

# Cruise Report

## HHUMTL22

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# HHUMTL22

The Arctic University Museum of Norway

R/V «Helmer Hanssen»

Tromsø–Longyearbyen

August 22–29, 2022

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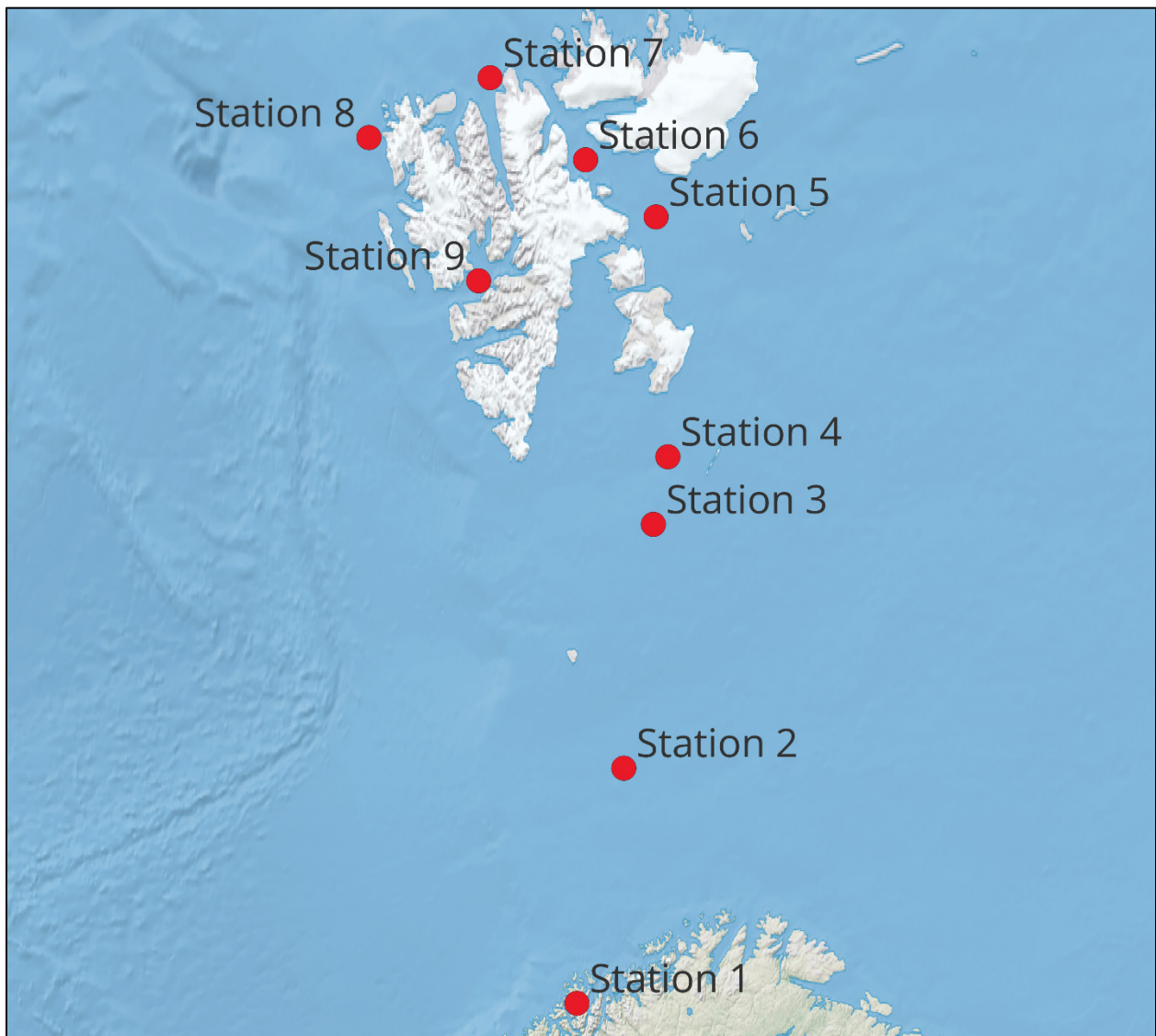


## Introduction

The HHUMTL22 cruise onboard R/V Helmer Hanssen was an initiative by The Arctic University Museum of Norway (UMAK) aimed at sampling marine fauna for the museum collections and various research projects undertaken at the museum. Researchers from the Swedish Museum of Natural History and the Department of Evolutionary Biology at the University of Vienna also participated in the cruise. Cruise leader was Andreas Altenburger (UMAK).

## Itinerary

The HHUMTL22 cruise embarked from Tromsø, Norway at 13:00 CET on Monday the 22<sup>nd</sup> of August 2022 and ended in Longyearbyen, Svalbard on Monday the 29<sup>th</sup> of August 2022 at 08.00 CET. The total distance travelled was about 900 nautical miles and the total time spent at sea amounted to 163 h (6 days 19 h). Travel and sample processing time during the cruise amounted to 143,5 h (5 days 23,5 h) while the time used for taking the samples was 19,5 h. In total, 9 stations were sampled (Fig. 1).



**Figure 1.** Map of Northern Norway, Svalbard and the Barents Sea. Red dots represent sampling stations.

## Project summaries

During the HHUMTL22 cruise, marine fauna for the following research projects was sampled.

1. Distribution and DNA barcoding of marine zooplankton along European coasts. Marine invertebrate animals such as annelids, mollusks, crustaceans, and many others commonly undergo a biphasic life cycle. Thereby, the usually benthic adult forms are antedated by free-swimming larvae that serve as dispersal stages. Since many of these larval types may live in the plankton for several weeks or even months, they may travel large distances by oceanic currents and thus may commence their adult life far from their parental habitat. While some marine invertebrates that exhibit larval stages develop taxon-specific structures in later larval stages (so-called secondary larvae), the primary larval type is often strikingly similar across distantly related taxa, as, e.g., exemplified in the trochophore-type larva of numerous lophotrochozoans or the nauplius of crustaceans. This makes determination of these minute animals – many of them are in the size range of around 100-500  $\mu\text{m}$  or even smaller - down to the species or genus level impossible, even by modern morphological studies. Therefore, DNA barcoding/metabarcoding using commonly available primers have established themselves as the current gold standard to efficiently assign such life cycle stages to their known adult kin. The present project is embedded in a large-scale approach to categorize and assess the biodiversity of invertebrate zooplankton species across major coastal oceanic regions of Europe using these methods in combination with molecular phylogenetic analyses. The results will form an important database for long-term studies revolving around population shifts and biodiversity loss of marine species in the light of ocean warming and acidification inflicted by the ongoing climate change. Samples are to be taken at selected sites from Southern to Northern Europe over the coming years. The northernmost part of the European continent around Northern Norway including Svalbard thereby constitutes a major landmark collecting site for a complete survey of European waters.
  - a. PI: Andreas Wanninger
  - b. Sampling gear: WP2 plankton nets (64 $\mu\text{m}$ , 180 $\mu\text{m}$ )
2. The project MIRevolution asks if there is one driving force of animal evolution that explains the immense diversity of life. And if this force can help us to understand the exceptional success of parasitic species that affect us? The underlying and very strong feature of both processes seems in fact to be very small: microRNAs. Since the discovery that they are found in all animals and regulate important biological processes about 20 years ago, these tiny fine-tuners of cellular programs are among the most studied molecules ever. However, with more than 16,000 annual publications in 2021, the rapidly growing microRNA field became riddled with contradicting reports that hindered novel discoveries and applications. In the recent research of Dr. Bastian Fromm, this was addressed with the microRNA gene database MirGeneDB and the foundations to transform the microRNA field from a qualitative research area to the quantitative level, and ask fundamental questions, were laid. In this TFS-project, Dr. Fromm and his group will use novel sequencing approaches, state of the art single cell experiments and take advantage of the unique biodiversity in Northern Norway and around Svalbard, to deepen the understanding of animal evolution. Using microRNAs, open questions in systematics and gene-regulation will be addressed. For MIRevolution the cruise will examine selected marine invertebrates for molecular analyses, genome sequencing and microRNA sequencing.

