Revised Supplementary Information

Short-term dynamics and interactions of marine protist communities during the spring-summer transition

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1. Supplementary Material

Environmental parameters. Temperature and salinity were determined immediately upon sampling in an on-board bucket by YSI (Yellow Springs, OH, USA). Chlorophyll a concentrations were determined via triplicate 0.5-1 L filtrations onto GF/F filter, frozen at -80C and extracted with 90% acetone and analyzed fluorometrically. Daily averages for precipitation, and wind speed were downloaded from http://www.wunderground.com/weather-forecast/US/CA/Catalina.html. Wave height was collected from the National Buoy Data Center from a buoy located in the San Pedro Channel (33°37' N 118° 19' W), 11 km from our sampling location. Nutrient analyses were performed at the Marine Science Institute Analytical Laboratory in Santa Barbara, CA, with recognized standard oceanographic protocols for nutrient autoanalyzers using a Lachat QuickChem 800 Flow Injection Nutrient Analyzer (Johnson et al, 1985).

Library preparation. Nested PCR (first amplifying with short barcoded 18S-only primers, then reamplifying with primers containing sequencing adapters) was required to amplify all samples, as we were unsuccessful attempting to create sequence-ready material when using the full-length primers alone. For the first PCR, 18S rDNA primers (V4F and V4RB) were used without adding adapters, barcodes/indexes and sequencing primers. This PCR consisted of an initial denaturation at 98°C for 1 min, 10 cycles of 30 s at 98°C, 30 s at 53°C and 30 s at 72°C, followed by 15 cycles of 10 s at 98°C, 30 s at 48°C, 30 s at 72°C, and a final extension at 72°C for 10 min. Nested PCR with different annealing temperatures was used to compensate the considerably lower annealing of the reverse primer compared to the forward primer (Stoeck et al. 2010; Balzano et al. 2015). 1 uL of the PCR product was used as a template for the second PCR, using the modified primers described above. The PCR conditions were: initial denaturation at 98°C for 1 min, 10 cycles of

30 s at 98°C, 30 s at 48°C, 30 s at 72°C, and a final extension at 72°C for 10 min. PCR reactions were then cleaned and concentrated with 1x (vol:vol) Agencourt AMPure XP magnetic beads (Beckman Coulter). Purified products from samples were pooled in equimolar concentrations. The pool was sent to the University of California Davis Genome Center and sequenced with generic sequencing primers on Illumina Miseq 2x300 chemistry.

Canonical Correspondence Analysis (CCA). To investigate the relationships between protist community composition and measured environmental variables, the CCA has been used (ter Braak, 1990). This ordination technique has been chosen rather than RDA (Redundancy Analysis) after a preliminary test performed with Detrended Correspondence Analysis which showed that species response to the selected environmental was unimodal and not linear ($p>0.05$) (Ramette, 2007).

Different variables were submitted to the forward selection procedure, in which the statistical significance of the term was tested by the unrestricted Monte Carlo permutation test (999 permutations). Explanatory variables with p-values greater than 0.05, were excluded from further analyses. The obtained ordination axes (based on community composition data) are linear combinations of environmental variables that best explain archaeal community structure data.

Variation partitioning was used to evaluate whether pure chemical variables affected the eukaryote community independently of the effect of physical variables. All explanatory variables were divided into three groups. Firstly, we separated the 'pure bottom-up' (A) effect as referring to the control by resources, including nutrients (nitrates + nitrites (NO_3^- + NO_2^-)), orthophosphates (PO_4^{3-}), silicate (SiO_3^{2-})). Secondly, we separated 'other chemical variables' (B) (pH) from the pure bottom-up variables. Thirdly, we generated a set of variables related to physical regulation

(Temperature, degree), dominant wave period (DPD, s); direction from which DPD is coming (MWD, degree), significant wave height (WVHT, m), average wave period (APD seconds), Wrigley wind speed average (WSPD, KmpH), Wrigley precipitation sum (cm) (Wrigley refers to the weather station at Wrigley Marine Science Center which is about 20km away from the sampling location). Each group of explanatory variables was tested independently as well as in combination. Additionally, Spearman's rank pairwise correlations between the environmental variables mentioned above helped to determine their significance for further ecological analysis.

Network analysis. Network characterization (structural cohesion and robustness) were evaluated using different topological indexes: degree, betweenness centrality and closeness centrality:

- **Degree** is the number of direct edges linked to the node n.
- **Betweeness centrality (Bn)** of the node n, defined as $Bn = \sum jk\ (\delta(j,n,k)/\delta(j,k))$, where j and k are nodes in the network different from the n, $\delta(j,k)$ is the total number of shortest path between j and k and $\delta(j,k,n)$ is the total number of shortest path between j and k that n lies on. Betweenness centrality of a node reflects the centrality of this node as direct route between two other nodes in the network (Yoon et al, 2006).
- **Closeness centrality C_c(n*)*** of a node n is defined as the reciprocal of the average shortest path length and is computed as follows: $C_c(n) = 1 / avg(L(n,m))$, where L(n,m) is the length of the shortest path between two nodes n and m (Newman, 2005). The closeness centrality measures how fast information spreads from n node to other reachable nodes in the network.

2. Supplementary Figures

Figure S1. Rank abundance curves of the 30 most abundant 18S OTUs generated from both Balzano and Stoeck primers showing strong difference in the relative abundance of Haptophytes OTUs (indicated with the symbol "*" on the plots)

