All data and code for: Peters et al. “Mesozooplankton grazing exerts a significant control on cyanobacterial harmful algal bloom (cHAB) growth in a large eutrophic lake”

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**Note:** The Lake Erie Plankton Abundance Survey (LEPAS) database is not publicly available. Some scripts extract from that database, which is not available here; however, all data required to conduct the analyses are available herein.

**Folders**

*01\_Data* – Raw data to run scripts, as well as output data from scripts

*02\_Script* – R scrips

*03\_Figures* – Figures generated for manuscript and to evaluate data

**R Script**

A description of all data used and outputs generated are described under the script which uses or generates them. Any product (csv, png, ect.) has the same initial number (e.g., “01\_”) as the script that generated it.

**00\_Mesozoop\_LEPAS\_2021\_36873\_biomass.R**

This script is not available because the script extracts directly from the LEPAS database. This script calculates mesozooplankton biomass (µg C L-1) at the field site during the grazing experiments. It also generates Figure 1 (zooplankton biomass) and Table 2 (relative biomass of major zooplankton taxa) in the manuscript.

*WBLE\_2021\_ZPgrazingexps\_ZPdens.csv*

Input data file-- ZP\_dens\_exp\_num\_L is the average zoop density in the experiment- calculated from the average of the zoop densities in each of the zoop treatments.

*00\_LEPAS\_WBLE\_2021\_36873\_FieldExp\_BMS\_ugCL.csv*

Output datafile created from R script—The calculated mesozooplankton biomass from the field site (36-873) during the experiments and average density and biomass of mesozooplankton in the experimental treatments.

*00\_WBLE\_2021\_LEPASzp\_Fig1.png*

Figure 1 in manuscript

*00\_Mesozoop\_percentTaxa\_LEPAS\_DensBMS\_2021nanopico\_36873.csv*

Data output used to create Table 2 in manuscript. Table 2 in the manuscript only shows zooplankton taxa with a relative biomass greater than 3%; this data file includes taxa with less than 3% relative biomass.

**01\_WBLE\_2021\_NanoPico\_calcBV.R**

Calculates autotrophic and heterotrophic biovolume of nano- and picoplankton from zooplankton grazing experiments. Nano- and picoplankton counts were conducted by Dan Peters via epifluorescence microscopy.

*NanoEAugCount.csv*

Input data file-- Raw data of nanoplankton (2-20 µm) counts from the August experiment.

*NanoESepCount.csv*

Input data file-- Raw data of nanoplankton (2-20 µm) counts from the September experiment.

*PicoEAugCount.csv*

Input data file-- Raw data of picoplankton (0.2 - < 2µm) counts from the August experiment.

*PicoESepCount.csv*

Input data file-- Raw data of picoplankton (0.2 - < 2µm) counts from the September experiment.

*00\_NanoPico\_WBLE\_2021\_SampleInfo.csv*

Input data file-- Sample information from the grazing experiments and epifluorescence microscopy counts, used to calculate biovolume.

*01\_WBLE\_2021\_NanoPico\_biovolume\_um3\_mL.csv*

Output datafile—calculated biovolume for autotrophic and heterotrophic pico- and nanoplankton. Units are µm3 mL-1.

**02\_WBLE\_2021\_NanoPico\_calcCR\_boot.R**

Calculates the mesozooplankton clearance rate for pico- and nanoplankton, as well as the pico- and nanoplankton growth rate via bootstrapping.

*00\_LEPAS\_WBLE\_2021\_36873\_FieldExp\_BMS\_ugCL.csv*

Input file of mesozooplankton field dens and bms (created in 00\_Mesozoop\_LEPAS\_2021\_36873\_biomass.R). Mesozooplankton biomass from the field site (36-873) during the experiments and average density and biomass of mesozooplankton in the experimental treatments.

*02\_CR\_growrate\_bms\_2021\_36873\_ZPgrazing\_boot100.csv*

Output file—calculated clearance rates (median, 10th percentile, 90th percentile) for pico- and nanoplankton.

**03\_InitialCollection\_NanoPico\_calcBV.R**

Calculates autotrophic and heterotrophic biovolume of nano- and picoplankton from samples collected from the field site during zooplankton grazing experiments. Nano- and picoplankton counts were conducted by Dan Peters via epifluorescence microscopy.

*NanoPico\_InitialCollection\_Count.csv*

Input data file-- Raw data of pico- and nanoplankton counts from samples collected from the field site.

