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The role of reproductive timing as a driver of genetic differentiation in populations of Pacific herring

Eleni L. Petrou
Univ. of Washington, United States, elpetrou@uw.edu

Todd Sandell
Washington Dept. of Fish and Wildlife, United States, todd.sandell@dfw.wa.gov

Dayv Lowry
Washington Dept. of Fish and Wildlife, United States, dayv.lowry@dfw.wa.gov

Lorenz Hauser
Univ. of Washington, United States, lhauser@uw.edu

Reproductive timing and geography influence genetic differentiation of Pacific herring

Eleni L. Petrou[1], Todd Sandell[2], Dayv Lowry[2], Lorenz Hauser[1]

1: University of Washington

2:Washington Department of Fish and Wildlife

Some important aspects of diversity

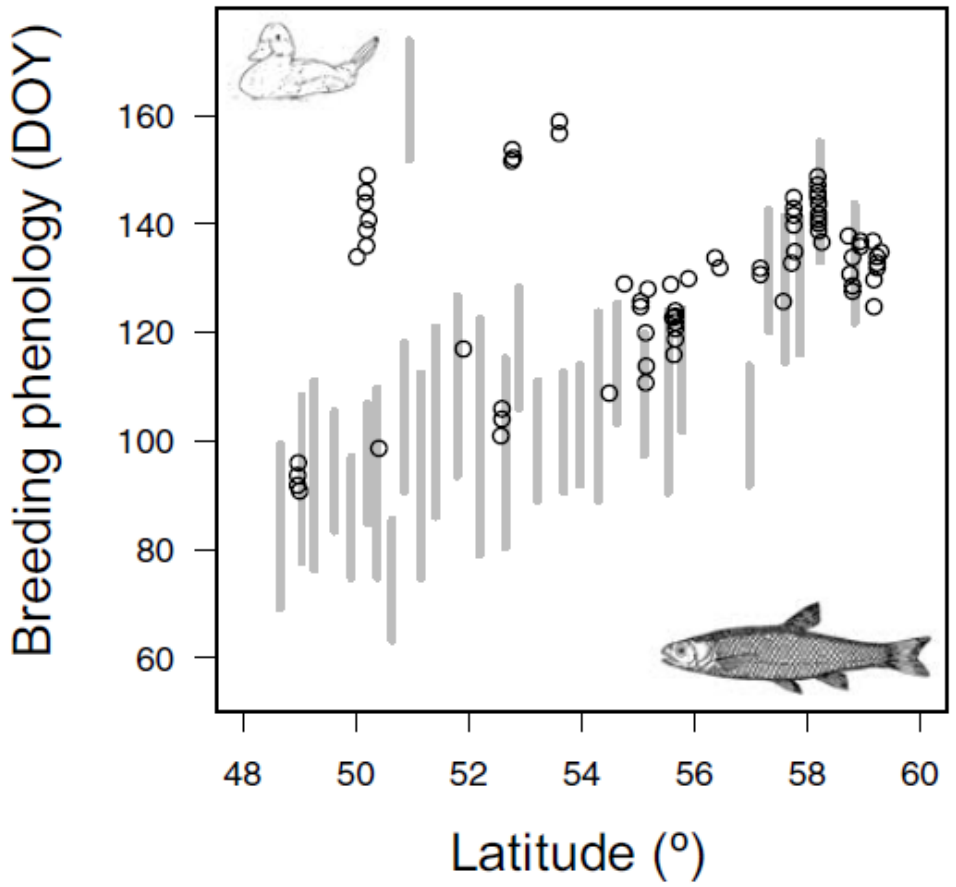
- Spatial distribution of populations
    - Especially when dispersal is limited
    - Demographic processes

Some important aspects of diversity

- Spatial distribution of populations
- Life history traits
- Contribute to stable productivity of wild populations (Siple and Francis, 2015)

Photos by Grant Callegari

Reproductive phenology is important life history trait



- Mediates ecological interactions:
  - Predation
  - Example: Scoters co-occur with spawning herring, eat eggs

Figure from Armstrong, et al. 2016; Data from Lok et al. 2012

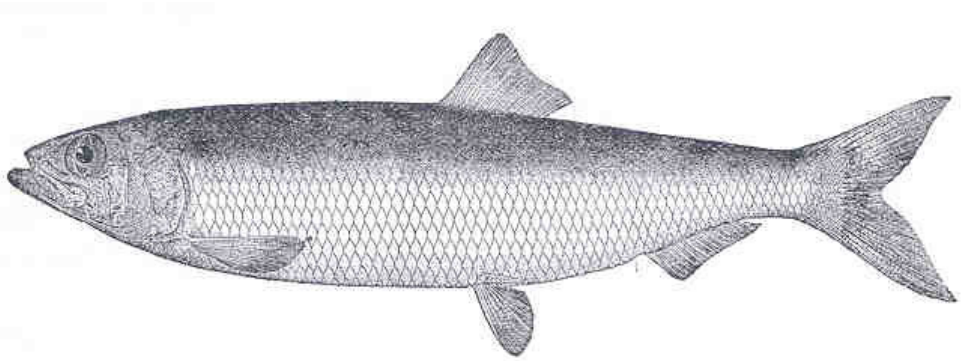
Reproductive phenology is important life history trait

Photo by Jonny Armstrong

- Evolution:
- Gene flow is limited between populations/individuals that reproduce at different times
- “Isolation by time”
  - Example: Sockeye from Cedar River (Hendry et al. 2005)

Reproductive timing in Pacific herring

- Salish Sea herring exhibit a wide diversity of spawn times:
  - Some populations start reproducing as early as January
  - Reproductive activity in the region continues through May

