# Hidden Diversity, Moving Stocks: Genomic Insights on Connectivity and Adaptation in Small Pelagics

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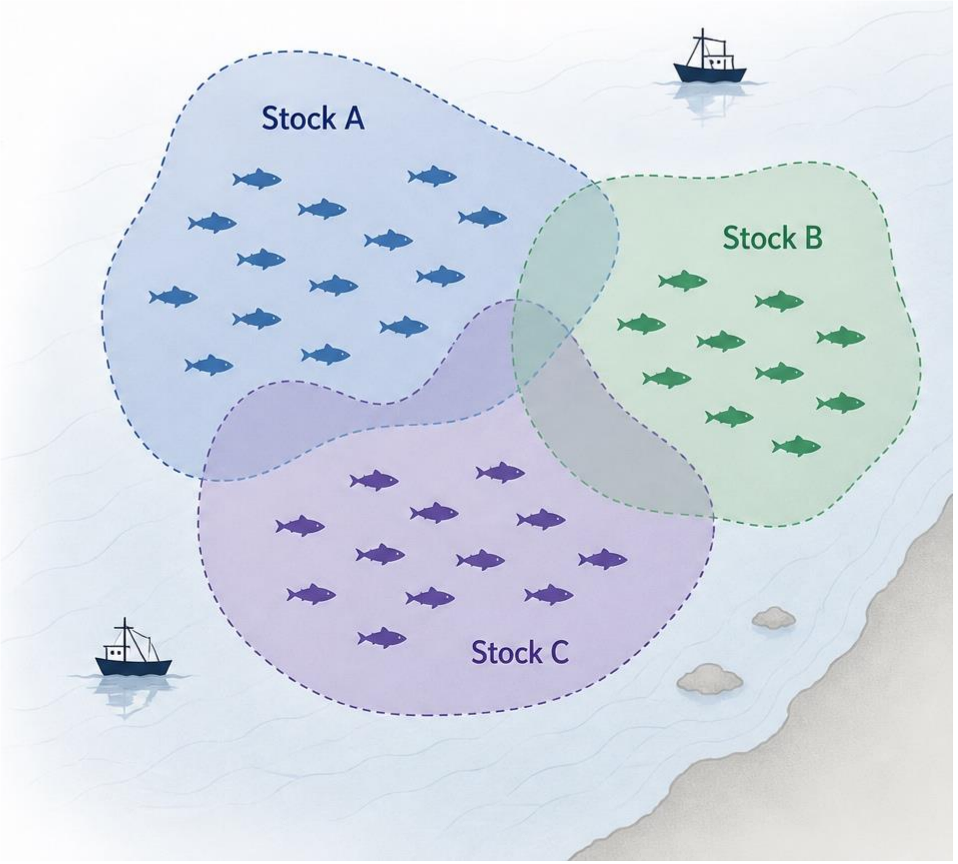
# Stock structure underpins key decisions

- Defines management units
- Determines how catch is allocated
- Shapes responses to environmental change



# Key processes are hard to observe directly

Especially in small pelagics

- Highly mobile species
- Variable recruitment
- Shifting distributions

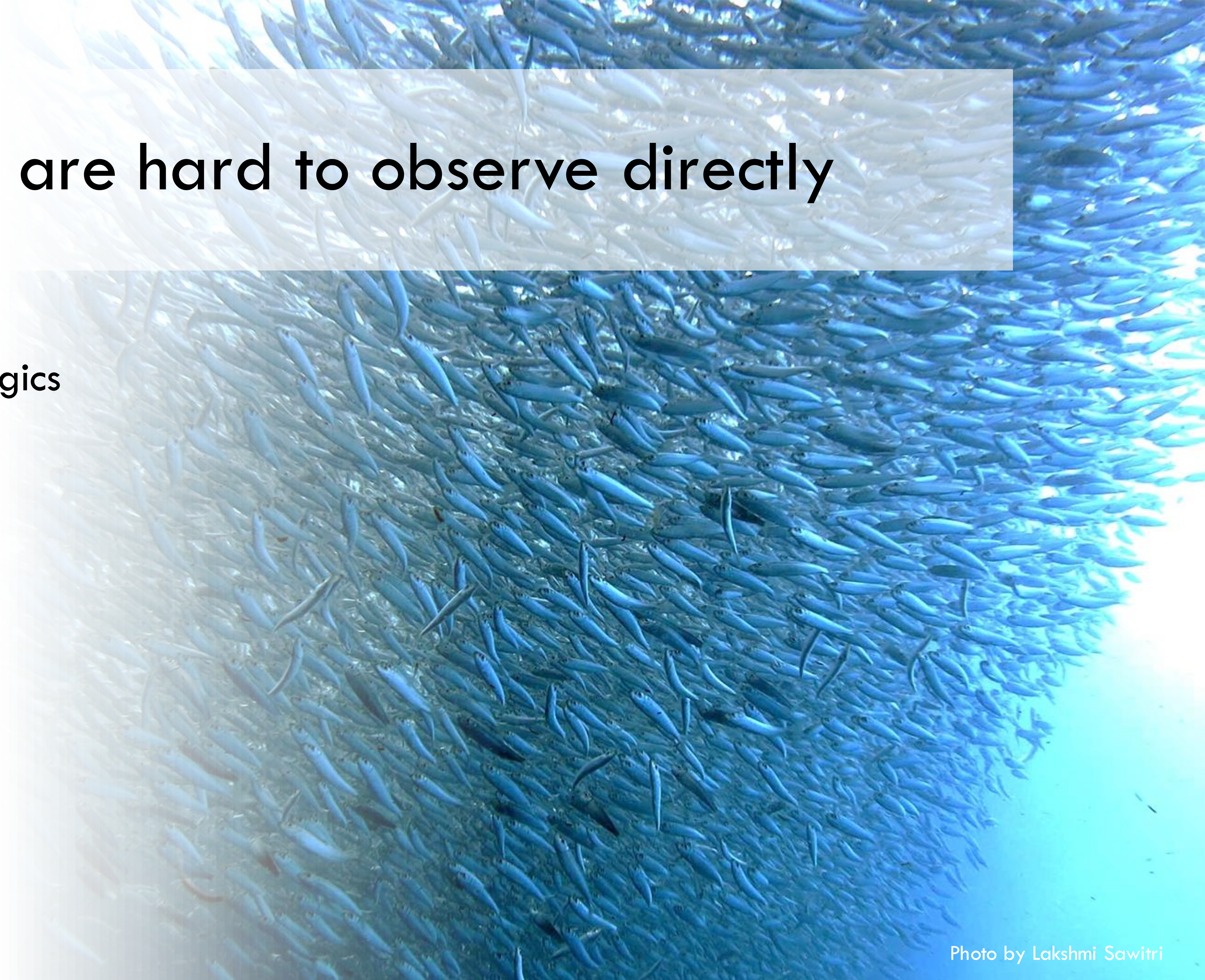
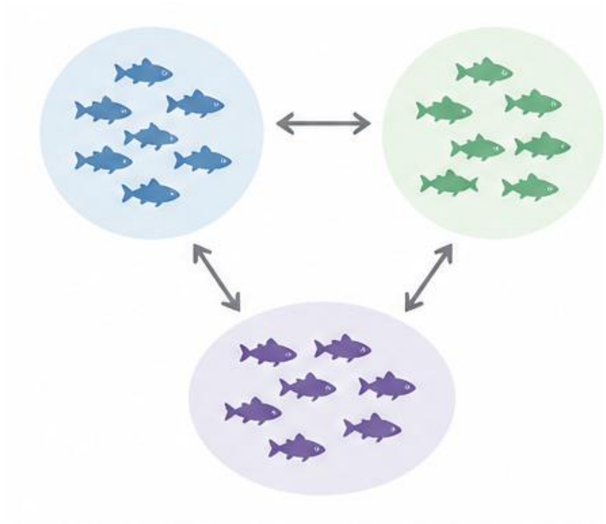


Photo by Lakshmi Sawitri

# What we need to assess

**Who interbreeds with whom**
(stock structure)



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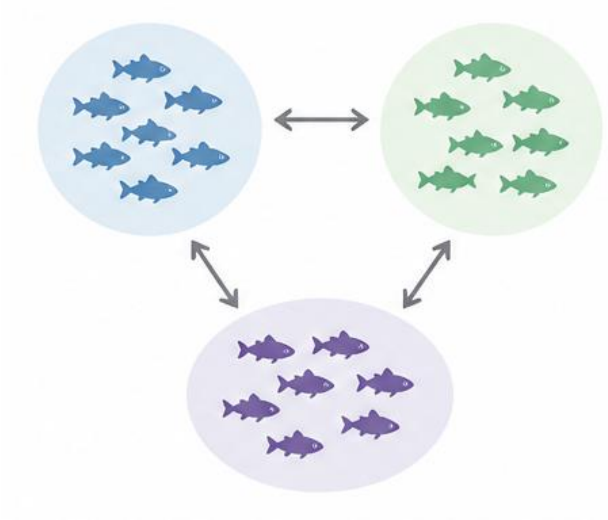
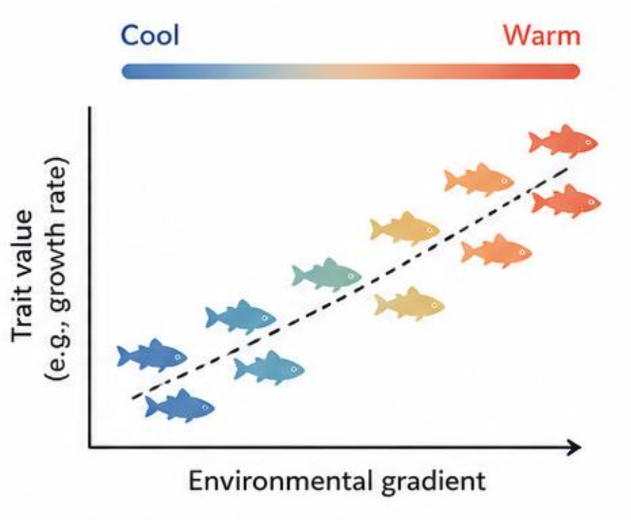


**How environmental responses vary**
(adaptation)



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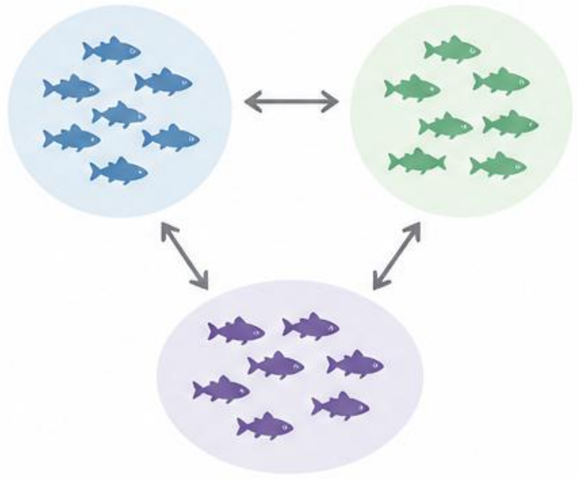

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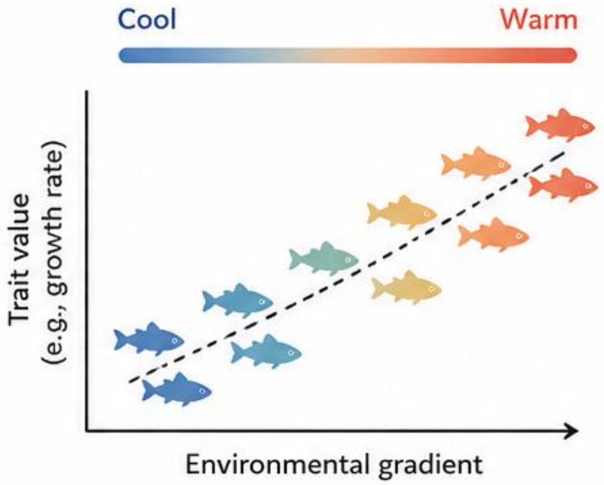
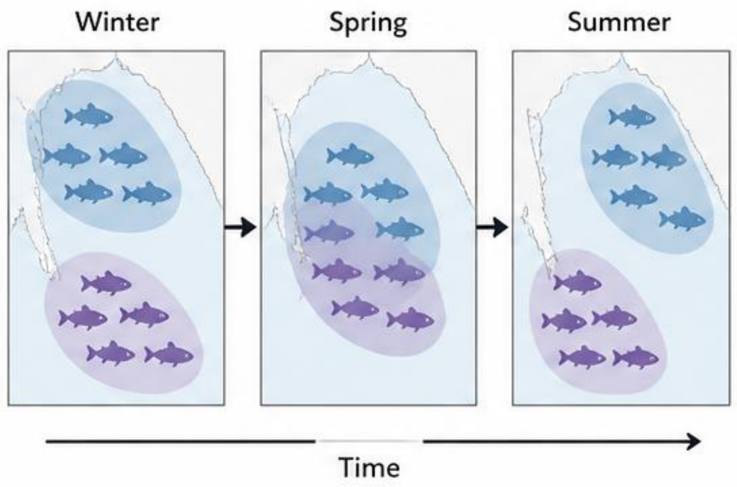


### Where different stocks occur through time and space

(mixing dynamics)



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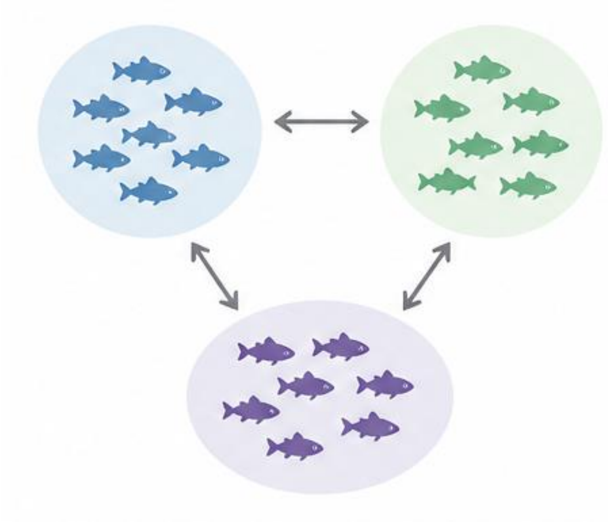

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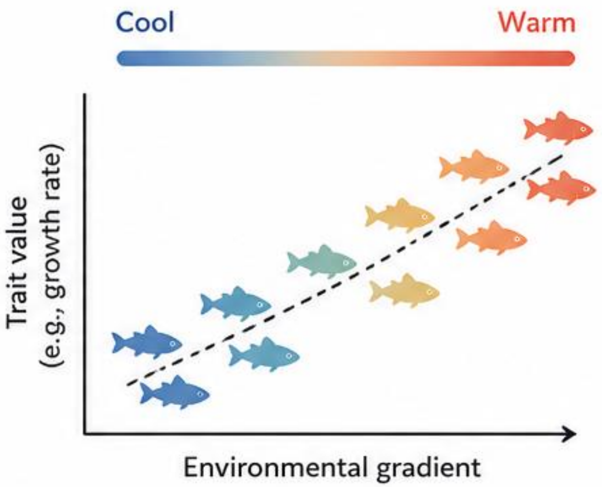

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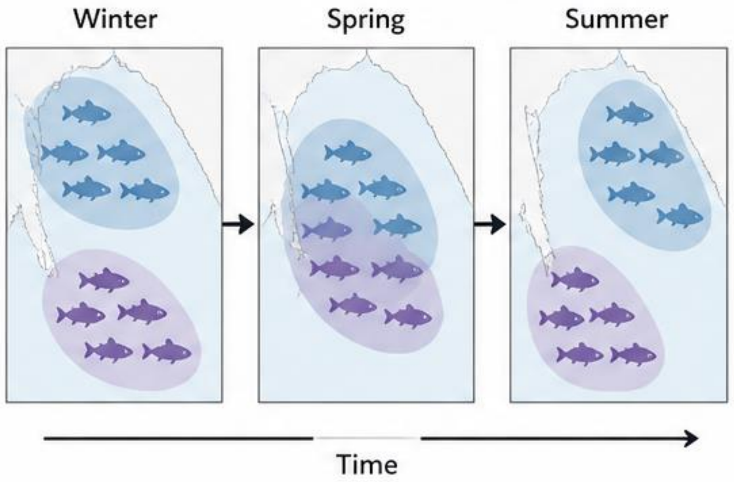


These underlying processes are essential for effective fisheries management

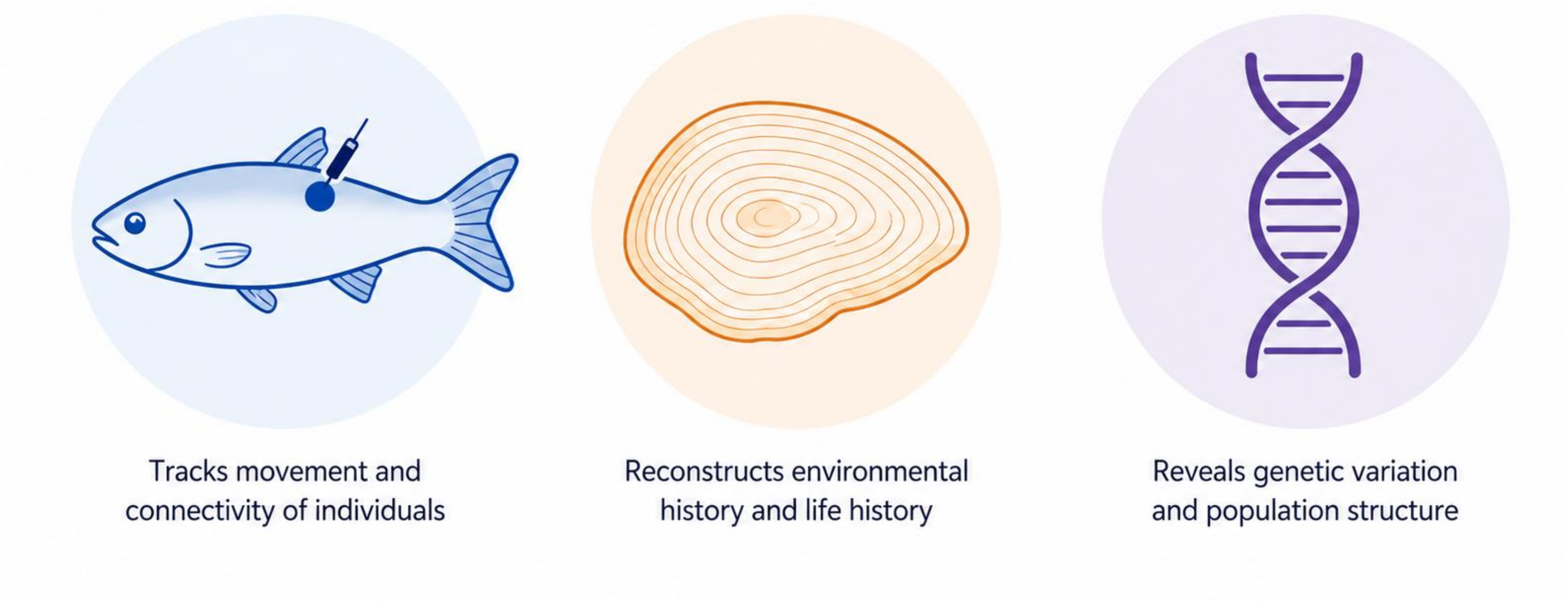
# Multiple complementary tools

Provide complementary views of connectivity and life history

Tagging

Otolith analysis

Genetics



Tracks movement and connectivity of individuals

Reconstructs environmental history and life history

Reveals genetic variation and population structure

Image: Google Maps)

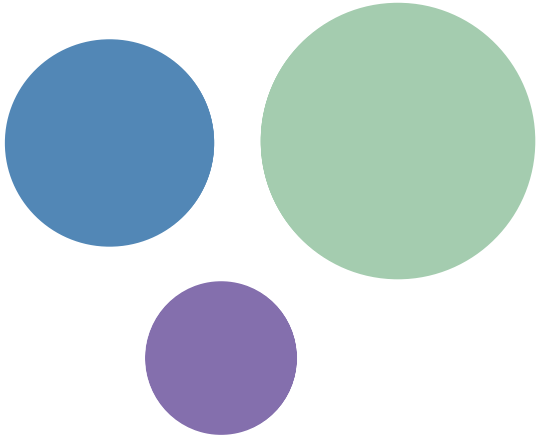
- Small population sizes
- Low dispersal/gene flow
- Strong differentiation

Image: Google Maps

- Large population sizes
- High dispersal/gene flow
- Weak differentiation

# Genomics adds the most value where signal is weakest

Small populations - low gene flow



Structure easy to detect

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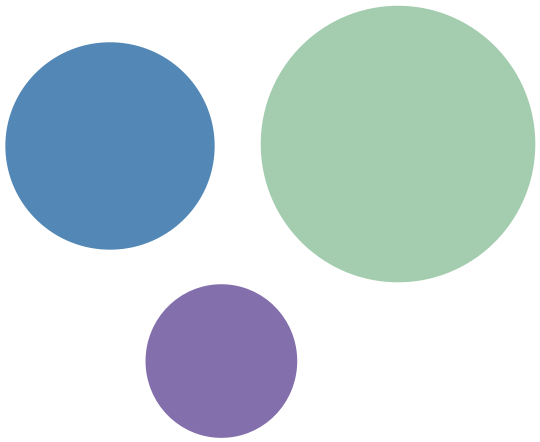

Structure easy to detect

## Large populations - high gene flow

Traditional markers often show “no structure”

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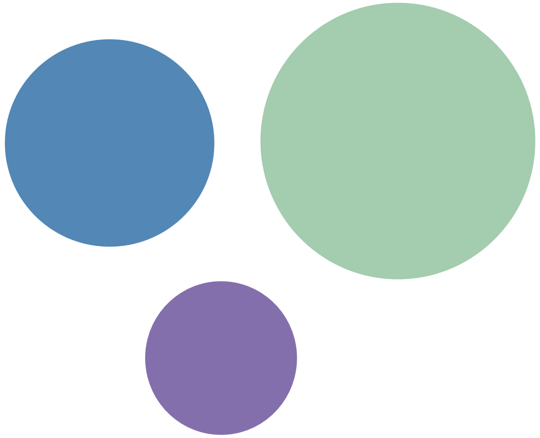

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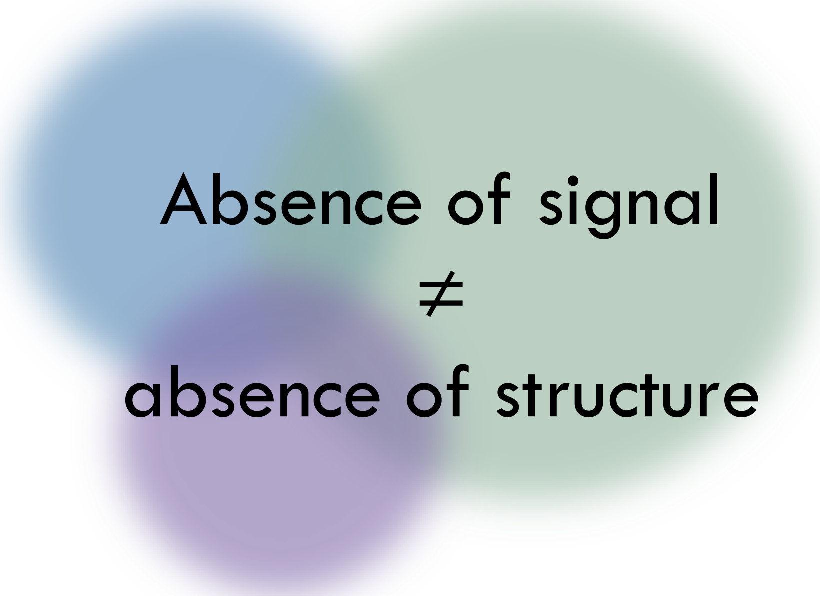

Absence of signal

≠

absence of structure

Traditional markers often show “no structure”

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# Genomes are big!

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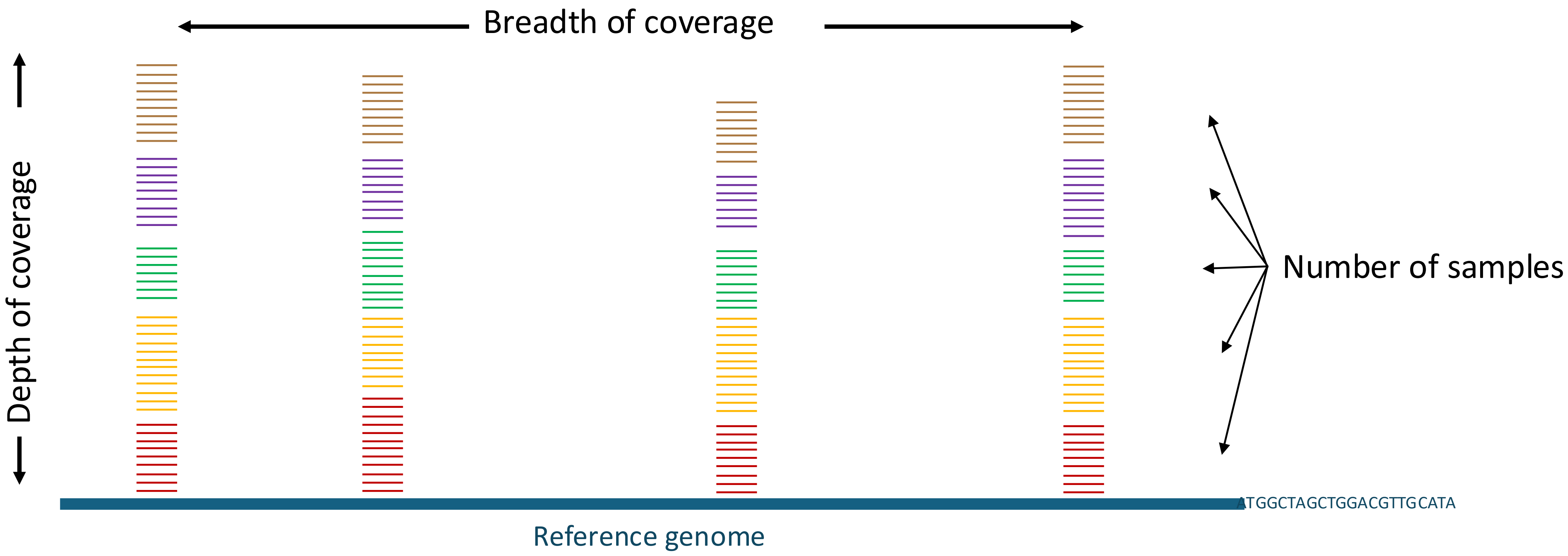
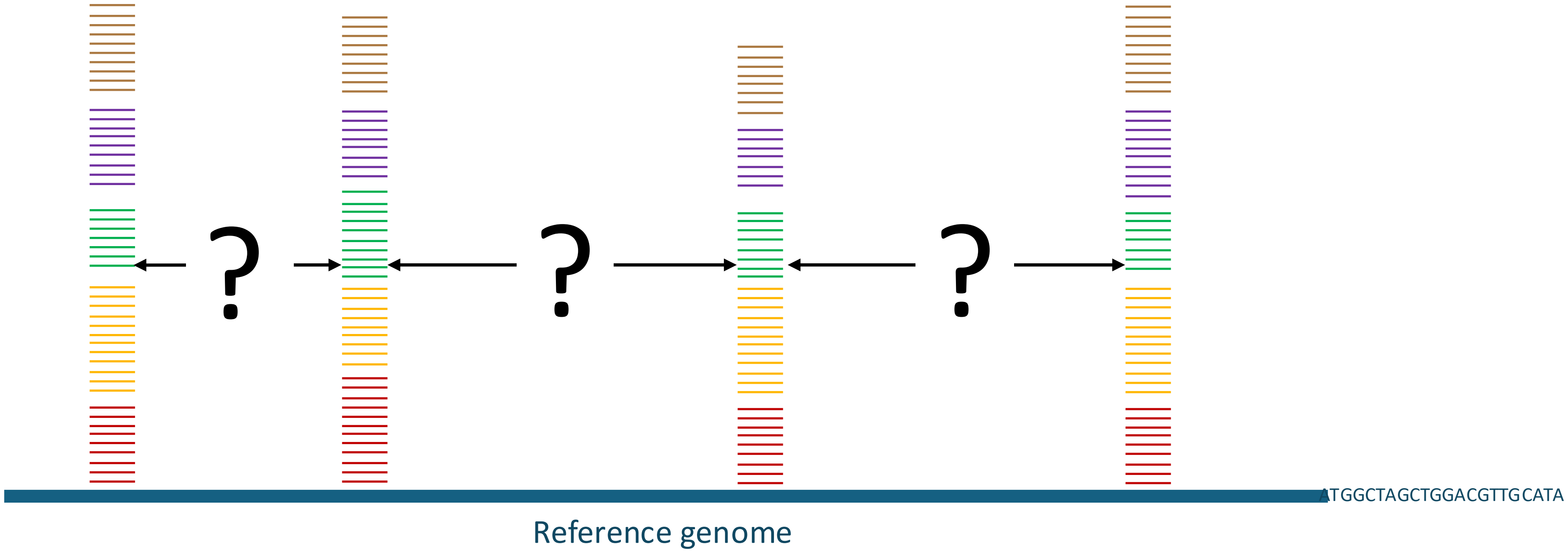
# RAD-seq approach or SNP chips



Adapted from https://sites.google.com/site/wiki4metagenomics/pdf/definition/coverage-read-depth

# RAD-seq approach or SNP chip

## What are we missing?



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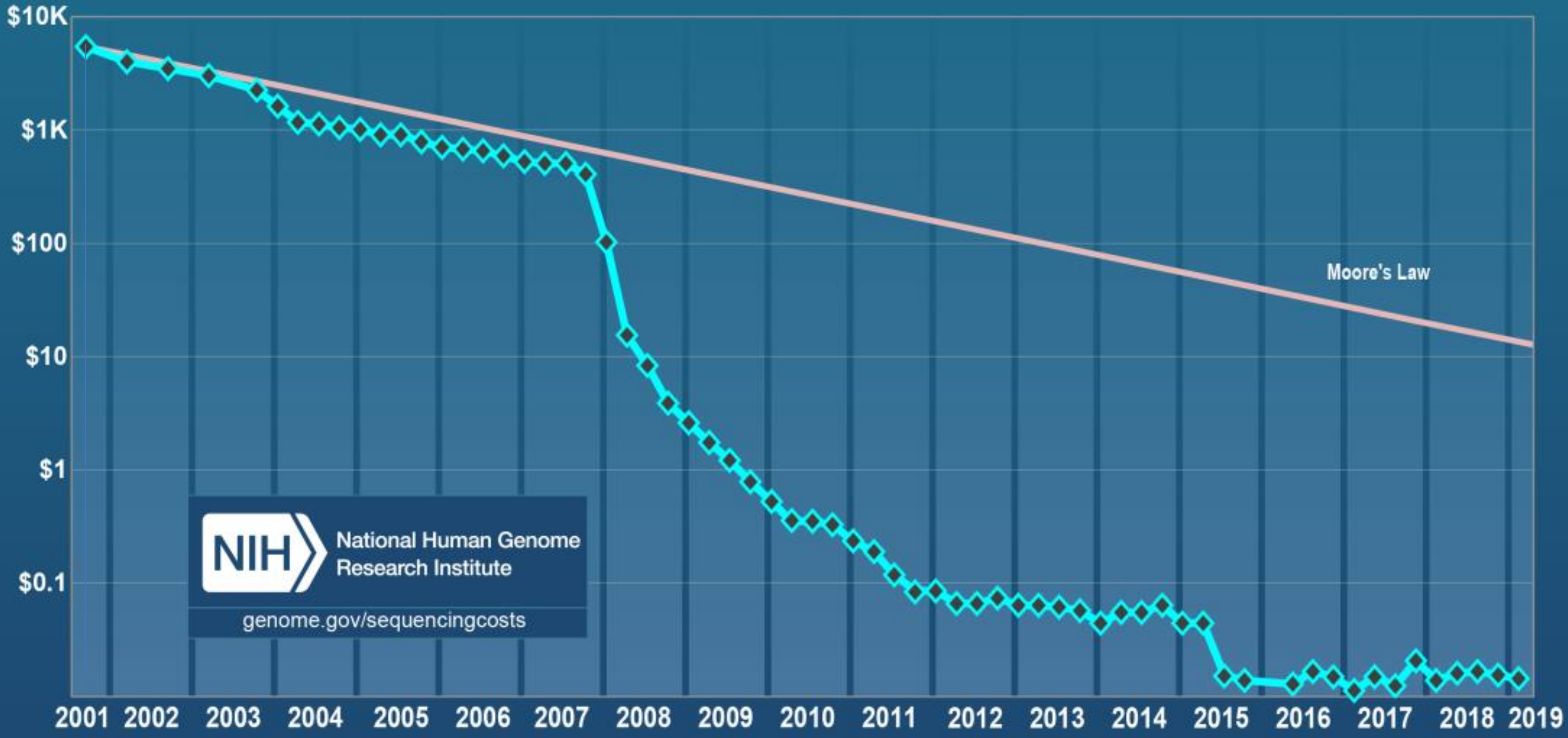
# Cost per Raw Megabase of DNA Sequence



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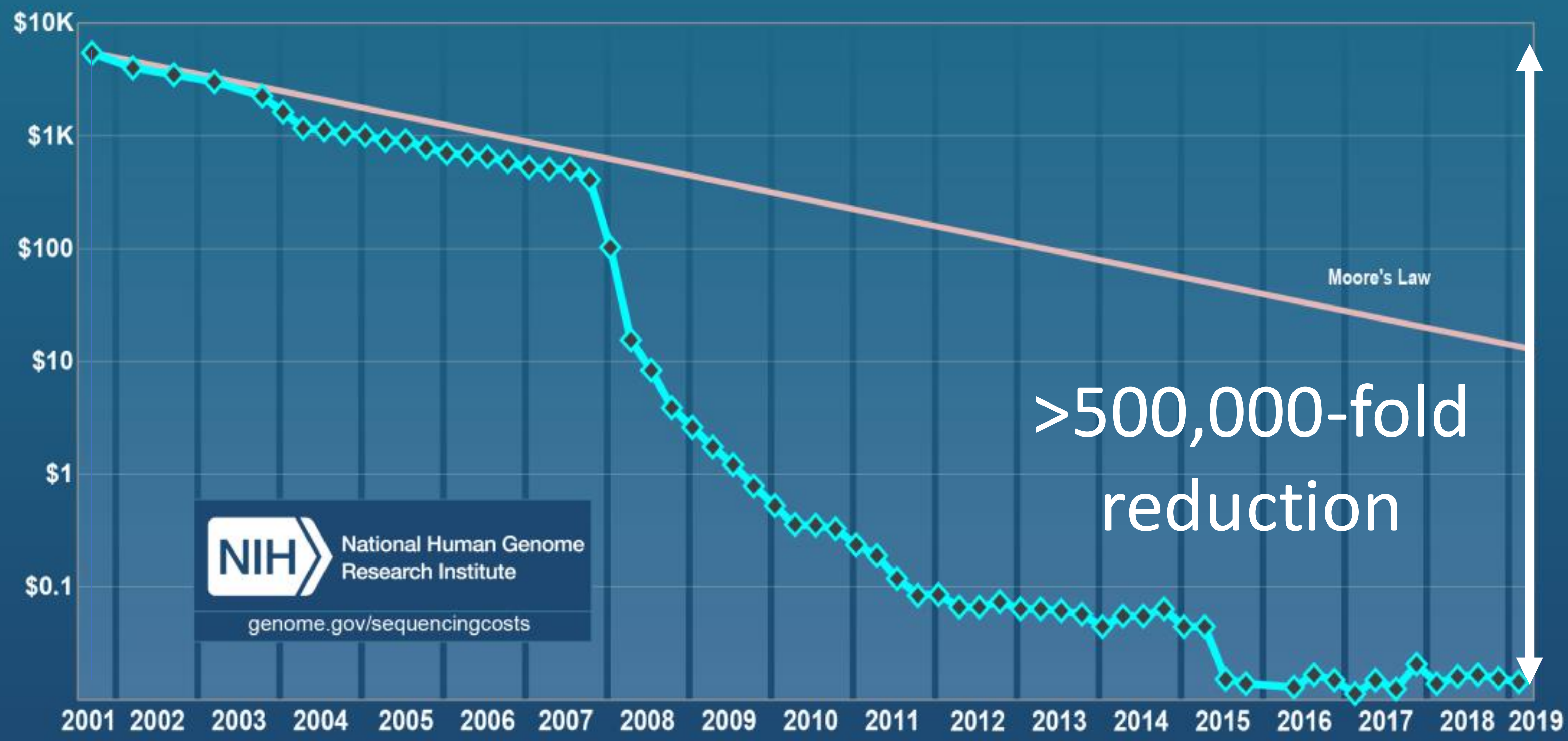
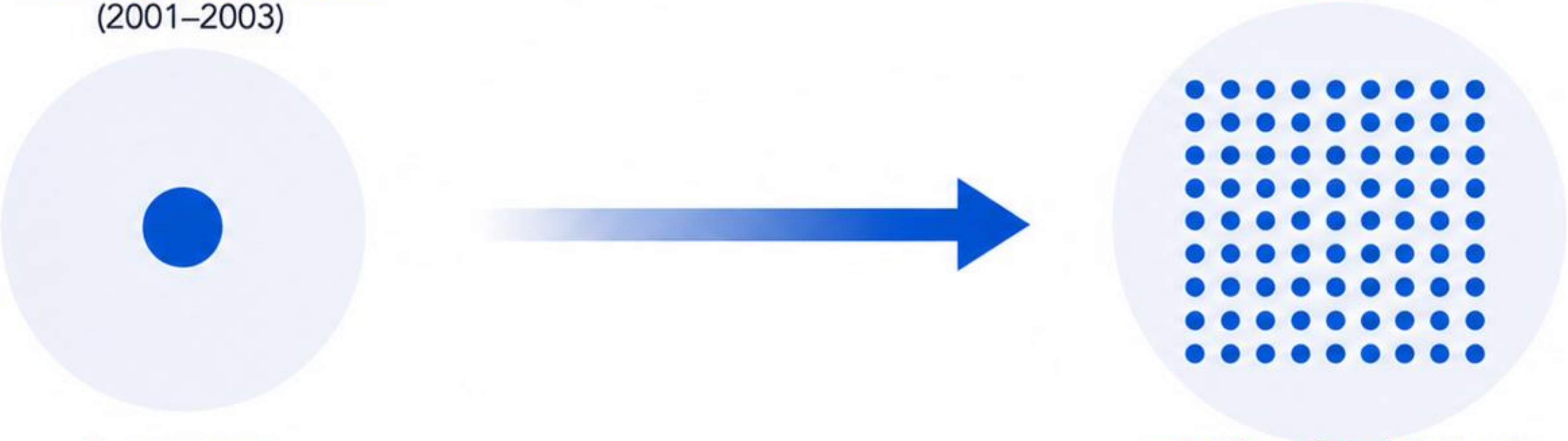


>500,000-fold reduction

# From one genome to thousands

ORDERS-OF-MAGNITUDE SHIFT IN SCALE



| THEN | NOW |
|---|---|
| Human Genome Project<br>(2001–2003) | Today |
| **1 genome** | **1000s of individuals** |
| $ ~$3 billion | $ ~$100–$1000 |
| >10 years | Days–weeks |
| Global effort (2,800 researchers) | Routine effort |

# From one genome to thousands

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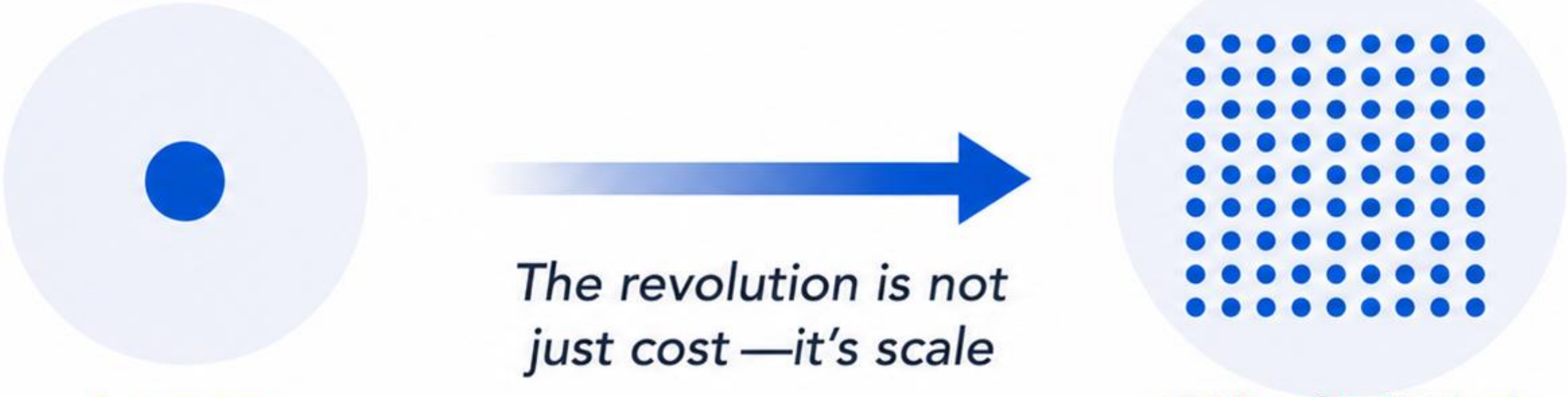

**THEN**

Human Genome Project
(2001–2003)

**1 genome**

- $ ~$3 billion
- >10 years
- Global effort (2,800 researchers)

*The revolution is not just cost —it's scale*

**NOW**

Today

**1000s of individuals**

- $ ~$100–$1000
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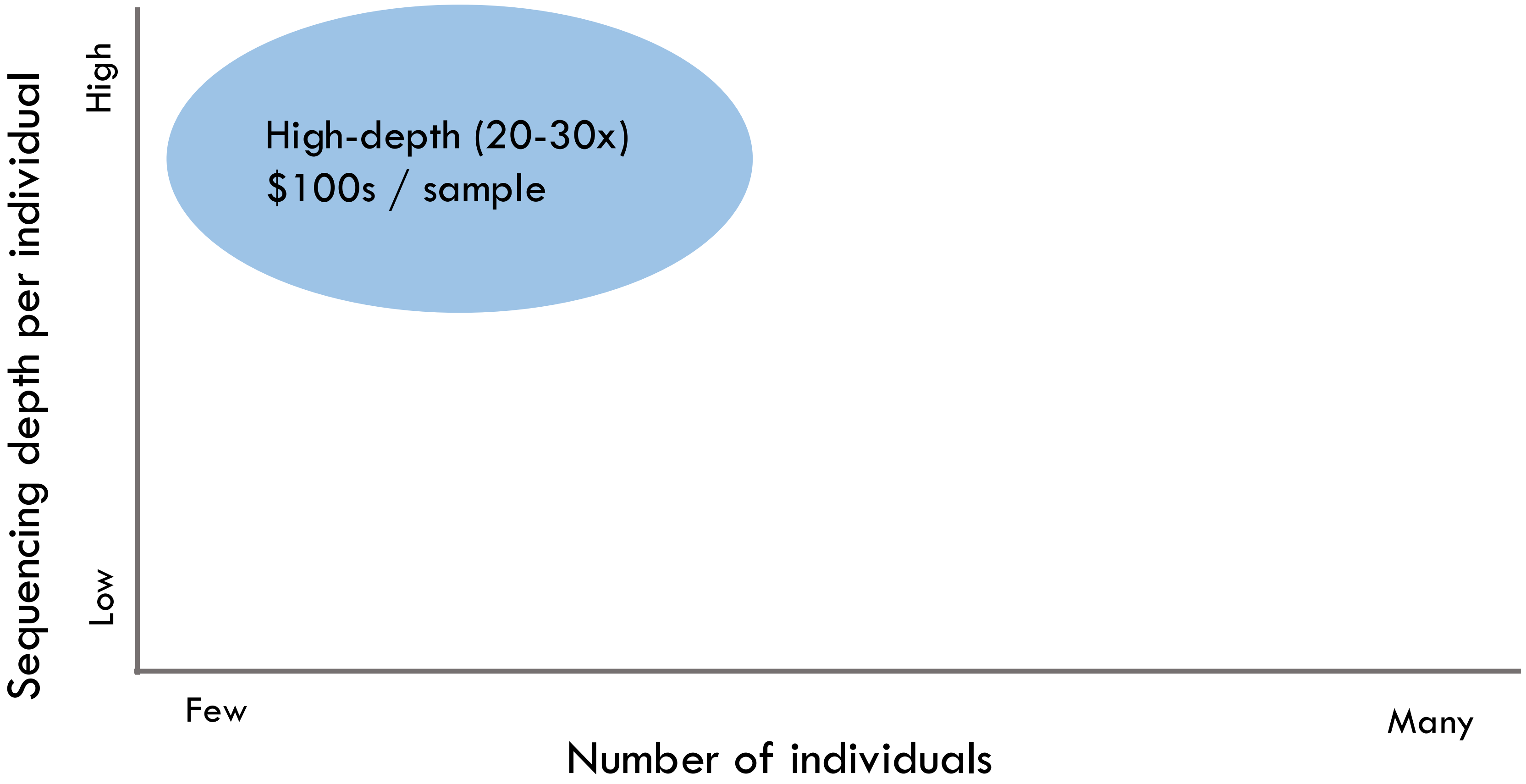
# Sequencing depth vs number of individuals



