High Resolution Growth Screen of Ruegeria pomeroyi Transporter Mutants Data September 2021 - June 2022 (C-CoMP Marine Bacterial Transporters project)

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Project
» Function and Importance of Marine Bacterial Transporters of Plankton Exometabolites (C-CoMP Marine Bacterial Transporters)

Program
» Center for Chemical Currencies of a Microbial Planet (C-CoMP)

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Abstract
High resolution growth screens were used to confirm the phenotype of Ruegeria pomeroyi DSS-3 transporter knockout mutants. Mutants which had demonstrated growth defects on a given substrate as sole carbon source during an initial growth screen were selected and used here. Each mutant was grown on the substrate(s) of interest along side a wildtype analog (pooled-TnSeq library). Growth curves were generated by reading the optical density at 600 nm hourly. The annotations of a transporter's cognate substrate was confirmed when the mutant of said transporter demonstrated significant defect relative to the wildtype analog on the substrate of interest.

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Coverage

Temporal Extent: 2021-09 - 2022-06

Dataset Description

Each column heading provides the treatment condition and replicate. The first 4 letters are substrate abbreviation (provided below) followed by the bacterial identifier. The bacterial identity is either "WT" indicating the wildtype analog (pooled-RBTnSeq library) or four numbers indicating the locus tag of the disrupted gene (e.g. "1234" represents a mutant of "SPO1234"). Finally, the underscore and lowercase letter ("_a", "_b", "_c", "_d") indicates the biological replicate.

Values are optical density at 600 nm.

Methods & Sampling

Methods & Sampling

Mutant cultures were pre-grown overnight in ½ YTSS medium with 50 mg ml-1 kanamycin. Screens were performed in L1 minimal medium (Guillard and Hargraves 1993) (dx.doi.org/10.17504/protocols.io.jvccn2w) modified to a salinity of 20 ppt and amended with ammonium (3 mM), kanamycin (50 mg ml-1), and phosphorus as PO43- at 36 mM. Overnight cultures of individual mutants were washed 3 times in substrate free medium. Four replicate 200 µl mutant cultures were prepared by inoculating 2 ml of washed overnight culture into 96 well plates containing 198 ml modified L1 medium and a single substrate at 8 mM carbon. As a positive control, four wells with the same medium were inoculated with washed overnight cultures of the pooled-RB-TnSeq library, used as a proxy for wild-type *R. pomeroyi* growth but harboring a transposon/kanamycin resistance gene insertion. Cultures were grown at 25oC in a Synergy H1 plate reader (BioTek, Winooski, VT, USA) shaking at 425 rpm for 68-72 h. OD600 readings were collected once each hour.

Data Processing Description

Data Processing Notes from Submitter:

The data were imported into Excel and compiled on a single sheet. Values are OD600, they have not been pathlength corrected, they have not been blank corrected. We recommend blanking each sample to its first time point.

BCO-DMO Processing Notes:

- Replaced spaces and special characters in column header names with underscores ("_")

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Data Files

File	
combinedgrowthcurves_bco_dmo3_23_2.csv	(Comma Separated Values (.csv), 35.34 KB) MD5:66bab205ed3cf81f5e5a42416fc32b5f
Primary data file for dataset ID 894179. File processed with laminar pipeline "894179_v1_high_resolution_screen_growth_curves" at path 894179/1/data/combinedgrowthcurves_bco_dmo3_23_2.csv	

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Related Publications

Schroer, W. F., Kepner, H. E., Uchimiya, M., Mejia, C., Rodriguez, L. T., Reisch, C. R., & Moran, M. A. (2023). Function and Importance of Marine Bacterial Transporters of Plankton Exometabolites. https://doi.org/10.1101/2023.01.19.524783

Results

Schroer, W. F., Kepner, H. E., Uchimiya, M., Mejia, C., Rodriguez, L. T., Reisch, C. R., & Moran, M. A. (2023). Functional annotation and importance of marine bacterial transporters of plankton exometabolites. ISME Communications, 3(1). https://doi.org/10.1038/s43705-023-00244-6
Results

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Parameters

Parameter	Description	Units
time_hours	Sample time	hours
thymWT_a	Thymidine wild type biological replicate a	units
thymWT_b	Thymidine wild type biological replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
thymWT_c	Thymidine wild type biological replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
thymWT_d	Thymidine wild type biological replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
thym0378_a	Thymidine locas tag 0378 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
thym0378_b	Thymidine locas tag 0378 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
thym0378_c	Thymidine locas tag 0378 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
thym0378_d	Thymidine locas tag 0378 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
thym0379_a	Thymidine locas tag 0379 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
thym0379_b	Thymidine locas tag 0379 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
thym0379_c	Thymidine locas tag 0379 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.

