

Coccolithophore bloom dynamics shape bacterioplankton communities in the northern Bay of Biscay

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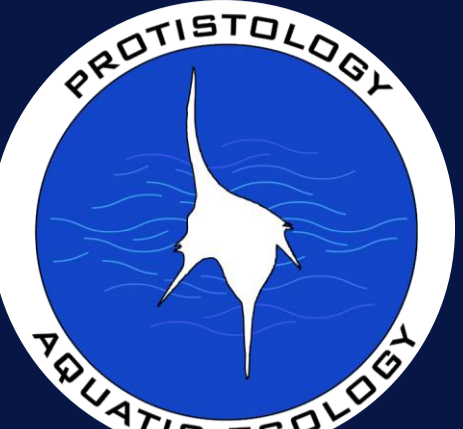


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Introduction & Aim

- Despite the importance of bacteria for the remineralisation and export efficiency of organic matter in the oceans, their specific roles in marine biogeochemical cycling remain largely unknown.
- The continental margins of the Bay of Biscay (W Europe) are characterized by intense phytoplankton blooms, which display a high degree of spatial and temporal complexity at various scales, shaped by local hydrodynamics and weather conditions.
- We performed a detailed analysis of **bacterial diversity** and **community dynamics during a diatom-coccolithophore bloom** in the Bay of Biscay in spring 2006. More specifically, we were interested in investigating the precise relationship between **bacterial diversity** and changes in **phytoplankton bloom stage and associated organic matter dynamics (especially Transparent Exopolymeric Particles – TEP)**.

Results

Stations 1, 2, 3, and 6 were characterized by a high coccolithophore biomass (Prymnesiophytes) with 1b (revisited after one week) showing a decrease in chl a, indicating the bloom's decay. In contrast, stations 4 (and especially 4b) and 7 were dominated by diatoms and to a lesser degree cryptophytes. Stations 6 & 8 had higher relative contributions of dinoflagellates.

