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Data Article

Seasonal gut contents of the eastern oyster, *Crassostreavirginica*, in the Rhode River, Chesapeake Bay, USA: Growth, phytoplankton and signature pigment data

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a b s t r a c t

A 2-year study was undertaken to understand feeding preferences of the eastern oyster *Crassostreavirginica* when growing in conditions of eutrophication and variable flow. Oysters were suspended in the Rhode River, a tributary of Chesapeake Bay, Maryland, USA, and a subset of these oysters was collected monthly, measured in height to determine growth, and the phytoplankton in their gut were examined both microscopically and using indicator pigments and compared with phytoplankton abundance and composition in the water column. The data herein summarize the oyster growth and the gut contents with respect to phytoplankton cell numbers and composition and with respect to signature pigments.

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Specification Table

Subject	Environmental science, Biological science
Specific subject area	Marine biology, animal physiology, ecology
Type of data	Table
How data were acquired	Microscope: Zeiss Axiovert 205 microscope at 40x or an Olympus phase-contrast compound microscope at 200X magnification High performance liquid chromatography: Hewlett Packard Series 1100 high-performance liquid chromatography (HPLC) system
Data format	Raw
Parameters for data collection	The data include 1) oyster growth reported as shell height; 2) phytoplankton enumerations for surface and bottom monthly samples from, and phytoplankton enumerations from the gut contents of 5 individual oysters collected monthly for 2 sequential monthly experiments over 2 years; 3) phytoplankton signature pigment data from surface and bottom samples from the river and from a single pooled gut content sample from the oysters collected monthly.
Description of data collection	The study was comprised of two individual experiments, each lasting ~1 year. In each, 100 adult *C. virginica* were suspended in cages. Each month, 5 oysters were removed and shell heights were measured to the nearest 1 mm using a caliper ruler. Oyster valves were separated and the samples of gut contents were collected and unpreserved material placed in a Sedgewick-Rafter plankton counting cell and allowed to settle for 15 minutes. Gut taxa were then grouped by phytoplankton functional group. After identifying cells from the gut, an equal aliquot from each oyster was then pooled into a combined gut sample which was subsequently analyzed for pigment composition using an HPLC system. Further details below.
Data source location	Latitude and longitude for collected samples/data: 38° 53 08 N, 76° 32 29 W
Data accessibility	With the article
Related research article	Weissberger, E.J. and P.M. Glibert. 2021. Diet of the eastern oyster, *Crassostrea virginica* , growing in a eutrophic tributary of Chesapeake Bay, Maryland, USA. Aquaculture Reports 20: 100655. https://doi.org/10.1016/j.aqrep.2021.100655

Value of the Data

- These data summarize both the individual, identifiable cells within oyster guts over 2 seasons and the phytoplankton signature and digestive pigments also in the guts. Data are also reported for the water column from which the oysters were collected. Comparatively few studies have quantified individual taxa to establish selectivity in natural populations of oysters, particularly in eutrophic waters.
- These data will be useful to oyster biologists and physiologists, as well as those interested in oyster restoration. Oyster restoration is often motivated by the promise of improved water quality conditions that extend from the filtration activity of oysters. Yet, if oyster feeding or growth is detrimentally affected by the environmental conditions or the community of phytoplankton within the water column, these ecosystem services will not be realized.
- These data were collected from a single site in Chesapeake Bay where eutrophic conditions are prevalent. Comparative studies will be valuable to fully understand the extent to which these findings can be generalized. These data may also be useful to modelers interested in projecting habitat conditions for oyster restoration.

1. Data Description

The data provided herein represent the complete data set for the analysis of the diet of the eastern oyster in eutrophic conditions as reported in Weissberger and Glibert [1]. The data in file 1 include the monthly shell height measurements and the phytoplankton identifications in

the water and in the oyster gut, and in file 2, the pigment compositional data in the water and in the oyster gut. In both files, data are reported by sampling date.

2. Experimental Design, Materials and Methods

Full details on experimental design, methodology and original sources can be found in the co-submitted paper [1] and are included below.

2.1. Oyster feeding

The study lasted 26 months, and was comprised of two individual experiments, each lasting ~1 year. The first experiment was initiated on September 26, 2010, and lasted through September 19, 2011, and the second experiment was initiated on September 29, 2011 and continued until December, 2012. In each experiment, 100 adult *C. virginica* were obtained from a commercial oyster grower, Marinetics, Inc., Cambridge MD, and divided among three cages (2.54 cm mesh). Cages were suspended from the Smithsonian Environmental Research Center dock, approximately 30 cm above the bottom of the Rhode River, a tributary of Chesapeake Bay.