- a. PI: Anju Angelina Hembrom
  - b. Sampling gear: WP2 plankton nets, triangular dredge, multi-corer, epibenthic sledge
3. Megafaunal benthic diversity in the Barents Sea and the Seas around Svalbard. Benthic megafauna comprises marine animals exceeding 0,5 – 1 cm in size. The benthic fauna plays an important role in marine ecosystems as recyclers of sedimented organic matter, and as link from the benthic to the pelagic food-webs. The benthic fauna in the Barents Sea is influenced by Atlantic and Arctic water masses. For this project benthic marine invertebrates were identified to their lowest taxonomical level and the findings will subsequently be published as a dataset to the Global Biodiversity Information Facility (GBIF). Some specimens were fixed and included in the marine invertebrate collection of the Arctic University Museum of Norway (UiT).
  - a. PI: Andreas Altenburger, Joel Vikberg Wernström
  - b. Sampling gear: WP2 plankton nets, triangular dredge, multi-corer, epibenthic sledge
4. Taxonomy of benthic meiofauna from the Barents Sea. Meiofauna is defined as the fraction of metazoans that pass through a 1 mm mesh size sieve but are retained by a 45 µm mesh. To investigate the biodiversity of meiofauna around Svalbard with a special focus on kinorhynchs, sea floor samples were taken with a multi-corer to explore the diversity of benthic meiofauna around Svalbard. Live kinorhynchs were collected for an attempt of culturing, a challenge that has so far not been solved by any research group. In addition, specimens of benthic meiofauna were sampled for the marine invertebrate collection of the Arctic University Museum of Norway.
  - a. PI: Joel Vikberg Wernström, Andreas Altenburger
  - b. Sampling gear: triangular dredge and multi-corer
5. Taxonomy, biodiversity and neuroanatomy of the taxon Pycnogonida (Arthropoda). Pycnogonida (sea spiders) are exclusively marine, benthic chelicerates. In many oceanic regions – including the Barents Sea and the waters around Svalbard – their biodiversity is incompletely documented and modern taxonomic studies integrating DNA sequencing and morphology are still scarce. During the cruise, benthic samples were checked for sea spiders and most of the specimens obtained were fixed for integrative taxonomic work at the University of Vienna. Beyond taxonomy, some of the samples taken will be used for invasive neuroanatomical studies seeking to shed light on structural transformations of the central nervous system during early chelicerate evolution.
  - a. PI: Georg Brenneis
  - b. Sampling gear: triangular dredge and epibenthic sledge
6. Evolution of nematodes. Early branching of the nematode tree as well as the relationships between nematodes and other seemingly closely related organisms remain unclear. The goal was to collect representatives from several early branching clades, including some enigmatic parasites from a sea urchin, *Strongylocentrotus drobachiensis*, for genomic sequencing. If successful, these newly generated genomes will be included in a broad phylogenomic study aimed to improve our understanding of the evolution of Ecdysozoa in general and nematodes in particular, mined for Hox genes in a study looking to understand

the evolution of homeodomains, and mined for genes involved in the evolution of parasitism.

- a. PI: Oleksandr Holovachov
  - b. Sampling gear: triangular dredge, multi-corer
7. Diversity of Monogenean and Digenean flatworms – parasites of fish in the North Sea. Historically, and understandably, most of the studies of fish parasites in the Nordic countries has been focused on commercial species of fish, while the remaining, and much more diverse fish species have been largely neglected. Seven species of fish were collected by a bottom trawl and one by a triangular dredge. All were dissected following standard techniques and gills and digestive system were examined for parasites. Seven species were infected at least in one of the examined organs. These parasites will be identified to species level, sequenced, and included in the current project “Taxonomy and systematics of digenic trematodes parasitizing fishes in Sweden” by Chahinez Bouguerche at the Swedish Museum of Natural History.
- a. PI: Oleksandr Holovachov
  - b. Sampling gear: triangular dredge, bottom trawl.

## Station details

22.08.2022

10:00, boarding of Helmer Hanssen (HH) in Tromsø (Fig. 2).



**Figure 2.** R/V Helmer Hanssen in Tromsø, prior to departure.

Until 12:00 unpacking and preparation of labs.

12:00, safety instructions and survival suit training.

13:00, departure from Tromsø.

### Station 1

14:40, HH station 1293. CTD at 69 46.811330 N, 19 15.290131 E, depth 70,67 m (Fig. 3). Water was taken from the CTD rosette's Niskin bottles and filtered to be used for preparation of 4% paraformaldehyde in filtered seawater (4% PFA/SW) for sample fixation.



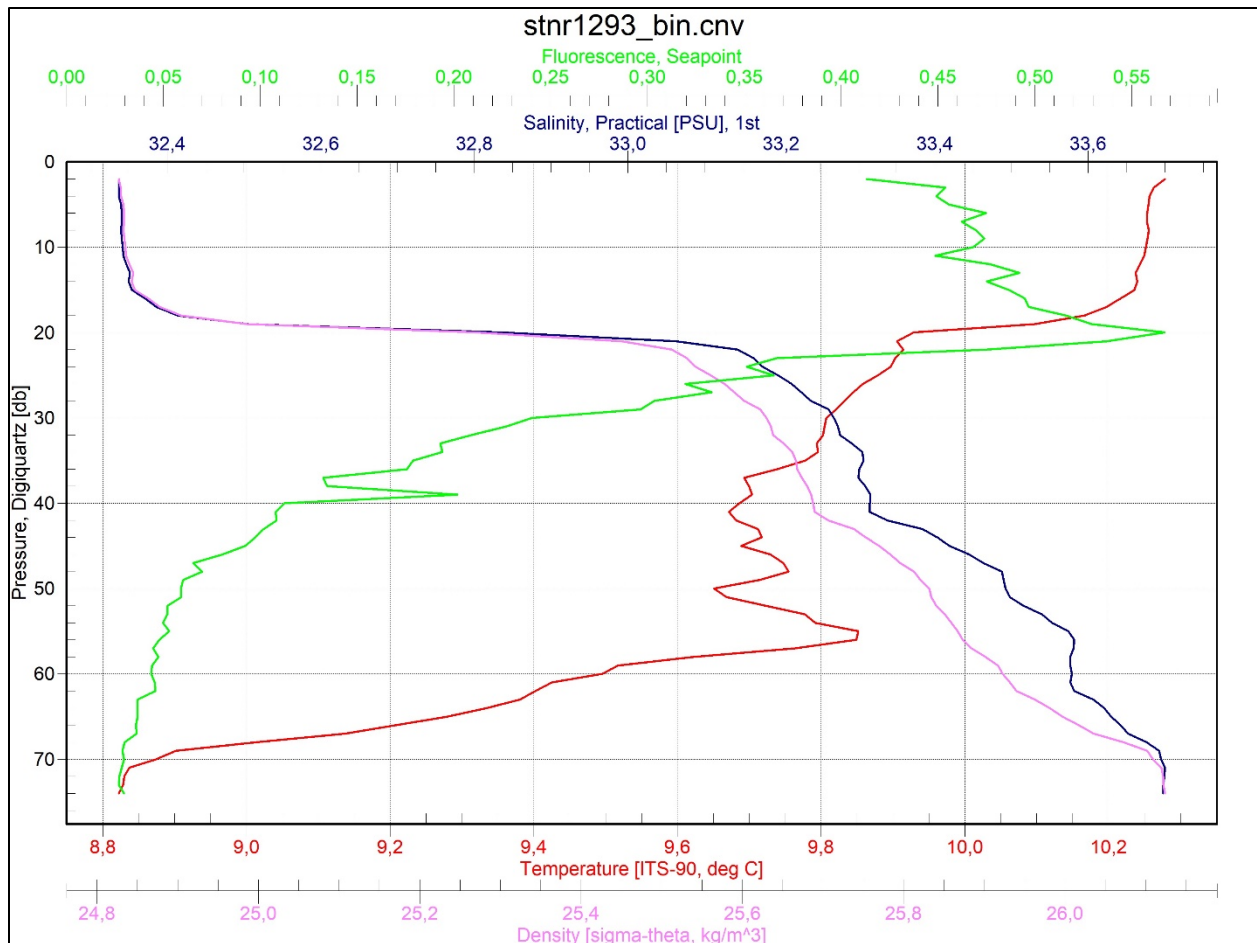


Figure 3. CTD output from Station 1 (HH station 1293).

15:01 – 15:11, HH station 1294, triangular dredge. Sediment was muddy with pebbles and stones. Fauna a mix of soft bottom and hard bottom. Many tunicates, a pycnogonid (*Nymphon* cf. *tenellum*), scaphopods, bivalves, gastropods, chitons, poriferans, annelids, sipunculids, sea urchins, brittle stars. In general, very diverse. One brachiopod (*Terebratulina retusa*) was fixed for genome and microRNA sequencing for the MIRevolution project. Scaphopods, chitons and sipunculids were fixed for DNA barcoding. The pycnogonid was fixed for taxonomic work. During the station it was realized that we forgot to bring ethanol and the epibenthic sledges from Havforskninginstituttet, hence we returned to Kailager in Tromsø to pick up the missing equipment and ethanol, which was done at 16.30.

