

# DNA barcoding of Arctic Chironomidae (Diptera)

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## Background

Chironomids are among the most abundant and species-rich insects in the Arctic, and species-specific habitat requirements for many species make them suitable for monitoring of Arctic environmental change. Since they are difficult to identify to species level based on morphology, this insect family is usually not utilized to its full potential in biodiversity assessments. DNA barcoding works well for identification of Chironomidae. Thus, a well-sampled barcode reference library for Arctic chironomids is a good start for common understanding of the taxonomy of this group, and a necessary step to use chironomids to monitor Arctic biodiversity change.



## Goals

This study provides a meta-data analysis of the currently available barcode data of Arctic Chironomidae in BOLD. Our goal is to compare coverage and quality of recorded diversity and investigate eventual biogeographic patterns.

## Methods

258 500 public Chironomidae COI sequences (> 500bp) from Canada, Alaska, Greenland, Iceland, and Norway were downloaded using the BOLD API. In addition, 10 900 sequences from our own projects in Arctic regions were added to the dataset. The dataset was filtered to include only records north of the southern tundra border, resulting in 65 000 georeferenced DNA barcodes.

## Results

The DNA barcodes formed 1520 BINs, yet only 572 species were named (Linnaean or interim names). Comparison of accumulation curves identifies huge differences in sampling effort (Fig. 1) as well as strategy: The data from Norway has been specifically selected to represent as many morphospecies as possible and not more than a few specimens per species have been sampled.

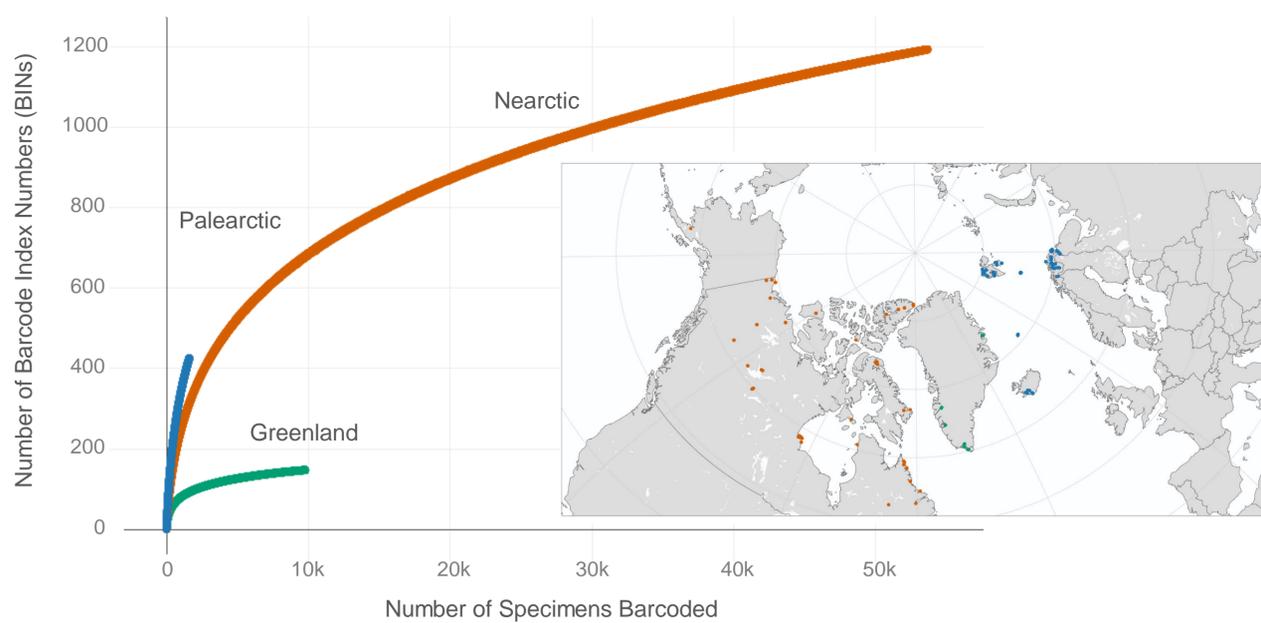


Figure 1. Sampling effort and accumulation curves of Chironomidae for the Palearctic, Nearctic, and Greenland (diversity is quantified with BINs).

Including all Canadian and all Norwegian chironomid records in BOLD increases the number of named species to 848 and the number of BINs to 4666 (Fig. 2).

Comparison of the unique and shared BINs between regions shows a large number of unique BINs for Canada. The numbers increase substantially when all Canadian and Norwegian records are included. The numbers of shared BINs between regions is fairly low.

Comparison of unique and shared named species show a Palearctic dominance, and a greater percentage of shared diversity between regions. The Palearctic dominance increases when all Canadian and Norwegian records are included.

The observed differences are likely caused by:

1. Different sampling efforts and strategies between regions.
2. Higher species-level identifications rates in barcoded material from Norway and Greenland.
3. A mismatch between the BIN boundaries and morphological species definitions.

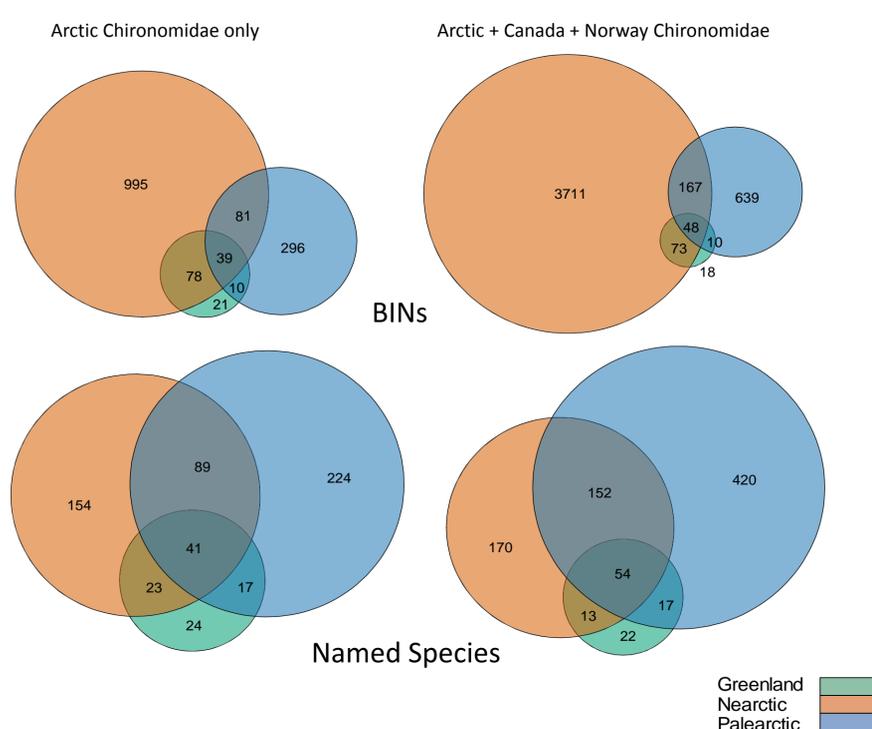


Figure 2. Distribution of Chironomidae taxa defined by BINs (top diagrams), or as named species (bottom diagram). Circle sizes are proportional to numbers.

## Acknowledgements

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