*03\_WBLE\_2021\_InitialCollection\_NanoPico\_BV.csv*

Output datafile—calculated biovolume for autotrophic and heterotrophic pico- and nanoplankton. Units are µm3 mL-1.

*03\_IC\_NanoPico\_biomass\_Fig3.png*

Figure 3 in manuscript.

**04\_WBLE\_2021\_NanoPico\_calcGR.R**

Calculates the mesozooplankton grazing rate, percent food growth consumed, and percent standing stock consumed for pico- and nanoplankton.

*00\_LEPAS\_WBLE\_2021\_36873\_FieldExp\_BMS\_ugCL.csv*

*02\_CR\_growrate\_bms\_2021\_36873\_ZPgrazing\_boot100.csv*

*03\_WBLE\_2021\_InitialCollection\_NanoPico\_BV.csv*

Input data files—generated from previous scripts.

*04\_2021\_36873\_CRGR\_bms\_NanoPico\_raw.csv*

Output datafile—calculated grazing rates (median, 10th percentile, 90th percentile), percent food growth consumed, and percent standing stock consumed for pico- and nanoplankton. Raw values (i.e., negative grazing rates) are included.

*04\_2021\_36873\_CRGR\_bms\_NanoPico.csv*

Output datafile—calculated grazing rates (median, 10th percentile, 90th percentile), percent food growth consumed, and percent standing stock consumed for pico- and nanoplankton. When the lower 10th percentile for the individual clearance rate is <0, this indicates there wasn't significant grazing, so the clearance rate and grazing rates are forced to zero.

**05\_WBLE\_2021\_chl\_calcCR\_boot.R**

Calculates the mesozooplankton clearance rate for total phytoplankton (chl-a), as well as the total phytoplankton (chl-a) growth rate via bootstrapping.

01\_2021\_WBLE\_ZP\_grazingZNR\_chl\_wide.csv

Input data file of chl-a measurements from the zooplankton grazing experiments. R script used to generate these data is available upon request.

*00\_ChlFluoro\_WBLE\_2021\_SampleInfo.csv*

Input data file-- Sample information for chl-a during the experiments—used to calculate chl-a grazing rates.

*00\_LEPAS\_WBLE\_2021\_36873\_FieldExp\_BMS\_ugCL.csv*

Input data file—generated in script 00\_Mesozoop\_LEPAS\_2021\_36873\_biomass.R

*05\_CR\_growrate\_est\_2021\_36873\_ZPgrazing\_chl\_bms\_boot100.csv*

Output file—calculated clearance rates (median, 10th percentile, 90th percentile) for chl-a.

**06\_WBLE\_2021\_chl\_calcGR.R**

Calculates the mesozooplankton grazing rate, percent food growth consumed, and percent standing stock consumed for total phytoplankton (chl-a).

*00\_ZP\_grazing\_field\_chl\_WBLE\_2021.csv*

Input data file—Chl-a measurements collected from the field site during the zooplankton grazing experiments.

*00\_LEPAS\_WBLE\_2021\_36873\_FieldExp\_BMS\_ugCL.csv*

*05\_CR\_growrate\_est\_2021\_36873\_ZPgrazing\_chl\_bms\_boot100.csv*

Input data files—generated from previous scripts.

*06\_2021\_36873\_CRGR\_chl\_raw.csv*

Output datafile—calculated grazing rates (median, 10th percentile, 90th percentile), percent food growth consumed, and percent standing stock consumed for total phytoplankton (chl-a). Raw values (i.e., negative grazing rates) are included.

*06\_2021\_36873\_CRGR\_chl.csv*

Output datafile—calculated grazing rates (median, 10th percentile, 90th percentile), percent food growth consumed, and percent standing stock consumed for total phytoplankton (chl-a). When the lower 10th percentile for the individual clearance rate is <0, this indicates there wasn't significant grazing, so the clearance rate and grazing rates are forced to zero.

**07\_WBLE\_2021\_fluoro\_calcCR\_boot.R**

Calculates the mesozooplankton clearance rate for different phytoplankton taxa (Cyanobacteria, Cryptophyta/Bacillariophyta, Chlorophyta; measured via the FluoroProbe) via bootstrapping. Also calculates the growth rate of these phytoplankton taxa via bootstrapping.

*03\_fluoroprobe\_exp\_phytogrps\_WBLE2021.csv*

Fluoroprobe data from the zooplankton grazing experiments, which measured the biomass of Cyanobacteria, Cryptophyta, Bacillariophyta, and Chlorophyta at the beginning and end of the experiments. R script used to generate these data is available upon request.

