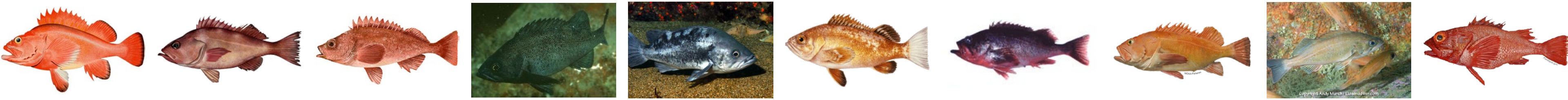


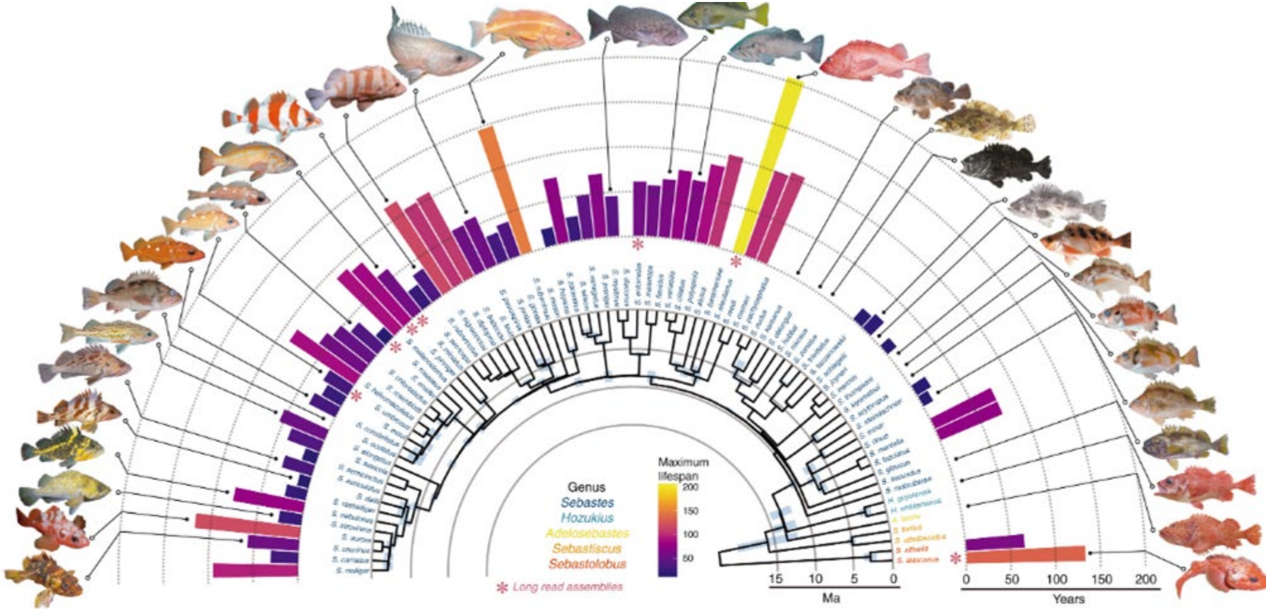
Genetic stock structure of multiple rockfish species across the West Coast: chaos reigns supreme?

