

# High resolution mass spectra for amphi-enterobactin related siderophores from *Vibrio harveyi* from laboratory experiments in 2017

**Website:** <https://www.bco-dmo.org/dataset/861194>

**Data Type:** experimental

**Version:** 1

**Version Date:** 2021-09-21

## Project

» [Iron uptake by marine bacteria: regulation and function of weak and strong siderophores](#) (Bacteria Iron Siderophores)

Contributors	Affiliation	Role
<a href="#">Morel, Francois</a>	Princeton University	Principal Investigator
<a href="#">McRose, Darcy</a>	Princeton University	Student, Contact
<a href="#">York, Amber D.</a>	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

## Abstract

High resolution mass spectra for amphi-enterobactin related siderophores from *Vibrio harveyi* from laboratory experiments in 2017. These data were published in McRose et al. (2018, Figs. S1, S4).

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## Coverage

**Temporal Extent:** 2017-01-01

## Acquisition Description

### Sampling and analytical procedures:

*V. harveyi* cells were cultured at 30C and shaken at 200 RPM in a fully chemically defined artificial seawater medium consisting of basic salts ( $3 \times 10^{-1}$  M NaCl,  $1.05 \times 10^{-2}$  M  $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$ ,  $5 \times 10^{-2}$  M  $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ ,  $4.85 \times 10^{-4}$  M  $\text{H}_3\text{BO}_3$ ) as well as  $1 \times 10^{-4}$  M  $\text{K}_2\text{HPO}_4$ ,  $6.51 \times 10^{-2}$  M glycerol,  $2.65 \times 10^{-8}$  M riboflavin,  $2.96 \times 10^{-6}$  M thiamine and Aquil trace metals without added Fe. Aquil trace metals contain 100 M EDTA, background Fe concentrations were determined by inductively coupled plasma MS (ICP-MS) to be  $\sim 100$  nM. Nitrogen was added as MEM essential and non-essential amino acids (Sigma M5550, 92 mL L<sup>-1</sup> ; Sigma M7145, 46 mL L<sup>-1</sup> ).

For quantification of siderophores  $\sim 200$  mL of *V. harveyi* overnight culture was centrifuged at 16,000 xg

for 6 minutes. Supernatant samples were decanted, filtered (0.2 m) and acidified with 0.1% formic acid. Samples were then extracted using Oasis HLB (Waters) columns with the following conditions: 20 mL methanol, 20 mL MilliQ H<sub>2</sub>O, 50 mL sample, 20 mL 0.03% trifluoroacetic acid, 10 mL 0.03% formic acid and final elution with 30 mL of 40% methanol. Cell pellets were extracted overnight (~18 hours) with 5 mL of 80% methanol with 0.1% formic acid. Four mL of the resulting supernatant was diluted to 20% methanol with acidic (0.1% formic acid) MilliQ and extracted using an HLB column: 20 mL methanol, 20 mL MilliQ, 16 mL sample, 20 mL MilliQ and elution with 30 mL of 100% methanol. Samples were dried under vacuum (SpeedVac, ThermoFisher) and resuspended in either 1 mL MilliQ (supernatants) or 1 mL of 80% methanol (pellets).

Amphi- enterobactins and breakdown products in the supernatant and pellets were determined by un-targeted HR- LC-MS/MS, using a C18 column (ACE 3 C18-AR, 1mm x 10cm, MAC MOD) coupled to an LTQ-Orbitrap XL mass spectrometer (ThermoFisher). Injected samples (20 µL) were separated (1 hr) under a gradient of solutions A and B (solution A: water + 0.1% FA + 0.1% acetic acid; solution B: acetonitrile + 0.1% FA + 0.1% acetic acid; gradient 0-100% B, flow rate 70 µL/min). Full-scan mass spectra were acquired in positive-ion mode ( $m/z = 160-1500$ ) with an experimental resolving power of  $R=60000$  ( $m/z=400$ ). MS/MS spectra were simultaneously acquired using CID in the Orbitrap targeting the two most abundant species in the full-scan spectrum.

Location: Laboratory experiments conducted at Princeton University.

## Processing Description

The MS/MS spectra of the identified putative siderophores were investigated using MS2Browser and Maven and only masses with the common characteristic product ion  $m/z = 224.0554$  were retained for further analysis. Structures for breakdown products were proposed based on the previously published amphi-enterobactin structure. Searches for serine-fatty acid tails were conducted by searching for the serine product ion ( $m/z=106.0499$ ) using MS2Browser.

