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Ambassador Story

Beyond the Bite: Mapping Arctic Mosquito Viromes with a Mobile Sequencing Lab

MOSQUITO team in Nuuk.

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Project MOSQUITO, Off-grid sequencing of mosquito viromes in Greenland

Research objectives

The overarching goal of this project is to **map mosquito and virus communities in Kobbefjord and other Arctic sites,** model the distribution of mosquito species and associated viruses under current climatic conditions, predict future changes in these distributions under climate change scenarios, and screen the viromes of Greenlandic mosquitoes. By mapping mosquito and virus communities in Arctic regions, the project provides essential baseline data on species composition and ecological interactions in polar ecosystems, where information remains sparse. Modeling current distributions in relation to climate helps clarify how environmental factors structure these communities, offering insights into Arctic ecosystem functioning. Predicting future changes under climate scenarios is particularly critical, as warming may shift species ranges, alter phenology, and foster novel host–virus interactions, potentially reshaping ecosystem dynamics. Finally, virome screening of Greenlandic mosquitoes will expand knowledge of microbial diversity in polar habitats, revealing cryptic biodiversity with ecological and evolutionary significance. The specific aim of this field campaign was to **optimize mosquito sampling and sequencing protocols** to ensure reliable data generation for subsequent mapping, modeling, and virome analyses. This included testing and refining methods for mosquito trapping, preservation, sample processing, and offline sequencing under Arctic field conditions.

Arrival to Nuuk and Kobbefjord

The project was scheduled to take place on July 7-14th, 2025. We, the project participants, were all from **University of Helsinki Department of Virology;** Dr Teemu Smura, expert in Next Generation Sequencing (NGS) and phylogeny, Dr Lorna Culverwell, expert on the field sampling of the mosquitoes and Dr Hanna Vauhkonen, expert in optimising the mobile laboratory procedures for NGS. All laboratory protocols were tested and optimised carefully before leaving to Greenland. We travelled to Nuuk via Reyakjavik. Unfortunately the flight to Nuuk was cancelled due to harsh weather conditions, resulting in loss of one field day and rescheduling of the project. Work, both field and laboratory-related, was conducted primarily at Kobbefjord Research Station. As the laboratory facilities were nonexistent, all necessary laboratory equipment, including pipettes, gloves and plasticware, had to be brought from Helsinki. The mobile laboratory included a **Bento Lab** benchtop labaratory, an Oxford Nanopore Technologies MinION Mk1D sequencer, a Qubit fluorometer for DNA concentration measurements, and a laptop for operating the MinION, all of which fitted in a cabin-size backpack.

Upon arrival in Nuuk, we spent one day preparing for the fieldwork in Kobbefjord, including shopping for grocery and collecting the first specimens. We also met with a local collaborator and reviewed his ongoing mosquito experiments, providing opportunities to discuss experimental design and share expertise.

Arriving to Nuuk one day behind schedule.


MOSQUITO team in Nuuk. From left Lorna (mosquito expert), Hanna (labrat), Teemu (bioinformatic wizard) and Viktor, the local collaborator.

Transportation between Nuuk and Kobbefjord was operated by a boat two or three times per week. As the duration of our stay in Kobbefjord was dominated by boat schedules, we ended up in spending four nights in Kobbefjord, form Thursday 10th to Monday 14th of July. As the research station was not in the reach of internet, both the software for sequencing and bioinformatic analysis had to be operatable offline. Luckily, we were pre-informed; Oxford Nanopore Technologies kindly provided an offline version of the software used in the MinION sequencing and base calls. Also the bioinformatic software and databases used in viral sequence detection were modified for offline use.

The University of Greenland in Nuuk.

Leaving the University for Kobbefjord Research Station. Note the plastic bagsfull of food supplies. Because the Kobbefjord buildings were not located near the boat mooring site, a rucksack would have been more practical for transporting labware and other necessitied than a suitcase.

The electricity of the research station was mainly provided by solar panels. However, to meet the energy requirements of the laboratory equipment on rainy days, a gasoline-fueled generator had to be operated. During two nights the power was lost resulting in premature termination of the sequencing run. In addition, only refrigerator-temperature storage was available in Kobbefjord, rendering us with uncertainty of the functionality of library production enzymes, as during the longer-than-expected stopover in Reykjavik our enzyme transport cooler was thawed into room temperature.

Boat arriving to Kobbefjord. Looking forward to spend time without internet or telephone.

Kobbefjord Reasearch station. Dormitory building on the left, main building (including lab room & kitchen space) and service building on the right, with e.g. power generator.

View from the dormitory building.

Collecting the sample specimens for NGS sequencing

As the mosquito season had not fully started, **the project scope was expanded to include both larval and adult samples.** Since one field day was lost due to flight cancellation, the immature stages were collected at a location near Nuuk (Kuanninnguit) on the day before the transportation to Kobbefjord. Scoops and nets were used in collecting larvae and pupae in puddles. At Kobbefjord Research Station, adult mosquitoes were sampled using Prokopack aspirators, however, as the mosquito season was delayed, more blackflies than mosquitoes were caught. Logistical challenges arose due to the absence of ethyl acetate and the lack of freezer facilities at Kobbefjord, complicating the processing of adult specimens.

