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# SEAFOAMS ASSOCIATED WITH PHAEOCYSTIS SP. BLOOM ACCUMULATE SAPROPHYTIC AND PARASITIC MICROORGANISMS FROM TERRESTRIAL ORIGIN

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**Abstract**

The community composition, structure, origin, and trophic functions of eukaryotic microorganisms on seafoam deposits (N = 30) and adjacent seawater (*N* = 32) were explored at the beach of Wimereux (North of France) during the *Phaeocystis globosa* spring bloom (March-May 2023), using high throughput sequencing of 18S rRNA marker gene. Our results notably showed that eukaryotic communities trapped in seafoams were different from communities in adjacent seawater. In particular, seafoams were rich in ASVs affiliated to saprobes and parasites compared to seawater, with a terrestrial origin for most of them.

## CONTEXT, MATERIAL AND METHODS

Seafoams, often associated with decaying marine algal blooms, are ubiquitous and increasingly acknowledged as a potential environmental issue (Lancelot 1995, Spilmont *et al.* 2009, Schilling & Zessner 2011, Peperzak and van Wezel 2023, Das *et al.* 2024, Seuront *et al.* 2024, Cazalis-Henry *et al.* 2025). The composition, structure, origin, and trophic functions of eukaryotes community trapped in seafoams are still, however, largely unexplored (Schilling & Zessner 2011, Das *et al.* 2024). Yet, such knowledge is essential for assessing the role of foams in the ecosystem functioning of the aquatic environment.

On the seashore of the eastern English Channel and North Sea during the spring bloom of *Phaeocystis globosa* (Haptophyte), a recurrent phenomenon of massive seafoam accumulation following agitated seawater and crashing waves is well documented (Lancelot 1995, Blaw *et al.* 2010, Peperzak and van Wezel 2023). Besides unpleasant visuals and odors (Lancelot 1995, Blaw *et al.* 2010), these seafoam deposits may concentrate pollutants (The Guardian 2023, Castagno 2025), various microorganisms (Schilling & Zessner 2011), and may provoke sediment anoxia (Spilmont *et al.* 2009). In addition, recent studies have reported that seafoams impair the behavior and metabolism of intertidal gastropods and are avoided by these organisms, which led to the identification

of a new taxis, i.e. aphrotaxis, coined from the ancient Greek word *aphrós*, 'seafoam' (Seuront *et al.* 2024, Cazalis-Henry *et al.* 2025).

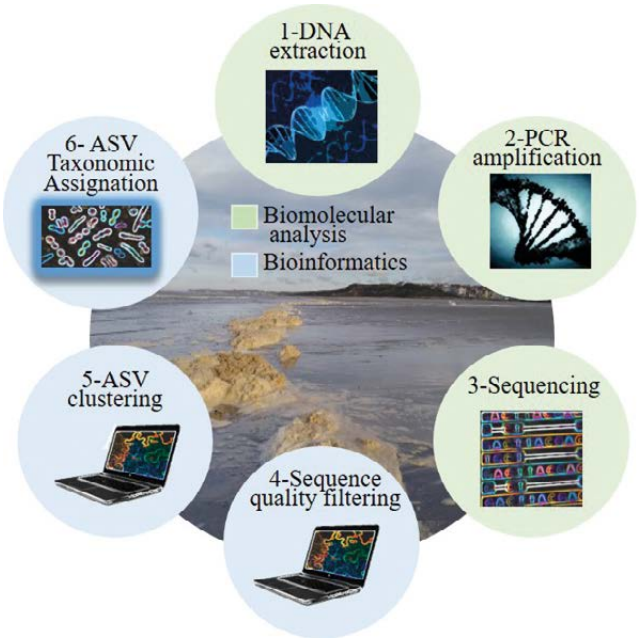


Figure 1. The different steps of the 18S rRNA gene Next Generation Sequencing.
*Figure 1. Les différentes étapes du 18S rRNA gene Next Generation Sequencing.*
ASV: Amplicon Sequence Variant, DNA: Deoxyribonucleic acid, PCR: Polymerase Chain Reaction.