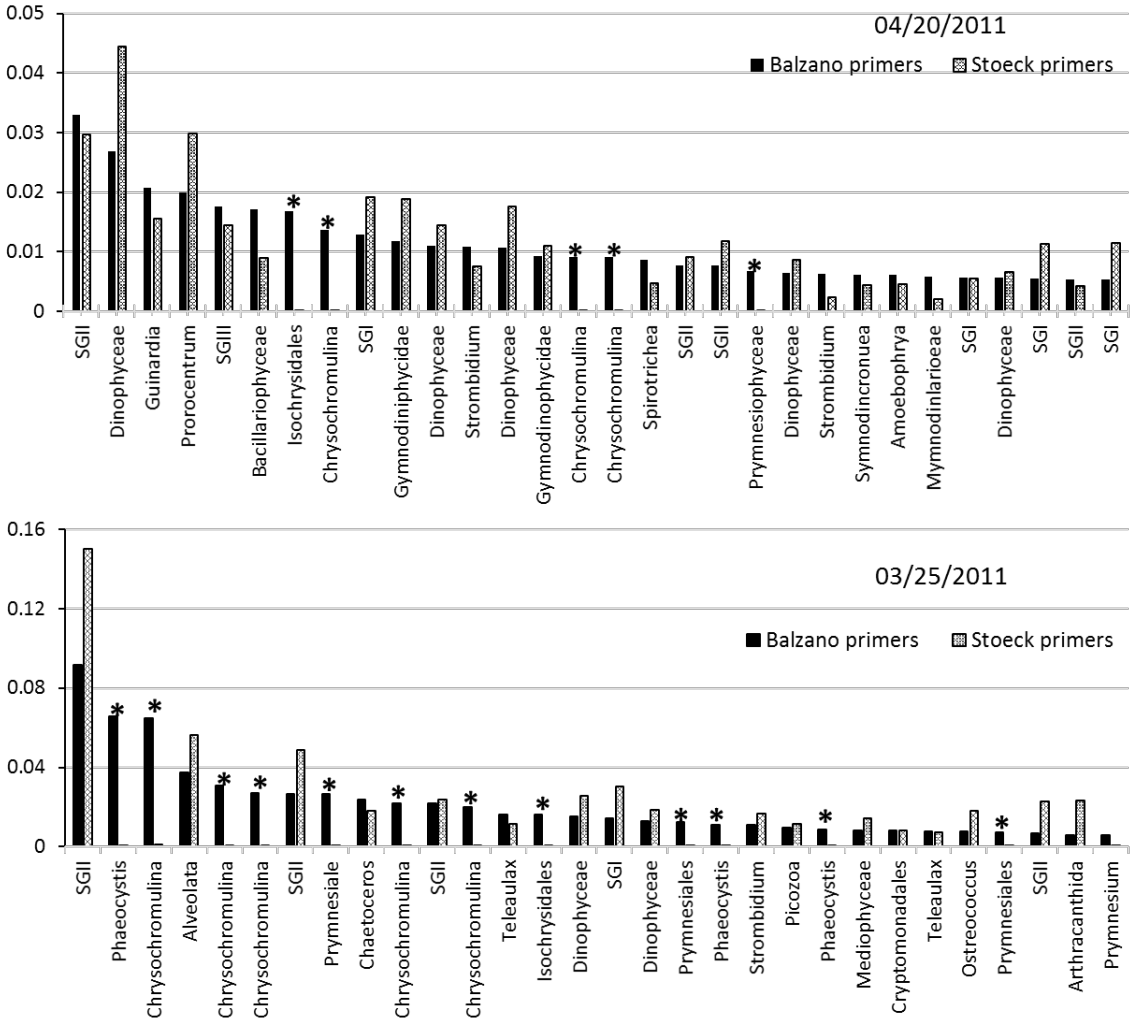
Figure S2. Temporal dynamics of environmental variables at SPOT location during the studied period.

Figure S3. Power-Law degree distribution of protist network indicating the number of OTUs (i.e. nodes) with the specific k degree (for k=1, 2,…,40).

Figure S4. Association networks showing the highest correlations between eukaryotic OTUs (Spearman correlation ≥ 0.8; $p<0.01$; $q<0.05$). Nodes colors and shapes correspond to main protist groups and their ecological behavior respectively.

Figure S5. Modular architecture of protist network according to AllegroMCODE analysis. Modules are decreasingly classified according to their score value.

Figure S6. Modules features as identified by AllegroMCODE analysis. Taxonomical abbreviations: A.: Azadinium; Ba.: Bathycoccus; C.: Chrysochromulina; K.: Karenia; L: Laboea; M.: Minidiscus; Mi.: Micromonas; P.: Prymnesium; Ph.: Phaeocystis; Pi: Picomonas; Pr.: Prorocentrum; Py.: Pyramimonas; S.: Syrachosphaera; St: Strombidium; T.: Teleaulax.



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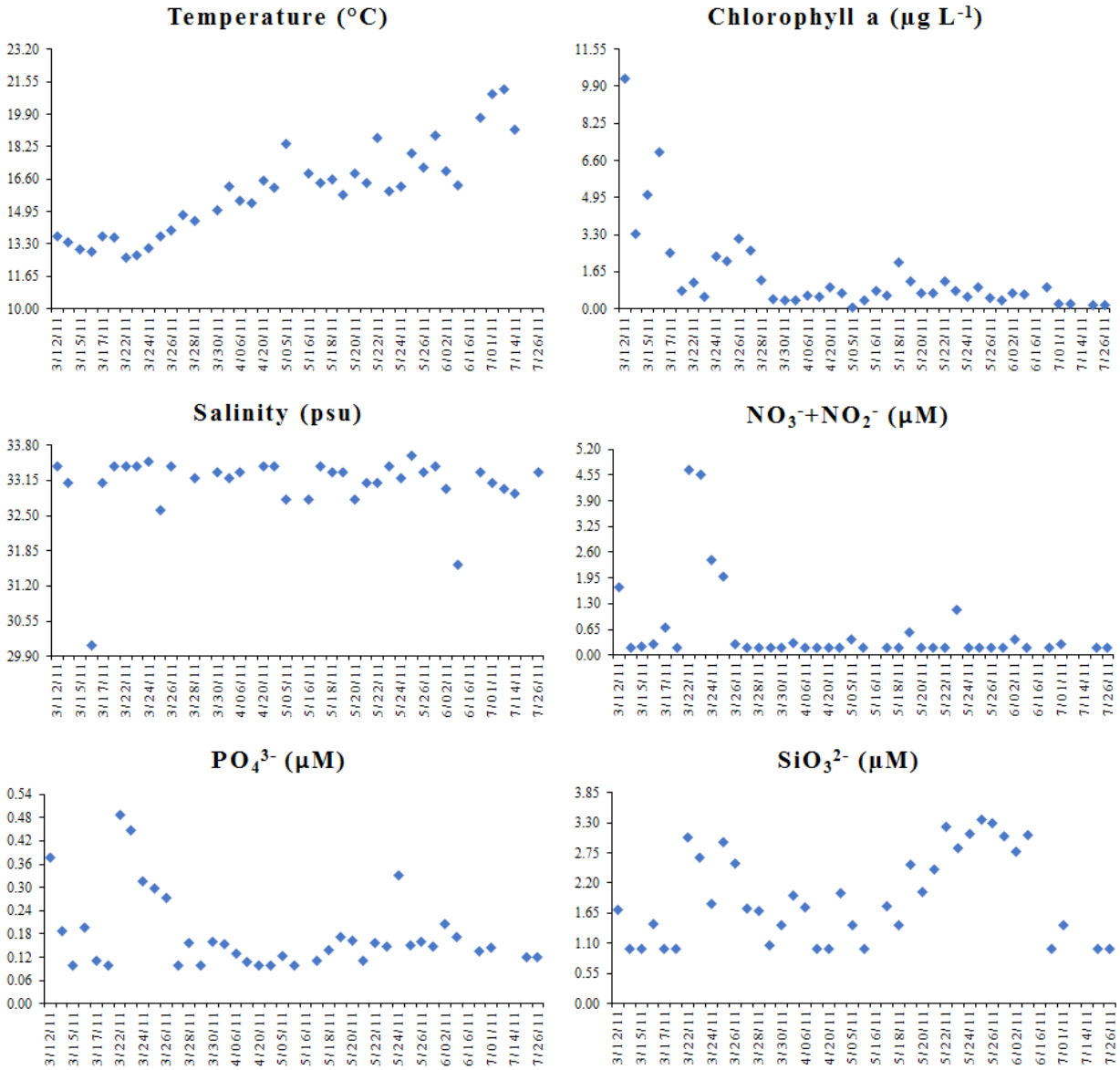

