.24	
<i>Cycloclasticus spirillensus</i>	<i>C.spi.</i>	0.23	<i>Lacinutrix gracilariae</i>	<i>L.gra.</i>	0.54	
<i>Flaviramulus ichthyoenteri</i>	<i>F.ich.</i>	0.32	<i>Lentibacter algarum</i>	<i>L.alg.</i>	0.32	
<i>Fluviicola taffensis</i>	<i>F.taf.</i>	0.17	<i>Lishizhenia caseinilytica</i>	<i>L.cas.</i>	0.25	
<i>Granulosicoccus antarcticus</i>	<i>G.ant.</i>	0.19	<i>Luminiphilus sylvensis</i>	<i>L.syl.</i>	0.38	
<i>Lentibacter algarum</i>	<i>L.alg.</i>	0.36	<i>Mesonia algae</i>	<i>M.alg.</i>	0.35	
<i>Lishizhenia caseinilytica</i>	<i>L.cas.</i>	0.15	<i>Methylophilus methylophilus</i>	<i>M.met.</i>	0.46	
<i>Luminiphilus sylvensis</i>	<i>L.syl.</i>	0.26	<i>Nisaea nitritireducens</i>	<i>N.nit.</i>	0.40	
<i>Mesonia algae</i>	<i>M.alg.</i>	0.36	<i>Novosphingobium acidiphilum</i>	<i>N.aci.</i>	0.31	
<i>Methylophilus methylophilus</i>	<i>M.met.</i>	0.31	<i>Owenweeksia hongkongensis</i>	<i>O.hon.</i>	0.37	
<i>Nisaea nitritireducens</i>	<i>N.nit.</i>	0.38	<i>Planktomarina temperata</i>	<i>P.tem.</i>	0.24	
<i>Novosphingobium acidiphilum</i>	<i>N.aci.</i>	0.35	<i>Reinekea aestuarii</i>	<i>R.aes.</i>	0.31	
<i>Owenweeksia hongkongensis</i>	<i>O.hon.</i>	0.37	<i>Salinirepens amamiensis</i>	<i>S.ama.</i>	0.25	
<i>Phaeocystidibacter marisrubri</i>	<i>P.mar.</i>	0.45	<i>Sedimenticola thiotaurini</i>	<i>S.thi.</i>	0.24	
<i>Planktomarina temperate</i>	<i>P.tem.</i>	0.22	<i>Sedimentitalea todarodis</i>	<i>S.tod.</i>	0.33	
<i>Polaribacter huanghezhanensis</i>	<i>P.hua.</i>	0.17	<i>Tenacibaculum aiptasiae</i>	<i>T.aip.</i>	0.21	
<i>Pseudohongiella spirulinae</i>	<i>P.spi.</i>	0.16				
<i>Tenacibaculum aiptasiae</i>	<i>T.aip.</i>	0.13				
<i>Thiohalobacter thiohalobacter</i>	<i>T.thi.</i>	0.18				
<i>Salinirepens amamiensis</i>	<i>S.ama.</i>	0.27				
<i>Sedimenticola thiotaurini</i>	<i>S.thi.</i>	0.32				
<i>Styela plicata</i>	<i>S.pli.</i>	0.17				
Uncultured Alpha-proteobacterium (OTU #2)	UAp#2	0.18				

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63 **Supplementary Table 6. Continued**

