Buoyant single cell densities of marine bacterial isolates in pure water, deuterated water and artificial seawater (Bacterioplankton single-cell growth project)

Website: https://www.bco-dmo.org/dataset/661577
Data Type: experimental
Version:
Version Date: 2016-10-19

Project
» Linking Single-Cell Growth Rates and Genomics (Bacterioplankton single-cell growth)

Contributors	Affiliation	Role
Polz, Martin	Massachusetts Institute of Technology (MIT)	Principal Investigator
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Dataset Description

Mass and density measurements of single cells from 8 microbial strains measured in pure water, deuterated water and artificial seawater.

These data are to appear in a paper entitled "Direct single-cell biomass estimates for marine bacteria via Archimedes' principle" by Nathan Cermak, Jamie W. Becker, Scott M. Knudsen, Sallie W. Chisholm, Scott R. Manalis, and Martin F. Polz. ISME Journal (In Press)

Methods & Sampling

We measured single cell buoyant mass (cell mass minus the mass of the fluid it displaces) using a suspended microchannel resonator. This is a custom-fabricated silicon microfluidic chip with a fluid-filled resonator. When a cell flows through the resonator in a fraction of a second, it briefly changes the resonator's total mass, which changes its resonant frequency. By tracking the resonator's resonant frequency, we can weigh single cells. The baseline frequency of the resonator is also proportional to the fluid density, and we quantify this relationship in advance using sodium-chloride solutions as density standards.

In this measurement, cells were grown in either 2216 marine broth (13B01) or dilute seawater-based media (all others). Cells were taken from exponential growth phase (except for 13B01 which was measured in both stationary and exponential phases) and fixed with either formaldehyde or glutaraldehyde.

Data Processing Description

BCO-DMO Processing:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- added 'cell_id' parameter name

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Data Files

File
cell_densities.csv (Comma Separated Values (.csv), 757.87 KB) MD5:d691fd86f920b7667dbff23f4d947923 Primary data file for dataset ID 661577

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Parameters

Parameter	Description	Units
strain	Bacterial strain	unitless
fluid	Type of fluid the cells were measured in: H2O is pure water; D2O is pure deuterated water; and ASW is artificial seawater (made from sea salts from sigma aldrich).	unitless
cell_id	Cell identification number	unitless
buoyantMass_fg	The cell's buoyant mass	femtograms (fg)
time_hr	The time elative to the start of the experiment at which the cell was measured	hours
baselineFrequency_hz	The resonator's baseline frequency at the time of measurement	hertz
fluidDensity_gpermL	The density of the fluid in which the cell was immersed; calculated based on the resonator's baseline frequency	grams/milliliter (g/ml)

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Suspended Microchannel Resonator
Dataset-specific Description	A custom-fabricated silicon microfluidic chip with a fluid-filled resonator to measure mass and density of single cells.
Generic Instrument Description	A high-precision instrument for measuring single-cell mass, volume, and density using one or two resonators connected by a serpentine fluidic channel. During operation of the dual SMR, a dilute cell population suspended in cell media, Fluid 1, is delivered to the sample bypass via pressure-driven flow (Figure 2A, Supplementary Figure 1), and single cells flow into the first SMR (SMR1) for the first buoyant mass measurement. The cells then travel through a microchannel to a cross-junction, where a second fluid of different density is introduced. After the cross-junction, cells continue through a long serpentine channel, which facilitates mixing of the two fluids. The cells next enter a second cantilever (SMR2) for a buoyant mass measurement in the mixed fluid, Fluid 2. As cells flow through each cantilever, a change in resonance frequency is recorded (Figure 2B), which is determined by each cell's buoyant mass in each cantilever's corresponding fluid. Reference: Bryan, A.K. et al. (2015) Measuring single cell mass, volume, and density with dual suspended microchannel resonators. Proc Natl Acad Sci USA 108: 10992–10996 doi:10.1073/pnas.1104651108. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3895367/

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Deployments

Polz_lab

Website	https://www.bco-dmo.org/deployment/661603
Platform	MIT
Start Date	2011-09-01
End Date	2016-12-31
Description	laboratory studies

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Project Information

Linking Single-Cell Growth Rates and Genomics (Bacterioplankton single-cell growth)

Coverage: Lab-based

Description from NSF award abstract:
Marine ecosystems are primarily microbial in nature. Microscopic organisms represent over 90% of biomass, including the major primary producers, and drive biogeochemical processes. Although this insight is merely 30 years old, it has led to concerted efforts in studying the structure and functioning of microbial communities in the ocean. Techniques are now available to estimate many key ecological parameters of microbial life; however, one fundamental gap is that estimates of microbial growth rates in the wild remain poorly constrained. Questions, which have largely remained unsolved, are:

What does the growth rate distribution look like for free-living microbes?

Which species grow at what rates?
How do environmental changes (e.g., nutrients, light) affect growth rates of different microbes?

To begin to address these questions, this project will develop a single-cell based system that allows coupled measurement of in situ growth rates and genomic characteristics. The suspended microchannel resonator (SMR) is a well-developed microfluidics-based mass-sensor that has sufficient resolution for measuring the natural range in size and growth rate of ocean microbes; here, this system will be adapted to enable: (i) capture and growth measurement of individual microbial cells in their native seawater microenvironment, (ii) genomic analysis of the same cells for which growth rates have been determined, and (iii) direct analysis of bacterioplankton communities obtained from mesocosm and natural ocean samples. This system is unique in that it couples quantitative growth rate determination and genomic identification of individual microbial cells in their natural microenvironment, and therefore promises to be applicable to the above questions.

Understanding what regulates bacterial growth on the single cell and population level is of fundamental importance in linking microbial diversity to function, and to model and predict carbon fluxes in the ocean. This project establishes a prototype system to couple determination of growth and genomics on the single cell level, for which no data currently exist. Future directions will include design of a system with increased throughput and capability of running onboard ship or autonomous sampling devices.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1129359

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