Supplementary information: Succession of protistan functional traits is influenced by bloom timing

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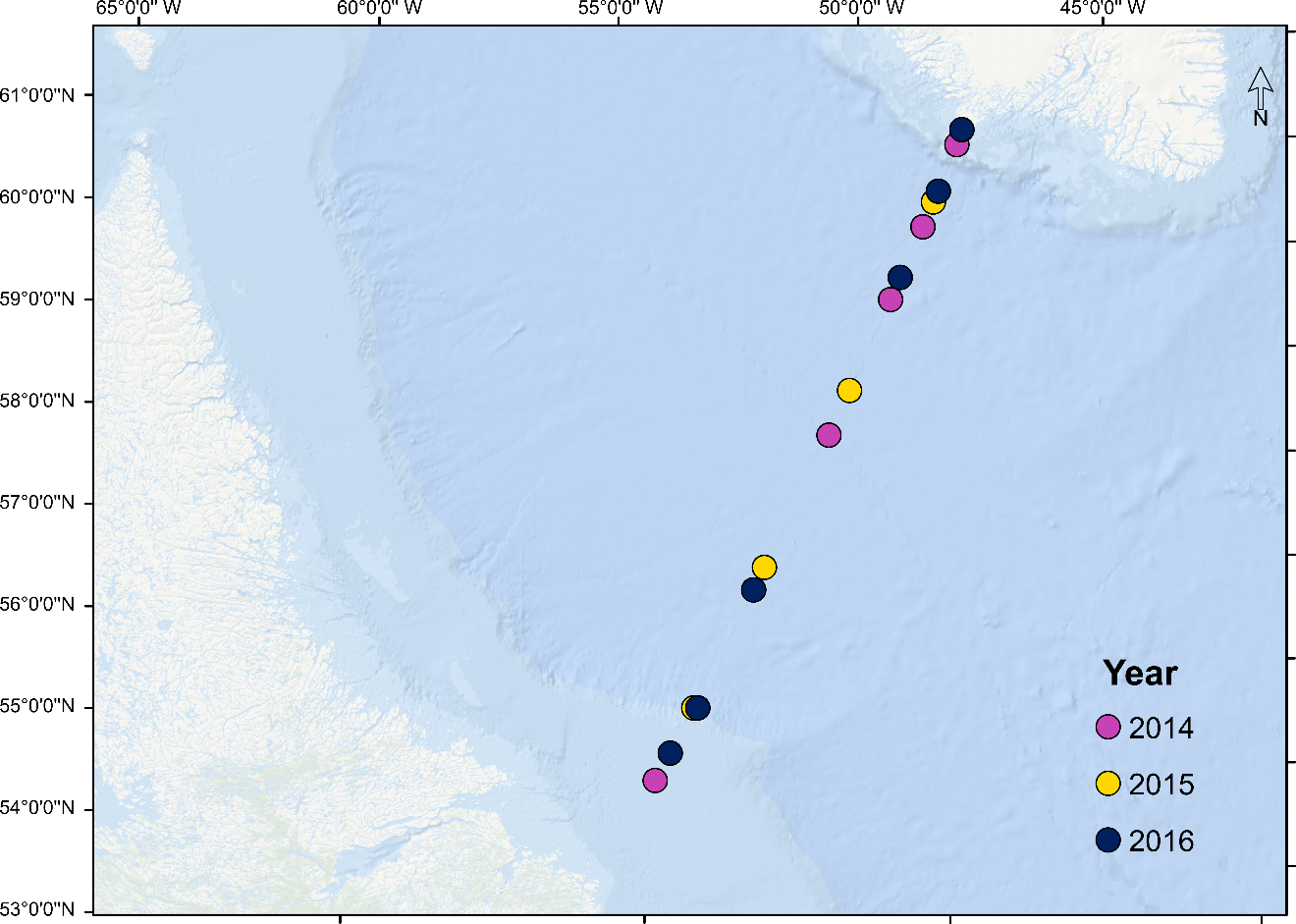


Figure S1. Map of the studied region. Colors indicate years. Note that station 8.5 (3rd from bottom) was sampled in 2015 and 2016.