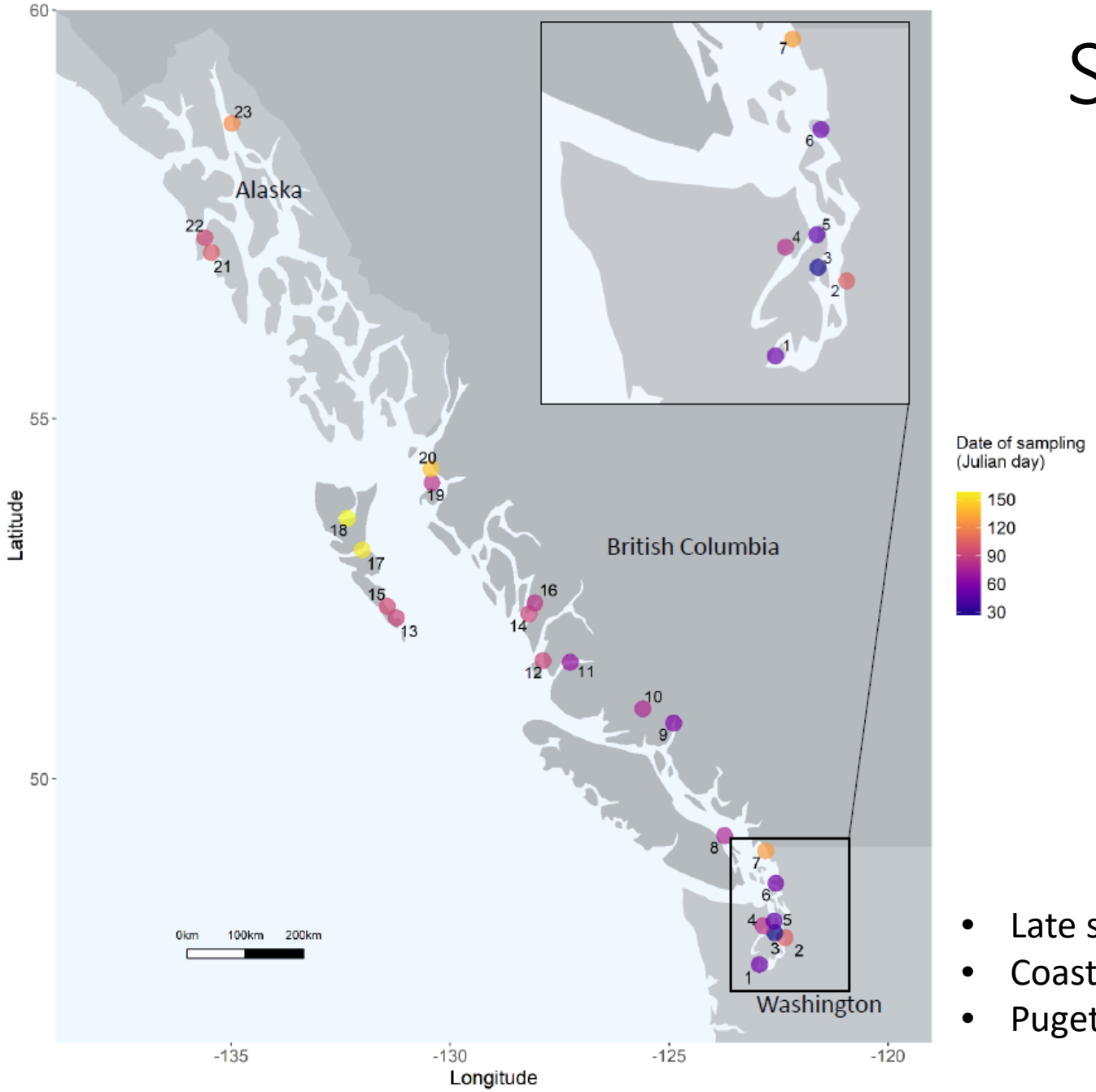


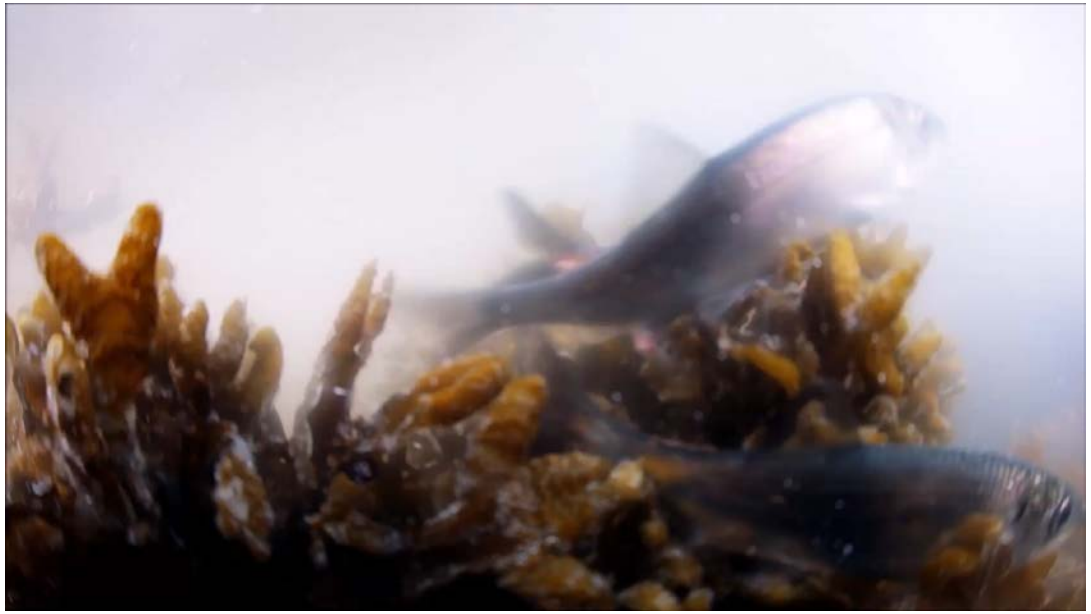
PACIFIC HERRING (*Clupea pallasi*).

Research Questions

- Do differences in spawn timing limit gene flow between populations?
- Is gene flow limited by geographic distance?

