

Alexander Kizyakov



# Characterisation of East Siberian Paleodiversity based on ancient DNA analyses of the Batagay megaslump exposure

[Jeremy Courtin](#)<sup>1</sup>, Amedea Perfumo<sup>1</sup>, Kathleen Stoof-Leichsenring<sup>1</sup> & Ulrike Herzs Schuh<sup>1,2,3</sup>

<sup>1</sup>Alfred-Wegener-Institute Helmholtz-Center for Polar and Marine Research, Polar Terrestrial Environmental Systems, Potsdam, Germany

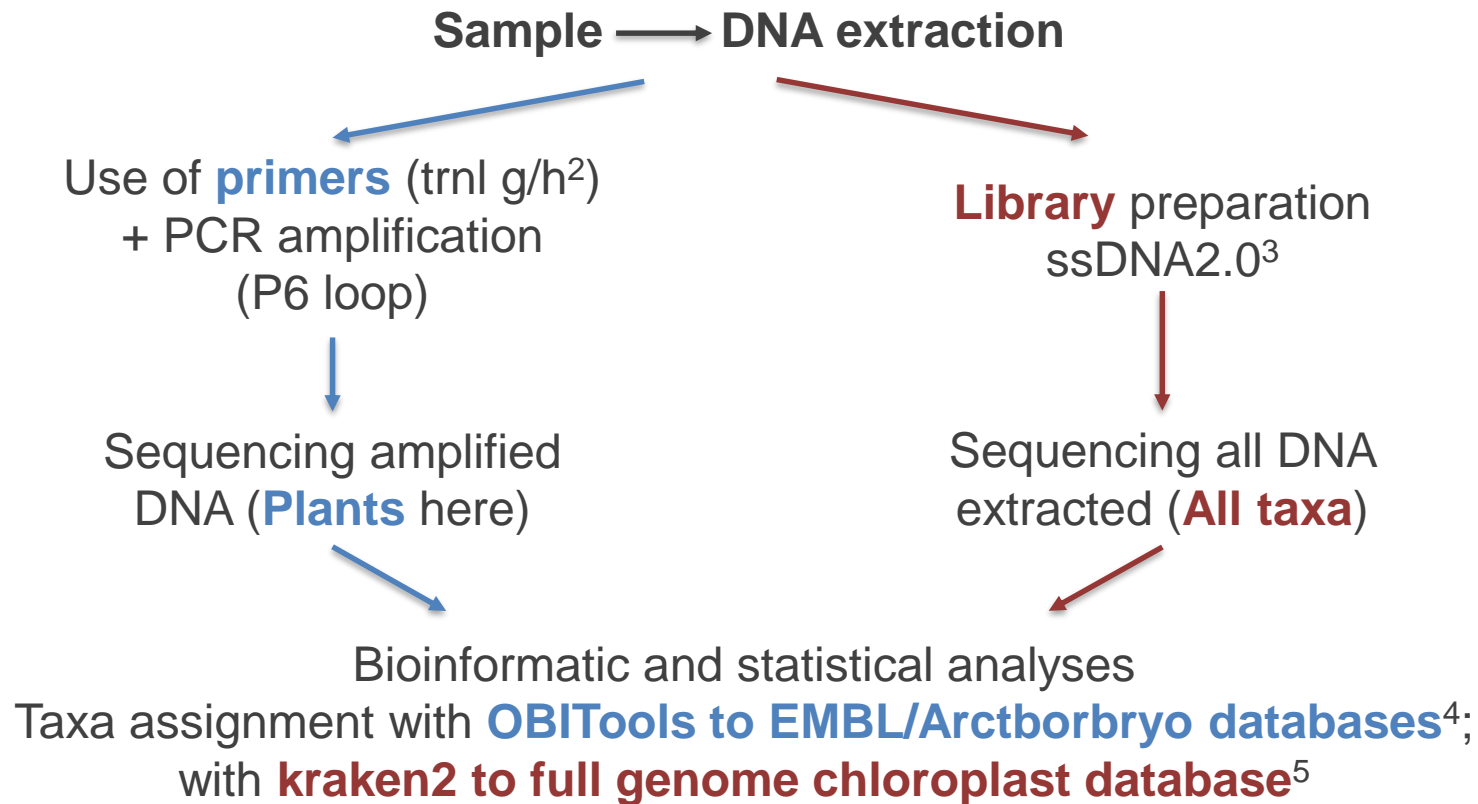
<sup>2</sup>Institute of Biology and Biochemistry, University of Potsdam, Potsdam-Golm, Germany