2016			2017			Classification
Factor	Abbreviation	Node size	Factor	Abbreviation	Node size	
<i>Acanthocystis turfacea</i> chlorella virus 1	AtcV1	0.30	<i>Acanthamoeba polyphaga</i> moumouvirus	ApmoV	0.76	NCLDV's
<i>Bathycoccus</i> sp. RCC1105 virus BpV1	BpV1	0.57	<i>Aureococcus anophagefferens</i> virus	AaV	0.67	
<i>Cafeteria roenbergensis</i> virus BV-PW1	CrVBV-PW1	0.65	<i>Bathycoccus</i> sp. RCC1105 virus BpV1	BpV1	0.37	
<i>Cedratvirus</i> A11	CV-A11	0.23	<i>Cafeteria roenbergensis</i> virus BV-PW1	CrVBV-PW1	0.56	
<i>Chrysochromulina ericina</i> virus	CeV	0.50	<i>Chrysochromulina ericina</i> virus	CeV	0.52	
<i>Diachasmimorpha longicaudata</i> entomopoxvirus	DleV	0.07	Dishui lake phycodnavirus 1	DlpV1	0.50	
<i>Diadromus pulchellus</i> ascovirus 4a	DpaV4a	0.10	<i>Emiliana huxleyi</i> virus 86	EhV86	0.55	
Dishui lake phycodnavirus 1	DlpV1	0.10	<i>Heterosigma akashiwo</i> virus 01	HaV01	0.63	
<i>Ectocarpus siliculosus</i> virus 1	EsV1	0.20	Megavirus chiliensis	McV	0.73	
<i>Emiliana huxleyi</i> virus 86	EhV86	0.36	<i>Micromonas</i> sp. RCC1109 virus MpV1	MpV1	0.40	
<i>Eptesipox</i> virus	EpV	0.63	<i>Micromonas pusilla</i> virus SP1	MpV-SP1	0.43	
European catfish virus	EcV	0.11	<i>Mimivirus terra2</i>	MVt2	0.70	
<i>Heterosigma akashiwo</i> virus 01	HaV01	0.22	<i>Mollivirus sibericum</i>	MsV	0.21	
Invertebrate iridovirus 22	IiV22	0.17	Only Syngen Nebraska virus 5	OSNV5	0.68	
Invertebrate iridescent virus 6	IiV6	0.16	<i>Ostreococcus lucimarinus</i> virus 1	OIV1	0.23	
<i>Lymphocystis</i> disease virus - isolate China	LdV	0.63	<i>Ostreococcus lucimarinus</i> virus OIV5	OIV5	0.35	
<i>Lymphocystis</i> disease virus Sa	LdVSA	0.08	<i>Ostreococcus tauri</i> virus 2	OtV2	0.30	
<i>Megavirus chiliensis</i>	McV	0.24	<i>Pandoravirus dulcis</i>	PdV	0.37	
<i>Micromonas</i> sp. RCC1109 virus MpV1	MpV1	0.36	<i>Pandoravirus inopinatum</i>	PiV	0.46	
<i>Micromonas pusilla</i> virus 12T	MpV12T	0.65	<i>Pandoravirus macleodensis</i>	PmV	0.17	
<i>Micromonas pusilla</i> virus SP1	MpV-SP1	0.36	<i>Pandoravirus neocaledonia</i>	PnV	0.48	
<i>Mimivirus terra2</i>	MVt2	0.63	<i>Pandoravirus quercus</i>	PqV	0.49	
<i>Ostreococcus lucimarinus</i> virus OIV5	OIV5	0.36	<i>Pandoravirus salinus</i>	PsV	0.51	
<i>Ostreococcus mediterraneus</i> virus 1	OmV1	0.25	<i>Phaeocystis globosa</i> virus	PgV	0.62	
Only Syngen Nebraska virus 5	OSNV5	0.58	Yellowstone lake mimivirus	YlmV	0.36	
<i>Ostreococcus tauri</i> virus OtV5	OtV5	0.13				
<i>Paramecium bursaria</i> chlorella virus 1	PbcV1	0.36				
<i>Paramecium bursaria</i> chlorella virus CVA-1	PbcV-CVA1	0.28				
<i>Paramecium bursaria</i> chlorella virus FR483	PbcV-FR483	0.26				
<i>Paramecium bursaria</i> chlorella virus NY2A	PbcV-NY2A	0.54				
<i>Paramecium bursaria</i> chlorella virus NYs1	PbcV-NYs1	0.39				
<i>Phaeocystis globosa</i> virus	PgV	0.63				
<i>Pandoravirus dulcis</i>	PdV	0.13				
<i>Pandoravirus macleodensis</i>	PmV	0.30				
<i>Pandoravirus quercus</i>	PqV	0.44				
<i>Pandoravirus salinus</i>	PsV	0.32				
<i>Ranavirus maximus</i>	RmV	0.30				
<i>Trichoplusia</i> ascovirus 2c	TaV2c	0.32				
<i>Taterapox</i> virus	TpV	0.13				
<i>Trichoplusia ni</i> ascovirus 2c	TnaV2c	0.32				
Yellowstone lake mimivirus	YlmV	0.23				
Yellowstone lake phycodnavirus 1	YlpV1	0.36				
Yellowstone lake phycodnavirus 3	YlpV3	0.45				
<i>Yokapox</i> virus	YpV	0.47				

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65

66 **Supplementary Table 7.** Description of LS correlations displayed of network analysis in Figure 7a.

