NERO

NUUK ECOLOGICAL RESEARCH OPERATIONS

7th Annual Report 2013

GEM

Greenland Ecosystem Monitoring

Aarhus University
DCE – Danish Centre for Environment and Energy

- Quantifying the influences of biogeochemical processes on carbon dynamics in Godthåbsfjord.
- Paleoclimate and sediment biogeochemistry.
- Otoliths and mussel shells as recorders of potential future pollution on a section from Nuuk to the proposed Isua iron-mine.
- Seasonality of marine mammals and background noise level in Godthåbsfjord.
- Quantifying grazing impact of krill and copepods in the Godthåbsfjord system.

Marine Chemistry Group

- Greenhouse gases (CO_2-CH_4-N_2O) dynamics within fjord sea ice.
- Underwater eddy correlation measurements of ice-ocean heat and mass exchange.
- Evolution and distribution of pH in natural first-year sea ice.
- Assessment of sea ice algae production in Kanajorusuit Fjord.
- Mercury transport and transformation across the sea ice environment.
- Circulation and exchange processes at the entrance to Godthåbsfjord.

Atmosphere Group

- Interactions between atmospheric processes and marine emissions of carbon.

Land and Freshwater Group

- Influence of environmental gradients on Arctic plant communities.
- Impact of shrub expansion and climate, and climate gradients on arthropod assemblages.
- Ecosystem patterns and processes at retreating glaciers.
- Snow cover in the Godthåbsfjord area 2007-2013.
- Fingerprints in lake sediments from retreating and expanding glaciers in a changing climate.
- Limnic ecosystem patterns and processes near retreating glaciers.
- Glacial activity and its consequences to terrestrial and limnic systems in Kobbefjord.
- Evolution potential. Arctic char and three-spined stickleback in Greenland.
- Carbon cycling in glacier forelands and the microbial terrestrial-atmospheric coupling.
- A millennium of changing environment in Godthåbsfjord.
- Permafrost – preserving the cultural heritage of Greenland in a changing climate.

For more information on the ASP partners, field campaigns and other activities please visit the website: http://asp-net.org/

6.2 Soil microarthropods collected in Kobbefjord and Zackenberg

Paul Henning Krogh, Peter Gjelstrup, Helena Wirta, Tomas Roslin, Zdenek Gavor, Elin Jørgensen, Niels Martin Schmidt, Henning Petersen, Katrine Raundrup, Josephine Nymand and Peter Aastrup

During the last few years, we have invested specific effort in generating a library of DNA barcodes *sensu* Hebert et al. (2003) for the microarthropod fauna of both BioBasis Nuuk and Zackenberg locations. Our prime objectives include generating a species identification tool for the benefit of all ecologists, creating the means for molecularly-based diet analysis and for quantifications of food web structure, and establishing the identity of microarthropod taxa encountered on both sides of Greenland.

Microarthropods collected during the barcoding campaign in 2012 were prepared according to the guidelines of BOLD (www.boldsystems.org) and submitted for sequencing in 2013 and 2014. Each specimen was photographed and subsequently placed in a well containing about 50 µl of 96% ethanol in a 96 well microplate. DNA extraction, amplification and sequencing were carried out by the Canadian Centre for DNA Barcoding (CCDB) following their standard procedures (CCDB, 2014). For both mites and collembolans, the primer set C_LepFolF/C_LepFolR was used for amplification. Collection details for each specimen together with its taxonomic assignment and its photograph are provided at the BOLD website. No physical vouchering was carried out for the sequenced specimen, but the species are in most cases available at Department of Bioscience, AU. When using the BOLD facility the Barcode Index Numbers (BIN) assigned to similar barcodes, guides the

Table 6.1 Collembola submitted for barcoding at CCDB by March 2014. Numbers in brackets indicates the number of individuals compiled from specific habitats within the Kobbefjord monitoring area (Krogh et al. 2013) or from the Zackenberg sampling location, ZA.