Sampling Locations

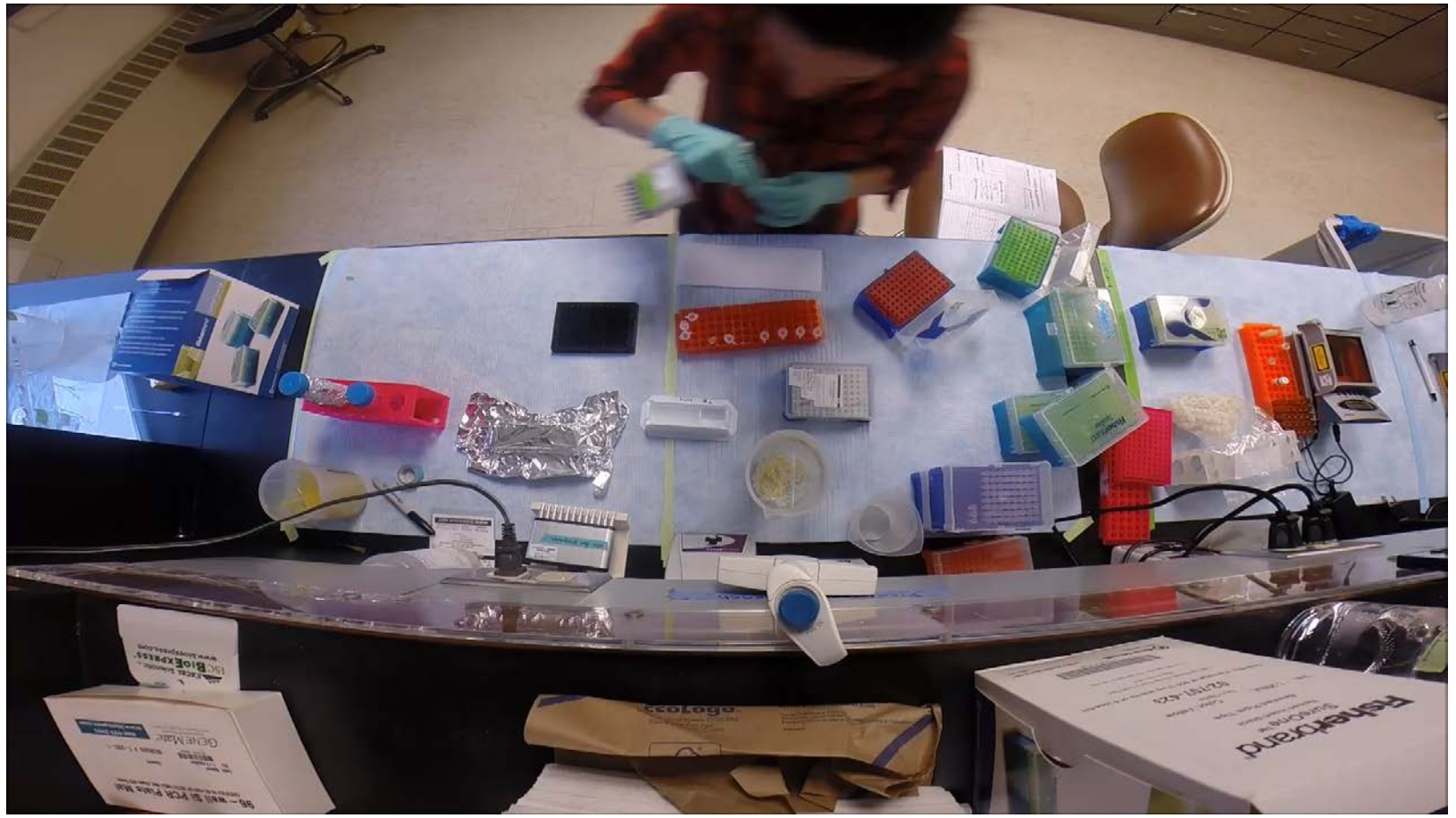




Video by Hakai Institute

- Late spawners
- Coastal vs. inlet spawners
- Puget Sound spawners

Summary of methods used



Video by Mary Fisher

Decontamination

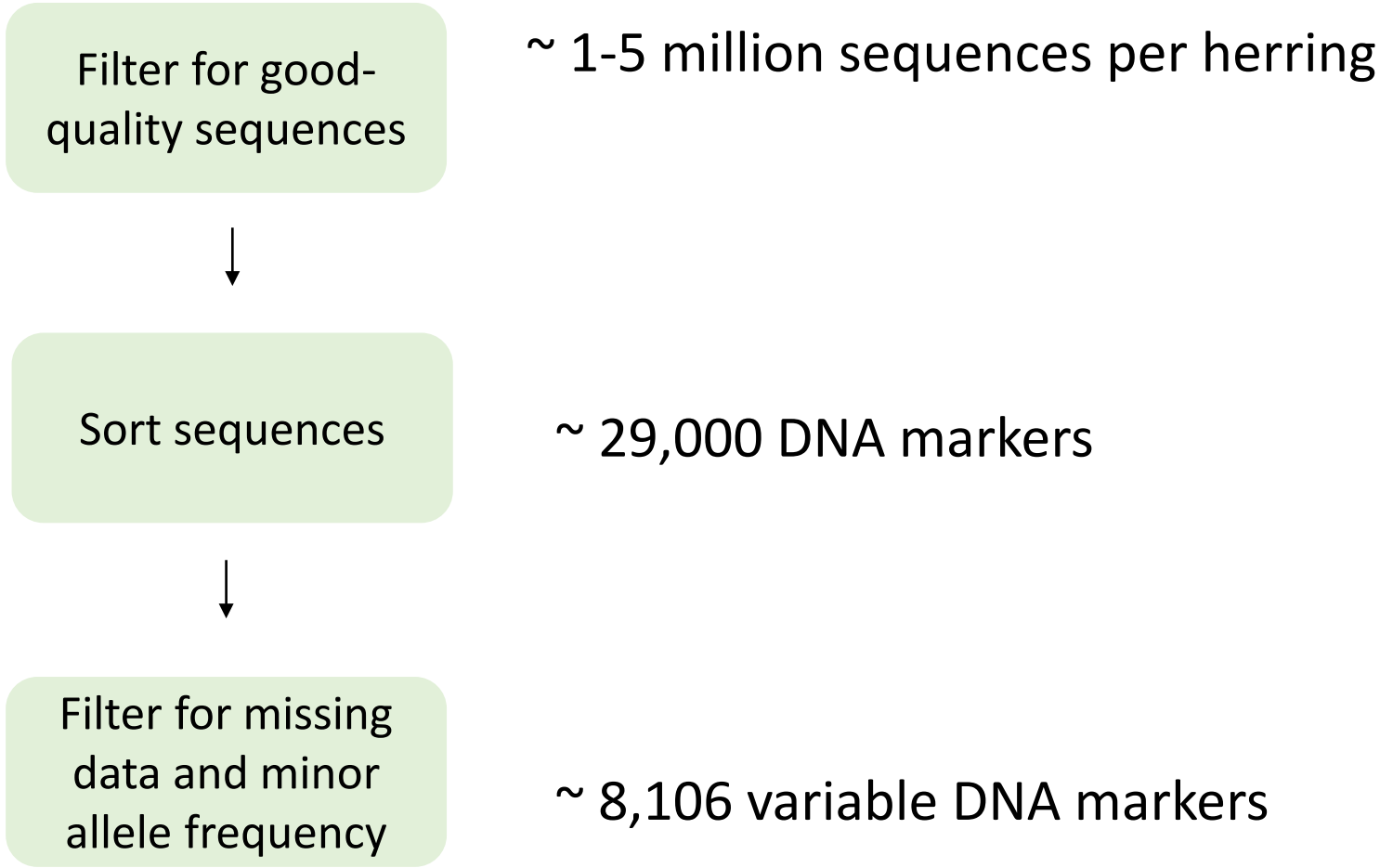
↓

DNA extraction

