

# DNA barcode libraries

## A treasure chest for alpha taxonomy

### Integrative taxonomy and systematics of *Allodia* Winnertz (Diptera, Mycetophilidae)

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#### Fungus gnats

- Family Mycetophilidae
- The larvae feed on fungal mycelium
- Exceptionally high diversity in northern boreal forests
- Many trans-Palaeartic and circumpolar species distributions

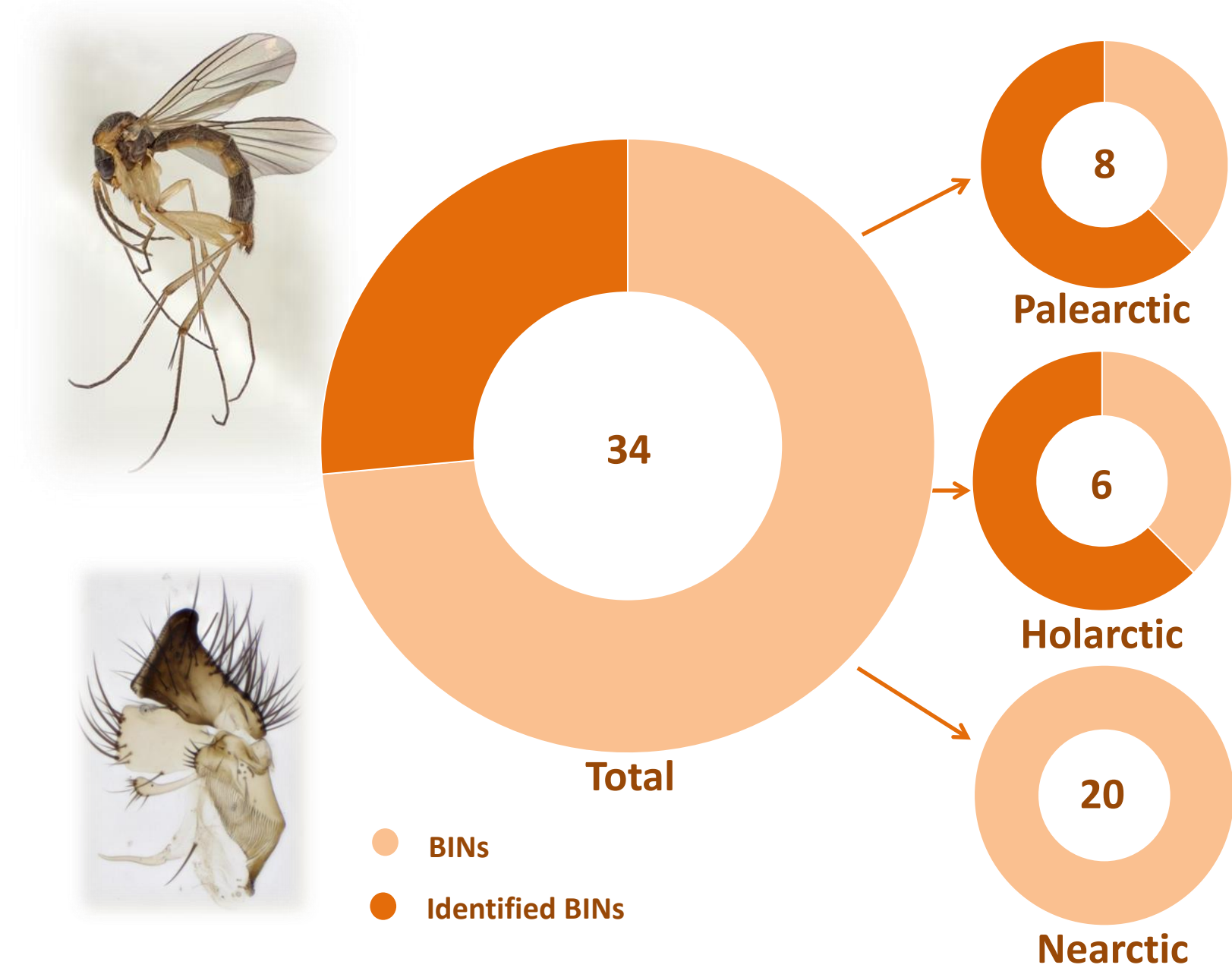
#### Background

- The taxonomic expertise of the Mycetophilidae has long traditions in Northern Europe
- The accumulated knowledge has been used to build up a reference library of DNA barcodes through The Norwegian Barcode of Life (NorBOL) initiative
- The Nearctic fauna is less known
- To explore relationships between the Palearctic and Nearctic fauna in more detail, we study the genus *Allodia*

#### Objective

The main objective is to investigate the species and species boundaries within *Allodia* s. str.

We will perform a review of the subgenus *Allodia* s. str. based on material from different parts of Europe and North America and comparing with type specimens and original descriptions.