Order	Species	Habitats
Entomobryomorpha	*Desoria olivacea*	Kaer (5)
	Desoria tshernovi	ZA (5)
	Folsomia bisetosa	ZA (5)
	Folsomia cf. near penicula	MArt2 (5)
	Folsomia quadrioculata	Sitka Østerild DK (2)[1], Urteli (5), ZA (5)
	Folsomia sexoculata	ZA (5)
	Isotomiella minor	MArt2 (5)
	Lepidocyrtus violaceus	Urteli (5)
	Parisotoma ekmani	ZA (5)
	Parisotoma notabilis	Urteli (5)
	Tetracanthella Arctica	MArt2 (5)
Neelipleona	*Megalothorax minimus*[2]	ZA (5)
Poduromorpha	*Ceratophysella denticulata*	ZA (5)
	Friesea quinquespinosa	ZA (5)
	Hypogastrura concolor	ZA (5)
	Neanura muscorum	MArt2 (5)
	Oligaphorura groenlandica	Kaer (5), ZA (5)
	Willemia anophthalma	MArt2 (5)
	Willemia scandinavica	ZA (2)
Symphypleona	*Sminthurides schoetti*	ZA (5)
	Sminthurinus aureus	ZA (5)

[1]Two specimen from a Danish spruce forest included for reference
[2]Formerly considered a symphypleonid

Table 6.2 Acari species submitted for barcoding to CCDB by March 2014. Numbers in brackets indicate the number of individuals compiled from specific habitats within the Kobbefjord monitoring area (Krogh et al. 2013) or from the Zackenberg sampling location, ZA.

Order	Species	Habitats
Oribatida	*Ceratoppia bipilis*	ZA (4)
	Brachychthonius sp.	MArt5 (4)
	Camisia lapponica	Kaer (2), MArt3 (3), ZA (2)
	Ceratoppia sp.	ZA (1)
	Ceratozetes sp.	Snow (3)
	Ceratozetes thienemanni	MArt3 (4)
	Diapterobates sp. nov.	ZA (4)
	Dissorhina ornata	Snow (4)
	Eupelops sp.	Kaer (1), Snow (2)
	Heminothrus longisetosus	MArt2 (3), MArt3 (1), Snow (1)
	Hermannia sp.	MArt2 (3)
	Hydrozetes sp.	Kaer (1)
	Liebstadia sp.	Kaer (1)
	Liochthonius alpestris	ZA (3)
	Liochthonius muscorum	Kaer (4)
	Melanozetes cf. meridianus nov. sp	Kaer (5), Snow (3)
	Microppia minus	MArt5 (4)
	Mucronothrus nasalis	Kaer (5)
	Mycobates tridactylus	MArt7 (5), ZA (4)
	Neonothrus sp. nov.	Kaer (5)
	Neonothrus sp. nov.	Kaer (5), ZA (5)
	Nothrus cf. borussicus	MArt3 (2)
	Opiella sp.	Kaer (2)
	Oppiella clavigera spp. nov.	ZA (4)
	Oribatula tibialis	MArt3 (3), ZA (3)
	Oromurcia bicuspidata	Snow (4)
	Plathynothrus thori	Kaer (4)
	Platynothrus capillatus	Urteli (5)
	Tectocepheus alatus	MArt5 (4)
	Tectocepheus tenuis	ZA (4)
Prostigmata	*Bdella* sp. 2	MArt3 (2)
	Bryobia sp.	ZA (2)
	Callidosom (cf.)	ZA (5)
	Erythraeus sp.	ZA (4)
	Erythraeus sp. larva	ZA (5)
	Eupodes sp.	ZA (2)
	Neomolgus sp.	ZA (2)
	Penthaleus sp.	ZA (2)
	Penthaleus sp. 2	ZA (2)
	Rhagidia sp.	MArt3 (2), ZA (1)
	Trombidium sp.	Kaer (1), Krat (3), MArt3 (1), ZA (4)
	Trombidium sp. z	ZA (3)

species identification and could possibly discover errors and synonymy of the barcoded specimen (Ratnasingham and Hebert, 2013).