## Table S1: Location, type of identification, sampling day and day of the peak chlorophyll-*a* for all stations

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Id** | **Station** | **Lat (°N)** | **Long (°E)** | **Year** | **Identification** | **Sampling (DOY)** | **Peak (DOY)** | **Days before peak** | **Onset of bloom (DOY)** |
| 400804 | L3\_05 | 54.49 | -54.75 | 2014 | Both | 133 | 164 | 31 | 157 |
| 400889 | L3\_9.5 | 55.34 | -53.9 | 2014 | Microscopy | 134 | 156 | 22 | 142 |
| 400563 | L3\_16.5 | 57.59 | -51.57 | 2014 | Microscopy | 131 | 148 | 17 | 133 |
| 400149 | L3\_17 | 57.8 | -51.33 | 2014 | Sequencing | 127 | 148 | 21 | 133 |
| 400244 | L3\_20 | 59.07 | -49.94 | 2014 | Both | 128 | 140 | 12 | 111 |
| 400467 | L3\_22 | 59.75 | -49.16 | 2014 | Both | 130 | 148 | 18 | 123 |
| 400365 | L3\_27.5 | 60.51 | -48.29 | 2014 | Both | 129 | 148 | 19 | 102 |
| 408395 | L3\_8.5 | 55.19 | -54.05 | 2015 | Both | 135 | 156 | 21 | 143 |
| 408491 | L3\_11.5 | 55.73 | -53.49 | 2015 | Microscopy | 136 | 132 | 4 | 125 |
| 407871 | L3\_14 | 56.54 | -52.68 | 2015 | Both | 129 | 140 | 11 | 117 |
| 408276 | L3\_15.5 | 57.18 | -52.01 | 2015 | Microscopy | 134 | 140 | 6 | 119 |
| 408231 | L3\_18 | 58.22 | -50.88 | 2015 | Both | 133 | 140 | 7 | 97 |
| 407968 | L3\_19.5 | 58.85 | -50.19 | 2015 | Microscopy | 130 | 140 | 10 | 111 |
| 408041 | L3\_23 | 59.98 | -48.9 | 2015 | Both | 131 | 140 | 9 | 82 |
| 408063 | L3\_28 | 60.57 | -48.23 | 2015 | Microscopy | 131 | 132 | 1 | 109 |
| 433946 | L3\_06 | 54.75 | -54.48 | 2016 | Sequencing | 136 | 172 | 36 | 131 |
| 433246 | L3\_8.5 | 55.19 | -53.97 | 2016 | Sequencing | 128 | 180 | 52 | 127 |
| 433318 | L3\_13.5 | 56.33 | -52.89 | 2016 | Sequencing | 129 | 172 | 43 | 126 |
| 433442 | L3\_20.5 | 59.28 | -49.71 | 2016 | Sequencing | 131 | 172 | 41 | 141 |
| 433643 | L3\_23.5 | 60.08 | -48.78 | 2016 | Sequencing | 133 | 180 | 47 | 141 |
| 433569 | L3\_28.5 | 60.65 | -48.15 | 2016 | Sequencing | 132 | 132 | 0 | 124 |