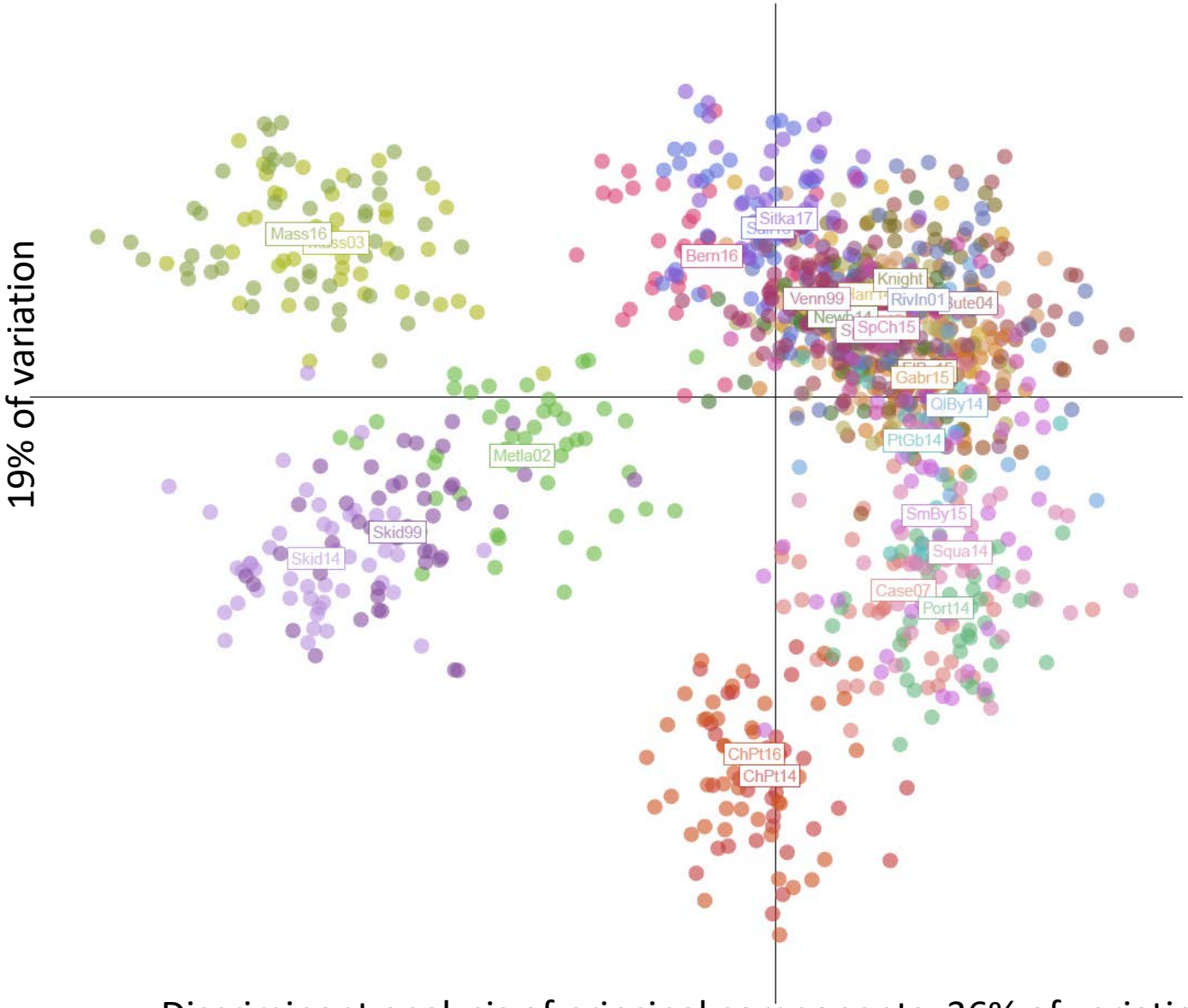
↓

RAD Sequencing

Summary of methods used

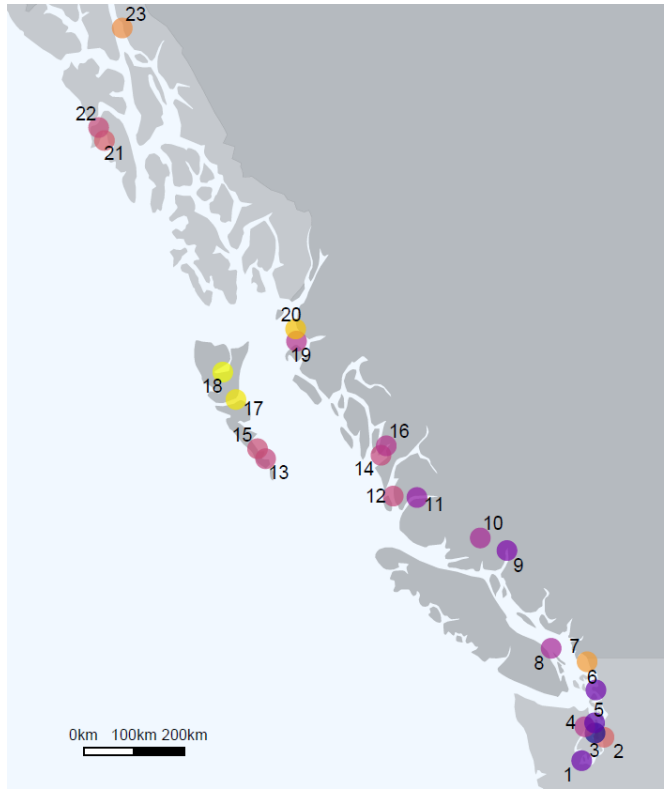


Population structure across the coast



19% of variation

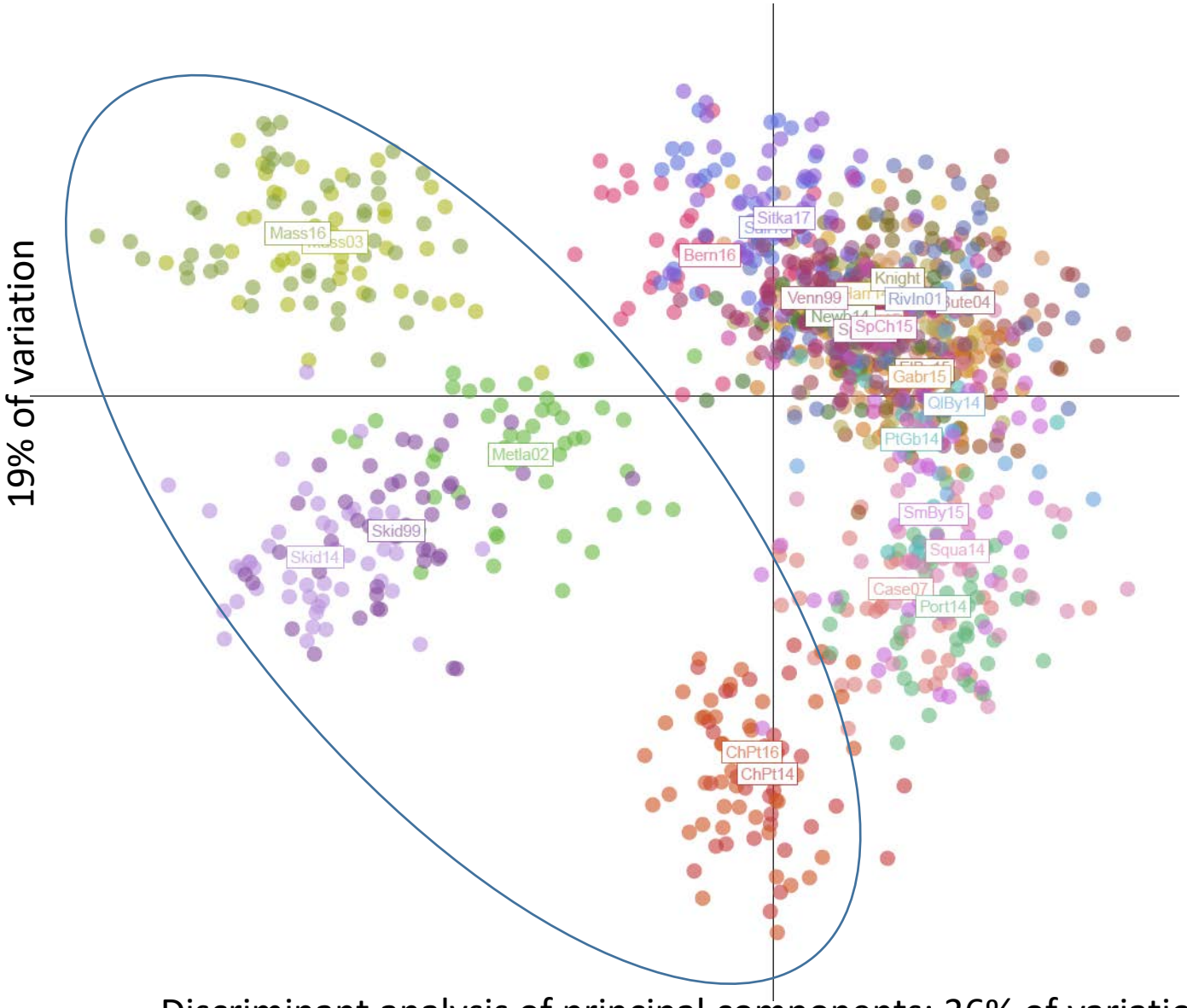
Discriminant analysis of principal components: 36% of variation