thym0379_d	Thymidine locas tag 0379 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cholWT_a	Choline wild type biological replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cholWT_b	Choline wild type biological replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cholWT_c	Choline wild type biological replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cholWT_d	Choline wild type biological replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
chol1087_a	Choline locas tag 1087 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
chol1087_b	Choline locas tag 1087 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
chol1087_c	Choline locas tag 1087 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
chol1087_d	Choline locas tag 1087 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
DMSPWT_a	DMSP wild type biological replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
DMSPWT_b	DMSP wild type biological replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
DMSPWT_c	DMSP wild type biological replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
DMSPWT_d	DMSP wild type biological replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
citrWT_a	Citrate wild type biological replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
citrWT_b	Citrate wild type biological replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.

citrWT_c	Citrate wild type biological replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
citrWT_d	Citrate wild type biological replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
DHPSWT_a	DHPS wild type biological replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
DHPSWT_b	DHPS wild type biological replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
DHPSWT_c	DHPS wild type biological replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
DHPSWT_d	DHPS wild type biological replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glosWT_a	Glucose wild type biological replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glosWT_b	Glucose wild type biological replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glosWT_c	Glucose wild type biological replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glosWT_d	Glucose wild type biological replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
xyloWT_a	Xylose wild type biological replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
xyloWT_b	Xylose wild type biological replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
xyloWT_c	Xylose wild type biological replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
xyloWT_d	Xylose wild type biological replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
taurWT_a	Taurine wild type biological replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.

taurWT_b	Taurine wild type biological replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
taurWT_c	Taurine wild type biological replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
taurWT_d	Taurine wild type biological replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
DMSP3186_a	DMSP locas tag 3186 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
DMSP3186_b	DMSP locas tag 3186 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
DMSP3186_c	DMSP locas tag 3186 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
DMSP3186_d	DMSP locas tag 3186 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
xylo0863_a	Xylose 0863 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
xylo0863_b	Xylose 0863 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
xylo0863_c	Xylose 0863 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
xylo0863_d	Xylose 0863 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
DHPS0591_a	DHPS locas tag 0591 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
DHPS0591_b	DHPS locas tag 0591 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
DHPS0591_c	DHPS locas tag 0591 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
DHPS0591_d	DHPS locas tag 0591 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glos0863_a	Glucose locas tag 0863 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glos0863_b	Glucose locas tag 0863 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.

glos0863_c	Glucose locas tag 0863 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glos0863_d	Glucose locas tag 0863 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
taur0676_a	Taurine locas tag 0676 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
taur0676_b	Taurine locas tag 0676 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
taur0676_c	Taurine locas tag 0676 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
taur0676_d	Taurine locas tag 0676 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
taur0674_a	Taurine locas tag 0674 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
taur0674_b	Taurine locas tag 0674 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
taur0674_c	Taurine locas tag 0674 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
taur0674_d	Taurine locas tag 0674 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glcNWT_a	GlcNAc biological wild type replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glcNWT_b	GLcNAc biological wild type replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glcNWT_c	GLcNAc biological wild type replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glcNWT_d	GLcNAc biological wild type replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glcN1839_a	GLcNAc locas tag 1839 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glcN1839_b	GLcNAc locas tag 1839 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glcN1839_c	GLcNAc locas tag 1839 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glcN1839_d	GLcNAc locas tag 1839 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.

sperWT_a	Spermidine biological wild type replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
sperWT_b	Spermidine biological wild type replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
sperWT_c	Spermidine biological wild type replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
sperWT_d	Spermidine biological wild type replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cadaWT_a	Cadaverine biological wild type replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cadaWT_b	Cadaverine biological wild type replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cadaWT_c	Cadaverine biological wild type replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cadaWT_d	Cadaverine biological wild type replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
putrWT_a	Putresceine biological wild type replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
putrWT_b	Putresceine biological wild type replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
putrWT_c	Putresceine biological wild type replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
putrWT_d	Putresceine biological wild type replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
ectoWT_a	Ectoine biological wild type replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
ectoWT_b	Ectoine biological wild type replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.

