# Zooplankton net haul metadata and specimen removal records collected from the R/V Gunnerus in the Tronheimsfjord, Norway during 2012 (Calanus Diapause project)

**Website**: https://www.bco-dmo.org/dataset/551905
**Version**: 2015-02-18

**Project**
» Identification of Diagnostic Markers of Diapause Preparation in the Copepod Calanus finmarchicus (Calanus_Diapause)

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## Dataset Description

This dataset consists of metadata associated with zooplankton net tows taken in Trondheimsfjord, Norway in spring 2012. A list of the specimens removed from the sample are also provided here.

### Methods & Sampling

Zooplankton samples were collected in Trondheimsfjord near Trondheim, Norway from 3 May to 11 June 2012 using a Sea-Gear 75-cm diameter ring net equipped with 150 micron mesh net and a cod end. Oblique tows were conducted over the upper ~50 m for nearly all tows. A close-open-close mechanism was used to collect zooplankton samples with the same net between roughly 250 and 350 m on three occasions. The volume filtered by the net was estimated using a General Oceanics flowmeter suspended in the center of the net mouth, and sample depths were measured using a SeaBird SBE39 depth-temperature recorder. Zooplankton samples were held on ice during transport back to the NTNU/SINTEF laboratory in Trondheim. Samples were live sorted to remove some late-stage Calanus finmarchicus, and then preserved in 5% buffered formalin. A small aliquot (subsample) of the bulk sample was removed and all taxa contained therein were enumerated. Species- or taxon-specific abundance of zooplankton was estimated from the raw counts, the subsample volume, sample volume, and the volume filtered by the net.

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## Data Files

| File |
| --- |
| **haul_meta.csv** (Comma Separated Values (.csv), 6.45 KB)<br>MD5:1b4cf70739f12028f6c85bf59b649925<br>Primary data file for dataset ID 551905 |

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## Parameters

| Parameter | Description | Units |
| --- | --- | --- |
| station | sampling location | unitless |
| cruise_name | cruise name assigned by PI | unitless |
| year | sampling year | yyyy |
| haul | plankton tow number | unitless |
| date | sampling date | yyyy-mm-dd |
| lat_start | latitude at start of haul; north is positive | decimal degrees |
| lon_start | longitude at start of haul; east is positive | decimal degrees |
| lat_end | latitude at end of haul; north is positive | decimal degrees |
| lon_end | longitude at end of haul; east is positive | decimal degrees |
| time_start | local time at start of haul | HH:MM:SS |
| time_end | local time at end of haul | HH:MM:SS |
| wire_out | meters of wire out | meters |
| depth_w | depth of water | meters |
| gear_type | type of sampling gear: ring = ring net | unitless |
| mesh | plankton net mesh size | microns |

| | | |
|---|---|---|
| net_diam | net diameter | meters |
| haul_type | type of haul: vertical or oblique | unitless |
| depth_start | depth at start of sample collection | meters |
| depth_end | depth at end of sample collection | meters |
| flow_serial_num | flow meter serial number | unitless |
| flow_count_start | initial flow count reading | unitless |
| flow_count_end | final flow count reading | unitless |
| flow_revolutions | number of flow count revolutions | revolutions |
| flow_cal_constant | flow meter calibration constant | meters/revolution |
| volume_haul | volume of water filtered during haul | cubic meters |
| taxa_removed_1 | taxa removed from sample (1) | unitless |
| num_removed_1 | Number removed from sample (1) | specimens |
| taxa_removed_2 | taxa removed from sample (2) | unitless |
| num_removed_2 | Number removed from sample (2) | specimens |
| taxa_removed_3 | taxa removed from sample (3) | unitless |
| num_removed_3 | Number removed from sample (3) | specimens |
| vol_subsample | volume of subsample | milliliters |
| vol_sample | sample volume | milliliters |
| processed_flag | flag designating sample processed: 1 = yes | unitless |

| | | |
|---|---|---|
| ISO_DateTime_Local_start | Local date and time in ISO format | YYYY-MM-DDTHH:MM:SS.xx |