● = 

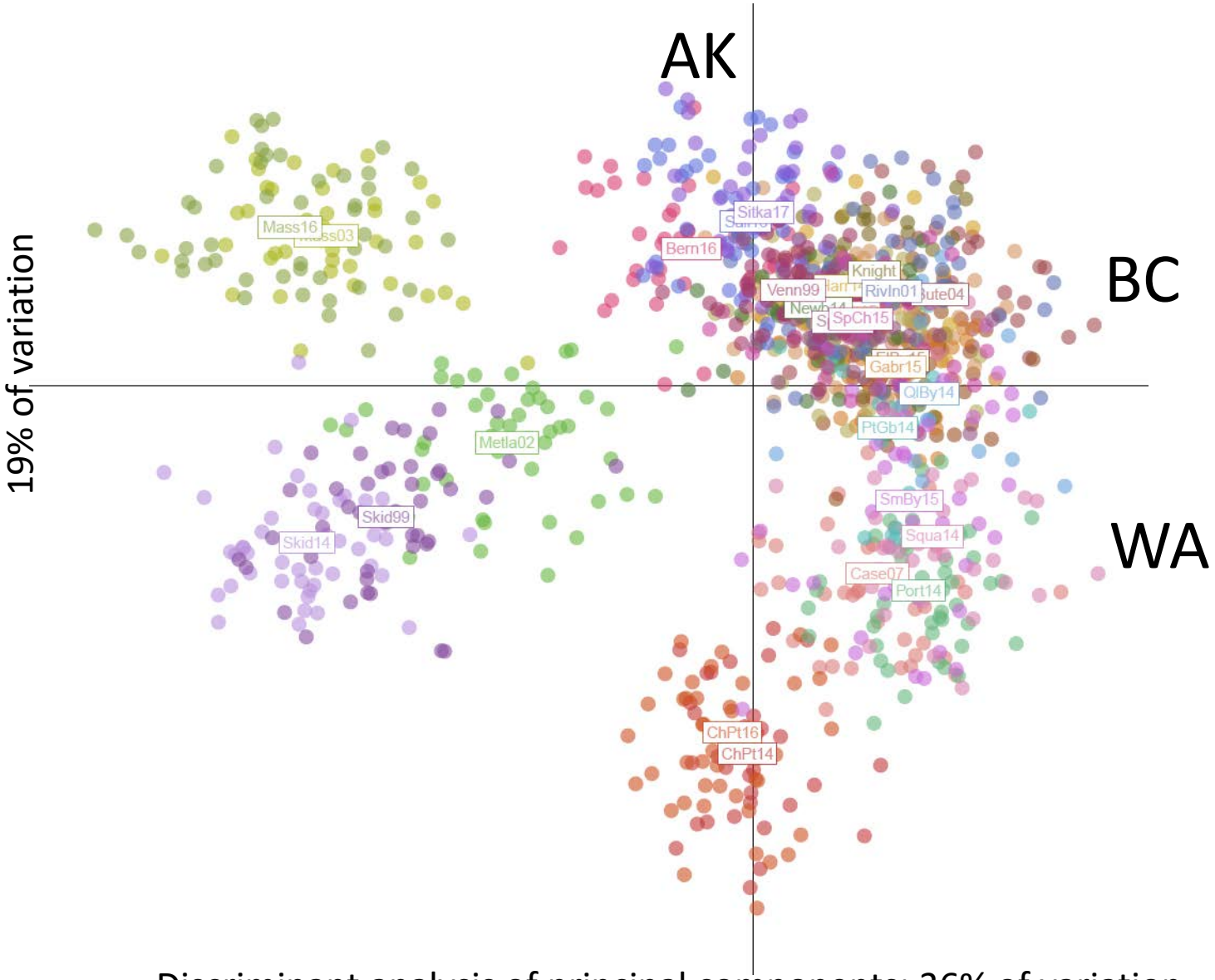
~ 8,000 DNA markers

Population structure across the coast



- Late-spawning populations are isolated (Small et al. 2005; Mitchell 2006; Beacham et al. 2008)

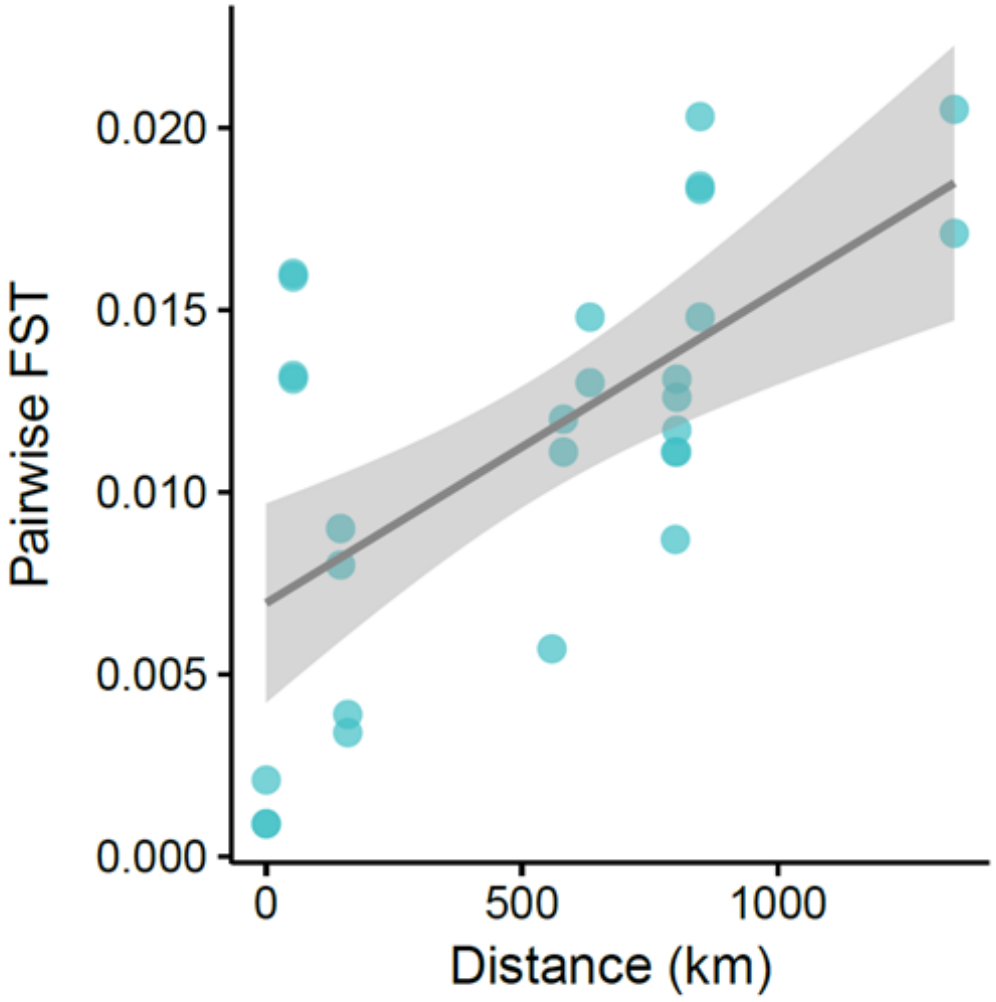
Population structure across the coast



- Late-spawning populations are isolated (Small et al. 2005; Mitchell 2006; Beacham et al. 2008)