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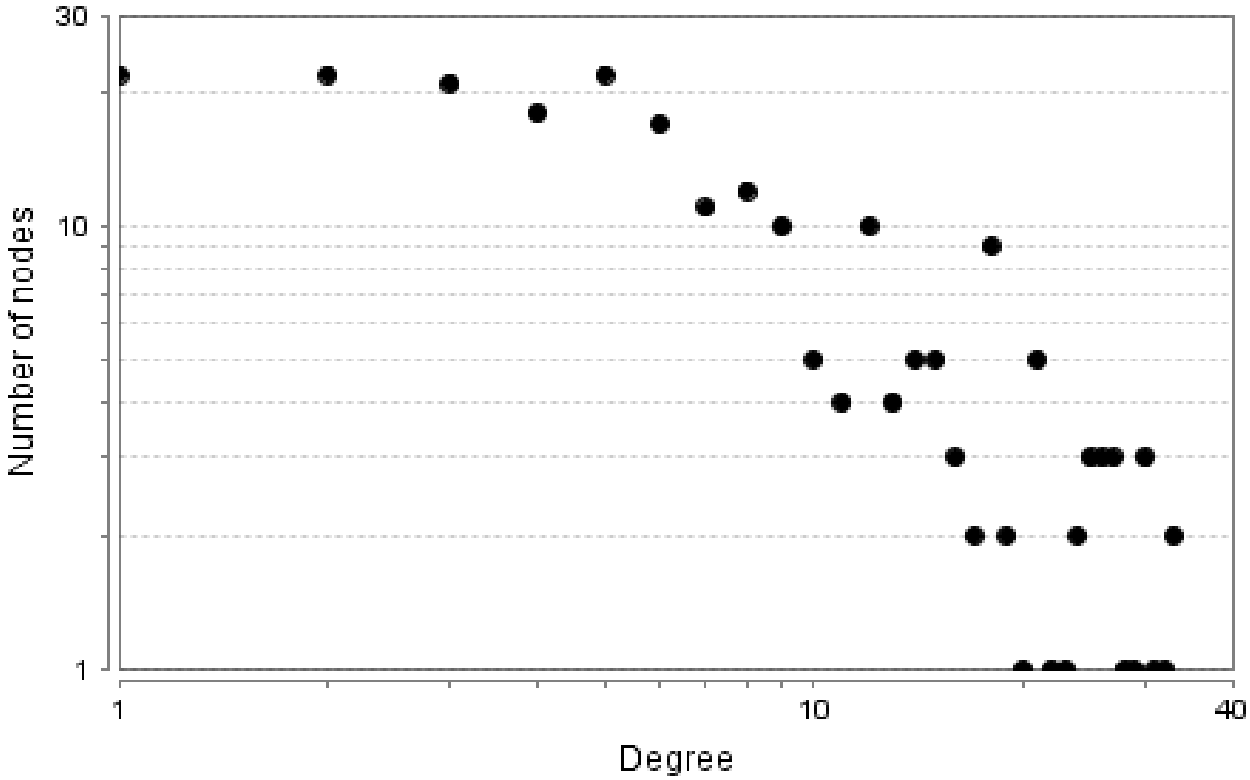

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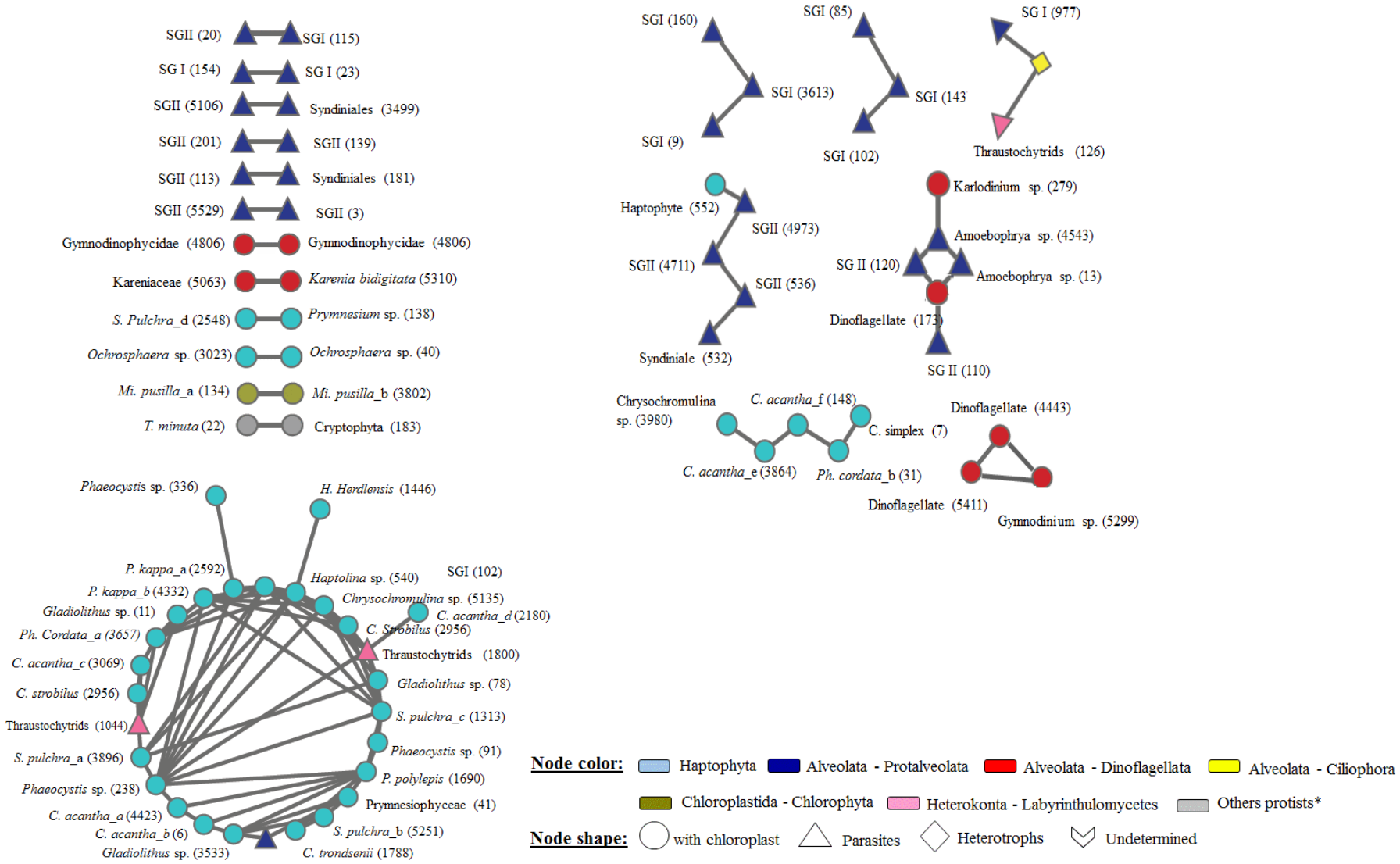


