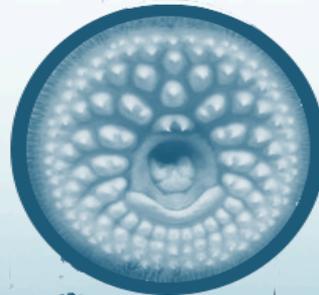


Population genomics of anadromous sea lamprey across its distributional range

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Supervisors: Margaret F. Docker, Colin Garroway (University of Manitoba)



The lab...

- Invasive sea lamprey population genomics
- Anadromous sea lamprey population genomics
- Sex determination in invasive sea lamprey
- Transcriptomics for genetic control



Current work

Reconstructing anadromous sea lamprey evolutionary history - implications for management & conservation

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Background



- Anadromous sea lamprey populations - of conservation concern in their native range on both sides of the Atlantic Ocean
- Genetic data can be used to uncover the evolutionary processes that gave rise to modern demography
- Informing management & conservation strategies
- Conservation of native sea lamprey populations

Mitochondrial DNA markers (Genner et al. 2012):

- Accumulation of genetic diversity - up to 125.000 years ago in European, and up to 500.000 years ago in North American sea lamprey
- East Atlantic/European population - lower genetic diversity and effective population size
- Scenario 1: Divergence early in evolutionary history prior to loss of shared genetic diversity followed by an environmentally-driven bottleneck in Europe ~125.000 years ago (also supported by Almada et al. 2008)
- Scenario 2: Colonization of Europe by North American migrants during the last 150.000 years

From genetics to genomics & a large scale sample collection for a deeper understanding of sea lamprey demography and population structure

Objectives

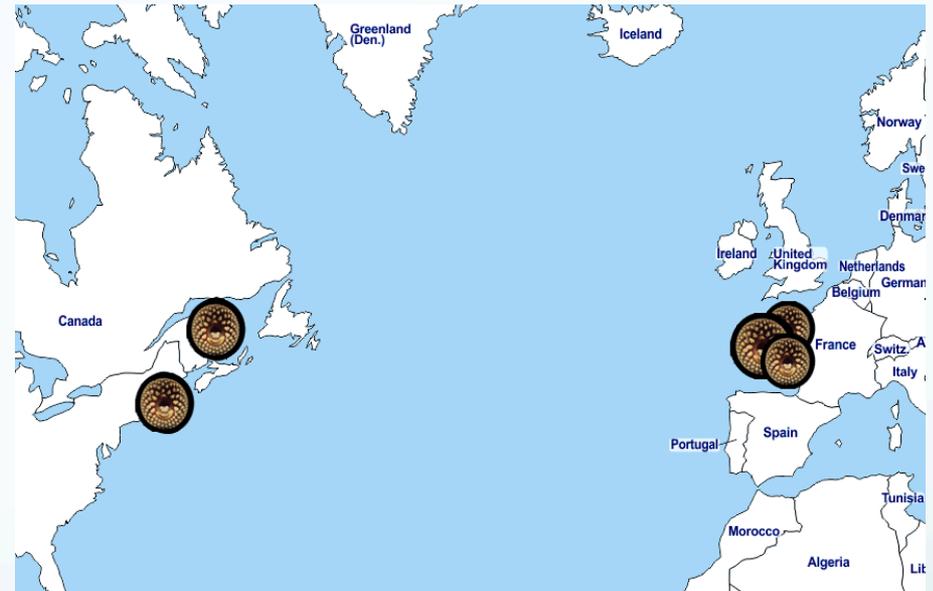
- Model evolutionary trajectory on a historic time scale
- Time the population split between North American and European coasts
- Estimate effective population size through time



Methods

Sequencing

- 45 anadromous sea lamprey samples
- West Atlantic: 24 specimens from New Brunswick (Richibucto River) & Massachusetts (Connecticut River)
- East Atlantic: 21 specimens from France (Rivers Scorff - 8, Oir - 7, Loire – 6)
- Whole-genome sequencing of $\sim 7X$ read depth
- Annotated sea lamprey genome (Smith et al. 2018) as a mapping reference
- $\sim 8.000.000$ variants after filtering