17:52, HH station 1295, plankton net WP 2, 180 µm, 69 46.565406 N, 19 14.428520 E, depth 55,93 m. Plankton net was lowered down to 50 m. Bulk fixation of plankton samples for metabarcoding.

18:07, HH station 1296, plankton net WP 2, 64 µm at 69 46.599232 N, 19 14.677683 E, 55,48 m depth. Plankton net was lowered down to 50 m. Up with 0,3 m/s. Bulk fixation of plankton samples for metabarcoding.

18:29, HH station 1297, triangular dredge, 69 46.544628 N, 19 14.308664 E for bulk fixation of mud as well as mud sampling for bubble and plot. One pycnogonid specimen (*Nymphon*



*grossipes*) was fixed for neuroanatomical study, with one of its legs being separately preserved in ethanol for taxonomic confirmation by DNA barcoding.

19:07, group meeting to plan the next day. The weather forecast indicated that the ship would pass through a storm during the following night and day. Consequently, no work was planned for the next day. The evening until 22:00 was spent getting the labs ready for the storm, photographing specimens from HH station 1294 and fixing them for the museum collection.

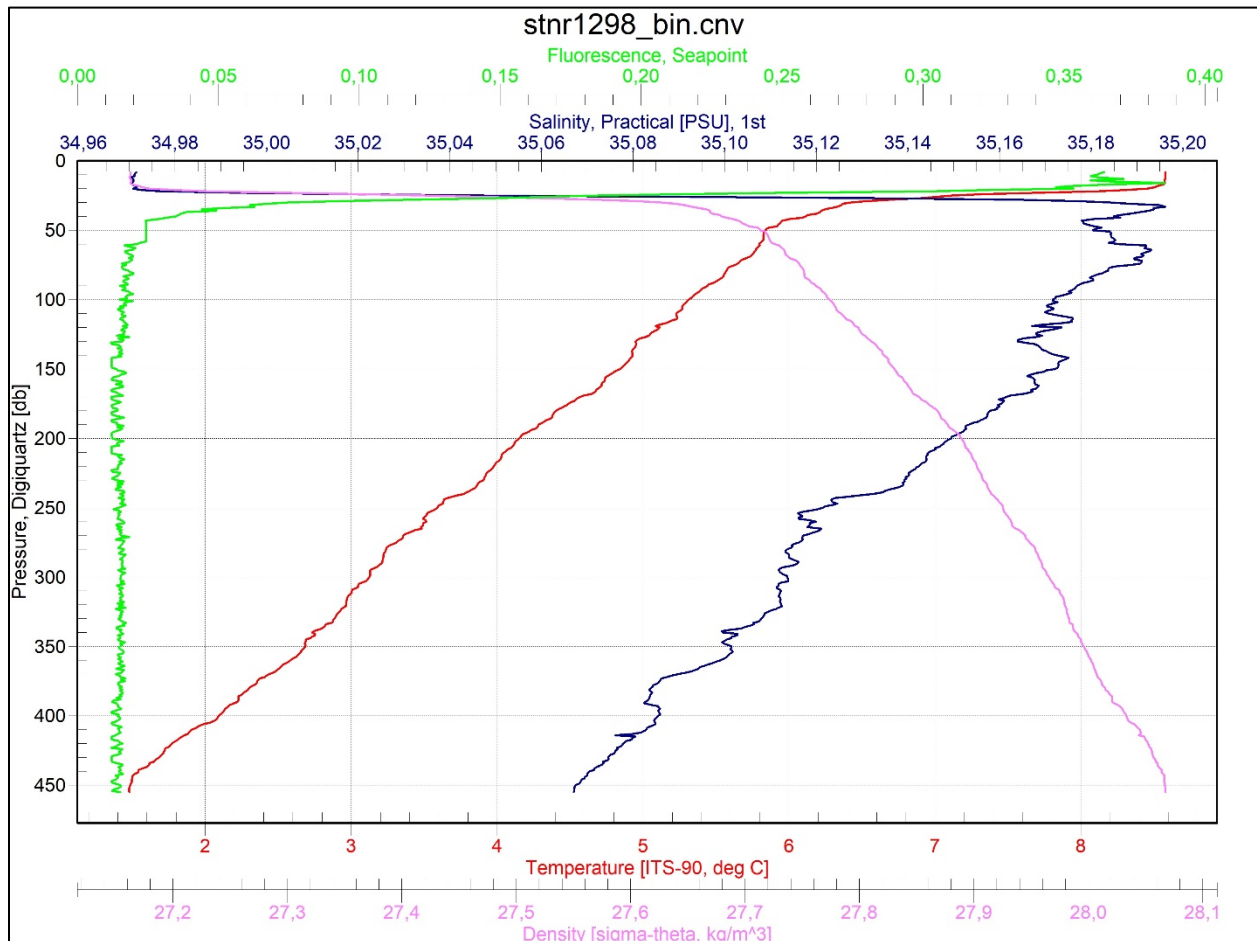
## 23.08.2022

Storm with waves up to 10 m. Everyone stayed in bed and waited for the sea sickness to disappear.

## 24.08.2022

### Station 2

8:59, HH station 1298, CTD at 73 03.788077 N, 21 18.808065 E, depth 457,45 m (Fig. 4). Water was taken from the CTD rosette's Niskin bottles and filtered to prepare 4% PFA/SW for fixation.



**Figure 4.** CTD output from Station 2 (HH station 1298).

9:32, HH station 1299, plankton net WP2 mesh size 64  $\mu\text{m}$  down to 450 m at 73 03.359989 N, 21 20.345687 E. Bulk fixation of plankton samples for metabarcoding.

10:20, HH station 1300, plankton net WP2 mesh size 180  $\mu\text{m}$  down to 450 m at 73 02.604550, N 21 19.705083 E. Bulk fixation of plankton samples for metabarcoding.

12:05, HH station 1301, epibenthic sledge down at 73 00.536707 N, 21 10.122484 E. Tubes (Foraminifera?), *Similipecten* sp., chaetognaths, brittle stars, crustaceans, *Terebratulina retusa*.

13:39, HH station 1302, epibenthic sledge at 72 59.253653 N, 20 58.445520 E, same as before. Various amphipod crustaceans from both sledge samples were preserved and will be examined for the presence of epibiotic nematodes.

15:00, transit to Station 3 and laboratory work with identification and fixation of sampled material. The *Terebratulina retusa* was fixed for the MIREvolution project. Select taxa (bivalves, chaetognaths, scaphopods, holothurian larvae/juveniles, one putative caudofauveate and one putative nemertean, cypris and veliger larvae, acoels and various annelids were fixed in ethanol and RNAlater for DNA barcoding, morphological analysis and transcriptomics.

25.08.2022

### Station 3

8:45, HH station 1303, CDT at 75 55.115157 N, 22 36.809925 E and a depth of 64.57 m (Fig. 5). Homogeneous waters. Water was taken from the CTD rosette's Niskin bottles and filtered to prepare 4% PFA/SW for fixation.