Sampling site near Nuuk. As one field day was lost, a day-trip was madeto find mosquito premature stages for sequencing in Kobbefjord. The mosquito expert catching the researchspecimens in the puddles with a scoop and net.

One of the sampling sites in Kobbefjord. Collecting adult mosquitoes with a vacuum-operated Prokopack aspirator.

During identification, we observed considerable morphological variation within larvae of *Ochlerotatus nigripes*, underlining the importance of rearing them to adults for accurate species identification. The second native mosquito species, *Ochlerotatus impiger*, was only observed in adult form due to differing developmental conditions.

Sorting out mosquitoes from hundreds of blackflies.

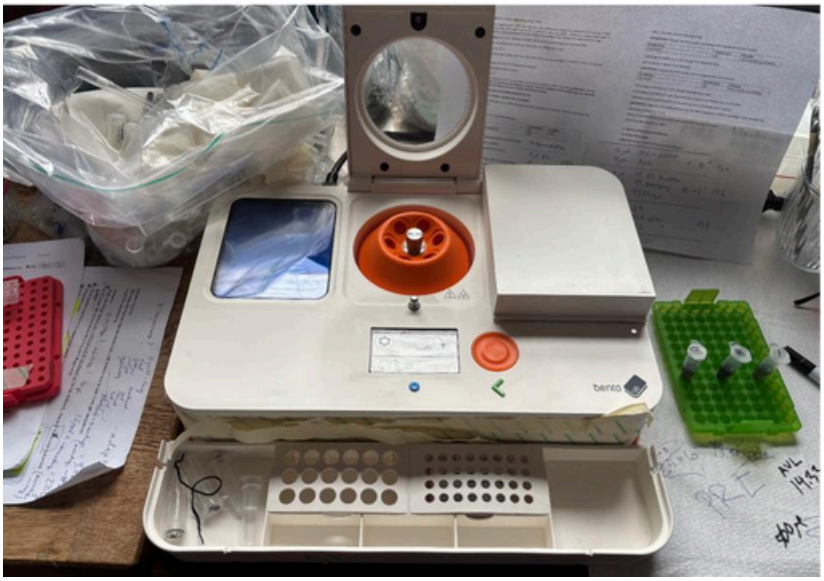
Kobbefjord. Species identification under the microscope.

Laboratory work; sample processing and sequencing

After species identification, the specimens were pooled in ten individuals in each. Species confirmation was done by our Mosquito Expert, aiming to have only one species in pool. Three pools at a time were processed for viral RNA extraction and library preparation for NGS. Viral RNA was extracted using Qiagen columns and libraries were produced using Template Switch (New England Biolabs) and Oxford Nanopore Rapid Barcode library kit. Sample handling and library preparation took approximately 9 hours. Altogether five successful sequencing runs were carried out on MinION Mk1D using R10.4.1 flow cells and MinKNOW software with FAST basecall.

Three pools were included in each run, lasting 9-14 hours. Three runs contained premature stages and two runs adult mosquitoes, both *Ochlerotetus nigripes* and *O. impiger*. Despite the overnight room temperature stopover in Reykjavik, the enzymes used for library preparations worked at least decently. The MinION flow cells were washed after run using Nanopore flow cell wash kit, transported back to Helsinki, and re-used for shorter runs later.

Pooling specimens for viral RNA extraction.



The portable benchtop Bento Lab with centrifuge and programmable PCR.

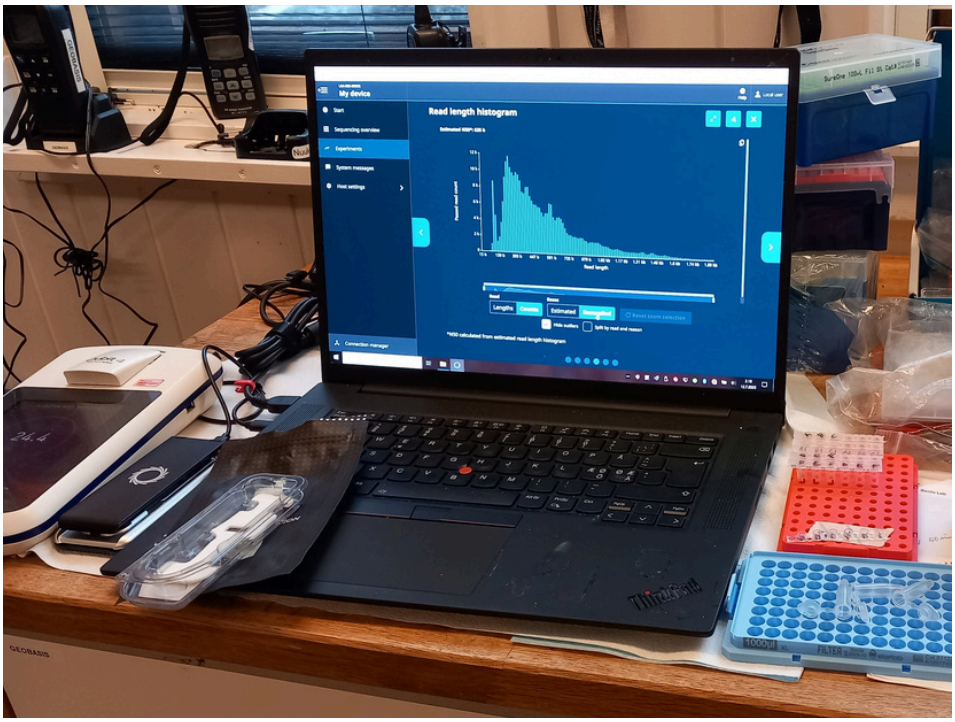
Data management.