BCO-DMO data manager processing notes:

\* Spectra pdf added to "Data Files" section

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## Data Files

File	Version
<b>High resolution mass spectra</b> filename: Vharveyi_Spectra.pdf (Portable Document Format (.pdf), 893.15 KB) MD5:0bd9d1ad3e69fc6a2748198c3cee0994 <i>High resolution mass spectra for amphi-enterobactin related siderophores from Vibrio harveyi.</i>	original

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## Related Publications

Clasquin, M. F., Melamud, E., & Rabinowitz, J. D. (2012). LC-MS Data Processing with MAVEN: A Metabolomic Analysis and Visualization Engine. *Current Protocols in Bioinformatics*.

doi:[10.1002/0471250953.bi1411s37](https://doi.org/10.1002/0471250953.bi1411s37)

*Methods*

McRose, D. L., Baars, O., Seyedsayamdost, M. R., & Morel, F. M. M. (2018). Quorum sensing and iron regulate a two-for-one siderophore gene cluster in *Vibrio harveyi*. *Proceedings of the National Academy of Sciences*, 115(29), 7581–7586. doi:[10.1073/pnas.1805791115](https://doi.org/10.1073/pnas.1805791115)

## Results

Naka, H., Reitz, Z. L., Jelowicki, A. L., Butler, A., & Haygood, M. G. (2018). Amphi-enterobactin commonly produced among *Vibrio campbellii* and *Vibrio harveyi* strains can be taken up by a novel outer membrane protein FapA that also can transport canonical Fe(III)-enterobactin. *JBIC Journal of Biological Inorganic Chemistry*, 23(7), 1009–1022. doi:[10.1007/s00775-018-1601-5](https://doi.org/10.1007/s00775-018-1601-5)

## Methods

Zane, H. K., Naka, H., Rosconi, F., Sandy, M., Haygood, M. G., & Butler, A. (2014). Biosynthesis of Amphi-enterobactin Siderophores by *Vibrio harveyi* BAA-1116: Identification of a Bifunctional Nonribosomal Peptide Synthetase Condensation Domain. *Journal of the American Chemical Society*, 136(15), 5615–5618. doi:[10.1021/ja5019942](https://doi.org/10.1021/ja5019942)

## Methods

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## Related Datasets

### References

Morel, F. (2021) **Amphi-enterobactins and related siderophore concentrations found in *Vibrio harveyi* supernatants and pellets from laboratory experiments in 2017.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2021-10-01 <http://lod.bco-dmo.org/id/dataset/861154> [[view at BCO-DMO](#)]

*Relationship Description: Concentrations from the same experiment these spectra were generated from.*

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### Parameters

*Parameters for this dataset have not yet been identified*

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### Instruments

<b>Dataset-specific Instrument Name</b>	LTQ-Orbitrap XL mass spectrometer (ThermoFisher)
<b>Generic Instrument Name</b>	Mass Spectrometer
<b>Generic Instrument Description</b>	General term for instruments used to measure the mass-to-charge ratio of ions; generally used to find the composition of a sample by generating a mass spectrum representing the masses of sample components.

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## Project Information

**Iron uptake by marine bacteria: regulation and function of weak and strong siderophores**

## (Bacteria Iron Siderophores)

**Coverage:** laboratory

NSF abstract:

Organic molecules that bind and transport iron are called siderophores. Because iron is an essential trace element for biological systems and exists at very, very low concentrations in the open ocean, siderophores perform a critical role in capturing iron for cellular function. It is known that marine bacteria can produce two different types of siderophores that either tightly bind iron or only weakly do so, with different ecological consequences. This researcher will leverage an exceptional career on metal-organism interactions to examine the unsolved question of exactly what environmental and biochemical conditions (for example the availability of iron) control bacterial production of various siderophores. Results will generate significant new understanding of a critical chemical oceanographic process, and cap this researcher's groundbreaking discoveries that have built to this project. Funding for this research will also support the advancement of women in science by both providing the highest quality training of a female scientist and providing the opportunity for her to host an oceanography booth at the Princeton Plasma Physics Lab's "Young Women in Science" conference.

This study will use *Vibrio harveyi* as a model organism to investigate a variety of questions surrounding the marine bacterial production of weak and strong siderophores. To start, the investigation will look into how siderophore production is controlled by varying iron availability and quorum sensing (i.e. a coordinated response correlated to population density and/or certain signaling molecules). This also includes in-depth investigation of the impact of life phase and biochemical changes with growth as they relate to coordinated use of weak and strong siderophores. Using established protocols for genetic manipulation of *V. harveyi*, the researcher plans to discover how varying combinations of weak and strong siderophores maximize the uptake of iron. The broader biogeochemical implications of this study to the field of chemical oceanography, with regard to the microbial use of, and cellular responses to, many essential micronutrients in the ocean would be to significantly influence understanding of elemental distributions beyond the specific study of iron and siderophore cycling in the ocean.

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### Funding

Funding Source	Award
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1657639</a>

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