ectoWT_c	Ectoine biological wild type replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
ectoWT_d	Ectoine biological wild type replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
sper3469_a	Spermidine locas tag 3469 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
sper3469_b	Spermidine locas tag 3469 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
sper3469_c	Spermidine locas tag 3469 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
sper3469_d	Spermidine locas tag 3469 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cada3469_a	Cadaverine locas tag 3469 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cada3469_b	Cadaverine locas tag 3469 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cada3469_c	Cadaverine locas tag 3469 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cada3469_d	Cadaverine locas tag 3469 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
putr3469_a	Putresceine locas tag 3469 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
putr3469_b	Putresceine locas tag 3469 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
putr3469_c	Putresceine locas tag 3469 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
putr3469_d	Putresceine locas tag 3469 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
ecto1147_a	Ectoine locas tag 1147 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.

ecto1147_b	Ectoine locas tag 1147 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
ecto1147_c	Ectoine locas tag 1147 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
ecto1147_d	Ectoine locas tag 1147 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
malaWT_a	Malate biological wild type replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
malaWT_b	Malate biological wild type replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
malaWT_c	Malate biological wild type replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
malaWT_d	Malate biological wild type replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
succWT_a	Succinate biological wild type replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
succWT_b	Succinate biological wild type replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
succWT_c	Succinate biological wild type replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
succWT_d	Succinate biological wild type replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
fumrWT_a	Fumarate biological wild type replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
fumrWT_b	Fumarate biological wild type replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
fumrWT_c	Fumarate biological wild type replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
fumrWT_d	Fumarate biological wild type replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
mala2626_a	Malate locus tag 2626 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.

mala2626_b	Malate locus tag 2626 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
mala2626_c	Malate locus tag 2626 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
mala2626_d	Malate locus tag 2626 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
mala2628_a	Malate locus tag 2628 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
mala2628_b	Malate locus tag 2628 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
mala2628_c	Malate locus tag 2628 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
mala2628_d	Malate locus tag 2628 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
mala2630_a	Malate locus tag 2630 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
mala2630_b	Malate locus tag 2630 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
mala2630_c	Malate locus tag 2630 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
mala2630_d	Malate locus tag 2630 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
succ2626_a	Succinate locus tag 2626 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
succ2626_b	Succinate locus tag 2626 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
succ2626_c	Succinate locus tag 2626 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
succ2626_d	Succinate locus tag 2626 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
succ2628_a	Succinate locus tag 2628 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
succ2628_b	Succinate locus tag 2628 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.

succ2628_c	Succinate locus tag 2628 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
succ2628_d	Succinate locus tag 2628 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
succ2630_a	Succinate locus tag 2630 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
succ2630_b	Succinate locus tag 2630 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
succ2630_c	Succinate locus tag 2630 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
succ2630_d	Succinate locus tag 2630 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
fumr2626_a	Fumarate locus tag 2626 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
fumr2626_b	Fumarate locus tag 2626 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
fumr2626_c	Fumarate locus tag 2626 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
fumr2626_d	Fumarate locus tag 2626 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
fumr2628_a	Fumarate locus tag 2628 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
fumr2628_b	Fumarate locus tag 2628 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
fumr2628_c	Fumarate locus tag 2628 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
fumr2628_d	Fumarate locus tag 2628 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.

fumr2630_a	Fumarate locus tag 2630 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
fumr2630_b	Fumarate locus tag 2630 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
fumr2630_c	Fumarate locus tag 2630 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
fumr2630_d	Fumarate locus tag 2630 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cystWT_a	Cysteate biological wild type replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cystWT_b	Cysteate biological wild type replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cystWT_c	Cysteate biological wild type replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cystWT_d	Cysteate biological wild type replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glycWT_a	Glycerol biological wild type replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glycWT_b	Glycerol biological wild type replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glycWT_c	Glycerol biological wild type replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glycWT_d	Glycerol biological wild type replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cyst3040_a	Cysteate locus tag 3040 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cyst3040_b	Cysteate locus tag 3040 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cyst3040_c	Cysteate locus tag 3040 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.

cyst3040_d	Cysteate locus tag 3040 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glyc0608_a	Glycerol locus tag 0608 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glyc0608_b	Glycerol locus tag 0608 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glyc0608_c	Glycerol locus tag 0608 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
glyc0608_d	Glycerol locus tag 0608 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cyst3041_a	Cysteate locus tag 3041 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cyst3041_b	Cysteate locus tag 3041 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cyst3041_c	Cysteate locus tag 3041 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
cyst3041_d	Cysteate locus tag 3041 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
isetWT_a	Isethionate biological wild type replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
isetWT_b	Isethionate biological wild type replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
isetWT_c	Isethionate biological wild type replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
isetWT_d	Isethionate biological wild type replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
iset2357_a	Isethionate locus tag 2357 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.