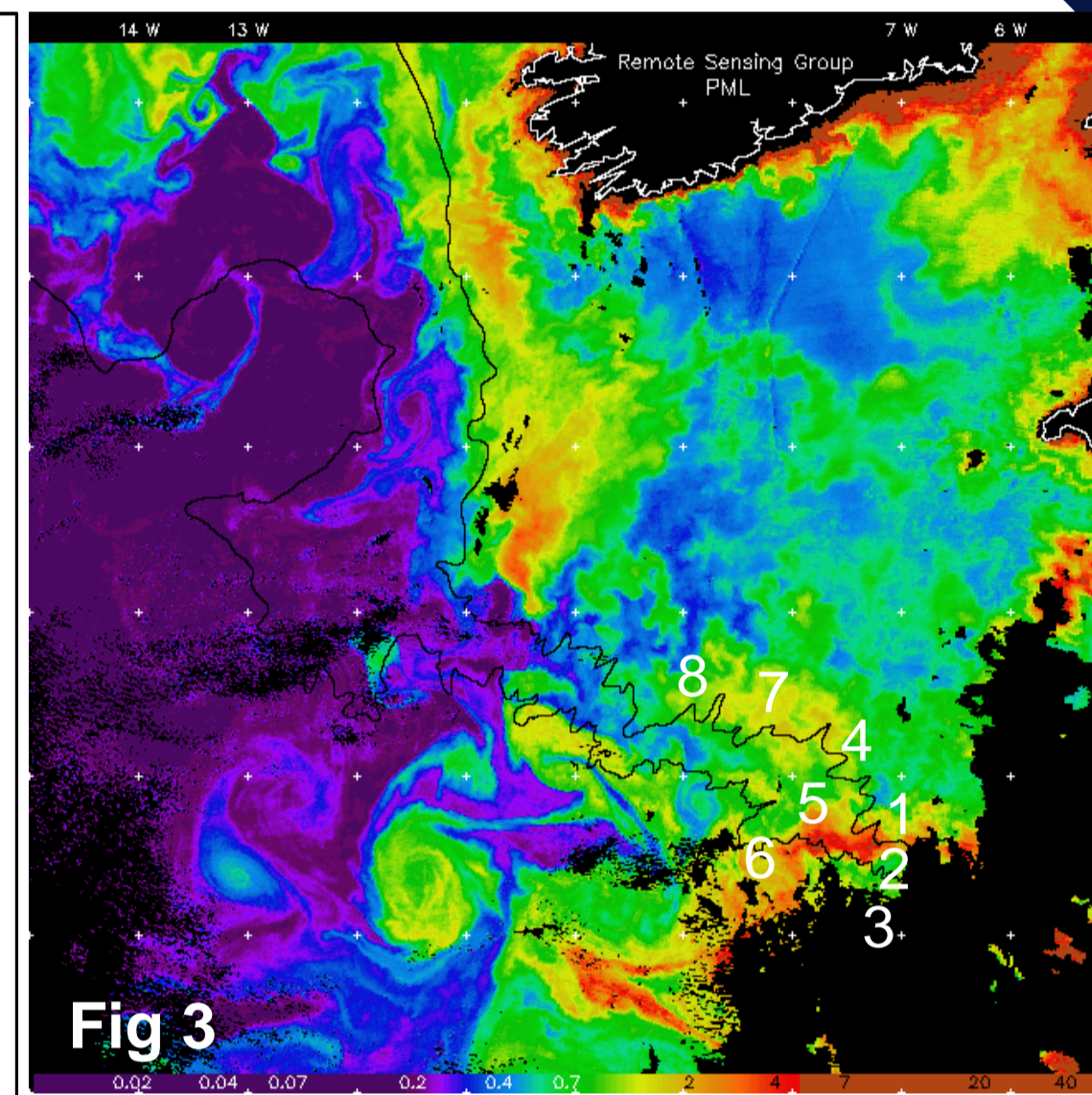
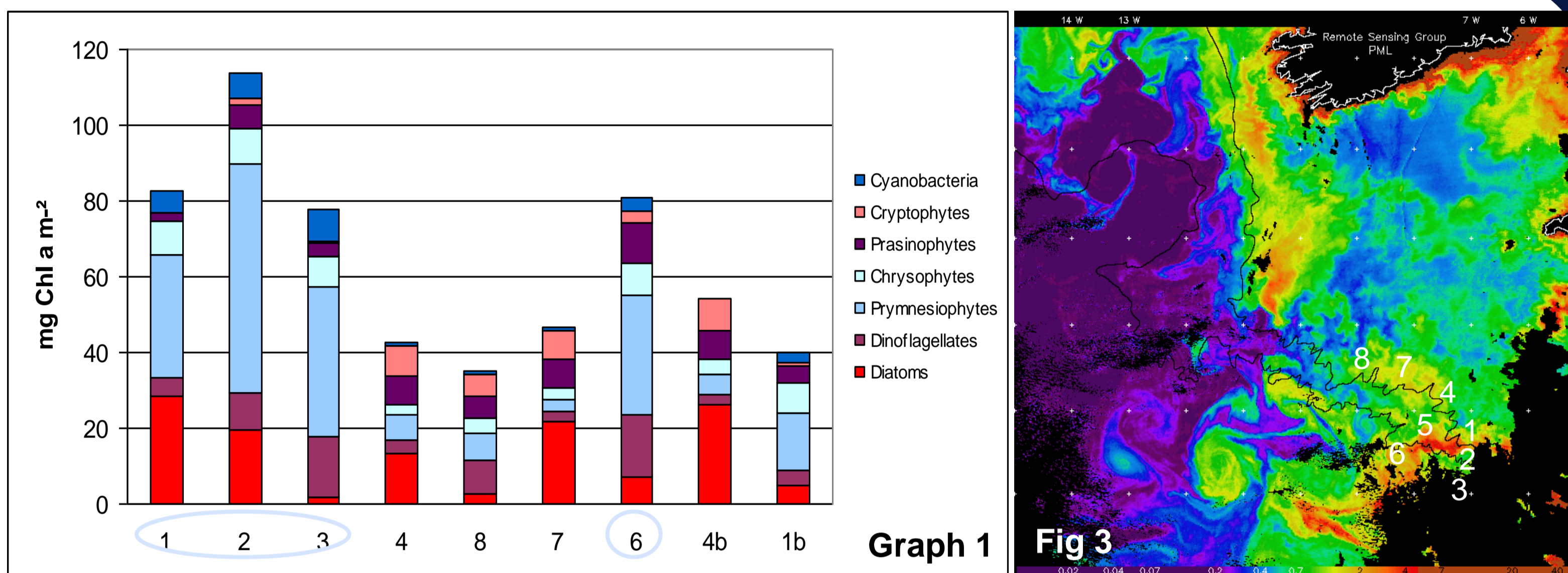