Note: DOY is day of year

Note 2: All stations were sampled at 2 m and 30 m deep

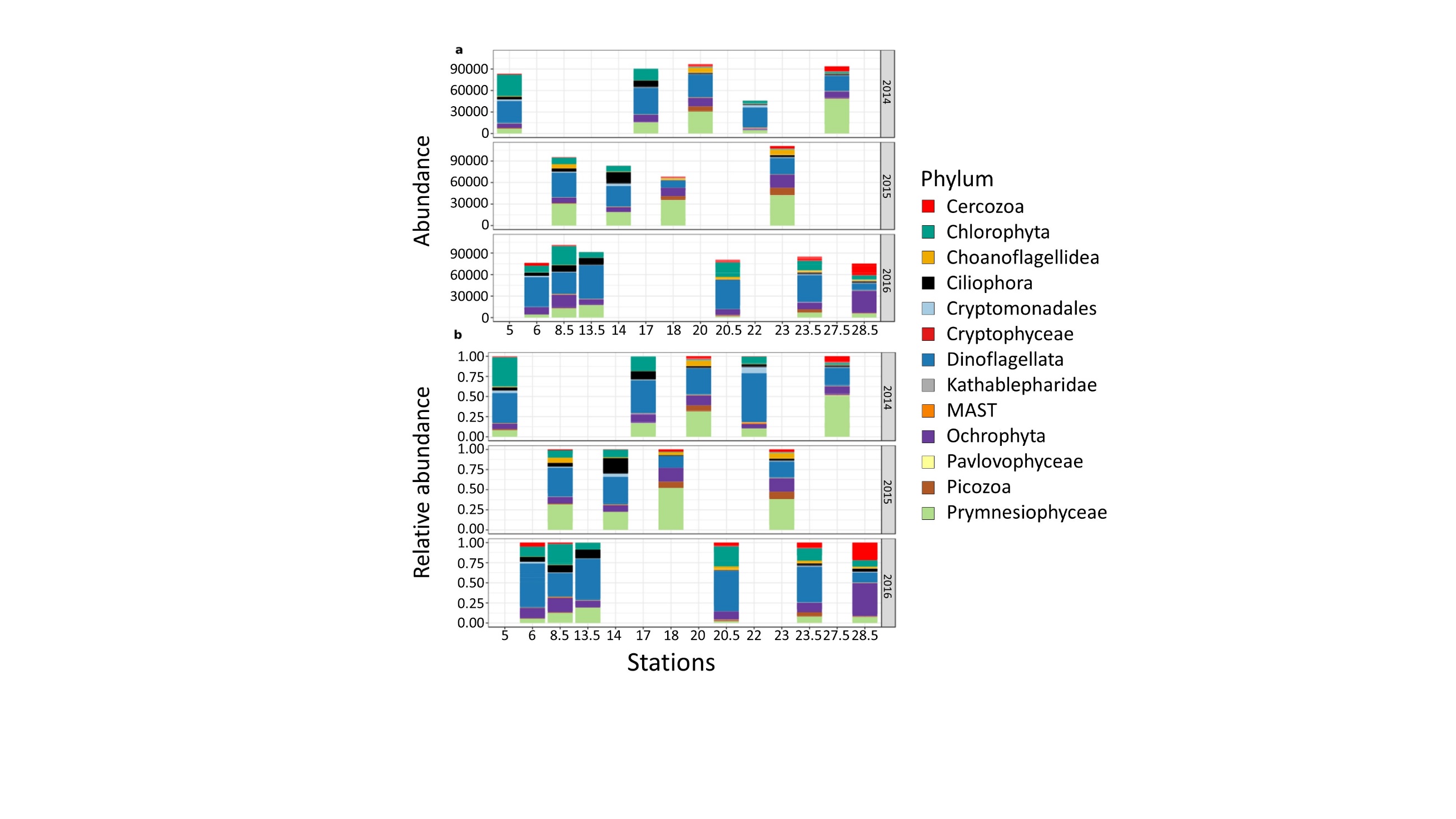


Figure S2. Total number of reads (a) and relative abundance (b) of the main protistan phyla detected at each station and for each year using 18SrRNA gene Illumina sequencing.