<sup>3</sup>Institute of Earth and Environmental Science, University of Potsdam, Potsdam-Golm, Germany

# Paleodiversity studied from DNA?

**Metabarcoding sequencing:** established method

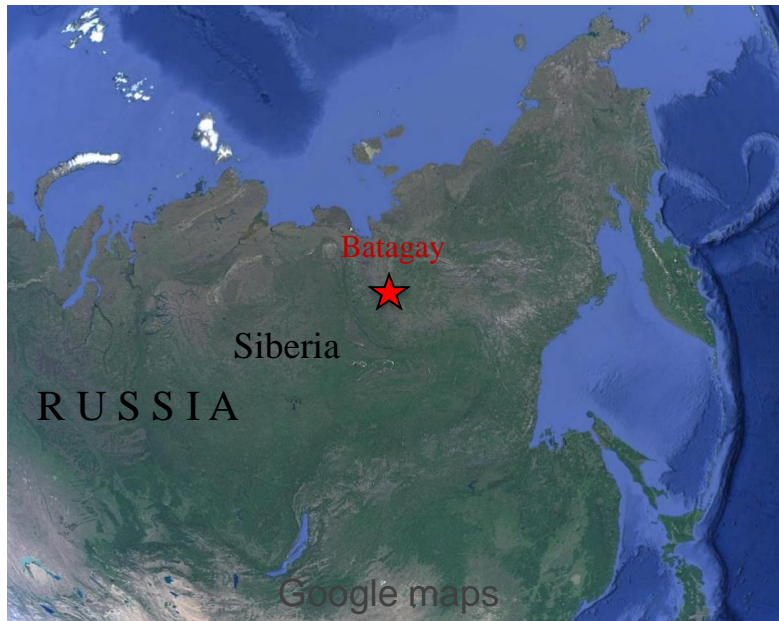
**Shotgun sequencing:** new method (few studies from environmental ancient DNA<sup>1</sup>)



**Can shotgun sequencing be used as a new robust proxy to investigate paleodiversity?**



# The study site: Batagay megaslump



- **World largest known thaw slump:**  
840m wide and ~55m deep in 2016<sup>6</sup>
- Exposes Holocene and Pleisocene permafrost formations **from MIS16 to MIS 1**<sup>7</sup>