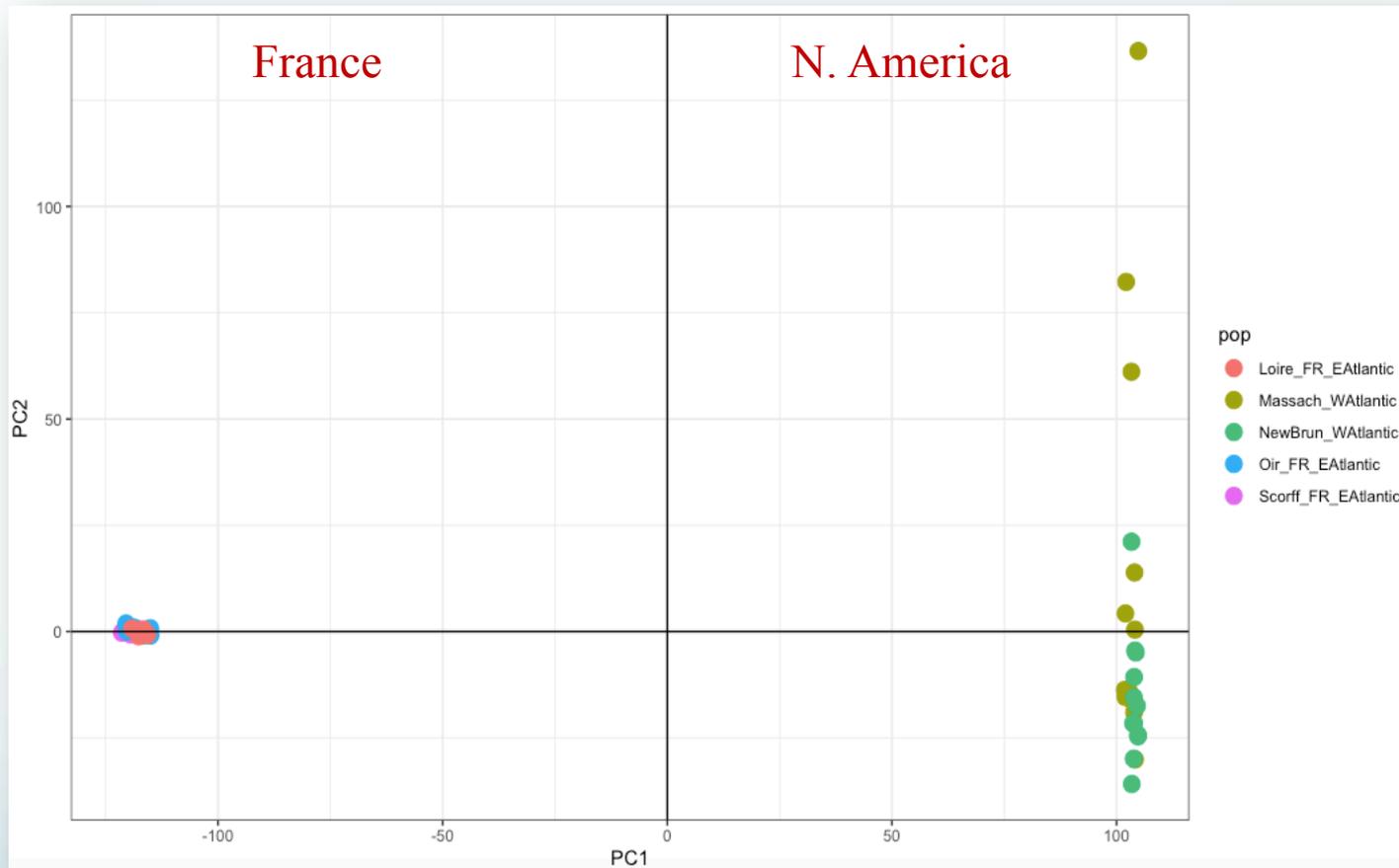


Population Genetic Analysis

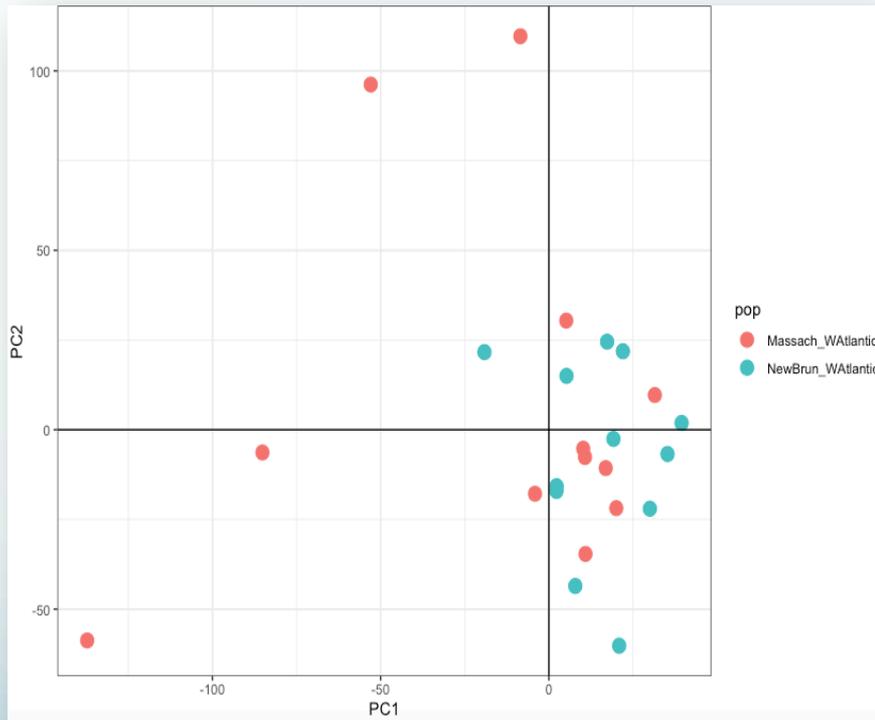
Fst estimates (Weir and Cockerham 1984) were used as a measure of between population genetic differentiation

- Significant genetic structure between East and West Atlantic coasts
- No significant genetic structure between North American populations (Massachusetts & New Brunswick) or between French populations (Rivers Oir, Loire & Scorff)

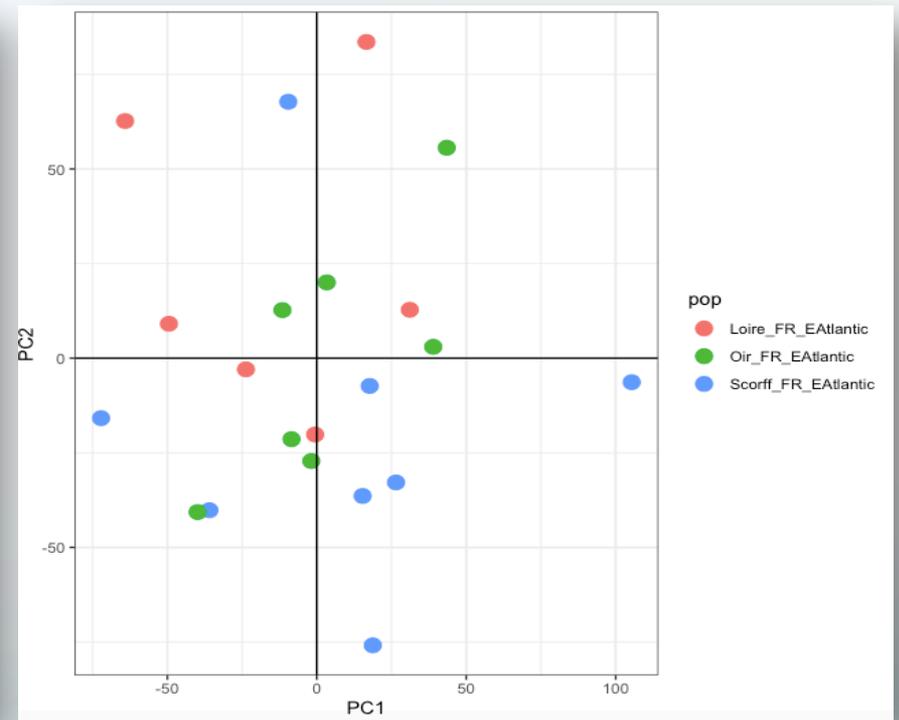
PCA plot of SNPs for whole dataset



PCA plot of North American populations



PCA plot of European populations



SMC++

- Sequentially Markovian coalescent approach SMC++ as seen in Terhorst et al. (2017)
- Uses rates of coalescence to infer effective population size across time
- Estimates time to most recent common ancestor across segments of the genome taking into account linkage disequilibrium
- 10 samples from French - East Atlantic population & 10 samples from North American - West Atlantic population