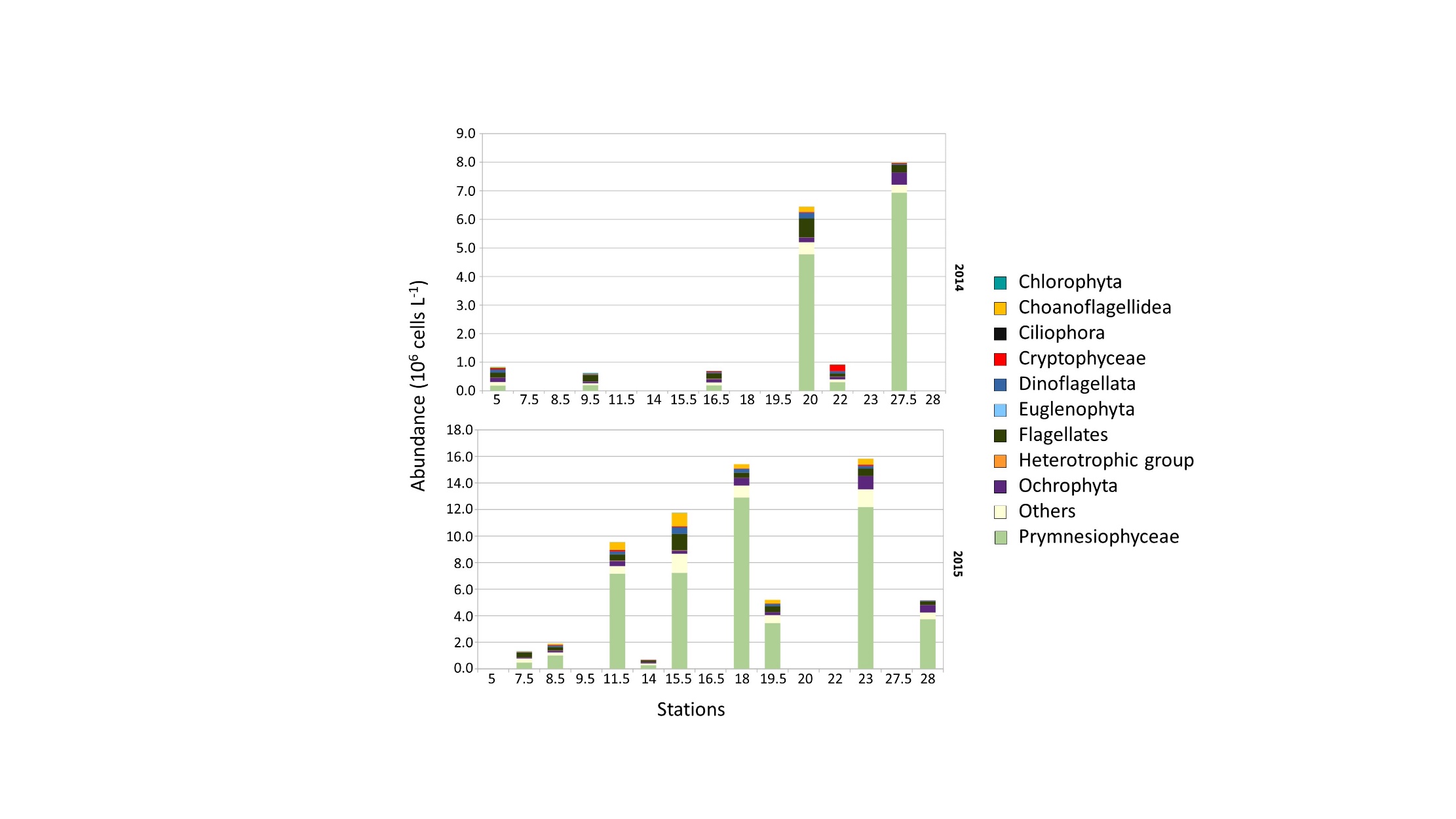


Figure S3. Total abundance of the main protistan phyla detected by microscopy at each station for 2014 (top) and 2015 (bottom).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Higher Rank** | **class** | **validName** | **No. Stations** | **Note** |
| Cercozoa | Incertae\_Sedis | Quadricilia | 1 | Classified as Cercozoa in 20181 |
| Chlorophyta | Chlorophyceae | Pachysphaera | 2 |  |
| Choanoflagellatea | Acanthoecida | Crucispina | 1 |  |
| Choanoflagellatea | Acanthoecida | Monosiga | 8 | Different species |
| Choanoflagellatea | Acanthoecida | Monosiga | 5 |
| Choanoflagellatea | Acanthoecida | Parvicorbicula | 1 | Different species |
| Choanoflagellatea | Acanthoecida | Parvicorbicula | 11 |
| Ciliophora | Intramacronucleata | Lohmanniella | 8 |  |
| Ciliophora | Intramacronucleata | Mesodinium | 4 |  |
| Ciliophora | Intramacronucleata | Uronema | 1 |  |
| Cryptophyta | Cryptomonadales\_cl | Hemiselmis | 2 |  |
| Cryptophyta | Cryptomonadales\_cl | Plagioselmis | 12 | Haploid stage of Teleaulax (found in 18S)2 |
| Dynophyta | Dinophyceae | Amphidinium | 14 | Different species |
| Dynophyta | Dinophyceae | Amphidinium | 3 |
| Dynophyta | Dinophyceae | Peridiniella | 4 | Different species |
| Dynophyta | Dinophyceae | Peridiniella | 1 |
| Dynophyta | Dinophyceae | Proterythropsis | 5 |  |
| Dynophyta | Dinophyceae | Torodinium | 1 |  |
| Euglenozoa | Euglenoidea | Eutreptiella | 1 |  |
| Haptophyta | Prymnesiales | Corymbellus | 9 | Colonial form of Chrysochromulina (found in 18S)3 |
| Haptophyta | Prymnesiophyceae\_cl | Phaeocystis\_haploid | 3 | Can't be differentiated from diploid stage using 18S |
| Ochrophyta | Dictyochophyceae | Apedinella | 3 |  |
| Ochrophyta | Diatomea | Arcocellulus | 6 |  |
| Ochrophyta | Raphidophyceae | Chattonella | 1 |  |
| Ochrophyta | Diatomea | Cylindrotheca | 1 |  |
| Ochrophyta | Dictyochophyceae | Dictyocha | 4 |  |
| Ochrophyta | Chrysophyceae | Dinobryon | 2 |  |
| Ochrophyta | Raphidophyceae | Heterosigma | 14 |  |
| Ochrophyta | Diatomea | Lennoxia | 2 |  |
| Ochrophyta | Diatomea | Membraneis | 1 |  |
| Ochrophyta | Xanthophyceaea | Meringosphaera | 6 | First sequenced in 20214 |
| Ochrophyta | Dictyochophyceae | Pseudopedinella | 6 | Different species |
| Ochrophyta | Dictyochophyceae | Pseudopedinella | 7 |
| Stramenopiles | Incertae\_Sedis | Commation | 6 | Classified as "MAST" in sequencing |
| Telonemia | Telonemea | Telonema | 6 | Different species; unique in this phylum |
| Telonemia | Telonemea | Telonema | 12 |

## Table S2: Taxa only found in microscopy

Note. 1. Yabuki and Ishida (2018); 2. Altenburger et al. (2020); 3. Estep and MacIntyre (1989); 4. Zlatogursky et al. (2021)

Some taxa identified in microscopy had other names in our sequencing database. For example, *Phaeocystis* was identified in both haploid and diploid stages which can’t be discriminated using 18S; *Corymbellus* (microscopy)is the colonial form of *Chrysochromulina* (18S) and *Plagioselmis* (microscopy) is the haploid form of *Teleaulax* (18S). Other taxa were first sequenced (Zlatogursky et al., 2021) or taxonomically classified (Yabuki and Ishida, 2018) after our sequencing database was made (SILVA v128, 2016).