Figure S4. Association networks showing the highest correlations between eukaryotic OTUs (Spearman correlation ≥ 0.8; $p<0.01$; $q<0.05$). Nodes colors and shapes correspond to main protist groups and their ecological behavior respectively. Taxonomical abbreviations: C.: Chrysochromulina; Mi.: Micromonas; P.: Prymnesium; Ph.: Phaeocystis; S.: Syrachosphaera; St: Strombidium; T.: Teleaulax.

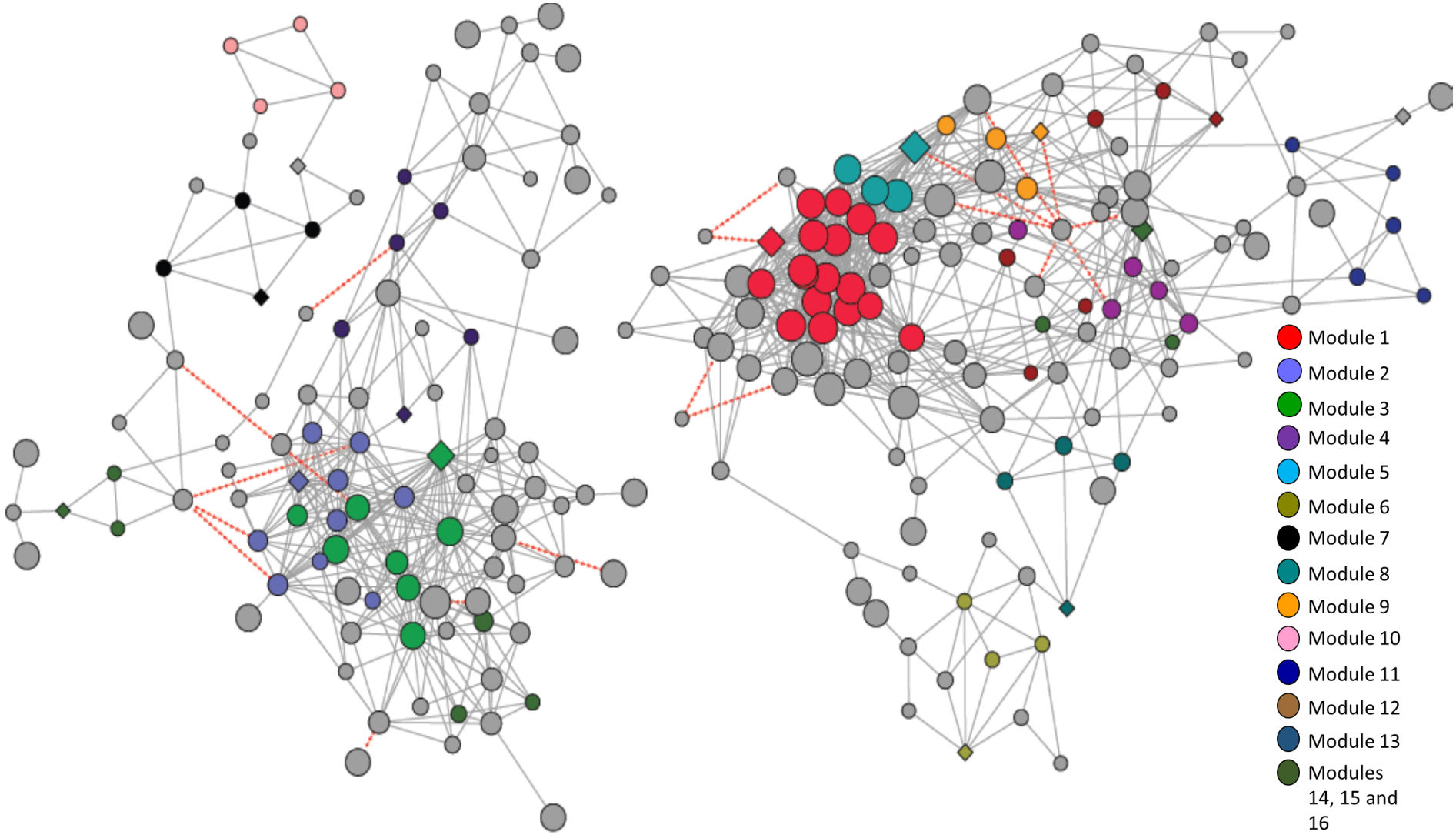
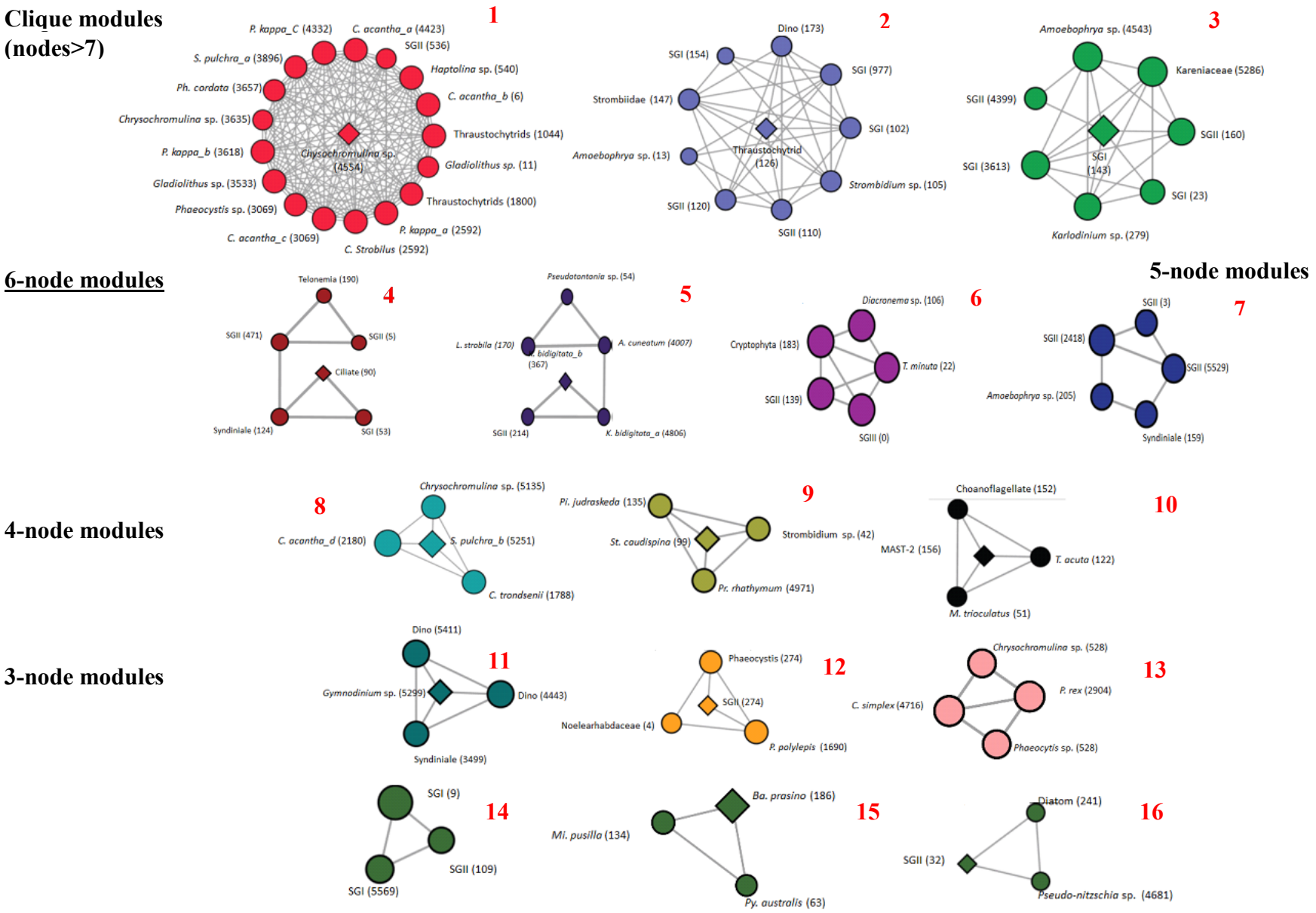