X	Y	LS	Xs	Ys	Length	Delay time (d)	SPCC	P _{SPCC}
Chl- <i>a</i>		0.727	2	1	16	4	0.706	0.002
DIP	<i>A.san.</i>	0.694	1	1	16	0	0.739	0.001
Sal.		-0.582	1	1	16	0	-0.866	0.000
Temp.		0.622	1	1	16	0	0.769	0.000
	PpV	-0.898	1	1	16	0	-0.834	0.000
	<i>H.rot.</i>	-0.684	1	1	16	0	-0.587	0.035
	<i>A.ste.</i>	-0.581	1	1	16	0	-0.510	0.075
	U.Str.	-0.857	1	1	17	0	-0.793	0.000
	<i>A.omo</i>	-0.610	1	1	17	0	-0.650	0.005
	<i>Amo.sp1.</i>	0.722	1	2	16	-2	0.594	0.015
	Oth.Syn.	-0.660	1	1	17	0	-0.823	0.000
	<i>N.aci.</i>	-0.660	1	1	17	0	-0.738	0.001
<i>A.san.</i>	UAp #2	0.665	1	1	16	0	0.679	0.003
	<i>A.ulv.</i>	-0.746	1	1	15	0	-0.753	0.001
	<i>P.mar.</i>	0.686	1	2	13	-2	0.575	0.020
	<i>M.alg.</i>	-0.684	1	3	15	-4	-0.812	0.000
	<i>F.taf.</i>	0.665	1	3	15	-2	0.595	0.025
	<i>S.ama.</i>	-0.706	1	1	16	0	-0.790	0.000
	<i>L.syl.</i>	-0.689	1	2	16	-2	-0.737	0.004
	<i>C.spi.</i>	-0.707	1	2	16	-2	-0.851	0.000
	<i>T.thi.</i>	-0.556	1	2	16	-2	-0.855	0.000
	EsV1	0.638	1	3	15	-4	0.502	0.067

67 Abbreviations: LS, local similarity; SPCC and P_{SPCC} are the Spearman's Correlation Coefficient and the
68 associated P-value, respectively for the OTUs listed. Delay indicates time-lag day. Xs and Ys note the day in
69 which the LS correlation begins, and 'Length,' indicates the length of the LS correlation in day.
70

71 **Supplementary Table 8.** Description of LS correlations displayed of network analysis in Figure 7b.

X	Y	LS	Xs	Ys	Length	Delay time (d)	SPCC	P _{SPCC}
pH	<i>B.pra.</i>	-0.712	1	1	15	0	0.717	0.019
	<i>S.tod.</i>	0.564	2	1	14	2	0.857	0.000
	<i>L.alg.</i>	-0.547	5	1	11	8	-0.895	0.000
	<i>T.aip.</i>	-0.501	1	1	15	0	-0.663	0.007
<i>B.pra.</i>	<i>B.arc.</i>	0.544	1	2	14	-2	0.739	0.003
	<i>E.tan.</i>	0.545	1	1	15	0	0.709	0.003
	OIV5	-0.541	1	1	15	0	-0.823	0.001
	OIV2	-0.555	5	4	11	2	-0.743	0.002

72 Abbreviations: LS, local similarity; SCC and P_{SCC} are the Spearman's Correlation Coefficient and the associated
73 P-value, respectively for the OTUs listed. Delay indicates time-lag day. Xs and Ys note the day in which the LS
74 correlation begins, and 'Length,' indicates the length of the LS correlation in day.
75

76 **Supplementary Table 9.** The list of the previous studies of algicidal bacteria.

