

# Exploring the phycosphere of *Emiliana huxleyi*: from bloom dynamics to microbiome assembly experiments

Mariana Câmara dos Reis<sup>1</sup>, Sarah Romac<sup>1</sup>, Florence Le Gall<sup>1</sup>, Dominique Marie<sup>1</sup>, Miguel José Frada<sup>2</sup>, Gil Koplovitz<sup>2</sup>, Thierry Cariou<sup>1</sup>, Nicolas Henry<sup>1</sup>, Colomán de Vargas<sup>1</sup>, and Christian Jeannot<sup>1</sup>

<sup>1</sup>Station Biologique de Roscoff

<sup>2</sup>Interuniversity Institute for Marine Sciences in Eilat

February 21, 2022

## Abstract

Coccolithophores have global ecological and biogeochemical significance as the most important calcifying marine phytoplankton group. The structure and selection of prokaryotic communities associated with the most abundant coccolithophore and bloom-forming species, *Emiliana huxleyi*, are still poorly known. In this study, we assessed the diversity of bacterial communities associated with an *E. huxleyi* bloom in the Celtic Sea, exposed axenic *E. huxleyi* cultures to prokaryotic communities derived from bloom and non-bloom conditions and followed the dynamics of their microbiome composition over one year. Bloom-associated prokaryotic communities were dominated by SAR11, Marine group II Euryarchaeota, Rhodobacterales and contained substantial proportions of known indicators of phytoplankton bloom demises such as Flavobacteriaceae and Pseudoalteromonadaceae. Taxonomic richness of replicated co-cultures resulting from natural communities with axenic *E. huxleyi* rapidly shifted and then stabilized over time, presumably by ecological selection favoring more beneficial populations. Recruited microbiomes from the environment were consistently dependent on the composition of the initial bacterioplankton community. Phycosphere-associated communities derived from the *E. huxleyi* bloom depth were highly similar to one another, suggesting deterministic processes, whereas cultures from non-bloom conditions show an effect of both deterministic processes and stochasticity. Overall, this work sheds new light on the importance of the initial inoculum composition in microbiome recruitment and elucidates the temporal dynamics of its composition and long-term stability.

## Hosted file

C:\selectlanguage{ngerman}âmara dos Reis et al. Manuscript.pdf available at <https://authorea.com/users/461680/articles/557316-exploring-the-phycosphere-of-emiliana-huxleyi-from-bloom-dynamics-to-microbiome-assembly-experiments>



