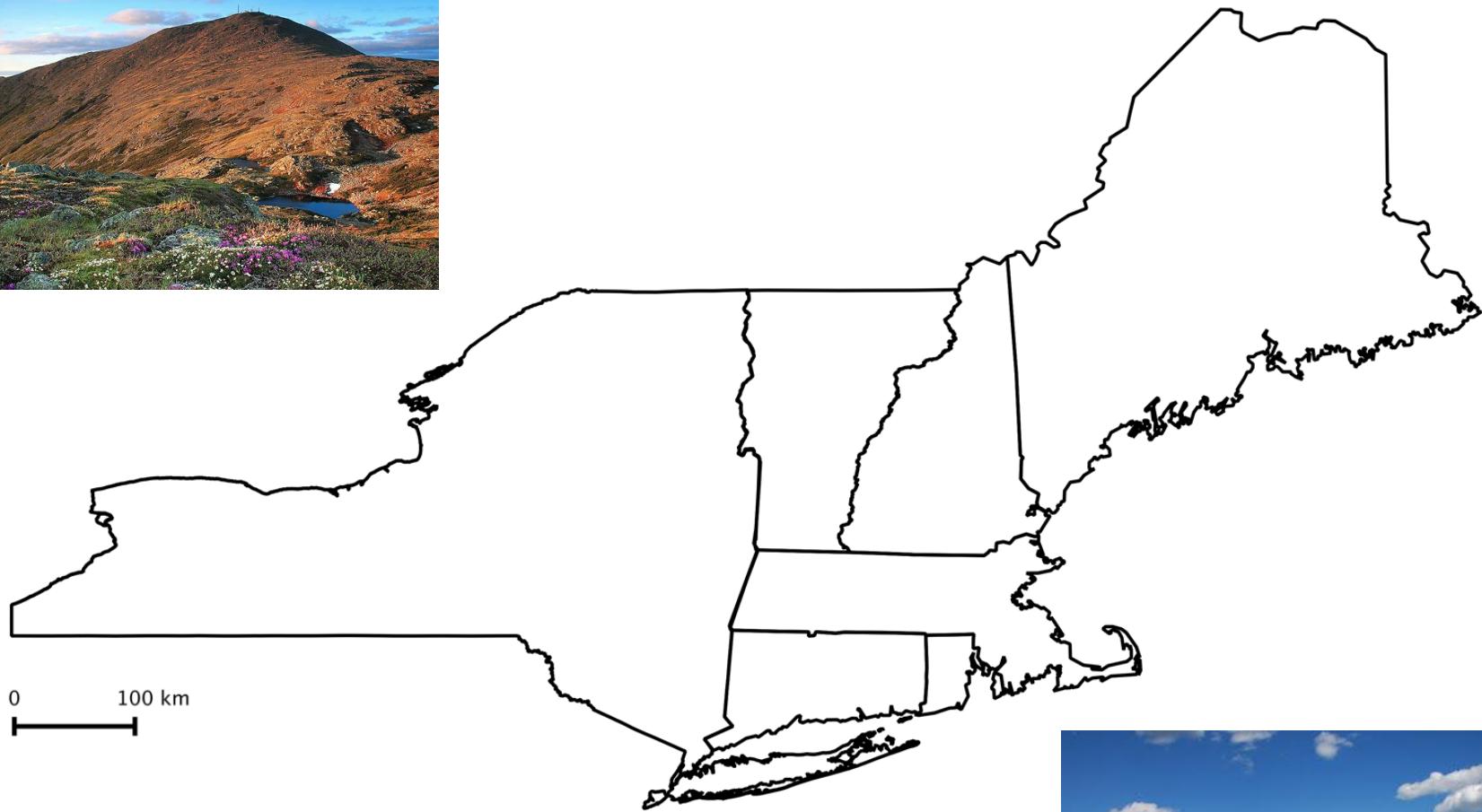


# Tracing the movement of the invasive alga *Nitellopsis obtusa* using genetic analyses

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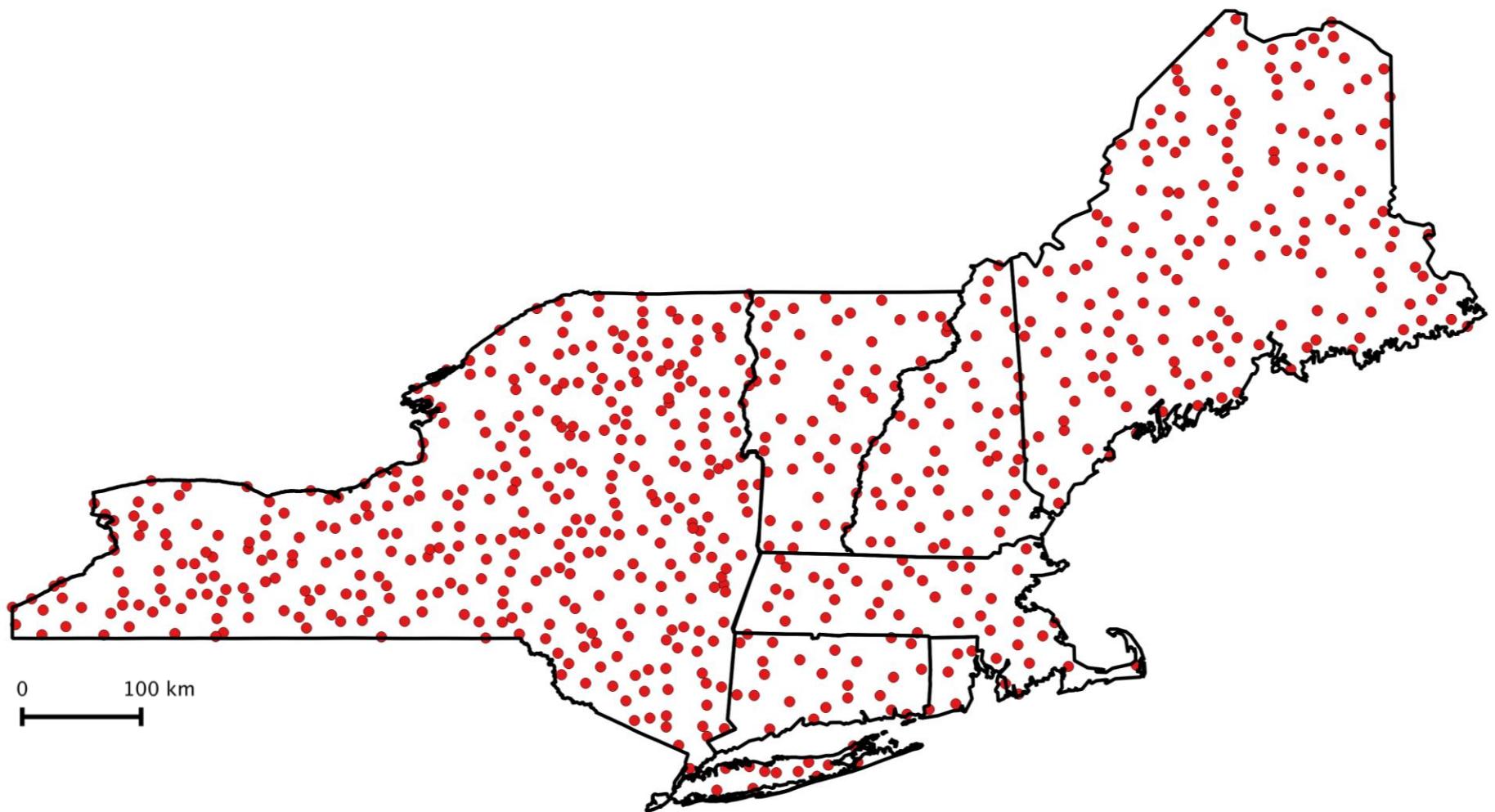
# Study Area