Figure S5. Modular architecture of protist network according to AllegroMCODE analysis. Modules are decreasingly classified according to their score value.



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3. Supplementary Tables

*Table S2 and S4 are presented in http://figshare.com/ and their access links are indicated in the legends.

Table S1. Percentage of coverage of both Balzano and Stoeck primers on different eukaryotes groups, according to SILVA test probe with zero mismatches allowed.

Table S2*. Relative abundance and dynamic of the 300 most abundant OTUs from which all the statistical analysis has been performed. Code correspond to OTU abbreviation name used to identify node in the network (Figure 4). **Data access link:** https://figshare.com/s/bf322a07e0ff7f4970f9

Table S3. Taxonomical and inferred ecological properties of the most abundant protist OTUs, each with a relative abundance of >2% in at least one sample. Chloroplastic trophic group point out potential mixotrophy. "na" indicates OTUs that were not available in the network because they did not display significant spearman correlation with other OTUs.

Table S4*. Bray-Curtis dissimilarity index estimated between samples showing the degree of PCC change between consecutive sampling time (days and weeks). **Data access link:** https://figshare.com/s/39afba10d1cb808b128a

Table S5. SIMPER results, showing the contribution ratio of most representatives OTUs between the five discriminate clusters.

Table S6. Canonical correspondence analysis of protist community structure data when constrained by nutrient, chemical and physical variables, respectively.

Table S7. General network properties of substructures (A) and (B), generated by Network Analyzer on Cytoscape.

Table S8. Main properties (cluster score, number of nodes, number of edges and OTU identity) of the different clusters discriminated by AllegroMCODE and presented in Figures S5 and S6.

Table S1. Percentage of coverage of both Balzano and Stoeck primers on different eukaryotes groups, according to SILVA test probe with zero mismatches allowed.

Eukaryotic groups	18S V4 Primers	
	Balzano et al, 2015	Stoeck et al, 2010
AB3F14RN1B12	33%	33%
Amoebozoa	62%	61%
Archaeplastida	75%	75%
BW-dinoclone28	100%	100%
Centrohelida	89%	89%
Cryptophyceae	77%	77%
D4P07G08	100%	100%
DH147-EKD10	61%	61%
DH147-EKD23	65%	65%
Haptophyta	**69%**	**1.90%**
Incertae Sedis	69%	69%
LG25-05	71%	71%
NAMAKO-1	100%	100%
Opisthokonta	45%	44%
Picozoa	73%	73%
RT5iin25	58%	58%
SA1-3C06	67%	67%
SAR	63%	63%