At the time of writing this report, sixteen of 22 collembolan species collected in 2012 (table 6.1) had been barcoded. All species seem to form well-defined and identifiable clades, with no cases of barcode-sharing among taxa (figure 6.2). Some taxa were characterised by surprisingly high levels of intraspecific variation, with sequence differences more than 5% within *Oligaphorura groenlandica* from Zackenberg, hence cryptic species diversity is suspected (figure 6.2); (Kimura 2-parameter distance). In *Folsomia quadrioculata*, individuals differed by as much as 19% (figure 6.3), which is still within the range of up to 20% (mean 14%) found for this species in BOLD[1]. Whether or not the species then corresponds to a single lineage or a larger species complex is then a topic worth further investigation. The genetically most variable species was *Megalothorax minimus* with up to 27% intraspecific

[1] www.boldsystems.org

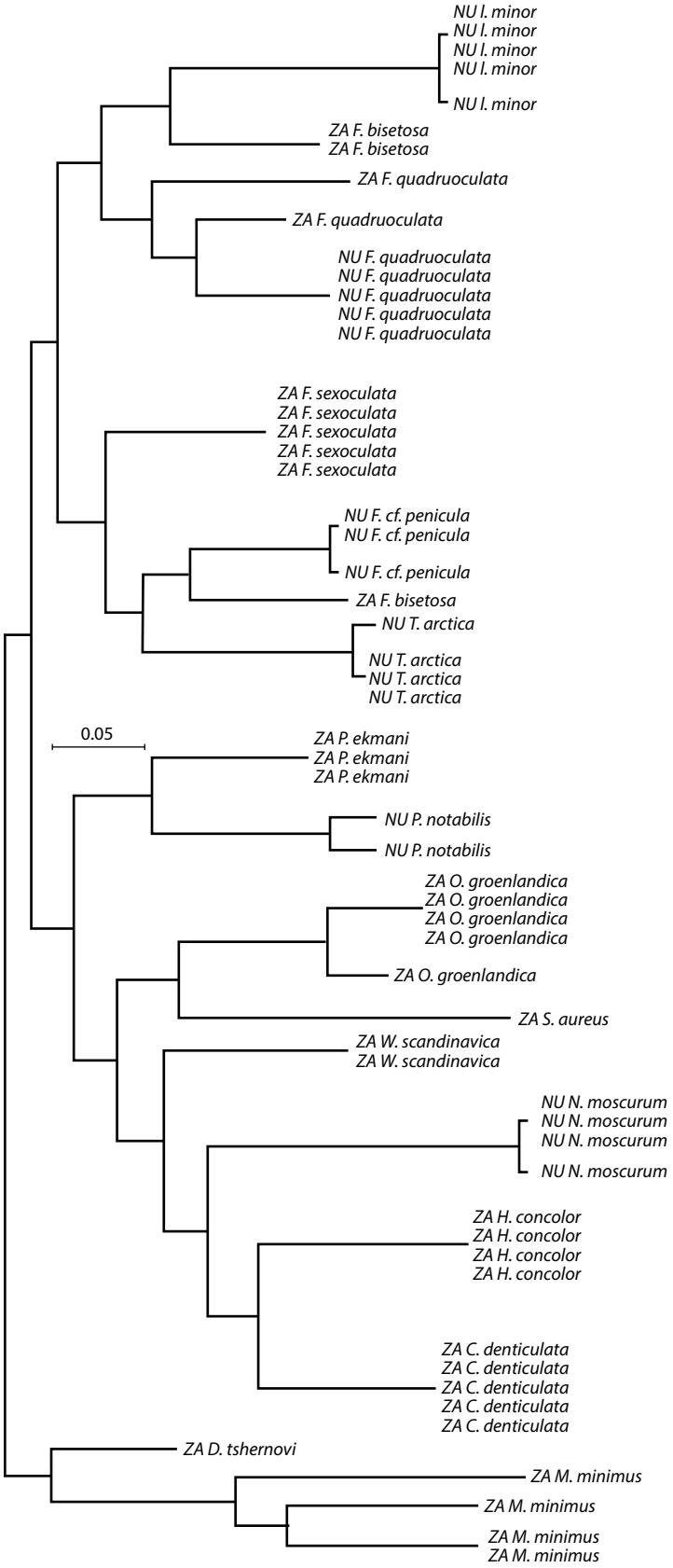

Figure 6.2 A cladogram showing the relationship among 58 COI sequences from 16 species of Collembola. The topology of the tree was reconstructed by MEGA version 6 (Tamura et al. 2013) as based on the K2P model (Kimura 1980). All nucleotide positions containing gaps and missing data were eliminated, resulting in a data set of 558 bp. Individual sequences derive from a total of 16 collembolan species identified by morphological criteria, with species designations shown at the end of each branch. ZA: Zackenberg; NU: Nuuk, Kobbefjord.