Everything works! Proud “lab rat” operating the mobile sequencing lab.

Mosquito viromes obtained by bioinformatic analysis

The diversity of mosquito viruses was assessed by mapping sequence reads against both the GenBank virus database and an in-house database, which was developed based on preliminary virome sequencing results from mosquitoes across Greenland. **Over 50 virus taxa were detected, including several divergent species and genera. Larvae and adults of the same mosquito species shared a significant proportion of virus taxa, suggesting vertical and/or environmental transmission of these (most likely insect-specific) viruses.**

However, a clear difference was observed between the virus communities found in *Ochlerotatus nigripes* and *O. impiger*, indicating host-dependent viral diversification. As a technical note, the number of virus taxa detected using the in-house database was significantly higher than those identified using publicly available databases. This is due to the presence of highly divergent viruses in Greenland. **These findings highlight that while bioinformatic analysis and annotation are feasible in field conditions, the number of taxa detected is highly dependent on prior knowledge of the local viral communities.**



The portable sequencer producing the first reads!

The bioinformatic wizard searching viruses with the offline in-house database.

The study of mosquito viromes in Greenland directly contributes to understanding polar ecosystems and biodiversity by revealing a previously underexplored component of Arctic ecological networks: the diversity of viruses associated with insects. **Over 50 virus taxa, including highly divergent and potentially endemic species, were detected, demonstrating that viral biodiversity in polar regions is both rich and largely undocumented.** The observation that larvae and adults of the same mosquito species share many virus taxa suggests the presence of vertical or environmental transmission pathways, highlighting the role of mosquitoes as integral vectors within local ecosystems. Additionally, the host-dependent differences in virus communities between *O. nigripes* and *O. impiger* indicate that even within a simple polar mosquito fauna, ecological interactions and host specificity drive viral diversification. Finally, the findings underscore the importance of building local reference databases to capture the unique biodiversity of polar regions. This demonstrates that Arctic ecosystems contain distinct viral communities, which are an essential yet often overlooked dimension of biodiversity. Understanding these interactions enhances our knowledge of ecosystem functioning, species relationships, and the potential impacts of environmental change in polar habitats.

Off-work activities in Kobberfjord

Kobbefjord resides in the end of the fjord and popular for day-trips. There are no other buildings outside the Research Station. The location is reachable by a 30-minute boat travel from Nuuk, approximately 25 kilometers in distance. During the weekend we saw many boats anchoring nearby, most probably enjoying fishing. As a hiking route starting from Nuuk goes near the Research Station, also hikers travelling on foot were observed. Despite the hours spent in lab we had a bunch of opportunities to enjoy the arctic nature and magnificient views nearby. The water of the fjord was unbelievably clear (and cold to swim in) and the tidal changes revealed seaweed, edible mussels and barnacles. Next time we have to remember to include garlic and other ingredients in the grocery list to enjoy moules marinière for dinner.

Morning coffee with a view over the fjord.

Enjoying the beauty of arctic nature and flora. *Rhodiola rosea.*

Arctic bog with *Rhododendron groenlandicum*.

Fish fiesta. Fresh cod straight from the fjord.

Plans for the next steps

The limited diversity of host species in Arctic regions offers a unique opportunity to study how microbial community composition influences the spread of viruses, either human-pathogenic or not. In Greenland, only two mosquito vector species — *Ochlerotatus nigripes* and *O. impiger* — and one known arthropod-borne human pathogen — Jamestown Canyon virus — have been identified. These relatively "simple" interaction networks provide a valuable framework for investigating the role of environmental factors, such as climate change, in shaping virus–virus interactions over time and across geographic space. To fully leverage the unique ecological setting of Greenland for virus ecology research, capacity building for local sequencing and bioinformatics infrastructure would be essential. Establishing field-based sequencing labs, training local personnel, and developing region-specific viral databases would significantly enhance the ability to monitor emerging viruses, understand transmission dynamics, and assess the impact of environmental changes such as climate warming. These efforts would also support real-time surveillance and rapid response to potential public health threats in remote Arctic communities.

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