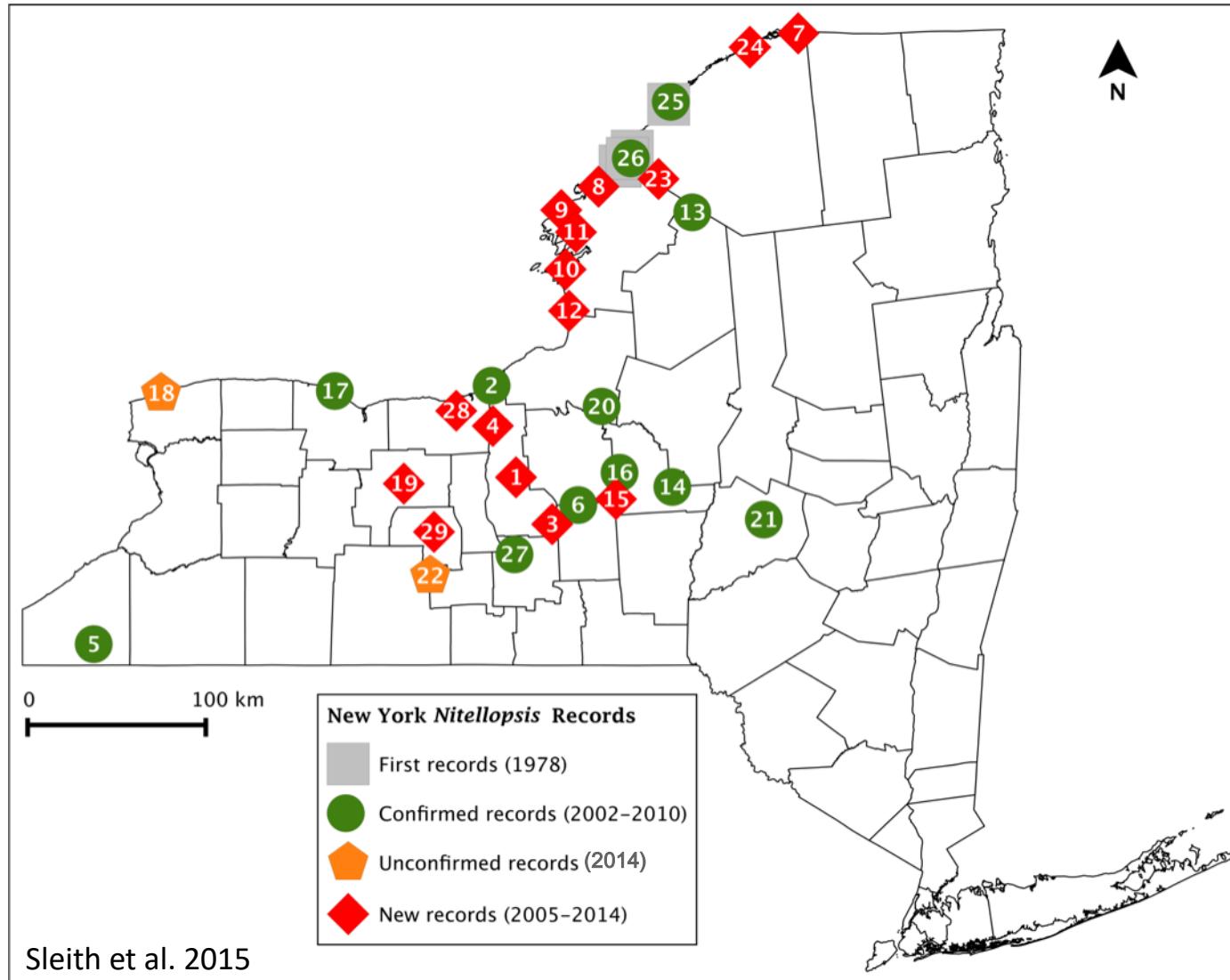
- 327,758 km<sup>2</sup> (a bit smaller than Germany)
- >15 ecoregions
- Barrier islands to alpine tundra