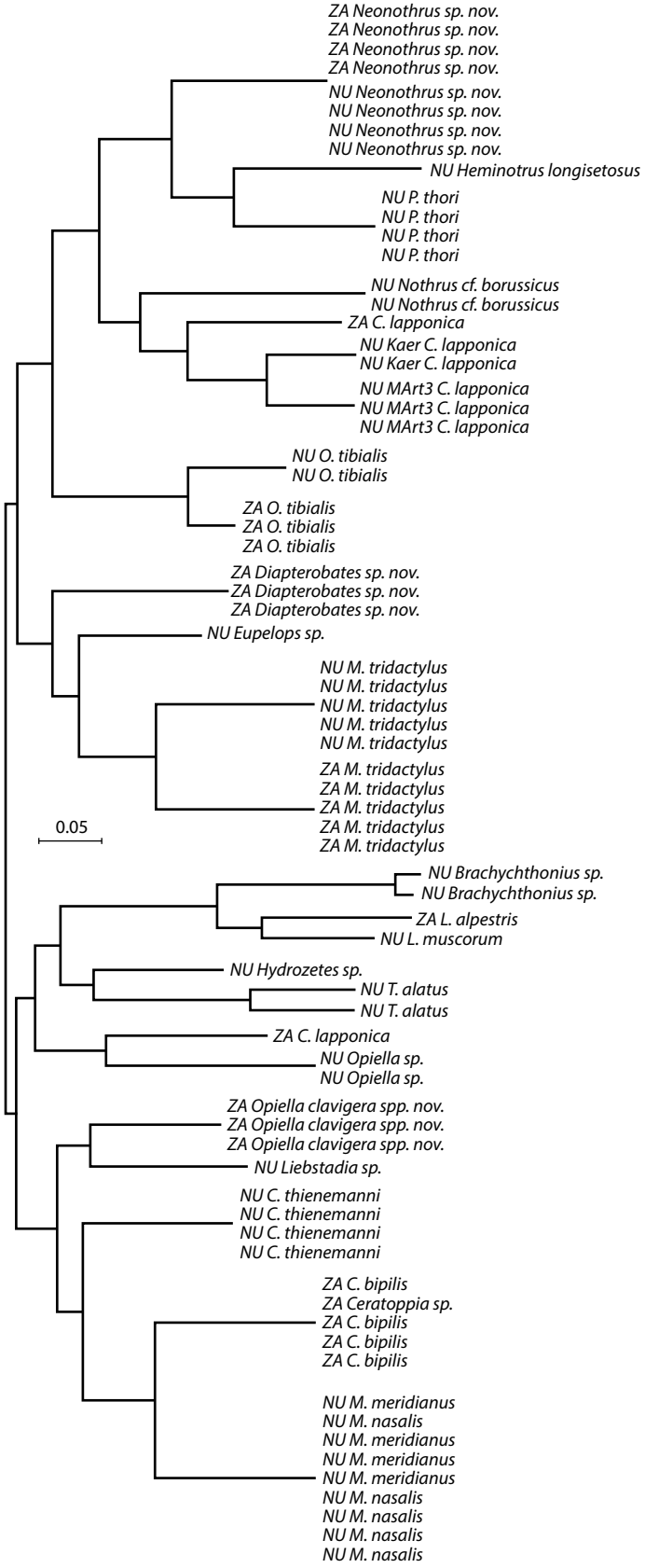

Figure 6.3 A cladogram showing the relationship among 73 COI sequences from oribatid mites. The topology of the tree was reconstructed by MEGA version 6 (Tamura et al. 2013) as based on the K2P model (Kimura 1980). All nucleotide positions containing gaps and missing data were eliminated, resulting in a data set of 606 bp. Individual sequences derive from a total of 23 mite species identified by morphological criteria, with species designations shown at the end of each branch. ZA: Zackenberg; NU: Nuuk, Kobbefjord.

