# Eukaryotic phytoplankton flow cytometric results from salp grazing incubations conducted on R/V Tangaroa cruise TAN1810 during Oct-Nov 2018

**Website**: https://www.bco-dmo.org/dataset/846664
**Data Type**: Cruise Results
**Version**: 1
**Version Date**: 2021-04-08

**Project**
» Collaborative Research: Quantifying trophic roles and food web ecology of salp blooms of the Chatham Rise (Salp Food Web Ecology)


| Contributors | Affiliation | Role |
|---|---|---|
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**Abstract**
This dataset includes eukaryotic phytoplankton flow cytometric results from salp grazing incubations in order to quantify food web flows through contrasting salp-dominated and salp-absent water parcels near the Chatham Rise off western New Zealand where salp blooms are a predictable phenomenon. Sampling was conducted on R/V Tangaroa (cruise TAN1810) during October-November 2018.

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## Coverage

**Spatial Extent**: **N**:-42.742 **E**:179.9428 **S**:-45.5503 **W**:174.095
**Temporal Extent**: 2018-10-23 - 2018-11-21

### Methods & Sampling

This dataset seeks to quantify food web flows through contrasting salp-dominated and salp-absent water parcels near the Chatham Rise off western New Zealand where salp blooms are a predictable phenomenon.

Paired 20-liter plankton kreisels or 30-liter pseudo-kreisels were gently filled (using silicon tubing) with mixed

layer seawater collected by CTD-Niskin rosette casts at ~22:00 local time. Salps for incubations were collected at ~23:00 local time using the salp net. The net was towed slowly and briefly (5-10 minutes) through the mixed layer. Healthy specimens, i.e., those that showed no physical damage, were then gently transferred (using a large ladle) into a bucket containing filtered surface seawater Specimens were further observed (15-30 minutes) to ensure they actively swam (i.e., that they appeared healthy). They were then transferred into one of the paired kreisels (+Salp treatment), while the second kreisel was used as a control treatment with prey only. We successfully collected and incubated S. thompsoni blastozooids and oozooids ranging in size from 50 – 128 millimeters. We also conducted three incubations with a chain of blastozooids (6-8 millimeter individuals) released by an oozooid inside of one of the plankton kreisels. We found that this was the only way to successfully obtain such small blastozooids in healthy conditions. We also incubated a 112-millimeter Thetys vagina oozooid.

Water was circulated within the kreisels using a peristaltic pump and silicon tubing. Just after salp transfer to the kreisels, initial samples for flow cytometry were taken from each experimental and control kreisel. Additional time points were taken approximately every 2 hours and analyzed in near real time to allow us to monitor salp grazing.Incubations typically lasted ~24 hours.

Samples from the salp incubations were analyzed at sea on a Becton-Dickinson Accuri C6 Plus flow cytometer to estimate the abundance and size of eukaryotic phytoplankton. Samples (~660 µL) were run live within ~1-2 h of collection, discriminating on the Chl a fluorescence signal. We estimated cell diameter from forward light scatter after developing a relationship based on analyses of multiple polystyrene bead sizes (0.99-10 µm diameter). We note that forward scatter is an imperfect proxy for equivalent spherical diameter, and thus the absolute cell sizes determined in our study should be assumed to have associated uncertainty.

For additional details on all methods, see Stukel et al. (in review).

Note: This dataset is also provided in .mat (MATLAB) format under Supplemental Files.

#### Data Processing Description

BCO-DMO Processing:
- Adjusted field/parameter names to comply with BCO-DMO naming conventions;
- Added a conventional header with dataset name, PI names, version date.

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## Data Files

| File | |
|---|---|
| **phytoplankton_flow_cytometry.csv** | (Comma Separated Values (.csv), 297.99 MB) MD5:47a4aa33600dff8d739226ee8a8c8865 |
| Primary data file for dataset ID 846664 | |

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## Supplemental Files

| File | |
|---|---|
| **FCMTable.mat** | (MATLAB Data (.mat), 63.83 MB) MD5:4b0c586c08520df15c1fafa1feff3987 |
| This is a copy of the dataset in .mat format. | |

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## Related Publications

Stukel, M.R., Décima, M., Selph, K.E. and Gutiérrez-Rodríguez, A. (2021), Size-specific grazing and competitive interactions between large salps and protistan grazers. Limnol Oceanogr, 66: 2521-2534. https://doi.org/10.1002/lno.11770
*Results*

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## Parameters

| Parameter | Description | Units |
|---|---|---|
| Stage | Stage of salp (oozooid/blastozooid) | unitless |
| Incubation | Incubation Number | number |
| SalpTL | Salp Total length | millimeters (mm) |
| NumSalps | Number of salps in the incubation | number |
| Temperature | Temperature of incubation | degrees Celsius |
| Vol_Kreisel | Volume of the plankton kreisel | liter |
| TimePoint | Time point of sample | unitless |
| TimeSinceStart | Time since the beginning of incubation | days |
| TreatmentControl | 1=+Salp Treatment, 2=Control Treatment | unitless |
| vol_FCM | Sample volume analyzed for FCM | milliliters (mL) |
| FSC | Forward scatter | arbitrary units |
| SSC | Side scatter | arbitrary units |
| Phyco | Phycoerythrin fluorescence | arbitrary units |
| Chl | Chlorophyll fluorescence | arbitrary units |
| ESD_fsc | Equivalent spherical diameter estimated from FSC | micrometer (um) |