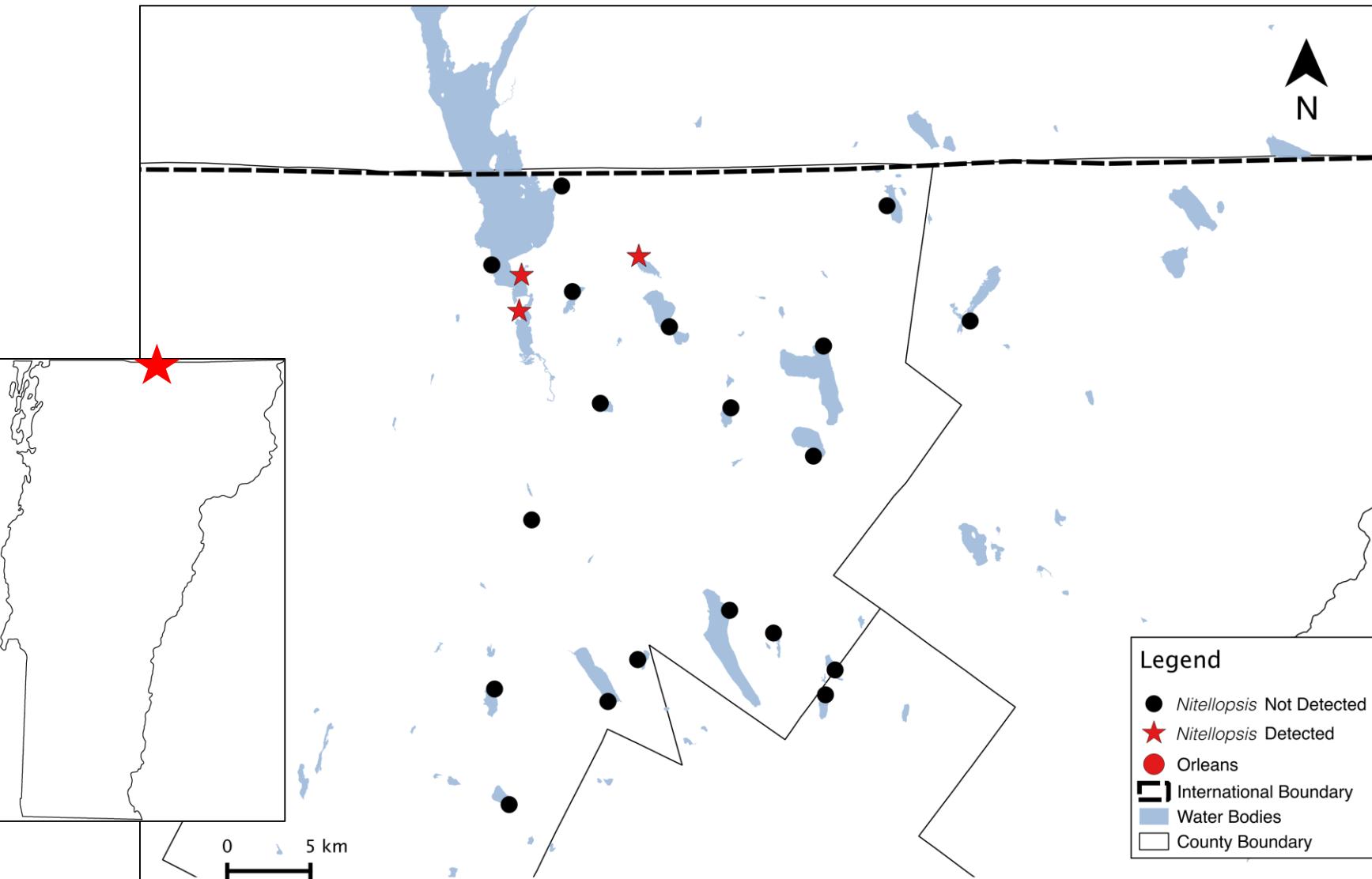
# 740 Sites



- 24,000 miles of driving = 1 trip around the equator



Starry Stonewort in 31 sites across 17 counties, 18 new records (red diamonds)



Starry Stonewort in 3 sites in Orleans County, Vermont

# Water Chemistry



- Temperature (C)
- Dissolved Oxygen (mg/L)
- Oxidation Reduction Potential (mV)
- pH
- Conductivity (uS/cm)

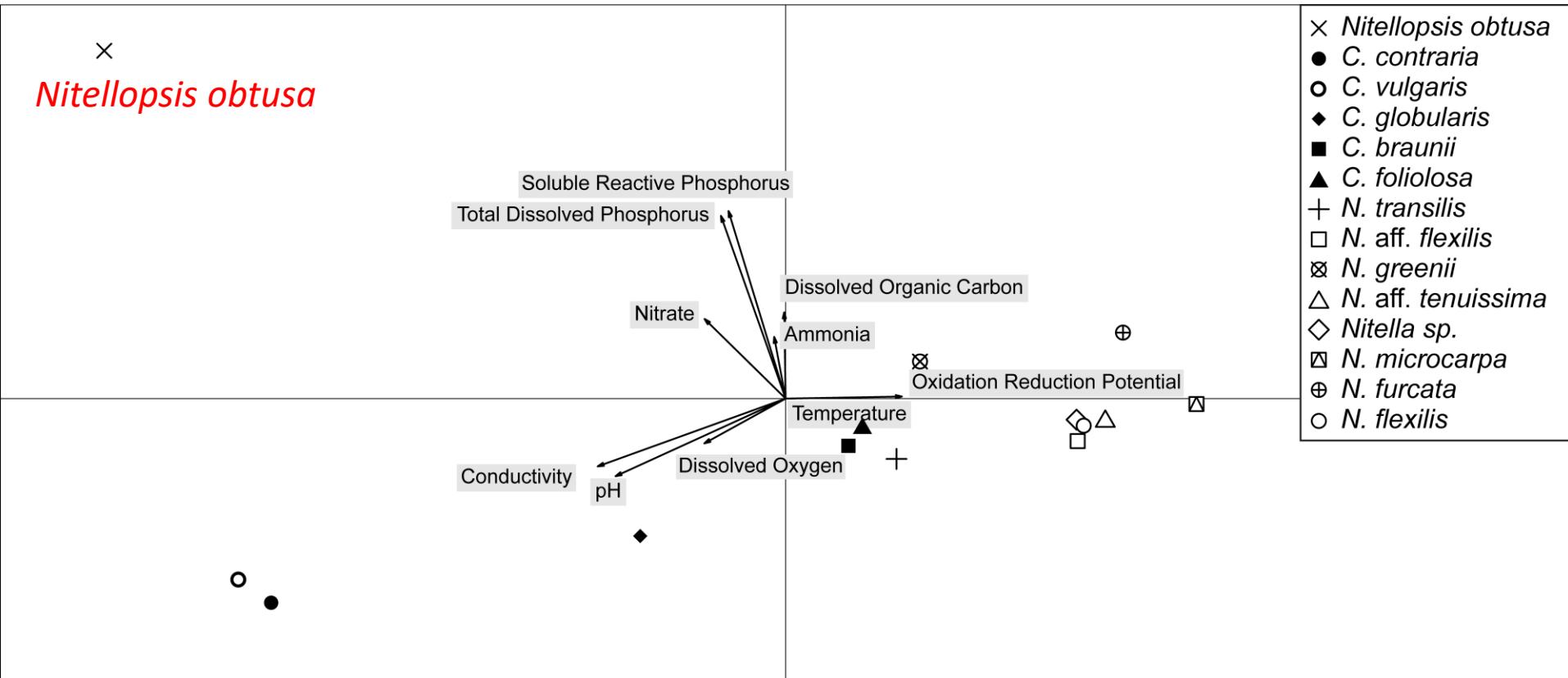


- Nitrogen from Ammonia (ug/L)
- Nitrogen from Nitrate (ug/L)
- SRP- Soluble Reactive Phosphate (ug/L)
- TDP- Total Dissolved Phosphorus (ug/L)
- DOC- Dissolved Organic Carbon (mg/L )
- Calcium (mg/L)
- Magnesium (mg/L)

# Species in OMI Space

High conductivity, basic,  
high nutrients

Low conductivity, acidic,  
high nutrients

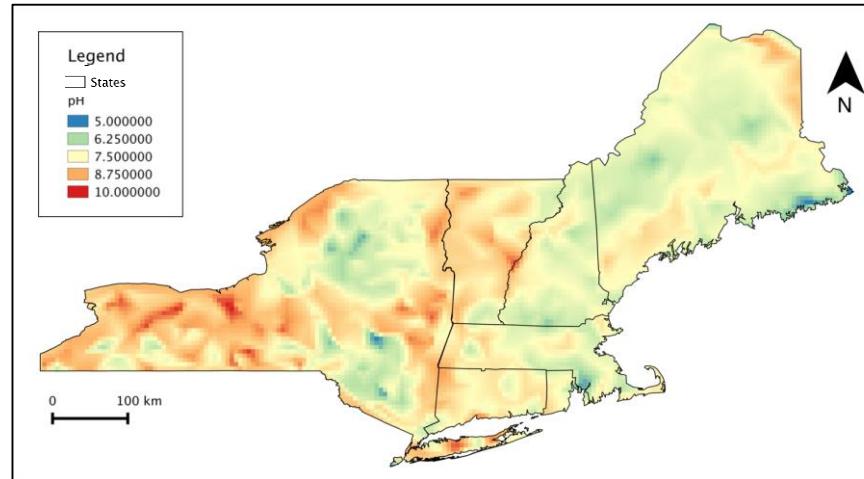
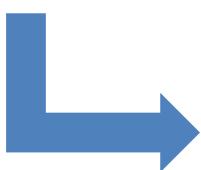
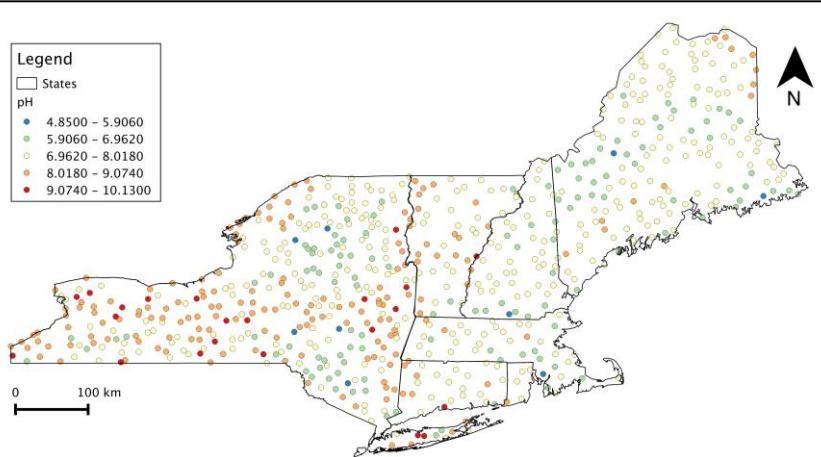


