

# Chlorophyll measurements from HHQ experiments conducted during the MesoHux mesocosm experiment, May 2017, Bergen, Norway

**Website:** <https://www.bco-dmo.org/dataset/753388>

**Data Type:** experimental

**Version:** 1

**Version Date:** 2019-01-23

## Project

» [Collaborative Research: Building a framework for the role of bacterial-derived chemical signals in mediating phytoplankton population dynamics](#) (HHQSignals)

| Contributors                       | Affiliation   | Role                      |
|------------------------------------|---|---------------------------|
| <a href="#">Harvey, Elizabeth</a>  | Skidaway Institute of Oceanography (SkIO)           | Principal Investigator    |
| <a href="#">Rowley, David</a>      | University of Rhode Island (URI)                    | Co-Principal Investigator |
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## Abstract

This dataset includes chlorophyll measurements from HHQ experiments conducted during the MesoHux mesocosm experiment, May 2017, Bergen, Norway. Microbial mesocosms were spiked with 2-heptyl-4-quinolone (HHQ).

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## Coverage

**Spatial Extent:** Lat:60.221 Lon:5.281

**Temporal Extent:** 2017-05-16 - 2017-05-31

## Dataset Description

This dataset includes chlorophyll measurements from HHQ experiments conducted during the MesoHux mesocosm experiment, May 2017, Bergen, Norway. Microbial mesocosms were spiked with 2-heptyl-4-quinolone (HHQ).

## Methods & Sampling

Water samples for chlorophyll extraction were collected either from the mesocosms via a 5 L Niskin or subsampled from experimental bottles. Chlorophyll samples were filtered in triplicate through a 25mm Glass Fiber Filter (GFF), and immediately extracted in 6 mL of ethanol for 12-18 hours in the dark at room temperature. After extraction, filters were removed from the sample, and the fluorescence of the sample was read on a Turner AU10. The sample was then acidified with 1 drop of 10% HCL and re-read on the same

instrument. The fluorometer was calibrated prior to using with a chlorophyll standard purchased from Sigma.

Mesocosm treatment for all HHQ experiments was as follows:

Redfield: N:P added in a 16:1 ratio during the first 3 days of the experiment, no shading

HHQ treatments here are as follows:

High HHQ - 100 ng mL<sup>-1</sup> (410 uM) added to triplicate 5L bottles.

DMSO control - equivalent (v:v) DMSO added to triplicate 5L bottles.

All bottles were incubated for 24h in a flow-through tank, that was shaded to mimic in situ conditions.

Chlorophyll samples were taken at T0 and T24 for all experiments.

Data were processed in Excel with statistics run in Excel, R, or Matlab.

## Data Processing Description

### BCO-DMO Processing Notes:

- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- reduced precision of total chlorophyll columns from (5 to 15) to 2 decimal places

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## Data Files

| File  |
|---|
| <b>chlorophyll.csv</b> (Comma Separated Values (.csv), 4.77 KB)<br>MD5:28df4bedc5ac8fc7d022a8513b0541d3 |
| Primary data file for dataset ID 753388   |

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## Parameters

| Parameter            | Description                                       | Units                               |
|----------------------|---|-------------------------------------|
| Date                 | sampling date formatted as Mon dd yyyy            | unitless                            |
| Sample               | sample identifier                                 | unitless                            |
| Experiment_num       | experiment number                                 | unitless                            |
| Time                 | time since start of experiment                    | hours                               |
| Replication          | replicate number                                  | unitless                            |
| Volume_Filtered_mL   | volume filtered                                   | milliliters (mL)                    |
| Extract_Volume_mL    | volume extracted                                  | milliliters (mL)                    |
| Dilution_Factor      | dilution factor                                   | unitless                            |
| F_o                  | initial fluorescence reading                      | Relative Fluorescence Units (RFU)   |
| F_o_blank            | initial fluorescence of control blank             | Relative Fluorescence Units (RFU)   |
| F_a                  | fluorescence after acidification                  | Relative Fluorescence Units (RFU)   |
| F_a_blank            | fluorescence of control blank after acidification | Relative Fluorescence Units (RFU)   |
| Total_chl_with_phaeo | total chlorophyll including phaeophytin           | micrograms chlorophyll/Liter (ug/L) |
| Total_ChI_no_phaeo   | total chlorophyll NOT including phaeophytin       | micrograms chlorophyll/Liter (ug/L) |