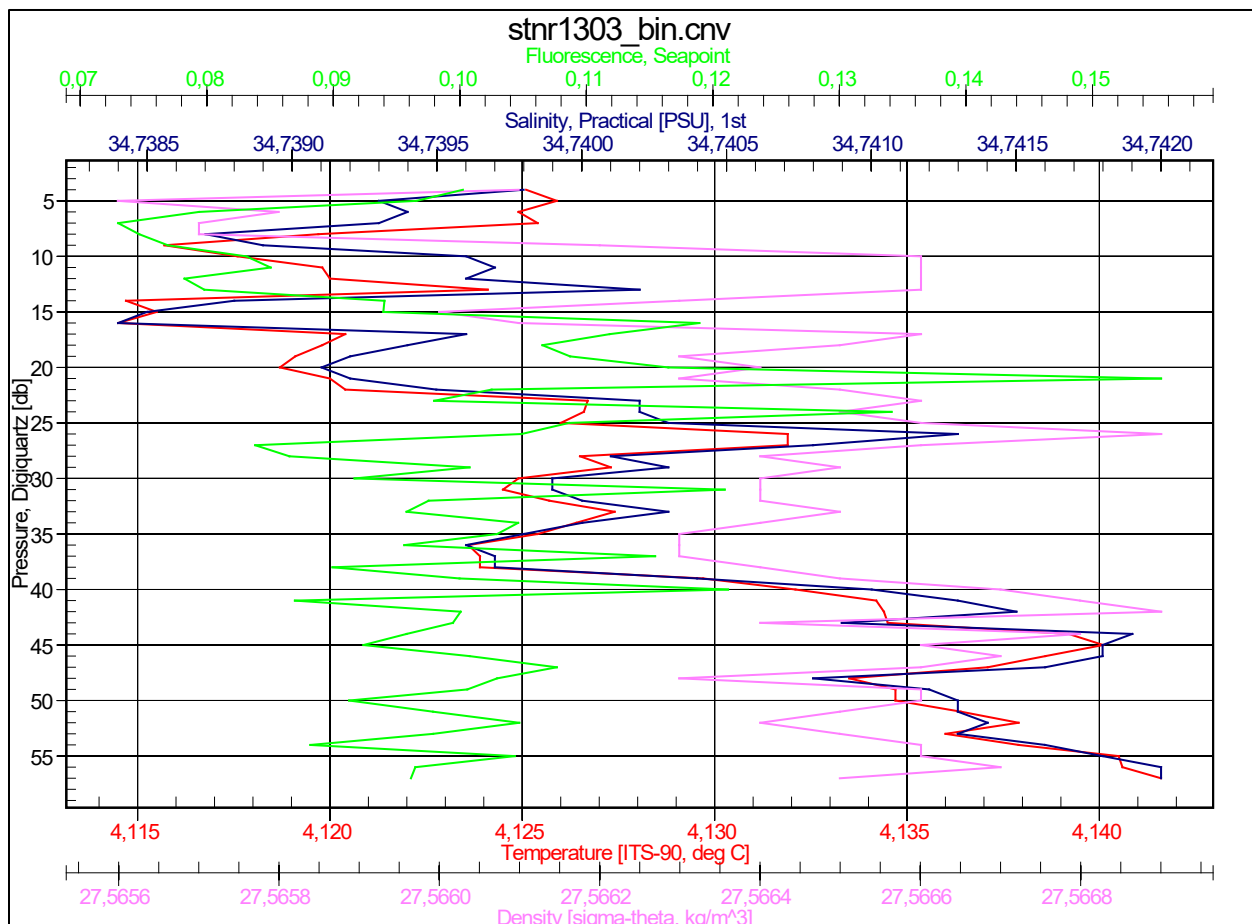
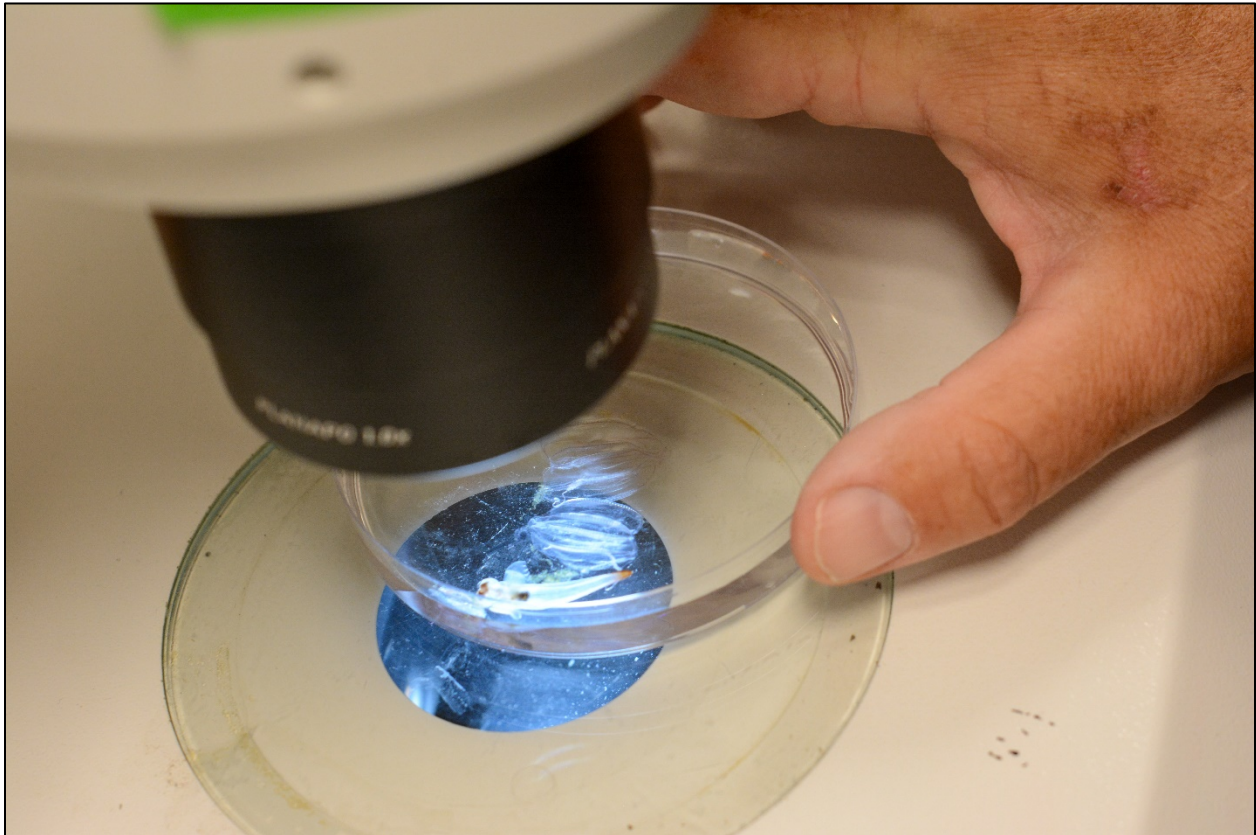


Figure 5. CTD output from Station 3 (HH station 1303).

8:45, HH station 1304, plankton net 180  $\mu\text{m}$ , vertical tow from bottom to surface, 75 55.036522 N, 22 36.527300 E. Bulk fixation of plankton samples for metabarcoding.

9:07, HH station 1305, plankton net 64  $\mu\text{m}$ , vertical tow from bottom to surface, 75 55.006063 N, 22 36.213258 E. Bulk fixation of plankton samples for metabarcoding. Fixation of one pteropod (Fig. 6) in 4 % PFA/SW for morphological analysis. Fixation of several ctenophores, small bivalves, zoea larvae and holothurian larvae/juveniles in 4% PFA/SW, ethanol and RNAlater for DNA barcoding, transcriptomics and morphological analysis.



**Figure 6.** Pteropod and ctenophores from Station 3.

9:27, HH station 1306, epibenthic sledge, 75 54.741750 N, 22 34.537739 E. The sledge came up empty because a big stone blocked the sampling opening.

9:53, HH station 1307, epibenthic sledge. 75 54.218892 N 22 31.167276 E. Few animals in the sledge, including *Sclerocrangon boreas*.

10:28, HH station 1308, triangular dredge (Fig. 7), at 75 53.662645 N, 22 27.006057 E. Shelly-gravel substrate. The dredge came up with a lot of shells, annelids (including scale worms), a few brittle stars, bryozoans, one nudibranch, and sipunculids, holothurians (incl. *Cucumaria frondosa*), *Pagurus* sp., *Buccinum* sp. and *Hyas araneus*. An assemblage of nematodes were collected and fixed for morpho-taxonomic studies. Meiofauna was extracted using  $\text{MgCl}_2$  anaesthesia, and 1 kamptozoon was preserved in 96% ethanol for sequencing and 2 others were preserved in 4% PFA/SW for morphological study, along with meiofaunal copepods and annelids.





Figure 7. Sorting of shelly gravel substrate from the triangular dredge at Station 3.

### Station 4

15:00, HH station 1309, CTD at 76 37.389029 N 23 15.006129 E and 162 m depth (Fig. 8). Water was taken from the CTD rosette's Niskin bottles and filtered to prepare 4% PFA/SW for fixation.