iset2357_b	Isethionate locus tag 2357 repilicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
iset2357_c	Isethionate locus tag 2357 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
iset2357_d	Isethionate locus tag 2357 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
iset2358_a	Isethionate locus tag 2358 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
iset2358_b	Isethionate locus tag 2358 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
iset2358_c	Isethionate locus tag 2358 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
iset2358_d	Isethionate locus tag 2358 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
butrWT_a	3-Hydroxybutyrate biological wild type replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
butrWT_b	3-Hydroxybutyrate biological wild type replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
butrWT_c	3-Hydroxybutyrate biological wild type replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
butrWT_d	3-Hydroxybutyrate biological wild type replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
carnWT_a	Carnitine biological wild type replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
carnWT_b	Carnitine biological wild type replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
carnWT_c	Carnitine biological wild type replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
carnWT_d	Carnitine biological wild type replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.

butr537A_a	3-Hydroxybutyrate locus tag 537A replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
butr537A_b	3-Hydroxybutyrate locus tag 537A replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
butr537A_c	3-Hydroxybutyrate locus tag 537A replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
butr537A_d	3-Hydroxybutyrate locus tag 537A replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
butr537B_a	3-Hydroxybutyrate locus tag 537B replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
butr537B_b	3-Hydroxybutyrate locus tag 537B replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
butr537B_c	3-Hydroxybutyrate locus tag 537B replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
butr537B_d	3-Hydroxybutyrate locus tag 537B replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
carn2995_a	Carnitine locus tag 2995 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
carn2995_b	Carnitine locus tag 2995 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
carn2995_c	Carnitine locus tag 2995 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
carn2995_d	Carnitine locus tag 2995 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
carn2996_a	Carnitine locus tag 2996 replicate a	Number of sequence counts (barcodes) that mapped to each gene in the treatment.

carn2996_b	Carnitine locus tag 2996 replicate b	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
carn2996_c	Carnitine locus tag 2996 replicate c	Number of sequence counts (barcodes) that mapped to each gene in the treatment.
carn2996_d	Carnitine locus tag 2996 replicate d	Number of sequence counts (barcodes) that mapped to each gene in the treatment.

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Instruments

Dataset-specific Instrument Name	Synergy H1 plate reader (BioTek, Winooski, VT, USA)
Generic Instrument Name	plate reader
Dataset-specific Description	Cultures were grown at 25oC in a Synergy H1 plate reader (BioTek, Winooski, VT, USA) shaking at 425 rpm for 68-72 h. OD600 readings were collected once each hour.
Generic Instrument Description	Plate readers (also known as microplate readers) are laboratory instruments designed to detect biological, chemical or physical events of samples in microtiter plates. They are widely used in research, drug discovery, bioassay validation, quality control and manufacturing processes in the pharmaceutical and biotechnological industry and academic organizations. Sample reactions can be assayed in 6-1536 well format microtiter plates. The most common microplate format used in academic research laboratories or clinical diagnostic laboratories is 96-well (8 by 12 matrix) with a typical reaction volume between 100 and 200 uL per well. Higher density microplates (384- or 1536-well microplates) are typically used for screening applications, when throughput (number of samples per day processed) and assay cost per sample become critical parameters, with a typical assay volume between 5 and 50 µL per well. Common detection modes for microplate assays are absorbance, fluorescence intensity, luminescence, time-resolved fluorescence, and fluorescence polarization. From: http://en.wikipedia.org/wiki/Plate_reader, 2014-09-0-23.

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Project Information

Function and Importance of Marine Bacterial Transporters of Plankton Exometabolites (C-CoMP Marine Bacterial Transporters)

Project:

Observing expression of marine bacterial transporter systems with transcriptomic or proteomic tools can provide valuable information about the metabolomic environment. However, these ‘omics approaches are limited by the low rate of transporter gene annotation. Here, a barcoded, arrayed, mutant library of the marine bacterium *Ruegeria pomeroyi* DSS-3 is employed in high throughput screens to identify the target substrates of 13 transporter systems. A set of 156 isolated putative transporter mutants were screened for growth on

minimal medium with 63 substrates, each as a sole carbon source. Mutants that demonstrated a growth defect on a specific substrate were selected for secondary, higher resolution, growth screening. Mutants that continued to demonstrate growth defect relative to the pooled-mutant library (pooled-BarSeq, used as an analog for wildtype) were screened for their ability to drawdown the target substate. Gene annotations were made when mutants of the given transporter demonstrated both growth and drawdown defects on the target substrate.