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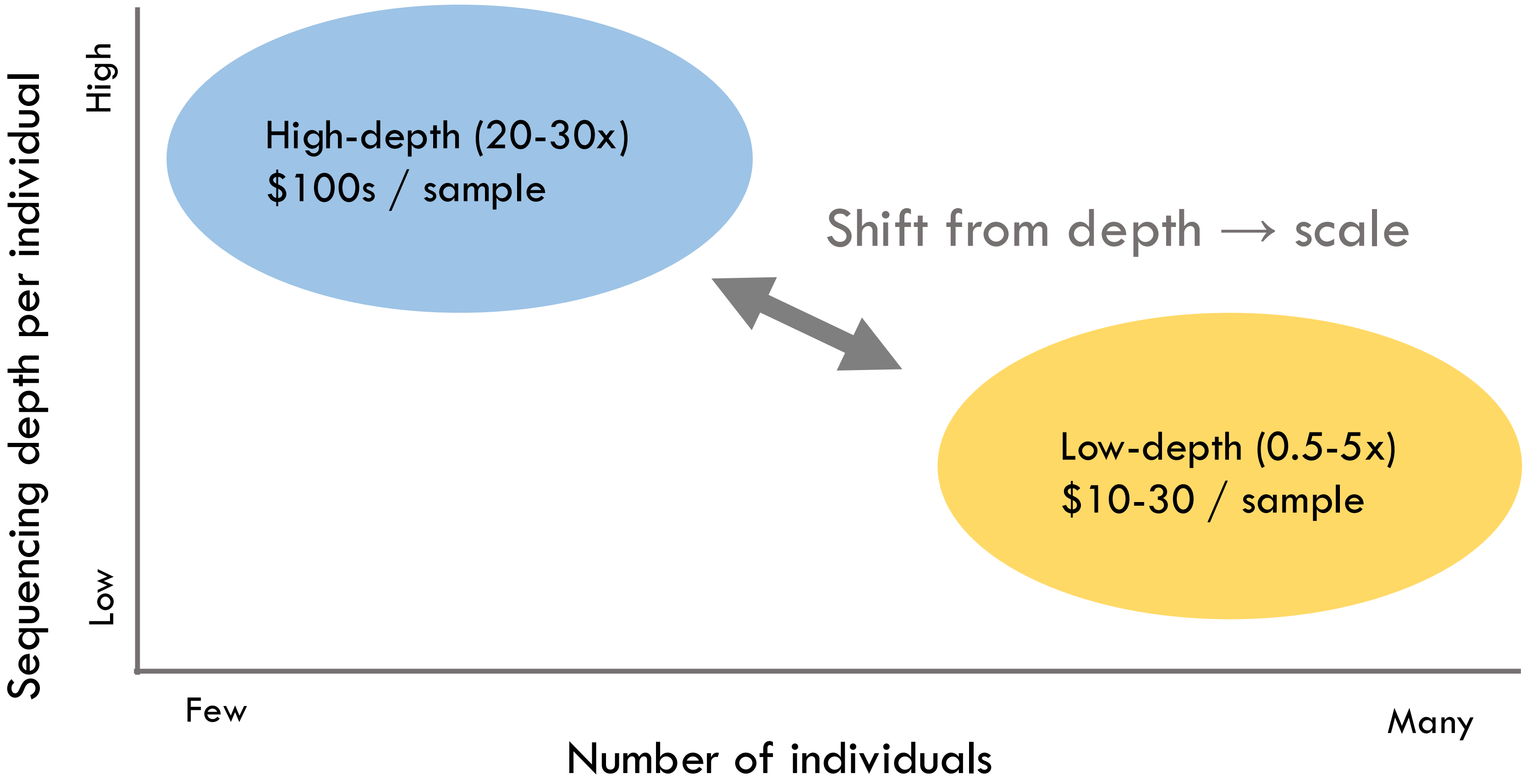
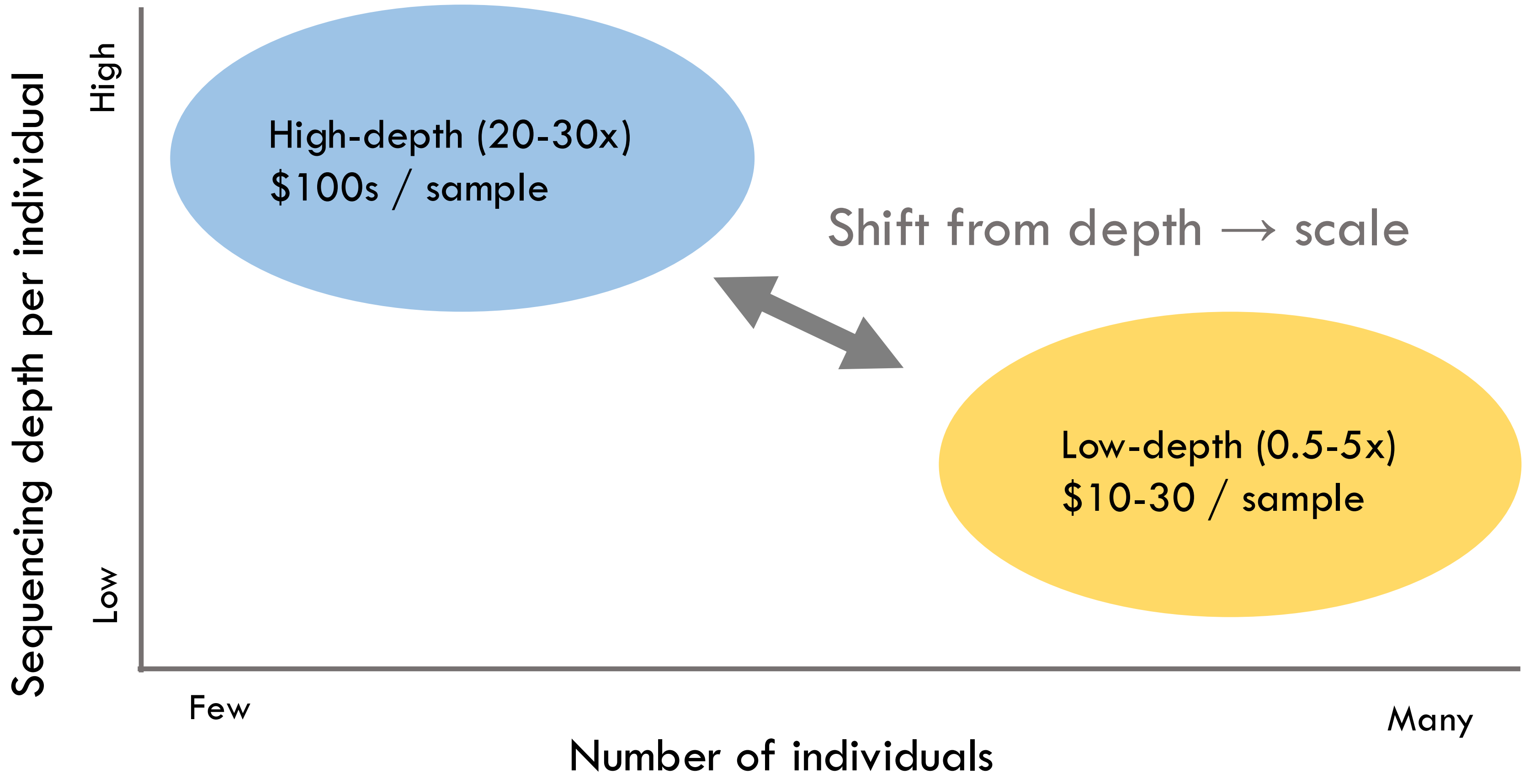


High-depth (20-30x)
$100s / sample

Shift from depth → scale

Low-depth (0.5-5x)
$10-30 / sample

# Sequencing depth vs number of individuals



Sequencing depth per individual

High

Low

High-depth (20-30x)
$100s / sample

Shift from depth → scale

Low-depth (0.5-5x)
$10-30 / sample

Few

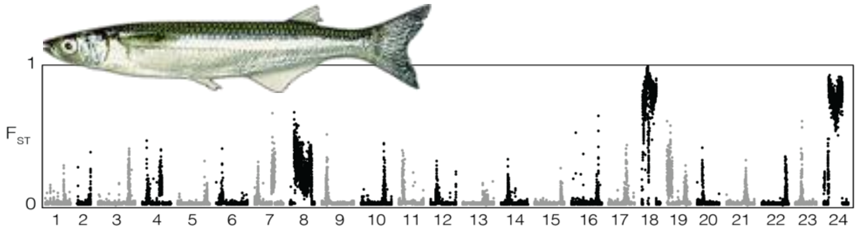
Many

Number of individuals

Power comes from sampling more individuals
- not sequencing each one more deeply

# Structure can be hidden in different ways

Strong adaptation despite homogeneous genomes



Atlantic silversides

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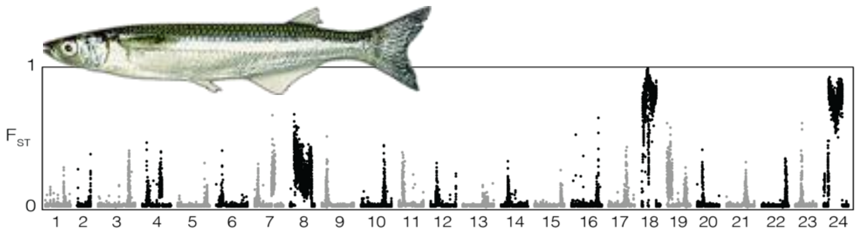
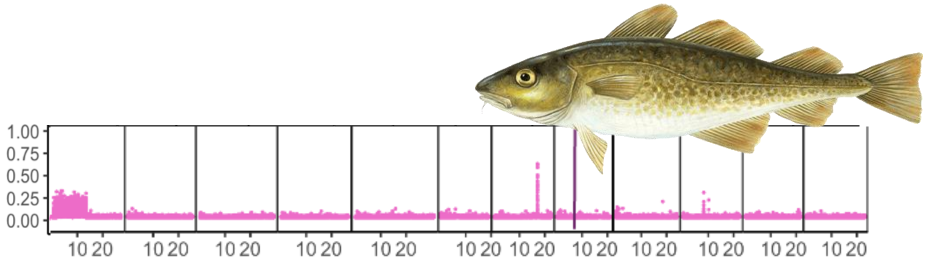


Atlantic silversides

Differences confined to small genomic regions



Atlantic cod

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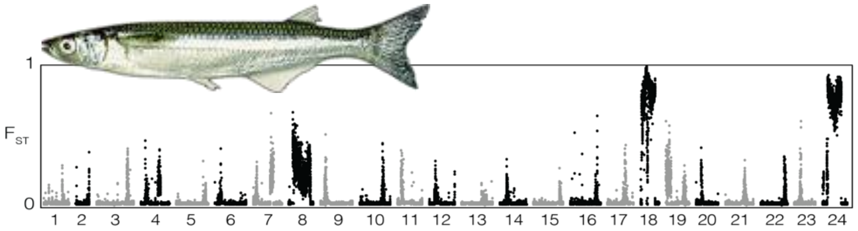
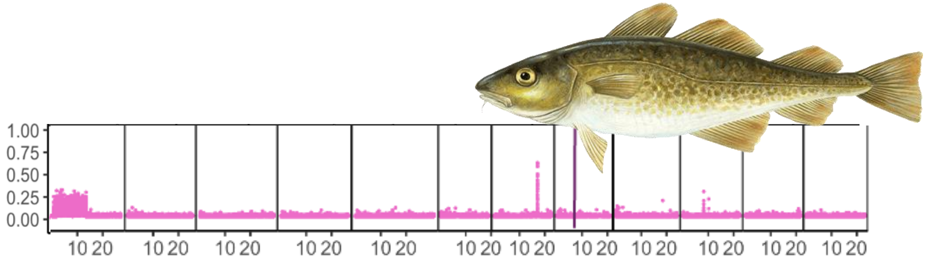
## Strong adaptation despite homogeneous genomes



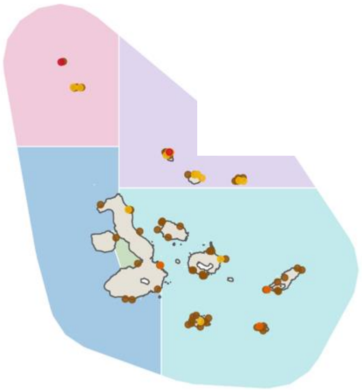
Atlantic silversides

## Differences confined to small genomic regions



Atlantic cod

## Cryptic mixing of distinct lineages



Brown sea cucumber

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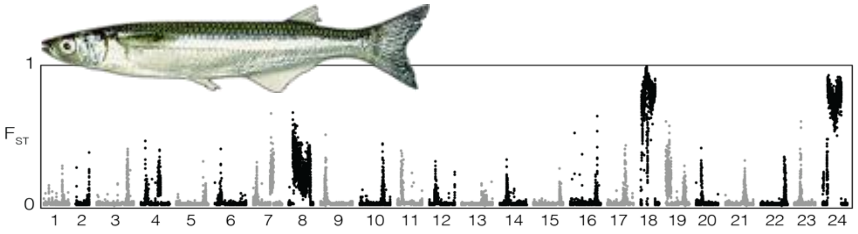

Atlantic silversides

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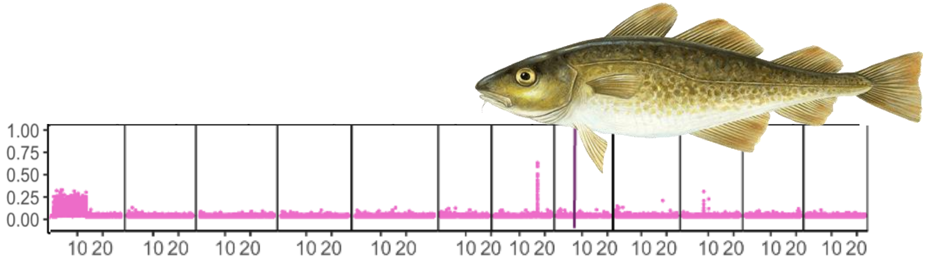

Atlantic cod

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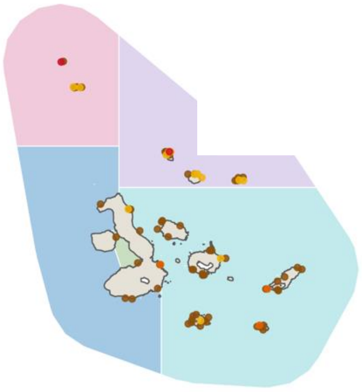
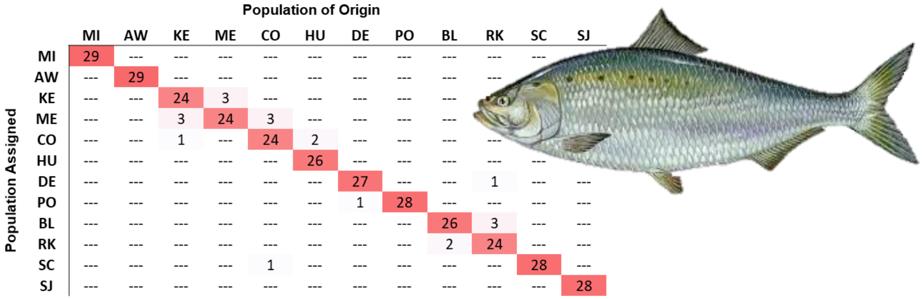


Brown sea cucumber

## Tracking who mixes with whom—and when



Population of Origin

| Population Assigned | MI | AW | KE | ME | CO | HU | DE | PO | BL | RK | SC | SJ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MI | 29 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | |
| AW | --- | 29 | --- | --- | --- | --- | --- | --- | --- | --- | | |
| KE | --- | --- | 24 | 3 | --- | --- | --- | --- | --- | | | |
| ME | --- | --- | 3 | 24 | 3 | --- | --- | --- | --- | | | |
| CO | --- | --- | 1 | --- | 24 | 2 | --- | --- | --- | --- | | |
| HU | --- | --- | --- | --- | --- | 26 | --- | --- | --- | --- | --- | |
| DE | --- | --- | --- | --- | --- | --- | 27 | --- | --- | 1 | --- | --- |
| PO | --- | --- | --- | --- | --- | --- | 1 | 28 | --- | --- | --- | --- |
| BL | --- | --- | --- | --- | --- | --- | --- | --- | 26 | 3 | --- | --- |
| RK | --- | --- | --- | --- | --- | --- | --- | --- | 2 | 24 | --- | --- |
| SC | --- | --- | --- | --- | 1 | --- | --- | --- | --- | --- | 28 | --- |
| SJ | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | 28 |

American shad

# Atlantic silverside *Menidia menidia*

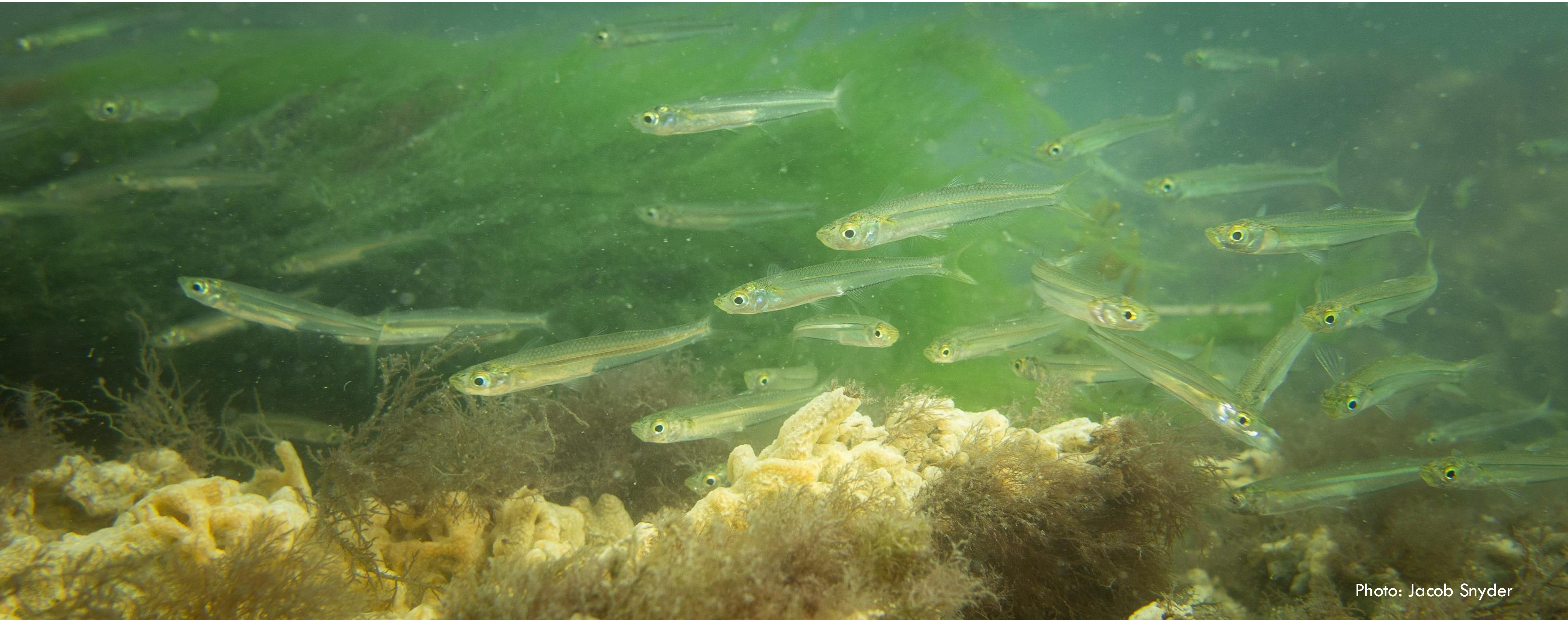
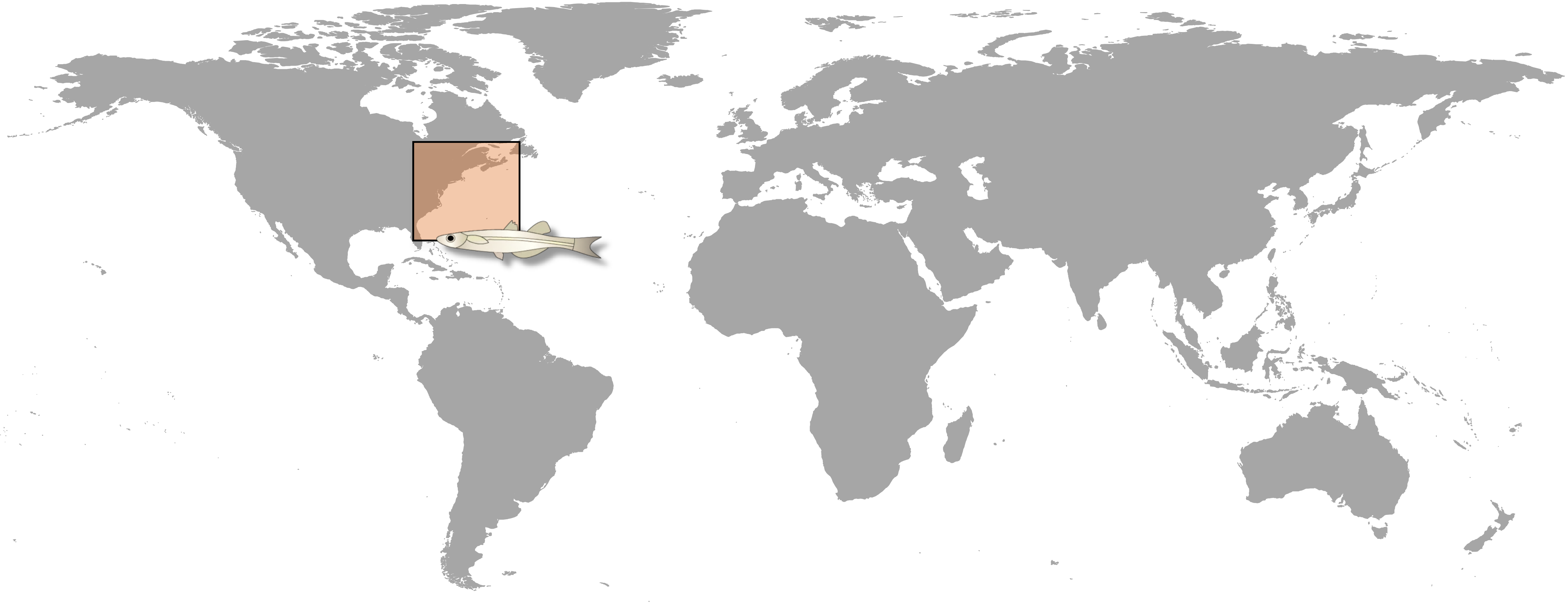
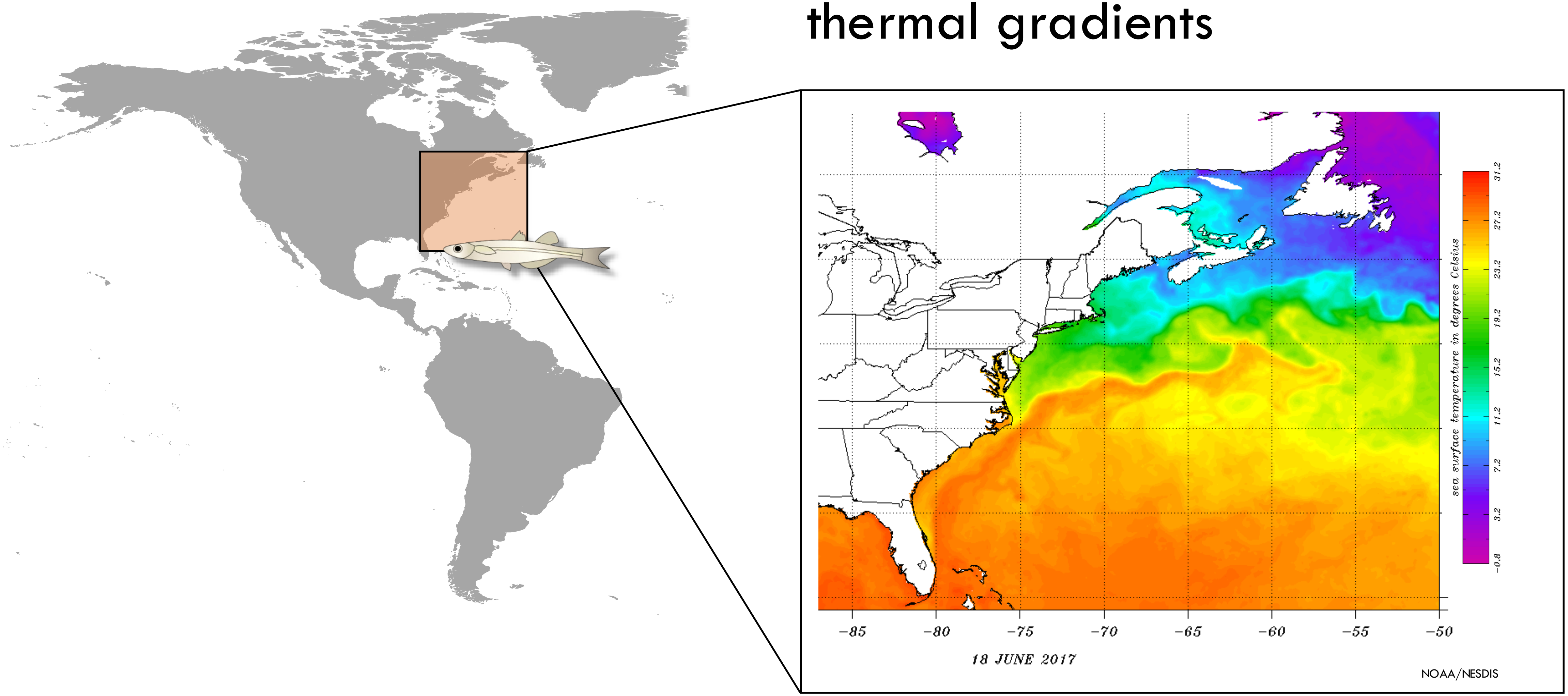


Photo: Jacob Snyder



# One of the world's steepest thermal gradients



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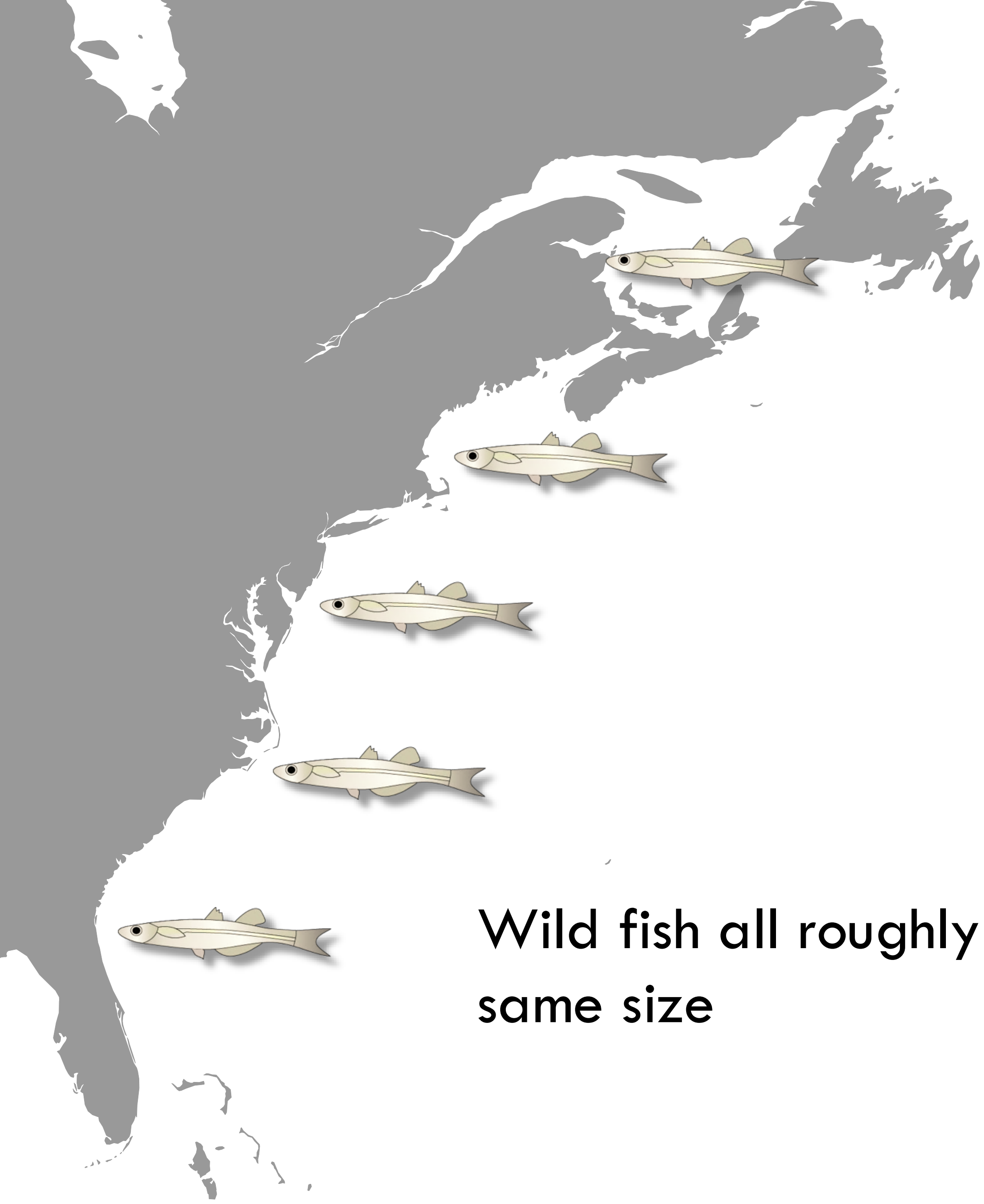
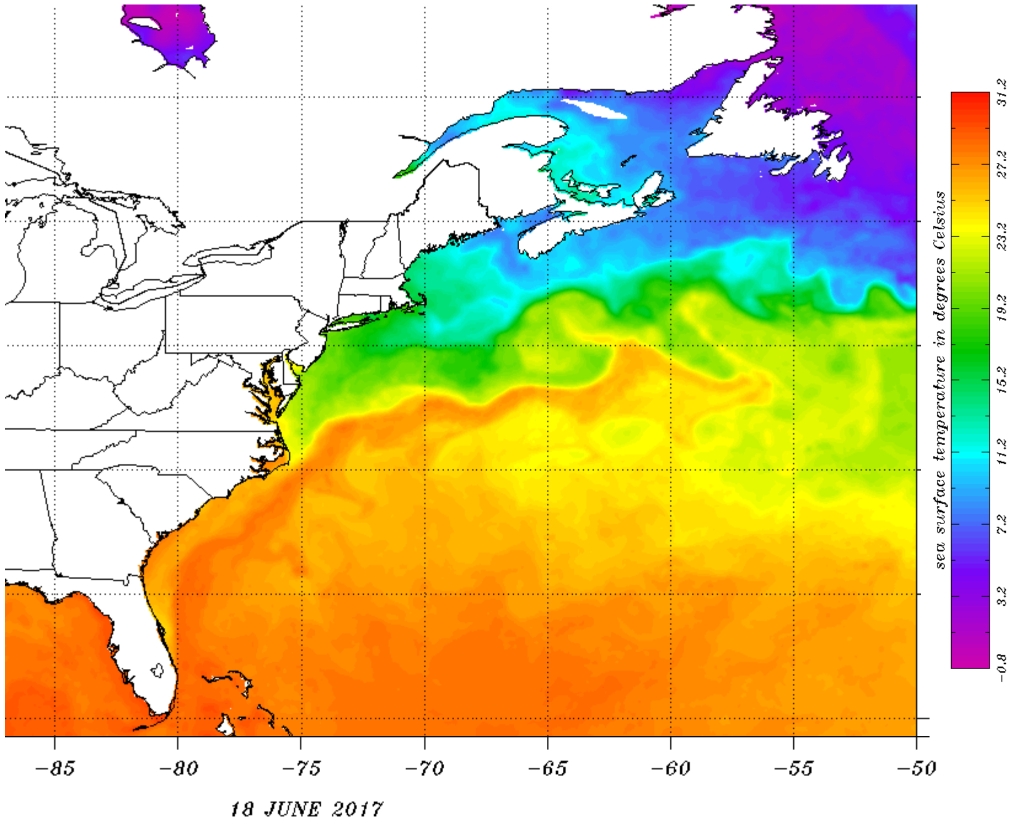
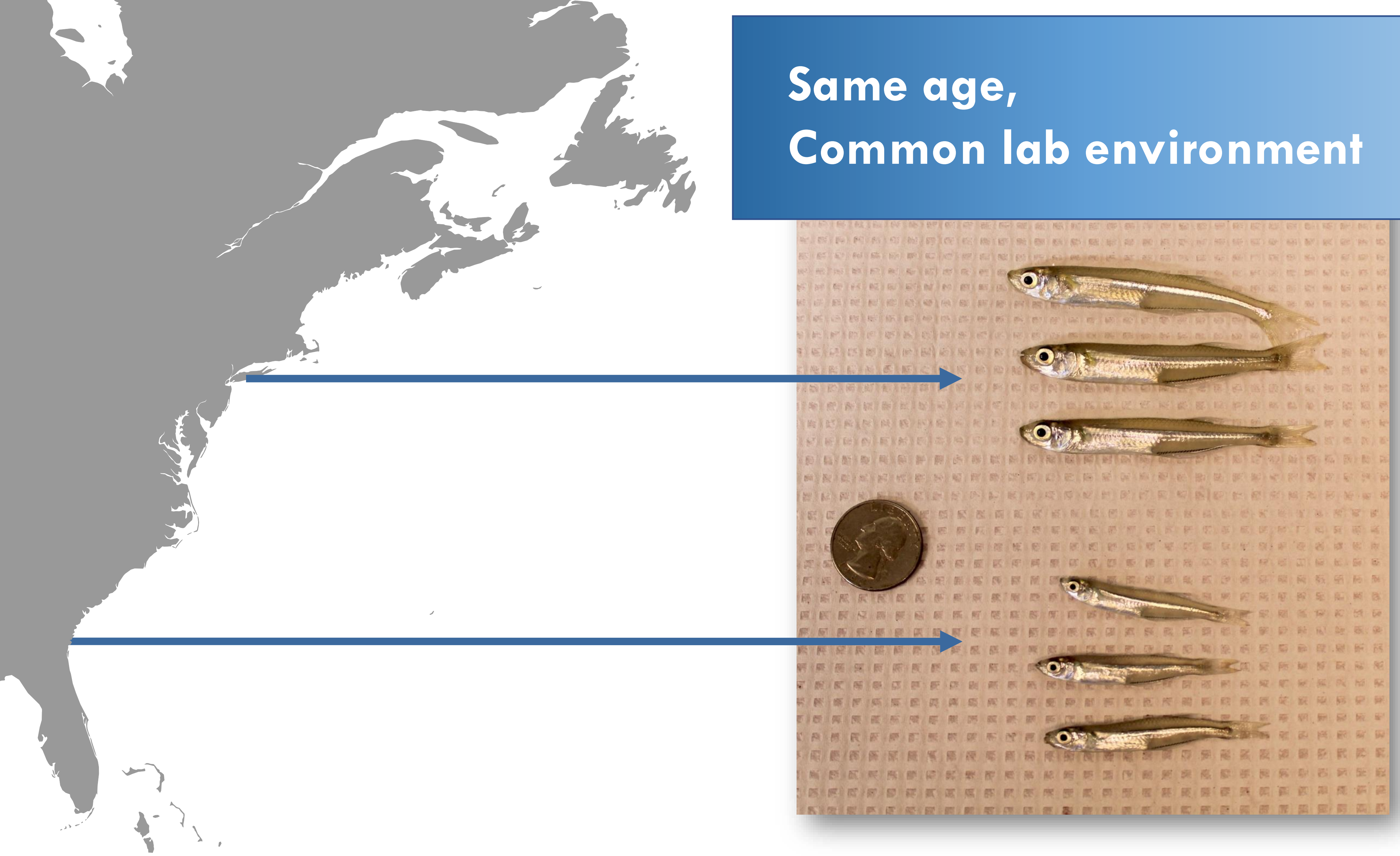


Wild fish all roughly the same size

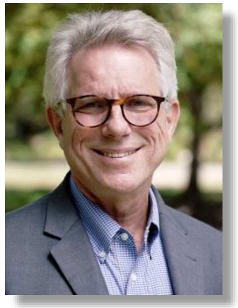


NOAA/NESDIS

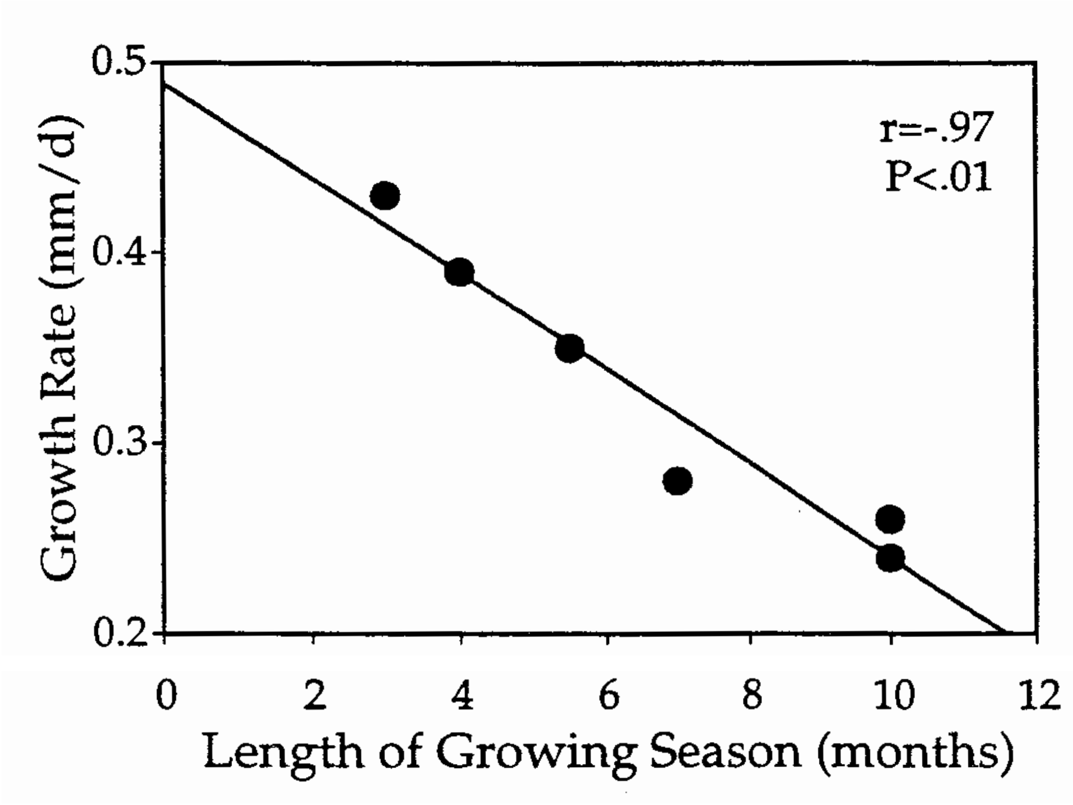
# Same age,
# Common lab environment



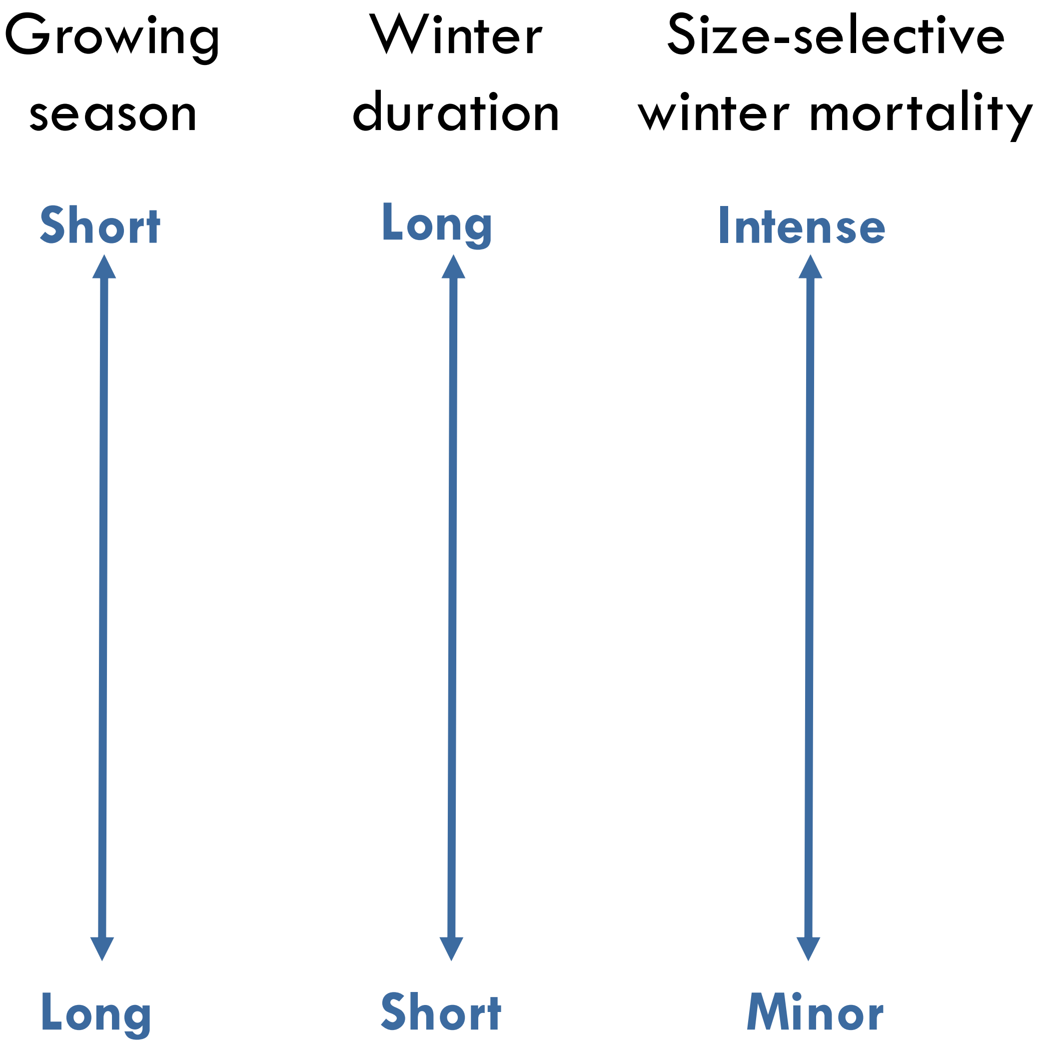
# Growth capacity is tightly correlated with latitude



David Conover et al.



Reproduced from Conover. 1998. Bull. Mar. Sci.