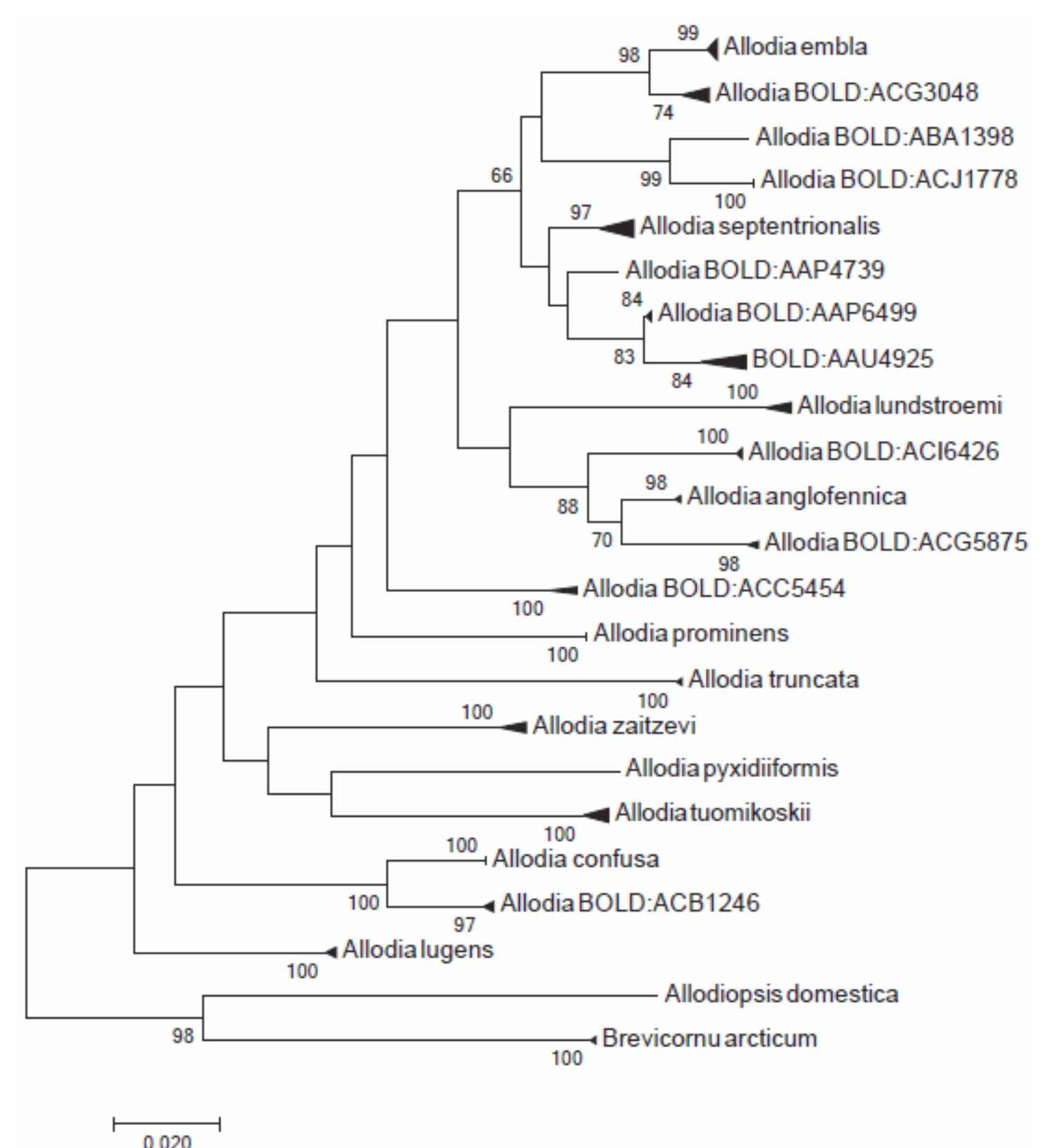
Overview of BINs of *Allodia* s. str.: Charts showing the number of operational taxonomic units in BOLD (Ratnasingham and Hebert 2007), based on the Barcode Index Number (BIN) system.