*00\_ChlFluoro\_WBLE\_2021\_SampleInfo.csv*

Input data file-- Sample information for chl-a during the experiments—used to calculate chl-a grazing rates.

*00\_LEPAS\_WBLE\_2021\_36873\_FieldExp\_BMS\_ugCL.csv*

Input data files—generated from previous script.

*07\_CR\_growrate\_est\_2021\_36873\_ZPgrazing\_fluoro\_boot100.csv*

Output file—calculated clearance rates (median, 10th percentile, 90th percentile) for different phytoplankton taxa (Cyanobacteria, Cryptophyta/Bacillariophyta, Chlorophyta).

**08\_WBLE\_2021\_fluoro\_calcGR.R**

Calculates the mesozooplankton grazing rate, percent food growth consumed, and percent standing stock consumed for different phytoplankton taxa (Cyanobacteria, Cryptophyta/Bacillariophyta, Chlorophyta; measured via the FluoroProbe).

*00\_fluoroprobe\_EarlyAugSept\_field\_WBLE2021.csv*

Input data file—Fluoroprobe measurements collected from the field site during the zooplankton grazing experiments.

*00\_fluoroprobe\_Cconversions.csv*

Input data file—Carbon conversion factors for the Fluoroprobe groups (Cyanobacteria, Cryptophyta/Bacillariophyta, Chlorophyta)

*07\_CR\_growrate\_est\_2021\_36873\_ZPgrazing\_fluoro\_boot100.csv*

*00\_LEPAS\_WBLE\_2021\_36873\_FieldExp\_BMS\_ugCL.csv*

Input data files—generated from previous scripts.

*08\_2021\_36873\_CRGR\_fluoro\_raw.csv*

Output datafile—calculated grazing rates (median, 10th percentile, 90th percentile), percent food growth consumed, and percent standing stock consumed for Cyanobacteria, Cryptophyta/Bacillariophyta, Chlorophyta. Raw values (i.e., negative grazing rates) are included.

*08\_2021\_36873\_CRGR\_fluoro.csv*

Output datafile—calculated grazing rates (median, 10th percentile, 90th percentile), percent food growth consumed, and percent standing stock consumed for Cyanobacteria, Cryptophyta/Bacillariophyta, Chlorophyta. When the lower 10th percentile for the individual clearance rate is <0, this indicates there wasn't significant grazing, so the clearance rate and grazing rates are forced to zero. Contains data to create Tables S2-S5.

**09\_WBLE\_2021\_ZPexp\_CRGR\_combinedata.R**

Combines grazing data calculated in previous scripts into a single data file.

*04\_2021\_36873\_CRGR\_bms\_NanoPico.csv*

*06\_2021\_36873\_CRGR\_chl.csv*

*08\_2021\_36873\_CRGR\_fluoro.csv*

Input data files—generated from previous scripts.

*09\_2021\_36873\_NanoPicoMS\_CRGR\_final.csv*

Output datafile—Mesozooplankton clearance rates, grazing rates, and percent food source consumed for all food sources (nano/pico plankton, total phytoplankton (chl-a), and Fluoroprobe groups (Cyanobacteria, Cryptophyta/Bacillariophyta, Chlorophyta).

**10\_WBLE\_2021\_ZPexp\_CRGR\_Figs4to6.R**

Makes Figures 4-6 in manuscript.

*09\_2021\_36873\_NanoPicoMS\_CRGR\_final.csv*

Input data file—generated from previous script.

*10\_WBLE\_2021\_Fig4\_bms\_083124.png*

Figure 4 in manuscript.

*10\_WBLE\_2021\_Fig5a\_062424.png*

Figure 5a in manuscript.

*10\_WBLE\_2021\_Fig5b\_062424.png*

Figure 5b in manuscript.

*10\_WBLE\_2021\_Fig6.png*

Figure 6 in manuscript.

***Script 11 was not used in the final draft of the manuscript, and therefore is not included here.***

**12\_NOAA\_HABcruise\_fieldsampling\_PAR\_cyanobms\_forMS.R**

Uses publicly available data from NOAA’s Great Lakes Environmental Research Laboratory (NOAA-GLERL) to create Figure S2. Also calculates Photosynthetically Active Radiation (PAR) in western Lake Erie to determine the PAR level for the grazing experiments.