Each month, 5 oysters were removed from the cages and returned to the laboratory for sampling. In the laboratory, shell heights were first measured to the nearest 1 mm using a caliper ruler. Then, the oyster valves were separated and the samples of gut contents were collected with disposable Pasteur pipettes. Given the natural environment from which the oysters were collected, it was not possible to sample pseudofeces. Unpreserved material collected from the gut was placed in a Sedgewick-Rafter plankton counting cell and allowed to settle for 15 minutes. Identification and counting were done with either a Zeiss Axiovert 205 microscope at 40x or an Olympus phase-contrast compound microscope at 200X magnification. Cells were identified to the lowest taxon possible. Gut taxa were then grouped by phytoplankton functional group. Microscopic identifications did not include material or taxa other than phytoplankton. In all, 130 individual oysters were sampled, dissected, and gut contents identified.

After identifying cells from the gut of each of the 5 oysters individually, an equal aliquot from each oyster was then pooled into a combined gut sample. This combined material was placed on a GF/F filter. Filters were frozen at −80 °C and subsequently analyzed for pigment composition using a Hewlett Packard Series 1100 high-performance liquid chromatography (HPLC) system according to Van Heukelem and Thomas [2] . The rationale for pigment analysis in addition to that of individual microscopic enumerations is that pigment signatures may yield insight into food ingested and digested even when cells were no longer identifiable. Changes in the ratio of selected, diagnostic pigments relative to chlorophyll *a* (chl *a*), and relative to the initial ratio of these pigments in the algal diet, were used as indices of cell passage through the gut. Pigment contents were normalized to chl *a* and the composition of fucoxanthin:chl *a* was taken as a measure of diatoms abundance, peridinin:chl *a* as a measure of peridinin-containing dinoflagellates, and zeaxanthin:chl *a* as a measure of cyanobacteria (e.g., [3,4]). Phaeophytin *a* and phaeophorbide *a* were used as the diagnostic indicators of the degradation of chl *a*. In total, 26 monthly pooled samples were analyzed for gut pigment composition, although data on the degradation pigments are only available for 12 of those 26 sets of samples (primarily from experiment 1 in 2011).

2.2. Phytoplankton community composition in water

At the time of oyster sampling, phytoplankton samples were also collected from the river for comparison with that in the gut composition samples. Whole water samples were collected

from near surface and near bottom at the site of the oyster cages and returned to the laboratory for near-immediate microscopic identification and enumeration of taxa present as above. In the laboratory, samples were inverted to mix and 1 ml was then transferred to a Sedgewick-Rafter chamber using a disposable glass Pasteur pipette. The chamber was examined on a Zeiss Axiovert 205 microscope at 40x. Cells were identified to the lowest taxon possible.

To compare the water column pigment composition with cell enumerations, the water samples were filtered, filters were frozen at −80 °C, and diagnostic pigments were subsequently analyzed by HPLC using the same techniques as described above [2].

2.3. Water quality and flow

Data that were also included in the analysis reported in Weissberger and Glibert [1], but not included here are monthly-collected dissolved and particulate nutrient data (concentrations of NO_3^-, NH_4^+, PO_4^{3-}, particulate nitrogen (PN), particulate phosphorus (PP) and particulate carbon (PC) and chlorophyll *a*) from a nearby site on the same river. These data are available through the Chesapeake Bay Monitoring Program (https://www.chesapeakebay.net/what/data). Note that these samples were not taken on the exact same dates as the oyster collections.

Other data included in the analysis reported in Weissberger and Glibert [1], but not included here are monthly river flow data. These data were downloaded from the USGS gaging site 01589795 at the adjacent South River (waterdata.usgs.gov).

Ethics Statement

Not applicable.

CRediT Authorship Statement

Eric J. Weissberger: Conceptualization, Data curation, Formal analysis, Funding acquisition, Investigation, Methodology, Visualization, Writing - original draft; **Patricia M. Glibert:** Investigation, Methodology, Writing - review & editing.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper. The views expressed in this article are the authors' own and do not necessarily represent the view of MD DNR. Any reference obtained to a specific product, process, or service does not constitute or imply an endorsement by the authors or their organizations.

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Supplementary Materials

Supplementary material associated with this article can be found in the online version at doi: 10.1016/j.dib.2021.107176.

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