Growing season

**Short**

**Long**

Winter duration

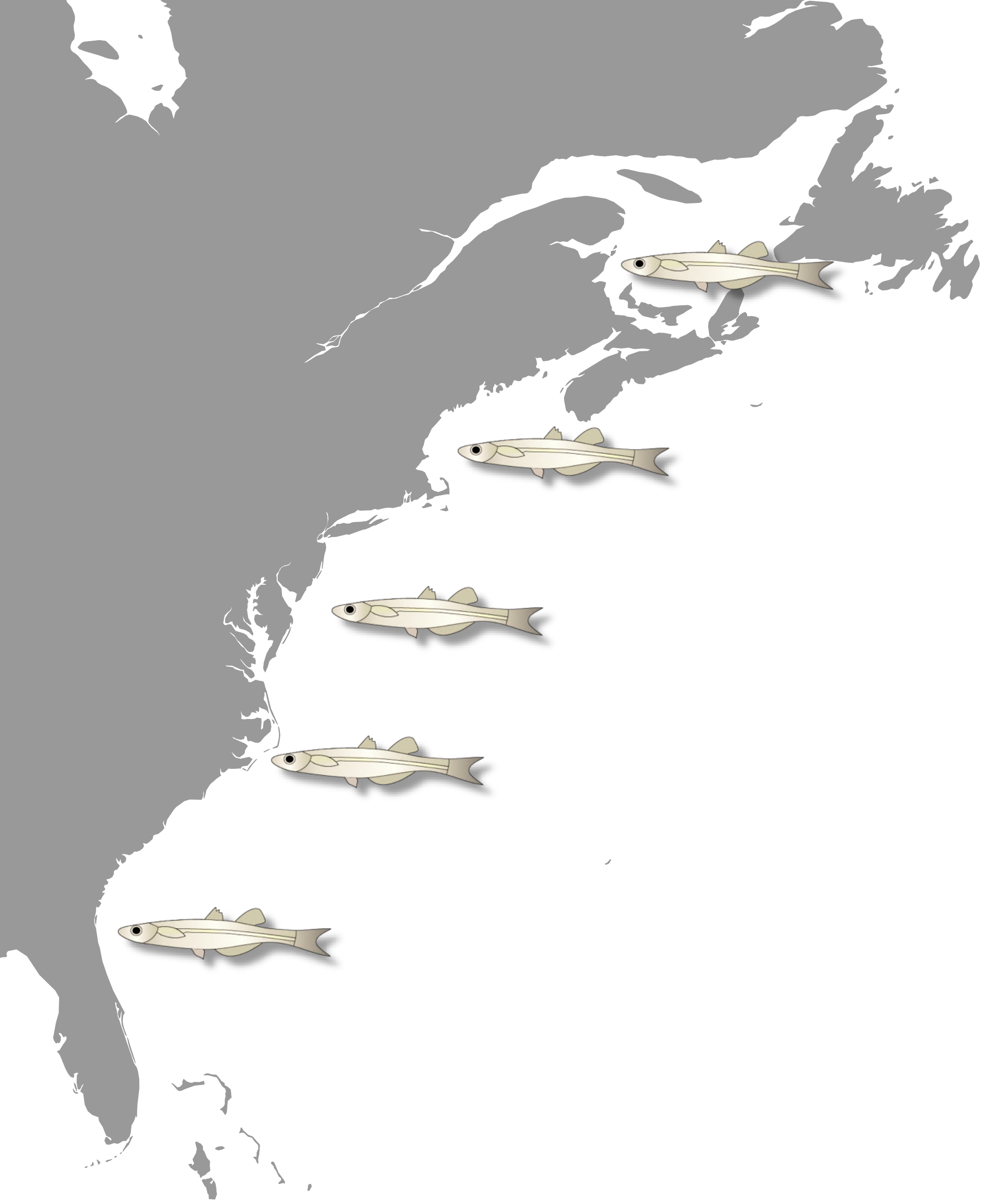
**Long**

**Short**

Size-selective winter mortality

**Intense**

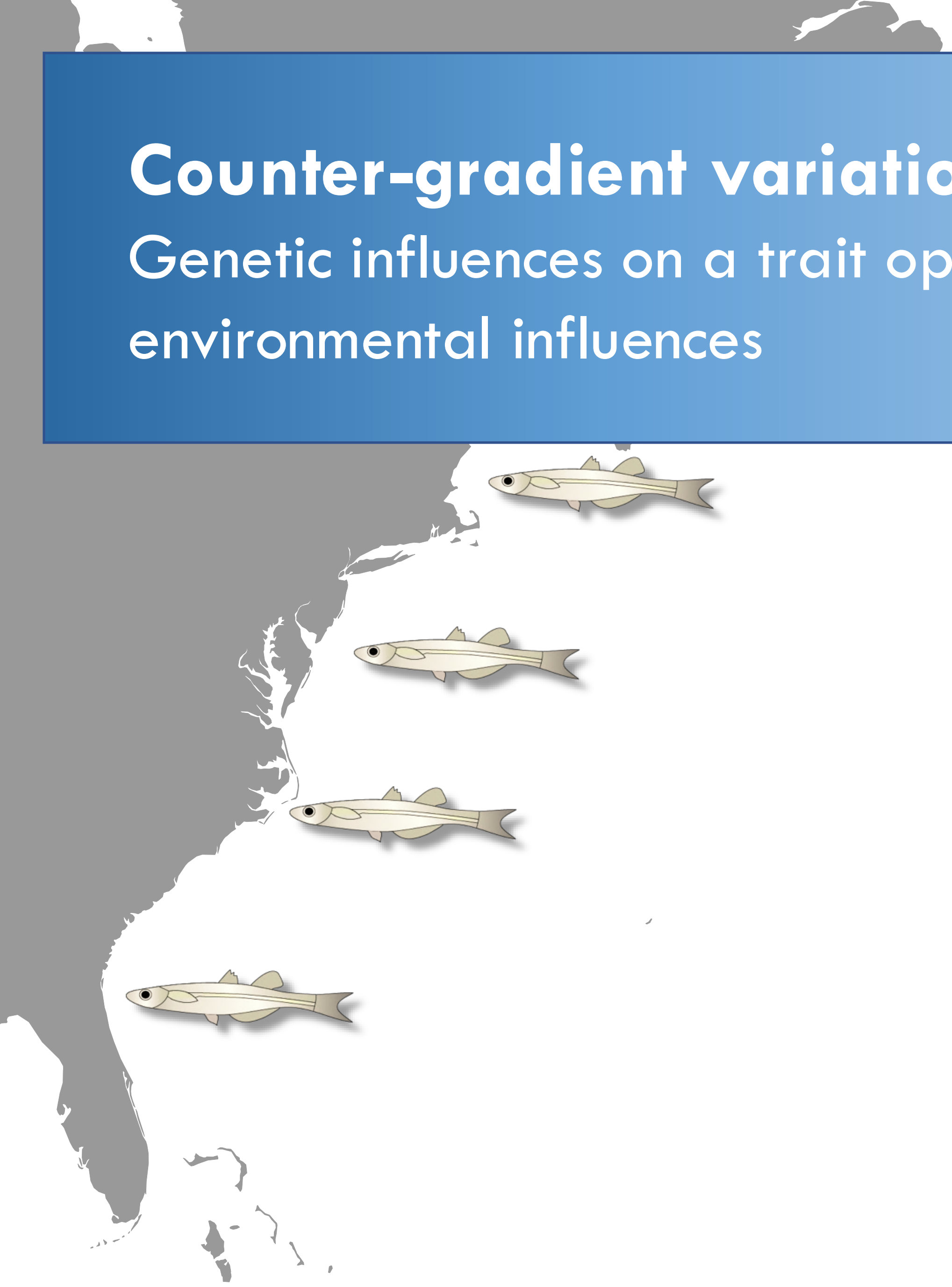
**Minor**



| Growing season | Winter duration | Size-selective winter mortality |
|---|---|---|
| **Short** | **Long** | **Intense** |
| **Long** | **Short** | **Minor** |

# Counter-gradient variation:

Genetic influences on a trait oppose environmental influences



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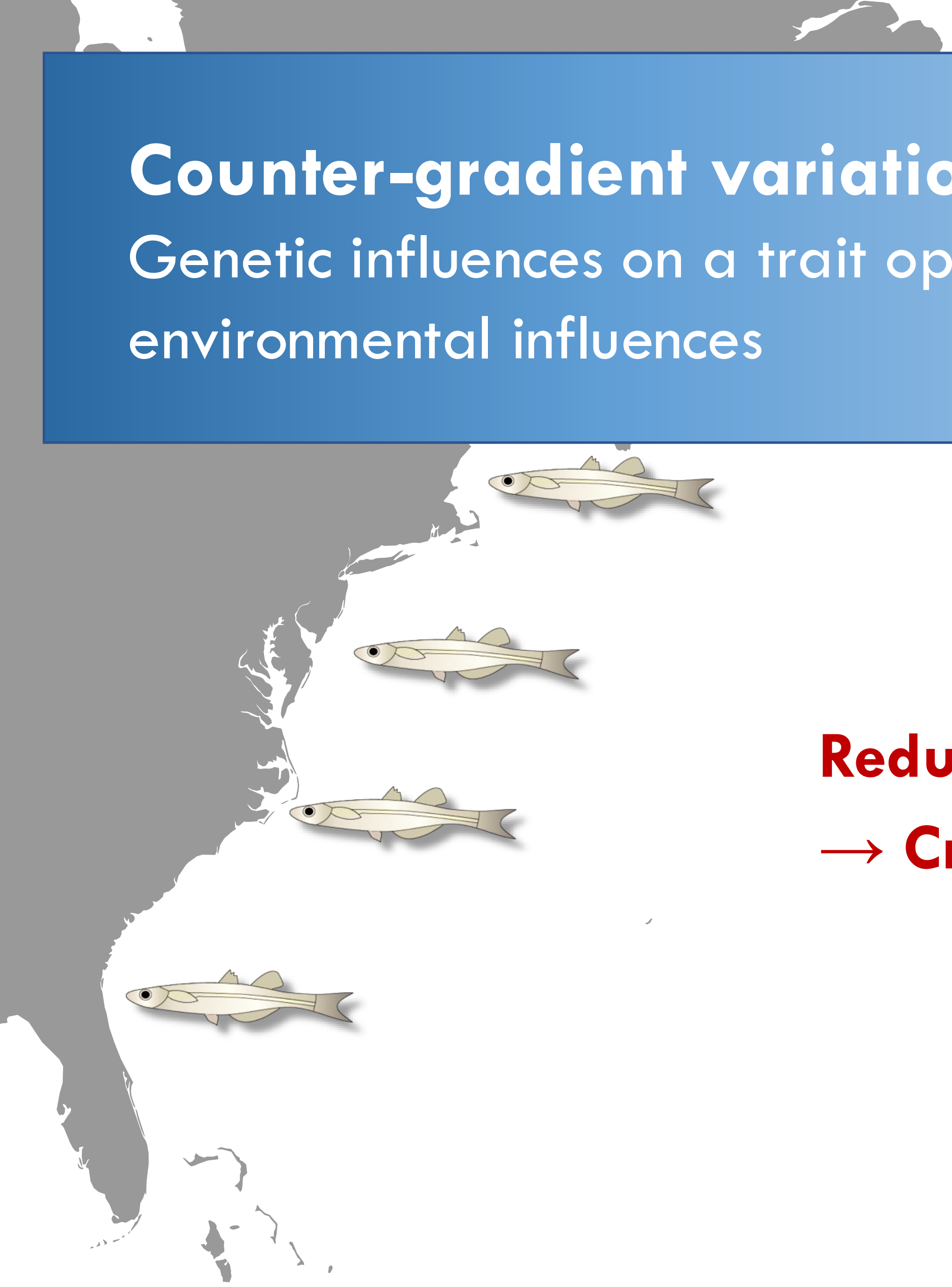


**Reduced phenotypic variation**

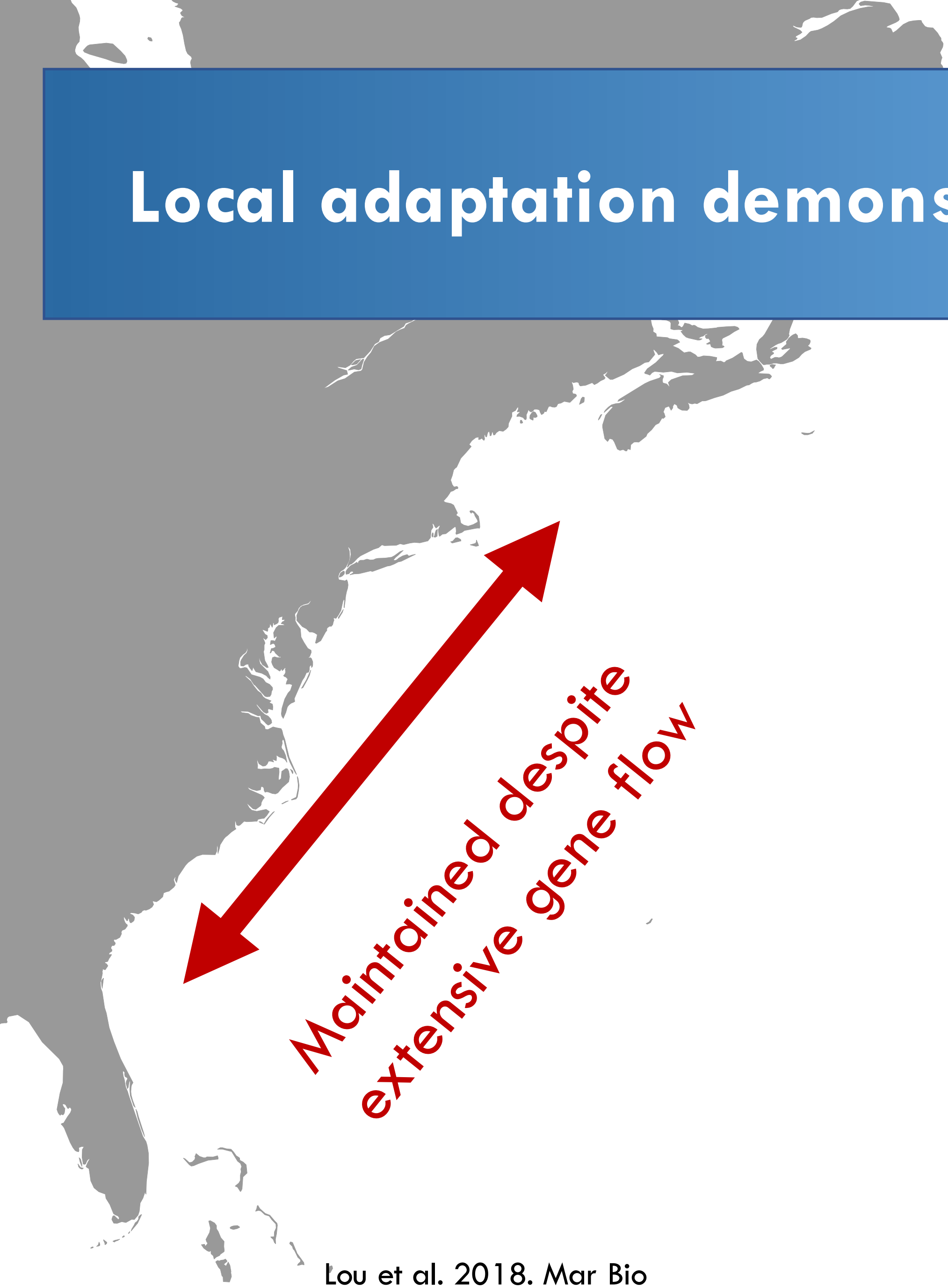
**→ Cryptic adaptive divergence**

# Local adaptation demonstrated in multiple correlated traits

**Other traits that vary with latitude:**

- Rates of energy consumption
- Metabolism
- Growth efficiency
- Lipid energy reserves
- Egg production rate
- Egg size and size of offspring at hatch
- Willingness to forage under threat of predation
- Number of vertebrae
- Levels of temperature-dep. sex determination

# Local adaptation demonstrated in multiple correlated traits



Lou et al. 2018. Mar Bio

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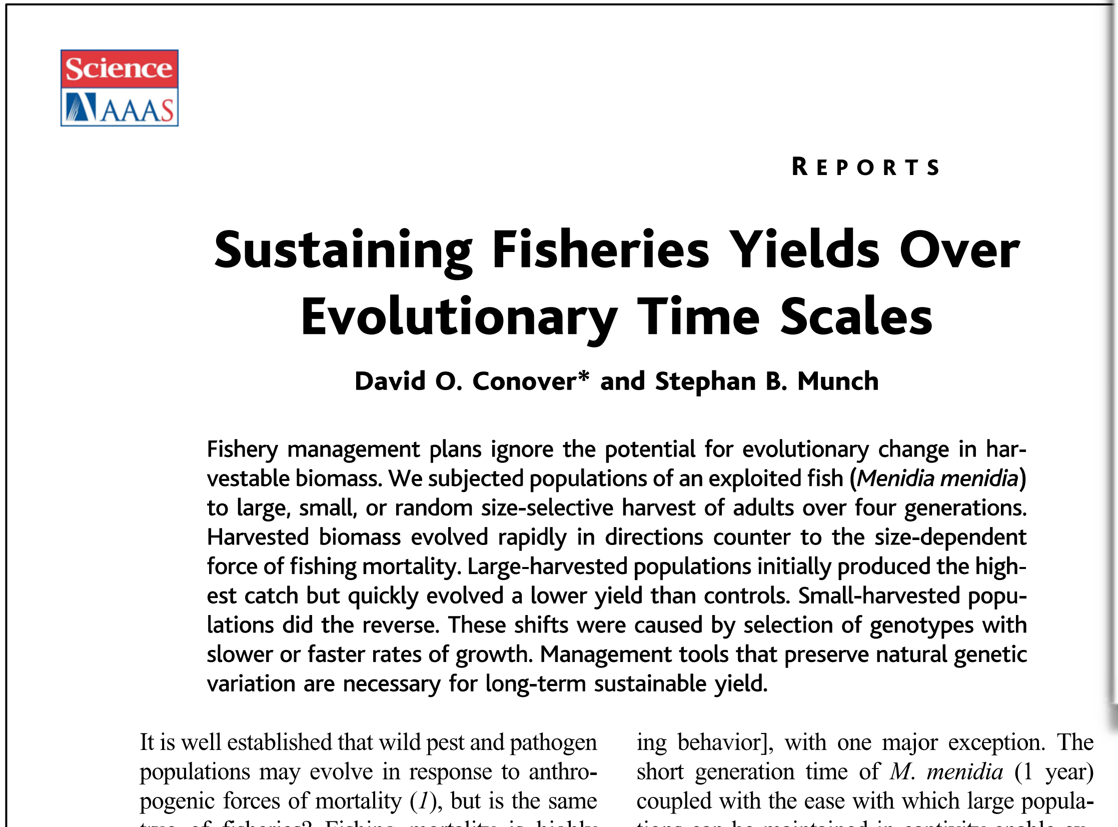
# Capacity for rapid evolution



Science AAAS

REPORTS

## Sustaining Fisheries Yields Over Evolutionary Time Scales

**David O. Conover* and Stephan B. Munch**

Fishery management plans ignore the potential for evolutionary change in harvestable biomass. We subjected populations of an exploited fish (*Menidia menidia*) to large, small, or random size-selective harvest of adults over four generations. Harvested biomass evolved rapidly in directions counter to the size-dependent force of fishing mortality. Large-harvested populations initially produced the highest catch but quickly evolved a lower yield than controls. Small-harvested populations did the reverse. These shifts were caused by selection of genotypes with slower or faster rates of growth. Management tools that preserve natural genetic variation are necessary for long-term sustainable yield.

It is well established that wild pest and pathogen populations may evolve in response to anthropogenic forces of mortality (*1*), but is the same

ing behavior], with one major exception. The short generation time of *M. menidia* (1 year) coupled with the ease with which large popula-

initially produced the highest total yield and mean weight of fish but then declined. Small-harvested populations started with low yield and then increased. By the fourth generation of

# Questions

- What is the genomic basis for the adaptive cline?

# Questions

- What is the genomic basis for the adaptive cline?
- Does the underlying genomic architecture help maintain local adaptation in spite of gene flow?

**Maria Akopyan**
UC Riverside

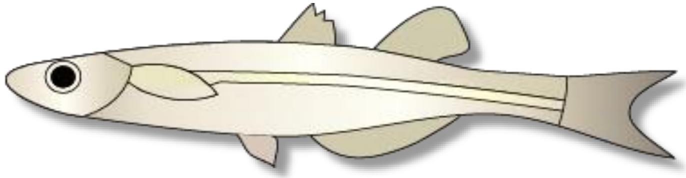
**Arne Jacobs**
U. Glasgow

**Aryn Wilder**
San Diego Zoo

**Anna Tigano**
DFO Canada

**Hannes Baumann**
U. Conn

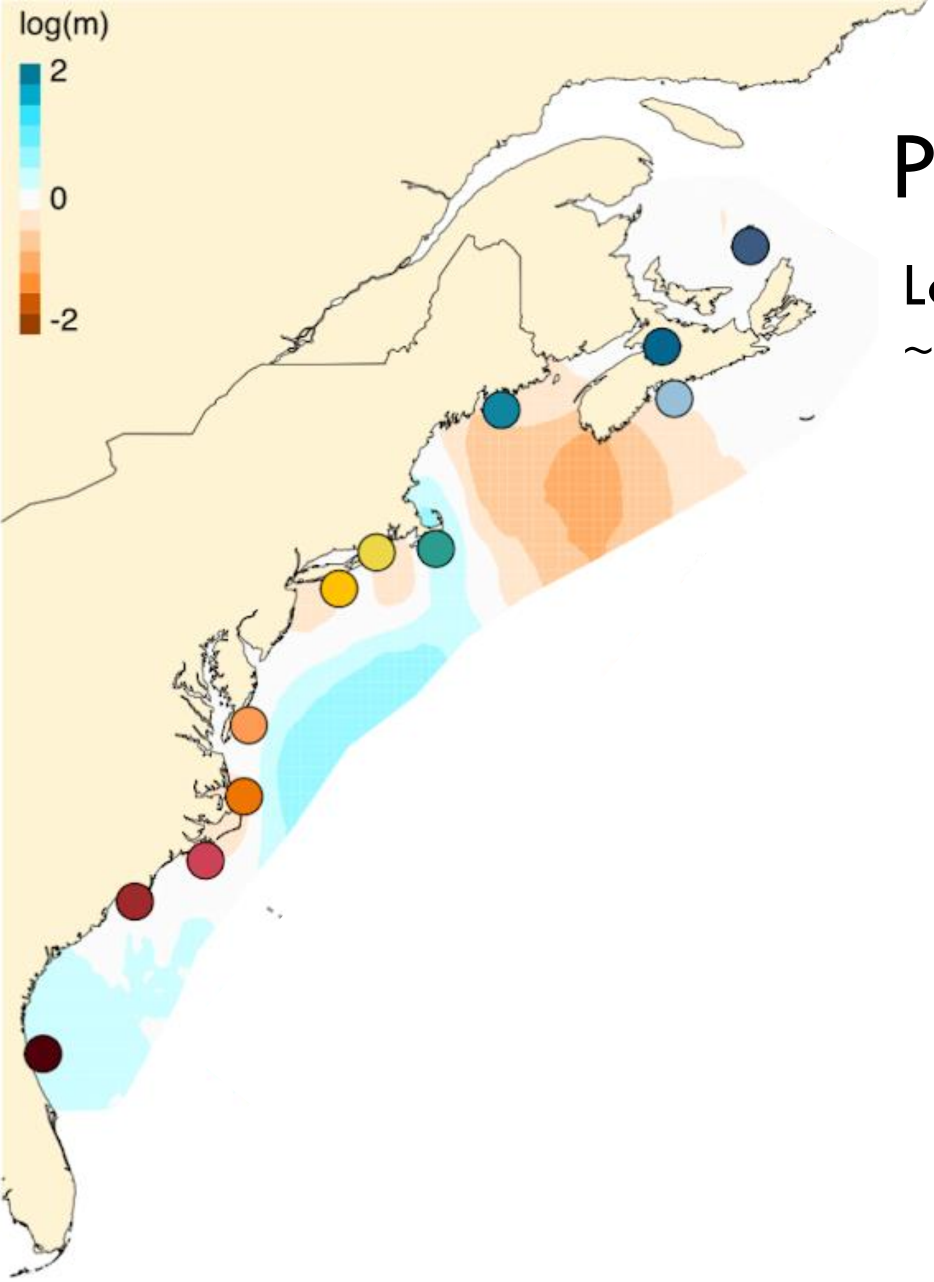
# Team silverside



# Population structure across latitudes

Low-coverage whole genome sequencing (lcWGS)

~1.3x for 50 individuals per population



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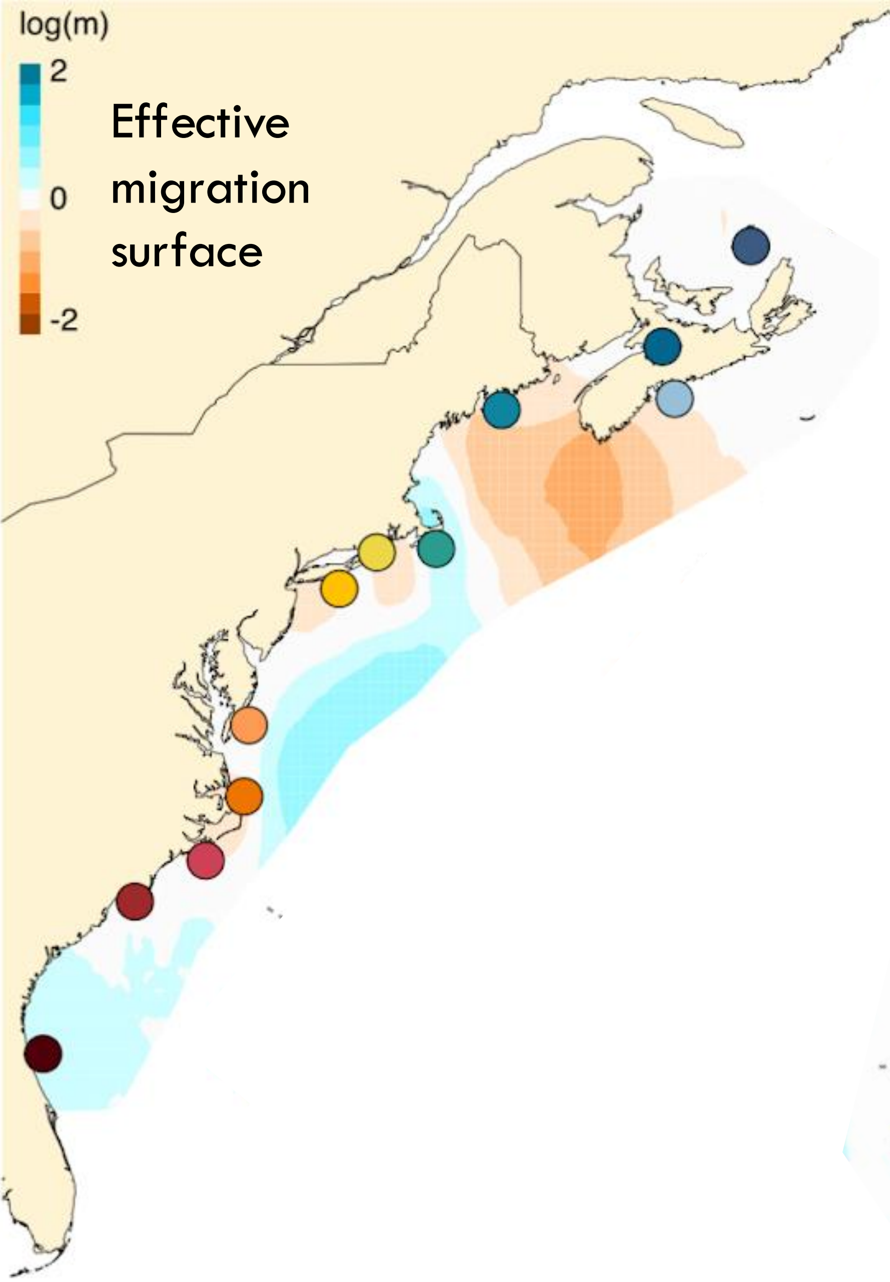
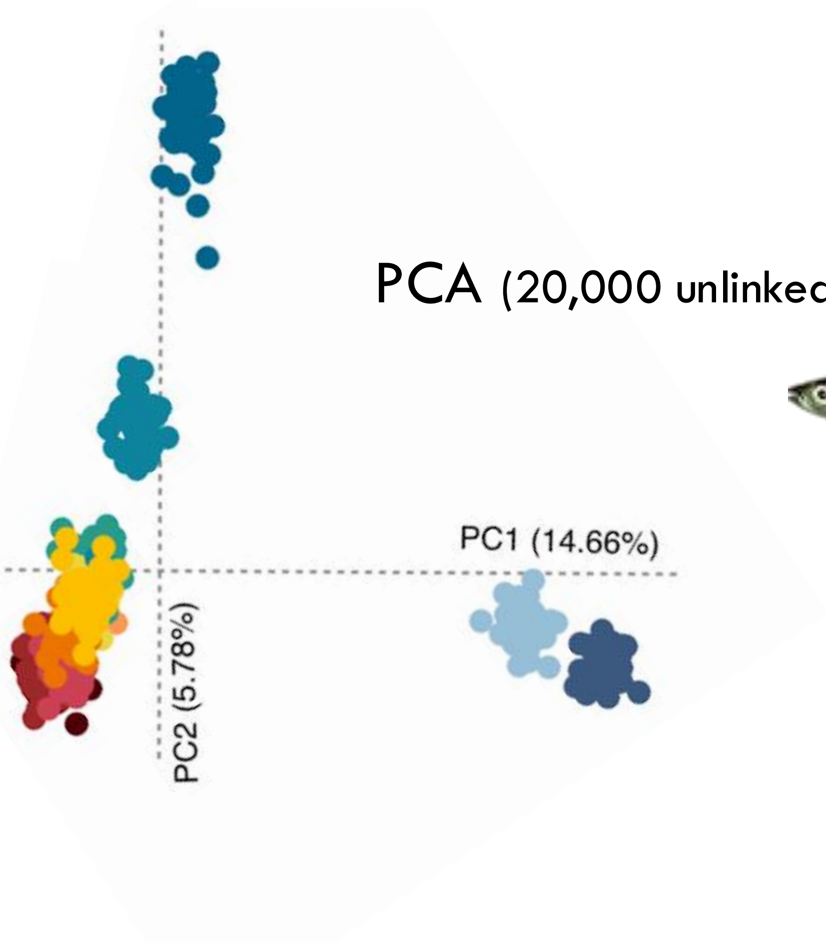


PCA (20,000 unlinked SNPs)



Akopyan et al. 2026. Science

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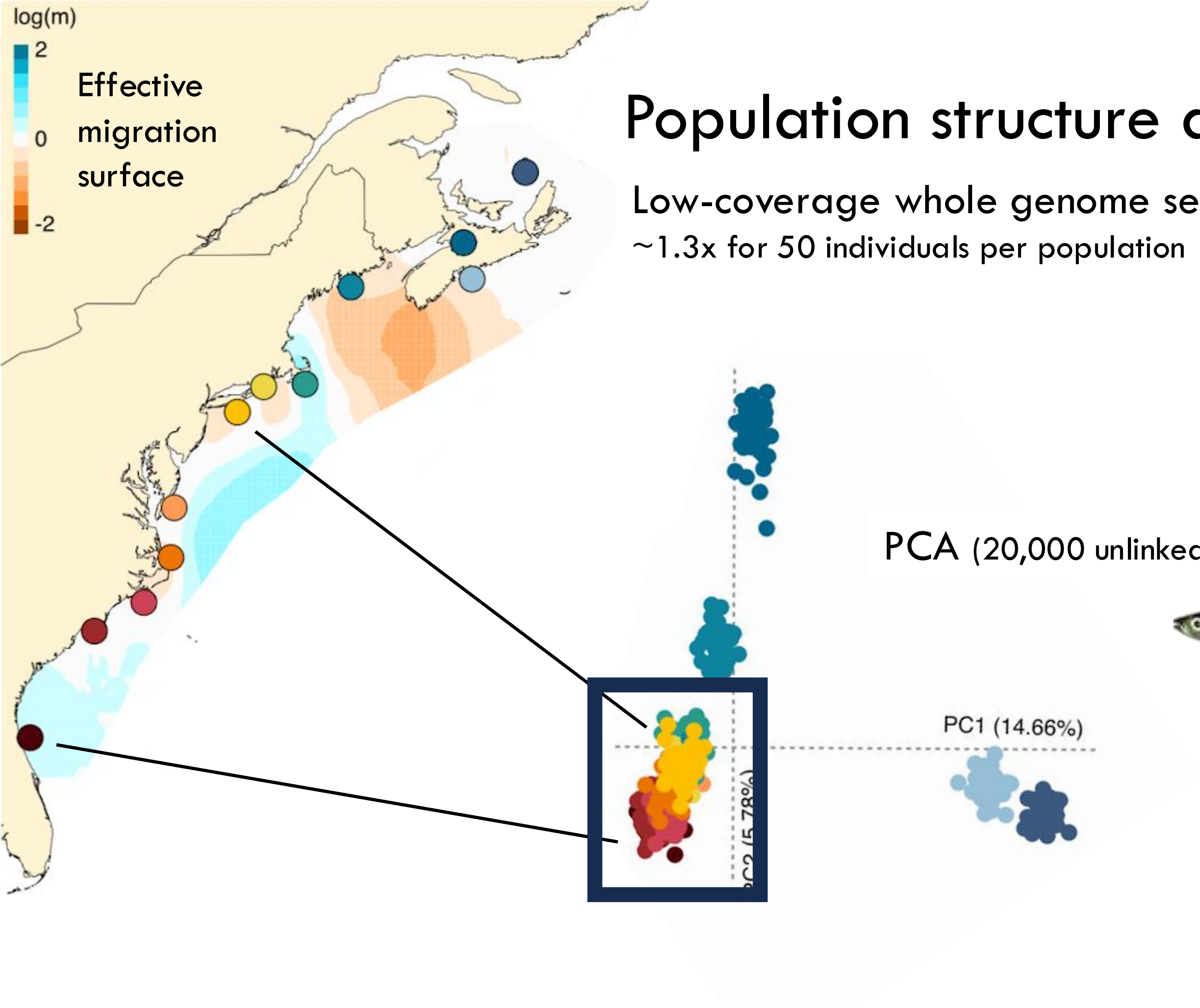
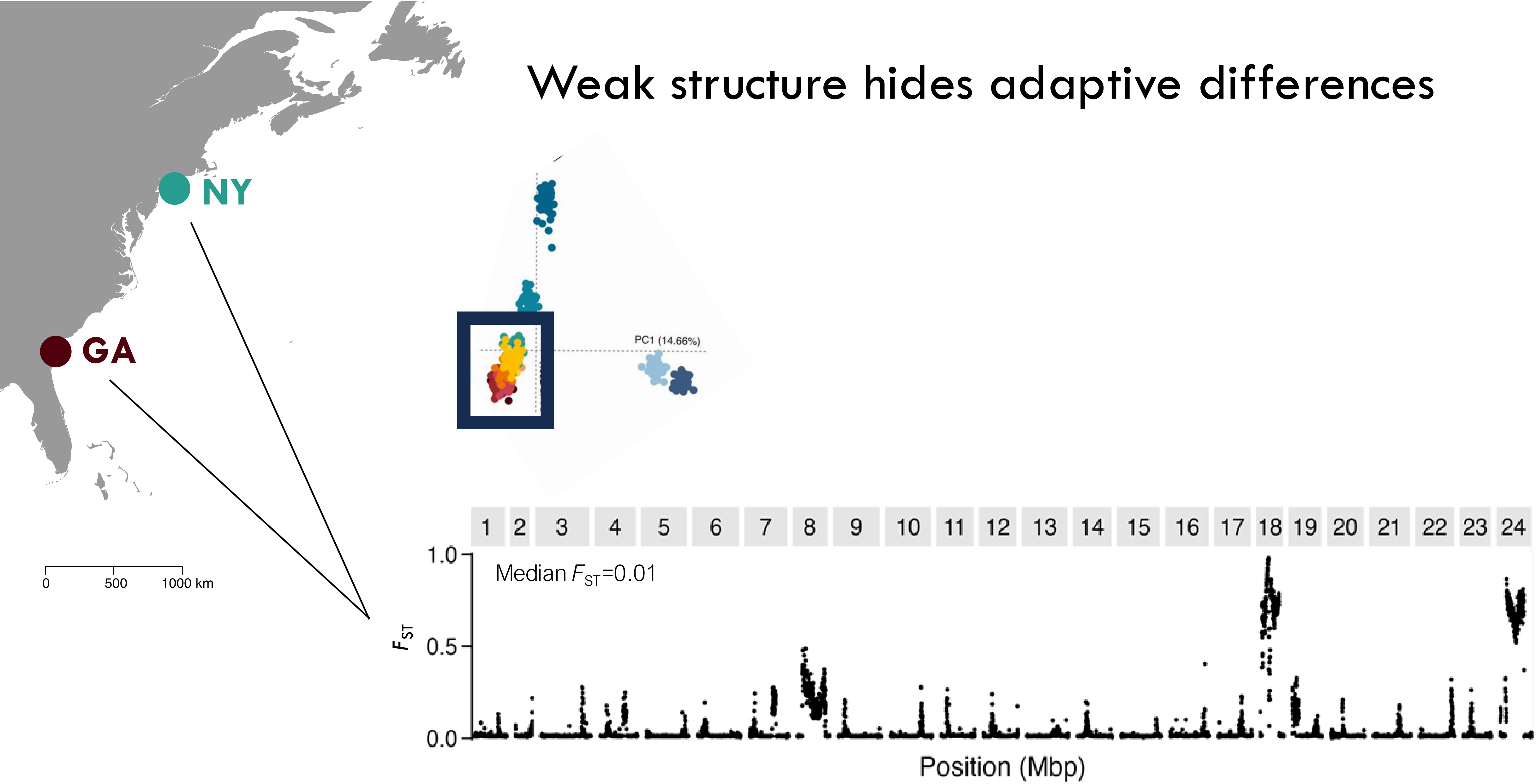


PCA (20,000 unlinked SNPs)

Akopyan et al. 2026. Science

# Weak structure hides adaptive differences



**LcWGS data**

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Akopyan et al. 2025. MBE

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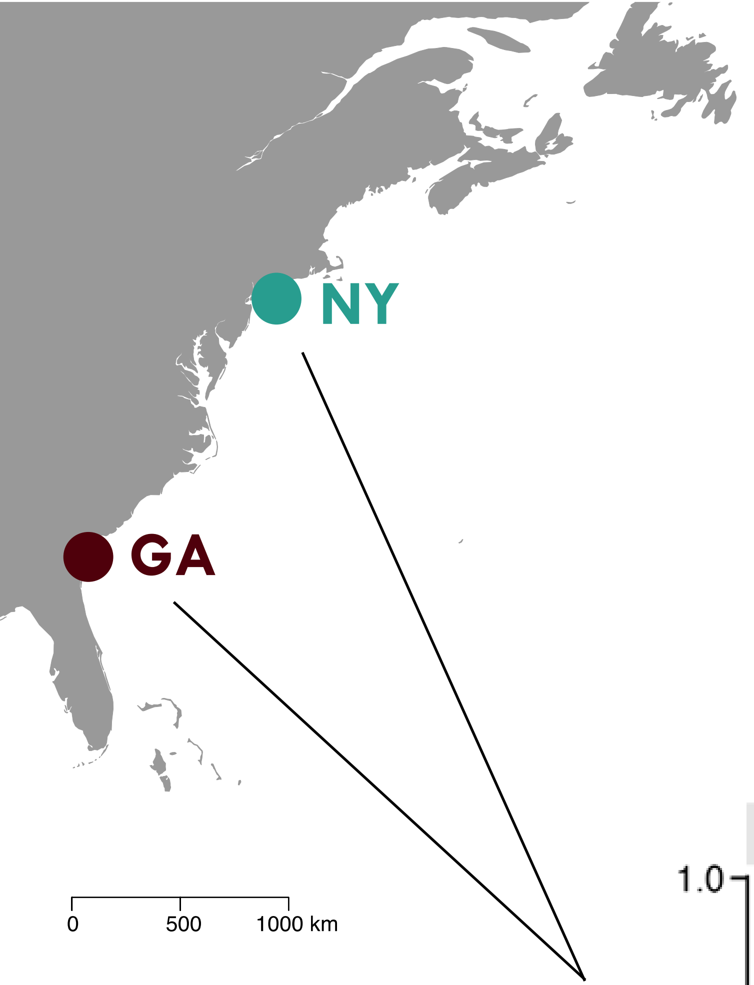

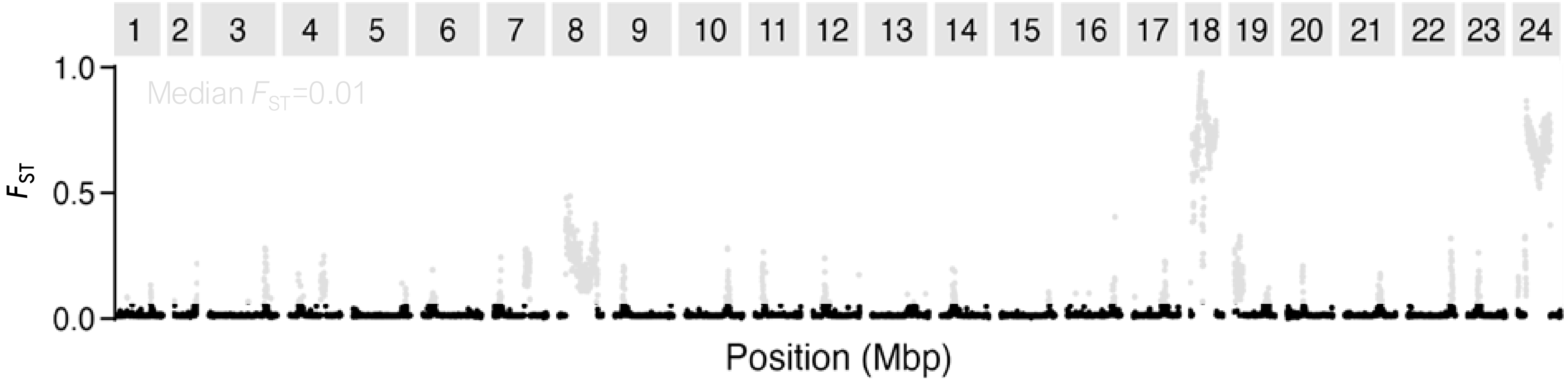

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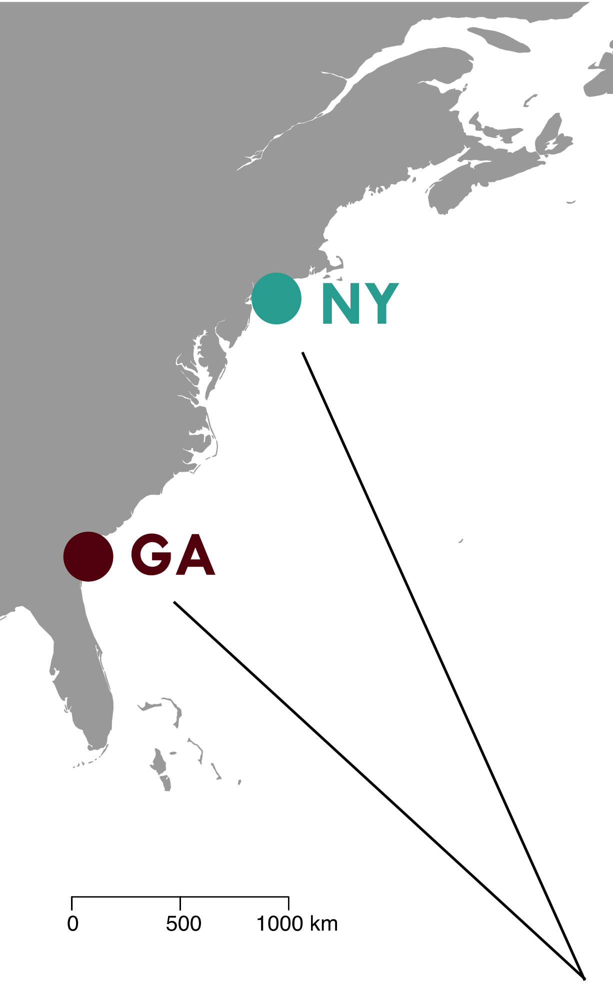

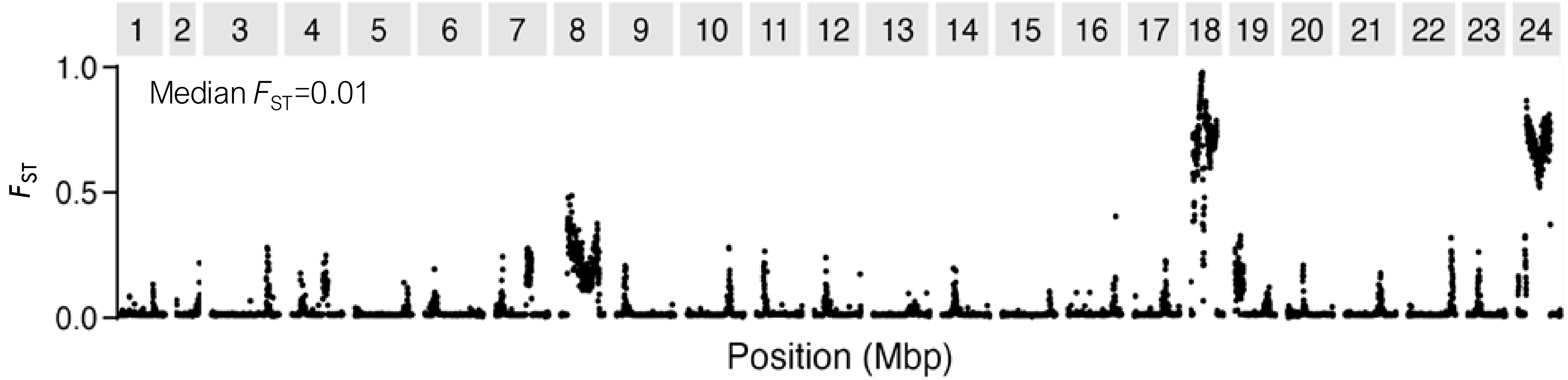

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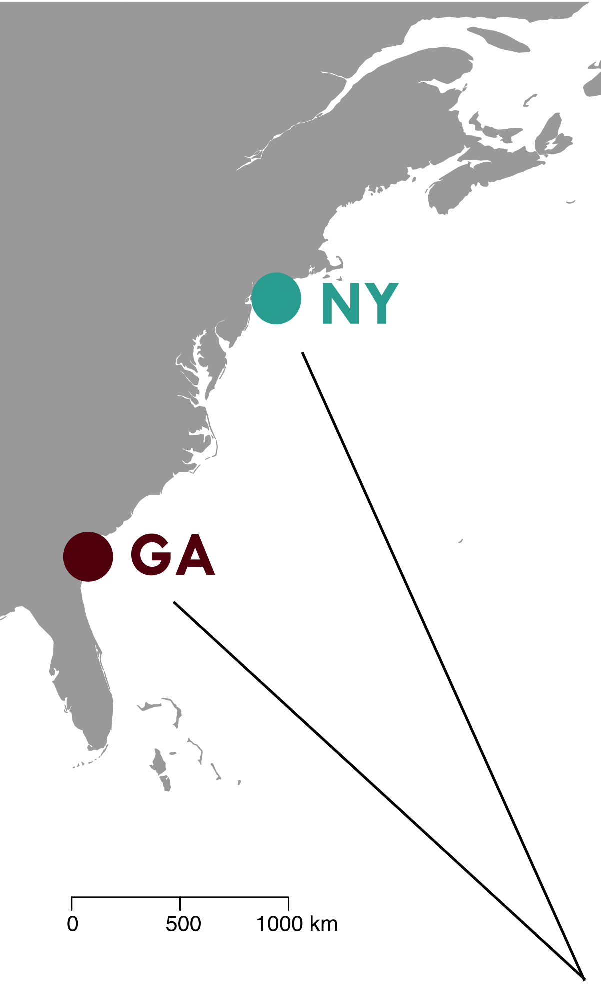
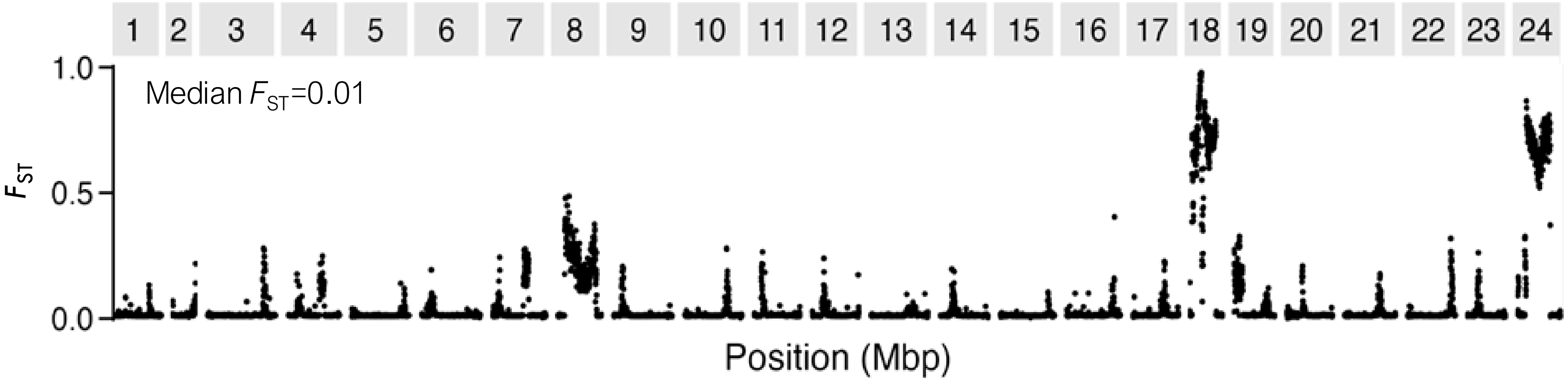
Akopyan et al. 2025. MBE

# Extreme ‘islands of divergence’

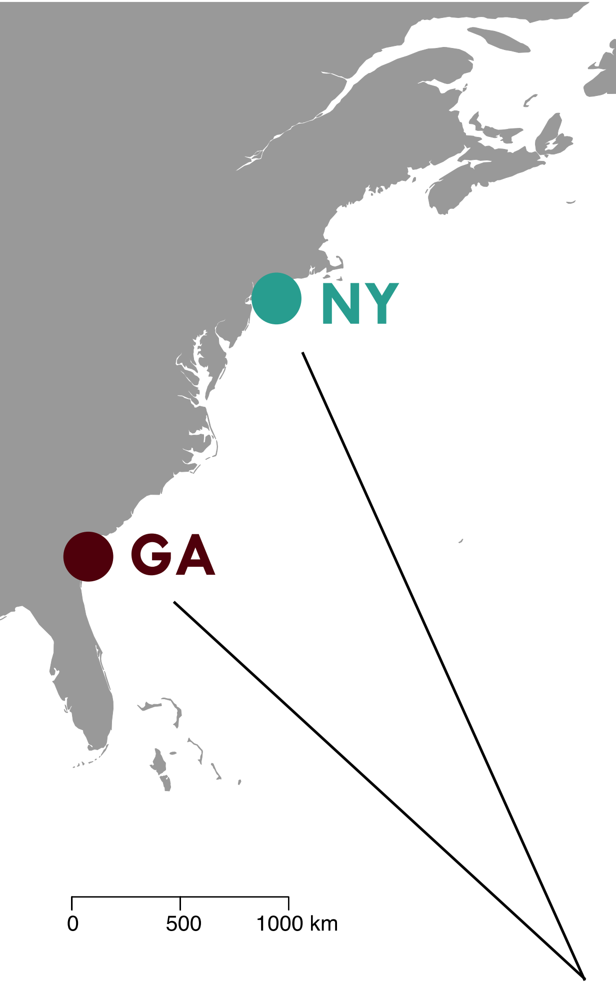
- Degree of differentiation
  (1000s of fixed SNPs)
- Genomic breath
  (>2/3 the length of multiple chromosomes)