High conductivity, basic,  
low nutrients

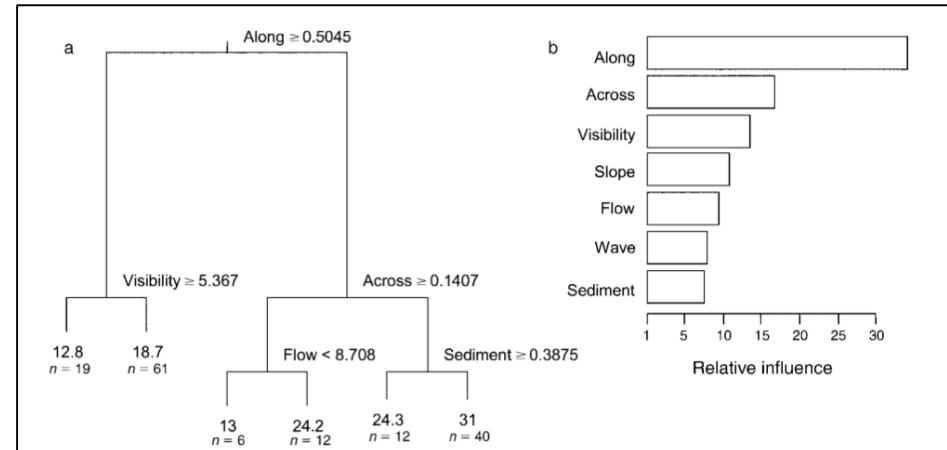
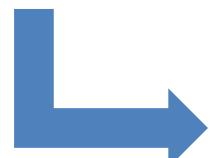
Low conductivity, acidic,  
low nutrients

# Modeling Methods

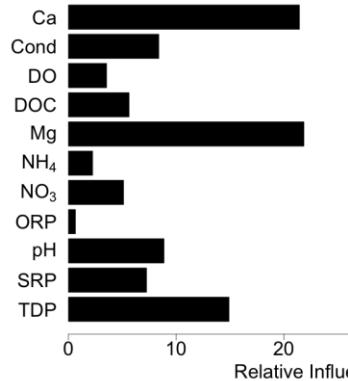
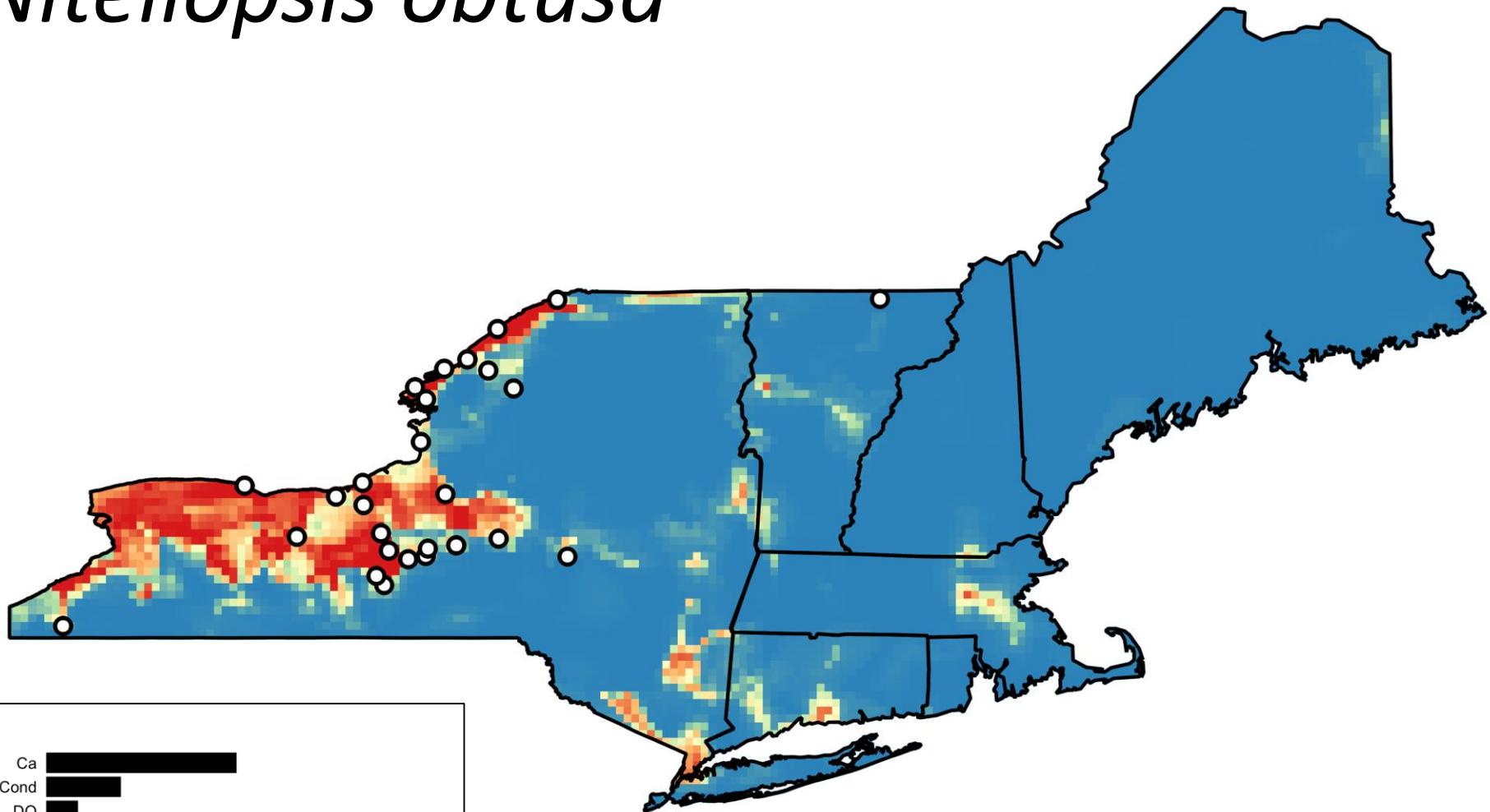
## Chemistry Point Data