variability, supporting the conclusion of Schneider et al. (2011) that this taxon is a species complex containing many species yet to be discovered. Nonetheless, as *M. minimus* is likely parthenogenetic, the variability observed may also reflect intraspecific differences between clones. Most of the collembolan species were still characterised by remarkably low levels of intraspecific variability (figure 6.2). Hence, beyond the variability mentioned above, haplotypes within species were either identical or differed by a few bp only (figure 6.2). This pattern brings confidence to our ecological investigation of these collembolan species at the Kobbefjord monitoring site, proving that morphologically-identified taxa are indeed valid species. On a more systematic note, it should be stressed that the tree shown in figure 6.2 is not providing any more generally valid phylogenetic hypothesis of Collembola, as e.g. species like the sminthurid *Sminthurinus aureus* (a symphypleonid) are here grouped together with the genetically distant poduromorph onychiurids.

Patterns observed within mites were more complex. Of the 41 mite species found in Kobbefjord and Zackenberg (table 6.2), 73 individuals have now been barcoded (figure 6.3). Here, a number of challenges were revealed by the sequencing exercise, as related partly to the morphologically-based identification of oribatids and partly to the barcoding itself. A few cases of barcode-sharing emerged, of which one was related to *Mucronothrus nasalis* – a species belonging to the primitive oribatid superfamily, Crotonoidea, of moss mites. This taxon is, from a systematic point of view, rather distant from the higher oribatids, but yet it shared its barcode with *Melanozetes meridianus* (figure 6.3) – and was grouped by BOLD into a single molecular taxonomic unit (MOTU) together with *Ghilarovizetes longisetosus* collected in Manitoba (Young et al. 2012) (BIN: BOLD:AAF907). For two other species, *Camisia lapponica* and *Mycobates tridactylus*, haplotypes encountered within the Kobbefjord area and Zackenberg proved distinctly different (figure 6.3), and only added material will show whether the taxa encountered in Western and Northeastern Greenland are indeed identical or not.

6.3 Comparing Late Holocene climate changes in low and high Arctic regions using lake sediments and annual rings of dwarf tundra shrubs records

Daniel Nývlt, Jiří Lehejček and Petra Polická

Due to lack of long instrumental climatic records and their spatial scarcity (Weijers et al. 2010) as well as missing written sources from the Arctic, paleoclimatological studies are important evidence of climatic variations in Polar Regions (AICA 2005). Our study aims to reconstruct past climate development prior instrumental measurements. We used two main approaches combining high-resolution record of responses for recent climate (dendroclimatology of dwarf tundra shrubs and record from lake sediments). In addition, soil characteristics and vegetation cover were recorded in order to display the current state of ecosystem to understand past changes better.

Multi-proxy record from lake sediments is combining litological (mainly grain-size composition), petrophysical (magnetic susceptibility), geochemical (determination of basic lithophile elements, organic and anorganic carbon and sulphur, possibly also stable isotopes), and biological proxy (pigments, biostratigraphy of different groups of organisms) approaches. Petrophysical and geochemical analysis were finalized recently. Remaining analysis is being processed at the moment. This will show climatic and environmental variability. For determination of the time development of sedimentation appropriate dating methods will be applied (AMS radiocarbon dating, OSL, ^{210}Pb and ^{137}Cs for the youngest parts of sediments accumulated in last centuries; see Nehyba et al. 2011).

Dendroclimatology of dwarf tundra shrubs (*Juniperus communis, Salix glauca, Alnus crispa*) will give up to three century long climatic record. The age of the oldest shrub (*Juniperus communis*) spans to 17th century. Using microtome knife and staining solutions the micropreparates were prepared (Gärtner and Schweingruber 2013) to obtain reliable information from this archive on the cell level. Subsequently, the digital photos were taken under microscope with 100x magnification (figure 6.4) and growth parameters (width of rings,