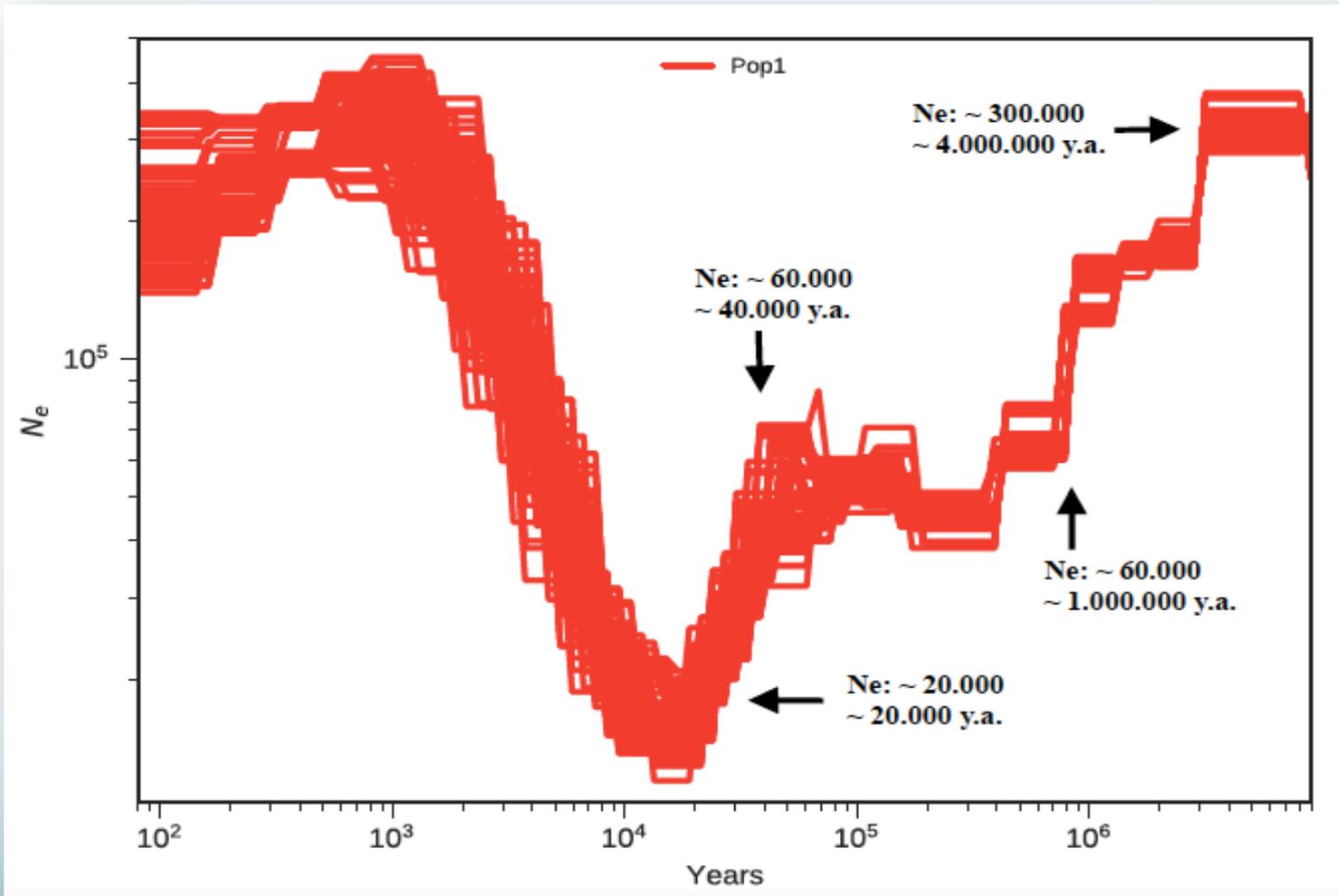
Preliminary results

Mutation rate

- Per generation mutation rate (per base pair) – important for running models
- Expected to be between $\sim 10^{-8}$ (Nikolic et al. 2019) $\sim 10^{-9}$ (Genner et al. 2012, Kuraku & Kuratani 2006)
- Anadromous sea lamprey mutation rate?