## Interpolated Chemistry Raster



# *Nitellopsis obtusa*



Low suitability      High suitability

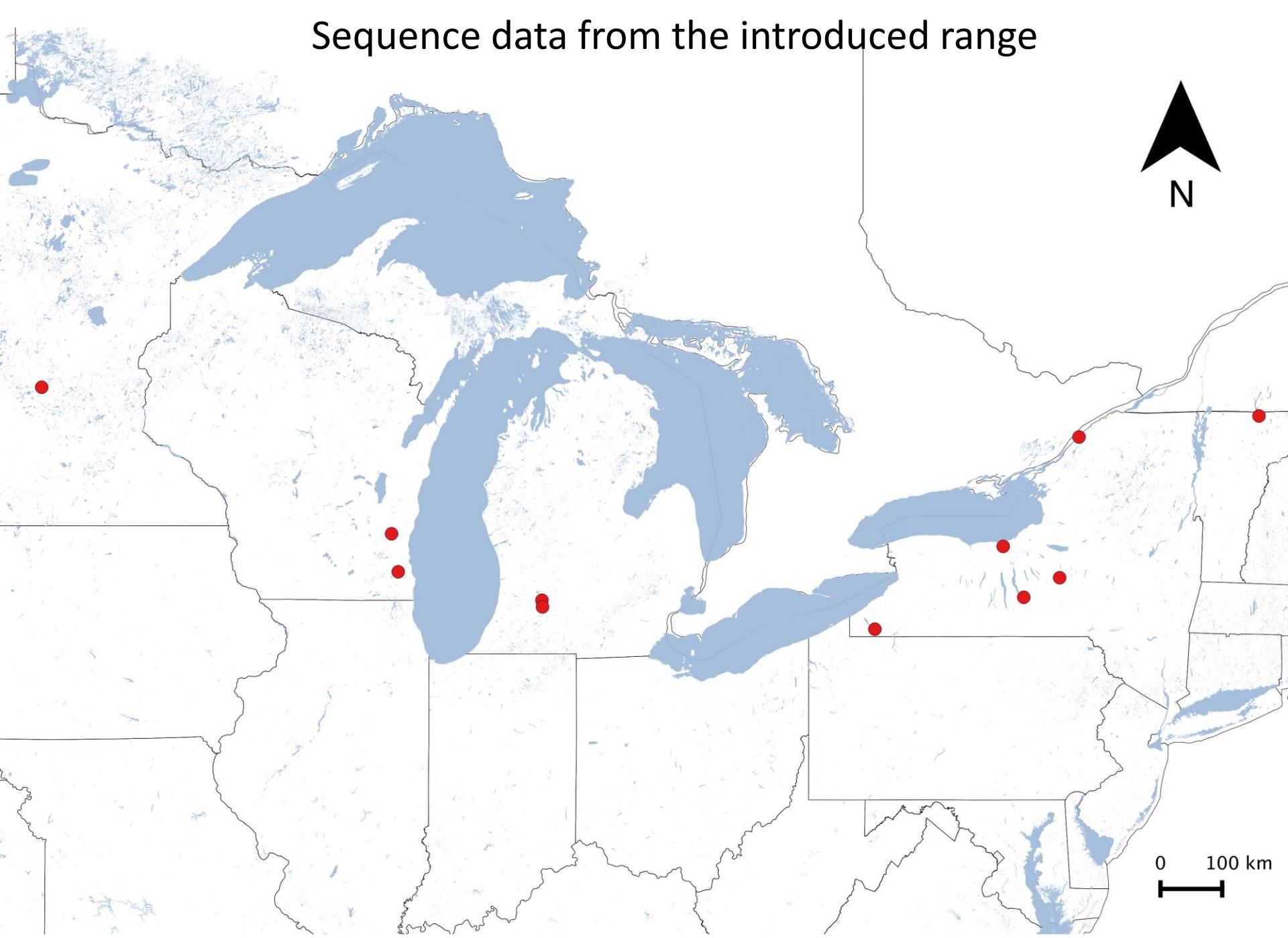
○ Occurrence Records

# Phylogeography

- Hypotheses
  - Introduced from Europe not Asia
  - Single introduction to North America with subsequent spread
  - Spread in North America is incremental in East to West direction