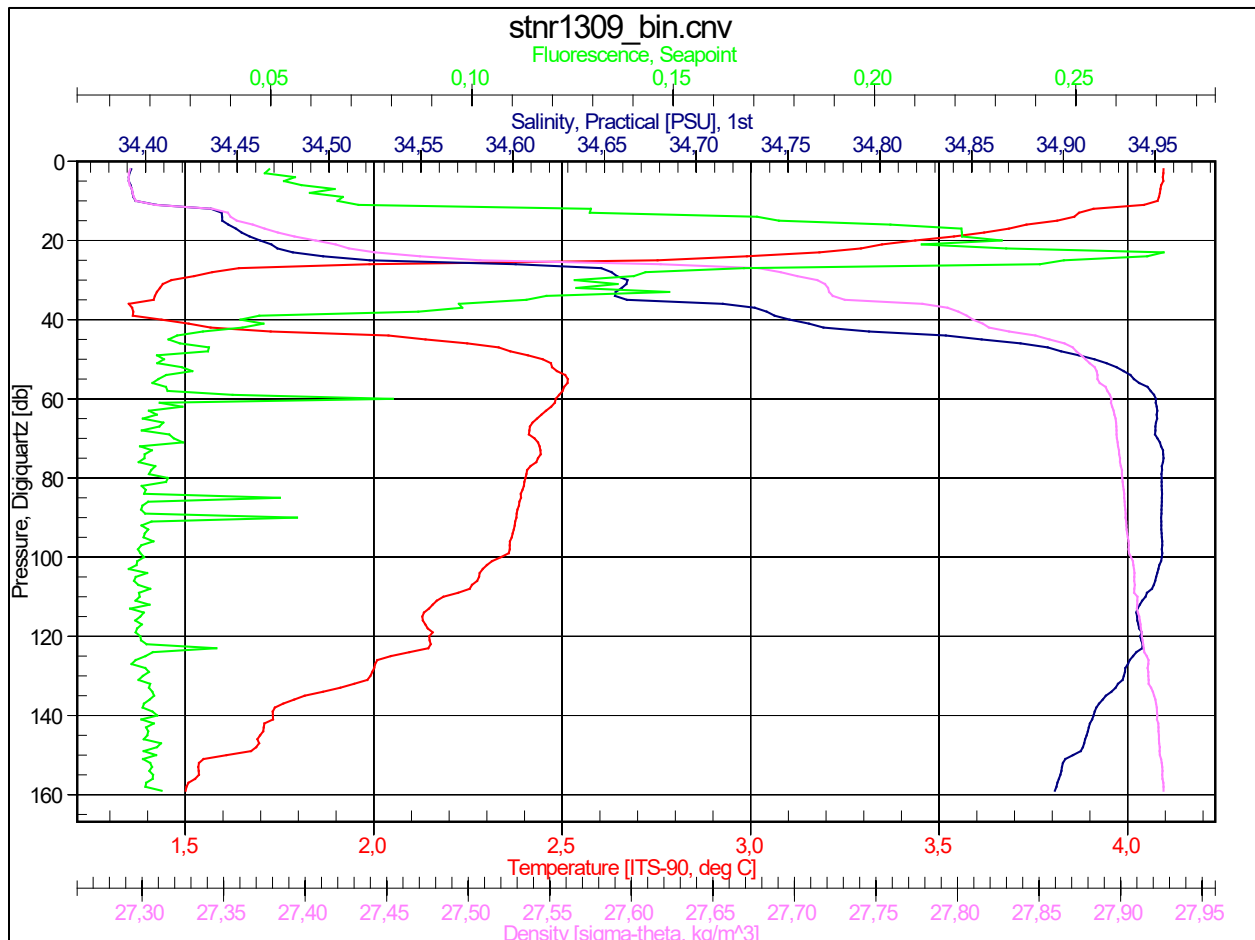


Figure 8. CTD output from Station 4 (HH station 1309).



15:11, HH station 1310, plankton net WP2, 64  $\mu\text{m}$ , at 76 37.410977 N, 23 14.805193 E, 150 m depth. Bulk fixation of plankton samples for metabarcoding.

15:33, HH station 1311, plankton net WP2, 180  $\mu\text{m}$ , at 76 37.441321 N, 23 14.658352 E, 150 m depth. Bulk fixation of plankton samples for metabarcoding. Fixation of pteropods in 4% PFA/SW and in RNALater for morphological analysis and transcriptomics. Fixation of selected taxa (holothurian larvae/juveniles, veliger larvae, mitraria larvae, acoels, ctenophore juveniles, one cubozoan) in 4% PFA/SW for morphological analysis.

16:04, HH station 1312, triangular dredge at 76 37.371260 N, 23 13.640811 E, 165 m depth. The dredge was full of mud. Species from the mud fixed in 96% EtOH for the museum collection: *Ctenodiscus crispatus*, *Drifa glomerata* (?), *Ophiura* sp. Bulk fixation of mud for meiofauna study at University of Vienna. Other species identified: *Spiochaetopterus* tubes, *Hormathia digitata*, *Astarte* sp. An assemblage of nematodes were fixed for morpho-taxonomic studies.

17:11, HH station 1313, multi corer (Fig. 9), 76 37.381056 N, 23 07.654756 E, 174 m depth. Excellent mud conditions. The upper 2 cm of each core were taken for extraction of meiofauna. An aplacophoran mollusc, *Chaetoderma nitidulum*, was preserved for possible molecular study. This sample had a more diverse nematode fauna than 1312, which were also fixed for morpho-taxonomic studies. Meiofauna was extracted using the 'bubble and blot' method. Plenty of kinorhynchans were found, and 40 were saved for the culturing attempt, 15 were preserved in SW and frozen for genomics, 10 fixed in RNALater and frozen for the MIRevolution project, and 3 were preserved in 4% PFA/SW for morphological study.



Figure 9. Multi corer being emptied at Station 4.

26.08.2022

### Station 5

9:05, HH station 1314, CTD at 78 51.276613 N 22 43.849367 E, 119 m depth (Fig. 10). Water was taken from the CTD rosette's Niskin bottles and filtered to prepare 4% PFA/SW for fixation.

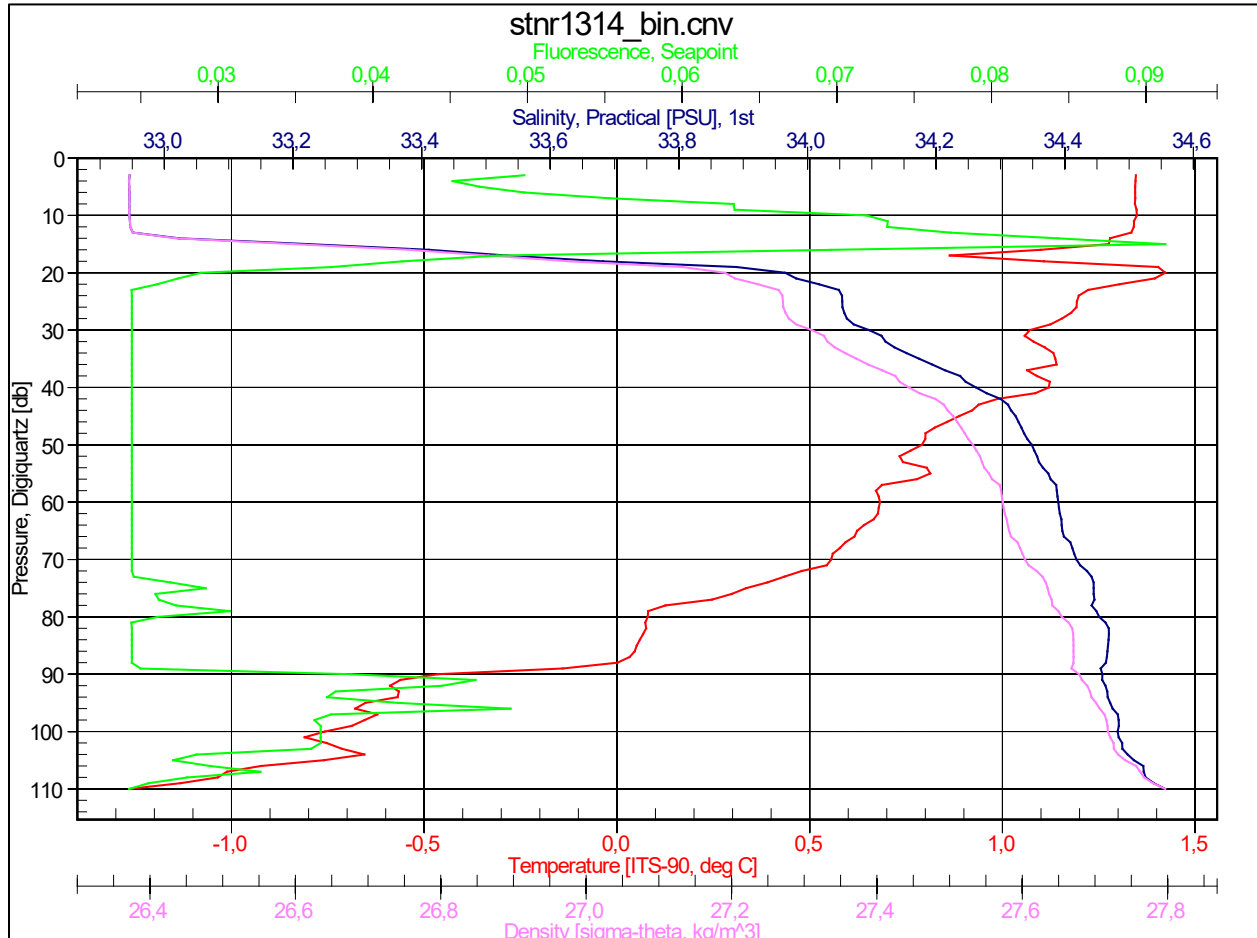


Figure 10. CTD output from Station 5 (HH station 1314).