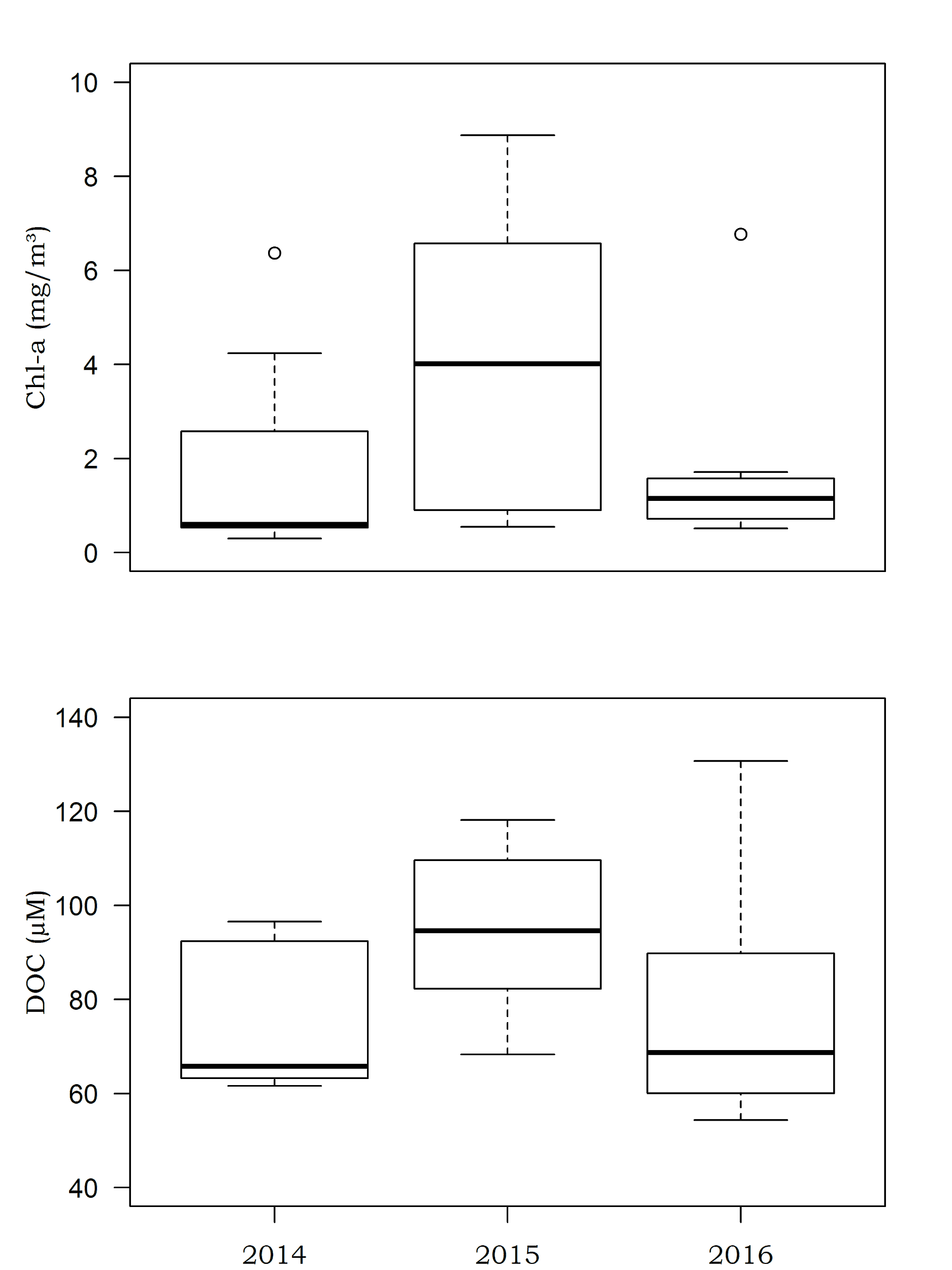


Figure S4. Box and whiskers plot of 5% and 95% (whiskers), 25% and 75% (box) and median (bold line) chlorophyll-*a* and DOC concentrations among years across all stations of the Atlantic Repeat Hydrography Line 7 west (AR7W) sampling line in the Labrador Sea.