Strain name	Genus	Phylum	Target phytoplankton	Killing Type	Reference
ACEM 21	<i>Cellulophaga</i>		Raphidophyceae, Dinoflagellate, Diatoms	Indirect	5
A5Y	<i>Cytophaga</i>		Raphidophyceae, Diatoms.	Direct	6
41-DBG2	<i>Cytophaga</i>		Dinoflagellate	Indirect	7
N/D	<i>Cytophaga</i>		Raphidophyceae,	Direct	8
MC8	<i>Cytophaga</i>		Raphidophyceae,	Direct	9
J18/M01	<i>Cytophaga</i>		Raphidophyceae, Diatoms.	Direct	10
LR2	<i>Cytophaga</i>		Dinoflagellate	Unknown	11
AA8-2	<i>Cytophaga</i>	Bacteriodetes	Dinoflagellate	Direct	12
AMA-01	<i>Cytophaga</i>		Dinoflagellate	Indirect	13
5N-3	<i>Flavobacterium</i>		Dinoflagellate	Indirect	14
C49	<i>Flavobacterium</i>		Raphidophyceae,	Unknown	15
SS98-5	<i>Saprospira</i>		Diatoms	Direct	16
SS-K1	<i>Saprospira</i>		Diatoms	Direct	17
ACEM 20	<i>Zobellia</i>		Raphidophyceae, Dinoflagellate	Indirect	5
Unknown	unknown		Diatoms	Unknown	18
K12	<i>Alteromonas</i>		Diatoms	Indirect	19
SR-14	<i>Alteromonas</i>		Diatoms	Indirect	20
ANSW2-2	<i>Alteromonas</i>		Dinoflagellate	Indirect	7
E401	<i>Alteromonas</i>		Raphidophyceae, Dinoflagellate	Indirect	21
MC27	<i>Alteromonas</i>		Raphidophyceae	Indirect	22
GY21	<i>Alteromonas</i>		Raphidophyceae	Indirect	22
GY9501	<i>Alteromonas</i>		Rap., Dinoflagellate	Indirect	23
S	<i>Alteromonas</i>		Raphidophyceae, Dinoflagellate, Diaotms.	Indirect	24
K	<i>Alteromonas</i>		Raphidophyceae, Dinoflagellate, Diaotms.	Indirect	24
D	<i>Alteromonas</i>		Raphidophyceae, Dinoflagellate, Diaotms.	Indirect	24
A25	<i>Pseudoalteromonas</i>		Diatoms	Indirect	25
A28	<i>Pseudoalteromonas</i>		Raphidophyceae, Diatoms	Indirect	26
Y	<i>Pseudoalteromonas</i>		Raphidophyceae, Dinoflagellate	Indirect	27
ACEM 4	<i>Pseudoalteromonas</i>	Gamma-proteobacteria	Raphidophyceae, Dinoflagellate	Indirect	5
R	<i>Pseudoalteromonas</i>		Raphidophyceae, Dinoflagellate, Diatoms	Indirect	24
AMA-02	<i>Pseudoalteromonas</i>		Dinoflagellate	Indirect	13
T827/2B	<i>Pseudomonas</i>		Diatoms	Indirect	28
LG-2	<i>Pseudomonas</i>		Dinoflagellate	Indirect	29
EHK-1	<i>Pseudomonas</i>		Dinoflagellate	Indirect	30
G42	<i>Pseudomonas</i>		Raphidophyceae	Unknown	15
O-2-2	<i>Pseudomonas</i>		Raphidophyceae, Dinoflagellate	Indirect	31
T27	<i>Vibrio</i>		Raphidophyceae, Dinoflagellate	Unknown	32
A47	<i>Vibrio</i>		Raphidophyceae	Unknown	15
B42	<i>Vibrio</i>		Diatoms	Unknown	15
C4	<i>Vibrio</i>		Raphidophyceae, Diatoms	Unknown	15
G62	<i>Vibrio</i>		Raphidophyceae, Dinoflagellate	Unknown	15
AMA-03	<i>Ruegeria</i>		Dinoflagellate	Indirect	13
IRI-60	<i>Shewanella</i>		Dinoflagellate	Direct	33
ACEM 32	<i>Bacillus</i>	Firmicutes	Raphidophyceae, Dinoflagellate	Indirect	5
SY-1	<i>Bacillus</i>		Dinoflagellate	Indirect	34
ACEM 22	<i>Planomicrobium</i>		Raphidophyceae, Dinoflagellate	Indirect	5
LG-1	<i>Micrococcus</i>	Actinobacteria	Dinoflagellate	Indirect	35
LG-5	<i>Micrococcus</i>		Dinoflagellate	Indirect	36
SY-13	<i>Micrococcus</i>		Dinoflagellate	Indirect	37
OT-1	<i>Kordia</i>		Diatoms	direct	38
H519S5-4	Unknown	Unknown	Raphidophyceae, Dinoflagellate., Diatoms	indirect	39
H605S5-15	Unknown		Raphidophyceae, Dinoflagellate, Diatoms	indirect	39
H605S5-22	Unknown		Raphidophyceae, Dinoflagellate, Diatoms	indirect	39

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