- Large-scale patterns of geographic differentiation

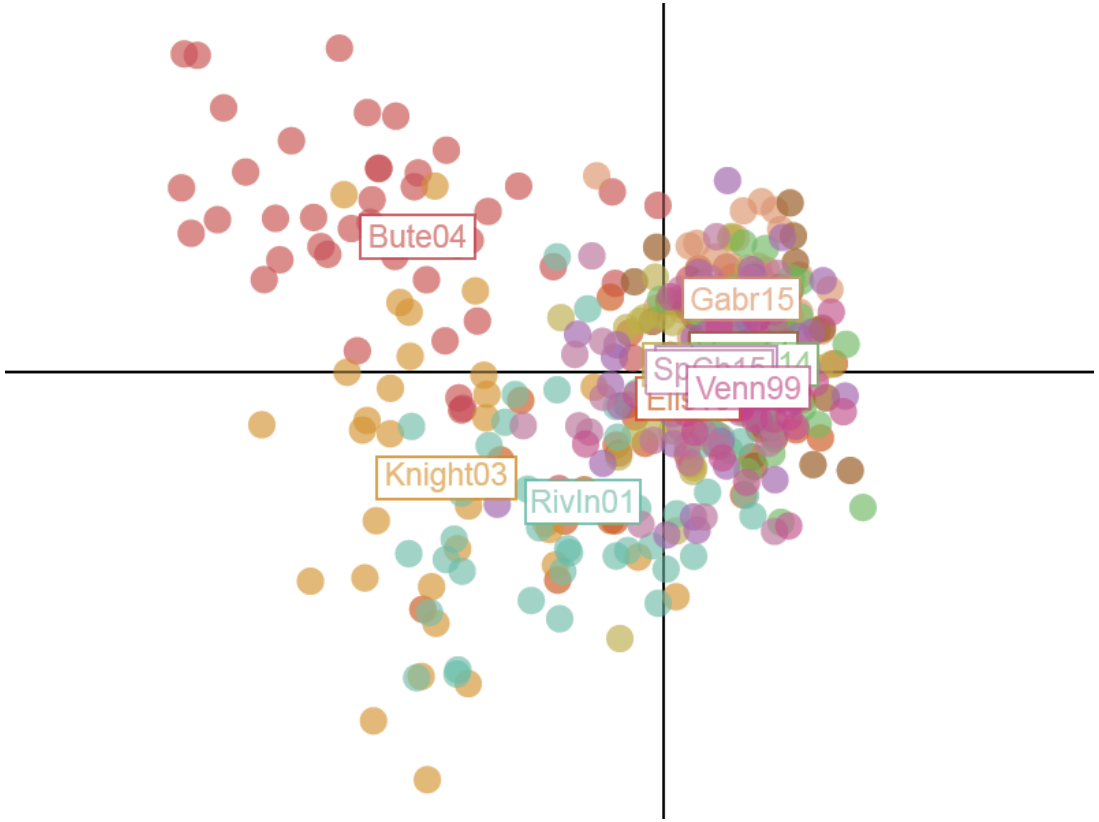
Late spawners: isolation by distance

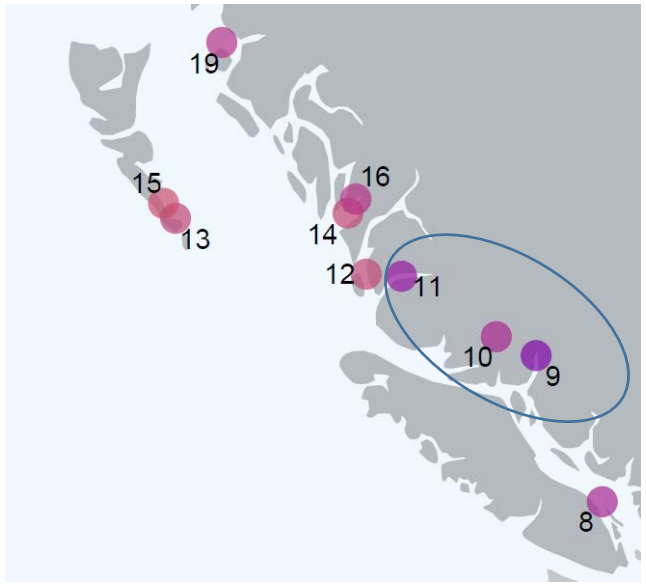


Adjusted R-squared = 0.37; p-value: 0.0004

- Dispersal distances are limited between late-spawning populations

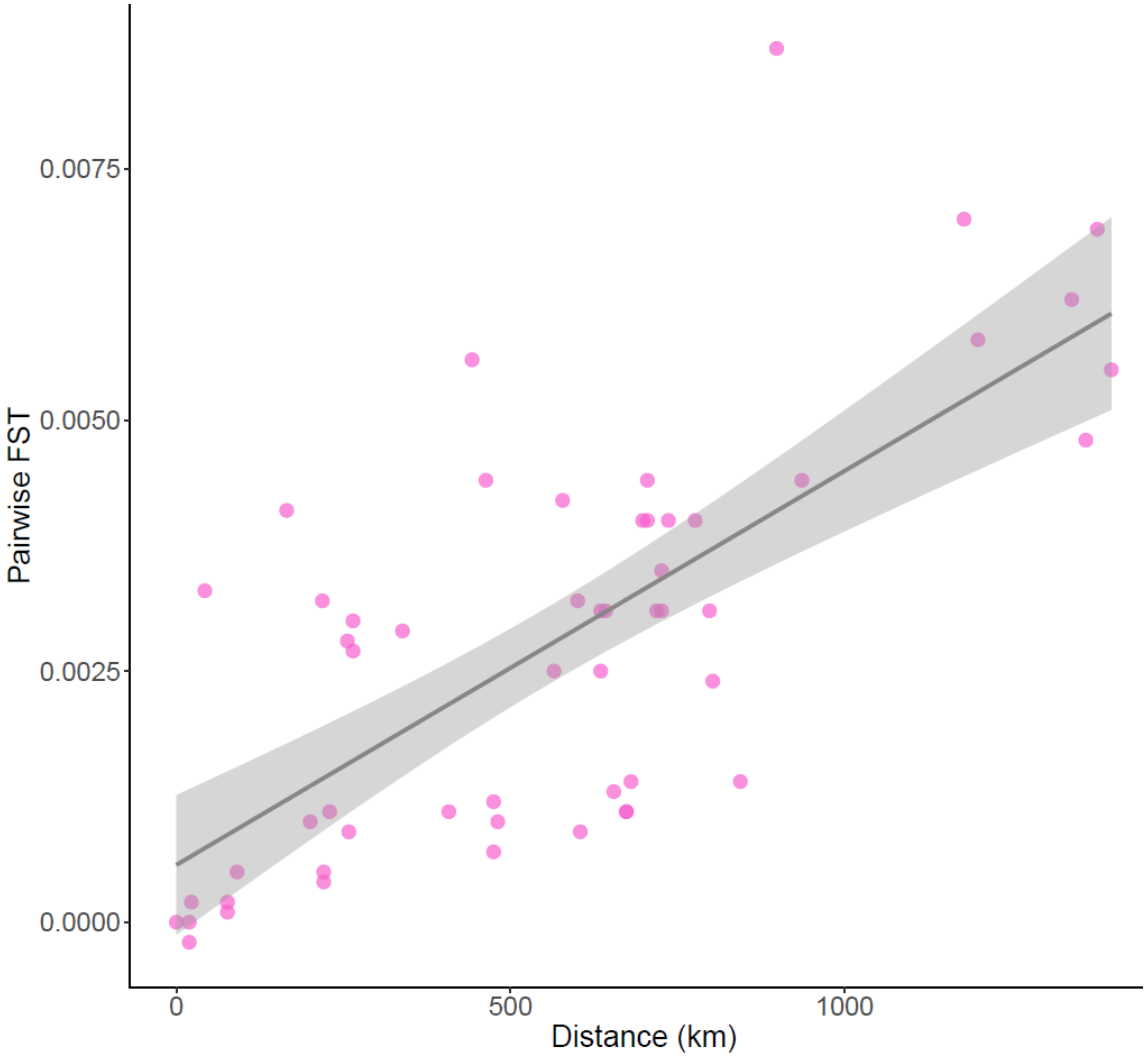
Population structure in British Columbia



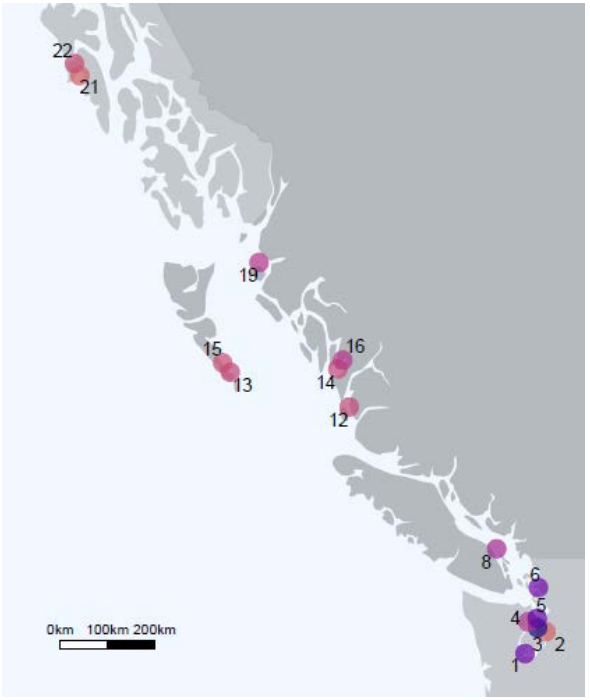


- Inlet populations are isolated (Beacham et al. 2008)