## Table S3: Adjusted R2 values from the variance partitioning on taxonomic composition and selected functional traits shown as percentages for each fraction.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Water mass (WM)** | **Year** | **Days before peak** | **WM+Year** | **DBP+WM** | **DBP+Year** | **DBP+Year+WM** | **Total** |
| **(DBP)** |
| **Taxonomic composition** | 8%\* | 4%\* | 0% | 1% | 9% | 8% | 0% | 30% |
| **Trophic strategy** | 10%\* | 14%\* | 0% | 0% | 27% | 11% | 0% | 62% |
| **Size (5 classes)** | 16%\*\*\* | 9%\* | 0% | 0% | 13% | 17% | 0% | 55% |
| **Motility** | 18%\* | 13%\* | 0% | 0% | 23% | 19% | 0% | 73% |
| **DMS** | 0% | 31%\*\* | 0% | 4% | 5% | 14% | 0% | 54% |

Note: DMS represent dimethylsulfoxide or dimethylsulfoniopropionate producers. \*, \*\* and \*\*\* represent partial RDA p-values of ≤ 0.05, ≤ 0.01 and ≤ 0.001, respectively.

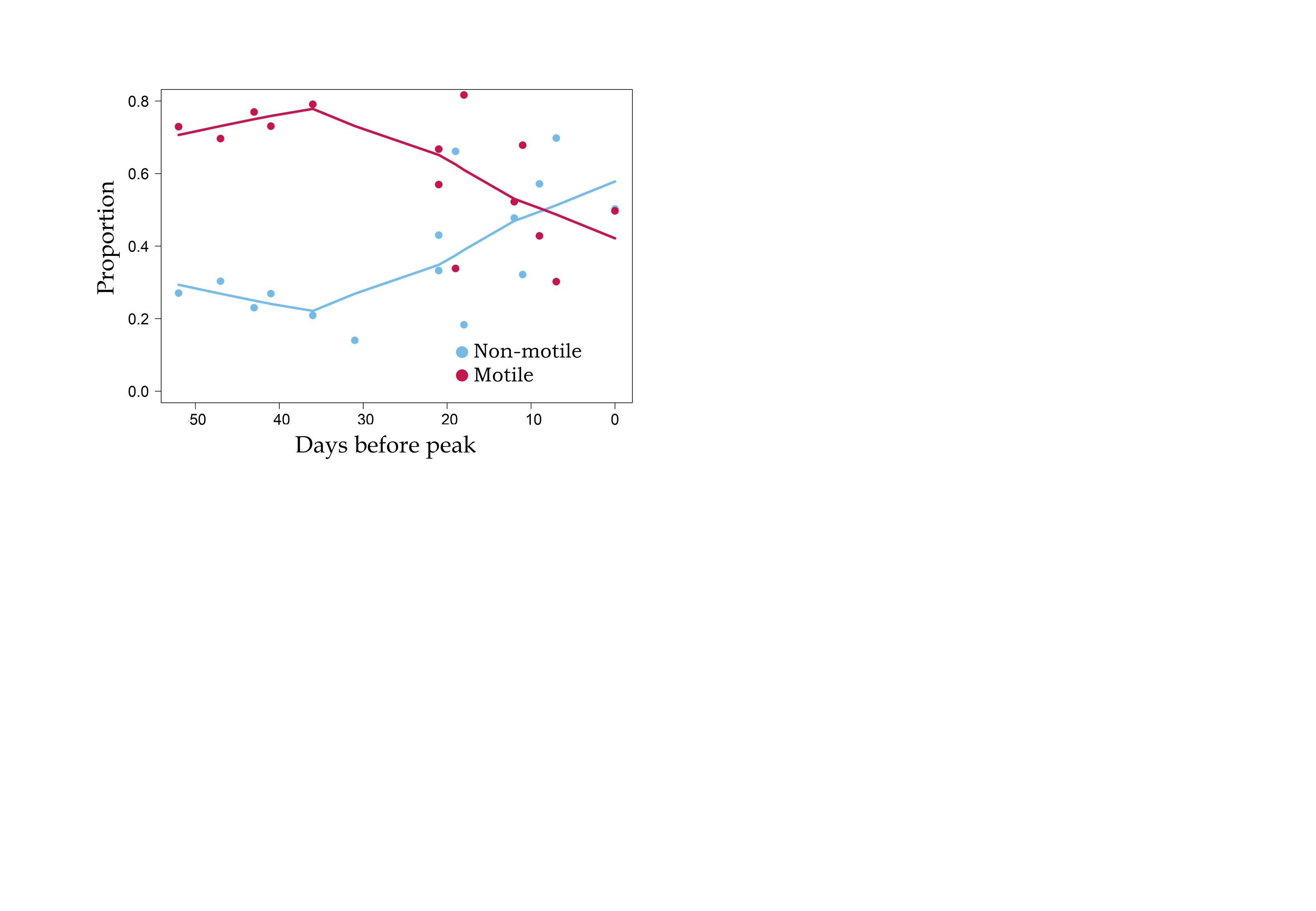


Figure S5. The smoothed (LOWESS function, stats core R package, 60% span) relationship between the proportion of motile protists and the number of days before peak.