Expedition in 2017, **5 samples for preliminary DNA investigation:**

Depth (m)	2.15	2.3	25.8	47.6	49.5
MIS	2	2	4	7-6	16

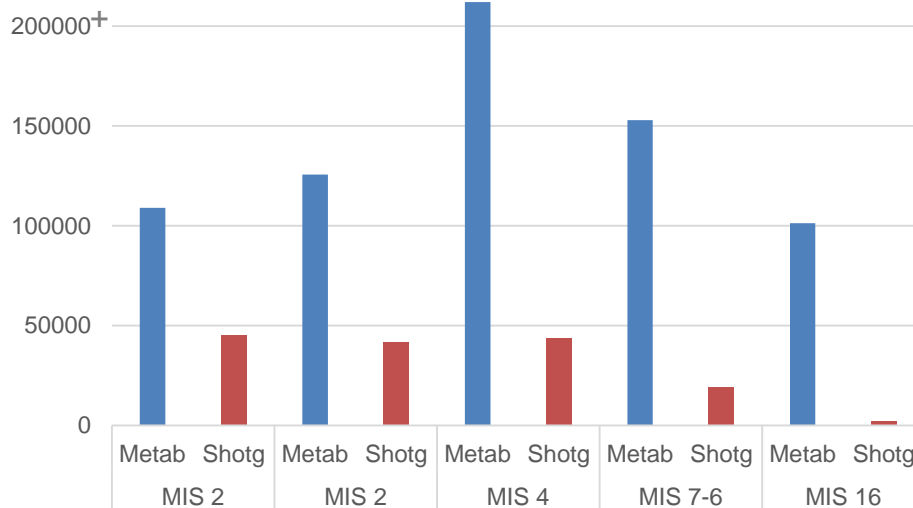
More samples recovered on a second expedition in 2019



# Past vegetation direct comparison

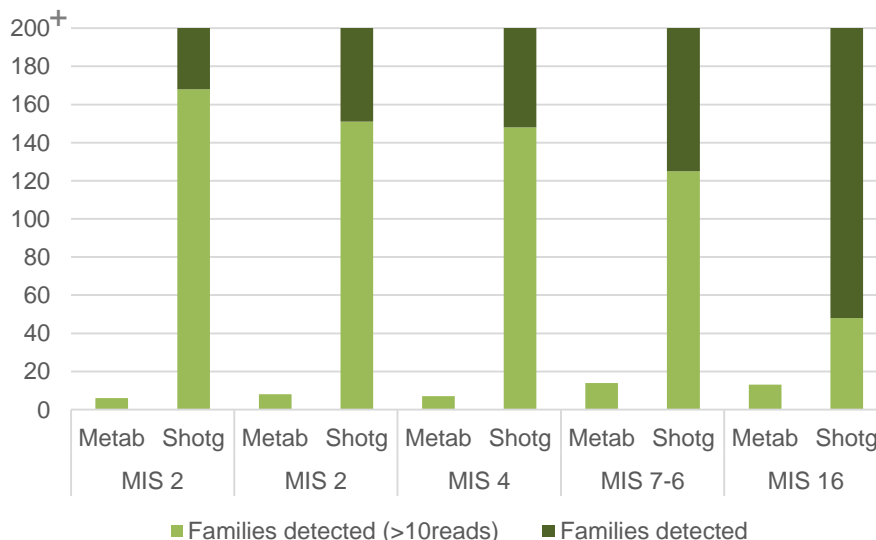


Reads assigned to plant taxa



- **Metabarcoding**: more reads assigned to plants and reads counts more consistent
- **Shotgun**: decrease in reads count with age and huge drop for MIS 16