In this study, we analyzed the community composition of eukaryotic microorganisms using high throughput sequencing of 18S rRNA marker gene on seafoam deposits (N = 30) and adjacent seawater (*N* = 32) at the beach of Wimereux (North of France) collected over the duration of the phytoplankton spring bloom, i.e. March-May 2023 (Fig. 1). A comparative analysis was performed to investigate differences between seafoam and seawater samples in microbial diversity, community structure, potential microbes origin along a seawater-land gradient, and trophic modes (e.g. autotroph, mixotroph, phagotroph, saprotroph, parasite). The origin and trophic modes were assessed according to available scientific literatures. Samples were also examined by light microscopy (Nikon Eclipse TE2000-S) and scanning electron microscopy (LEO 438 VP).

## RESULTS AND DISCUSSION

Our results notably showed that eukaryotic communities trapped in seafoams were different from communities in adjacent seawater. Indeed, only 10 % of Amplicon Sequence Variants (ASVs, the molecular equivalent of species) were common between the two habitats (Fig. 2A). The result of diversity analysis showed that seafoams accommodate a greater richness of eukaryotic ASVs compared to seawater. These results support the hypothesis that seafoam is a transition habitat and is strongly influenced by interactions with (i) seawater and wave action, (ii) sands during seafoam formation and accumulation, and (iii) the continent under