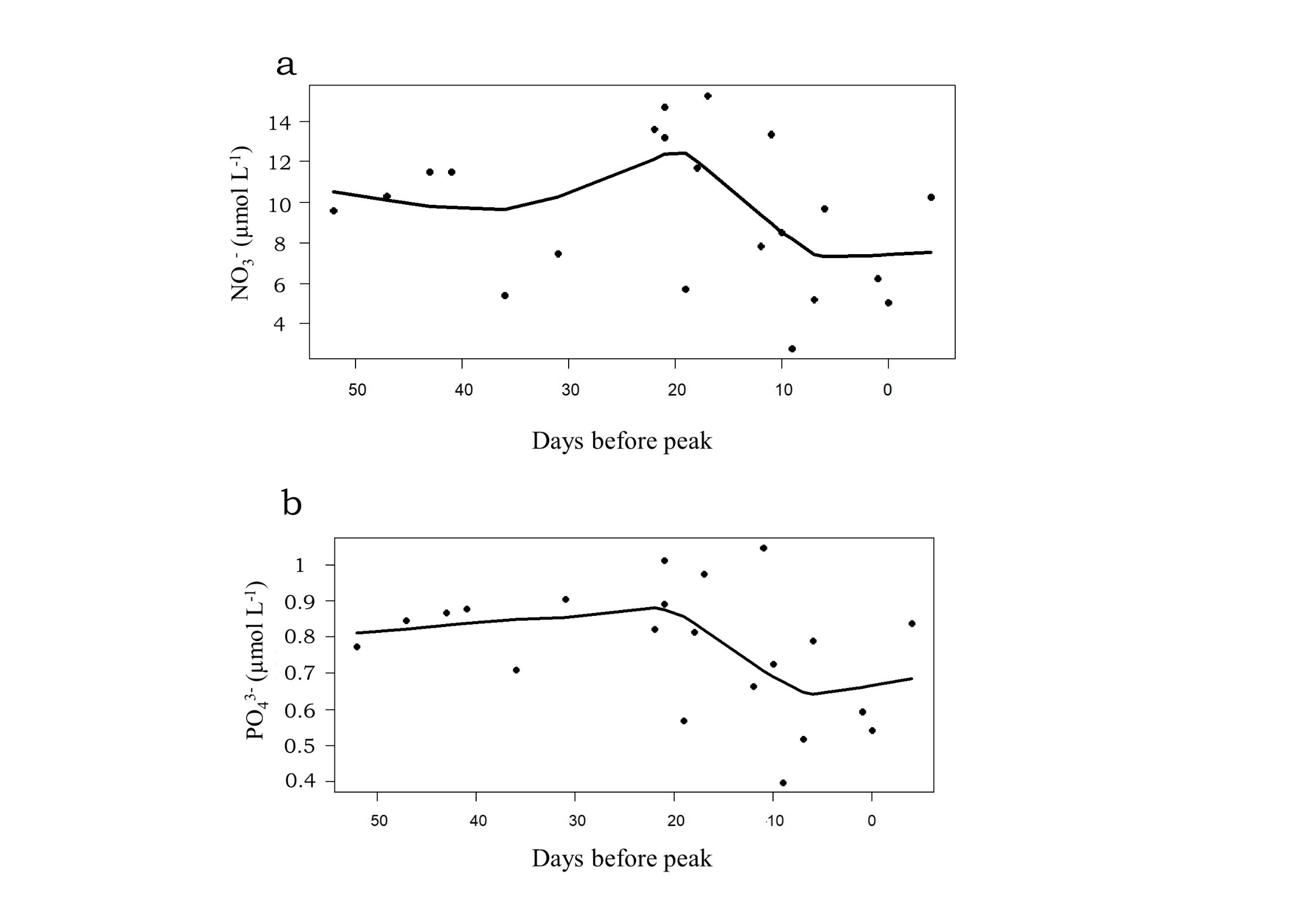


Figure S6. The smoothed (LOWESS function, stats core R package, 60% span) relationship between nitrate (a) and phosphate (b) concentrations the number of days before peak.