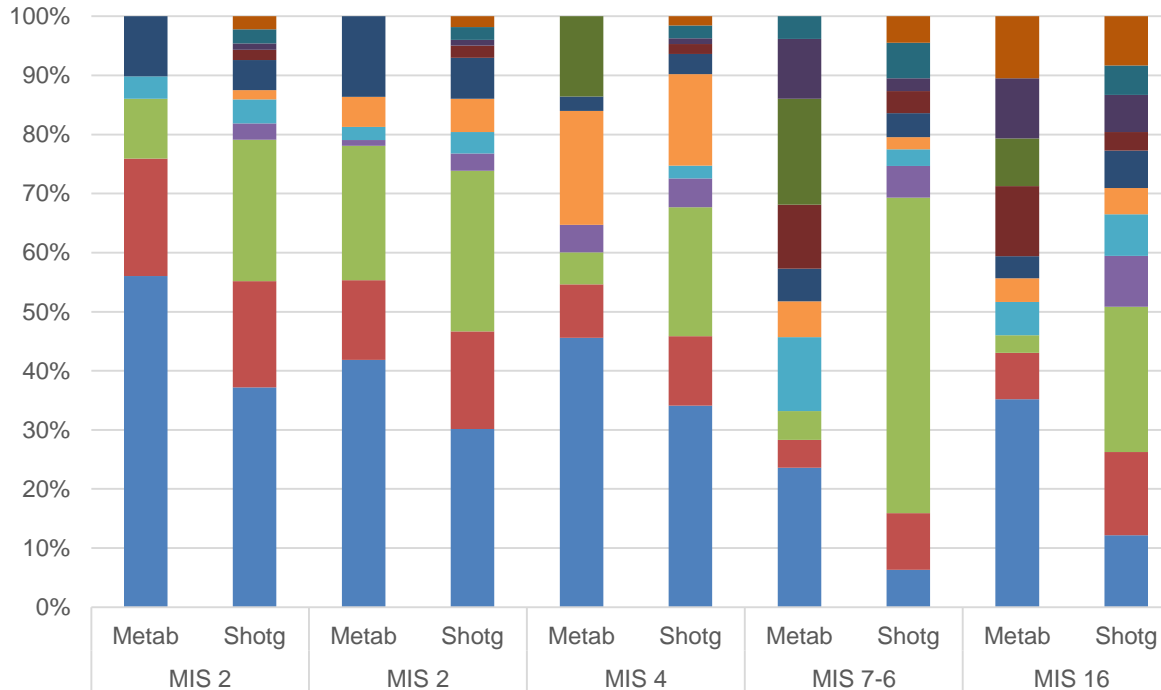
Number of plant families detected



- More families detected with shotgun in all samples
- In the shotgun: many plant taxa detected by **less than 10 reads**

**Shotgun detect more plant taxa with less reads**

# Past vegetation direct comparison

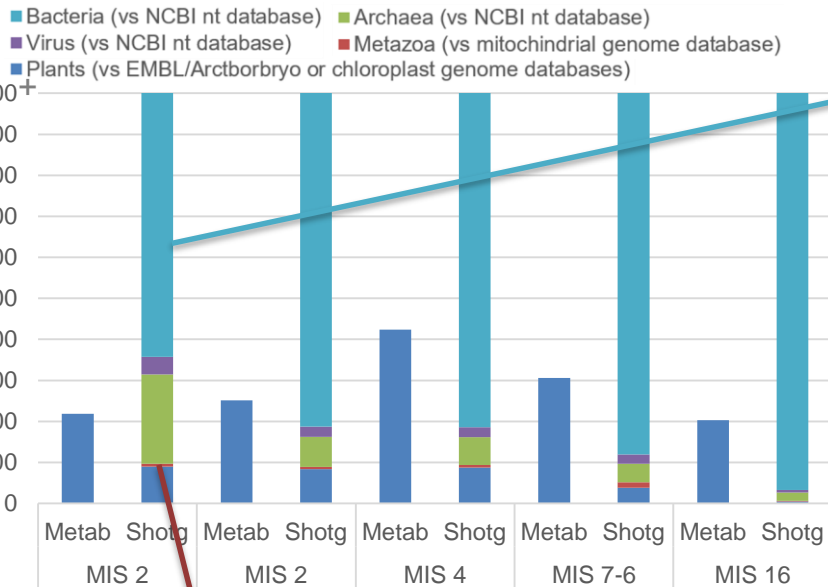


Comparison between samples of relative proportion for the 12 most represented plant families present in both methods