**LcWGS data**
~1.3x for 50 individuals per population

Akopyan et al. 2025. MBE



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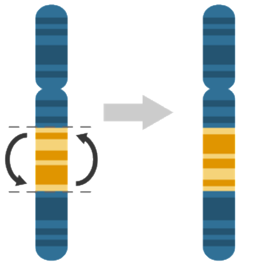
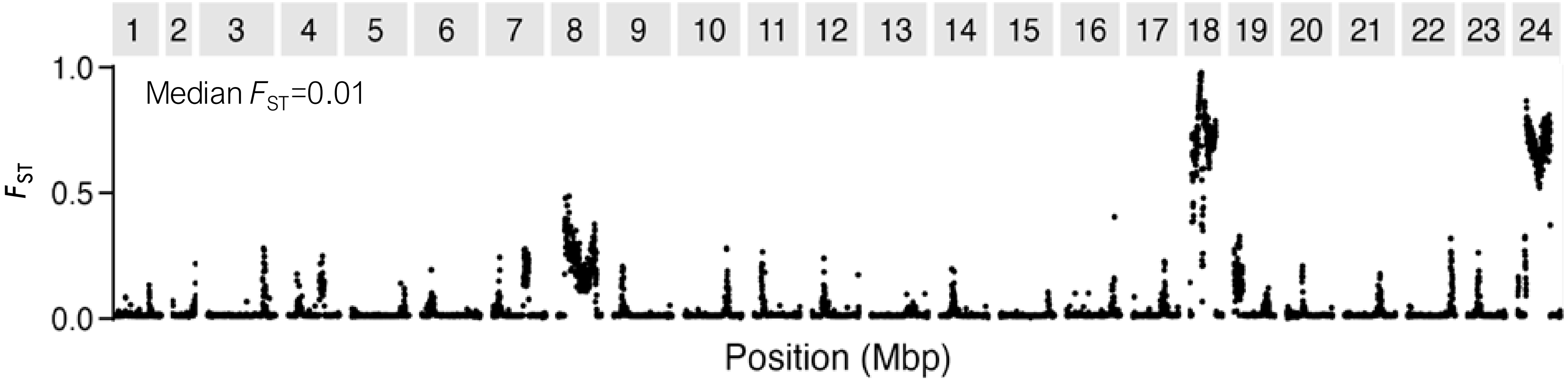
Chromosomal inversions





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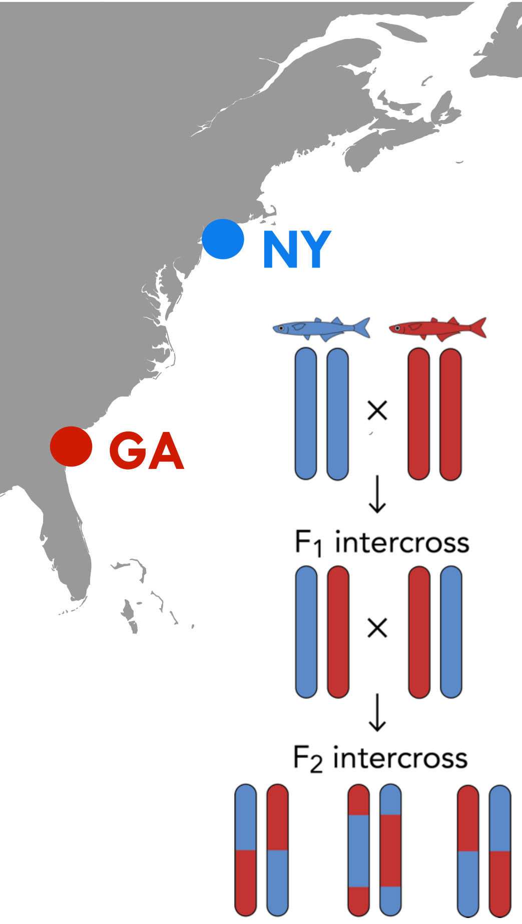
~1.3x for 50 individuals per population

Akopyan et al. 2025. MBE

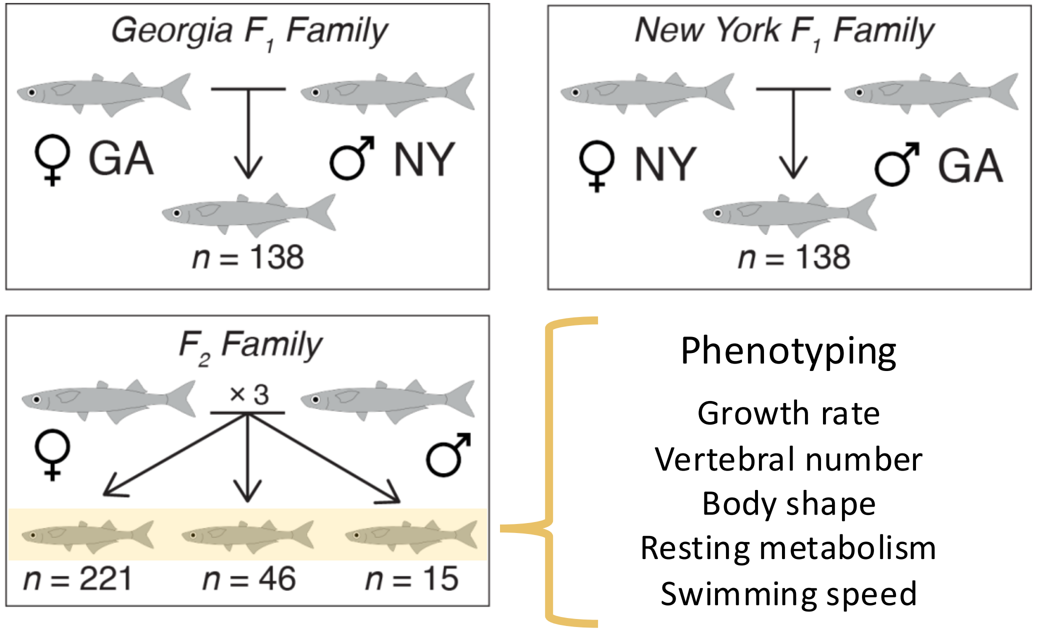
# QTL mapping to link genotype to phenotype



wild caught $F_0$ generation

$F_1$ generation

$F_2$ generation



## Genotyping

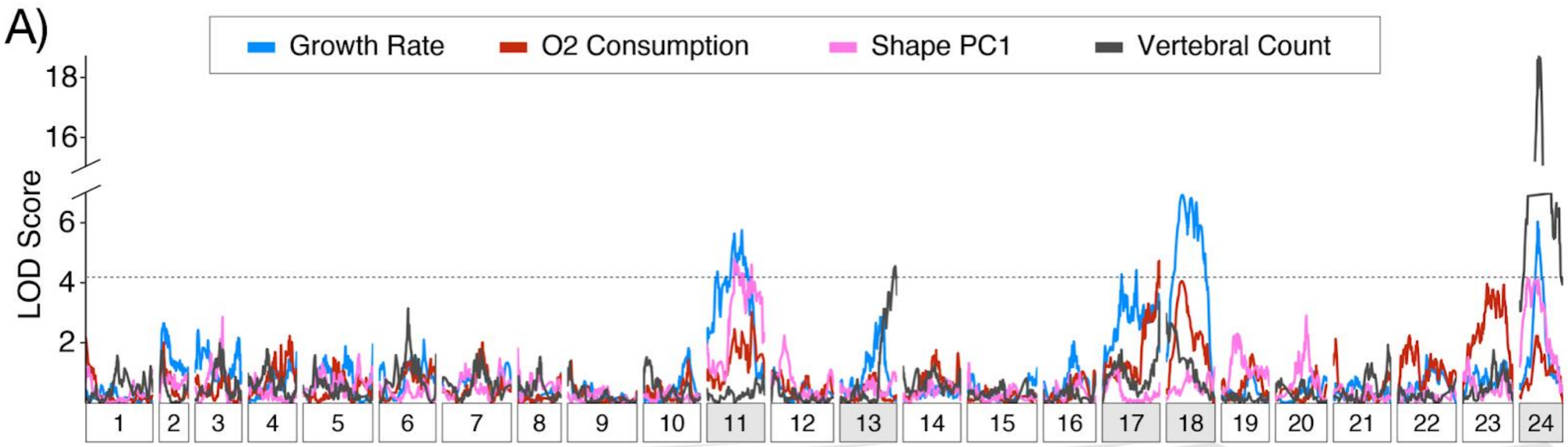
- ddRAD, *n*=568, 5 families
- ~50K SNPs @ 15X coverage

★ mapped to GA genome

## Phenotyping

Growth rate
Vertebral number
Body shape
Resting metabolism
Swimming speed

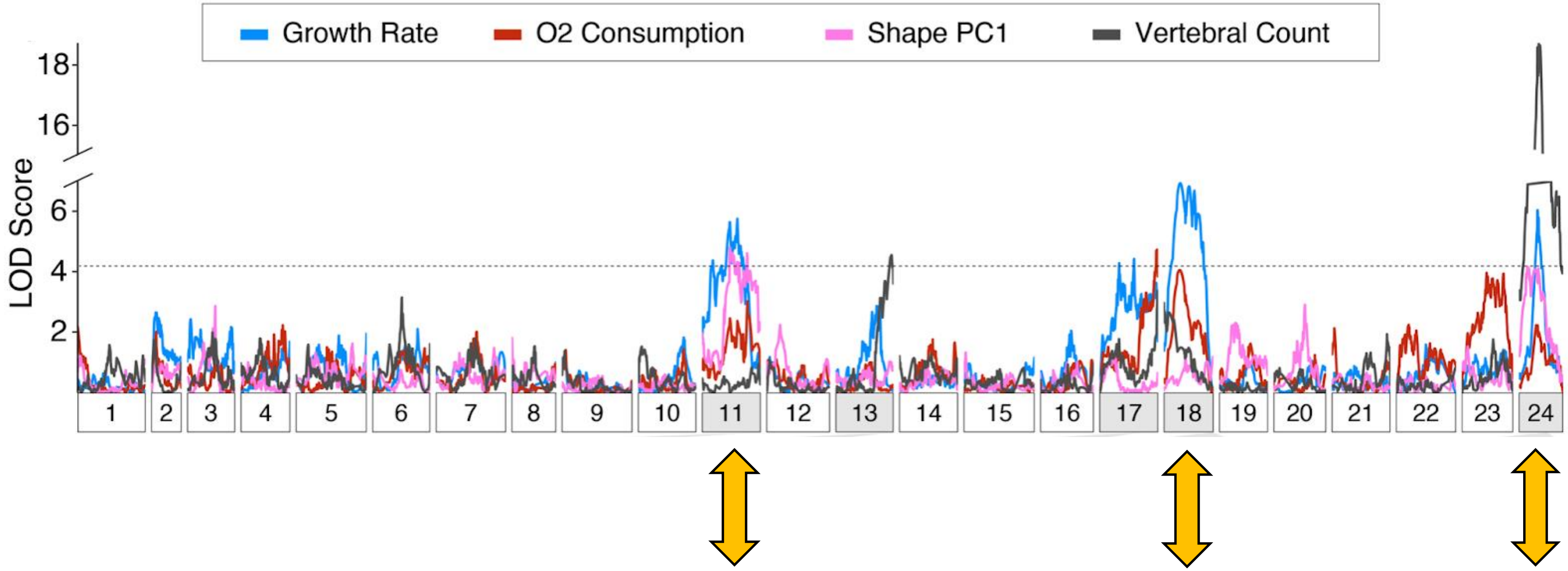
# Multiple traits map to the same genomic locations



Eight significant QTL on five chromosomes for four traits

Akopyan et al. 2026. Science

# Strongest QTL signals coincide with inversions

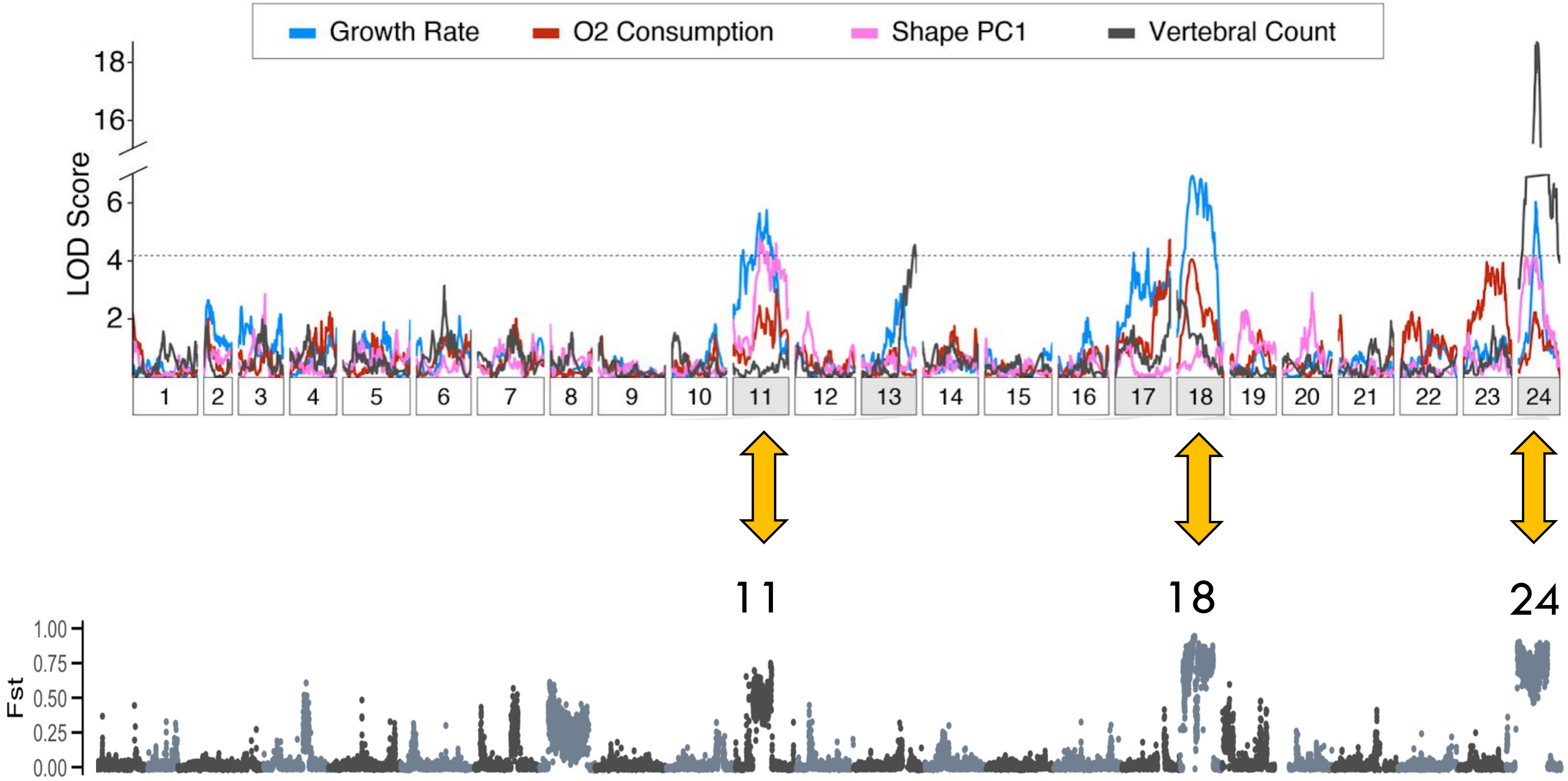


QTL signal

11 18 24 Major inversion

Akopyan et al. 2026. Science

# Strongest QTL signals coincide with inversions
# - and the blocks of strongest differentiation



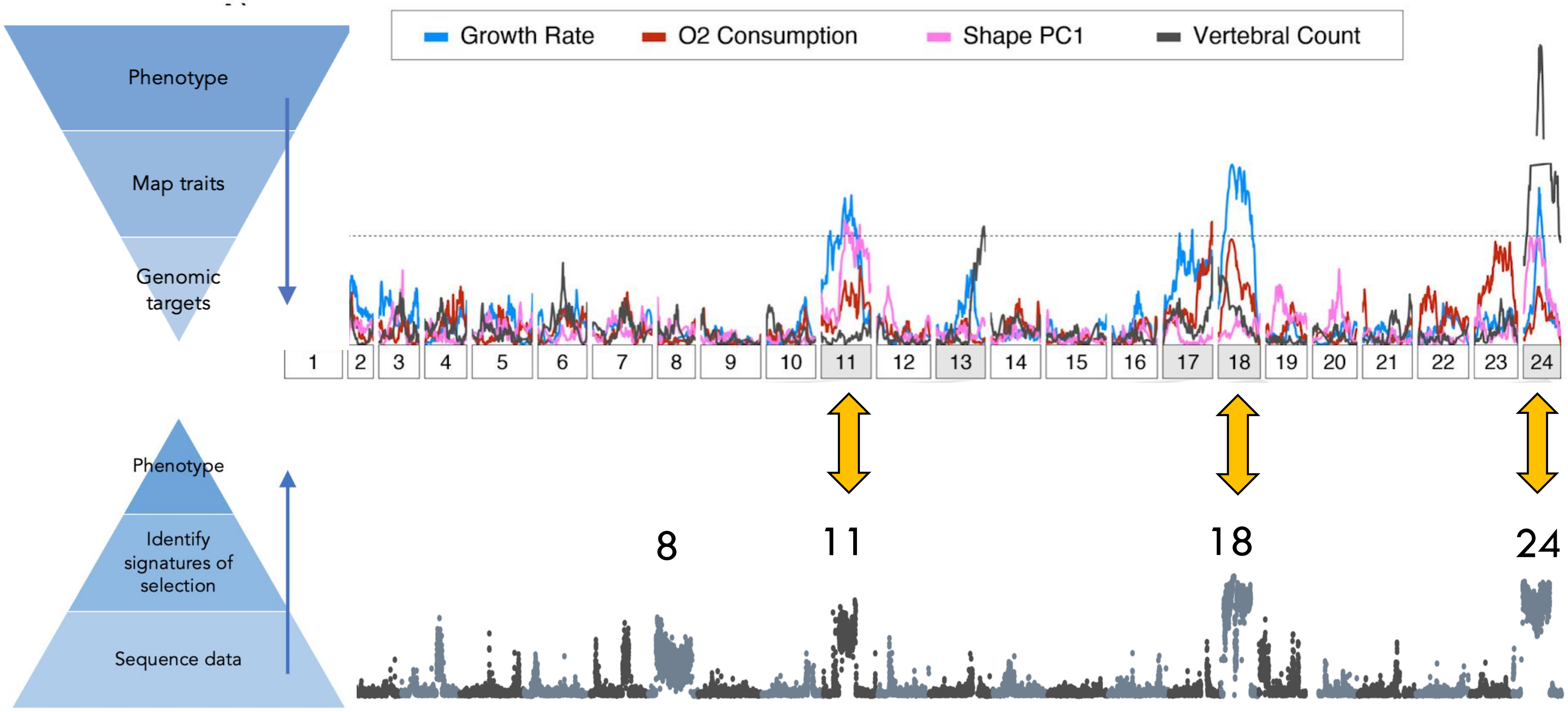
QTL signal

Major inversion

Geographic $F_{ST}$

Akopyan et al. 2026. Science

# Inversions play a crucial role in local adaptation

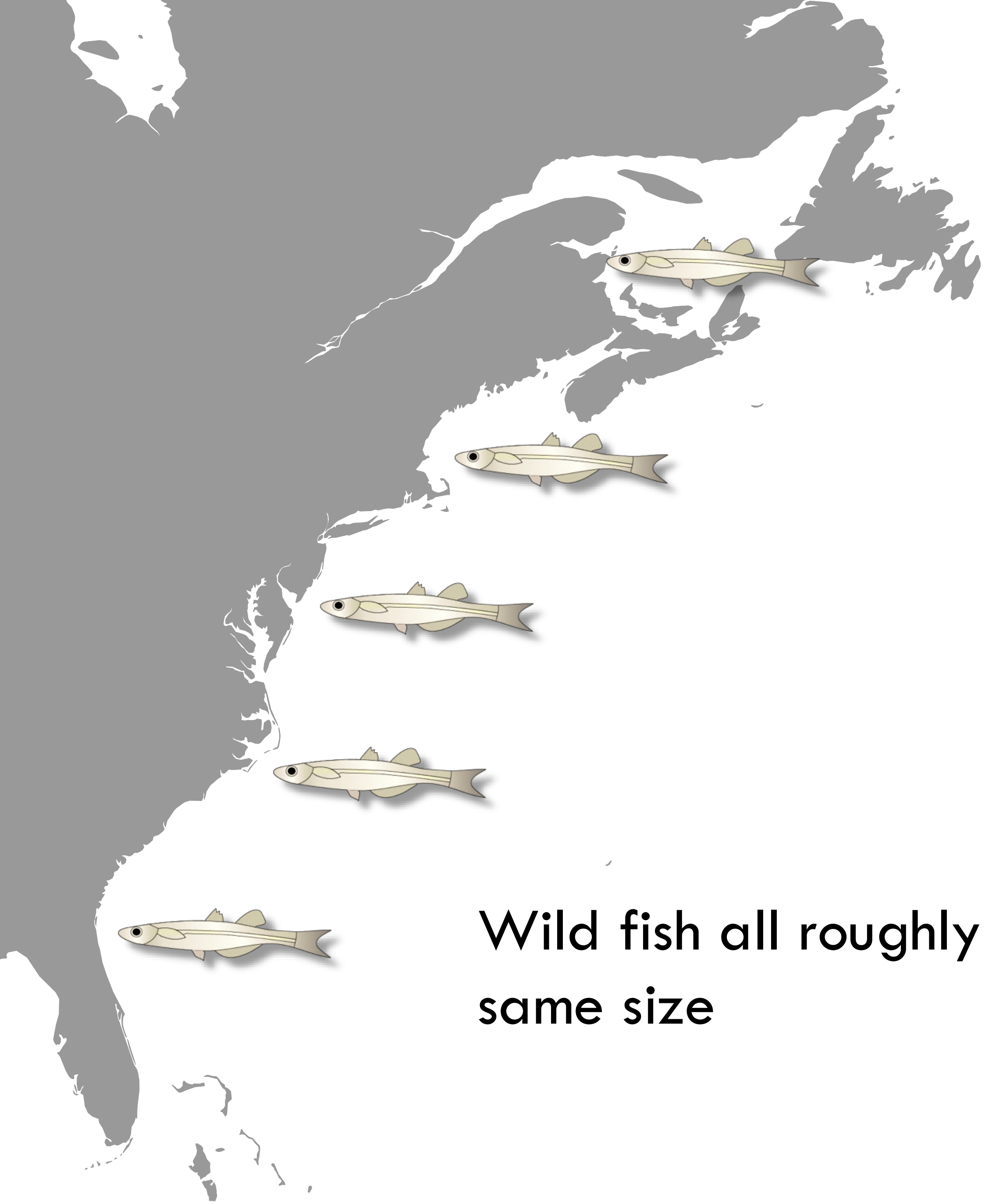


QTL signal

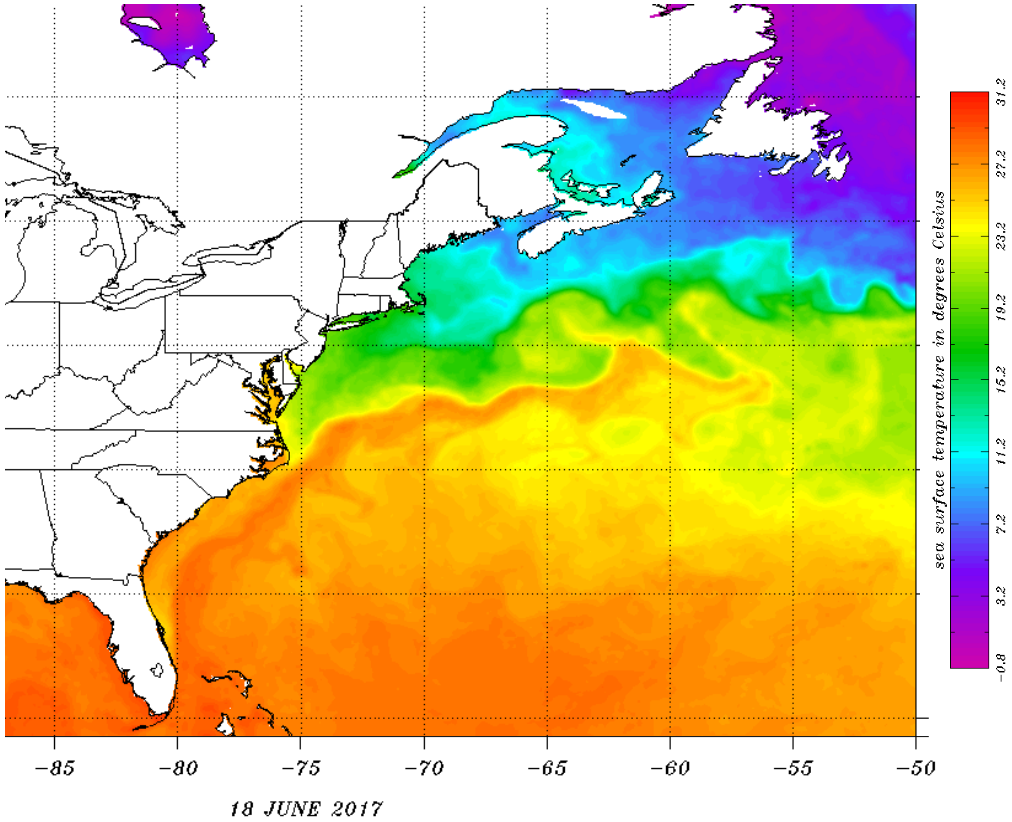
Major inversion

Geographic $F_{ST}$

# One of the world’s steepest thermal gradients

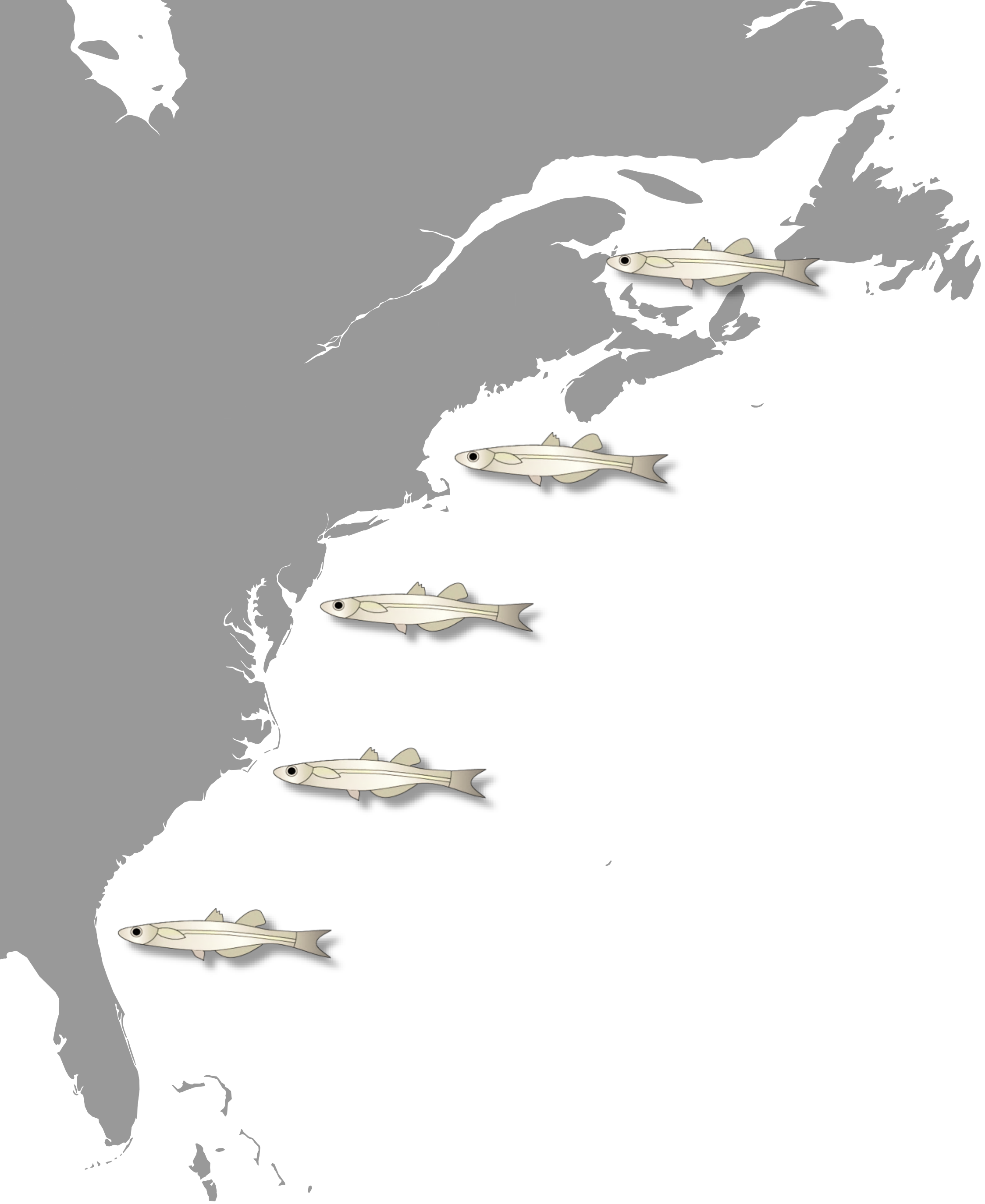


Wild fish all roughly the same size

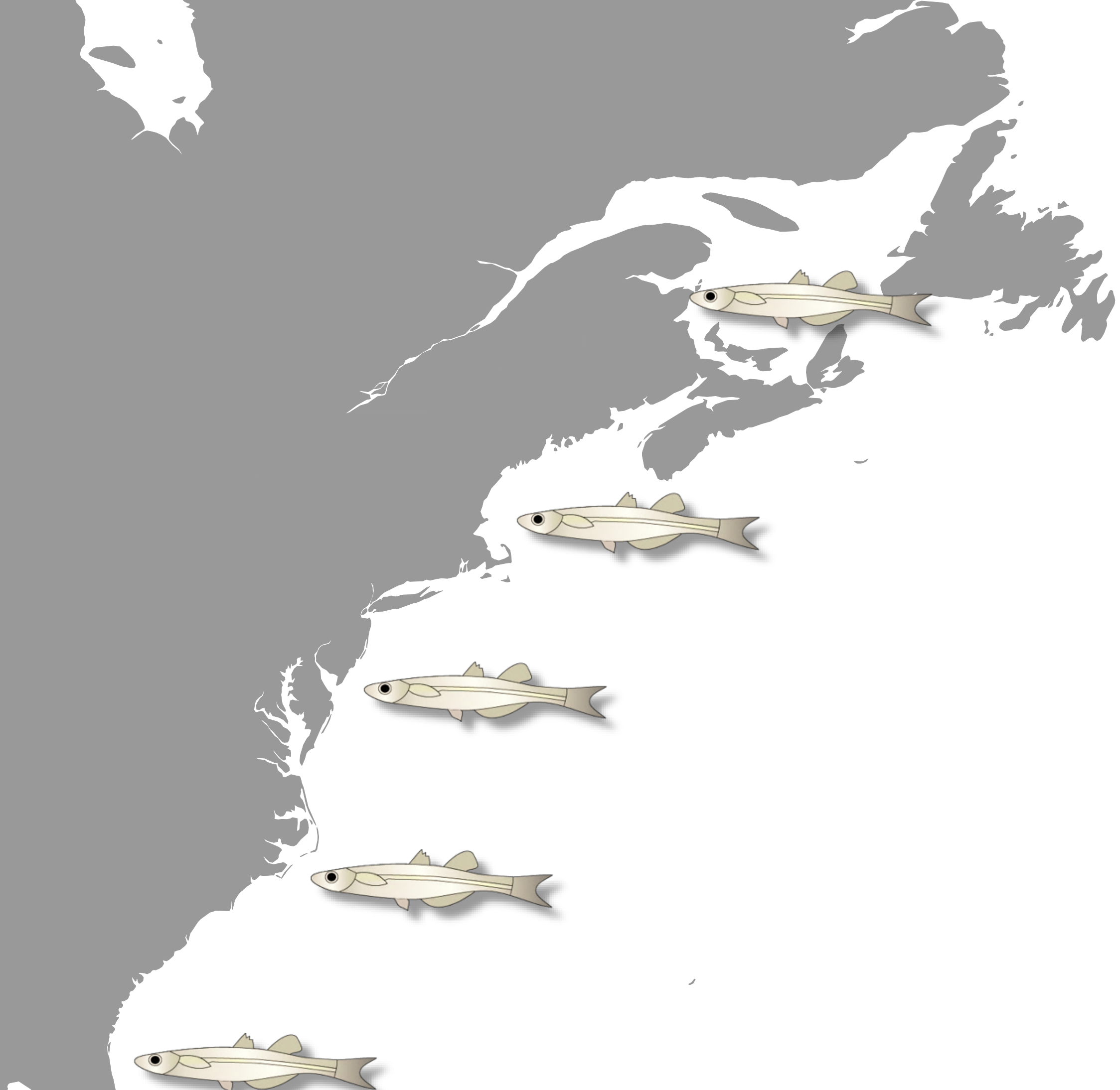


18 JUNE 2017

NOAA/NESDIS

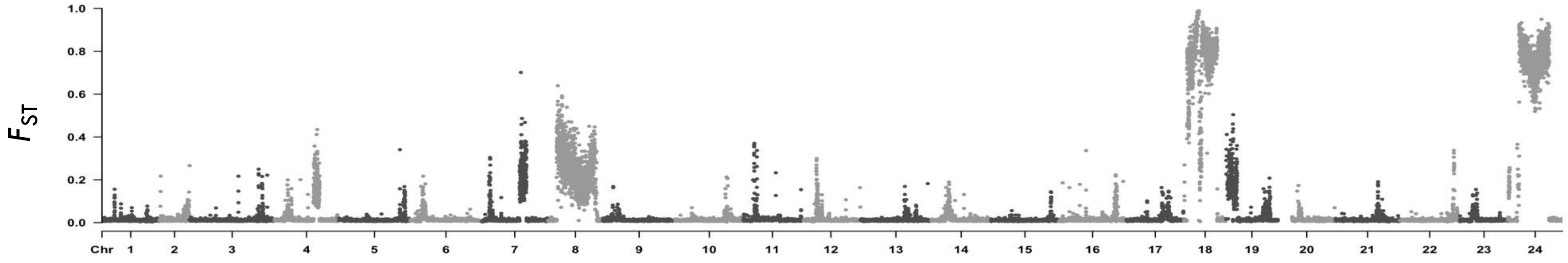


# Common garden experiments



## Common garden experiments

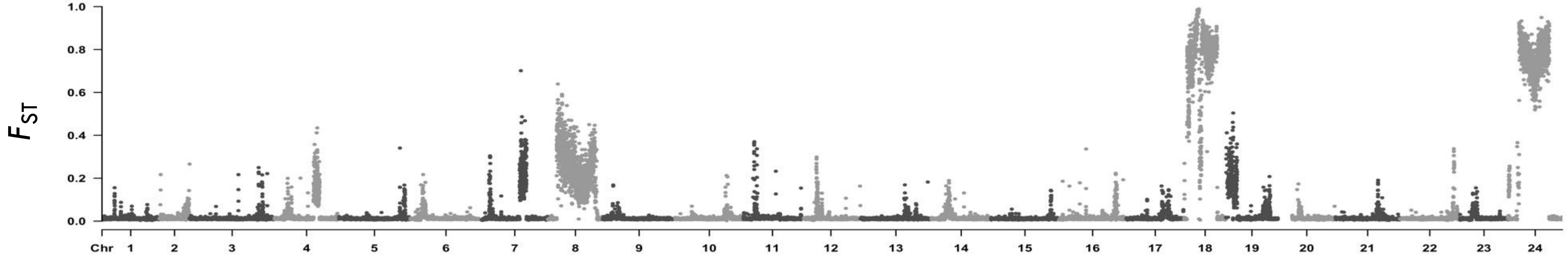
## Whole genome sequencing



Striking cryptic diversity uncovered

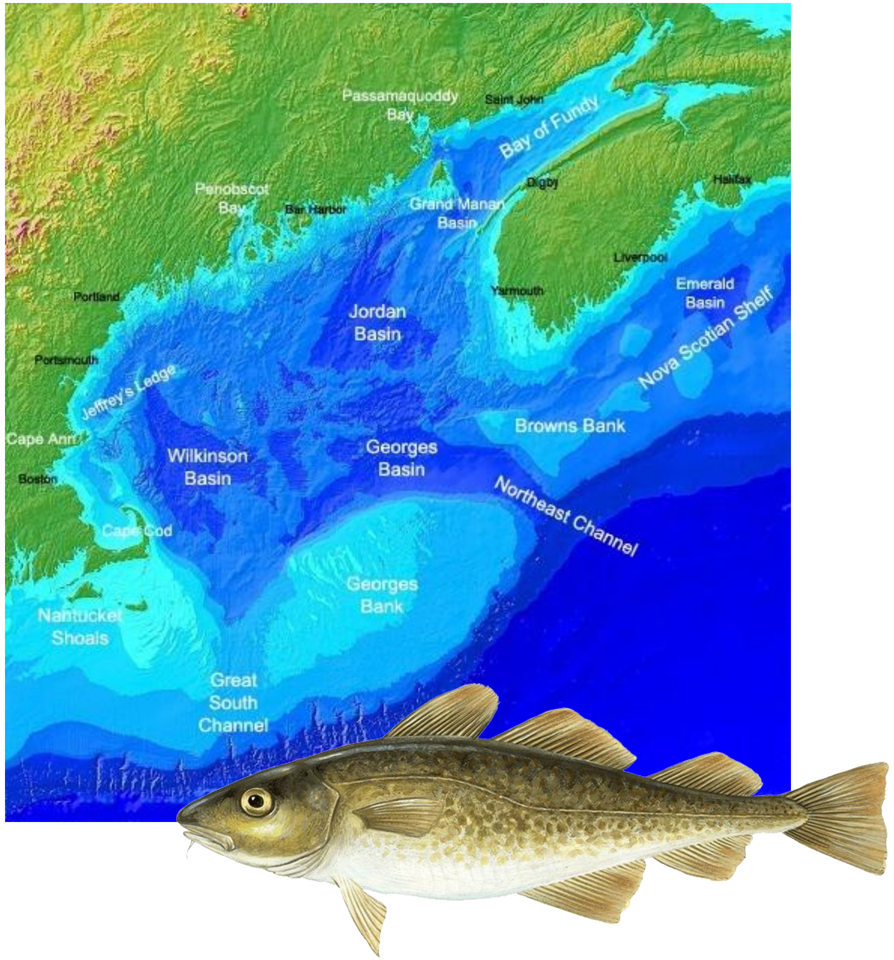
## Common garden experiments

## Whole genome sequencing



# Adaptive divergence in Atlantic cod in the Gulf of Maine

1. Use genomic analyses to characterize structure of active cod spawning populations in US waters
2. Identify adaptive genetic differences among populations



## Collaborators


Adrienne Kovach

University of New Hampshire


Gemma Clucas

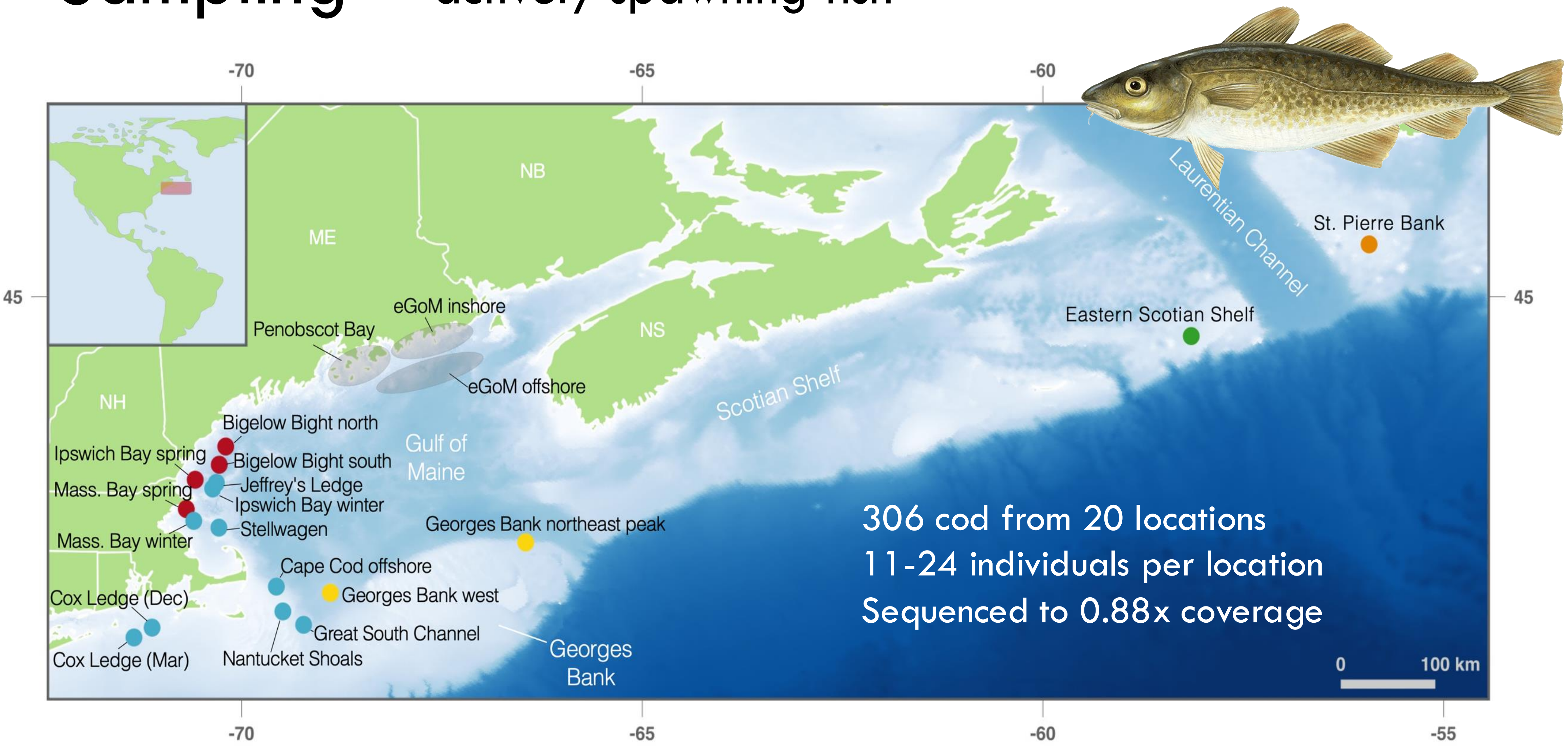
University of New Hampshire


Nicolas Lou

Cornell University

Sea Grant
New Hampshire

# Sampling – actively spawning fish

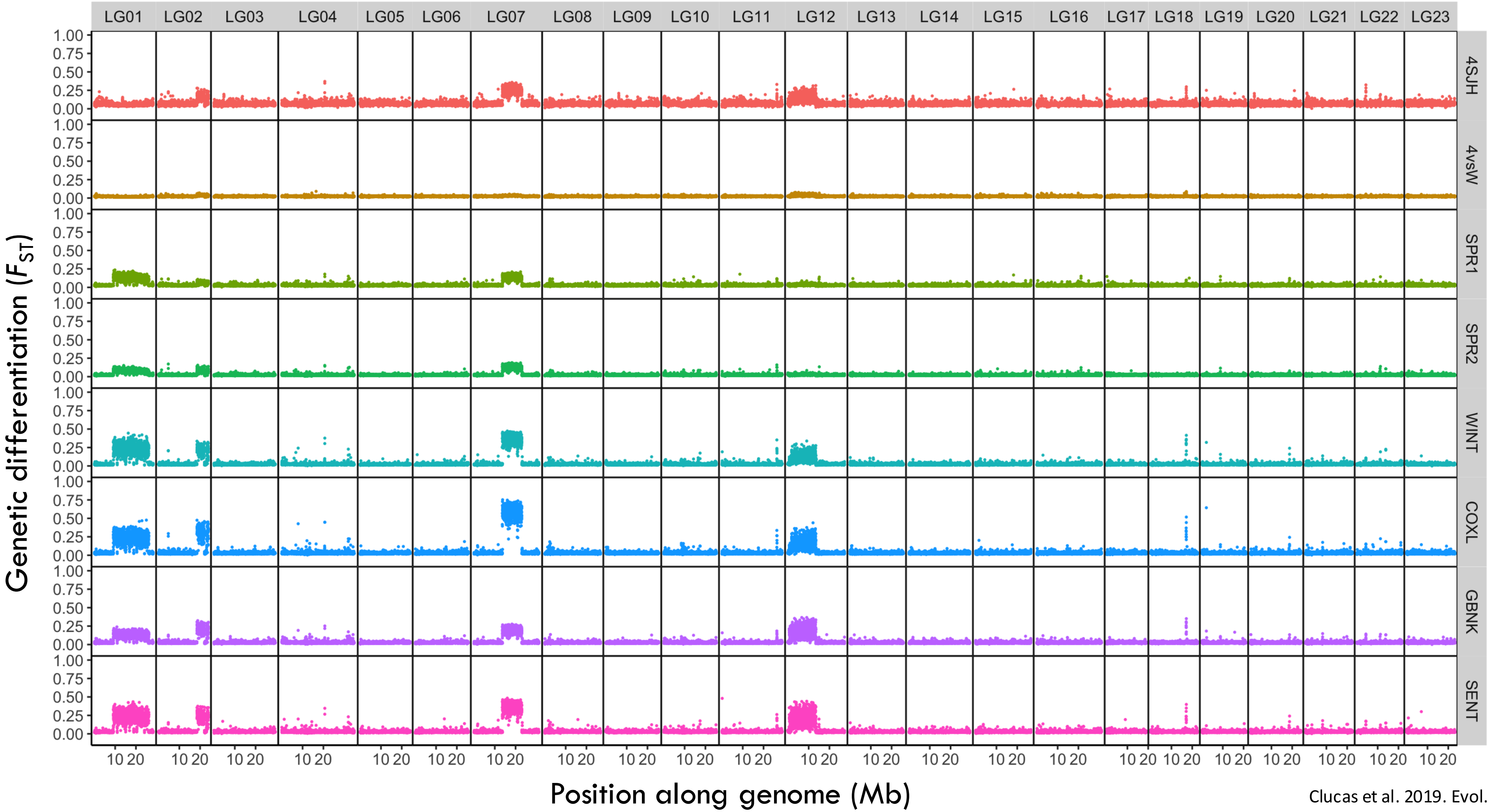


306 cod from 20 locations

11-24 individuals per location

Sequenced to 0.88x coverage

# Pairwise comparisons to St. Pierre Bank, Canada (15 kb windows)



Clucas et al. 2019. Evol. Appl.