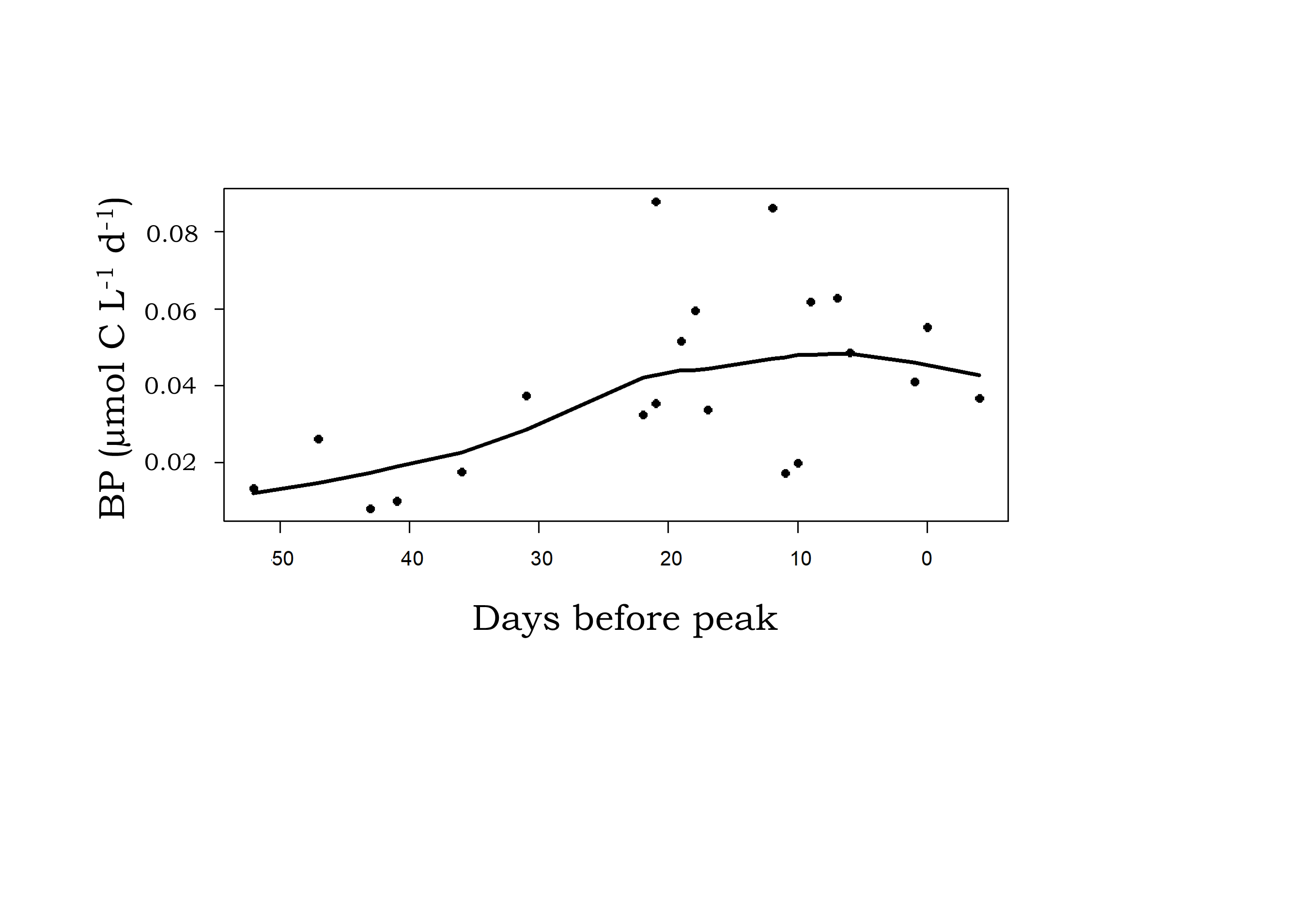


Figure S7. The smoothed (LOWESS function, stats core R package, 60% span) relationship between bacterial biomass production and the number of days before peak.

**References**

Altenburger, A., Blossom, H.E., Garcia-Cuetos, L., Jakobsen, H.H., Carstensen, J., Lundholm, N., et al. (2020). Dimorphism in cryptophytes—The case of Teleaulax amphioxeia/Plagioselmis prolonga and its ecological implications. *Science Advances* 6(37)**,** eabb1611. doi: 10.1126/sciadv.abb1611.

Estep, K.W., and MacIntyre, F. (1989). Taxonomy, life cycle, distribution and dasmotrophy of Chrysochromulina: a theory accounting for scales, haptonema, muciferous bodies and toxicity. *Marine Ecology Progress Series* 57(1)**,** 11-21.

Yabuki, A., and Ishida, K.-i. (2018). An Orphan Protist Quadricilia rotundata Finally Finds Its Phylogenetic Home in Cercozoa. *Journal of Eukaryotic Microbiology* 65(5)**,** 729-732. doi: <https://doi.org/10.1111/jeu.12502>.

Zlatogursky, V.V., Shɨshkin, Y., Drachko, D., and Burki, F. (2021). The long-time orphan protist Meringosphaera mediterranea Lohmann, 1902 [1903] is a centrohelid heliozoan. *The Journal of Eukaryotic Microbiology* 68(5)**,** e12860. doi: 10.1111/jeu.12860.