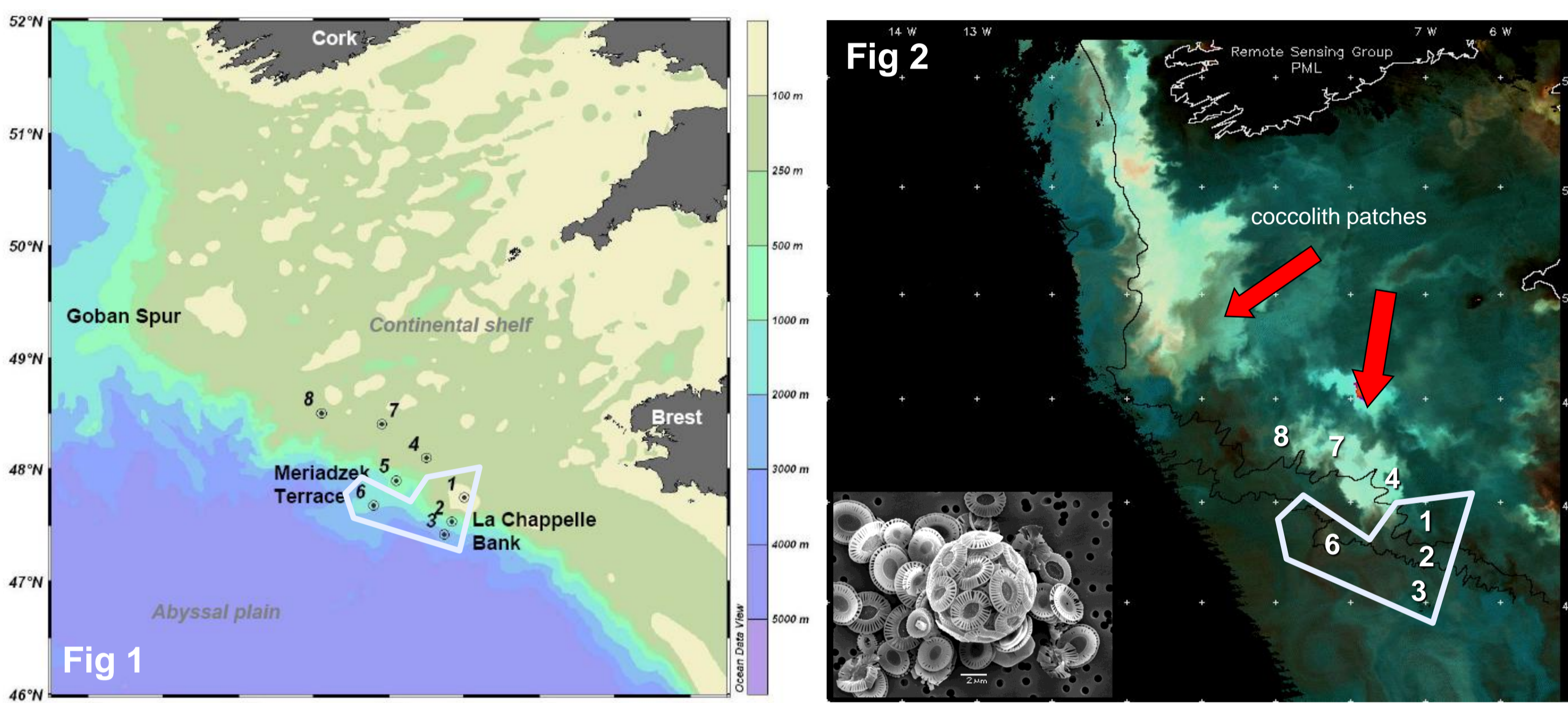