East Atlantic Population - France

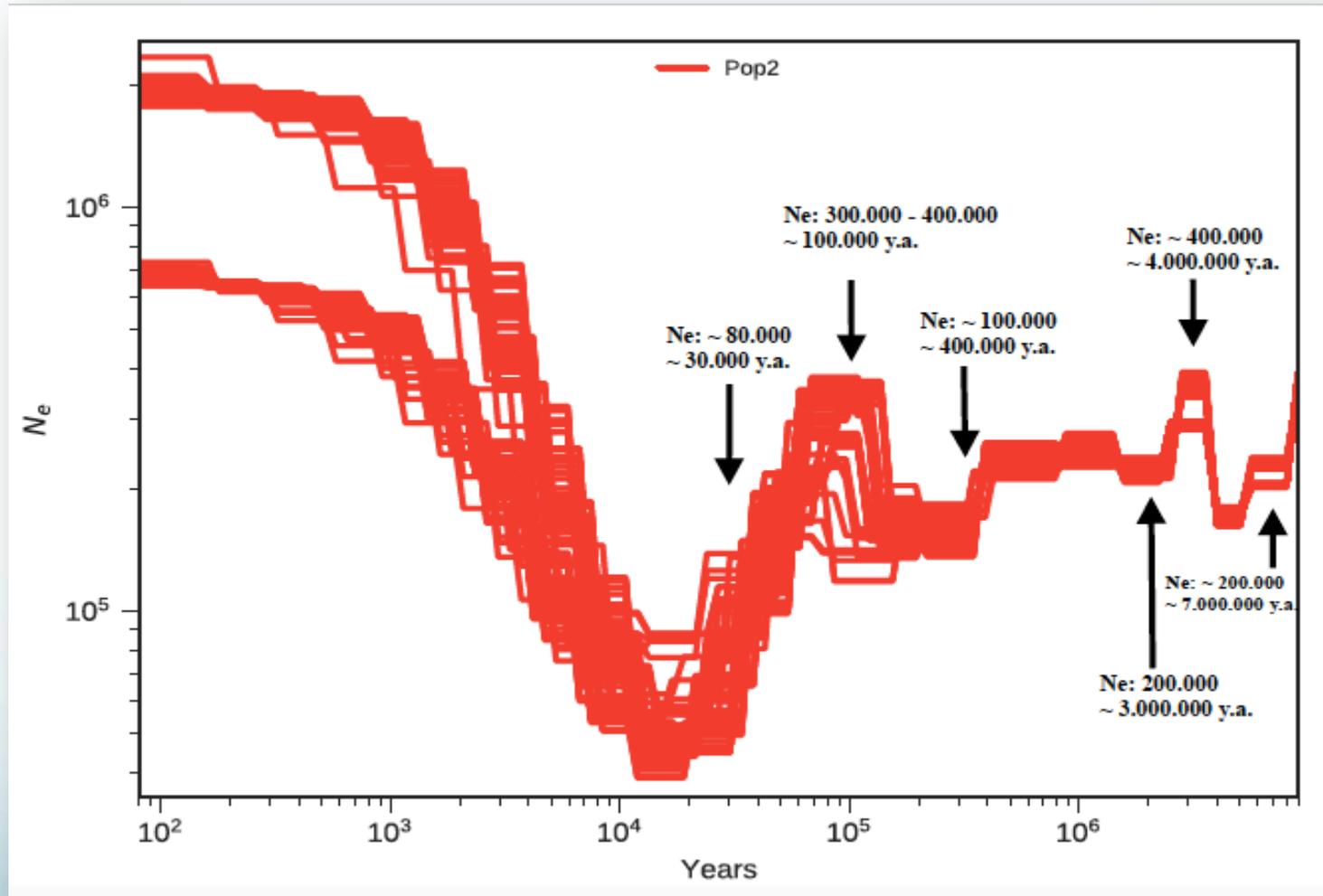
(Per generation mutation rate: 10^{-9} for 20 sample subset)