March & April spawners: isolation by distance

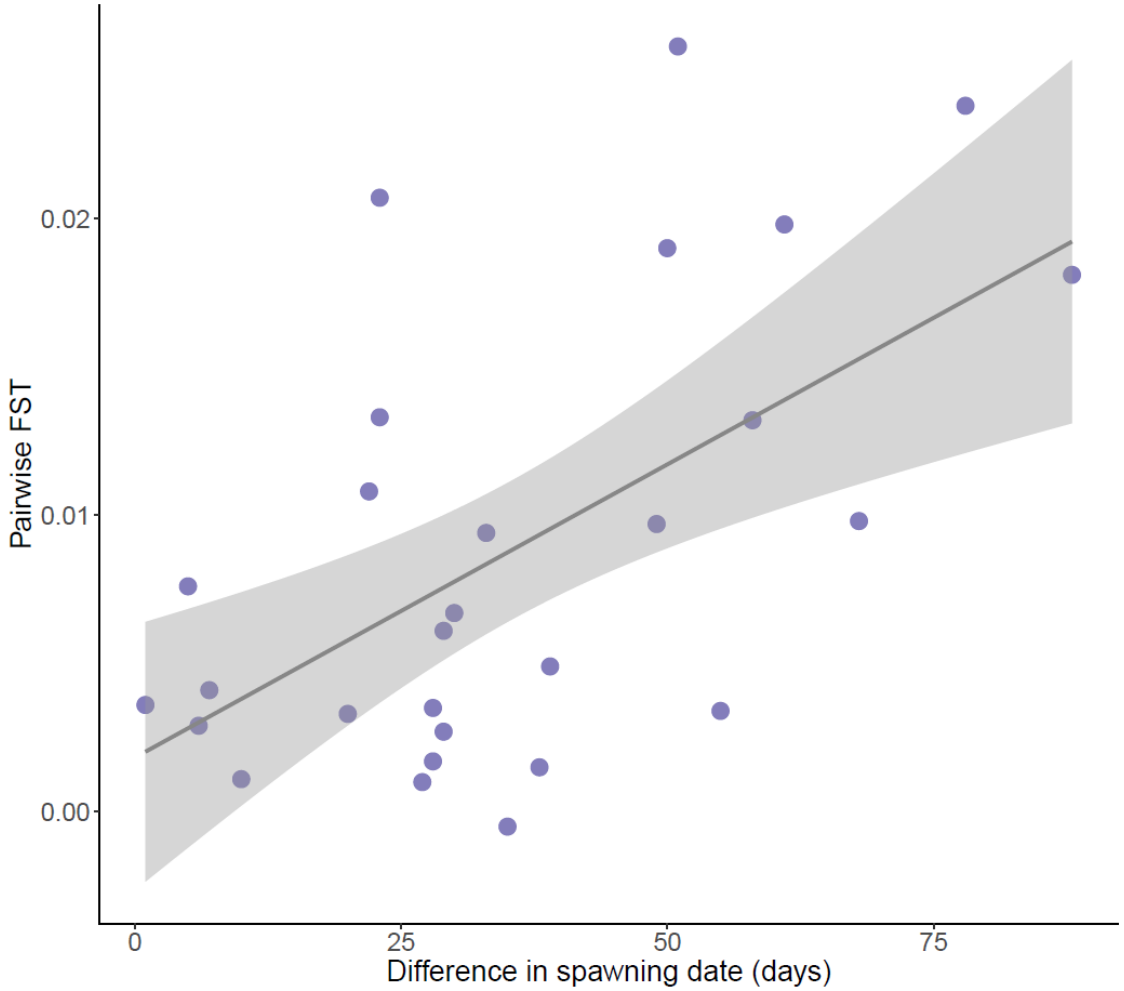


Adjusted R-squared = 0.50; p-value: 10^{-09}



- Dispersal distances are limited by geographic distance separating populations
- Even at modest spatial scales (~200 km)

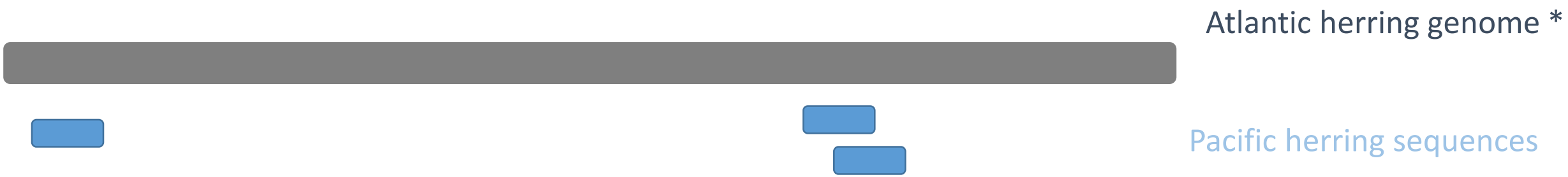
Spawn timing drives genetic differentiation in the Salish Sea



Adjusted R-squared = 0.31; p-value: 0.001

- Early and diverse spawning
- Spawn timing limits dispersal between populations in Salish Sea

What more can we learn from RAD sequencing?



Thyroid- stimulating hormone (*TSHb*)

- "Master regulator of seasonal reproduction"
- Triggers photoperiod-induced reproduction in mammals, birds, fish
- Spring & autumn Atlantic herring: different alleles for *TSH receptor****

Nuclear envelope protein (*SYNE2*)

- Influences development of photoreceptors in retina
- Spring & autumn Atlantic herring: different alleles of *SYNE2***

* Barrio et al. 2016
** Lamichhaney, Fuentes-Pardo, et al. 2017

Summary

- Dispersal distance is:
- Limited over moderate geographic scales (100s of km)
- Limited by temporal differences in spawn timing
  - Even among primary spawners

Implications for conservation and management

- Conserve:
  - Populations with diverse spawn timing
  - Spatial diversity of spawning populations across the coast
- If local extinction occurs -> neighboring populations recolonize

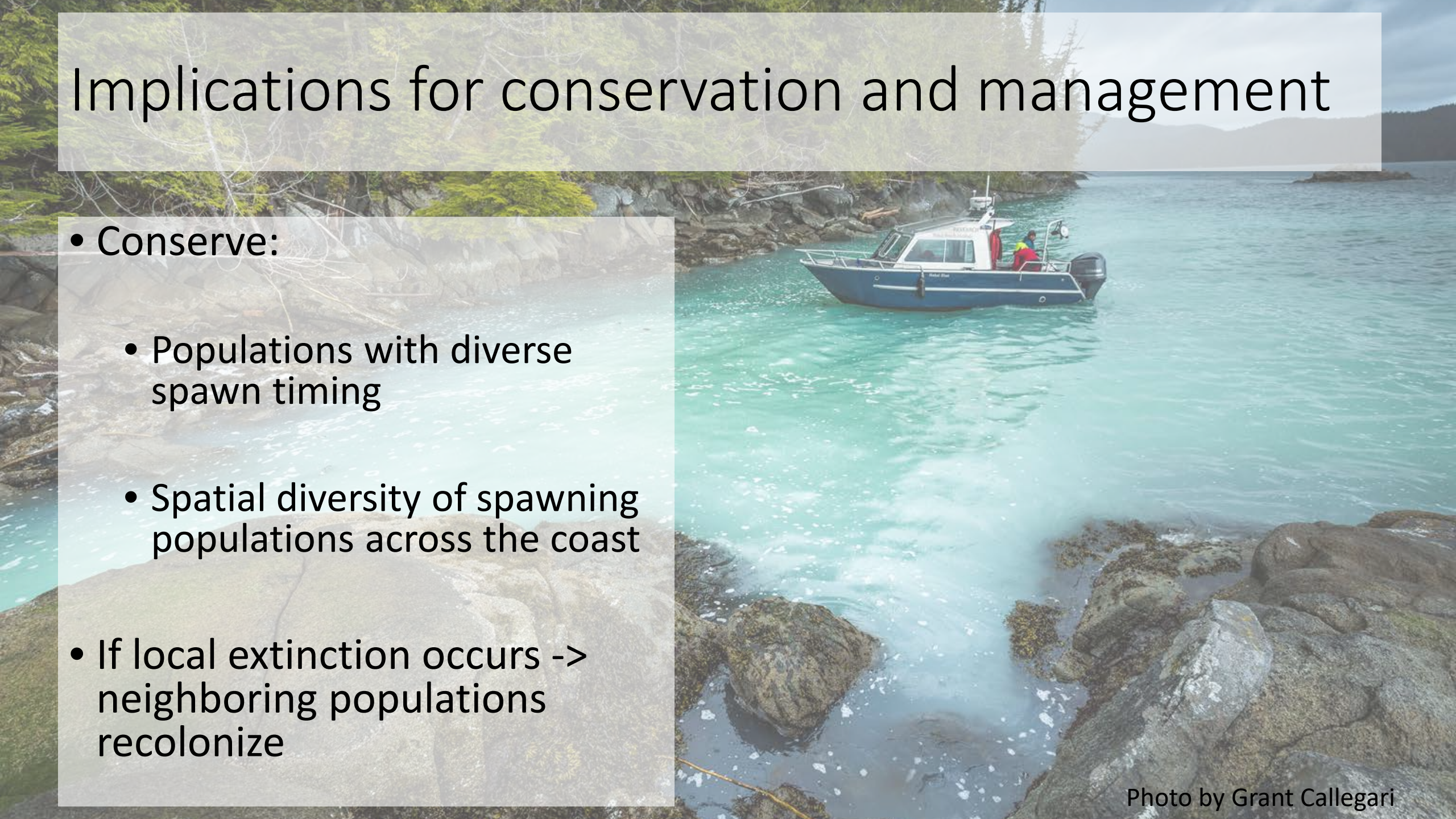
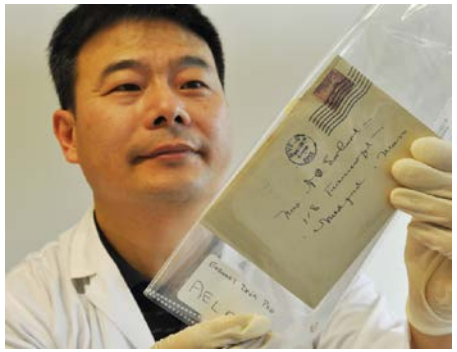