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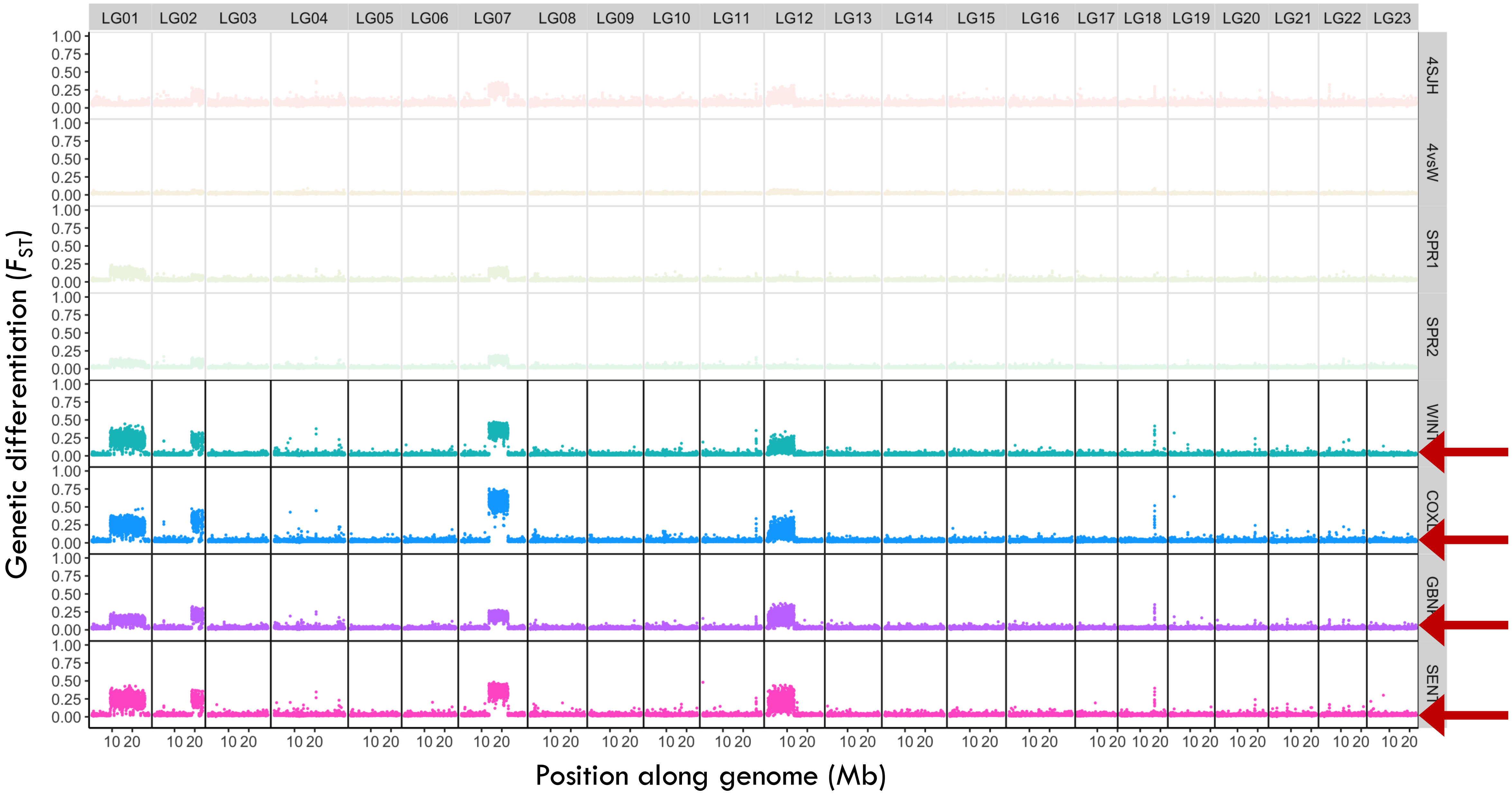

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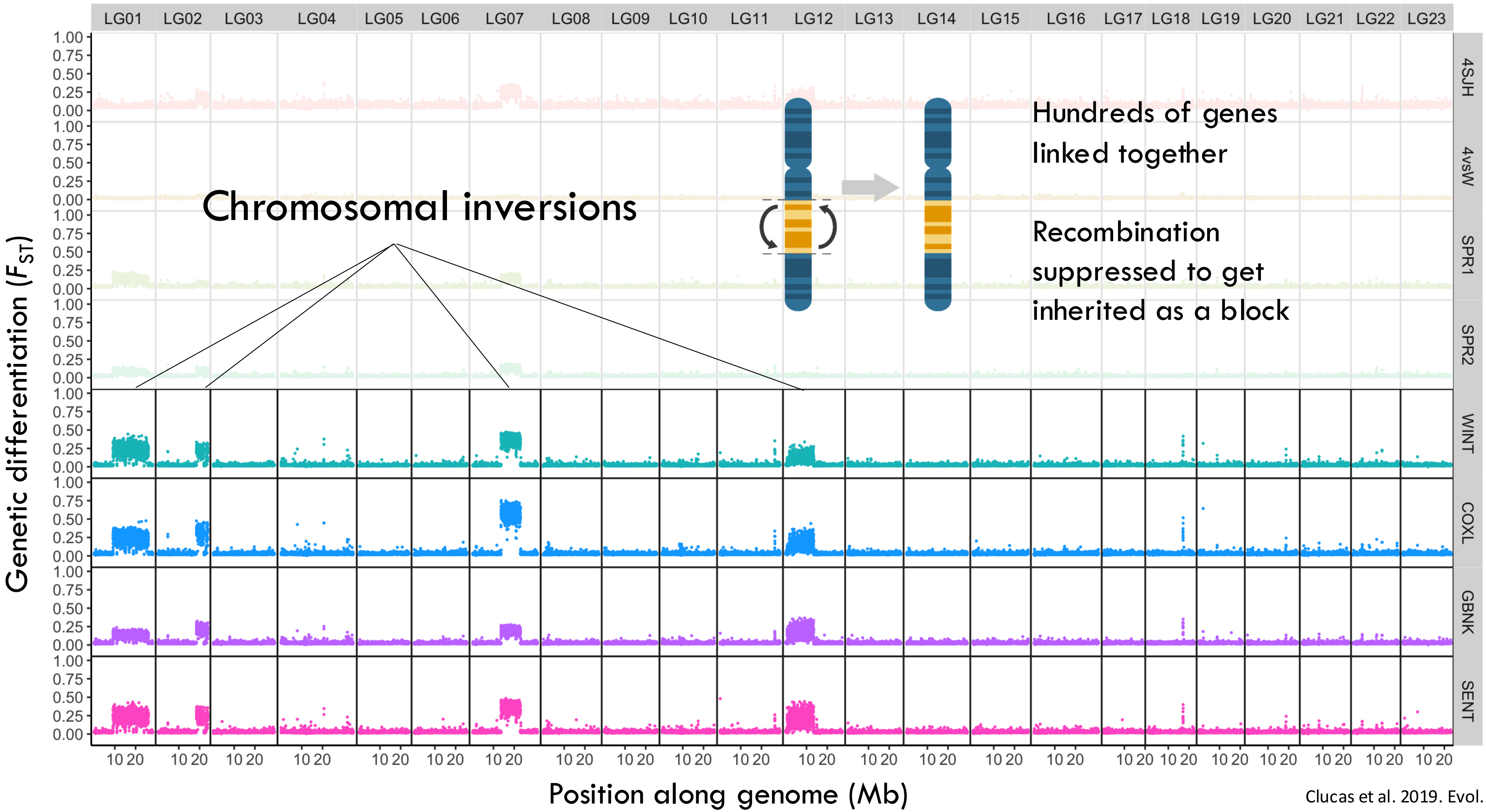


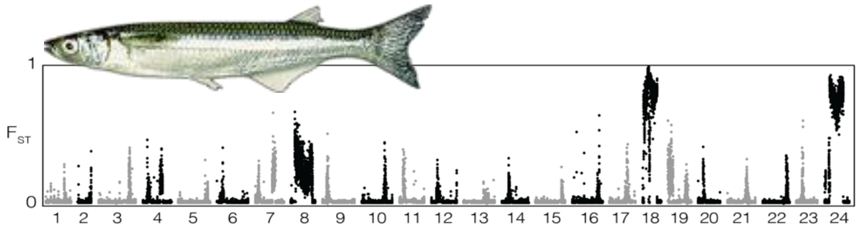
Chromosomal inversions

Hundreds of genes linked together

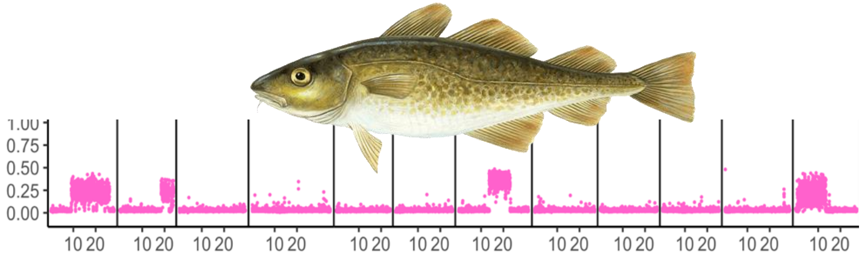
Recombination suppressed to get inherited as a block

Clucas et al. 2019. Evol. Appl.

# Chromosomal inversions everywhere!



Atlantic silversides



Clucas et al. 2019. Evol. Appl.

Atlantic cod

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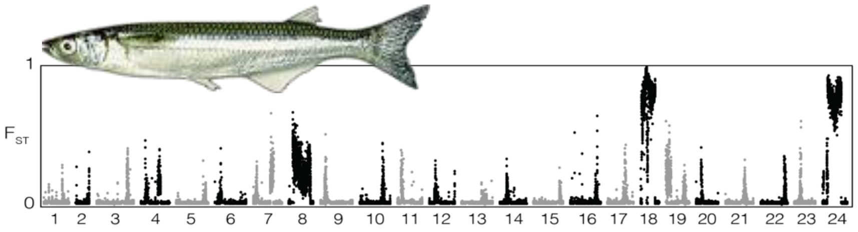
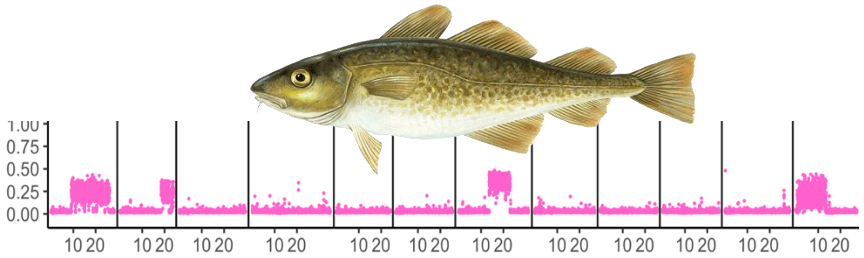


Atlantic silversides



Clucas et al. 2019. Evol. Appl.

Atlantic cod

Locally Adaptive Inversions Modulate Genetic Variation at Different Geographic Scales in a Seaweed Fly

Claire Mérot,*[1] Emma L. Berdan,[2] Hugo Cayuela,[1,3] Haig Djambazian,[4] Anne-Laure Ferchaud,[1]
Ragoussis,[4] Maren Wellenreuther,[5,6] and Louis Bernatchez[1]

e et des Systèmes (IBIS), Université Laval, Québec, Canada
s, Science for Life Laboratory, Stockholm University, Stockholm, Sweden
usanne, Lausanne, Switzerland
anada
lson, Nelson, New Zealand
uckland, New Zealand
om.

Received: 29 September 2021 | Revised: 25 October 2021 | Accepted: 26 October 2021
DOI: 10.1111/mec.16258

NEWS AND VIEWS

Perspective

Ready on arrival: Standing variation at a chromosomal inversion contributes to rapid adaptation in an invasive marine crab

Joshua A. Thia

Bio21 Institute, School of BioSciences, University of Melbourne, Victoria, Australia

**Correspondence**
Joshua A Thia, Bio21 Institute, School of BioSciences, University of Melbourne, Victoria, Australia.
Emails: joshua.thia@unimelb.edu.au; josh.thia@live.com

In this issue of M
tecture of adapt
vasive species is
that they will h
initially small fo
tionary factors t
endeavour of in
crab in its invasi
duction into Ca
spite low diversi
variation in tem
sion. This invers
of green crabs a
demonstrate th
tlenecks if varia
introduced popu
sions acting as l

*Molecular Ecology*

**ORIGINAL ARTICLE**

Inversions Dominate Evolution in the European Sardine (*Sardina pilchardus*) Amid Strong Gene Flow

Stephen J. Sabatino[1,2] | M. Pilar Cabezas[3,4] | Paulo Pereira[1,2] | Susana Garrido[5,6] | António M. Santos[1,2,7] | Miguel Carneiro[1,2] | Paulo T. Santos[2,7] | Bruno Louro[8] | Cymon J. Cox[8] | Adelino V. M. Canário[8] | Ana Veríssimo[1,2]

[1]CIBIO-InBIO, Research Center in Biodiversity and Genetic Resources, University of Porto, Vairão, Portugal | [2]BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Vairão, Portugal | [3]Centre of Molecular and Environmental Biology (CBMA) and ARNET—Aquatic Research Network, Department of Biology, University of Minho, Gualtar Campus, Braga, Portugal | [4]Institute of Science and Innovation for Bio-Sustainability (IB-S), University of Minho, Gualtar Campus, Braga, Portugal | [5]Portuguese Institute for sea and Atmosphere (IPMA), Lisbon, Portugal | [6]Marine and Environmental Sciences Centre (MARE), Faculty of Sciences, University of Lisbon, Lisbon, Portugal | [7]Faculty of Sciences, University of Porto, Porto, Portugal | [8]Algarve Centre for Marine Sciences (CCMAR/CIMAR), Gambelas Campus, University of Algarve, Faro, Portugal

**Correspondence:** Stephen J. Sabatino (sjsabatino@gmail.com)

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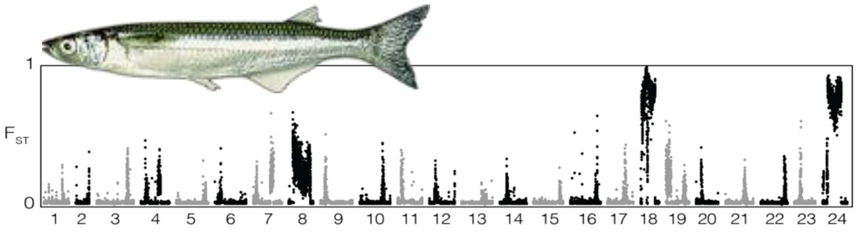
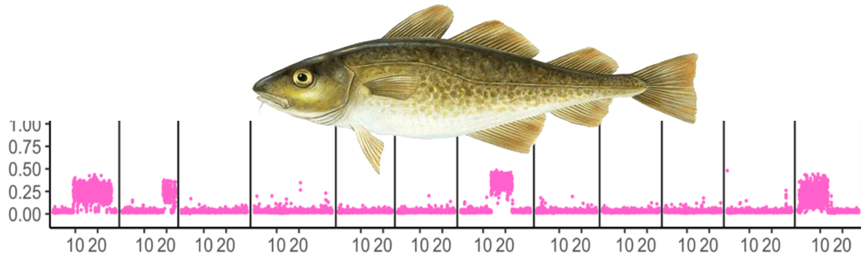
**Keywords:** adaptation | climate change | life-history evolution | population genetics—empirical | wildlife management

**ABSTRACT**
Inversions can play key roles in the genetic architecture of adaptation, but the scale of their effects across different species remains poorly understood. Here, we use whole-genome sequencing and demographic modelling to investigate the influence of inversions on the population genomics of the r-selected European sardine (*Sardina pilchardus*). Allele frequency differences from millions of SNPs across 34 populations spanning the species' range were analysed. Genomic scans identified several extreme outlier regions overlapping large inversions (29–52 Mbp), collectively representing over half the genome. Our findings suggest these inversions correlate with locally adapted life-history strategies. First, SNPs within outlier regions containing inversions exhibited striking allele frequency differences between Atlantic and Mediterranean sardines, which differ in key adaptive life-history traits. In the Atlantic, inversion allele frequencies varied latitudinally, while in the Mediterranean, they shifted longitudinally.

# Chromosomal inversions everywhere!



Atlantic silversides



Clucas et al. 2019. Evol. Appl.

Atlantic cod

Locally Adaptive Inversions Modulate Genetic Variation at Different Geographic Scales in a Seaweed Fly

Claire Mérot,*[1] Emma L. Berdan,[2] Hugo Cayuela,[1,3] Haig Djambazian,[4] Anne-Laure Ferchaud,[1]
Ragoussis,[4] Maren Wellenreuther,[5,6] and Louis Bernatchez[1]

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MOLECULAR ECOLOGY WILEY

NEWS AND VIEWS

Perspective

Ready on arrival: Standing variation at a chromosomal inversion contributes to rapid adaptation in an invasive marine crab

Joshua A. Thia

Bio21 Institute, School of BioSciences, University of Melbourne, Victoria, Australia

Correspondence
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Emails: joshua.thia@unimelb.edu.au; josh.thia@live.com

In this issue of M
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Molecular Ecology

WILEY

MOLECULAR ECOLOGY

ORIGINAL ARTICLE

Inversions Dominate Evolution in the European Sardine (*Sardina pilchardus*) Amid Strong Gene Flow

Stephen J. Sabatino[1,2] | M. Pilar Cabezas[3,4] | Paulo Pereira[1,2] | Susana Garrido[5,6] | António M. Santos[1,2,7] |
Miguel Carneiro[1,2] | Paulo T. Santos[2,7] | Bruno Louro[8] | Cymon J. Cox[8] | Adelino V. M. Canário[8] | Ana Veríssimo[1,2]

Biodiversity and Genetic Resources, University of Porto, Vairão, Portugal | [2]BIOPOLIS Program in Genomics,
IBIO, Vairão, Portugal | [3]Centre of Molecular and Environmental Biology (CBMA) and ARNET—Aquatic Research
University of Minho, Gualtar Campus, Braga, Portugal | [4]Institute of Science and Innovation for Bio-Sustainability
r Campus, Braga, Portugal | [5]Portuguese Institute for sea and Atmosphere (IPMA), Lisbon, Portugal | [6]Marine and
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ised: 7 May 2025 | **Accepted:** 30 June 2025

Barton

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ange | life-history evolution | population genetics—empirical | wildlife management

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cally adapted life-history strategies. First, SNPs within outlier regions containing inversions exhib-
ited striking allele frequency differences between Atlantic and Mediterranean sardines, which differ in key adaptive life-history

## Talks this afternoon:

**(Invited) (ECOP) Chromosomal inversions and selection shape the population structure of Pacific herring COPY**

2:35 PM – 3:00 PM

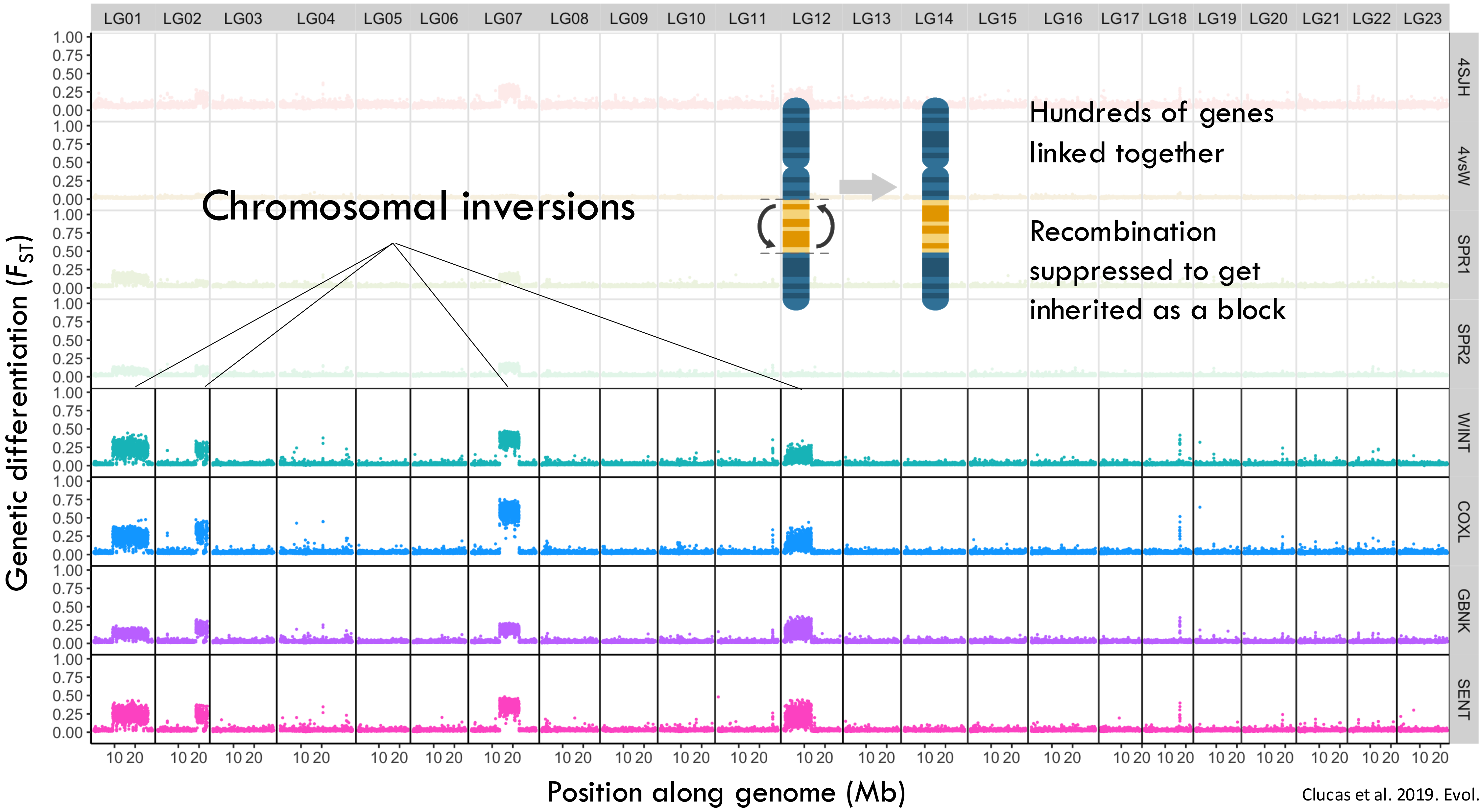
**Speaker: Eleni Petrou**

**(ECOP) Multiple chromosomal inversions reveal the evolutionary history of lineage divergence and admixture in the European sardine**

3:00 PM – 3:15 PM

**Speaker: Marina Puebla-Aparicio**

# Pairwise comparisons to St. Pierre Bank, Canada (15 kb windows)



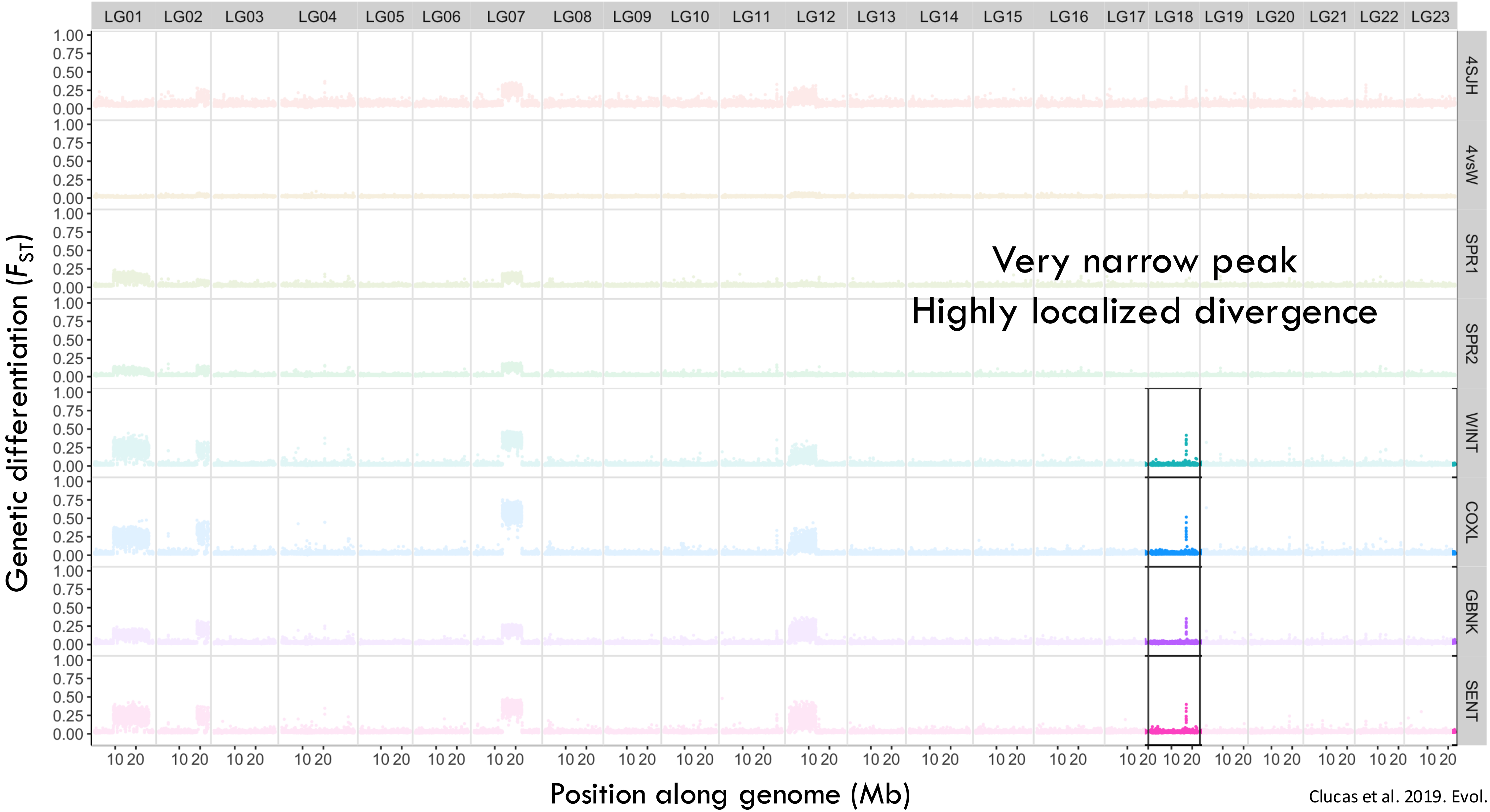
Chromosomal inversions

Hundreds of genes linked together

Recombination suppressed to get inherited as a block

Clucas et al. 2019. Evol. Appl.

# Pairwise comparisons to St. Pierre Bank, Canada (15 kb windows)

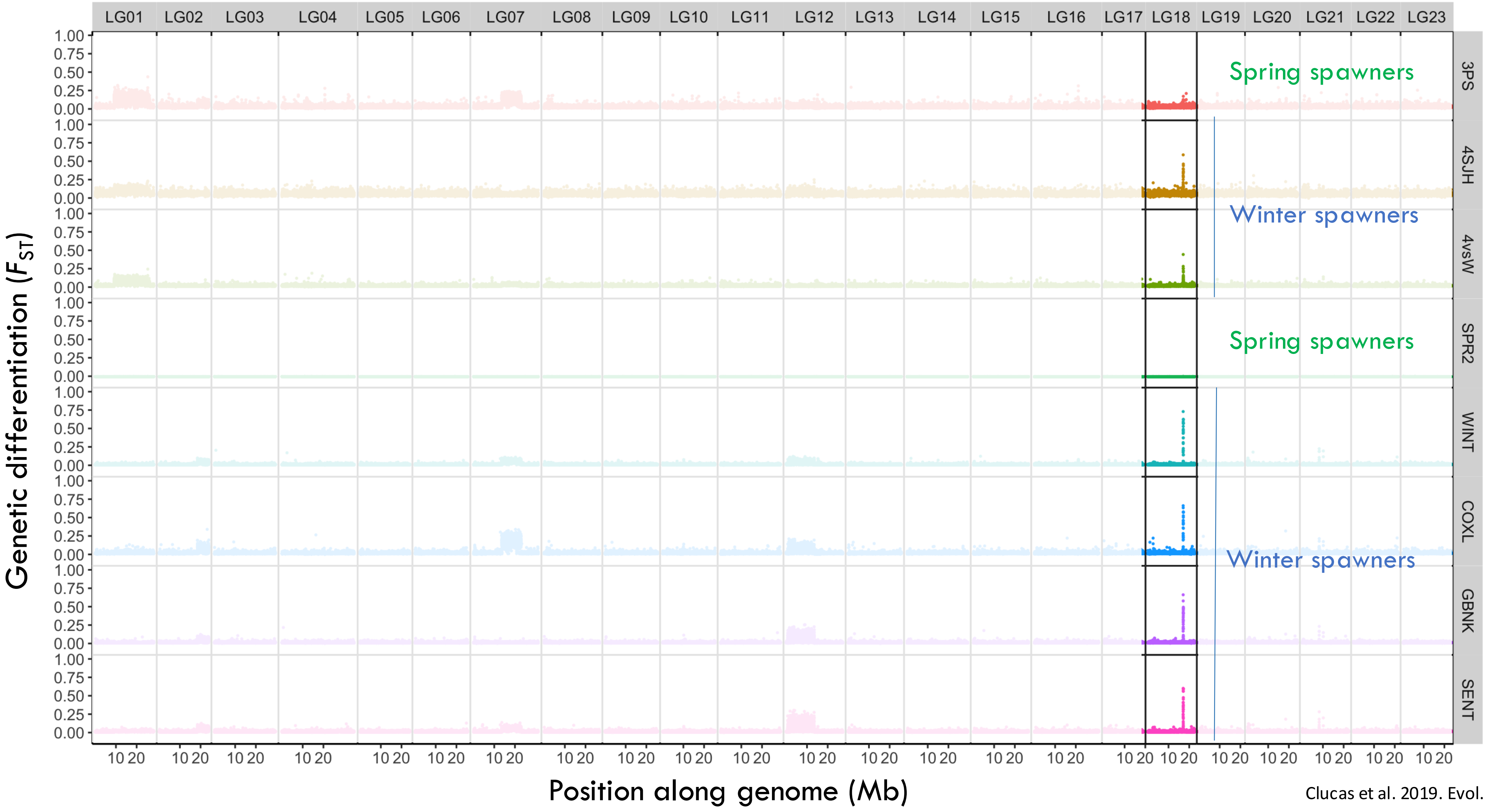


Very narrow peak

Highly localized divergence

Clucas et al. 2019. Evol. Appl.

# Pairwise comparisons to the wGoM spring spawners (5 kb windows)



Spring spawners

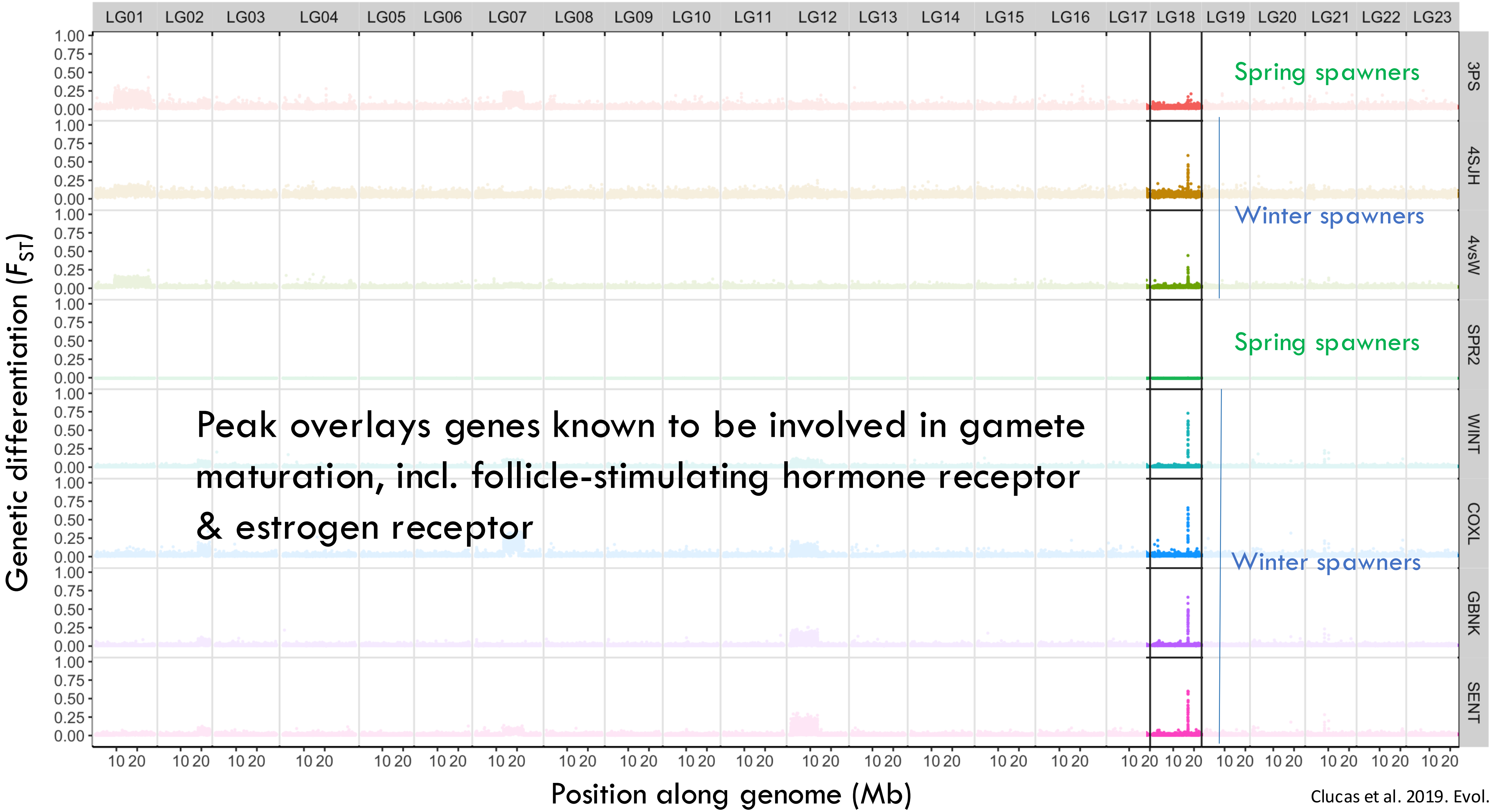
Winter spawners

Spring spawners

Winter spawners

Clucas et al. 2019. Evol. Appl.

# Pairwise comparisons to the wGoM spring spawners (5 kb windows)



Spring spawners

Winter spawners

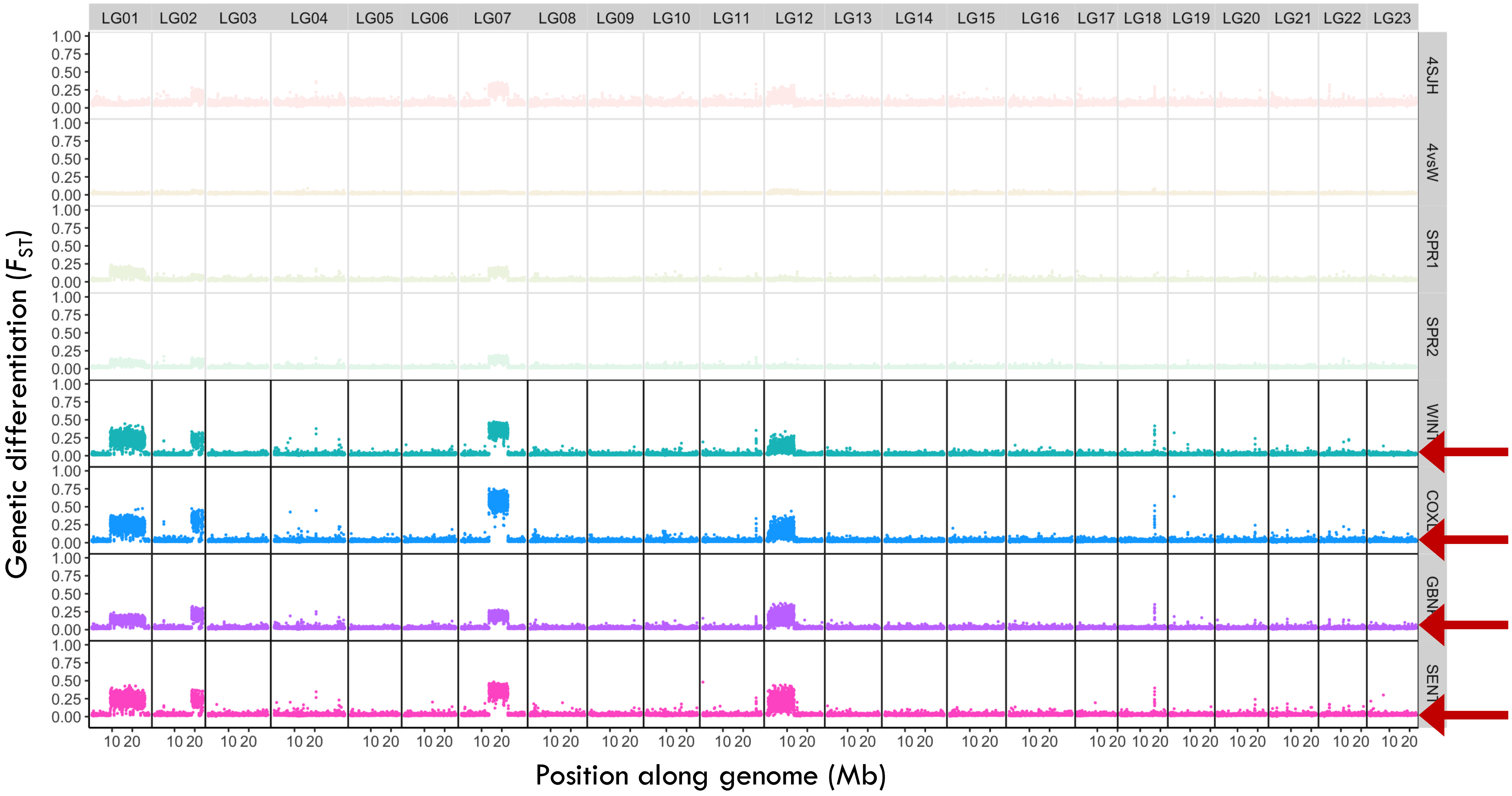
Spring spawners

Winter spawners

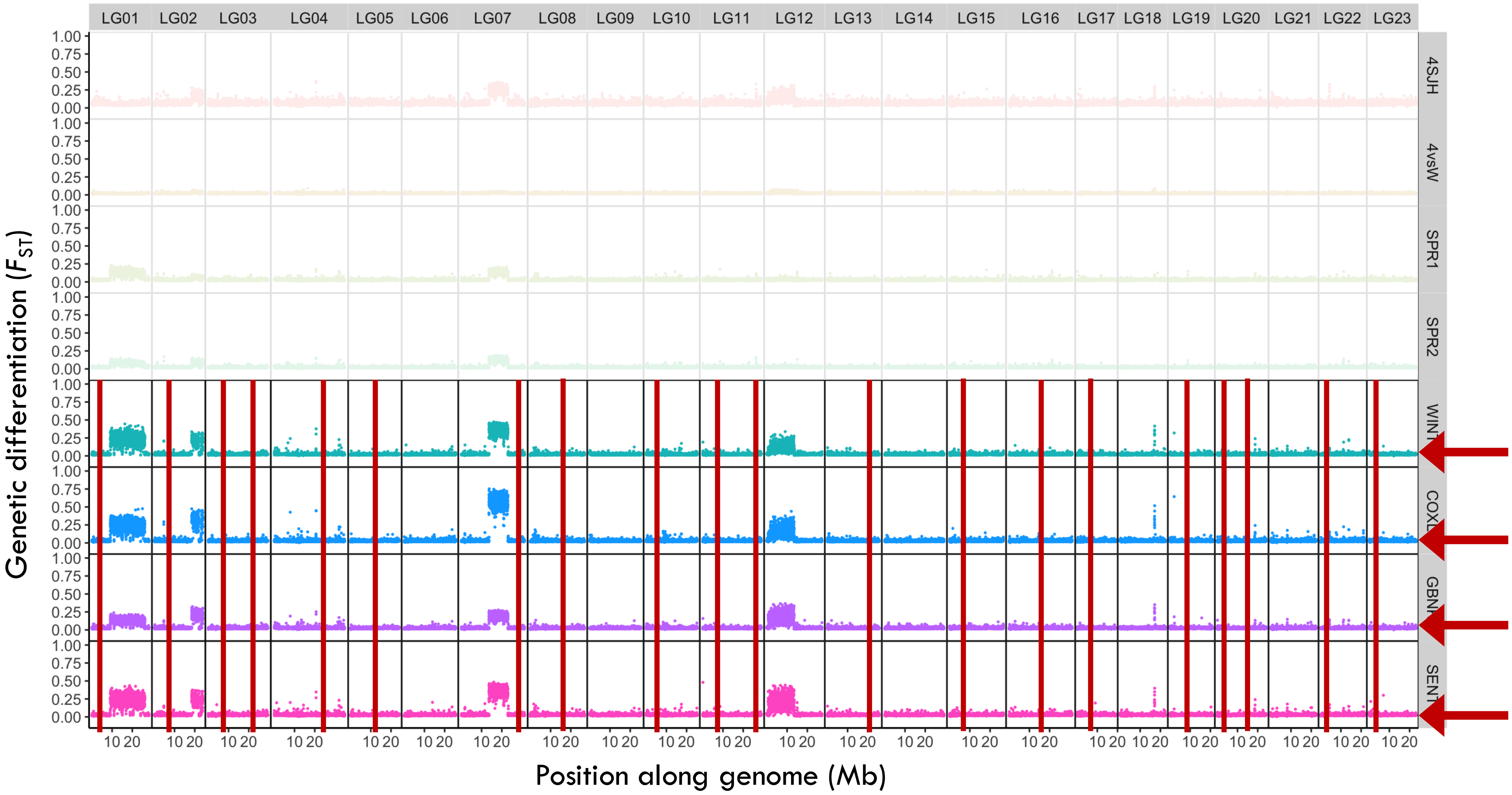
Peak overlays genes known to be involved in gamete maturation, incl. follicle-stimulating hormone receptor & estrogen receptor

Clucas et al. 2019. Evol. Appl.

# Pairwise comparisons to St. Pierre Bank, Canada (15 kb windows)



# Sampling with 20 random markers could miss differentiated regions



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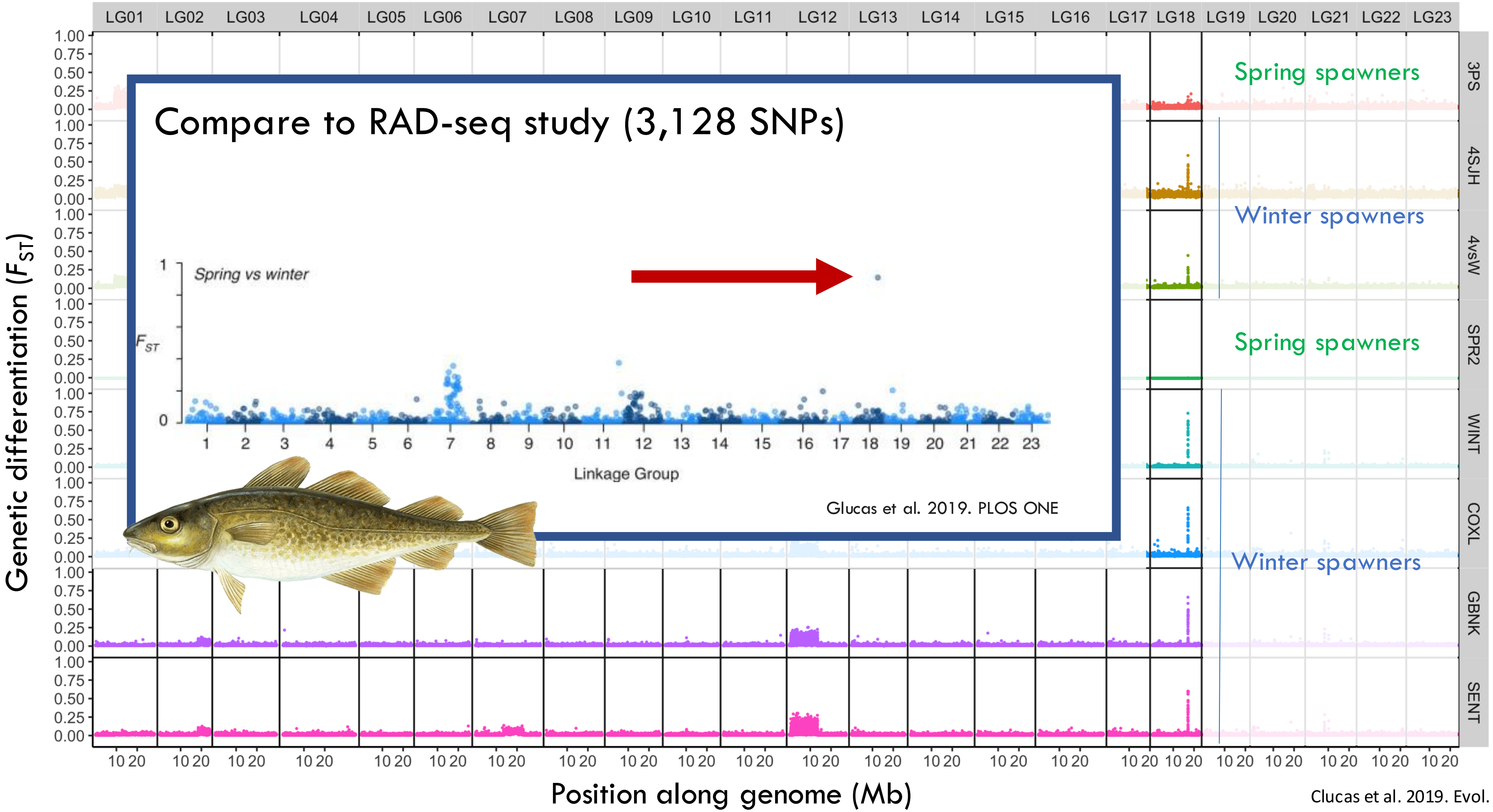
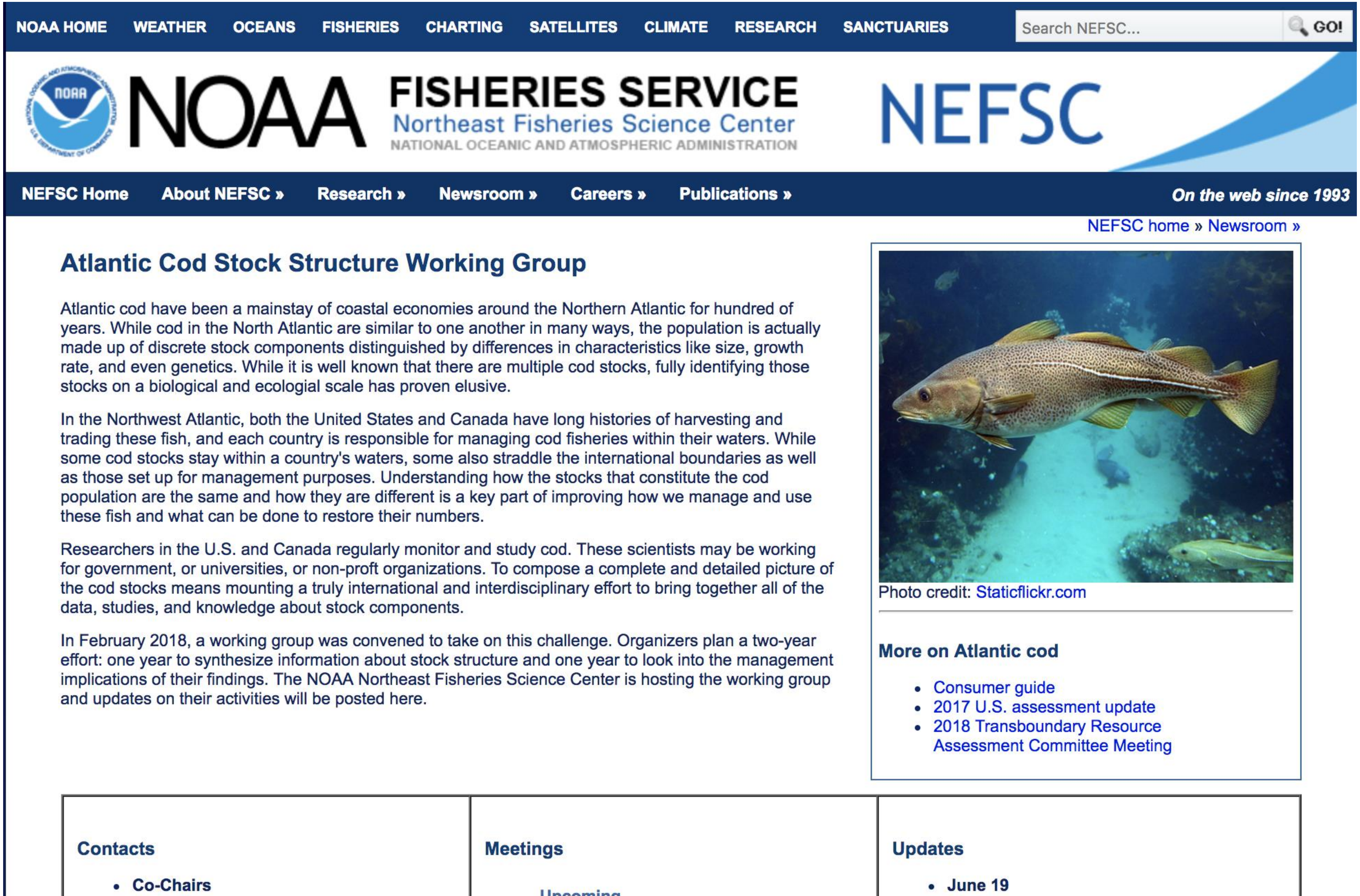


## Compare to RAD-seq study (3,128 SNPs)

Glucas et al. 2019. PLOS ONE

Clucas et al. 2019. Evol. Appl.