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## Instruments

| | |
|---|---|
| **Dataset-specific Instrument Name** | Flow Meter |
| **Generic Instrument Name** | Flow Meter |
| **Dataset-specific Description** | General Oceanics flowmeter |
| **Generic Instrument Description** | General term for a sensor that quantifies the rate at which fluids (e.g. water or air) pass through sensor packages, instruments, or sampling devices. A flow meter may be mechanical, optical, electromagnetic, etc. |

| | |
|---|---|
| **Dataset-specific Instrument Name** | Ring Net |
| **Generic Instrument Name** | Ring Net |
| **Dataset-specific Description** | Sea-Gear 75-cm diameter ring net equipped with 150 micron mesh net and a cod end |
| **Generic Instrument Description** | A Ring Net is a generic plankton net, made by attaching a net of any mesh size to a metal ring of any diameter. There are 1 meter, .75 meter, .25 meter and .5 meter nets that are used regularly. The most common zooplankton ring net is 1 meter in diameter and of mesh size .333mm, also known as a 'meter net' (see Meter Net). |

| | |
|---|---|
| **Dataset-specific Instrument Name** | Temperature and depth recorder |
| **Generic Instrument Name** | Water Temperature Sensor |
| **Dataset-specific Description** | SeaBird SBE39 depth-temperature recorder |
| **Generic Instrument Description** | General term for an instrument that measures the temperature of the water with which it is in contact (thermometer). |

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## Deployments

**Baumgartner_fjord_2012**

| | |
|---|---|
| **Website** | https://www.bco-dmo.org/deployment/551934 |
| **Platform** | R/V Gunnerus |
| **Start Date** | 2012-05-03 |
| **End Date** | 2012-06-11 |
| **Description** | Zooplankton sampling on the RV Gunnerus (102') and RV Calanus (~22') out of the Norwegian University of Science and Technology (NTNU). Sampling by day trips in Trondheimsfjord. |

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## Project Information

**Identification of Diagnostic Markers of Diapause Preparation in the Copepod Calanus finmarchicus (Calanus_Diapause)**

**Coverage**: Trondheimfjord (near Trondheim, Norway)

*Extracted from the NSF award abstract:*

Oceanic copepods in the family Calanidae, such as *Calanus finmarchicus*, are among the most abundant animals on the planet, and they serve a key role in marine food webs by transferring energy from phytoplankton to higher trophic levels. The life history of these copepods has been well-studied, but fundamental questions remain about the regulation of an important period of dormancy called diapause. In the last juvenile stage of development, *C. finmarchicus* either proceed to the terminal molt (i.e., molt into adults) or vertically migrate to depth and initiate diapause. This divergence in developmental pathways has critical implications for *C. finmarchicus* population dynamics, but is difficult to study experimentally because *C. finmarchicus*, like all other copepods in the family Calanidae, do not reliably enter diapause in the laboratory. In addition, most temperate populations of calanoid copepods have multiple generations in a single year with variability in the timing of reproduction and development that causes significant heterogeneity in age structure. Thus, field sampling of these heterogeneous populations yields a mixture of copepods that are preparing for diapause, are preparing for the terminal molt, or are not yet preparing for either fate. Studies of diapause preparation in such populations are extremely difficult.

To enable direct investigation of the factors that influence diapause initiation, we require markers that reliably predict the fate of individual copepods (entry into diapause or continued maturation to adulthood) within heterogeneous populations. Fortunately, the fjord population of *C. finmarchicus* off the coast of Norway during the late spring is remarkably synchronous and is comprised of juvenile copepods that are all destined to undergo diapause. This project will use high-throughput 454 pyrosequencing to identify genes that change in expression as these copepods progress toward diapause. In collaboration with Norwegian researchers, the investigators will also rear copepods in a unique continuous culture and conduct additional transcriptional profiling to identify genes that change in expression as copepods prepare for the terminal molt. Comparison of gene expression patterns in the wild and cultured populations will enable the principal investigators to develop robust markers of diapauses preparation that can be used to study diapause initiation in more heterogeneous temperate populations.

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## Funding

| Funding Source | Award |
|---|---|
| NSF Division of Ocean Sciences (NSF OCE) | OCE-1132567 |

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