Going back in Time →

West Atlantic Population – North America

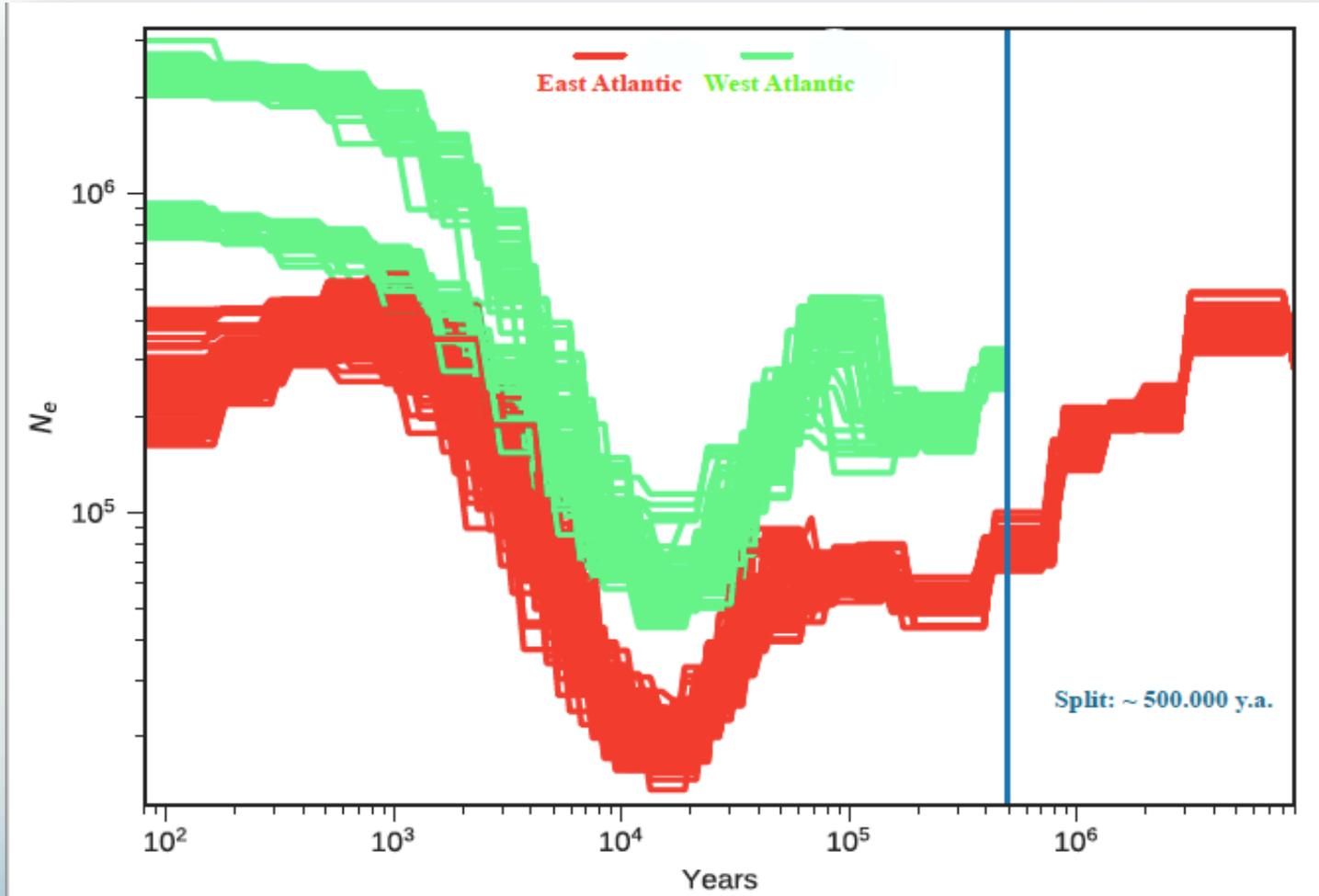
(Per generation mutation rate: 10^{-9} for 20 sample subset)