Photo by Grant Callegari

Many thanks to:

Collaborators

CCIRA


Dongya Yang


Dana Lepofsky


Madonna Moss


Robert Kopperl


Carolyn Tarpey

Funding Sources

Questions?

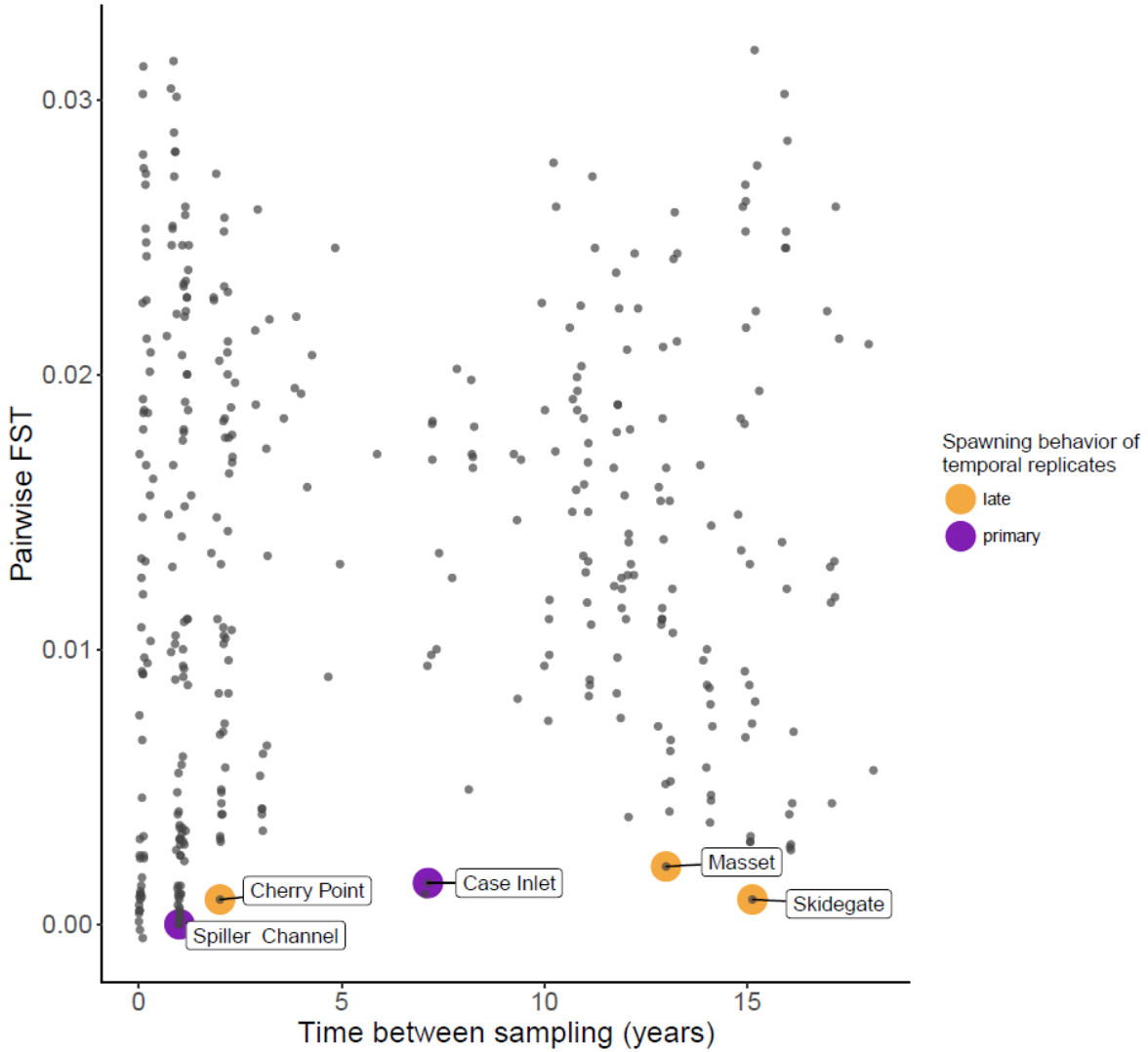






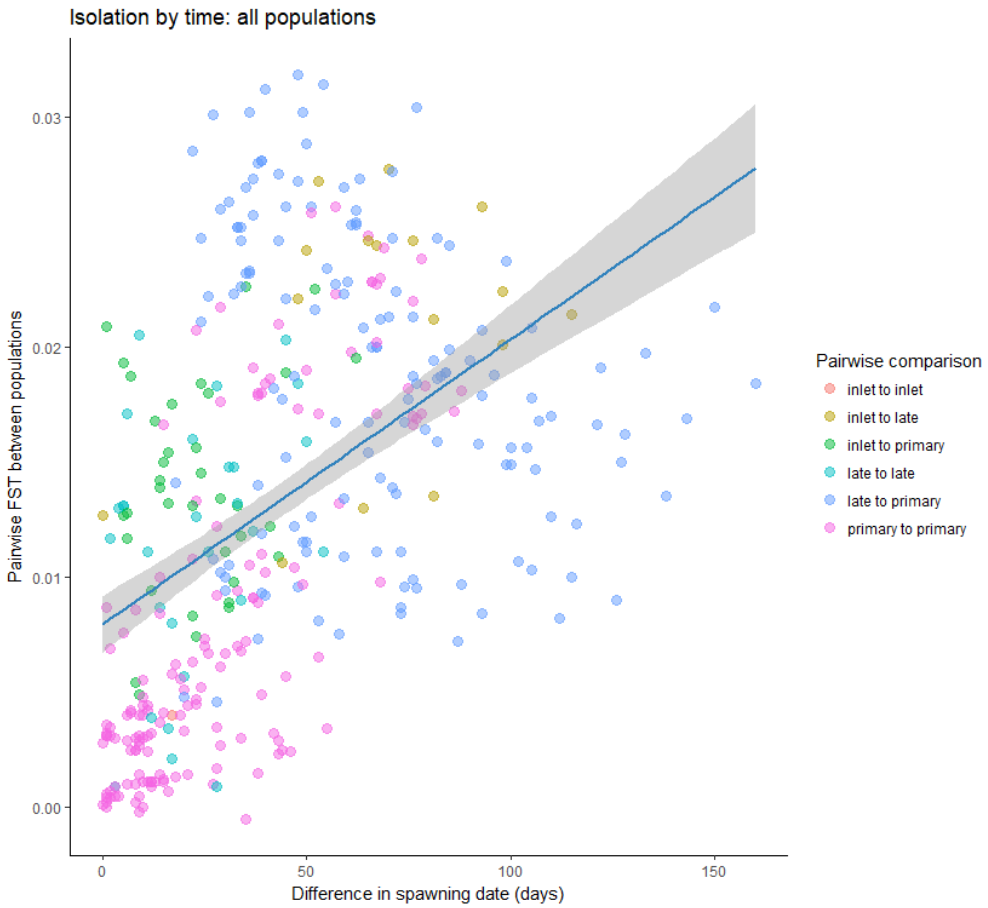


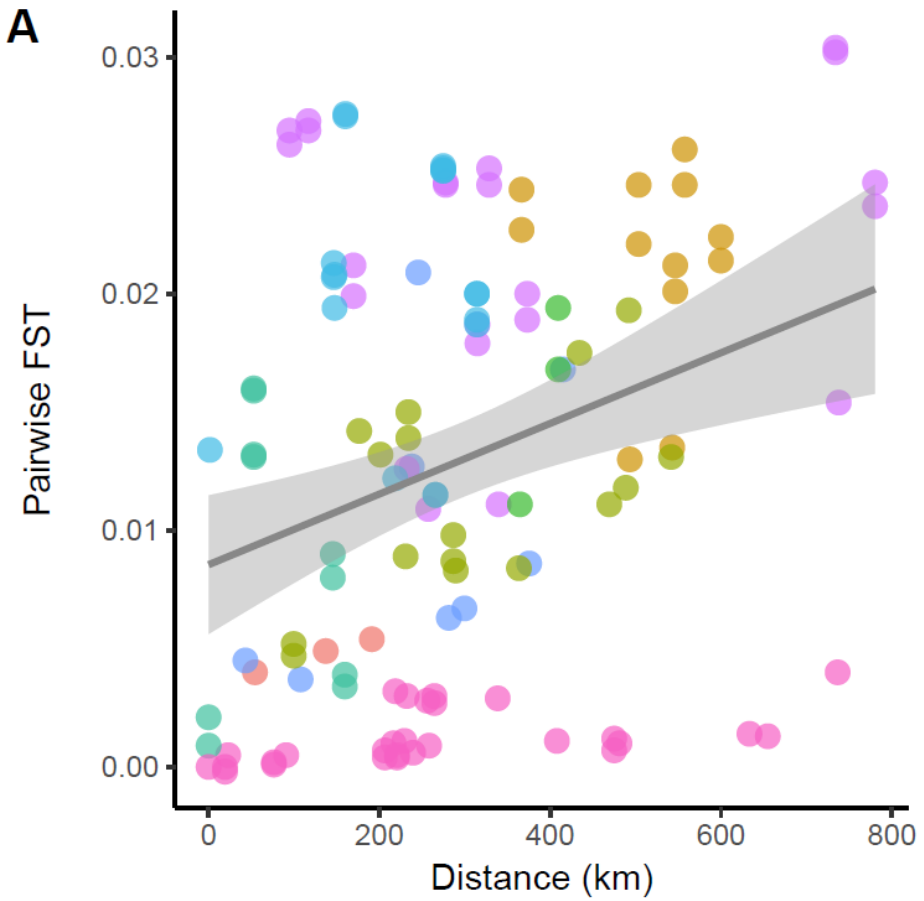
What can we learn from temporal replicates?



- Allele frequencies stable over time
- Homing behavior in terms of spawning season

IBT and IBD all pops



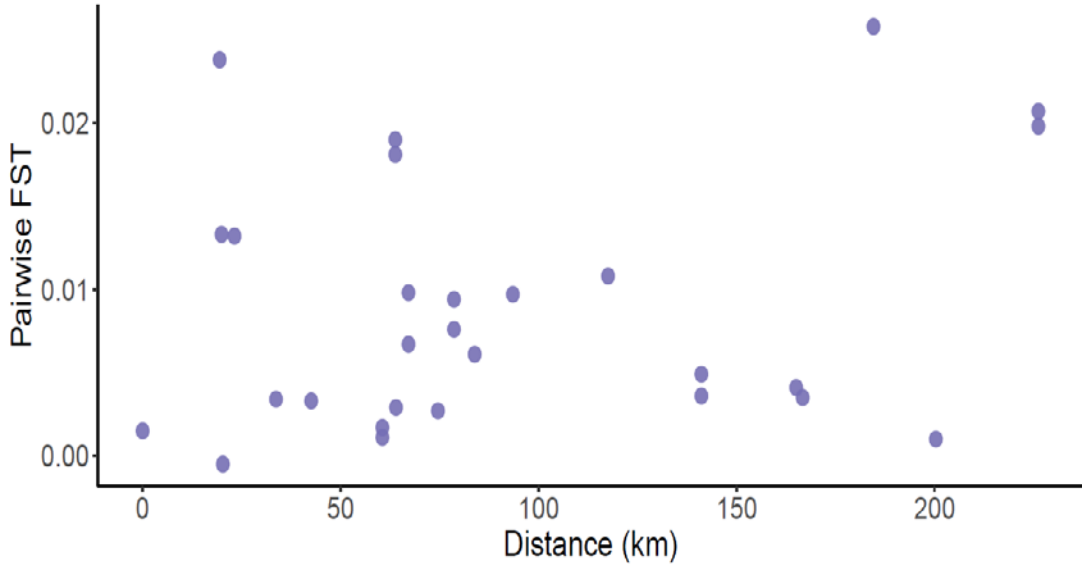


IBD in Salish Sea?

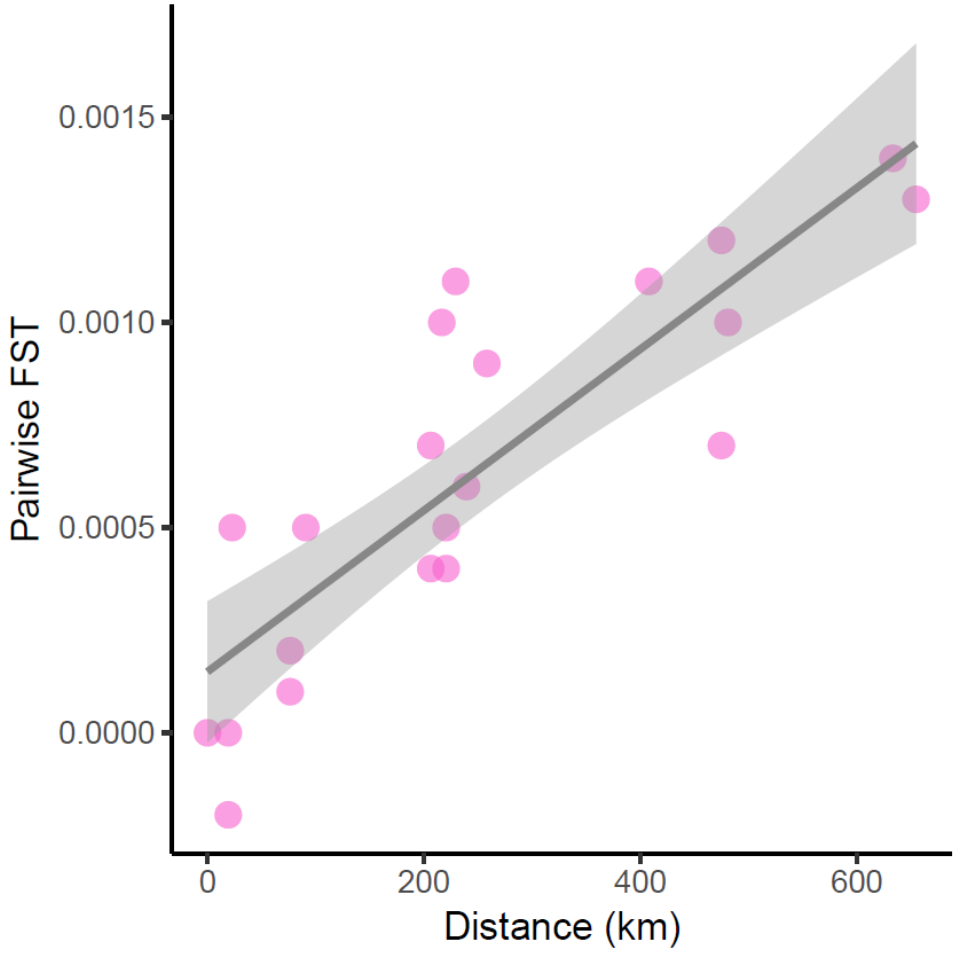
- Small spatial scale
- Dispersal is limited (FST ≠ 0)

  BUT

- Not correlated to geographic distance separating populations



BC primary spawners: isolation by distance



adjusted R-squared = 0.71, p-value = 9 e-07

- Dispersal is limited by geographic distance
- Even at modest spatial scales!

Key notes about IBD

- When dispersal is restricted, we expect to observe increase in genetic diff with increasing geo distance.
- IBD should develop most quickly in 1-d systems and short distances.
- At migration-drift equilibrium, no variation in IBD slope should be observed across the spp range (Hutchinson & Templeton 1999)
- IBD slope depends on geographic scale considered (Bradbury and Bentzen 2007)

Abstract

- **The role of reproductive timing as a driver of genetic differentiation in populations of Pacific herring**
- Eleni L. Petrou, Todd Sandell, Dayv Lowry, Lorenz Hauser
- There is growing recognition that maintaining diversity in life history traits contributes to the sustainable management of wild populations. One important life history characteristic is reproductive phenology, and it has been shown that differences in the timing of reproduction can act as a barrier to gene flow between populations. If the difference in reproductive timing determines the level of connectivity, one would expect that genetic differentiation between populations would increase as a function of difference in reproductive date. This pattern, known as “isolation by time” (IBT), has been observed in wild populations of salmonids containing early and late runs. Pacific herring in the Salish Sea also exhibit a wide diversity of spawn times; some populations start reproducing as early as January and reproductive activity in the region continues through May. Here, we test whether these temporal differences in reproduction influence the genetic population structure of herring. We collected adult herring from seven different locations in the Salish Sea during active spawning events (N = 48 per site). Samples were sequenced using a restriction site-associated (RAD) approach and approximately 3,000 polymorphic loci were genotyped in each sample. We found a positive correlation between genetic differentiation and difference in spawn date, with evidence of migration between populations with similar spawn timing. Several loci exhibited exceptionally steep gradients in allele frequencies, including one locus linked to the photoperiodic regulation of reproduction. Our discovery of IBT in Pacific herring support the adaptive significance of spawn timing and underscore the importance of conserving spawning time diversity in Puget Sound herring.