9:17, HH station 1315, plankton net WP2, 180  $\mu$ m mesh size, 110 m depth at 78 51.260868 N, 22 43.198704 E. Bulk fixation of plankton samples for metabarcoding.

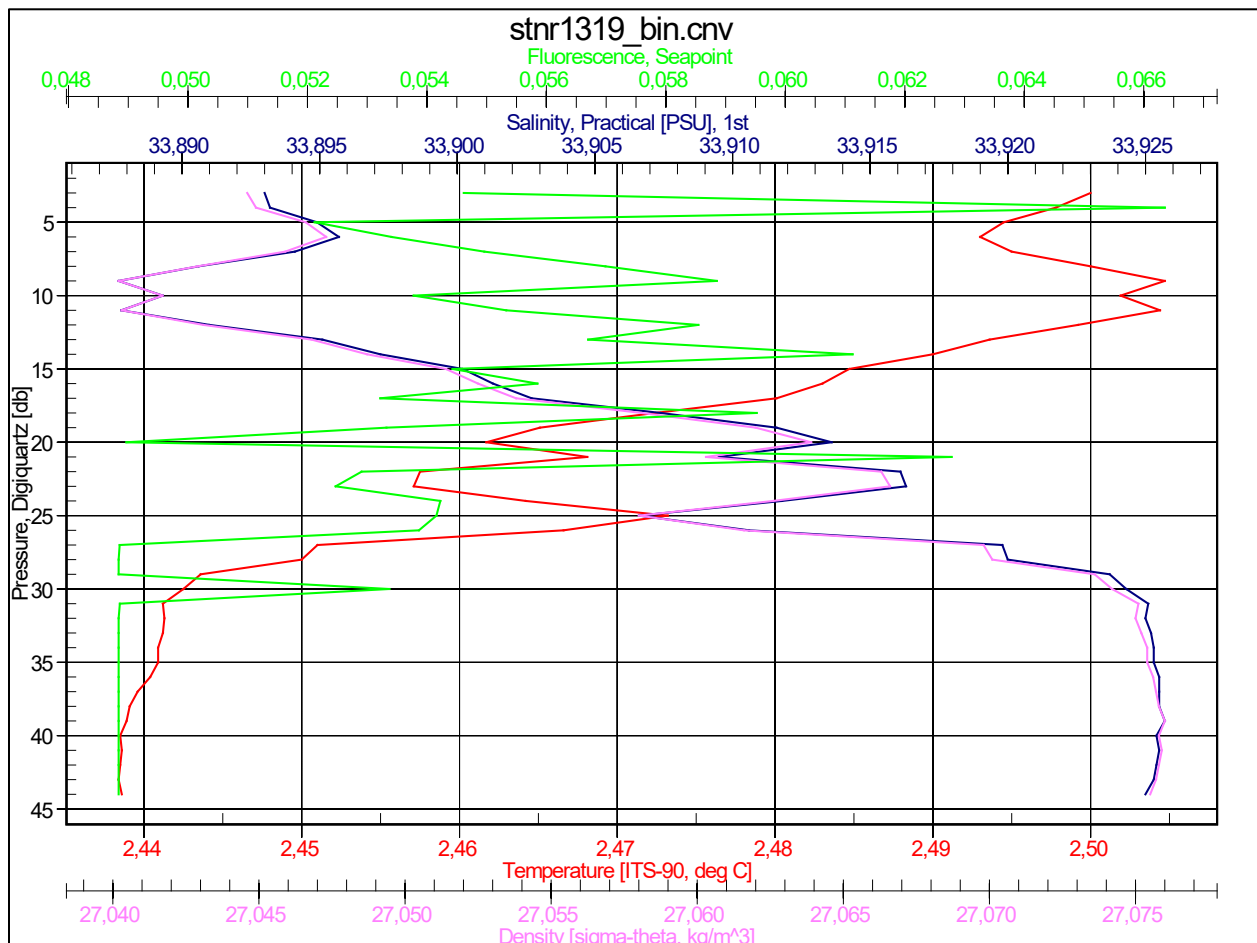
9:34, HH station 1316, plankton net WP2, 64  $\mu$ m mesh size, 110 m depth at 78 51.219198 N, 22 42.333865 E. Bulk fixation of plankton samples for metabarcoding and fixation of selected taxa in 4% PFA for morphological analysis. Low phytoplankton content in the sample, predominately crustaceans (cypris larvae and various copepods) and ctenophores.

10:01, HH station 1317, triangular dredge at 78 51.549856 N, 22 39.875775 E, at 119 m depth. Muddy substrate with *Ctenodiscus crispatus*, *Ophiura* sp., *Hormathia digitata*, Pectinariidae, and six large pycnogonid specimens (*Nymphon* cf. *tenellum*). One pycnogonid was fixed for genome and microRNA sequencing, the remaining five specimens were preserved for taxonomic and neuroanatomical studies. One pycnogonid was also fixed for the MIRevolution project. Accidentally collected in the dredge, an eelpout fish (*Lycodes gracilis*) was examined for parasites – a monogenean flatworm was found on its gills.

11:07, HH station 1318, multi corer at 78 52.363538 N, 22 35.725148 E, at 122 m depth. Good mud for extraction of meiofauna, which was done using the 'bubble and blot' method. Kinorhyncha were fixed for the MIRevolution project (11 specimens in RNALater), morphological examinations (3 specimens in 4% PFA/SW), and genomics (10 specimens). An assemblage of nematodes were fixed for morpho-taxonomic studies.

## Station 6

16:02, HH station 1319, CTD at 79 19.760405 N, 19 37.949692 E and 47,75 m depth (Fig. 11). Water was taken from the CTD rosette's Niskin bottles and filtered to prepare 4% PFA/SW for fixation. Almost no fluorescence, hence no phytoplankton. Therefore, only 64 µm mesh in subsequent plankton tows.



**Figure 11.** CTD output from Station 6 (HH station 1319).

16:08, HH station number 1320, plankton WP2, 64 µm mesh size at 79 19.805455 N, 19 37.988058 E and 40 m depth. Bulk fixation of plankton samples for metabarcoding. Almost no plankton in the net, few crustaceans, ctenophores and tintinnid ciliates.

16:23, HH station number 1321, triangular dredge (Fig. 12), at 79 19.924680 N, 19 37.590741 E and 45 m depth. Shells with stones. Crustaceans, brachiopods, gastropods, ascidians, bivalves and small pycnogonids clinging to arborescent bryozoans. Identified and photographed taxa: *Eucratea loricata*, *Solaster* sp., *Gersemia rubiformis*. *Eucratea loricata* and the bryozoan



*Hemithiris psittacea* were fixed for the MIRevolution project. Eight juvenile and subadult pycnogonids of the genus *Nymphon* (Nymphonidae), seven (sub)adults of the genus *Eurycyde* (Ascorhynchidae), and seven juveniles and subadults of the genus *Pseudopallene* (Callipallenidae) were preserved for taxonomic and neuroanatomical studies. Nematodes were extracted from a large sponge that was collected by the dredge – a yet unidentified species of Leptosomatidae was transported alive and will be used for genome sequencing. Other nematodes were fixed for morpho-taxonomic studies. Meiofauna was extracted using the  $MgCl_2$  method, and many halacarid mites in addition to some harpacticoid copepods and annelids were preserved in 96% ethanol for sequencing and 4% PFA/SW for morphological study.



**Figure 12.** Sorting of shells with stones from the triangular dredge substrate at Station 6.

27.08. 2022

Station 7

8:16, HH station 1322, CDT at 79 58.597201 N, 15 26.372198 E, 183 m depth (Fig. 13). Water was taken from the CTD rosette's Niskin bottles and filtered to prepare 4% PFA/SW for fixation.