## Atlantic Cod Stock Structure Working Group

Atlantic cod have been a mainstay of coastal economies around the Northern Atlantic for hundred of years. While cod in the North Atlantic are similar to one another in many ways, the population is actually made up of discrete stock components distinguished by differences in characteristics like size, growth rate, and even genetics. While it is well known that there are multiple cod stocks, fully identifying those stocks on a biological and ecologial scale has proven elusive.

In the Northwest Atlantic, both the United States and Canada have long histories of harvesting and trading these fish, and each country is responsible for managing cod fisheries within their waters. While some cod stocks stay within a country's waters, some also straddle the international boundaries as well as those set up for management purposes. Understanding how the stocks that constitute the cod population are the same and how they are different is a key part of improving how we manage and use these fish and what can be done to restore their numbers.

Researchers in the U.S. and Canada regularly monitor and study cod. These scientists may be working for government, or universities, or non-proft organizations. To compose a complete and detailed picture of the cod stocks means mounting a truly international and interdisciplinary effort to bring together all of the data, studies, and knowledge about stock components.

In February 2018, a working group was convened to take on this challenge. Organizers plan a two-year effort: one year to synthesize information about stock structure and one year to look into the management implications of their findings. The NOAA Northeast Fisheries Science Center is hosting the working group and updates on their activities will be posted here.

Photo credit: Staticflickr.com

### More on Atlantic cod

- Consumer guide
- 2017 U.S. assessment update
- 2018 Transboundary Resource Assessment Committee Meeting

### Contacts

- Co-Chairs

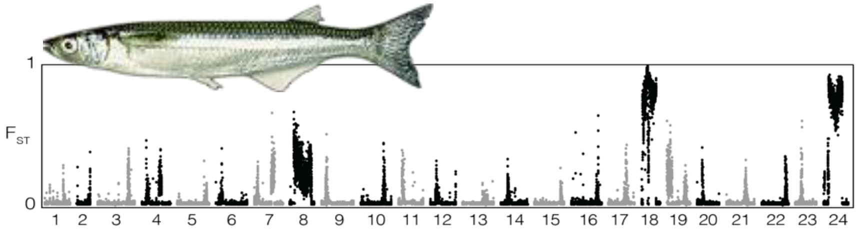
### Meetings

### Updates

- June 19

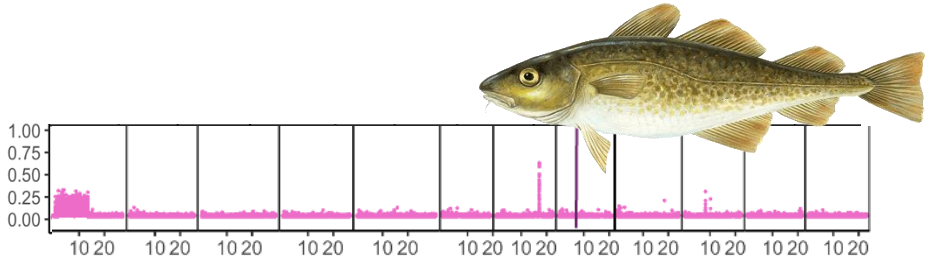
# Differentiation often limited to parts of the genome

## Strong adaptation despite homogeneous genomes



Atlantic silversides

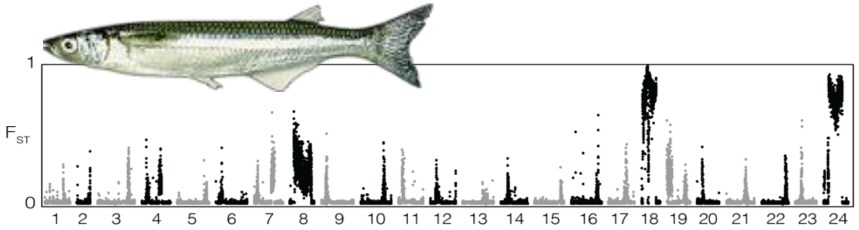
## Differences confined to small genomic regions



Atlantic cod

# Differentiation often limited to parts of the genome

Strong adaptation despite homogeneous genomes



Atlantic silversides

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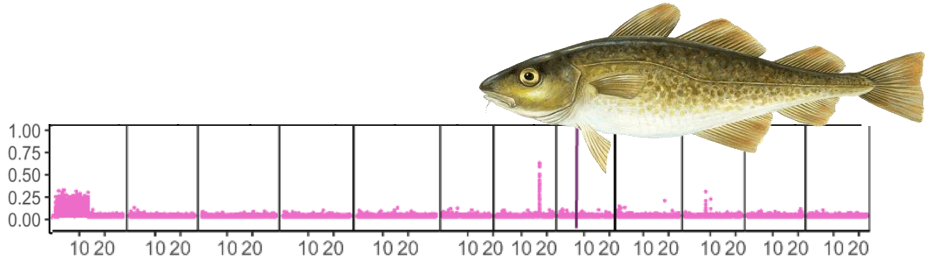


Atlantic cod

Surprising mixture of lineages can also occur

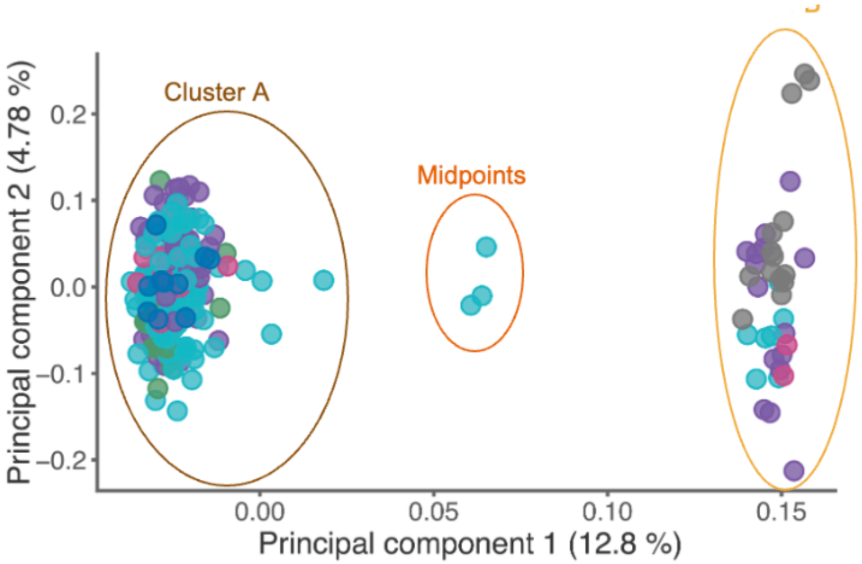
# Sea cucumbers in the Galapagos islands

## Mixture of local and mainland-connected lineage

Jaime Ortiz-Pachar

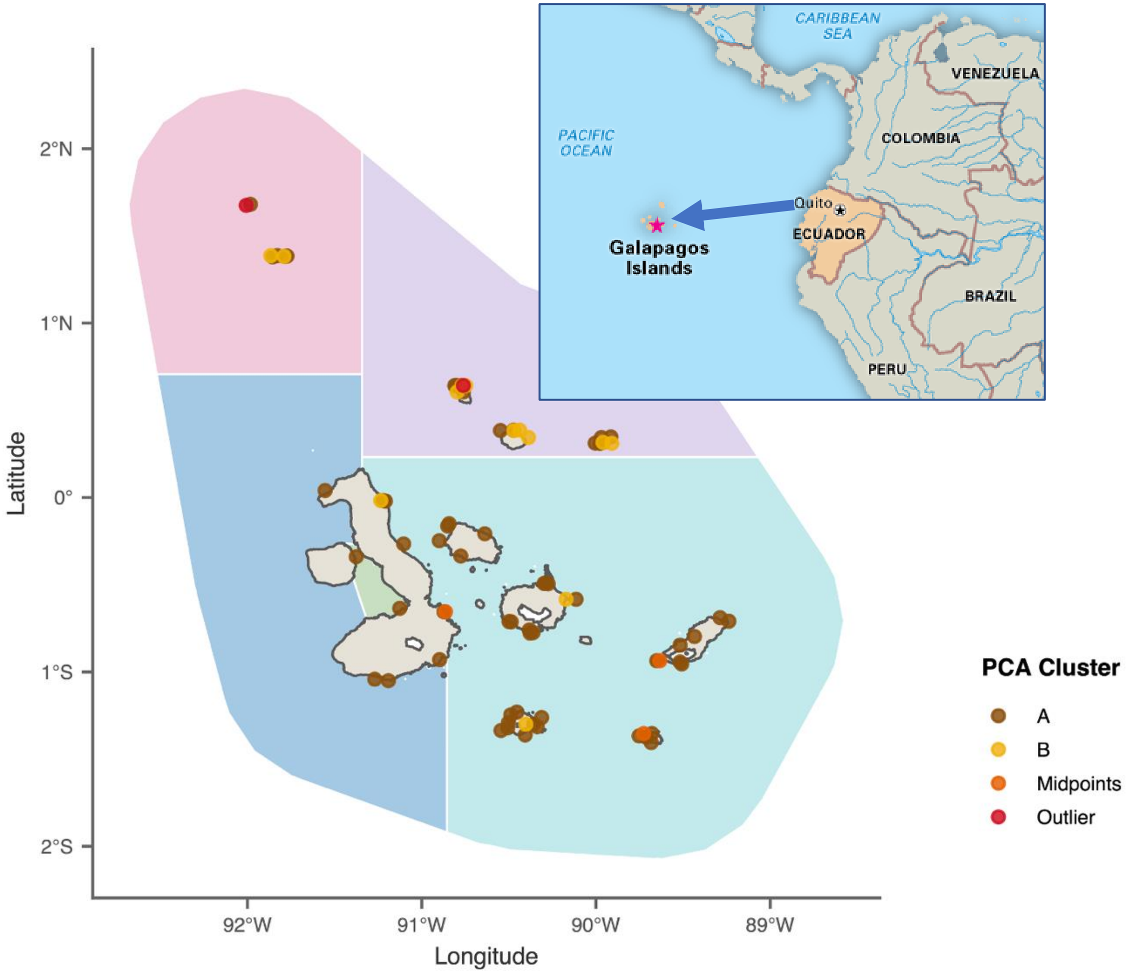
# Sea cucumbers in the Galapagos islands

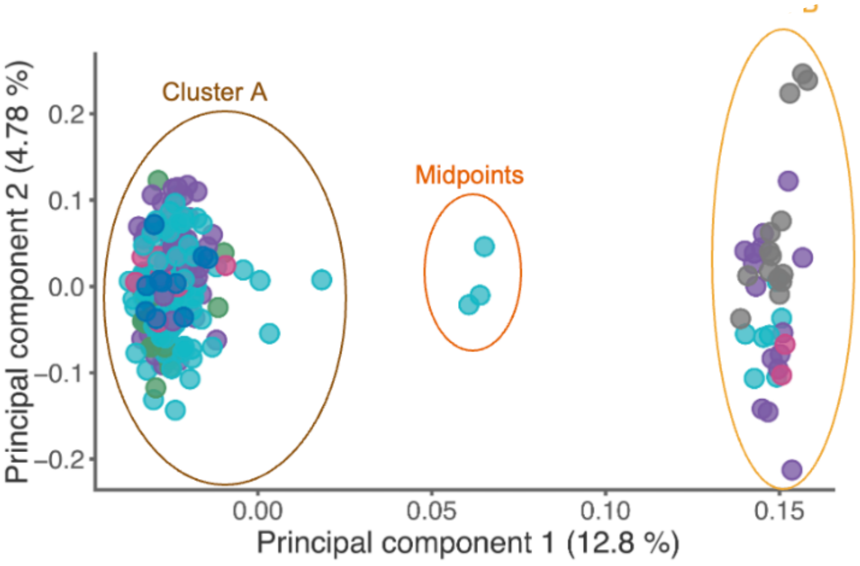
## Mixture of local and mainland-connected lineage



# Sea cucumbers in the Galapagos islands

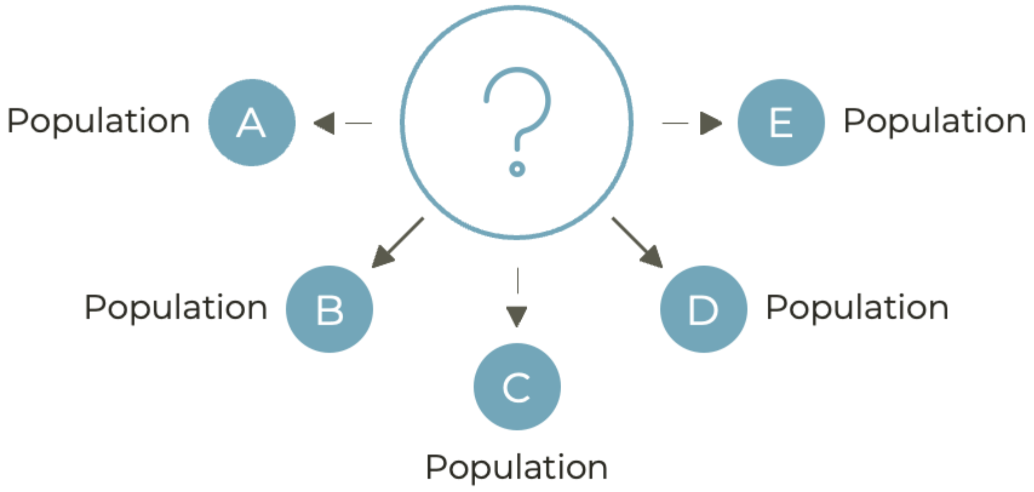
## Mixture of local and mainland-connected lineage

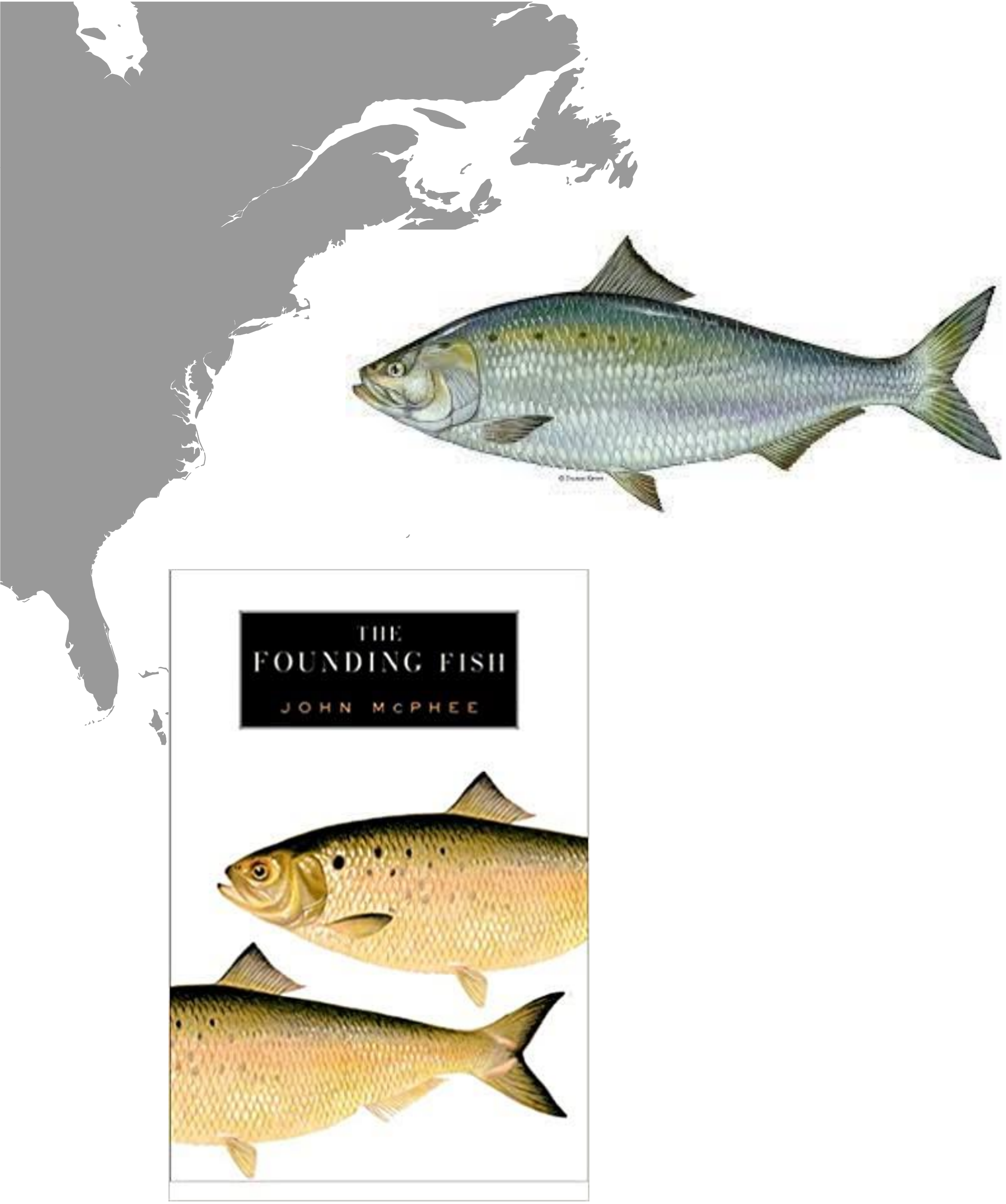




# From hidden structure to measurable mixing

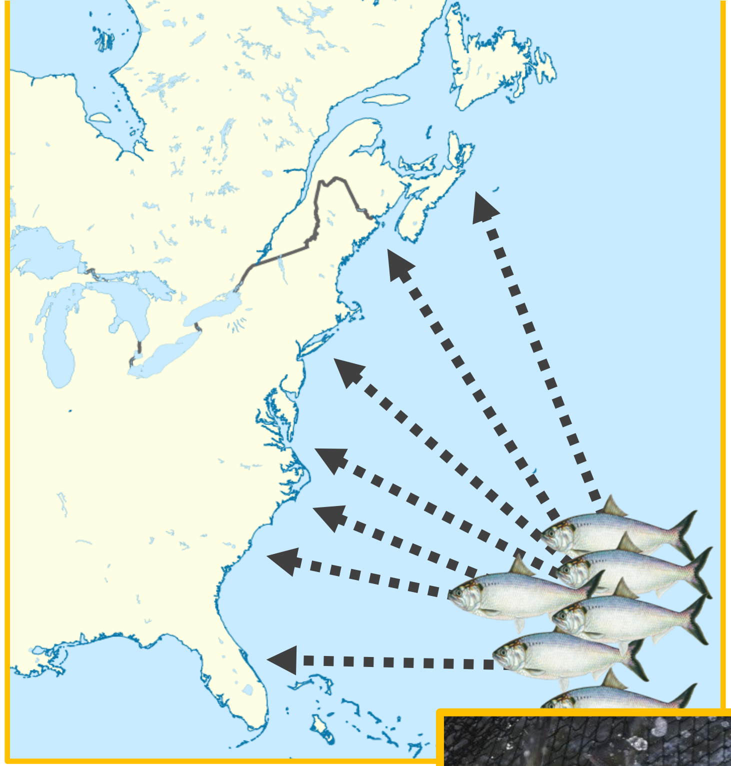
- Subtle and cryptic structure is common
- Management decisions depend on who mixes with whom – and when
- We need to assign individuals to their origin





# American shad

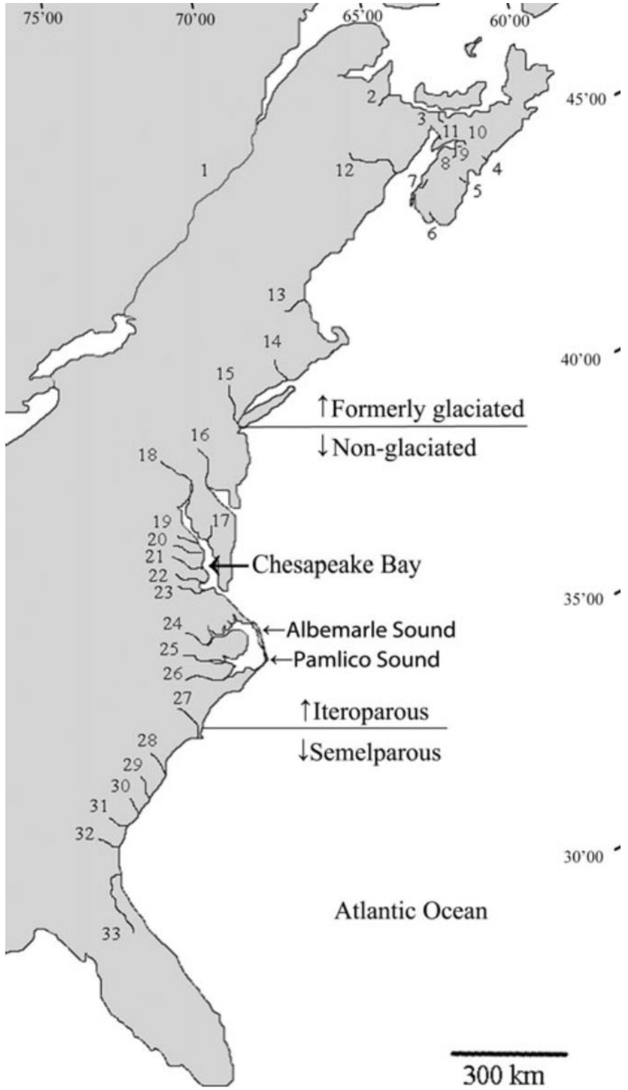
- Called “the founding” fish because of historical abundance
- Now decimated in many places, but some remaining fisheries

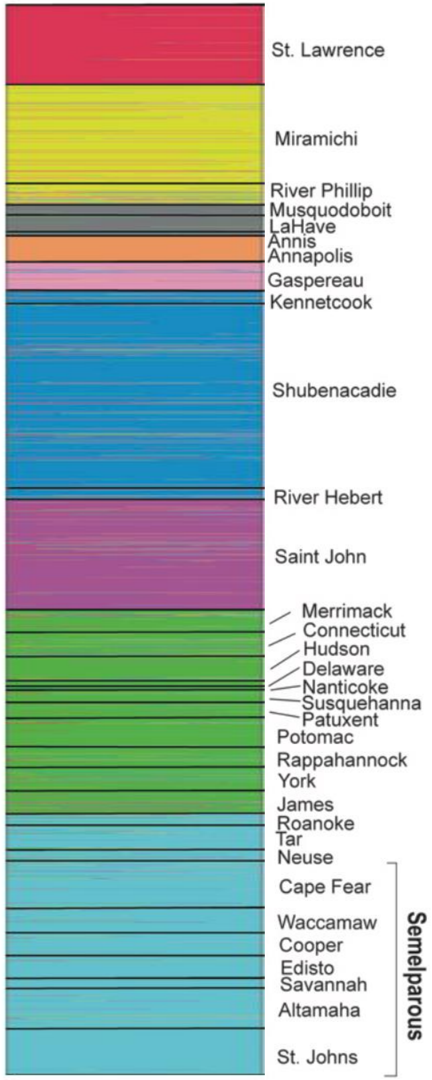


# American shad

- Called "the founding" fish because of historical abundance
- Now decimated in many places, but some remaining fisheries
- Interest in assigning marine bycatch to population

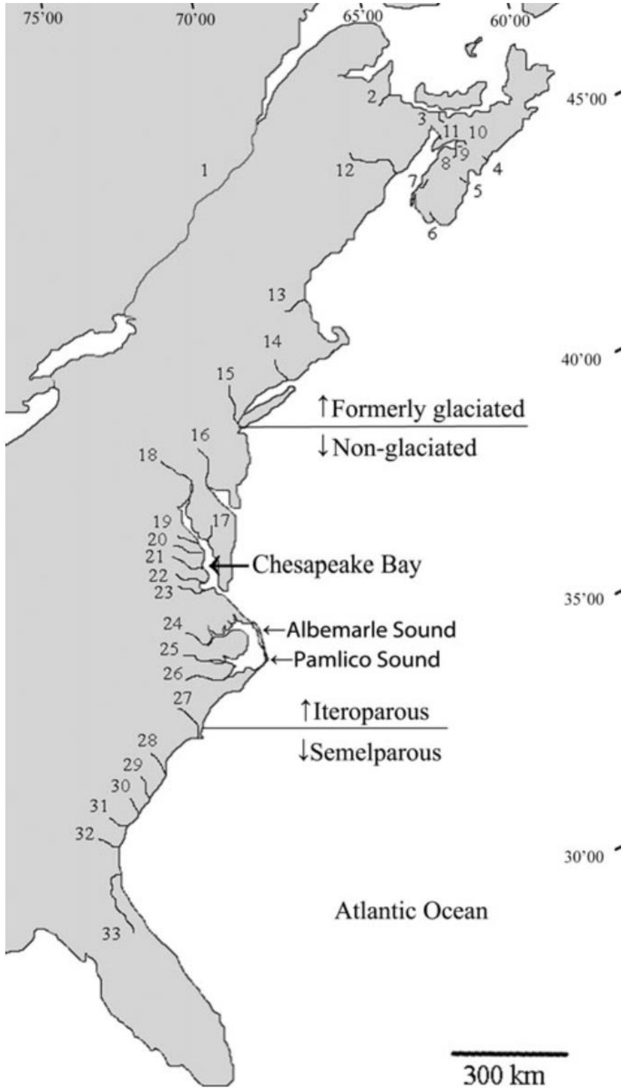
# Limited population differentiation in US waters with microsatellites

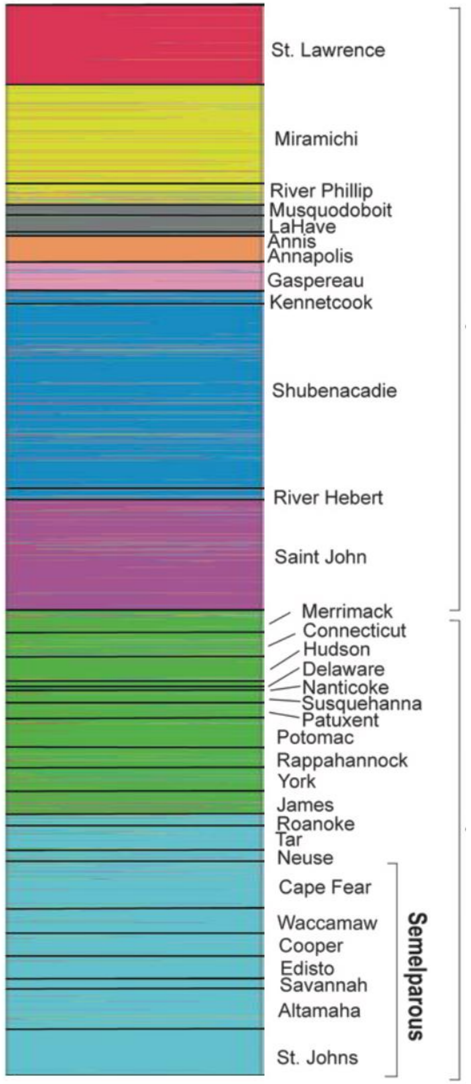




Hasselmann et al. 2013, Waldman et al. 2014

# Limited population differentiation in US waters with microsatellites



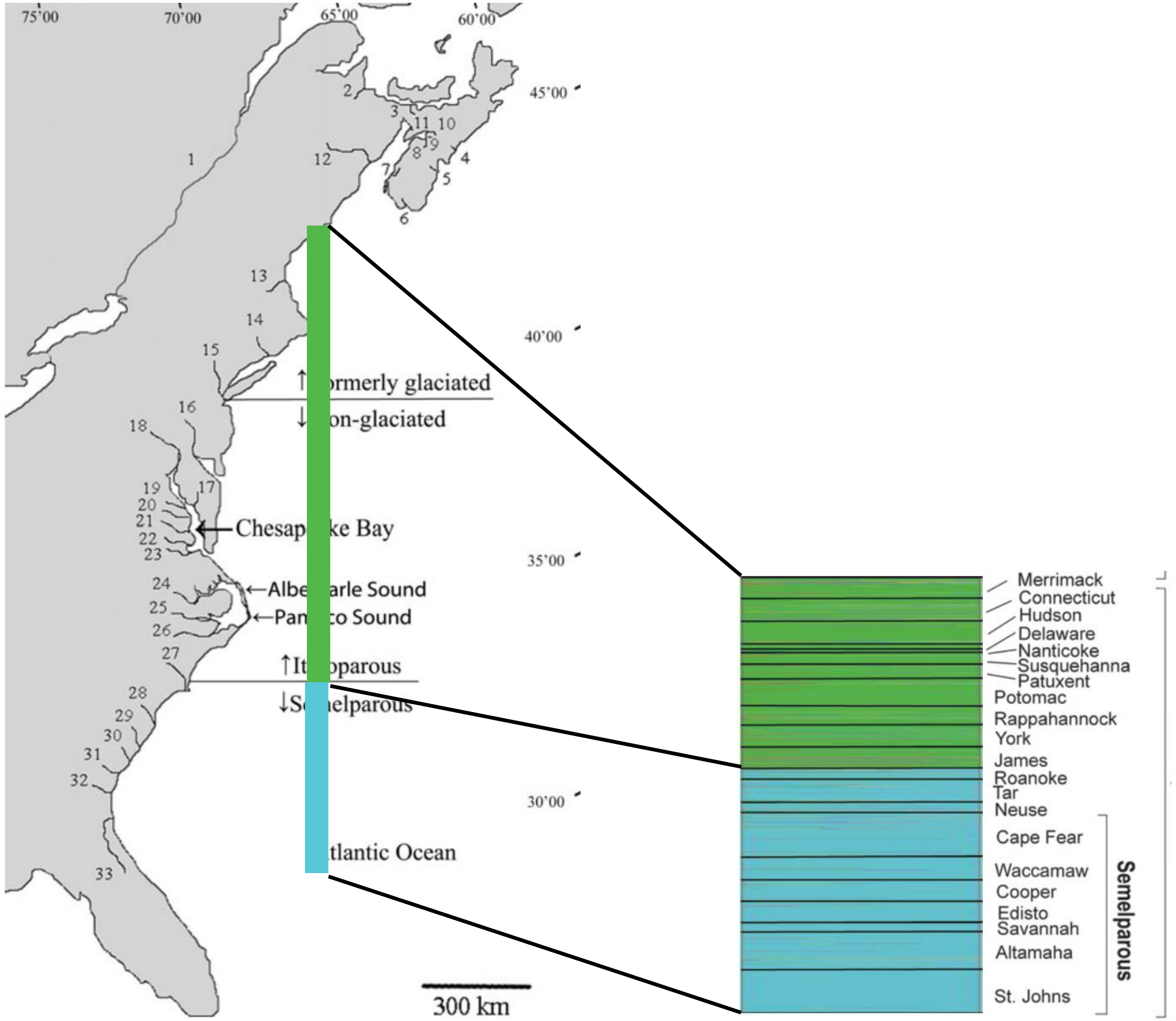


Canadian populations

U.S. populations

Hasselmann et al. 2013, Waldman et al. 2014

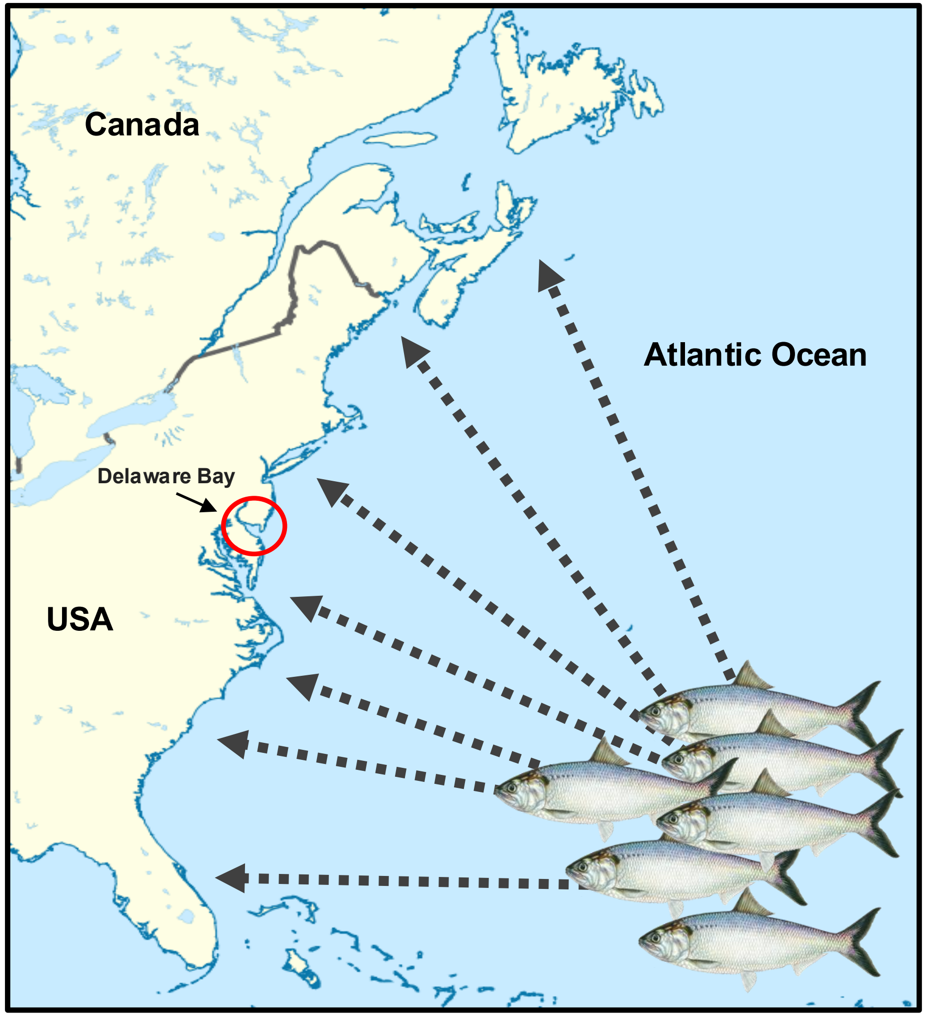
# Limited population differentiation in US waters with microsatellites



U.S. populations

Hasselmann et al. 2013, Waldman et al. 2014

# Microsatellite assignment

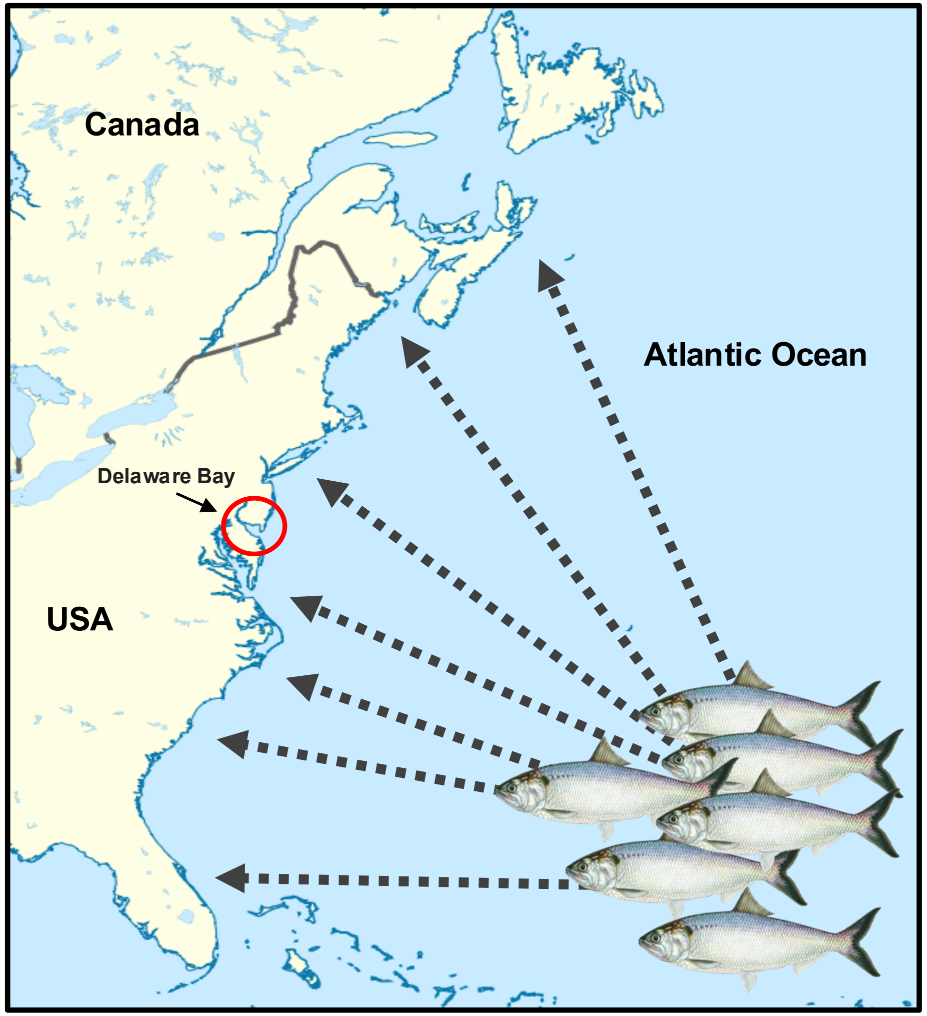


## Resolving Contribution of American Shad Mixed Stock Fishery in Lower Delaware River and Bay: 2017-2020 collection evaluation

Meredith L. Bartron and Lauren M. Prasko
USFWS Northeast Fishery Center, Lamar, PA

| Collection location | Sample size | Correct assignment |
|---|---|---|
| Narraguagus | 50 | 0.88 |
| Penobscot | 93 | 0.37 |
| Androscoggin | 48 | 0.19 |
| Kennebec | 24 | 0.04 |
| Sheepscot | 23 | 0.04 |
| Saco | 50 | 0.10 |
| Merrimack | 49 | 0.10 |
| Connecticut | 54 | 0.15 |
| Hudson | 200 | 0.47 |
| Delaware | 198 | 0.43 |
| Susquehanna | 48 | 0.19 |
| Potomac | 49 | 0.22 |
| Tar | 38 | 0.16 |
| Cooper | 48 | 0.92 |

# Microsatellite assignment



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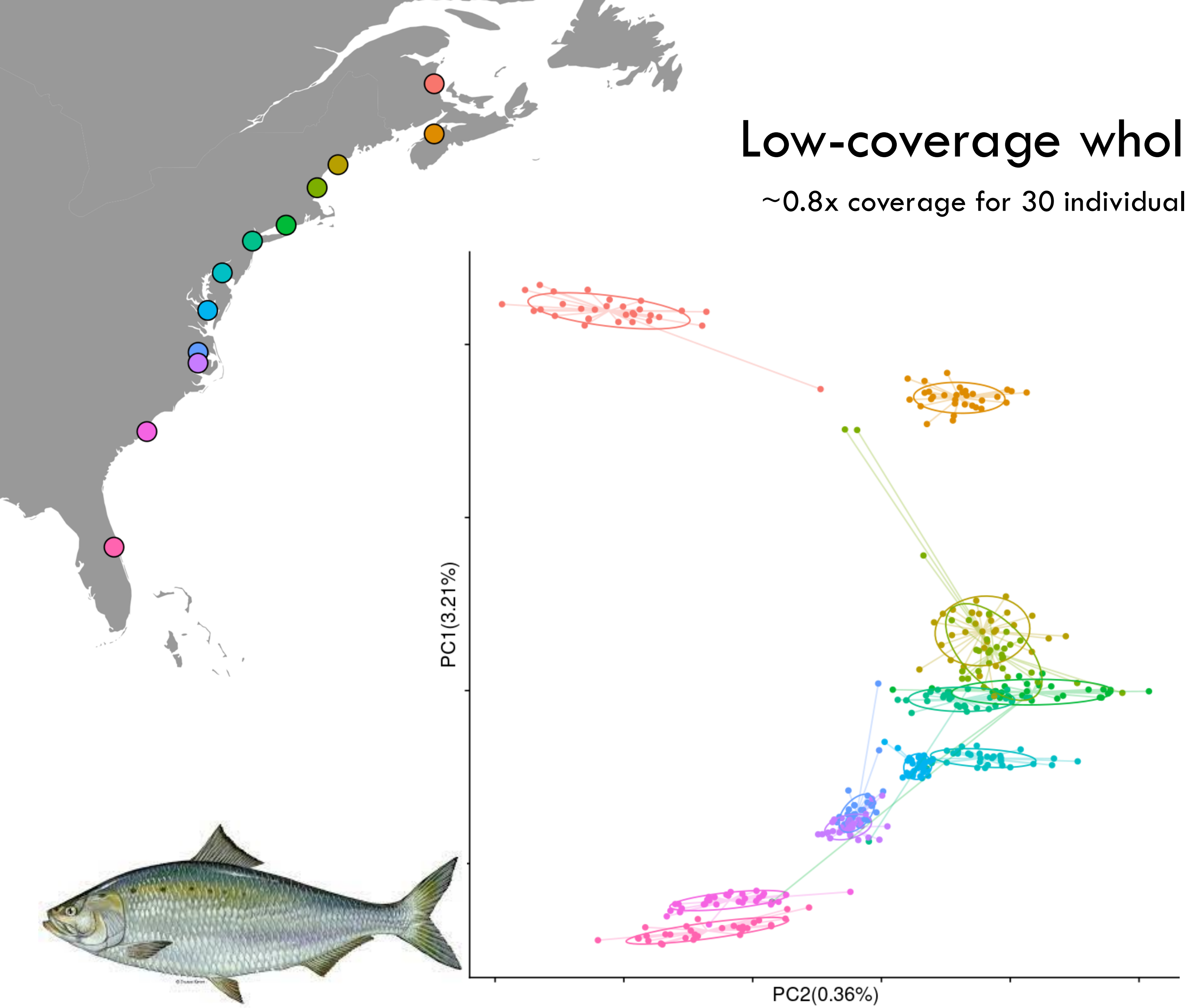
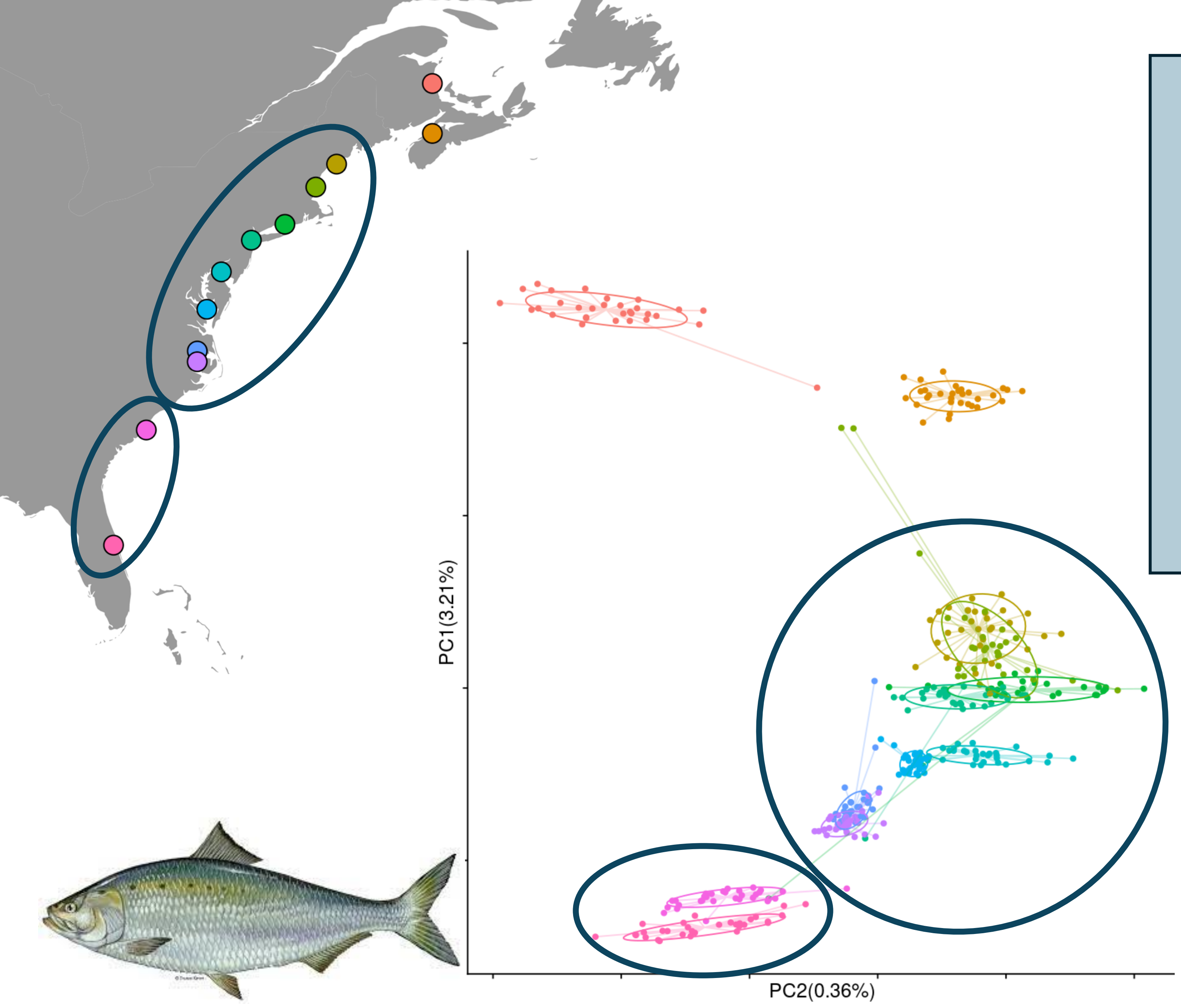
Mean: 30.2%
Range: 4 - 92%