*00\_lake\_erie\_habs\_field\_sampling\_results\_2012\_2018\_v2.csv*

Input data file— Physical, chemical, and biological water quality data collected from a small boat in western Lake Erie, Great Lakes from 2012-05-15 to 2018-10-09. Accessed via https://www.ncei.noaa.gov/archive/accession/0187718 on 10/01/2020.

*00\_lake\_erie\_habs\_field\_sampling\_results\_2019.csv*

Input data file— Physical, chemical, and biological water quality data collected from a small boat in western Lake Erie, Great Lakes from 2019-04-30 to 2019-10-07. Accessed via https://www.ncei.noaa.gov/archive/accession/0209116 on 10/01/2020.

*12\_WE2\_HABscruise\_chl\_phyco\_FigS2.png*

Figure S2 in manuscript.

**13\_SuppFig3\_fluoroprobetime.R**

Creates Supplementary Figure 3—Fluoroprobe data by major group (Cyanobacteria, Cryptophyta, Bacillariophyta, Chlorophyta), measurements are taken every three seconds by the Fluoroprobe.

*InitialCollection\_2021\_ZPexps\_rawdata4.csv*

Input data file—Fluoroprobe data collected from the field site during two experiments. One experiment (6/29/21) was conducted during low/no cHABs, and the other experiment (10/4/21) was conducted during the cHAB event, which were used to make Figure S3.

*13\_WBLE\_Fluoroprobe\_SuppFige3.png*

Figure S3 in manuscript.

**14\_WBLE\_2021\_chla\_field\_Fig2b.R**

Creates Figure 2b—Chl-a measurements collected from the field during the mesozooplankton grazing experiments.

*00\_ZP\_grazing\_field\_chl\_WBLE\_2021.csv*

Input data file-- Chl-a measurements collected from the field during the mesozooplankton grazing experiments

*14\_WBLE\_FieldChla\_Fige2b.png*

Figure 2b in manuscript.

**15a\_LEPAS\_phyto\_lengths\_NanoPicoMS\_Fig2a\_FigS5.R**

Calculates phytoplankton biomass <200 µm, collected from the Lake Erie Plankton Abundance Study (LEPAS) for script 15b (which creates Figure 2a). Also creates Figure S5, which shows phytoplankton biomass by genus for phytoplankton less than 200 µm.

*03b\_LEPAS\_phyto\_biomass\_09012024.csv*

Input data file—Phytoplankton biomass of each genus, collected and enumerated via LEPAS protocols. The script used to generate these data is not available, as it extracts directly from the LEPAS database.

*03b\_LEPAS\_phyto\_RawLengths.csv*

Input data file—Individual lengths of each phytoplankton genus identified via LEPAS protocols. As per protocols, only the first 20 lengths of each genus are measured per sample. These data were used to determine the proportion of each genus greater than and less than 200 µm, in order to determine the phytoplankton biomass less than 200 µm in each field sample.

*15a\_LEPAS\_phyto\_bms\_less200um\_2021\_36873.csv*

Output file—Biomass of major phytoplankton taxa (Cyanobacteria, Cryptophyta, Bacillariophyta, Chlorophyta) from field collections taken during the grazing experiments.

*15a\_LEPAS\_phyto\_bms\_less200um\_per\_2021\_36873.csv*

Output file—Percent biomass of each genus per major taxonomic group (Cyanobacteria, Cryptophyta/Bacillariophyta, Chlorophyta) less than 200 µm.

*15a\_LEPASphyto\_AugSep\_bms\_less200um\_FigS5.png*

Figure S5 in manuscript.

**15b\_LEPASphyto\_fluoro\_less200um\_combine\_graphs.R**

Creates Figure 2a—biomass of phytoplankton groups estimated via the Fluoroprobe and light microscopy.

*15a \_LEPAS\_phyto\_bms\_less200um\_2021\_36873.csv*

Input data file—Phytoplankton biomass at the field site during the mesozooplankton grazing experiments. Phytoplankton was collected and enumerated according to Lake Erie Plankton Abundance Study (LEPAS) protocols. Input data is phytoplankton less than 200um, which was calculated in 15a\_LEPAS\_phyto\_lengths\_NanoPicoMS\_Fig2a.R.

*00\_fluoro\_phyto\_bms\_ugCL\_less200um\_2021\_36873.csv*

Input data file—phytoplankton biomass less than 200 µm, as measured by the Fluoroprobe. Lake Erie water from site 36-873 was sieved through a 200um sieve for the grazing experiments prior to measurements.

*15b\_LEPASflouro\_comb\_less200um\_C\_ugL\_2021\_36873\_Fig2a.png*

Figure 2a in manuscript.