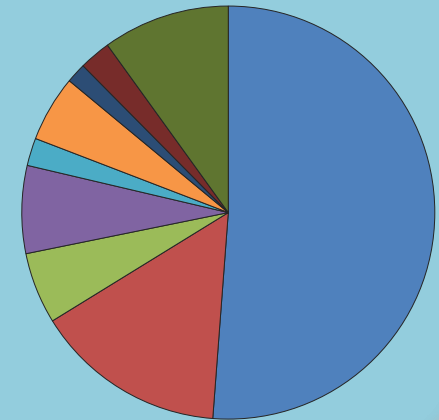
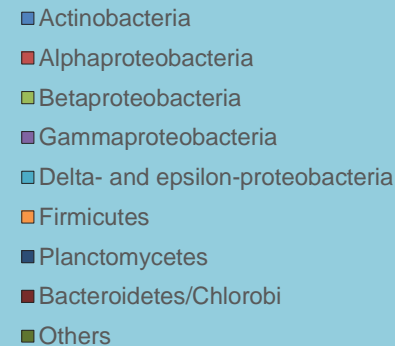
- **Similar signal** between methods: **same overrepresented families** (e.g. Asteraceae or Poaceae) and **similar trends** between samples
- **Some differences** though: e.g. Fabaceae, always more represented with shotgun and some signal only present in metabarcoding (e.g. Pinaceae)

**Shotgun signal is as relevant as metabarcoding one: similar ecological conclusions can be drawn with both methods**

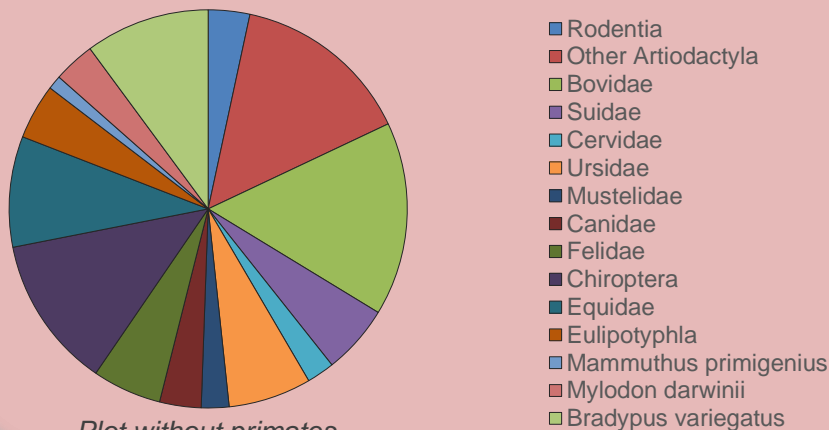
# Shotgun provides more



## Bacterial reads assigned vs NCBI nt database



## Mammals reads assigned vs Metazoan mitochondria genome database



**Zoom in Bacteria:** typical phylum for permafrost samples

**Zoom in Mammals:** typical pleistocene taxa such as Mammuthus or Mylodon

**Shotgun provides also relevant information on other kingdoms**

# References

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- <sup>1</sup>**Parducci, L. et al.** (2019) „Shotgun Environmental DNA, Pollen, and Macrofossil Analysis of Lateglacial Lake Sediments From Southern Sweden“, *Frontiers in Ecology and Evolution*, 7, 189.
- <sup>2</sup>**Taberlet, P. et al.** (2007) „Power and limitations of the chloroplast trnL (UAA) intron for plant DNA barcoding“, *Nucleic Acids Research*, 35(3).
- <sup>3</sup>**Gansauge M. T. et al.** (2017) „Single-stranded DNA library preparation from highly degraded DNA using T4 DNA ligase“, *Nucleic Acids Research*, 45(10).
- <sup>4</sup>**Boyer, F. et al.** (2015) „OBITOOLS: a UNIX-inspired software package for DNA metabarcoding“, *Molecular Ecology Resources*, 16.
- <sup>5</sup>**Wood, D. E. et al.** (2019) „Improved metagenomic analysis with Kraken 2“, *Genome Biology*, 20.
- <sup>6</sup>**Opel, T. et al.** (2018) „Middle and Late Pleistocene climate and continentality inferred from ice wedges at Batagay megaslump in the Northern Hemisphere's most continental region, Yana Highlands, interior Yakutia“, *Climate of the Past Discussion*, 1-32.
- <sup>7</sup>**Murton, J. B. et al.** in preparation