# Low-coverage whole genome sequencing

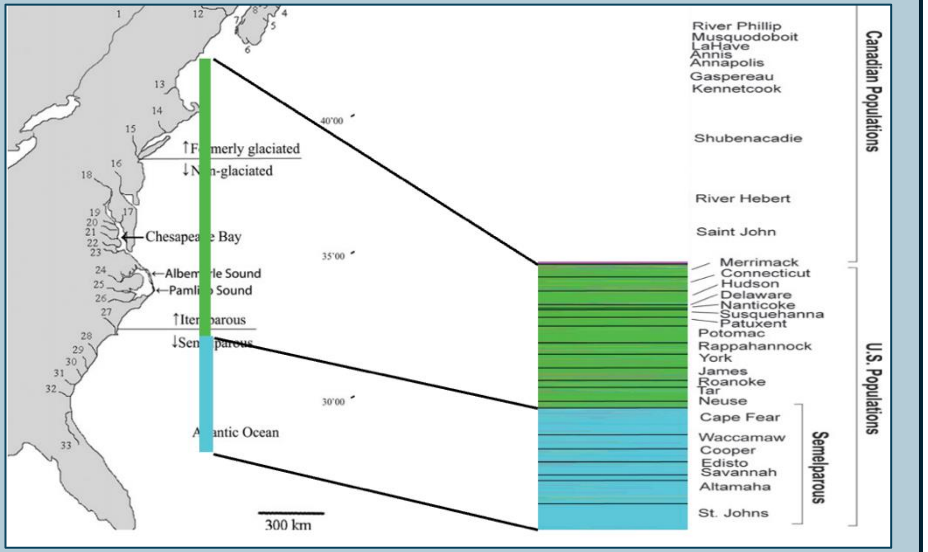
~0.8x coverage for 30 individuals per location



Ryan Franckowiak

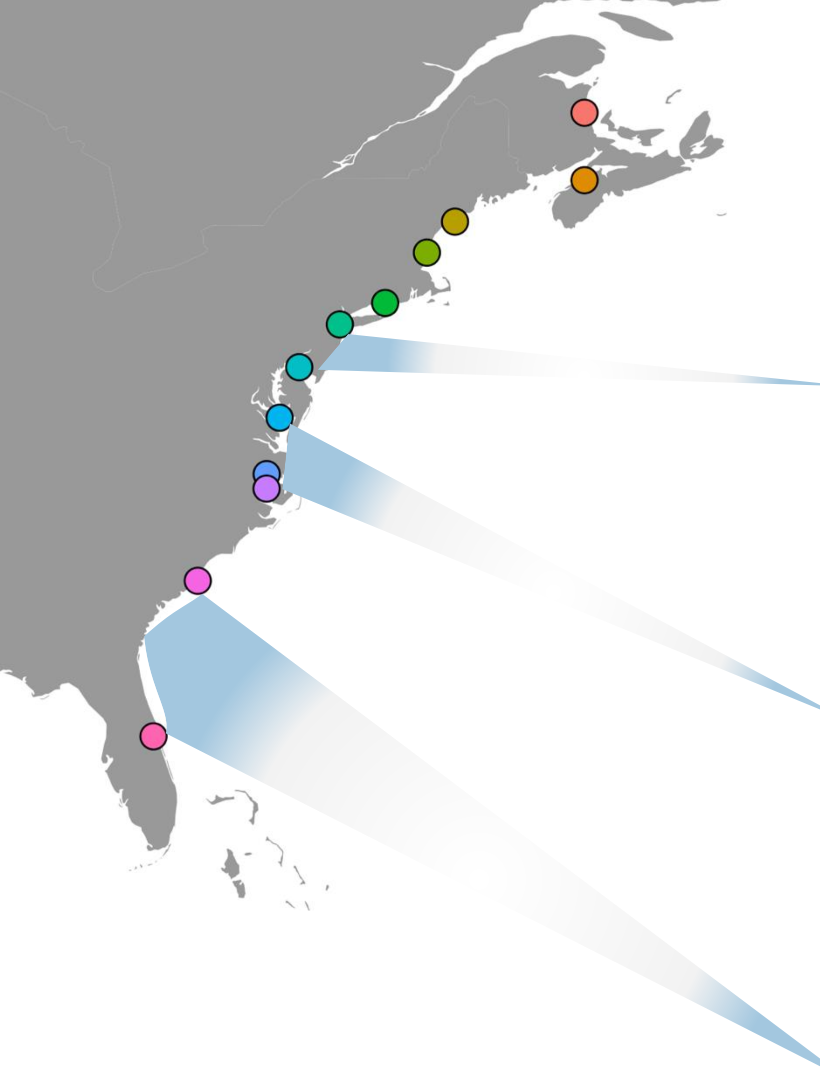


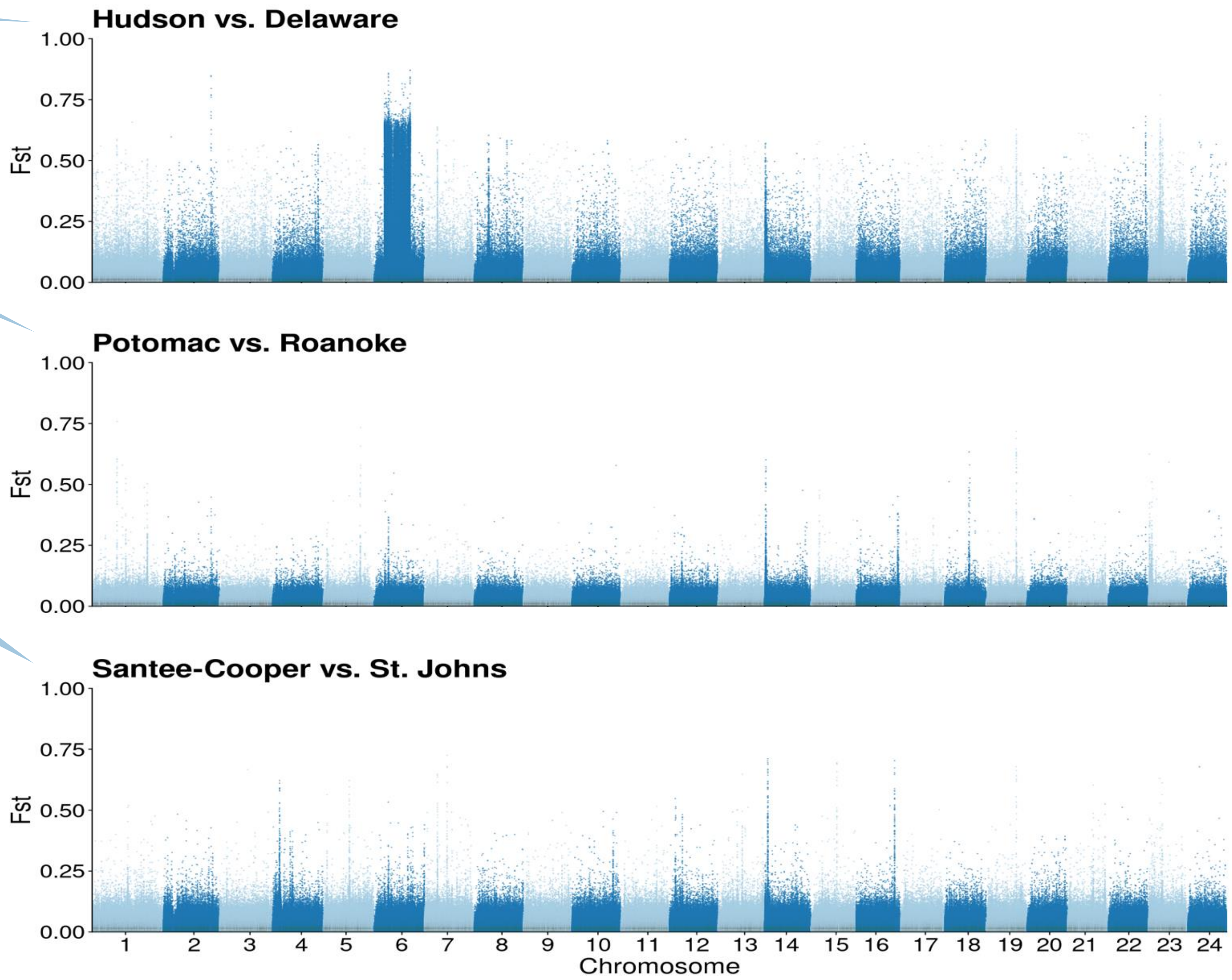
## Microsatellite results



Increased population resolution in US waters

# Pairwise comparisons of differentiation among neighboring populations

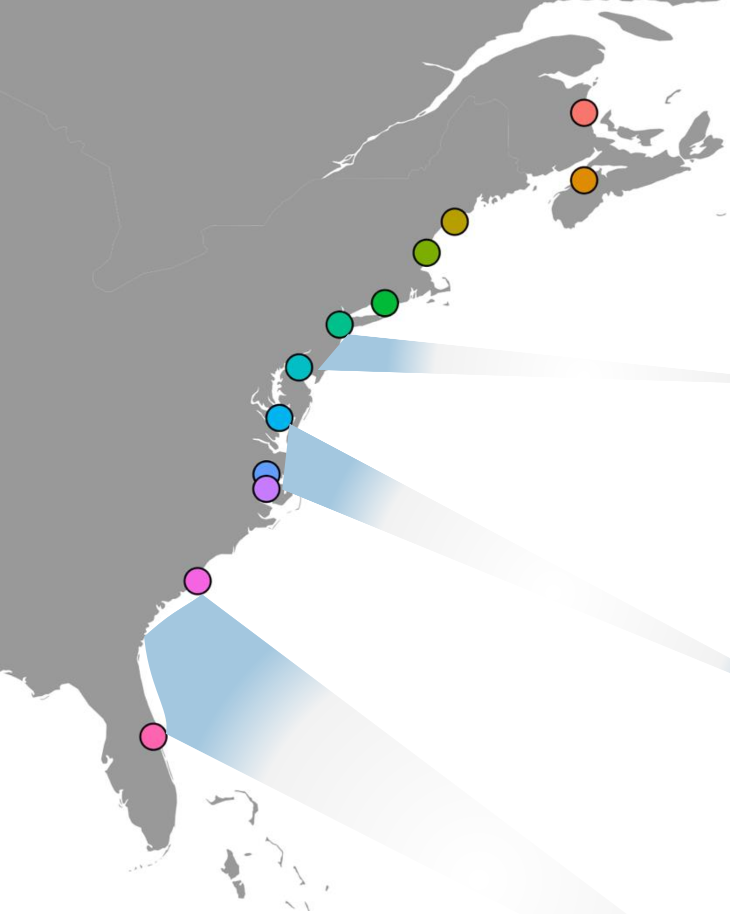


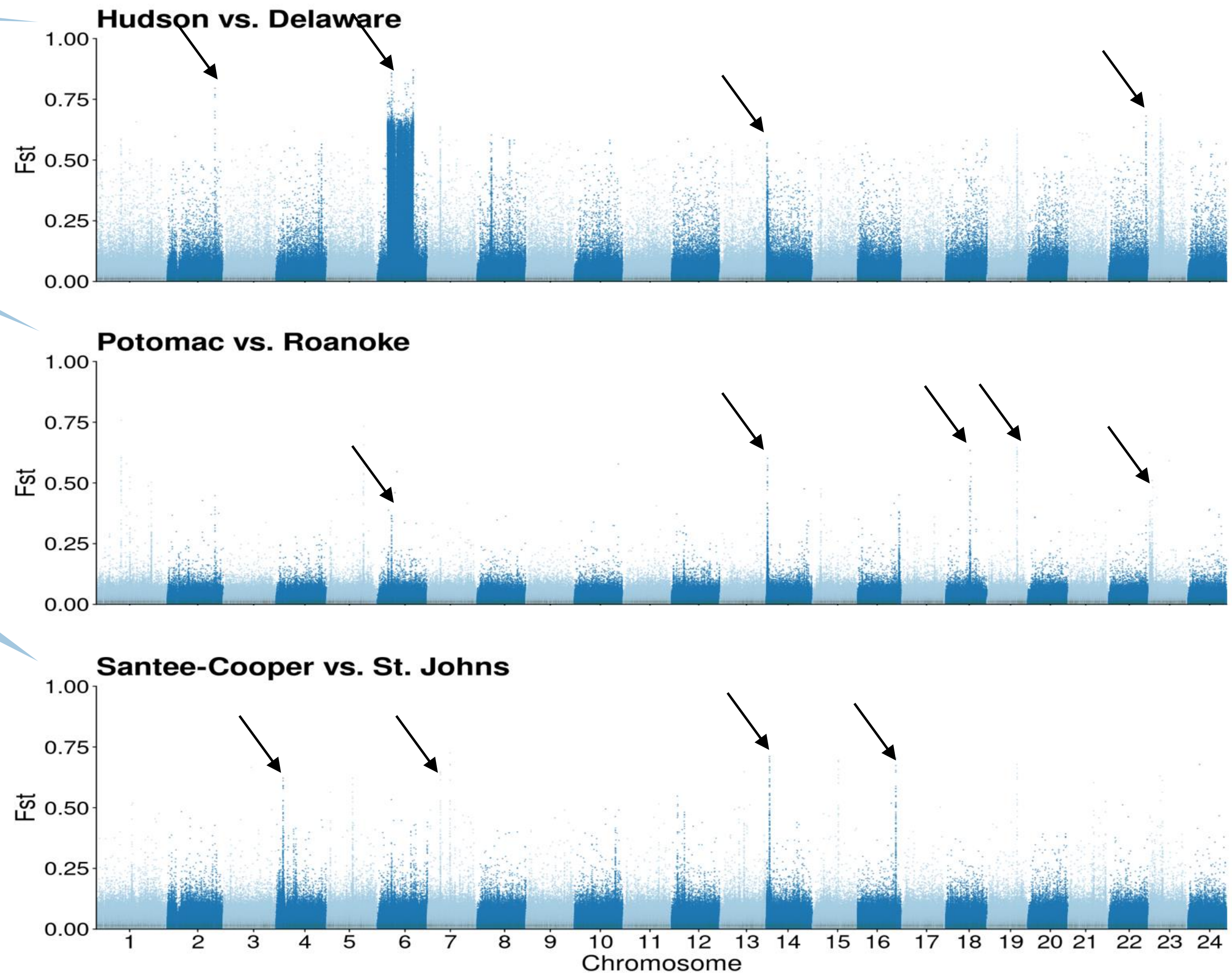

Hudson vs. Delaware

Potomac vs. Roanoke

Santee-Cooper vs. St. Johns

# Selecting markers from the biggest peaks should improve power for assignment





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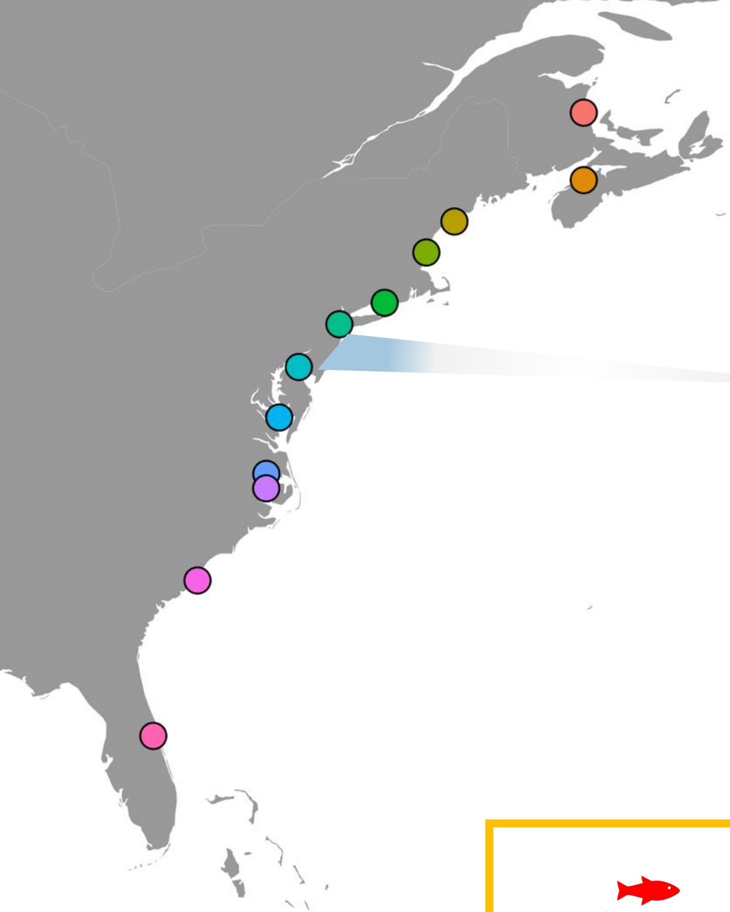

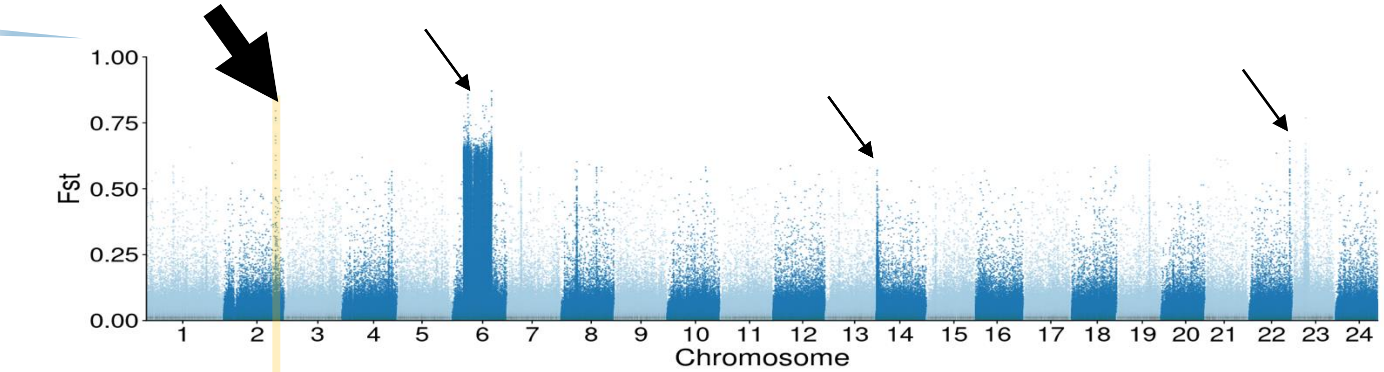

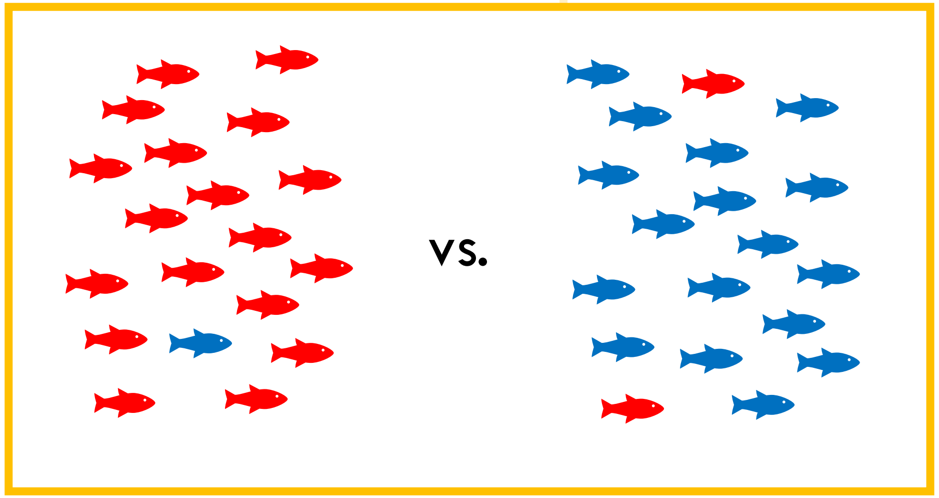

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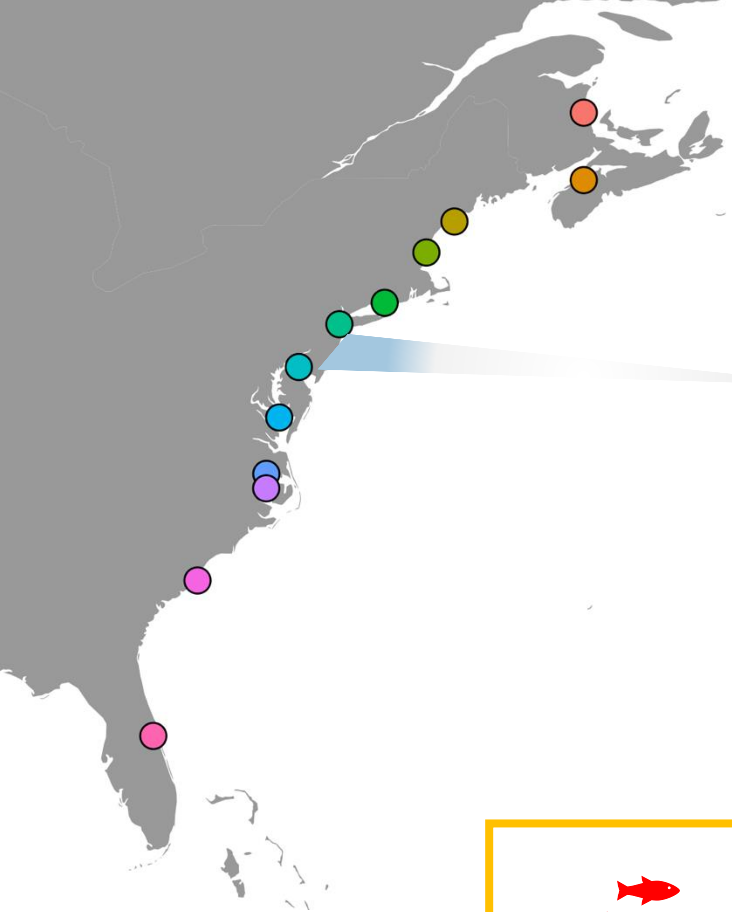
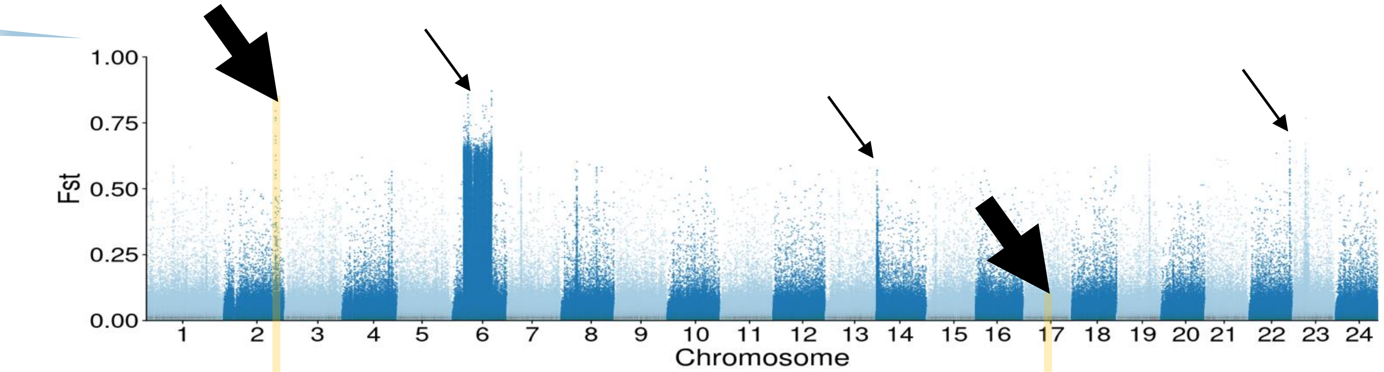
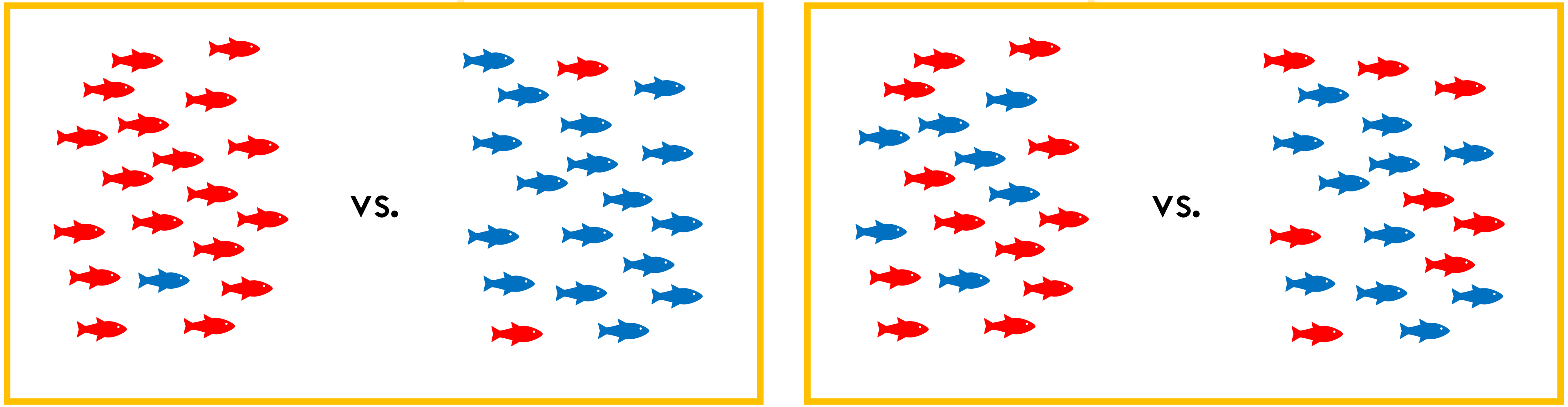






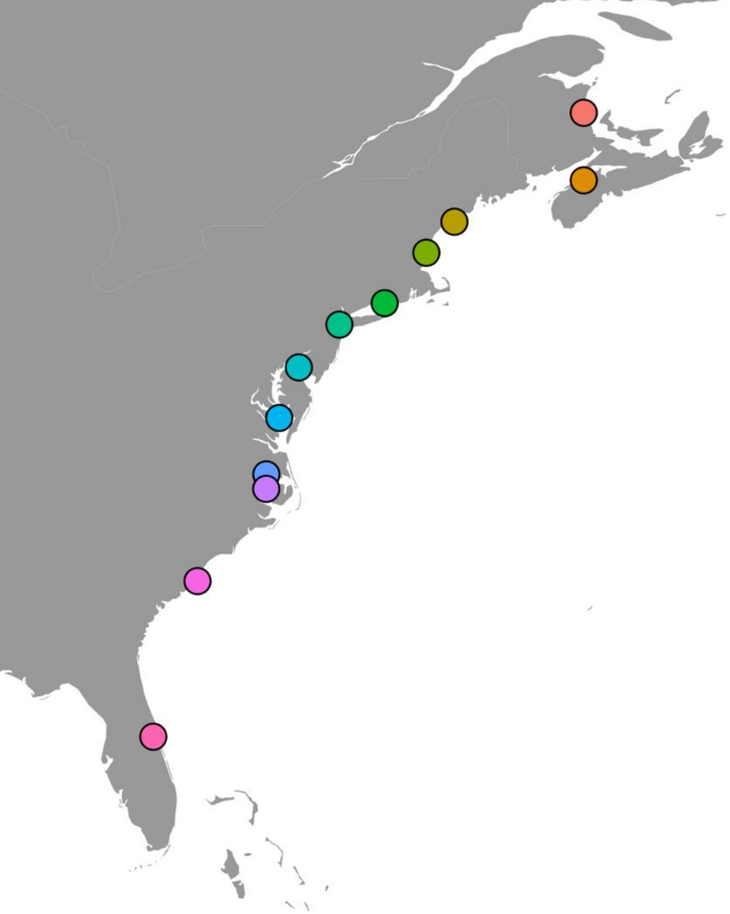
# Marker panel

## GT-seq (highly multiplexed amplicon sequencing)

578 top-ranked SNPs screened

248 retained for genotyping

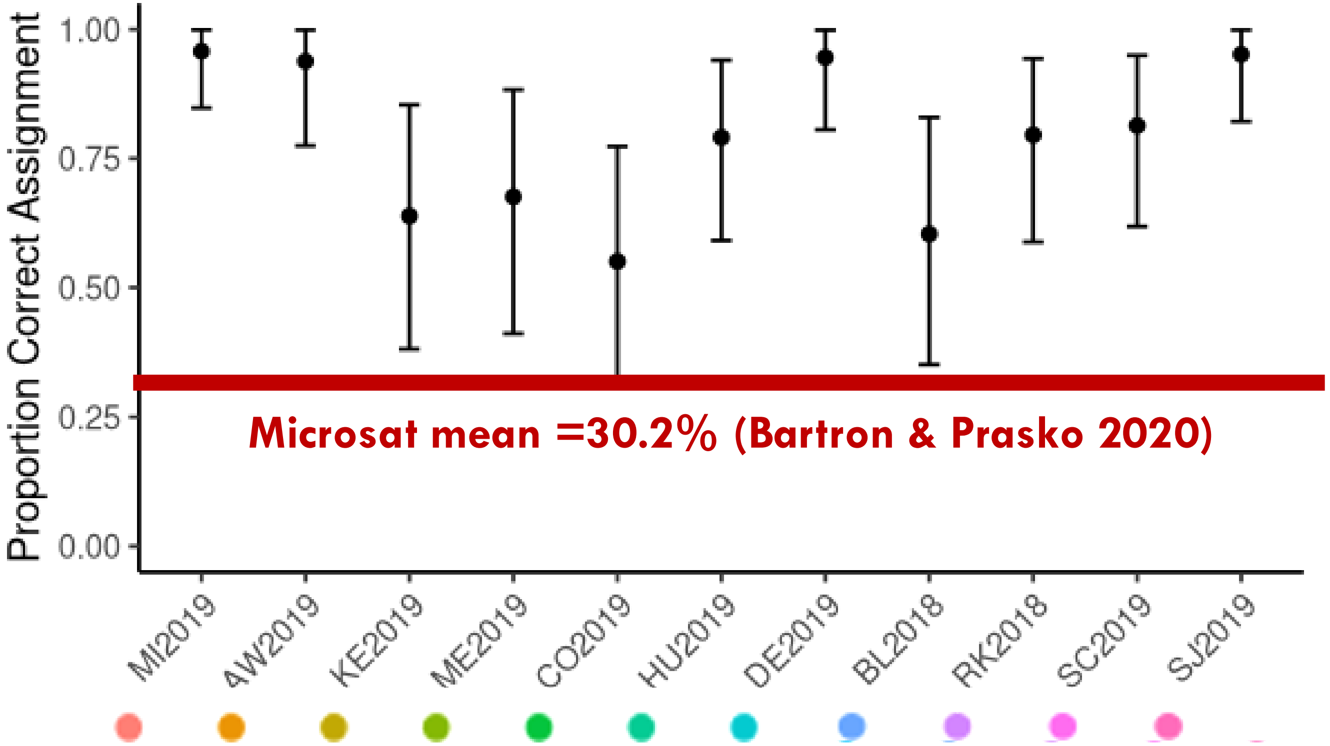
107 microhaplotypes (100bp) genotyped
(average 4.2 SNPs per microhaplotype, 2-9 alleles)



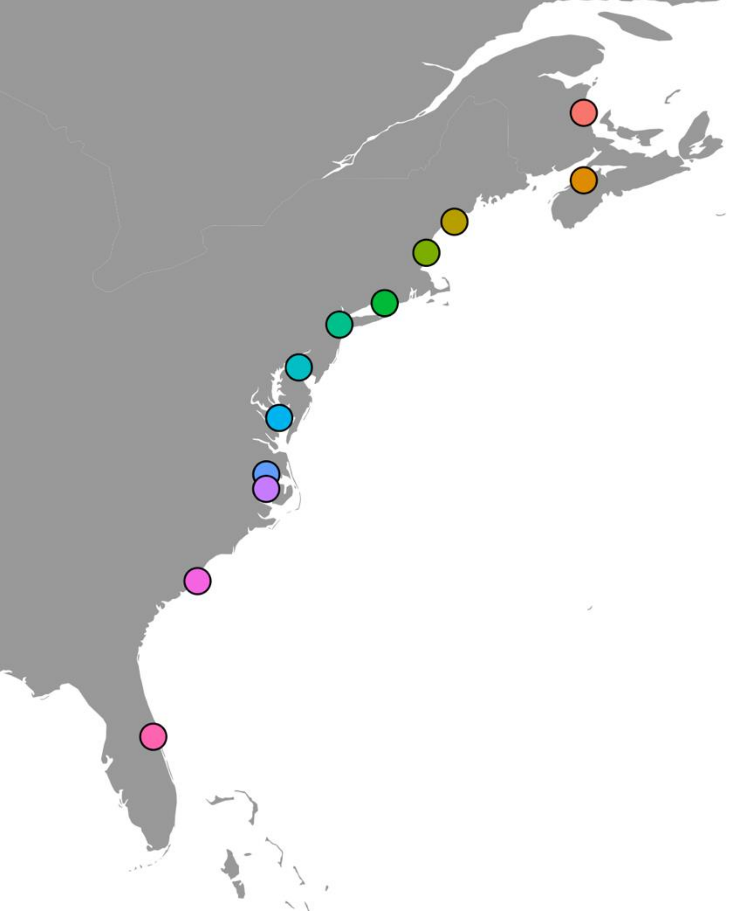
# Performance of GT-seq panel

SNP selection based on 30 training individuals from each population
Assignment success assessed for 20 separate in-year test individuals

Leave-one-out assignment with different simulated mixture proportions



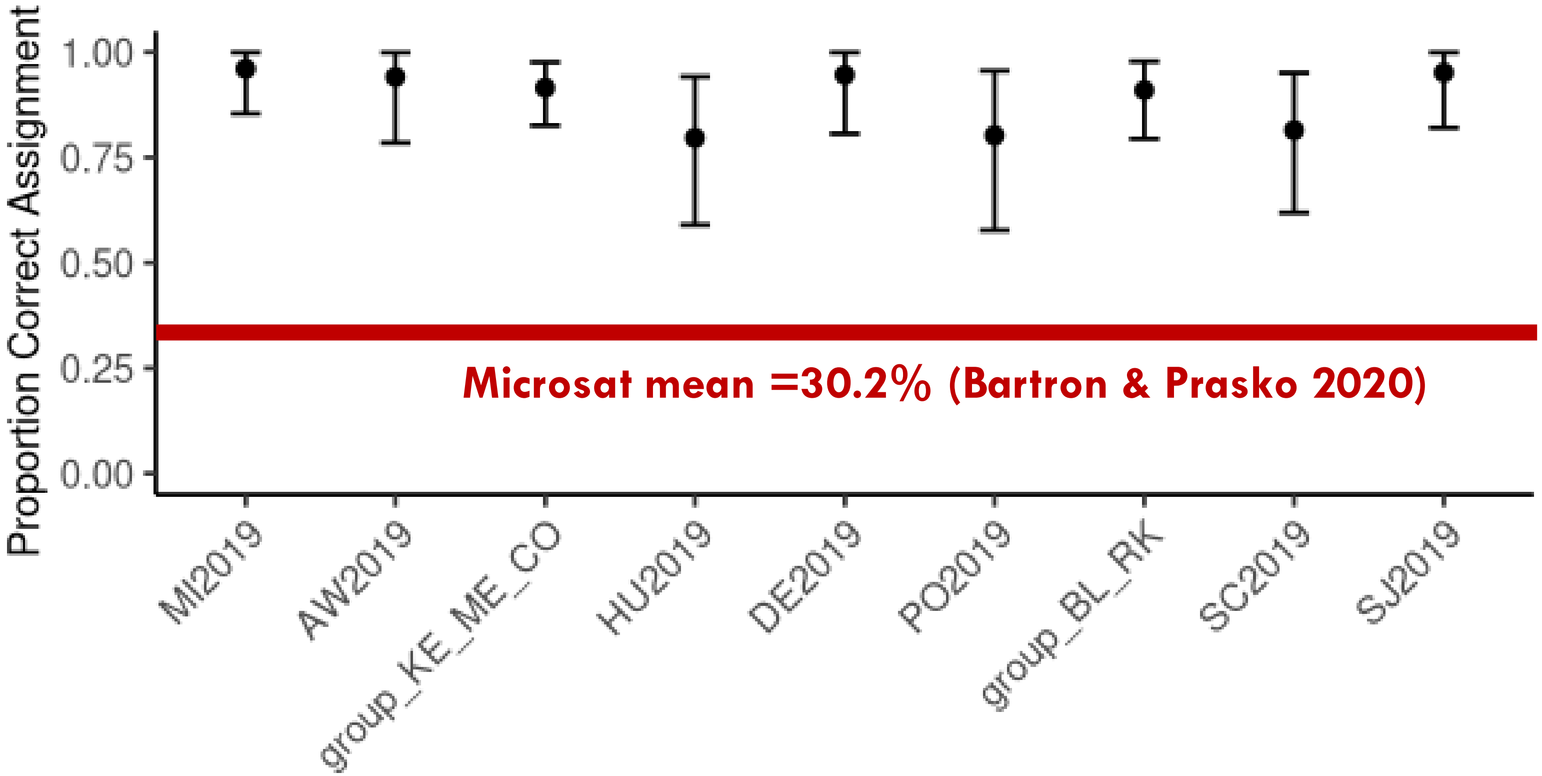
**Microsat mean =30.2% (Bartron & Prasko 2020)**



# Performance of GT-seq panel

SNP selection based on 30 training individuals from each population
Assignment success assessed for 20 separate in-year test individuals

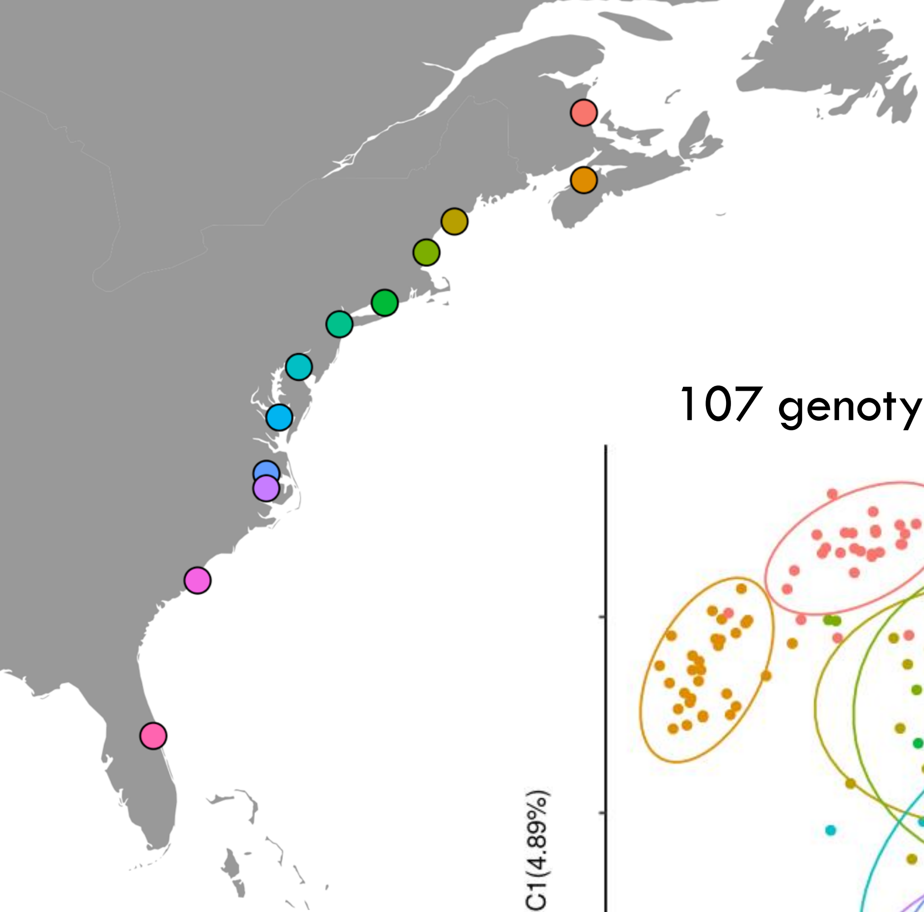
Leave-one-out assignment with different simulated mixture proportions



**Microsat mean =30.2% (Bartron & Prasko 2020)**

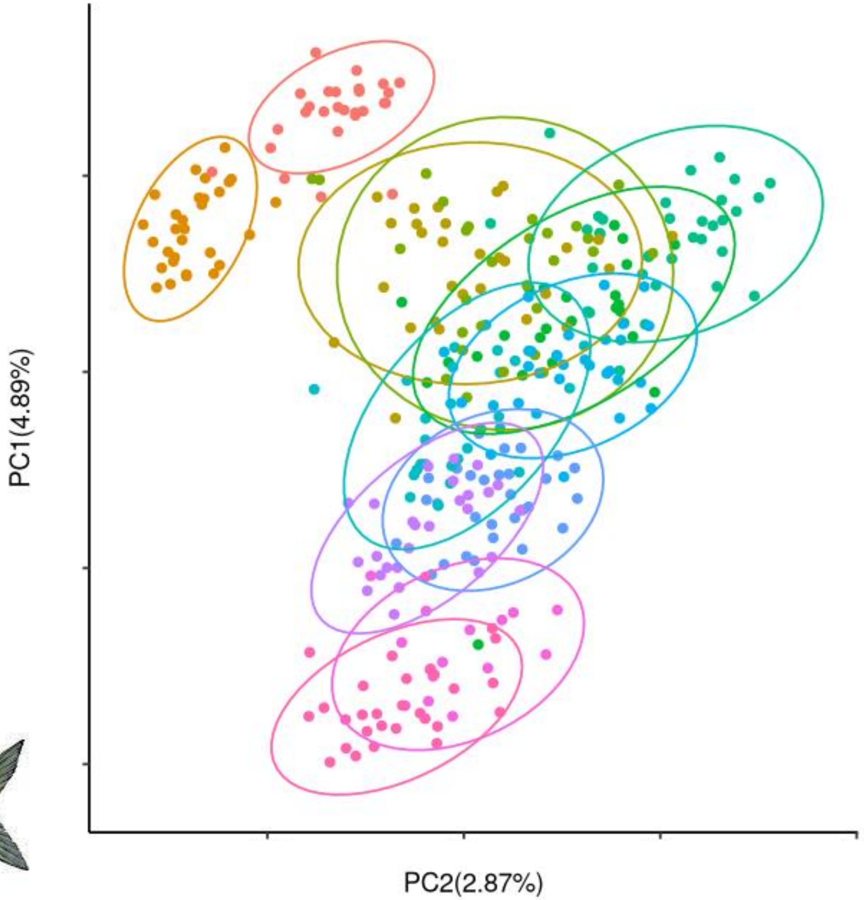
# Downsides of genotyping panel

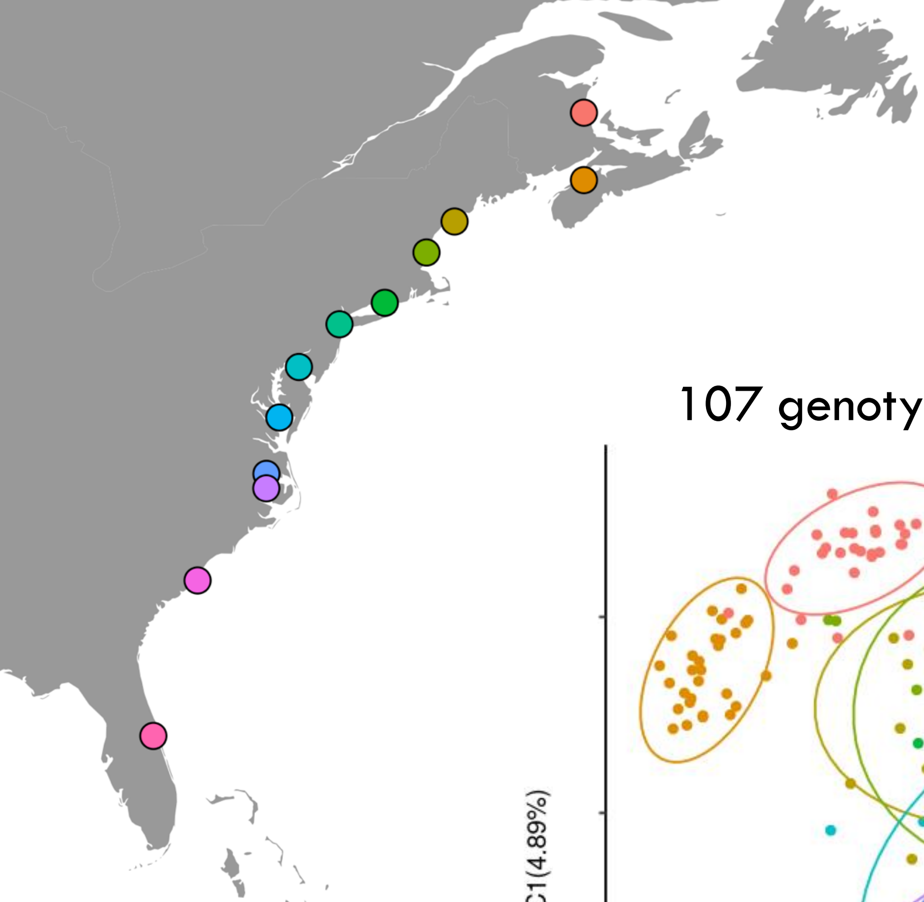
- Costly to develop
- Ascertainment bias based on which populations are included
- Large investment in targeted primers
- Does not capture the full variation