## Instruments

|   |   |
|---|---|
| <b>Dataset-specific Instrument Name</b> | Turner AU10 fluorometer   |
| <b>Generic Instrument Name</b>          | Fluorometer   |
| <b>Generic Instrument Description</b>   | A fluorometer or fluorimeter is a device used to measure parameters of fluorescence: its intensity and wavelength distribution of emission spectrum after excitation by a certain spectrum of light. The instrument is designed to measure the amount of stimulated electromagnetic radiation produced by pulses of electromagnetic radiation emitted into a water sample or in situ. |

|   |   |
|---|---|
| <b>Dataset-specific Instrument Name</b> | 5 L Niskin  |
| <b>Generic Instrument Name</b>          | Niskin bottle   |
| <b>Dataset-specific Description</b>     | Used to collect water samples.  |
| <b>Generic Instrument Description</b>   | A Niskin bottle (a next generation water sampler based on the Nansen bottle) is a cylindrical, non-metallic water collection device with stoppers at both ends. The bottles can be attached individually on a hydrowire or deployed in 12, 24, or 36 bottle Rosette systems mounted on a frame and combined with a CTD. Niskin bottles are used to collect discrete water samples for a range of measurements including pigments, nutrients, plankton, etc. |

## Project Information

### **Collaborative Research: Building a framework for the role of bacterial-derived chemical signals in mediating phytoplankton population dynamics (HHQSignals)**

**Coverage:** Bergen, Norway

#### *NSF Award Abstract:*

Bacteria and phytoplankton play a central role in the modification and flow of materials and nutrients through the marine environment. While it has been established that interactions between these two domains are complex, the mechanisms that underpin these interactions remain largely unknown. There is increasing recognition, however, that dissolved chemical cues govern these microbial interactions. This project focuses on establishing a mechanistic framework for how bacterially derived signaling molecules influence interactions between phytoplankton and bacteria. The quorum-sensing (QS) molecule, 2-heptyl-4-quinolone (HHQ) will be used as a model compound for these investigations. Previously published work suggests that exposure to very low levels of HHQ results in phytoplankton mortality. Gaining a mechanistic understanding of these ecologically important interactions will help to inform mathematical models for the accurate prediction of the cycling of material through the marine microbial loop. This work initiates a new, hybrid workshop-internship

undergraduate research program in chemical ecology, with a focus

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Interactions between phytoplankton and bacteria play a central role in mediating biogeochemical cycling and microbial trophic structure in the ocean. The intricate relationships between these two domains of life are mediated via excreted molecules that facilitate communication and determine competitive outcomes. Despite their predicted importance, identifying these released compounds has remained a challenge. The PIs recently identified a bacterial QS molecule, HHQ, produced by globally distributed marine gamma-proteobacteria, which induces phytoplankton mortality. The PIs therefore hypothesize that bacteria QS signals are critical drivers of phytoplankton population dynamics and, ultimately, biogeochemical fluxes. This project investigates the timing and magnitude of HHQ production, and the physiological and transcriptomic responses of susceptible phytoplankton species to HHQ exposure, and quantifies the influence of HHQ on natural algal and bacterial assemblages. The work connects laboratory and field-based experiments to understand the governance of chemical signaling on marine microbial interactions, and has the potential to yield broadly applicable insights into how microbial interactions influence biogeochemical fluxes in the marine environment.

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## Funding

| Funding Source   | Award                       |
|--|-----------------------------|
| <a href="#">NSF Division of Ocean Sciences (NSF OCE)</a> | <a href="#">OCE-1657898</a> |

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