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OTU number_Closest relative	Taxonomical affiliation	Blast similarity (%)	Trophic group	Cytoscape Network Analyzer					
				Sub-structure Network	Degree	Closeness cetrality	Betweenness centrality	Clustering coefficient	AllegroMCODE Module
46_*Scrippsiella trochoidea*	Dinophyceae	98	Undetermined	A	2	0.23	0.016	0	Unclustered
5495_*Gymnodinium dorsalisulcum*	Dinophyceae	99	Chloroplast	na	na	na	na	na	na
18_*Lingulodinium polyedrum*	Dinophyceae	100	Chloroplast	na	na	na	na	na	na
5563_*Scrippsiella* sp.	Dinophyceae	99	Undetermined	A	1	0.18	0	0	Unclustered
5063_Kareniaceae	Dinophyceae	99	Chloroplast	A	5	0.22	0.02	0.4	Unclustered
4971_*Prorocentrum rhathymum*	Dinophyceae	99	Chloroplast	B	6	0.2	0.042	0.4	Cluster 7
44_*Scrippsiella* sp.	Dinophyceae	100	Chloroplast	na	na	na	na	na	na
2894_*Gymnodinium gutula*	Dinophyceae	100	Heterotroph	A	1	0.18	0	0	Unclustered
5_SGII	Syndiniales	100	Parasite	na	na	na	na	na	na
9_SGI	Syndiniales	99	Parasite	A	6	0.27	0.0004	0.8	Cluster 14
0_SGIII	Syndiniales	99	Parasite	B	12	0.34	0.06	0.32	Cluster 4
32_SGII	Syndiniales	98	Parasite	A	3	0.21	0.06	0.33	Cluster 16
5529_SGII	Syndiniales	99	Parasite	B	4	0.23	0.002	0.33	Cluster 11
1_SGI	Syndiniales	99	Parasite	na	na	na	na	na	na
5569_SGI	Syndiniales	99	Parasite	A	6	0.28	0.0004	0.8	Cluster 14
5106_SGII	Syndiniales	99	Parasite	B	1	0.38	0	0	Unclustered
13_*Amoebophrya* sp.	Syndiniales	99	Parasite	A	12	0.34	0.01	0.48	Cluster 2 (Clique)
57_SGII	Syndiniales	99	Parasite	A	7	0.29	0.0016	0.71	Unclustered
2453_*Amoebophrya* sp.	Syndiniales	98	Parasite	A	8	0.3	0.0024	0.53	Unclustered
20_SGII	Syndiniales	98	Parasite	B	3	0.25	0.005	0	Unclustered

OTU number_Closest relative	Taxonomical affiliation	Blast similarity (%)	Trophic group	Cytoscape Network Analyzer					
				Sub-structure Network	Degree	Closeness cetrality	Betweenness centrality	Clustering coefficient	AllegroMCODEModule
30_SGIII	Syndiniales	99	Parasite	A	8	0.32	0.07	0.6	Unclustered
3613_SGI	Syndiniales	100	Parasite	A	21	0.34	0.04	0.4	Cluster 3 (clique)
23_SGI	Syndiniales	100	Parasite	A	12	0.35	0.009	0.57	Cluster 3 (clique)
24_SGI	Syndiniales	99	Parasite	A	4	0.29	0	1	Unclustered
2418_SGII	Syndiniales	99	Parasite	B	5	0.27	0.03	0.1	Cluster 11
4681_*Pseudo-nitzschia* sp.	Diatomea	100	Autotroph	A	3	0.26	0.016	0	Cluster 16
15_*Chaetoceros* sp.	Diatomea	97	Autotroph	na	na	na	na	na	na
26_*Guinardia striata*	Diatomea	100	Autotroph	B	15	0.35	0.05	0.3	Unclustered
36_*Leptocylindrus convexus*	Diatomea	100	Autotroph	na	na	na	na	na	na
4203_*Protaspis grandis*	Cercozoa	99	Parasite	S	2	0.2	0.006	0	Unclustered
10_*Cryothecomonas longipes*	Cercozoa	98	Parasite	S	1	0.25	0	0	Unclustered
4334_*Cryothecomonas aestivalis*	Cercozoa	99	Heterotroph	A	2	0.2	0	1	Unclustered
14_*Acanthometron* sp.	Radiolaria	100	Heterotroph	na	na	na	na	na	na
60_*Larcopyle butschlii*	Radiolaria	100	Heterotroph	na	na	na	na	na	na
3618_*Prymnesium Kappa*	Haptophyta	99	Chloroplast	B	33	0.38	0.04	0.49	Cluster 1 (clique)
128_Syrchosphaerales	Haptophyta	98	Chloroplast	na	na	na	na	na	na
6_*Chrysochromulina acantha*	Haptophyta	100	Chloroplast	B	**30**	0.67	0.06	0.51	Cluster 1 (clique)
71_*Phaeocyctis jahnii*	Haptophyta	99	Chloroplast	na	na	na	na	na	na
16_*Phaeocyctis globosa*	Haptophyta	100	Chloroplast	na	na	na	na	na	na
3980_*Chrysochromulina* sp.	Haptophyta	99	Chloroplast	B	8	0.49	0.0002	0.92	Unclustered
7_*Chrysochromulina simplex*	Haptophyta	99	Chloroplast	B	2	0.42	0	1	Unclustered
1788_*Chrysochromulina trondsenii*	Haptophyta	100	Chloroplast	B	25	0.37	0.037	0.46	Cluster 5
5135_*Chrysochromulina* sp.	Haptophyta	98	Chloroplast	B	14	0.53	0.0007	0.92	Cluster 5
145_*Chrysochromulina* sp.	Haptophyta	100	chloroplast	A	4	0.28	0.0015	0.33	Unclustered
17_*Ostreococcus lucimarinus*	Chlorophyta	99	Chloroplast	na	na	na	na	na	na

Table S5. SIMPER results, showing the contribution ratio of most representatives OTUs between the five discriminate clusters.

SIMPER_Cluster I

OTUs#	OTUs iD	Group	Cluster I_II	Cluster I_III	Cluster I_IV	Cluster I_V
4203	4203_Protaspis_grandis	Cercozoa		0.269		
10	10_Cryothecomonas_longipes	Cercozoa		0.0809		
13	13_Amoebophrya_sp.	Syndiniales	0.0121	0.0164	0.0164	0.0164
14	14_Acanthometron_sp.	Radiolaria	0.0127	0.0144	0.014	0.0145
0	0_SGIII	Syndiniales		0.0133	0.0126	0.0135
5287	5287_Kareniaceae	Dinophyceae	0.0107	0.0132		0.0137
4681	4681_Pseudo-Niszchia	Diatomea		0.0127		
9	9_SGI	Syndiniales		0.0117	0.0128	0.0155
46	46_Scrippsiella_trochoidea	Dinophyceae		0.0115		0.0353
3618	3618_Prymnesium_Kappa	Haptophyta	0.0339	0.0107		0.0146
5495	5495_Gymnodinium_dorsalisulcum	Dinoflagellates				0.143
18	18_Lingulodinium_polyedrum	Dinophyceae				0.131
5563	5563_Scrippsiella_sp	Dinophyceae			0.0256	0.0982
4	4_Noelearhabdaceae	Haptophyta			0.0101	0.0133
1788	1788_Chrysochromulina_trondsenii	Haptophyta				0.00994
111	111_Gonyaulax_spinifera_	Dinophyceae				0.00951
5135	5135_Chrysochromulina_sp._	Haptophyta				0.0093
149	149_Alexandrium_fundeynse	Dinophyceae				0.00923
15	15_Chaetoceros_sp	Diatomea			0.0429	
4971	4971_Prorocentrum_rhathymum_	Dinophyceae			0.0301	
71	71_Phaeocyctis_jahnii	Haptophyta			0.0157	
5063	5063_Kareniaceae	Dinophyceae			0.0125	
48	48_Unassigned	Unassigned			0.0115	
7	7_Chrysochromulina_simplex	Haptophyta	0.012			
6	6_Chrysochromulina_acantha_	Haptophyta	0.0113			