# Principal Components Analysis

107 genotyped microhaplotypes





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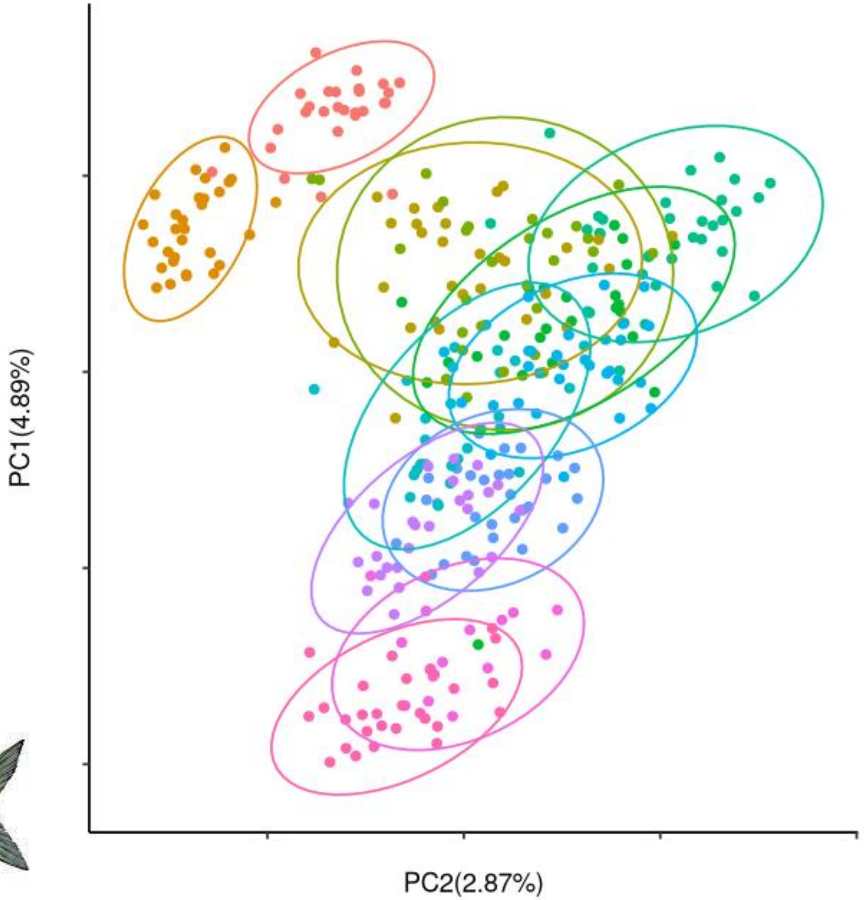
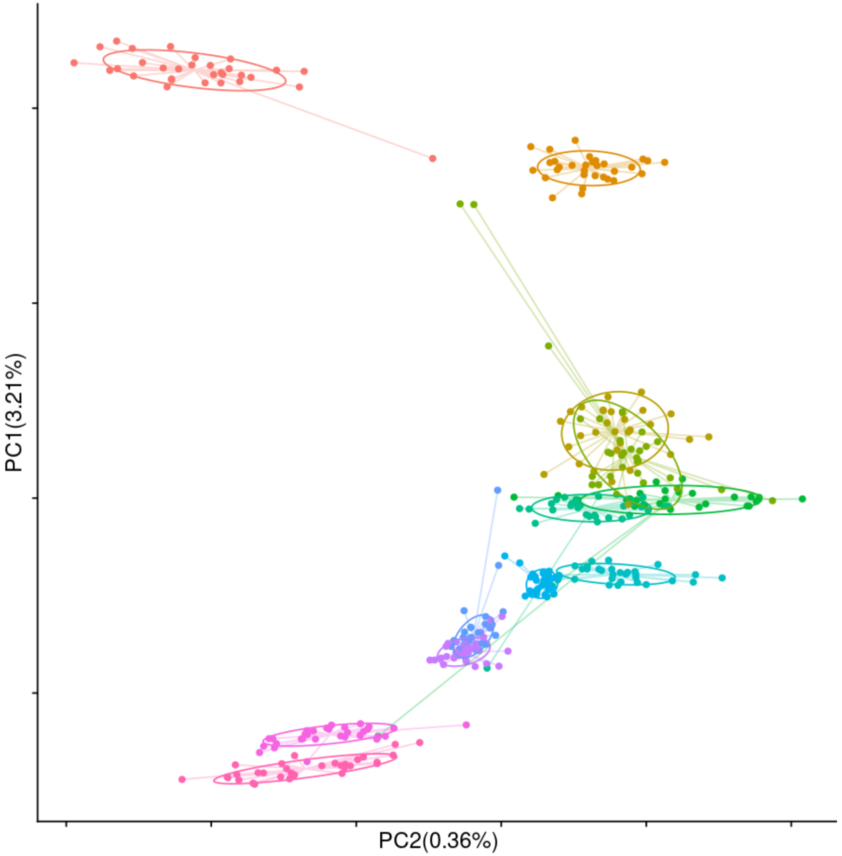
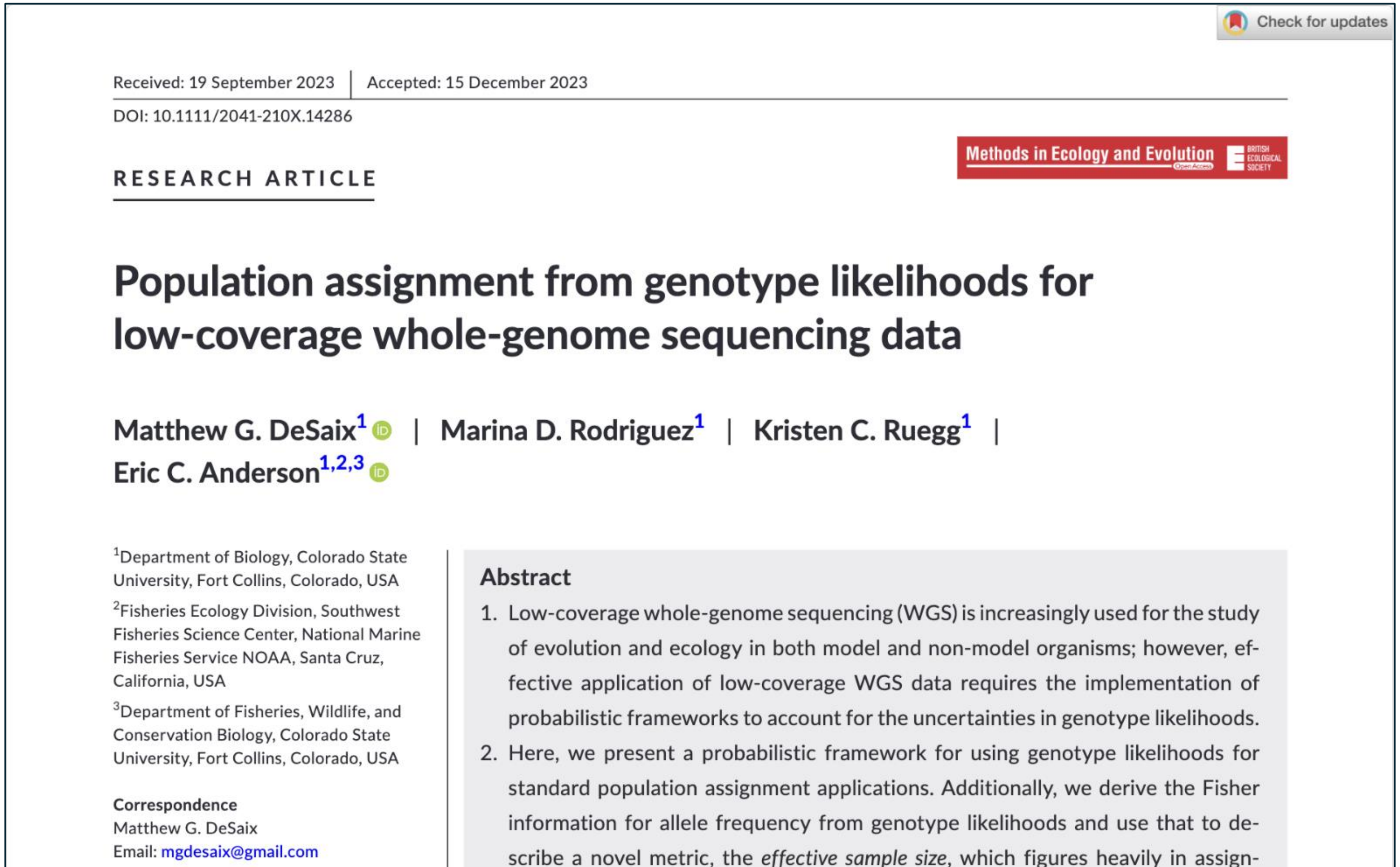


lcWGS (~0.8x), 12 million SNPs



# Assignment based directly on low-coverage whole genome data



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Methods in Ecology and Evolution
BRITISH ECOLOGICAL SOCIETY

RESEARCH ARTICLE

## Population assignment from genotype likelihoods for low-coverage whole-genome sequencing data

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**Eric C. Anderson**[1,2,3]

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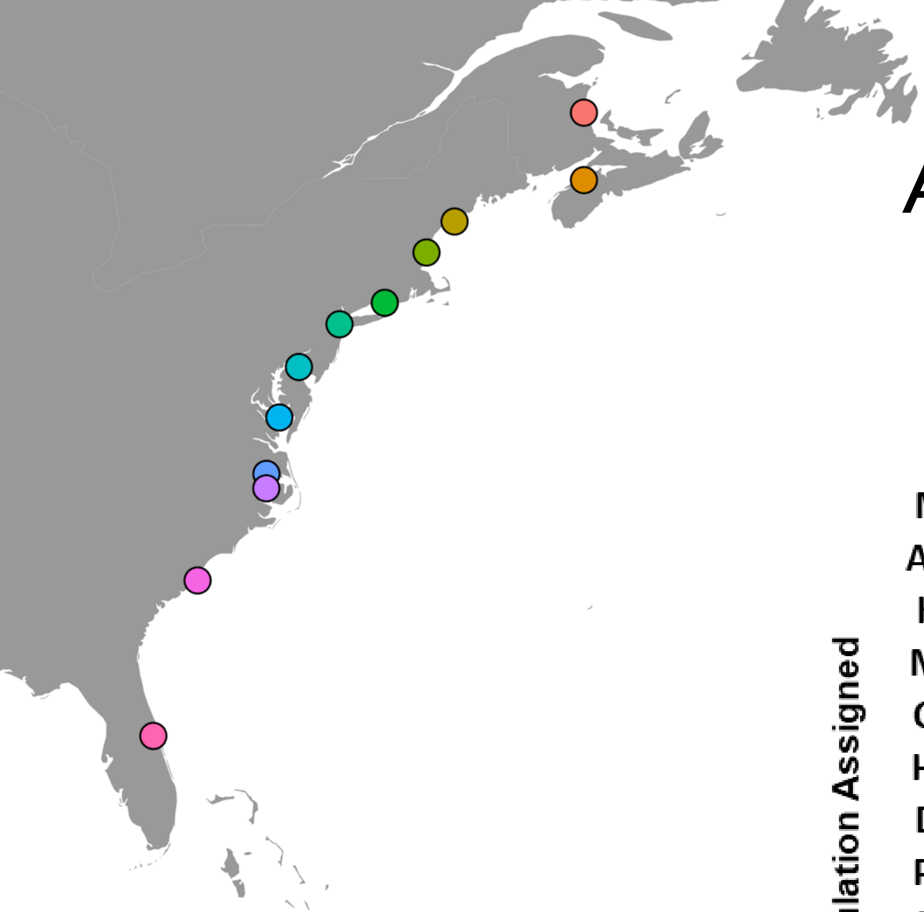
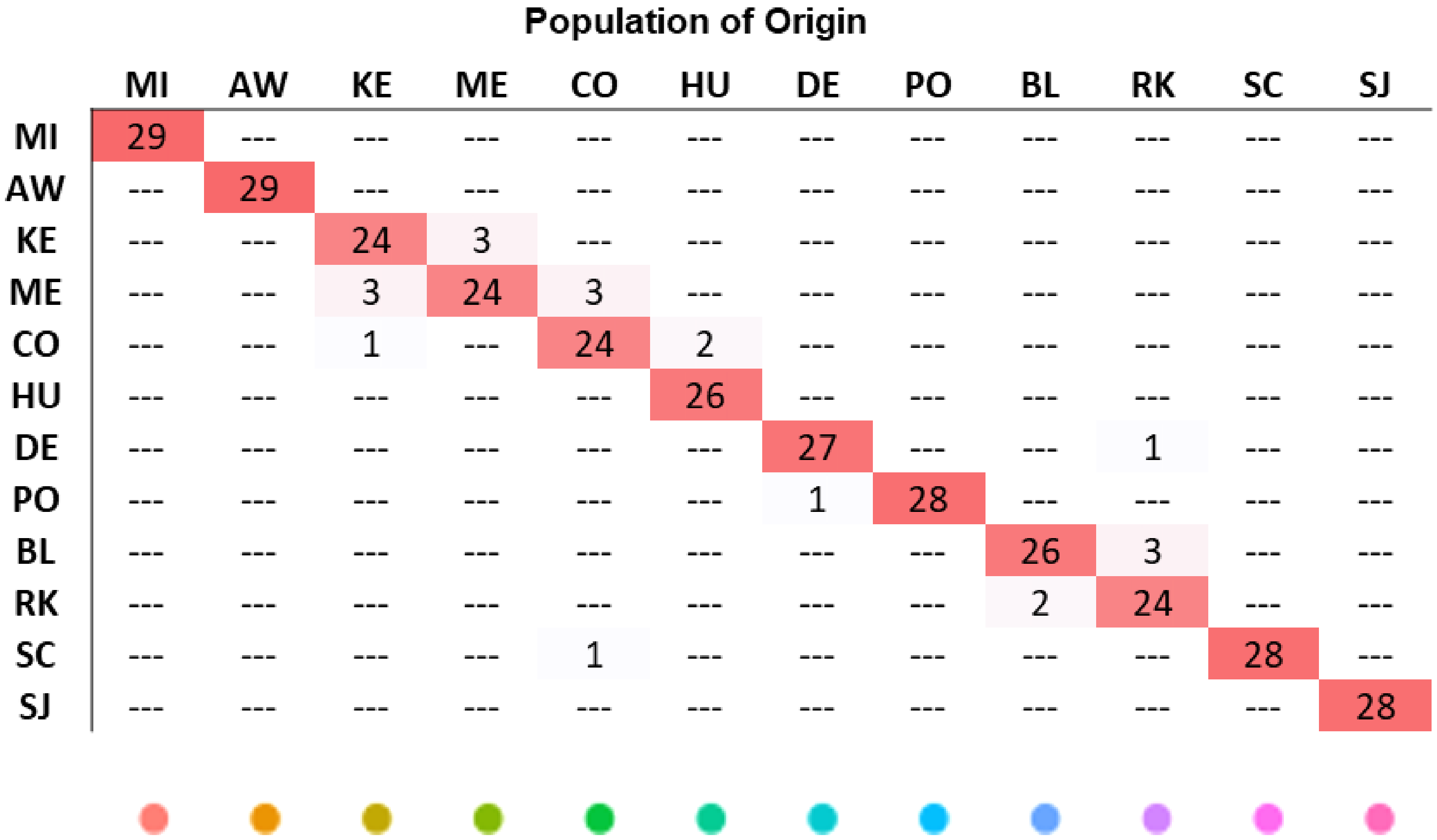
**Abstract**

1. Low-coverage whole-genome sequencing (WGS) is increasingly used for the study of evolution and ecology in both model and non-model organisms; however, effective application of low-coverage WGS data requires the implementation of probabilistic frameworks to account for the uncertainties in genotype likelihoods.
2. Here, we present a probabilistic framework for using genotype likelihoods for standard population assignment applications. Additionally, we derive the Fisher information for allele frequency from genotype likelihoods and use that to describe a novel metric, the *effective sample size*, which figures heavily in assign-



# Assignment from low-coverage data

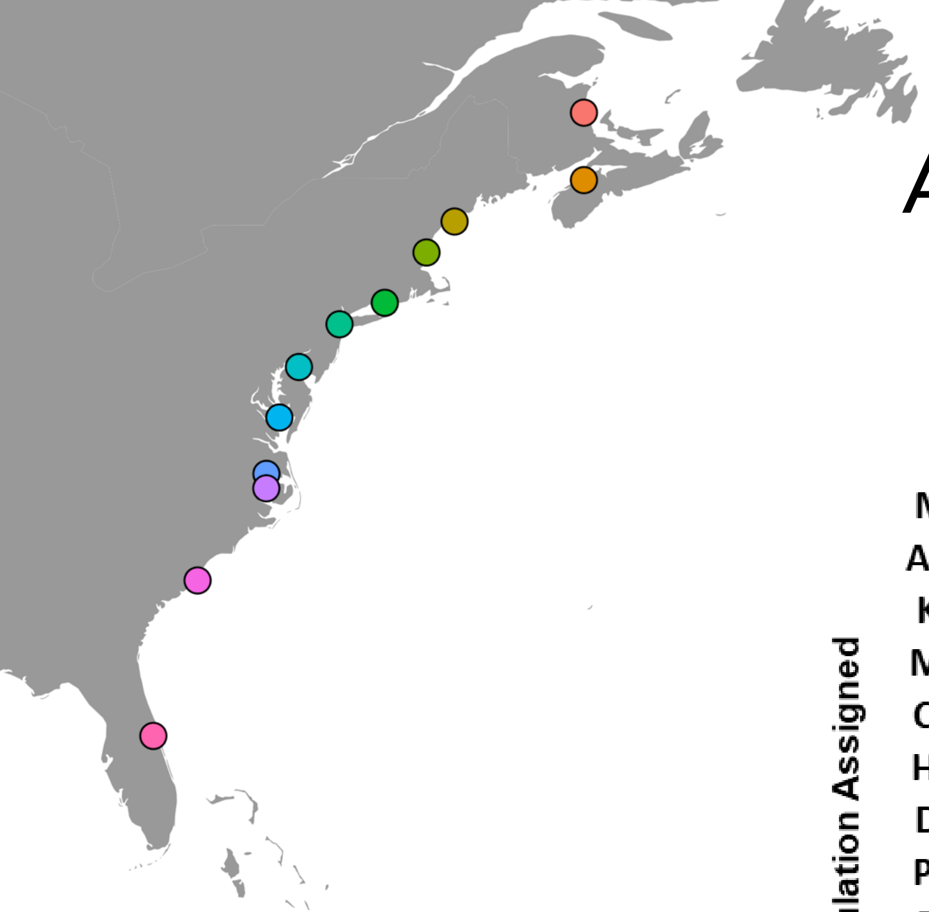
## Standardized effective sample size



Population of Origin

| Population Assigned | MI | AW | KE | ME | CO | HU | DE | PO | BL | RK | SC | SJ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MI | 29 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| AW | --- | 29 | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| KE | --- | --- | 24 | 3 | --- | --- | --- | --- | --- | --- | --- | --- |
| ME | --- | --- | 3 | 24 | 3 | --- | --- | --- | --- | --- | --- | --- |
| CO | --- | --- | 1 | --- | 24 | 2 | --- | --- | --- | --- | --- | --- |
| HU | --- | --- | --- | --- | --- | 26 | --- | --- | --- | --- | --- | --- |
| DE | --- | --- | --- | --- | --- | --- | 27 | --- | --- | 1 | --- | --- |
| PO | --- | --- | --- | --- | --- | --- | 1 | 28 | --- | --- | --- | --- |
| BL | --- | --- | --- | --- | --- | --- | --- | --- | 26 | 3 | --- | --- |
| RK | --- | --- | --- | --- | --- | --- | --- | --- | 2 | 24 | --- | --- |
| SC | --- | --- | --- | --- | 1 | --- | --- | --- | --- | --- | 28 | --- |
| SJ | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | 28 |

All individuals (~3.5x lcWGS) assigned based on genotype likelihoods at ~7million SNPs with leave-one-out



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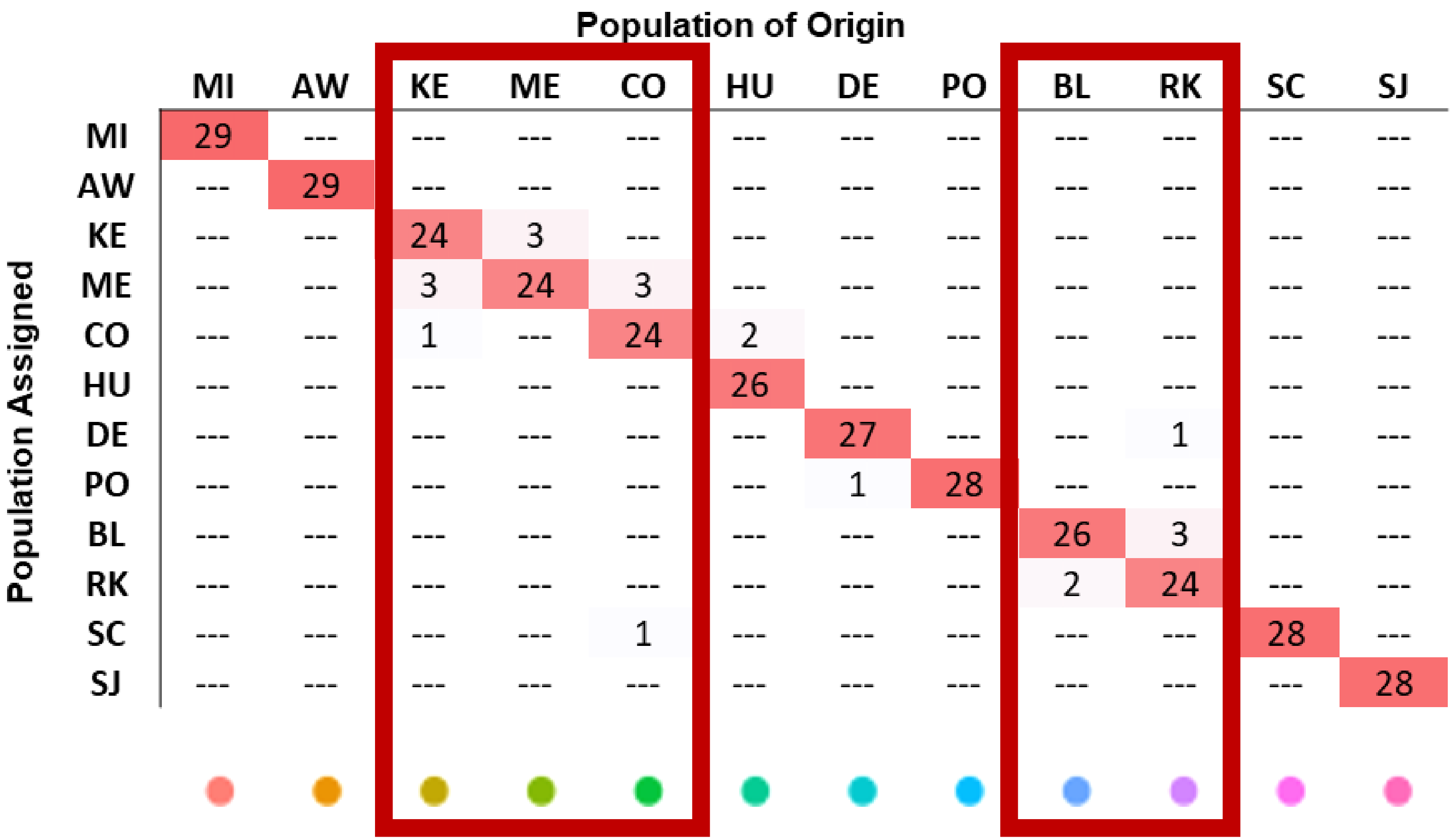
Standardized effective sample size



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| **RK** | --- | --- | --- | --- | --- | --- | --- | --- | 2 | 24 | --- | --- |
| **SC** | --- | --- | --- | --- | 1 | --- | --- | --- | --- | --- | 28 | --- |
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| | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● |

All individuals (~3.5x lcWGS) assigned based on genotype likelihoods at ~7million SNPs with leave-one-out

# How low can we go?

- Analysis on prior data has retained near-perfect assignment when down-sampling to 0.01x sequencing depth
  (DeSaix et al. 2023. Molecular Ecology , DeSaix et al. 2024. Methods in Ecology and Evolution)

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# Cost comparison

**GT-seq (200-400 markers)**

- Cost for library prep and sequencing ~$6

**LcWGS (millions of markers)**

- Library prep: ~$7
- Sequencing test sample: $0.1

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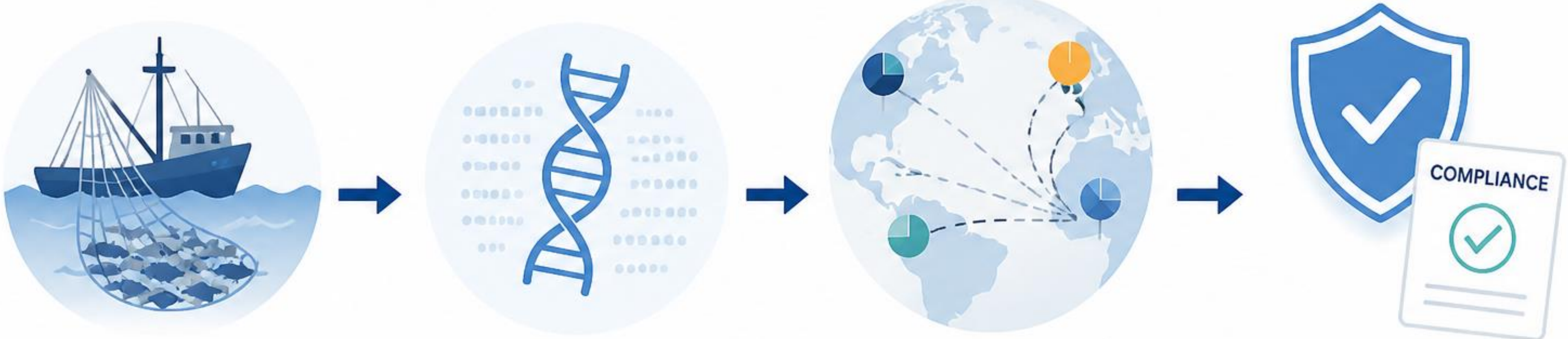
Routine running costs very similar

Assignment from whole genome data often more powerful

# Combatting illegal fishing

## INCREASING RESOLUTION IN ASSIGNMENT TESTING



**Sample from catch**

Fish harvested in unknown location

**Genomic assignment**

High-resolution genetic data assigns fish to its likely population of origin

**Origin identified**

Determine where the fish came from and whether the catch is authorized

**Inform enforcement**

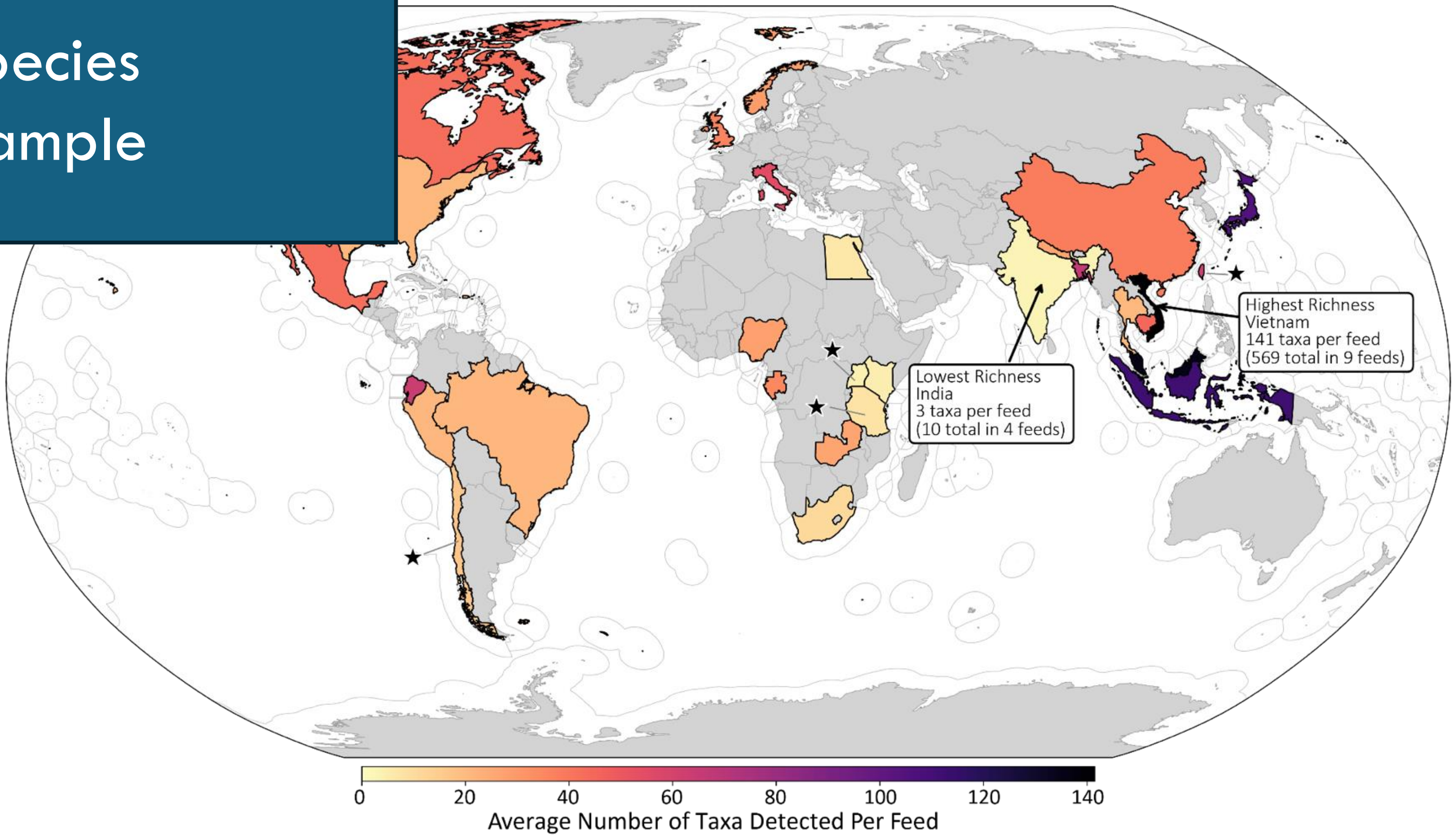
Science-based evidence supports compliance and helps deter illegal fishing

Higher resolution assignment provides the power to trace catch to its source—*helping ensure sustainable fisheries and protect ocean resources.*

# Genomics as a forensic tool

- Trace biological material through supply chains

Average number of fish species detected per aquafeed sample



Baetscher et al. in prep

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Pavel Dimens
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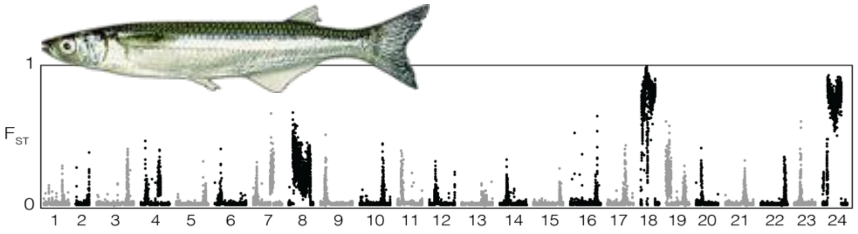
NEW YORK STATE OF OPPORTUNITY
Department of Environmental Conservation

Sea Grant

Cornell University

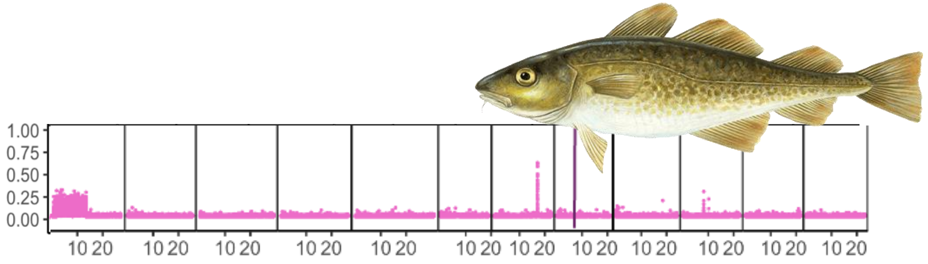
# Structure can be hidden in different ways

## Strong adaptation despite homogeneous genomes



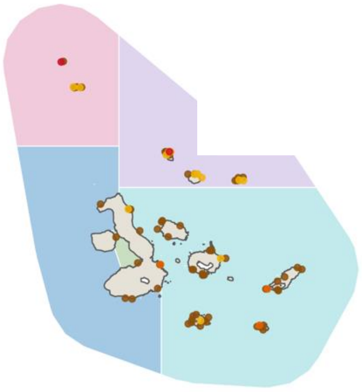
Atlantic silversides

## Differences confined to small genomic regions



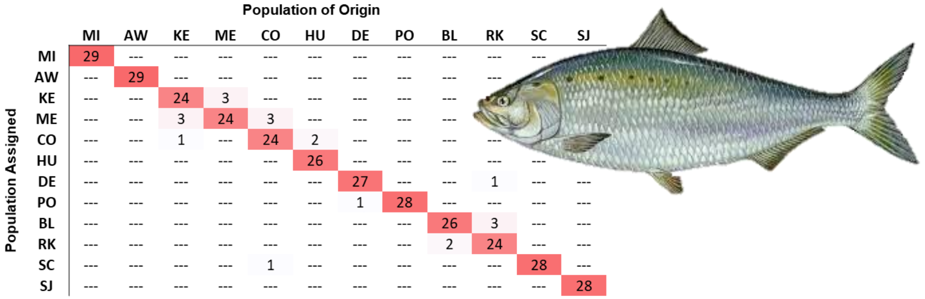
Atlantic cod

## Cryptic mixing of distinct lineages



Brown sea cucumber

## Tracking who mixes with whom—and when



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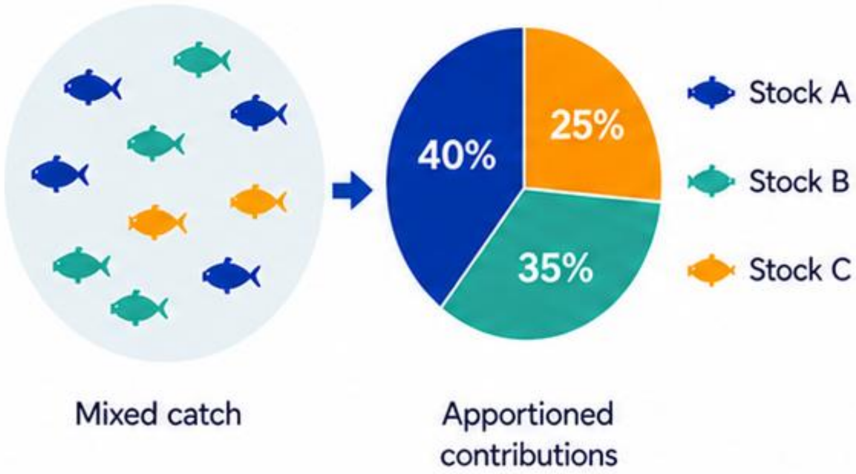
American shad

# From science to decisions

## 1 Mixed-stock fisheries



Quantify the contribution of each stock to mixed fisheries.

Genomic insights provide the resolution needed to turn complex data into **actionable information** for sustainable management.

# From science to decisions

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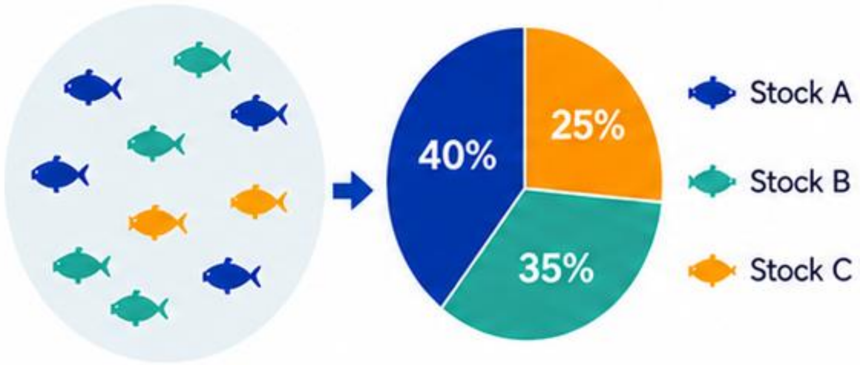
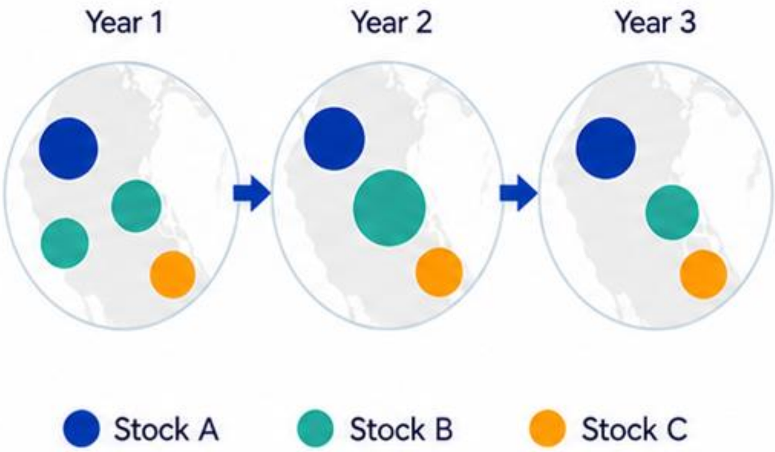


Mixed catch

Apportioned contributions

Quantify the contribution of each stock to mixed fisheries.

## 2 Shifting distributions



Monitor and adapt to changes in the composition of stocks through time.

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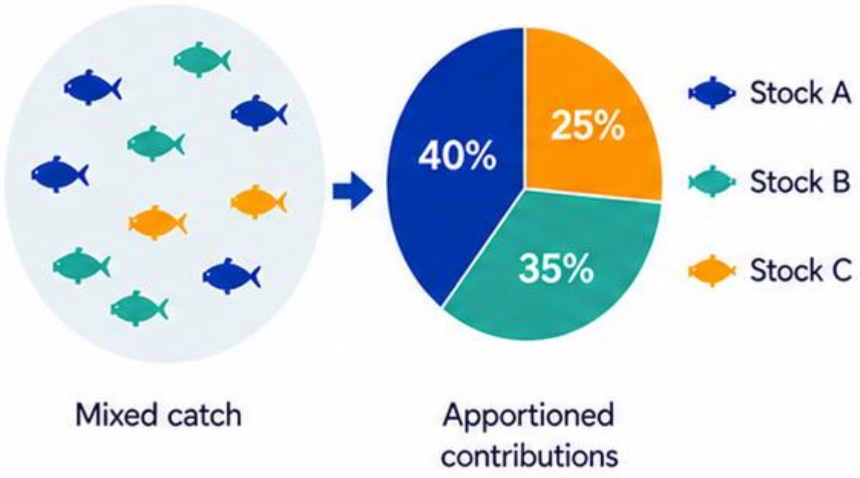

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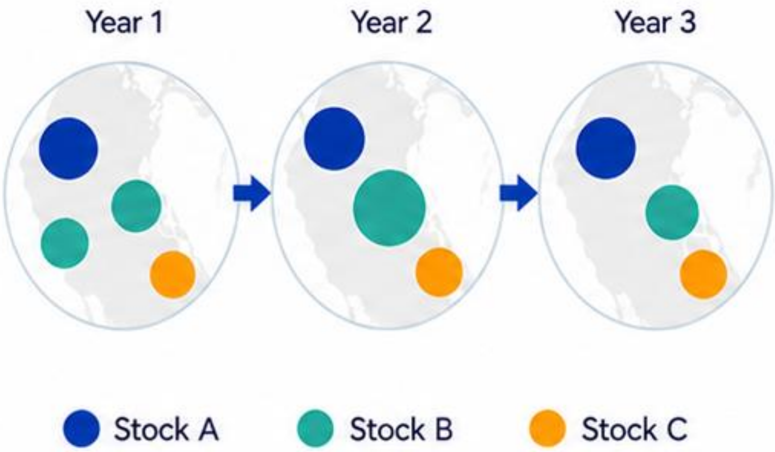

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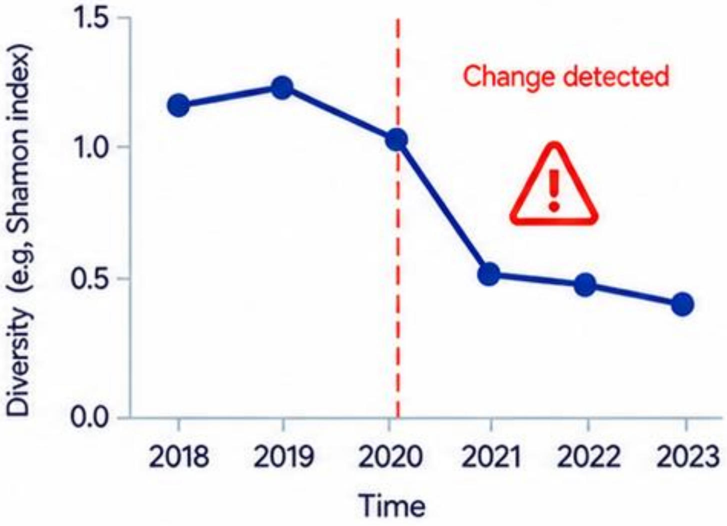
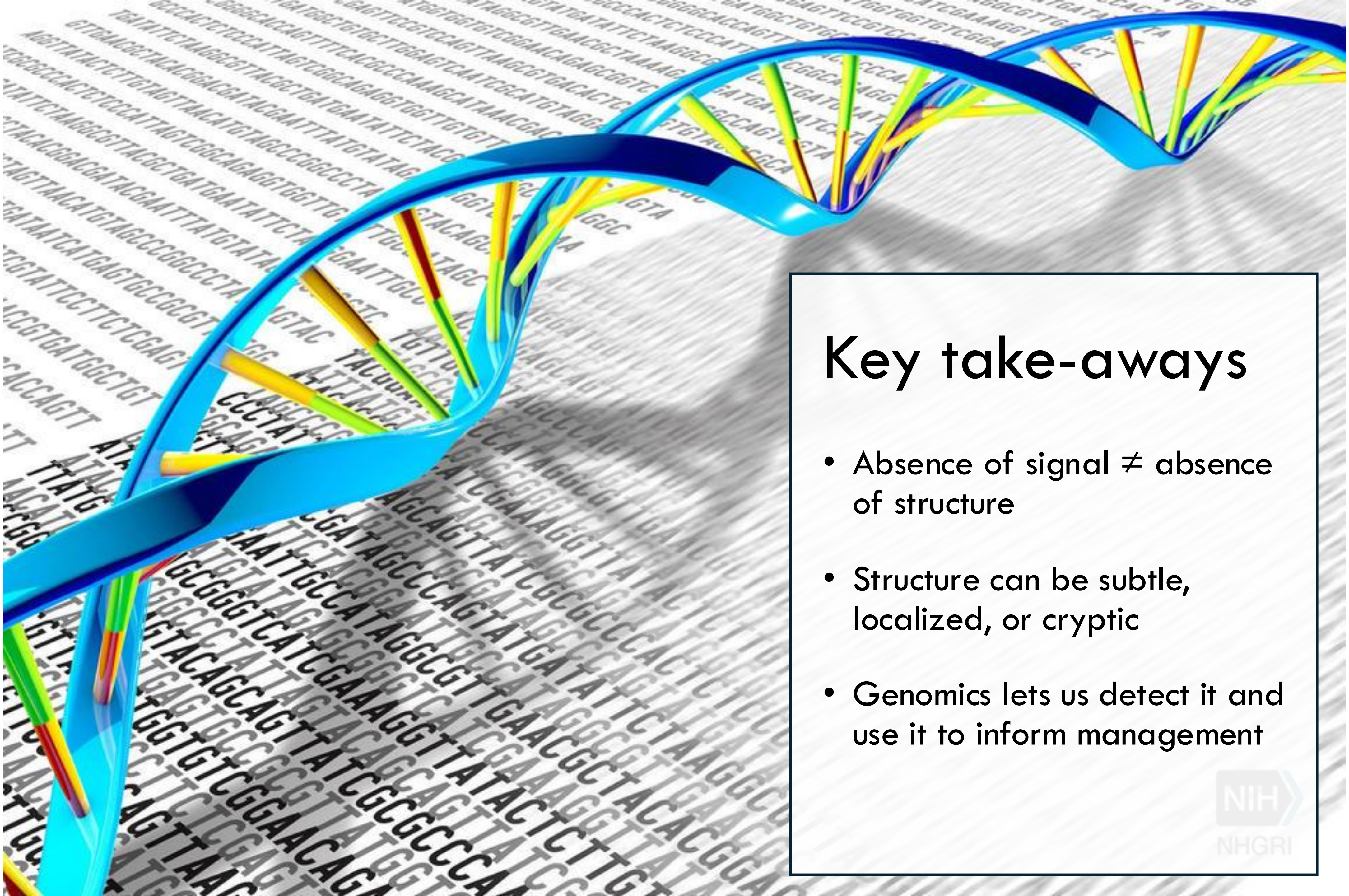
## 3 Early warning



Detect changes early to inform management and conservation.

Genomic insights provide the resolution needed to turn complex data into **actionable information** for sustainable management.



# Key take-aways

- Absence of signal ≠ absence of structure
- Structure can be subtle, localized, or cryptic
- Genomics lets us detect it and use it to inform management