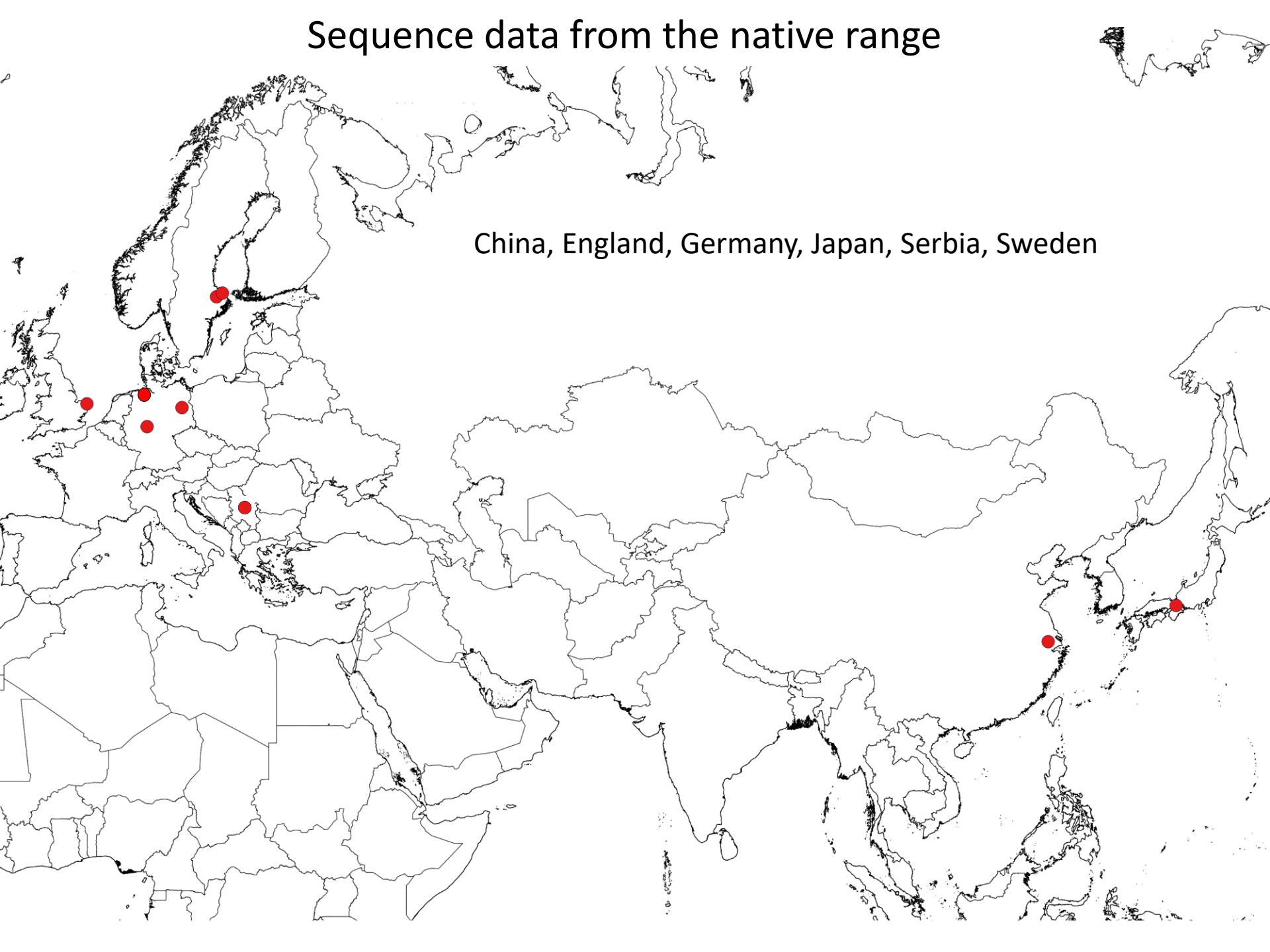


# Sequence data from the introduced range



# Sequence data from the native range

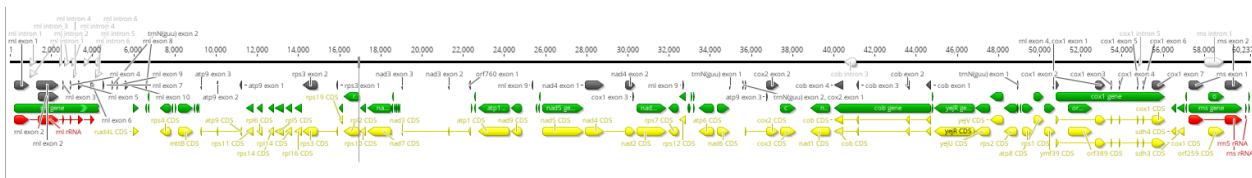
China, England, Germany, Japan, Serbia, Sweden



# Organellar Genome Sequencing

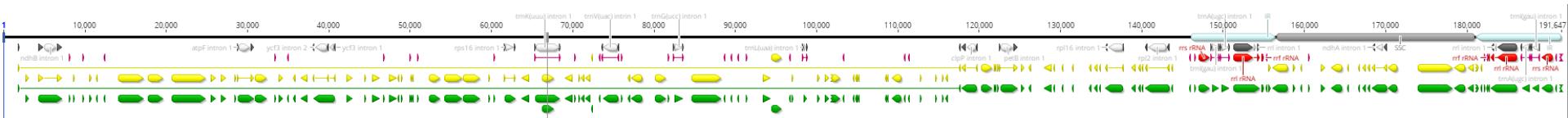
- Mitochondrial and plastid genomes
- Illumina whole genome approach
- Assemble *de novo* and annotate in Geneious

## MT



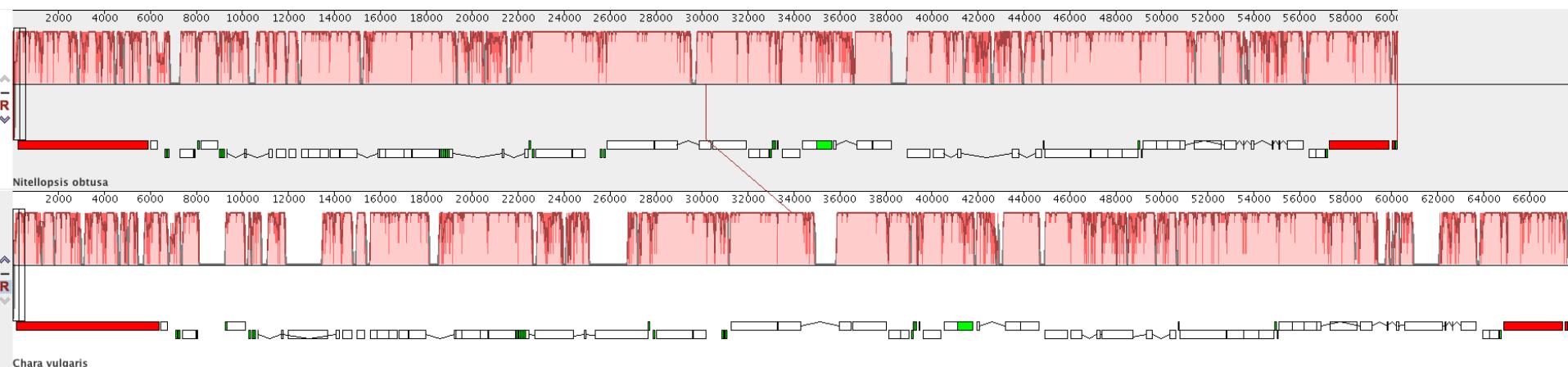
- 60,237 bp
- 70 genes
- 24 introns

## CP



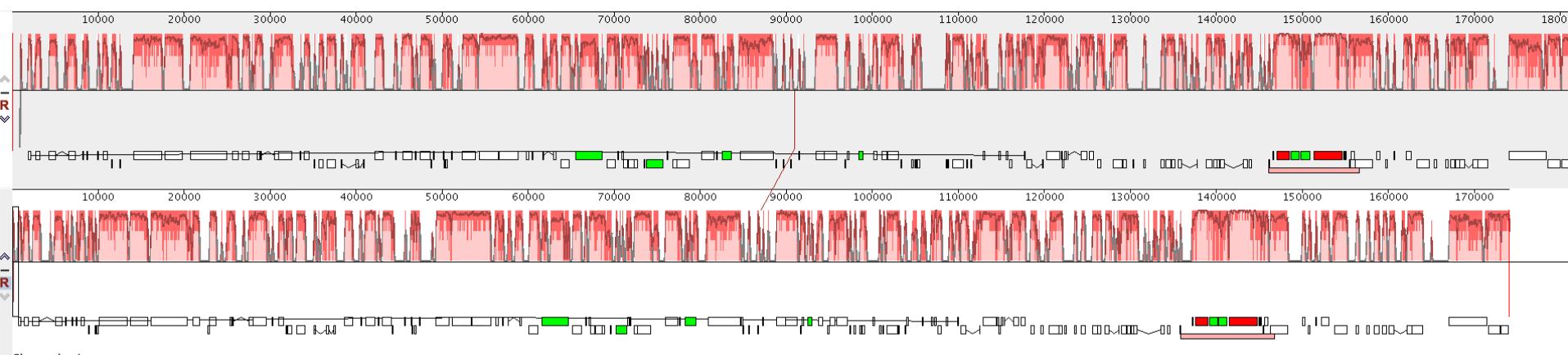
- 191,647 bp
- 2 inverted repeat regions
- 97 genes
- 20 introns