Wes Larson
Laura Timm
Nicolas Lou
Greg Owens
Peter Sudmant

wes.larson@noaa.gov

Characteristics of rockfish

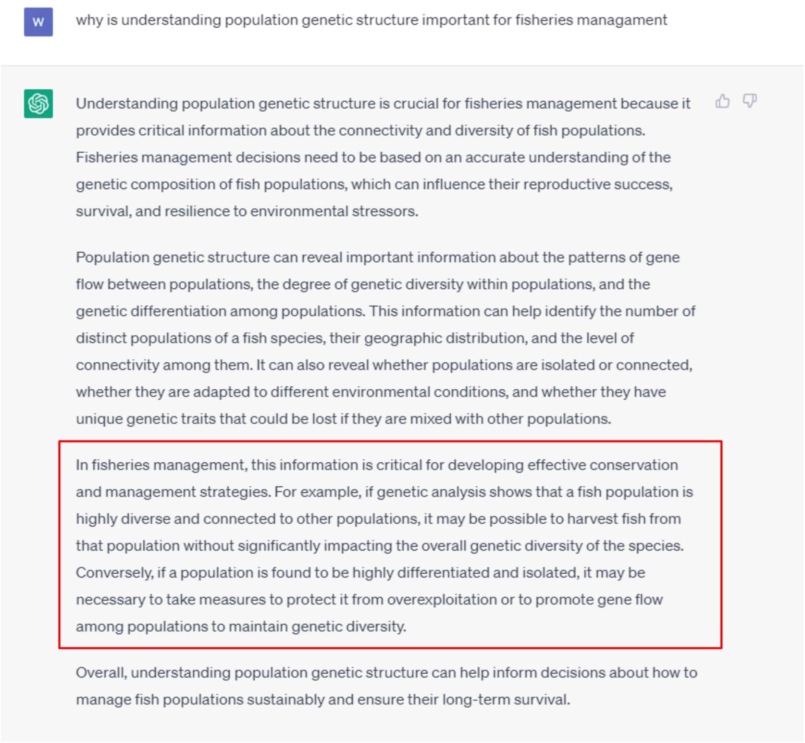
- Extreme diversity: life span, habitat, ecological niche
- Livebearer: mate choice
- Valuable fisheries species



Kohlora et al. 2021

Goal: understand population genetic structure of commercially important rockfish across Alaska

Why should we care about genetic structure for fisheries management?



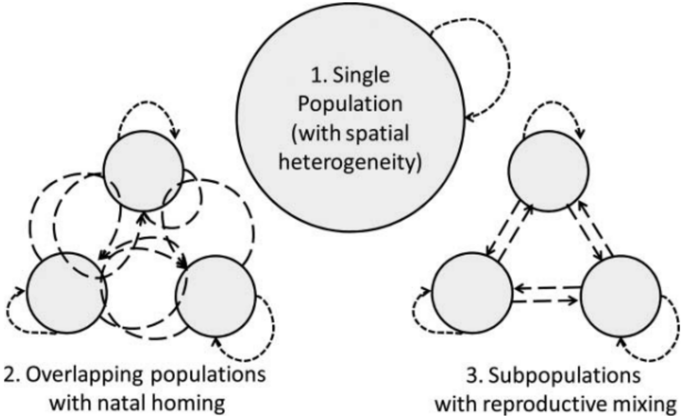
W why is understanding population genetic structure important for fisheries managament

Understanding population genetic structure is crucial for fisheries management because it provides critical information about the connectivity and diversity of fish populations. Fisheries management decisions need to be based on an accurate understanding of the genetic composition of fish populations, which can influence their reproductive success, survival, and resilience to environmental stressors.

Population genetic structure can reveal important information about the patterns of gene flow between populations, the degree of genetic diversity within populations, and the genetic differentiation among populations. This information can help identify the number of distinct populations of a fish species, their geographic distribution, and the level of connectivity among them. It can also reveal whether populations are isolated or connected, whether they are adapted to different environmental conditions, and whether they have unique genetic traits that could be lost if they are mixed with other populations.

In fisheries management, this information is critical for developing effective conservation and management strategies. For example, if genetic analysis shows that a fish population is highly diverse and connected to other populations, it may be possible to harvest fish from that population without significantly impacting the overall genetic diversity of the species. Conversely, if a population is found to be highly differentiated and isolated, it may be necessary to take measures to protect it from overexploitation or to promote gene flow among populations to maintain genetic diversity.

Overall, understanding population genetic structure can help inform decisions about how to manage fish populations sustainably and ensure their long-term survival.

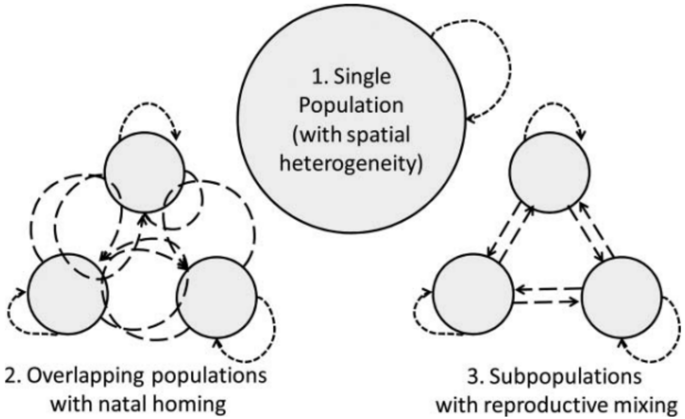


Goethel, Quinn, Cadrin 2011

ChatGPT

Why should we care about genetic structure for fisheries management?