Going back in Time →

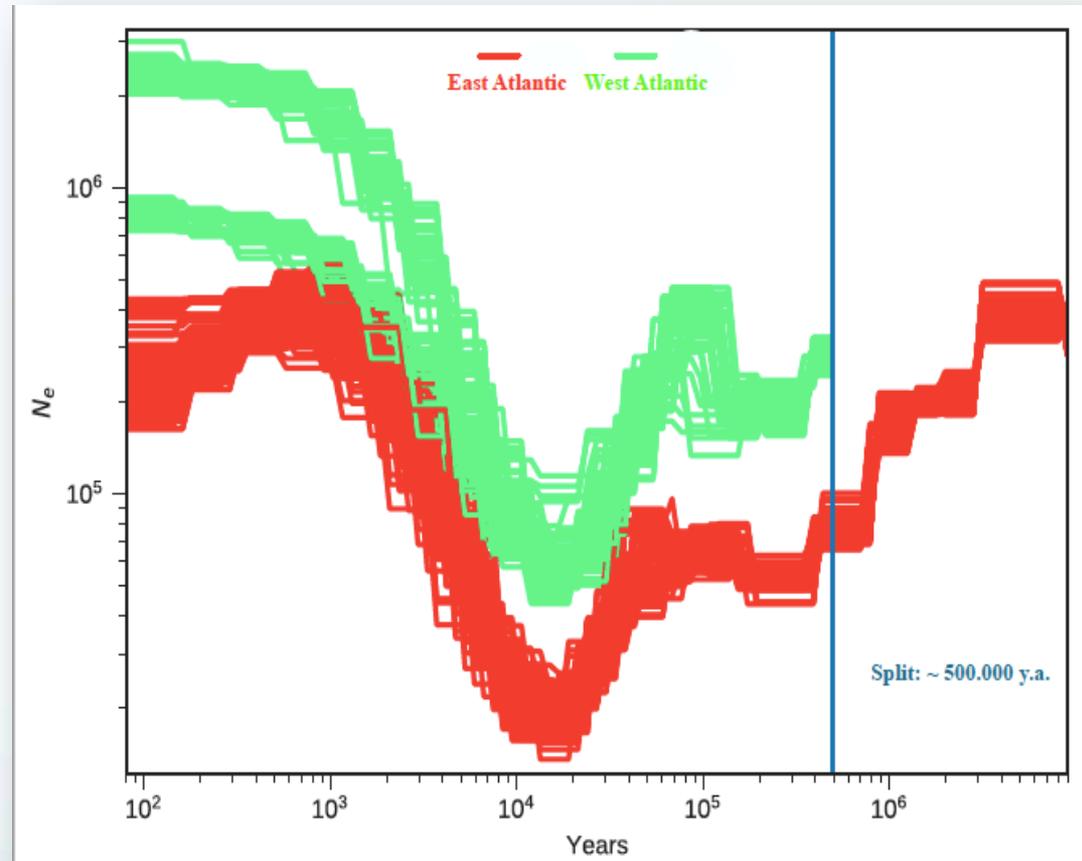
Split

(Per generation mutation rate: 10^{-9} for 20 sample subset)



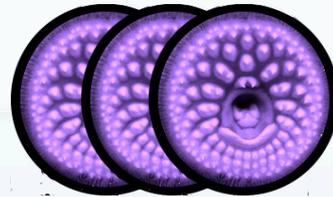
Going back in Time →

- Population split time estimated at ~500.000 years ago
- E. Atlantic (France): $N_e \sim 20.000$
W. Atlantic(N.America): $N_e \sim 80.000$
- W. Atlantic $N_e > E. Atlantic N_e$
- Colonization of Europe by North American migrants?
- Implications for conservation?
- Interpretation in regards to other diadromous species population splits in the North Atlantic, connection to past climatic events