#### Approach

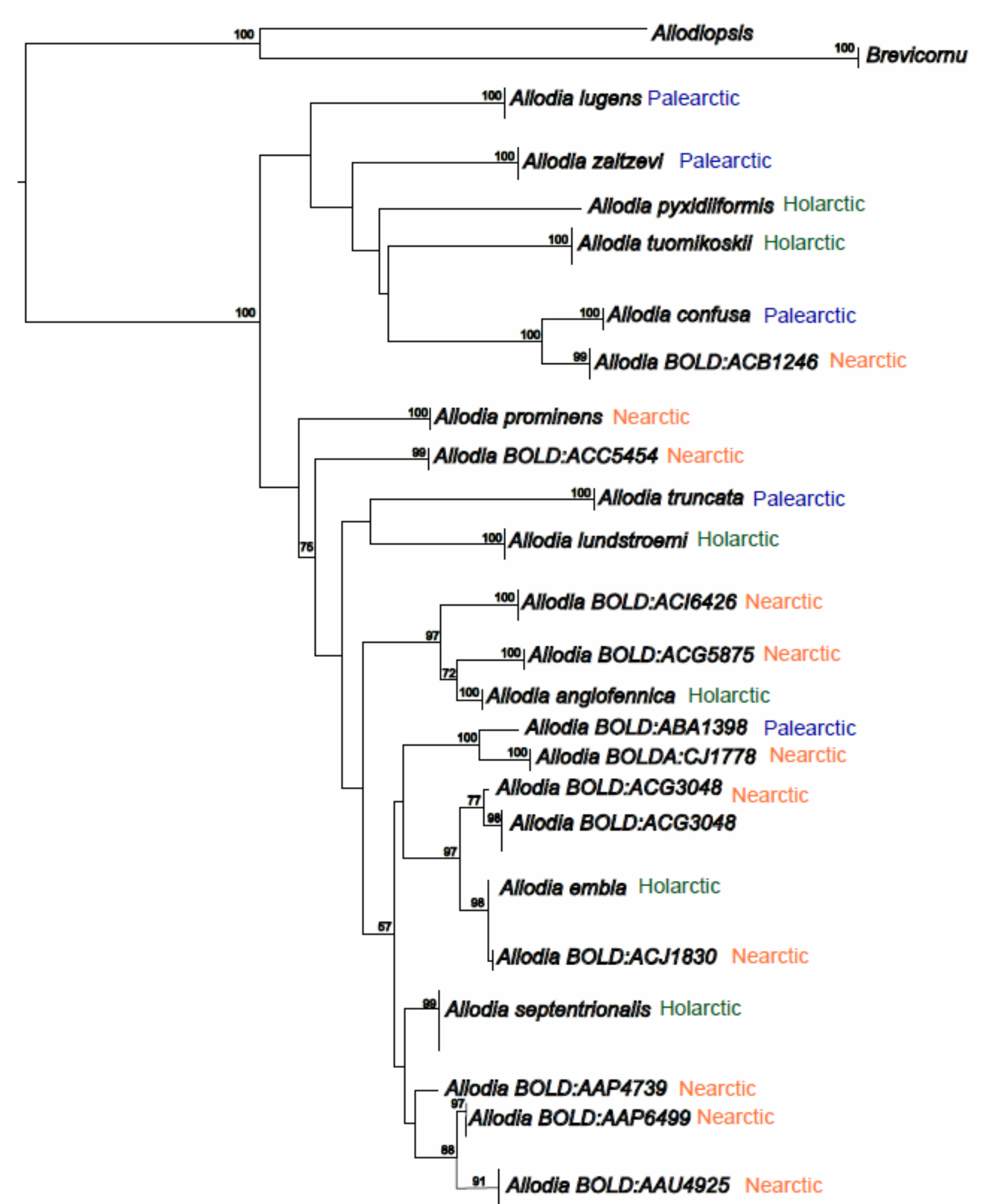
- Operational taxonomic units produced by the BIN system (Ratnasingham and Hebert 2013)
- The validity of species will be considered using an integrative approach, using data from cytochrome oxidase subunit 1 (CO1), the internal transcribed spacer 2 (ITS2) and morphology
- Material:
  - Centre for Biodiversity Genomics, University of Guelph
  - The Natural History Museum in Oslo
  - Tromsø Museum

#### Results

- The results presented here are based on the first preliminary data on morphology, CO1 sequences and ITS2 sequences



**COI gene tree:** Using Maximum likelihood. Analyses were conducted in MEGA version 7 (Kumar, Stecher and Tamura 2015). Based on 61 CO1 sequences, representing 21 *Allodia* species and 2 outgroup species. Bootstrap support shown next to nodes.



**CO1 and ITS2 tree:** Maximum likelihood analysis computed by RAxML. Based on 61 CO1 sequences and 61 ITS2 sequences, concatenated. Bootstrap support above 50 shown above branches.

#### References

Kumar, S, Stecher G, and Tamura K (2015) MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. *Molecular Biology and Evolution*.

Ratnasingham, S. & Hebert, P. D. N. (2007). BOLD: The Barcode of Life Datasystem (<http://www.barcodinglife.org>). *Molecular Ecology Notes* 7: 355-364.

Ratnasingham, S. & Hebert, P. D. N. (2013). A DNA-Based Registry for All Animal Species: The Barcode Index Number (BIN) System. *PLoS ONE* 8(7):1-16.

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