In addition to the isolated mutant screens, the pooled barcoded transposon mutant library (pooled-BarSeq) was grown on minimal medium with selected substrates, each as sole carbon source, such that the relative enrichment or depletion of each mutant could demonstrate its fitness cost associated with the loss of each disrupted gene when grown on each substrate. The results of pooled-BarSeq screens had mixed consistency with the isolated mutant screens, demonstrating the value of isolated mutants for transporter annotation.

Program:

The Center for Chemical Currencies of a Microbial Planet (C-CoMP) integrates research, education and knowledge transfer activities to develop a mechanistic understanding of surface ocean carbon flux within the context of a changing ocean and through increased participation in ocean sciences. C-CoMP supports science teams that merge biology, chemistry, modeling, and informatics to close long-standing knowledge gaps in the identities and dynamics of organic molecules that serve as the currencies of elemental transfer between the ocean and atmosphere.

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Program Information

Center for Chemical Currencies of a Microbial Planet (C-CoMP)

Website: https://ccomp-stc.org/

Coverage: North Atlantic, BATS, global/other

Functions carried out by microscopic inhabitants of the surface ocean affect every aspect of life on our planet, regardless of distance from the coast. Ocean phytoplankton are responsible for half of the photosynthesis on Earth, the first step in a complex system that annually withdraws 50 billion metric tons of carbon from the atmosphere to sustain their growth. Of this, 25 billion metric tons participate in a rapid cycle in which biologically reactive material is released into seawater and converted back into carbon dioxide by marine bacteria within hours to days. The chemical-microbe network at the heart of this fast cycle remains poorly constrained; consequently, its primary currencies and controls remain elusive; its sensitivities to changing ocean conditions are unknown; and its responses to future climate scenarios are not predictable. The Center for Chemical Currencies of a Microbial Planet (C-CoMP) integrates research, education and knowledge transfer activities to develop a mechanistic understanding of surface ocean carbon flux within the context of a changing ocean and through increased participation in ocean sciences. C-CoMP supports science teams that merge biology, chemistry, modeling, and informatics to close long-standing knowledge gaps in the identities and dynamics of organic molecules that serve as the currencies of elemental transfer between the ocean and atmosphere. C-CoMP fosters education, outreach, and knowledge transfer activities that engage students of all ages, broaden participation in the next generation of ocean scientists, and extend novel open-science approaches into complementary academic and industrial communities. The Center framework is critical to this mission, uniquely facilitating an open exchange of experimental and computational science, methodological and conceptual challenges, and collaborations that establish integrated science and education partnerships. With expanded participation in ocean science research and ocean literacy across the US society, the next generation of ocean scientists will better reflect the diverse US population.

Climate-carbon feedbacks on the marine carbon reservoir are major uncertainties for future climate projections, and the trajectory and rate of ocean changes depend directly on microbial responses to temperature increases, ocean acidification, and other perturbations driven by climate change. C-CoMP research closes an urgent knowledge gap in the mechanisms driving carbon flow between ocean and atmosphere, with global implications for predictive climate models. The Center supports interdisciplinary science teams following open and reproducible science practices to address: (1) the chemical currencies of

surface ocean carbon flux; (2) the structure and regulation of the chemical-microbe network that mediates this flux; and (3) sensitivity of the network and its feedbacks on climate. C-CoMP leverages emerging tools and technologies to tackle critical challenges in these themes, in synergy with existing ocean programs and consistent with NSF’s Big Ideas. C-CoMP education and outreach activities seek to overcome barriers to ocean literacy and diversify participation in ocean research. The Center is developing (1) initiatives to expand ocean literacy in K-12 and the broader public, (2) ocean sciences undergraduate curricula and research opportunities that provide multiple entry points into research experiences, (3) post-baccalaureate programs to transition undergraduates into graduate education and careers in ocean science, and (4) interdisciplinary graduate student and postdoctoral programs that prepare the next generation of ocean scientists. The C-CoMP team includes education faculty who evaluate the impacts of education and outreach activities and export successful STEM initiatives to the education community. C-CoMP is revolutionizing the technologies for studying chemical transformations in microbial systems to build understanding of the outsized impact of microbes on elemental cycles. Open science, cross-disciplinary collaborations, community engagement, and inclusive practices foster strategic advances in critical science problems and STEM initiatives. C-CoMP science, education, and knowledge-transfer themes are efficiently addressed through a sustained network of scientists addressing critical research challenges while broadening the workforce that will tackle multi-disciplinary problems with academic, industrial and policy partners.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

The Program's Data Management Plan (DMP) is available as a PDF document.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-2019589
Simons Foundation (Simons)	542391

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