Future work

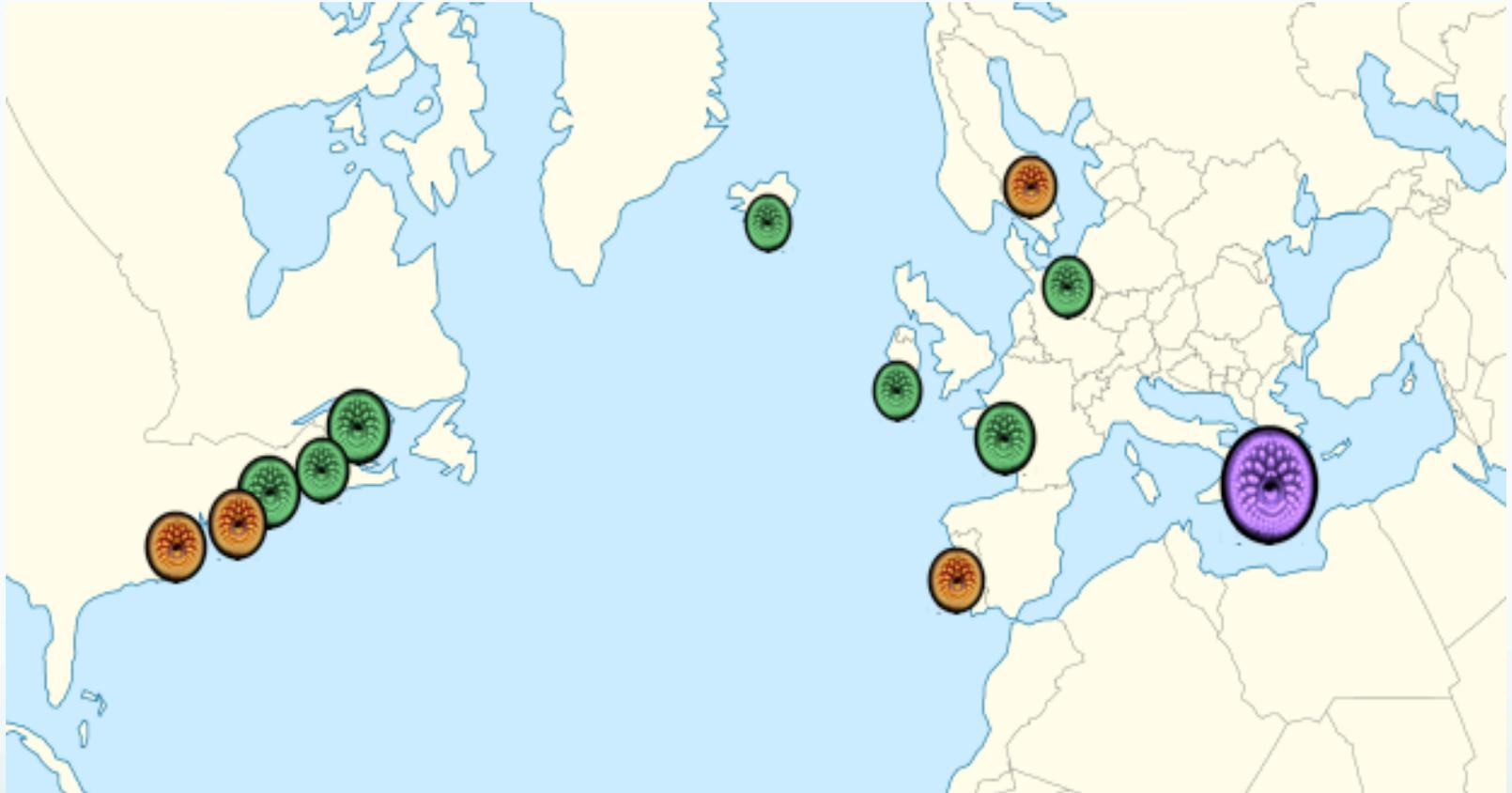
Fine-scale population structure of
anadromous sea lamprey & signals of
adaptation



Objectives

- Finer scale population structure and connectivity within and between East & West Atlantic coasts
- Signals of adaptation and their relation to environmental/human caused variables
- Interpretation of data in regards to localized sea lamprey management & conservation

Sample set



Already have



Collaboration underway



Seeking

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To be continued...

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