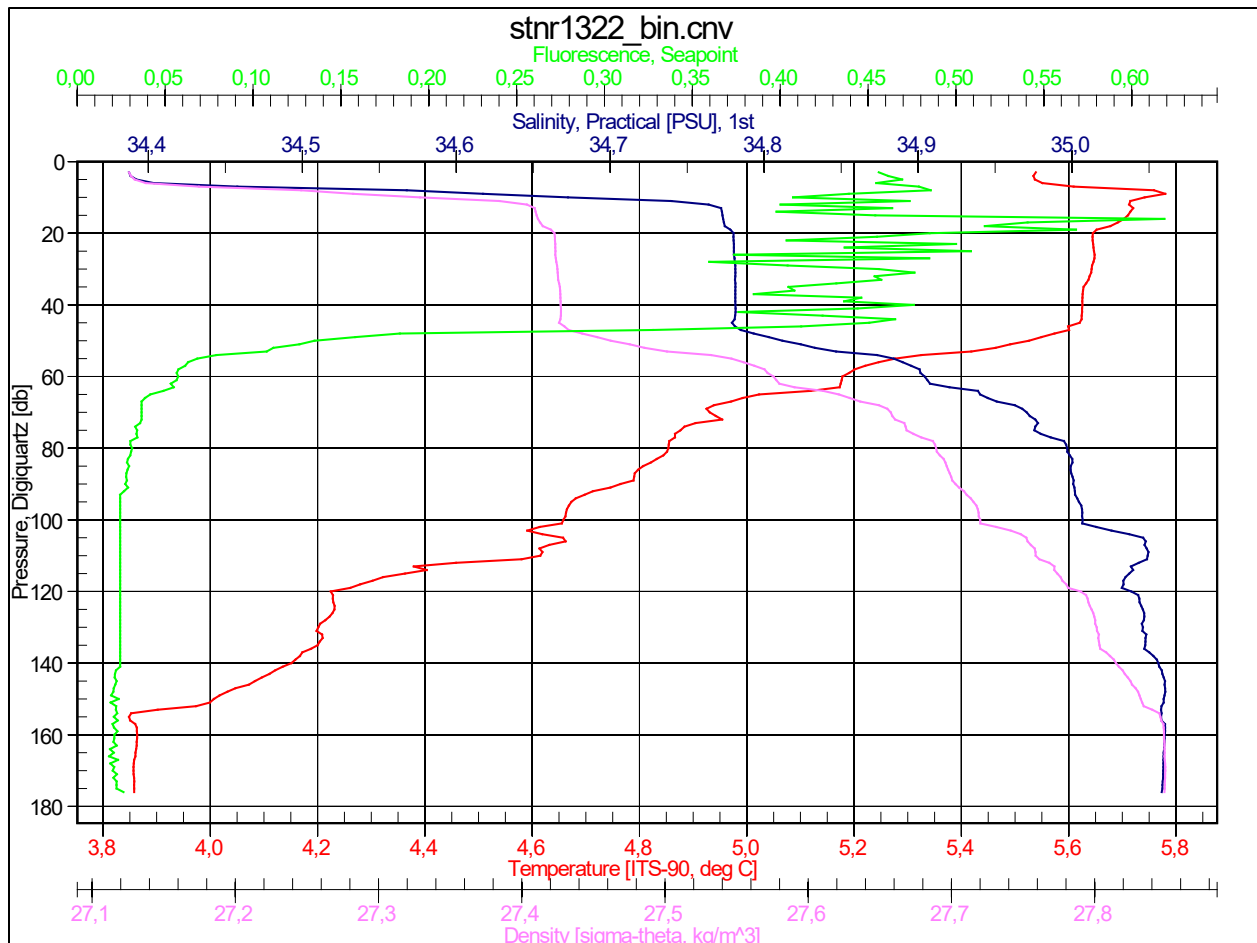


Figure 13. CTD output from Station 7 (HH station 1322).

8:32, HH station 1323, plankton net WP2, mesh size 64  $\mu\text{m}$ , at 79 58.576517 N, 15 26.137312 E, 183 m depth. Very full plankton net. Bulk fixation of plankton samples for metabarcoding.

8:57, HH station 1324, plankton net WP2, mesh size 180  $\mu\text{m}$ , at 79 58.719574 N, 15 25.990968 E, 181 m depth. Again, very full net. Bulk fixation of plankton samples for metabarcoding.

9:46, HH station 1325, bottom trawl (Fig. 14), at 79 59.860558 N, 15 27.879328 E, and 170 m depth. *Anarhichas minor* (spotted wolffish), *Anarhichas lupus* (Atlantic wolffish), *Gadus morhua* (Atlantic cod), *Mallotus villosus* (capelin), *Sebastes viviparus* (Norway redfish), *Leptoclinus maculatus* (Daubed shanny), *Lumpenus lampretæiformis* (Snakeblenny) and *Hippoglossoides platessoides* (American plaice) were examined for parasites. All fish except capelin had parasitic flatworms (Monogenea or Digenea) either on the gills or in the digestive system, usually in both places and more than one species. A total of 17 flatworm species were collected, 16 trematodes and one monogenean. The American plaice and the Atlantic cod, respectively, hosted four and six different species of trematodes each. The most exceptional findings were the rare blood parasites *Aporocotyle simplex* Odhner, 1900, for which molecular data remains unavailable to date despite its evolutionary and taxonomic importance; and two new species *Derogenes* n. sp. 1 from the American plaice and *Derogenes* n. sp. 2 from the cod. A list of parasites includes: *Helicometra plovornini* Issaitchikov, 1928 from *Sebastes viviparus*; *Helicometra insolita* Polyanski, 1955 from *Leptoclinus maculatus*; *Aponurus laguncula* Looss, 1907 from *Lumpenus*



*lampretæformis*; *Stringotrema ovacatum* (Køie, Thulin, 1994) from *Anarchias lupus*; *Brachyenteron pycnorganum* (Rees, 1953) from *Anarchias minor*; *Aporocotyle simplex* Odhner, 1900, *Stringophorus furciger* (Olsson, 1868), *Stenakron vetustum* Stafford, 1904 and *Derogenes* n. sp. 1 from *Hippoglossoides platessoides*; *Hemiurus luehei* Odhner, 1905, *Hemiurus communis* Odhner, 1905, *Hemiurus levinseni* Odhner, 1905, *Lecithaster gibbosus* (Rudolphi, 1802), *Derogenes* n. sp. 2 and unidentified *Derogenidae* from *Gadus morhua*. Abnormally large monocytilid Monogenea were collected on the gills of both species of wolffish. One of the large monogenean specimens will be used for mitochondrial genome sequencing.

