From bloom to foam: tracing the role of *phaeocystis* in marine gel formation

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Marine ecosystems harbor complex biochemical processes that are vital to the global carbon cycle[1,2]. A key component in this cycle is the generation of particulate organic carbon (POC), particularly through marine gels formed during algal blooms[3]. Our study focuses on *Phaeocystis*, a cosmopolitan, bloom-forming alga known for its foam production[4]. Under optimal conditions, *Phaeocystis* exudes excess energy as glucans and mucopolysaccharides. These molecules help form a gel matrix that facilitates colony formation and attracts specific bacterial communities. Post-bloom, the lysis of *Phaeocystis* colonies releases large quantities of carbohydrate-rich dissolved organic matter (DOM) into the water. This DOM serves as a precursor for transparent exopolymer particles (TEP), leading to marine gel and foam formation[5–7].

Our objective was to delineate and quantify the relationship between late-stage *Phaeocystis* blooms and TEP concentrations. We wanted to assess the metabolic contribution of *Phaeocystis* to the overall expression of genes involved in carbohydrate synthesis. We utilized a multidisciplinary approach, combining metatranscriptomics with measurements of ecosystem properties and abiotic factors. We organised a sampling campaign with the R/V Simon Stevin targeting two distinct ecosystem states during diel cycles: a *Phaeocystis globosa* bloom and a post-bloom ecosystem state. We measured primary production, phyto- and zooplankton community abundance and taxonomy via high-throughput automated microscopy, alongside microeukaryotic species' metabolic activity through metatranscriptomic analysis.

We captured a late-stage *Phaeocystis* bloom near Ostend harbour, and a post-bloom ecosystem 46.60 km northeast. Preliminary findings indicate significantly higher TEP concentrations during the late-stage *Phaeocystis* bloom compared to the non-*Phaeocystis* dominated ecosystem. Notable differences were also observed in the composition and abundance of phyto- and zooplankton communities. The *Phaeocystis* dominated ecosystem exhibited elevated nutrient loadings, dissolved oxygen, dissolved carbon, and turbidity. Successful RNA extraction and short-read sequencing have set the stage for the ongoing metatranscriptomic data analysis.

Thoroughly understanding these processes is vital for better grasping the global carbon cycle and the ecological impacts of algal blooms. This research provides detailed insights in the intricate connections between microbial processes and global biogeochemical dynamics.

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