Table S5. Continued

SIMPER_Cluster III

OTUs#	OTUs iD	Group	Cluster III_I	Cluster III_II	Cluster III_IV	Cluster III_V
4203	4203_Protaspis_grandis	Cercozoa	0.27	0.27	0.27	0.27
5495	5495_Gymnodinium_dorsalisulcum	Dinoflagellates				0.14
18	18_Lingulodinium_polyedrum	Dinophyceae				0.13
5563	5563_Scrippsiella_sp	Dinophyceae			0.03	0.11
10	10_Cryothecomonas_longipes	Cercozoa	0.08	0.08	0.08	0.08
46	46_Scrippsiella_trochoidea	Dinophyceae	0.01	0.01	0.01	0.02
4681	4681_Pseudo-Niszchia	Diatomea	0.01	0.01		0.01
4	4_Noelearhabdaceae	Haptophyta				0.01
111	111_Gonyaulax_spinifera_	Dinophyceae				0.01
149	149_Alexandrium_fundeynse	Dinophyceae				0.01
15	15_Chaetoceros_sp	Diatomea			0.04	
4971	4971_Prorocentrum_rhathymum_	Dinophyceae			0.03	
71	71_Phaeocyctis_jahnii	Haptophyta			0.02	
5063	5063_Kareniaceae	Dinophyceae			0.02	
5287	5287_Kareniaceae	Dinophyceae			0.02	
48	48_Unassigned	Unassigned			0.01	
13	13_Amoebophrya_sp.	Syndiniales	0.02			
14	14_Acanthometron_sp.	Radiolaria	0.01			
0	0_SGIII	Syndiniales	0.01			
5287	5287_Kareniaceae	Dinophyceae	0.01			
9	9_SGI	Syndiniales	0.01			
3618	3618_Prymnesium_Kappa	Haptophyta		0.04		
6	6_Chrysochromulina_acantha_	Haptophyta		0.02		
5135	5135_Chrysochromulina_sp._	Haptophyta		0.02		
7	7_Chrysochromulina_simplex	Haptophyta		0.01		
3980	3980_Chrysochromulina_sp._	Haptophyta		0.01		
5	5_SGII	Syndiniales		0.01		
1788	1788_Chrysochromulina_trondsenii	Haptophyta		0.01		
1	1_SGI	Syndiniales		0.01		

Table S5. continued

SIMPER_Cluster IV

OTUs#	OTUs iD	Group	Cluster IV_I	Cluster IV_II	Cluster IV_III	Cluster IV_V
4203	4203_Protaspis_grandis	Cercozoa			0.267	
10	10_Cryothecomonas_longipes	Cercozoa			0.0798	
15	15_Chaetoceros_sp	Diatomea	0.0429	0.0372	0.0418	0.0422
5563	5563_Scrippsiella_sp	Dinophyceae	0.0256	0.0316	0.0343	0.0725
4971	4971_Prorocentrum_rhathymum_	Dinophyceae	0.0301	0.0315	0.0316	0.0319
71	71_Phaeocyctis_jahnii	Haptophyta	0.0157	0.0125	0.0205	0.0214
5063	5063_Kareniaceae	Dinophyceae	0.0125	0.0185	0.018	0.0198
5287	5287_Kareniaceae	Dinophyceae		0.0146	0.0172	0.0176
48	48_Unassigned	Unassigned	0.0115	0.0119	0.0119	0.0119
46	46_Scrippsiella_trochoidea	Dinophyceae			0.00983	0.0337
5495	5495_Gymnodinium_dorsalisulcum	Dinoflagellates				0.142
18	18_Lingulodinium_polyedrum	Dinophyceae				0.127
4681	4681_Pseudo-Niszchia	Diatomea		0.0105		0.0102
16	16_Phaeocyctis_globosa	Haptophyta				0.0102
111	111_Gonyaulax_spinifera_	Dinophyceae				0.00943
149	149_Alexandrium_fundeynse	Dinophyceae				0.0091
13	13_Amoebophrya_sp.	Syndiniales	0.0164			
14	14_Acanthometron_sp.	Radiolaria	0.014			
9	9_SGI	Syndiniales	0.0128			
0	0_SGIII	Syndiniales	0.0126			
4	4_Noelearhabdaceae	Haptophyta	0.0101	0.0101		
3618	3618_Prymnesium_Kappa	Haptophyta		0.0412		
5135	5135_Chrysochromulina_sp._	Haptophyta		0.015		
6	6_Chrysochromulina_acantha_	Haptophyta		0.0125		
3980	3980_Chrysochromulina_sp._	Haptophyta		0.0106		
1788	1788_Chrysochromulina_trondsenii	Haptophyta		0.0103		
7	7_Chrysochromulina_simplex	Haptophyta		0.0103		