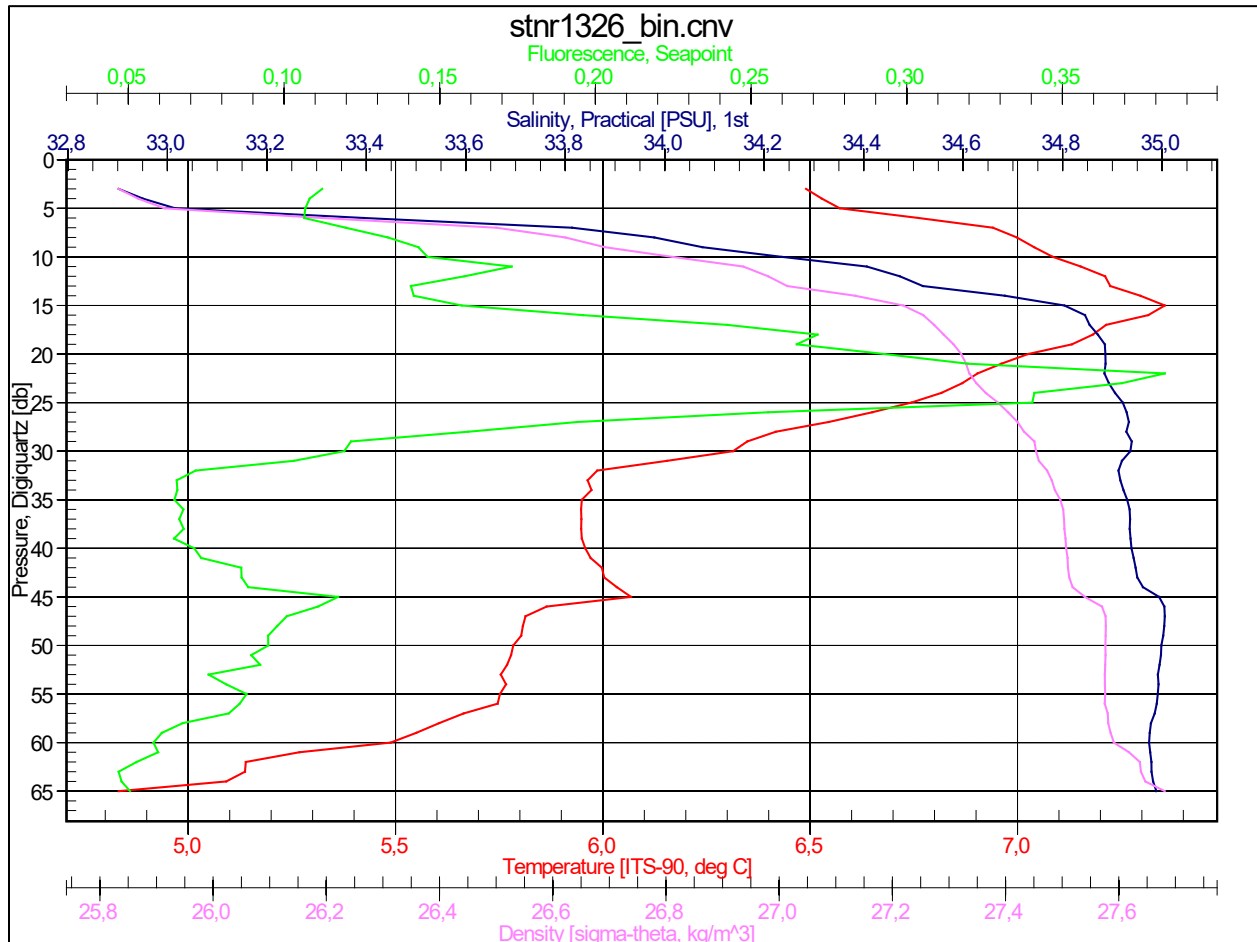


Figure 14. Partial contents of bottom trawl at station 7.



## Station 8

21:34, HH station 1326, CTD at 79 30.512400 N, 10 06.707600 E, 71.6m depth (Fig. 15). Water was taken from the CTD rosette's Niskin bottles and filtered to prepare 4% PFA/SW for fixation.



**Figure 15.** CTD output from Station 8 (HH station 1326).

21:42, HH station 1327, plankton net WP2, 180  $\mu\text{m}$ , at 79 30.536180 N, 10 06.666177 E, 71,45 m depth. Bulk fixation of plankton samples for metabarcoding.

21:52, HH station 1328, plankton net WP2, 64  $\mu\text{m}$ , at 79 30.585851 N, 10 06.380057 E, 72,57 m depth. Bulk fixation of plankton samples for metabarcoding. Many small gastropods (pteropods?), pluteus larvae, copepods, decapod larvae, chaetognaths, annelid larvae, some water fleas (Cladocera), appendicularians, no ctenophores. Chaetognaths were fixed in 4% PFA/SW for taxonomic confirmation, they were also fixed for genome and microRNA sequencing for the MIRevolution project.

28.08.2022

## Station 9

12:16, HH station 1329, CTD at 78 17.920438 N, 14 56.080027 E, 226 m depth (Fig. 16). Water was taken from the CTD rosette's Niskin bottles and filtered to prepare 4% PFA/SW for fixation.

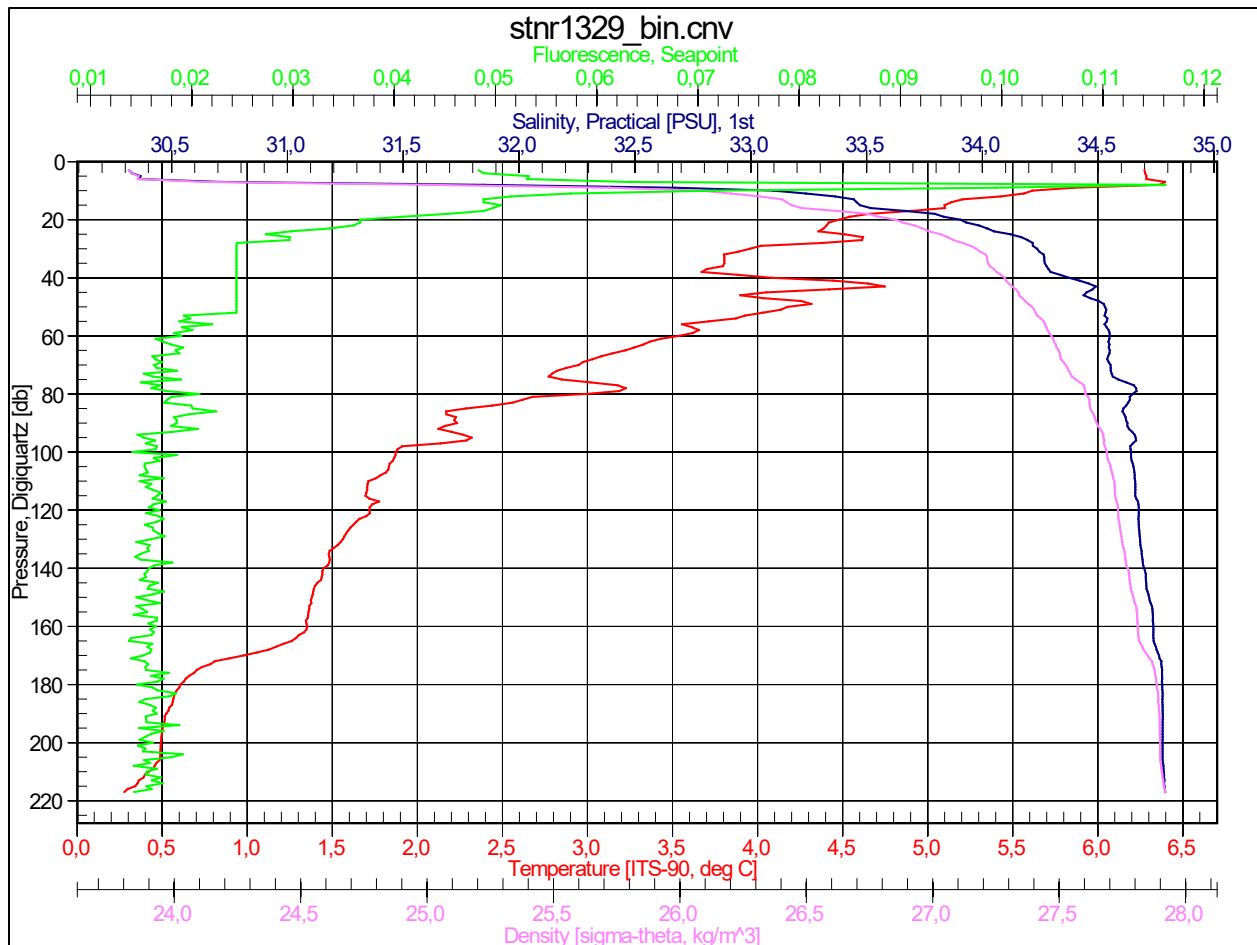


Figure 16. CTD output from Station 9 (HH station 1329).

12:31, HH station 1330, plankton net WP2, 64  $\mu\text{m}$  mesh, at 78 17.910046 N, 14 55.393644 E, 224 m depth. Bulk fixation of plankton samples for metabarcoding.

12:55, HH station 1331, plankton net WP2, 180  $\mu\text{m}$  mesh, at 78 17.871406 N, 1454.341419 E, 220 m depth. Bulk fixation of plankton samples for metabarcoding.

29.08.2022

8:00, arrival in Longyearbyen, disembarkation and organizing shipments of equipment and samples.

## Permits

Relevant permits for the fieldwork were applied for prior to the cruise. These included an application to the governor of Svalbard regarding fieldwork in Svalbard (RiS-1D12021A1) and an application to the Norwegian Directorate of Fisheries for permission to trawl (21/16250). Both activities were granted permission within the boundaries of the law.



## Outreach

Several cruise participants engaged in outreach activities during and after the cruise. For instance, O. Holovachov shared images and findings on [Twitter](#) and C. S. Hansen documented the scientific activities of the cruise in photographs and video for use in teaching and outreach at UMAK.

## Miscellanea

CTDs and plankton nets were always lowered until 10 m above echo-sounder-depth (SIMRAD EK60). Several seabirds and marine mammals were sighted during the cruise, including northern fulmars, black-legged kittiwakes, glaucous gulls, one ivory gull, great skuas, Arctic skuas, Arctic terns, Atlantic puffins, Brünnich's guillemots, scattered little auks, minke and fin whales, white-beaked dolphins and walrus.

Cabin list		Daily schedule	
Andreas A	505	Breakfast	07:30 – 08:00
Anju Angelina	214	Cake	10:00
Joel	213	Lunch	13:30 – 14:00
Hans Georg	216	Cake	17:00
Andreas W	211	Group meeting	19:00
Oleksandr	323	Dinner	19:30 – 20:30
Elisabeth	212	Meeting with captain	20:00 and as needed
Christel	215		

## Acknowledgements

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## Appendices

Appendix 1. Cruise log.