## *Nitellopsis obtusa*



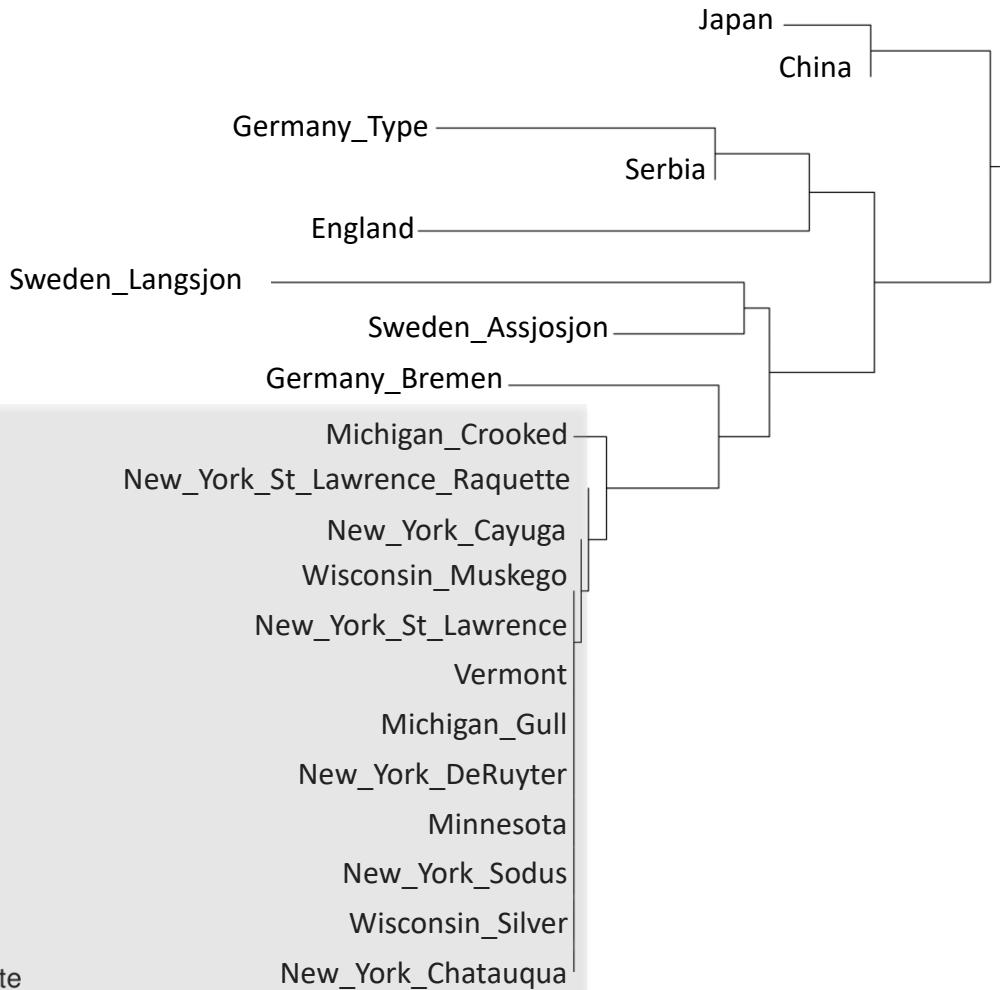
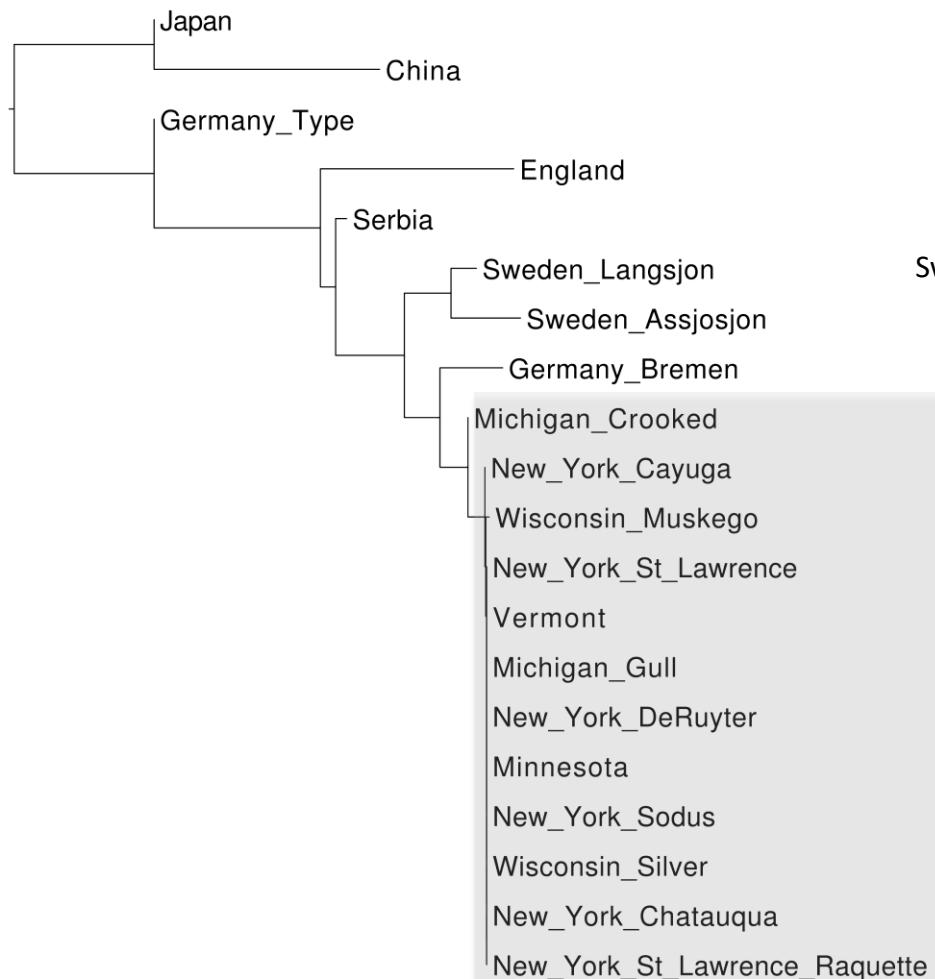
## *Chara vulgaris*