Fig. 1. Study area; oceanographic stations are denoted by numbers. **Fig. 2.** Backscatterance remote sensing image. Light-coloured patches represent suspended coccoliths in the watercolumn (courtesy of Steve Groom, PML). **Fig. 2 inset.** Scanning electron microscope image of an *Emiliania huxleyi* coccosphere shedding its coccoliths.

Fig. 3. SeaWiFS remote sensing image of chl a concentrations. **Graph. 1.** Depth-integrated chl a concentrations partitioned over algal groups. **Graph. 2&3.** PCA ordinations of the free-living (2) and the particle-associated (3) BCC. Bold arrows represent environmental variables significantly ($p < 0.05$) correlated with the variation in BCC.

The blue polygons in figs. 1, 2 and graphs 2, 3 indicate the stations with coccolithophore bloom



Average relative abundance of dominant bacterial DGGE phylotypes

Free-living fraction

Phylotype	Species	Abundance (%)
aProt_5	uncult. α -Proteobacterium	18%
Pubique	<i>Pelagibacter ubique</i>	13%
SAR86_1	uncult. γ -Proteobacterium	10%
18.2	no clone available	8%
SAR86_2	uncult. γ -Proteobacterium	7%
yProt_2	uncult. γ -Proteobacterium	6%

Particle-associated fraction

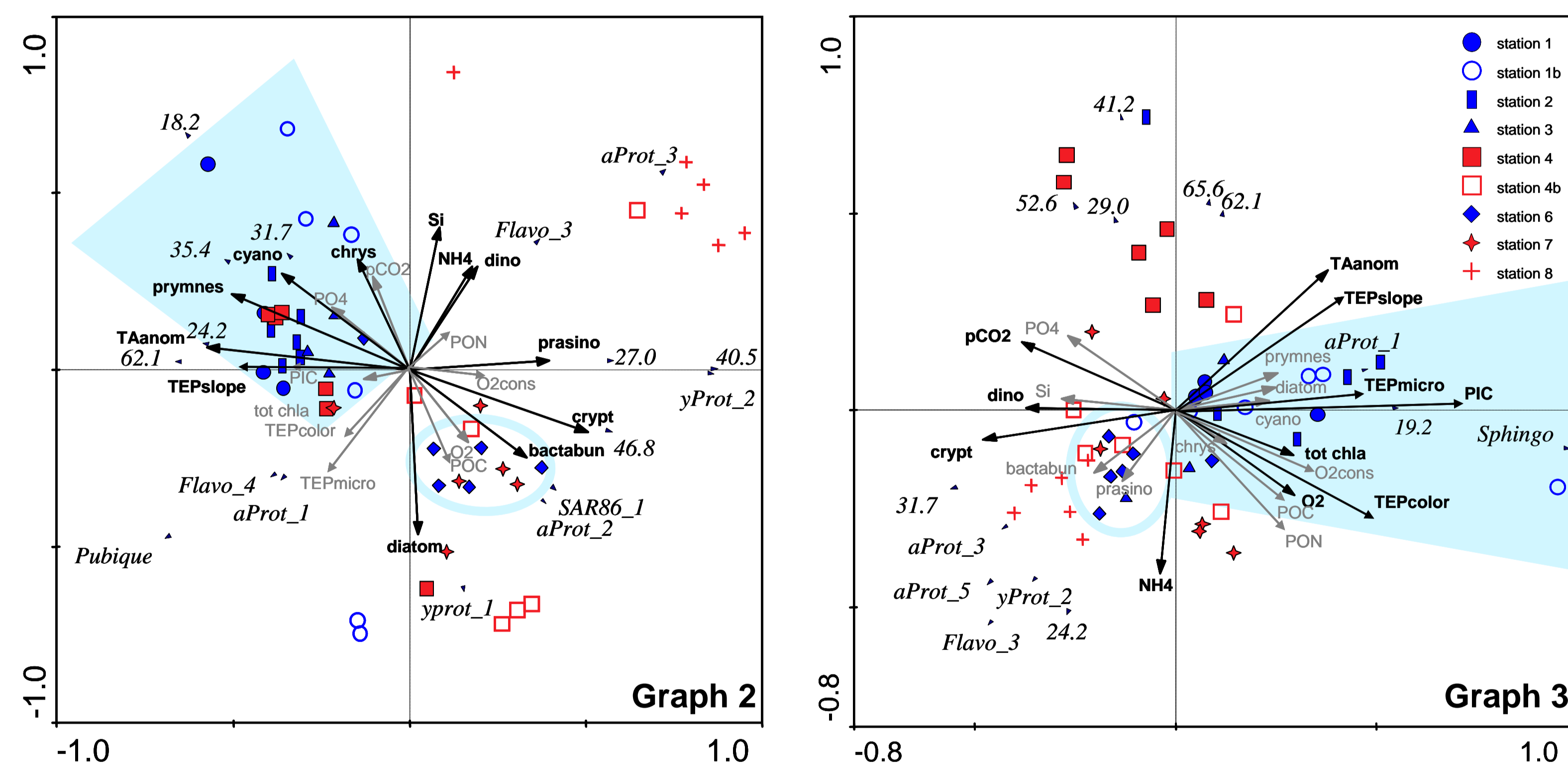
Phylotype	Species	Abundance (%)
Sphingo	<i>Saprospiraceae</i> sp.	19%
24.2	no clone available	11%
aProt_5	uncult. α -Proteobacterium	8%
Pubique	<i>Pelagibacter ubique</i>	8%
41.2	no clone available	5%
Flavo_4	<i>Ulviabacter</i> sp.	5%

