

## ARCDYN: Exposing the long-term dynamics of Arctic ecosystems From samples to sequences



Tomas Roslin<sup>1,2</sup>, Tea Huotari<sup>1</sup>, Yinqiu Ji<sup>3</sup>, Niels Martin Schmidt<sup>4</sup>, Otso Ovaskainen<sup>1</sup> & Douglas W. Yu<sup>3,5</sup>

1) University of Helsinki, Finland; 2) Swedish University of Agricultural Sciences, Sweden; 3) Kunming Institute of Zoology, China; 4) Aarhus University, Denmark; 5) University of East Anglia, UK



Our work has revealed an Arctic teeming with life, where species are bound closely together by live interactions. Wirta et al. 2015. Ecology and Evolution 5: 3842–3856 The Biobasis programme at Zackenberg, Northeast Greenland, has collected a unique record of community response to Arctic warming: for two decades, full arthropod assemblages have been sampled with standardised yellow pitfall traps.

During the last seven years, we have used a variety of methods to document all macroscopic, terrestrial species present in the area.



Our work has yielded a library of all species present, and molecular tools to identify them. Wirta et al. 2016. Molecular Ecology Resources 16: 809–822.



Most transports in and out of Zackenberg occur by Twin Otter planes, with a single ship arriving per summer.





We combine molecular tools for identifying species with the massive collection accumulated over two decades.



15-20

Lars Holst Hans

The samples are transported to Aarhus for storage at the museum.

The samples contain almost 1 Million arthropods, so new molecular tools are a prerequisite for ever identifying them. These tools will also allow new ways of continuing the time series.



To extract DNA from the samples, arthropods are first dried, then soaked in lysis buffer.

DNA is purified before sequencing by using a purification kit. After the DNA extration, arthropods are returned to the collection.

The samples are sequenced on the Illumina HiSeq 2500 platform, and the sequences generated are compared with our reference library.

Overall, our work yields a record of which species have been active during which week in which year. The data document changes in Artic community composition over 20 years, including changes in species composition and in species-level phenology. By relating the changes observed to interannual variation in abiotic variables, we explore the drivers of current change. By relating the structure of the interaction network and the functional role of different taxa, we ask whether functionally important species are also sensitive to climate change. Our prime interest is in how communities and associated ecosystem functions change with progressing Arctic change.