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## Instruments

| | |
|---|---|
| **Dataset-specific Instrument Name** | |
| **Generic Instrument Name** | Flow Cytometer |
| **Dataset-specific Description** | Becton-Dickinson Accuri C6 Plus flow cytometer |
| **Generic Instrument Description** | Flow cytometers (FC or FCM) are automated instruments that quantitate properties of single cells, one cell at a time. They can measure cell size, cell granularity, the amounts of cell components such as total DNA, newly synthesized DNA, gene expression as the amount messenger RNA for a particular gene, amounts of specific surface receptors, amounts of intracellular proteins, or transient signalling events in living cells. (from: http://www.bio.umass.edu/micro/immunology/facs542/facswhat.htm) |

| | |
|---|---|
| **Dataset-specific Instrument Name** | |
| **Generic Instrument Name** | Niskin bottle |
| **Generic Instrument Description** | A Niskin bottle (a next generation water sampler based on the Nansen bottle) is a cylindrical, non-metallic water collection device with stoppers at both ends. The bottles can be attached individually on a hydrowire or deployed in 12, 24, or 36 bottle Rosette systems mounted on a frame and combined with a CTD. Niskin bottles are used to collect discrete water samples for a range of measurements including pigments, nutrients, plankton, etc. |

| | |
|---|---|
| **Dataset-specific Instrument Name** | salp net |
| **Generic Instrument Name** | Plankton Net |
| **Generic Instrument Description** | A Plankton Net is a generic term for a sampling net that is used to collect plankton. It is used only when detailed instrument documentation is not available. |

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## Deployments

**TAN1810**

| | |
|---|---|
| **Website** | https://www.bco-dmo.org/deployment/757070 |
| **Platform** | R/V Tangaroa |
| **Start Date** | 2018-10-23 |
| **End Date** | 2018-11-21 |

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## Project Information

**Collaborative Research: Quantifying trophic roles and food web ecology of salp blooms of the Chatham Rise (Salp Food Web Ecology)**

**Coverage**: East of New Zealand, Chatham Rise area

*NSF Award Abstract:*
Salps are unique open-ocean animals that range in size from a few millimeters to greater than twenty centimeters, have a gelatinous (jelly-like) body, and can form long chains of many connected individuals. These oceanic organisms act as oceanic vacuum cleaners, having incredibly high feeding rates on phytoplankton and, unusual for consumers of their size, smaller bacteria-sized prey. This rapid feeding and the salps' tendency to form dense blooms, allows them move substantial amounts of prey carbon from the surface into the deep ocean, leading to carbon dioxide removal from the atmosphere. However, salps are often considered a trophic dead-end, rather than a link, in the food web due to the assumption that they themselves are not consumed, since their gelatinous bodies are less nutritious than co-occurring crustacean prey. Along with this, salp populations are hypothesized to be increasing due to climate change. This proposal addresses these questions: 1) Do salps compete primarily with crustaceans (as in the prevailing paradigm) or are they competitors of single-celled protists, which are the dominant grazers of small phytoplankton? 2) Do salp

blooms increase the efficiency of food-web pathways from tiny phytoplankton to fisheries production in nutrient-poor ocean regions?

This project will support the interdisciplinary education of a graduate student who will learn modeling and laboratory techniques in the fields of biological and chemical oceanography and stimulate international collaborations between scientists in the United States and New Zealand. Additionally, several Education and Outreach initiatives are planned, including development of a week-long immersive high school class in biological oceanography, and education modules that will serve the "scientists-in-the schools" program in Tallahassee, FL.

It is commonly assumed that salps are a trophic sink. However, this idea was developed before the discovery that protists (rather than crustaceans) are the dominant grazers in the open ocean and was biased by the difficulty of recognizing gelatinous salps in fish guts. More recent studies show that salps are found in guts of a diverse group of fish and seabirds and are a readily available prey source when crustacean abundance is low. This proposal seeks to quantify food web flows through contrasting salp-dominated and salp-absent water parcels near the Chatham Rise off western New Zealand where salp blooms are a predictable phenomenon. The proposal will leverage previously obtained data on salp abundance, bulk grazing impact, and biogeochemical significance during Lagrangian experiments conducted by New Zealand-based collaborators. The proposal will determine 1) taxon- and size-specific phytoplankton growth rate measurements, 2) taxon- and size-specific protozoan and salp grazing rate measurements, 3) compound specific isotopic analysis of the amino acids of mesozooplankton to quantify the trophic position of salps, hyperiid amphipods, and other crustaceans, 4) sediment traps to quantify zooplankton carcass sinking rates, and 5) linear inverse ecosystem modeling syntheses. Secondary production and trophic flows from this well-constrained ecosystem model will be compared to crustacean-dominated and microbial loop-dominated ecosystems in similarly characterized regions (California Current, Costa Rica Dome, and Gulf of Mexico).

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.

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## Funding


| Funding Source | Award |
|---|---|
| NSF Division of Ocean Sciences (NSF OCE) | OCE-1756465 |
| NSF Division of Ocean Sciences (NSF OCE) | OCE-1756610 |


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