Particle-associated (PA) and free-living (FL) bacterial assemblages differ in composition, with a high relative abundance of *Sphingobacterium* typical of PA fraction and α - and γ -Proteobacteria common in the FL BCC.

PCA's of the bacterial community composition (BCC) of both

the FL and PA fractions show a tight clustering of the samples of the coccolithophore dominated stations 1, 1b, 2, and 3 (highlighted in blue). However, station 6 associates with that of the diatom dominated stations 4b and 7, while station 4 (FL) clusters with the coccolithophore dominated stations. Stations 4 (PA) and 8 (FL) each display a station-specific BCC.

The BCC in both FL and PA fractions seems to be related to different driving forces, with **variation in FL BCC correlating with phytoplankton community composition** and **variation in PA BCC more strongly related to TEP dynamics**. Typical TEP-associated phylotypes could be identified (*Sphingo*, aProt_1, 19.2).



Conclusions & Prospects

- FL and PA BCC have a different species composition and are related to different environmental factors, with PA communities more strongly relating to TEP dynamics than to phytoplankton composition.
- Although the bacterial communities show congruence with the phytoplankton dynamics, transitional bloom conditions and local hydrodynamic and biological features (such as grazing and lysis) could account for the observed discrepancies between BCC and the nature of phytoplankton community (e.g. BCC at stations 4 and 6).
- Mesocosm tracer experiments are currently being set-up to investigate the specific role of bacteria in TEP and sugar dynamics.

Material & Methods

During 2006 oceanographic campaign, the upper 80 m of the water column were sampled at 6 depths for bacterial DNA (size-fractionated at 3 μ m), microplankton, pigments, and various environmental variables. Stations 1, 4, 7, and 8 were located on the Bay of Biscay shelf area, and stations 2, 3, and 6 were on the shelf slope. Two stations - stations 1 and 4 - were sampled twice at a about week interval. Bacterial community composition was assessed by Denaturant Gradient Gel Electrophoresis and clone libraries (16 S rRNA gene) and analyzed using Principal Components Analysis (PCA) Phytoplankton community composition were analysed by microscopy and chemotaxonomic partitioning of HPLC data.

PEACE project URL: <http://www.co2.ulg.ac.be/peace>

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