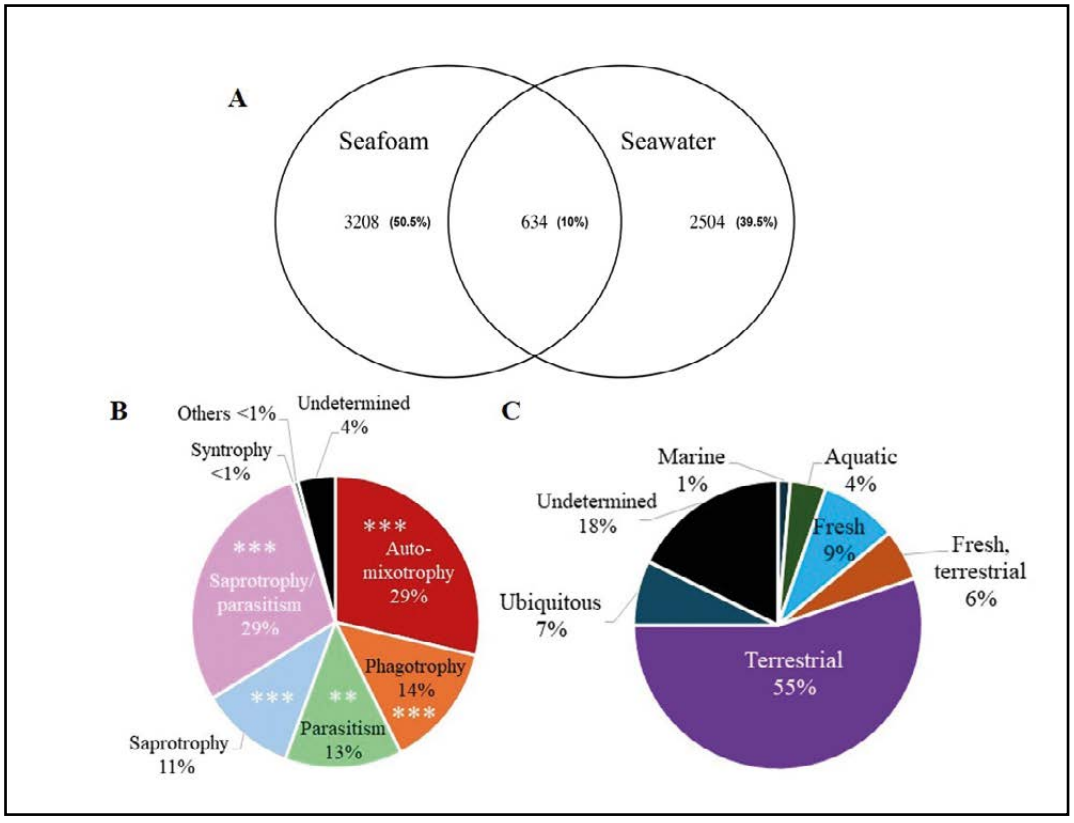


Figure 2. Comparison of eukaryotic communities between seafoam and adjacent seawater.
*Figure 2. Comparaison des communautés eukaryotiques dans la mousse marine et l'eau de mer.*
**A.** Venn diagram showing the number of shared and unique ASVs (Amplicon Sequence Variant) among seafoam and seawater; and **B&C.** The mean proportion (%) in seafoam of the different trophic modes of the eukaryotic ASVs and sources of saprobes and parasites (sea-continent gradient). Comparison between seafoam and seawater: (Mann-Witney test). *p<0.05, **p<0.005, ***p<0.0001.