## *Nitellopsis obtusa*



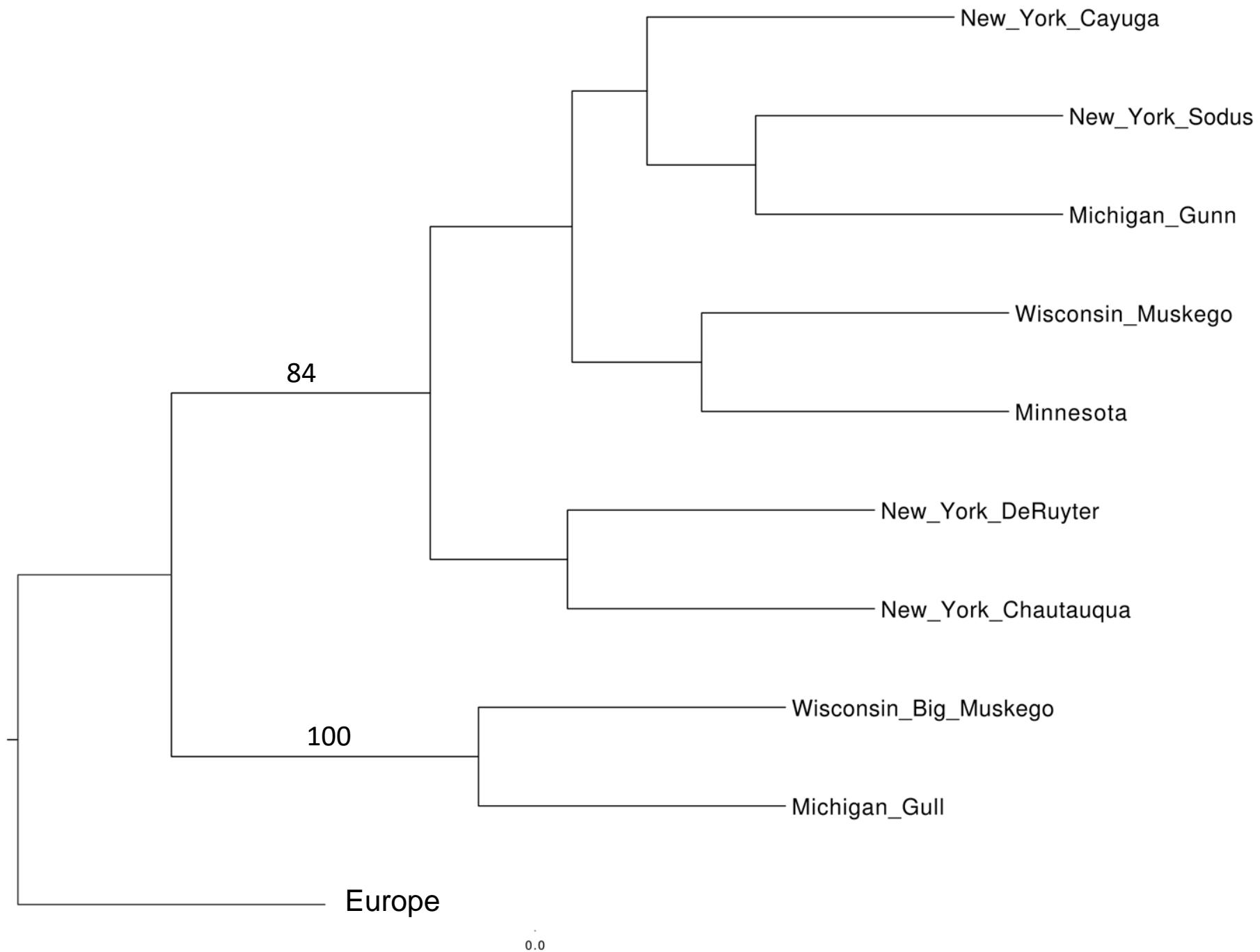
## *Chara vulgaris*

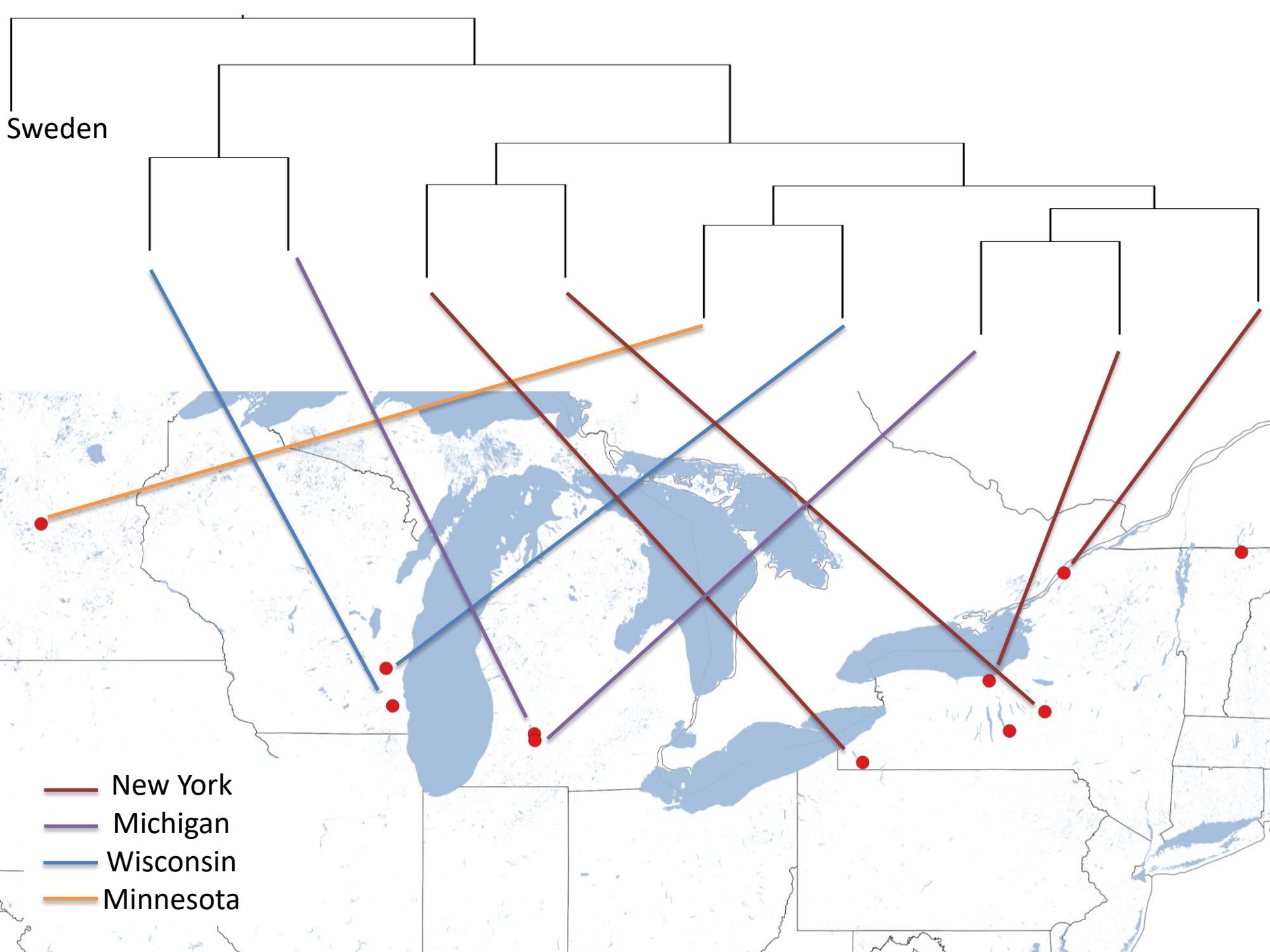
- Strict map to reference
- MAFFT Alignment
- Neighbor-Joining (Tamura-Nei)



# Genotyping by Sequencing

- Sequences flanking areas of restriction sites
- Reduces complexity of genome
- More variable than organellar sequencing
- Identified single nucleotide polymorphisms (SNPs) across nuclear genome
- ipyrad pipeline used for processing data





# Conclusions

- *Nitellopsis obtusa* is still being reported from new localities in North America
- Occurs in unique chemical environment
- Is associated with higher concentrations of calcium and magnesium
- Introduced from Europe
- Complicated pattern of spread

# Acknowledgements

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