Table S5. continued

SIMPER_Cluster V						
OTUs#	OTUs iD	Group	Cluster V_I	Cluster V_II	Cluster V_III	Cluster V_IV
4203	4203_Protaspis_grandis	Cercozoa			0.27	
5495	5495_Gymnodinium_dorsalisulcum	Dinoflagellates	0.14	0.14	0.14	0.14
18	18_Lingulodinium_polyedrum	Dinophyceae	0.13	0.13	0.13	0.13
5563	5563_Scrippsiella_sp	Dinophyceae	0.10	0.10	0.11	0.07
10	10_Cryothecomonas_longipes	Cercozoa			0.08	
46	46_Scrippsiella_trochoidea	Dinophyceae	0.04	0.04	0.02	0.03
4681	4681_Pseudo-Niszchia	Diatomea			0.01	0.01
4	4_Emiliania_huxley/Gephyrocapsa_r	Haptophyta			0.01	
111	111_Gonyaulax_spinifera_	Dinophyceae	0.01		0.01	0.01
149	149_Alexandrium_fundeynse	Dinophyceae	0.01	0.01	0.01	0.01
5287	5287_Kareniaceae	Dinophyceae	0.01	0.01		0.02
15	15_Chaetoceros_sp	Diatomea				0.04
4971	4971_Prorocentrum_rhathymum_	Dinophyceae				0.03
71	71_Phaeocyctis_jahnii	Haptophyta				0.02
5063	5063_Kareniaceae	Dinophyceae				0.02
48	48_Unassigned	Unassigned				0.01
16	16_Phaeocyctis_globosa	Haptophyta				0.01
13	13_Amoebophrya_sp.	Syndiniales	0.02			
9	9_SGI	Syndiniales	0.02			
3618	3618_Prymnesium_Kappa	Haptophyta	0.01	0.05		
14	14_Acanthometron_sp.	Radiolaria	0.01			
0	0_SGIII	Syndiniales	0.01			
4	4_Noelearhabdaceae	Haptophyta	0.01	0.01		
1788	1788_Chrysochromulina_trondsenii	Haptophyta	0.01	0.01		
5135	5135_Chrysochromulina_sp._	Haptophyta	0.01	0.02		
6	6_Chrysochromulina_acantha_	Haptophyta		0.02		
7	7_Chrysochromulina_simplex	Haptophyta		0.02		
3980	3980_Chrysochromulina_sp._	Haptophyta		0.02		
5	5_SGII	Syndiniales		0.01		
1	1_SGI	Syndiniales		0.01		

Table S6. Canonical correspondence analysis of protist community structure data when constrained by nutrient, chemical and physical variables, respectively.

Environmental variables	**Physico-chemical variables**		**Physical variables**		**Chemical variables**		**Nutrient**	
p value	0.031		**0.137**		<0.0001		0.003	
Total Inertia	4.177		4.177		4.177		4.177	
Sum of all canonical eigenvalues	1.297				0.565		0.447	
Explained variance	**31.04**				**13.52**		**11.29**	
Axix	Axis 1	Axis 2	Axis 1	Axis 2	Axis 1	Axis 2	Axis 1	Axis 2
Eigenvalues	0.393	0.240			0.610	0.564	0.360	0.126
Cumulative percentage variance of:								
species data	30.289	48.794			16.900	32.523	17.481	33.464
species-environment relation	9.402	15.147			14.610	28.126	15.507	29.686

Table S7. General network properties of Substructures (A) and (B), generated by Network Analyzer on Cytoscape.

Network characteristics	Substructure A	Substructre B
Diameter	11	10
Short path length	3.93	3.51
Average neighbors	6.76	10.3
Total number of nodes	103	125
Network density	0.07	0.08
Total number of edges	643	348
Number of negative edges	7	11

Table S8. Main properties (cluster score, number of nodes, number of edges and OTU identity) of the different clusters discriminated by AllegroMCODE and presented in Figures S5 and S6.

ID	Cluster ID	Nodes colors	Score	Nodes	Edges	Node_IDs
1	Cluster 1		8	18	144	3635_Chrysochromulina_sp.; 1044_Thraustochytriidea_sp.; 4554_Chrysochromulina_sp.; 540_Haptolina_sp.; 2592_Prymnesium_kappa; 3069_Chrysochromulina_acantha_A; 2956_Chrysochromulina_strobilus; 4423_Chrysochromulina_acantha_B; 3657_Phaeocystis_cordata; 6_Chrysochromulina_acantha_C; 4332_Prymnesium_kappa_A; 3618_Prymnesium_Kappa_B; 3896_Syracosphaera_pulchra; 11_Gladiolithus_sp.; 1800_Thraustochytriidea_sp.; 3533_Gladiolithus_sp.; 336_Phaeocystis_sp.; 536_SGII
2	Cluster 2		3,4	10	34	154_SGI; 977_SGI; 126_Thraustochytriidea_sp.; 173_Dinoflagellates; 102_SGI; 13_Amoebophrya_sp.; 105__Strombidium_sp; 147_Strombidiidae; 120_SGII; 110_SGII
3	Cluster 3		2,625	8	21	23_SGI; 4399_SGII; 4543_Amoebophrya_sp.; 3613_SGI; 5286_Kareniaceae; 160_SGII
4	Cluster 4		1,6	5	8	0_SGIII; 106_Diacronema_sp.; 139_SGII; 22_Teleaulax_minuta; 183_Cryptophyta; 143_SGI; 279_Karlodinium_sp.

Table S8. Continued.

ID	Cluster ID	Nodes colors	Score	Nodes	Edges	Node_IDs
5	Cluster 5		1,5	4	6	5135_Chrysochromulina_sp.; 5251_Syracosphaera_pulchra; 1788_Chrysochromulina_trondsenii; 2180_Chrysochromulina_acantha
6	Cluster 6		1,5	4	6	51_Minidiscus_trioculatus; 122_Teleaulax_acuta; 156_MAST-2; 152_Choanoflagellida_sp.
7	Cluster 7		1,5	4	6	4971_Prorocentrum_rhathymum; 99_Strombidium_caudispina; 135_Picomonas_judraskeda; 42_Strombidium_sp.
8	Cluster 8		1,5	4	6	5411_Dinoflagellates; 3499_Syndiniales; 4443_Dinoflagellates; 5299_Gymnodinium_sp.
9	Cluster 9		1,25	4	5	274_SGII; 4_Noelearhabdaceae; 1690_Prymnesium_aff._Polylepis; 91_Phaeocystis_sp.
10	Cluster 10		1,25	4	5	4716_Chrysochromulina_simplex; 528_Chrysochromulina_sp.; 3020_Phaeocystis_sp.; 2904_Phaeocytis_rex

Table S8. Continued.

ID	Cluster ID	Nodes colors	Score	Nodes	Edges	Node_IDs
11	Cluster 11		1,2	5	6	3_SGII; 2418_SGII; 5529_SGII; 205_Amoebophrya_sp; 159_Syndiniales
12	Cluster 12		1,167	6	7	190_Telonemia; 5_SGII; 90_Ciliates; 53_SGI; 4711_SGII; 124_Syndiniales
13	Cluster 13		1,167	6	7	54_Pseuditononia_sp.; 170_Laboea_strobila; 4007_Azadinium_cuneatum; 367_Gymnodiniphycidae; 4806_Gymnodiniphycidae; 214_SGII
14	Cluster 14		1	3	3	5569_SGI; 9_SGI; 109_SGII
15	Cluster 15		1	3	3	134_Micomonas_pusilla; 186_Bathycoccus_prasinos; 63_Pyramimonas_Australis
16	Cluster 16		1	3	3	32_SGII; 4681_Pseudo-Niszchia; 241_Diatoms