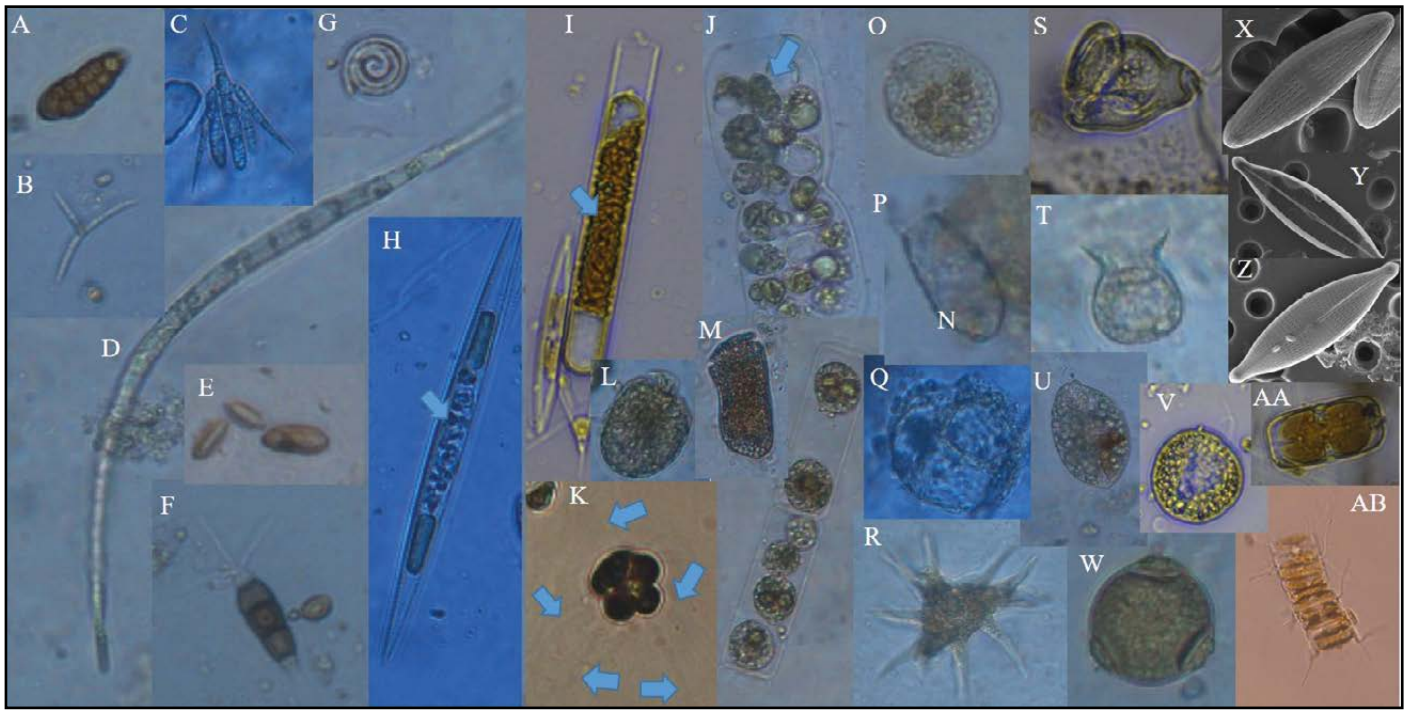


Figure 3. Example of abundant eukaryotic organisms found exclusively in seafoam deposits on the Wimereux beach.
*Figure 3. Exemples d'eucaryotes abondants recensés uniquement dans la mousse déposée sur la plage de Wimereux.*
Fungal conidia (A-J) of **A:** *Alternaria* sp. (Dothideomycetes), **B&C:** *Alatospora acuminata* and *Tetracladium. maxilliforme* (Leotiomycetes), **D:** *Amniculicola longissima* (Dothideomycetes), **E:** *Cladosporium* sp. (Dothideomycetes), **F:** *Neopestalotiopsis clavispora* (Sordariomycetes), **G:** *Neohelicosporium griseum* (Dothideomycetes), **H-I:** oomycete parasitoids, **J:** Chytrid-like in the diatom *Amphiprora*; **K:** *Micractinium pusillum* (Trebouxiophyceae, Chlorophyta); **L-M:** Dinophyceae (**L:** *Sinophysis* sp. ; **M:** *Apicoporus glaber*), **N-Q:** Cercozoa (Rhizaria) (**N:** *Cryothecomonas* sp. in the diatom *Guinardia delicatula*, **O:** Cryomonadida, **P:** Silicofilosea, and **Q:** *Ebria tripartita*); **R:** naked amoeba (Amoebozoa) ; **S:** Zoothamnium sp. (Peritrichia, Ciliata); **T:** *Strombidium* sp. (Oligotrichea, Ciliata); **U:** Euglenid; **V:** *Chlamydomonas* sp. (Chlamydomonadaceae, Chlorophyta) ; **W:** Pollen grain of *Betula_papyrifera* (Archaeplastida), and **X-AB:** the diatoms (Stramenopile, **X:** *Navicula perminuta*, **Y:** *N. gregaria*, **Z:** *N. veneta*, **AA:** *Parlibellus delognei*, and **AB:** *Attheya armata*). Not at scale.

the action of winds, precipitation and animals (Gobet *et al.* 2012, Whitman *et al.* 2014, Probandt *et al.* 2018, Okamoto *et al.* 2022). In addition, seafoams act as a sticky, sponge-like matrix trapping enormous organic contents.

More importantly, when considering the trophic modes of microorganisms, seafoams have 7-fold more ASVs affiliated to saprobes and parasites (corresponding to 53% of all ASVs, Fig. 2B) compared to seawater. However, considering the predominant land-origin of saprobes and parasites (i.e. associated to trees, lichens, plants including vegetables, soil, human gut and skin, and fresh water; 87% of the total ASVs, Fig. 2C), their viability in the intertidal zone and seafoam remain unknown. Such unknown also apply to about 25% of auto- mixotrophs, including pollen and remains of wild and cultivated terrestrial plants. Interestingly, certain fungi, amoeba, Rhizaria, dinoflagellates, ciliates, pollen, euglenid, chlorophytes and diatoms were present only in seafoams (Fig. 3), which may indicate that seafoam acts as selective filters accumulating species and taxa otherwise present at very low concentration in the bulk phase seawater, hence below the detection limits of our analytical approach.

## CONCLUSION

Eukaryotic communities in seafoams are distinct from those in adjacent seawater. Given that seafoams typically occur at the sea-land interface, the seafoam-trapped eukaryotic communities were enriched by organisms originating from land, especially saprobes and parasites. Future studies are needed to investigate their variability as well as their biological activity in a habitat different from the ones they originated from.

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