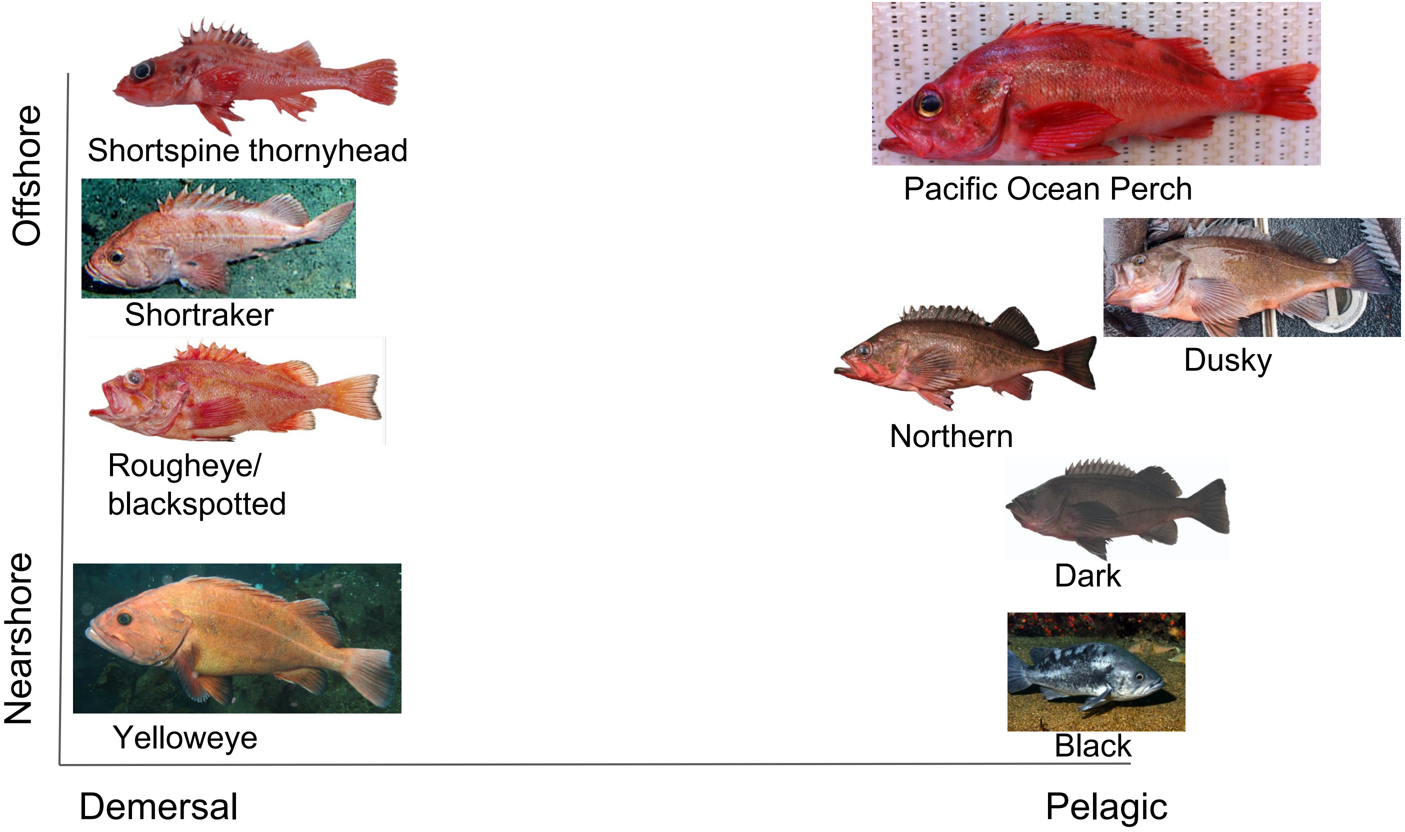
- Population genetics provides information on the degree of gene flow (i.e. migration) among populations
- Understanding how populations are demographically connected is vital for managing them sustainably
- We use genetic markers (here SNPs from whole genome resequencing) to assess genetic differentiation among individuals



Goethel, Quinn, Cadrin 2011

ChatGPT

Study species



Offshore

Nearshore

Shortspine thornyhead

Shortraker

Rougheye/
blackspotted

Yelloweye

Pacific Ocean Perch

Dusky

Northern

Dark

Black

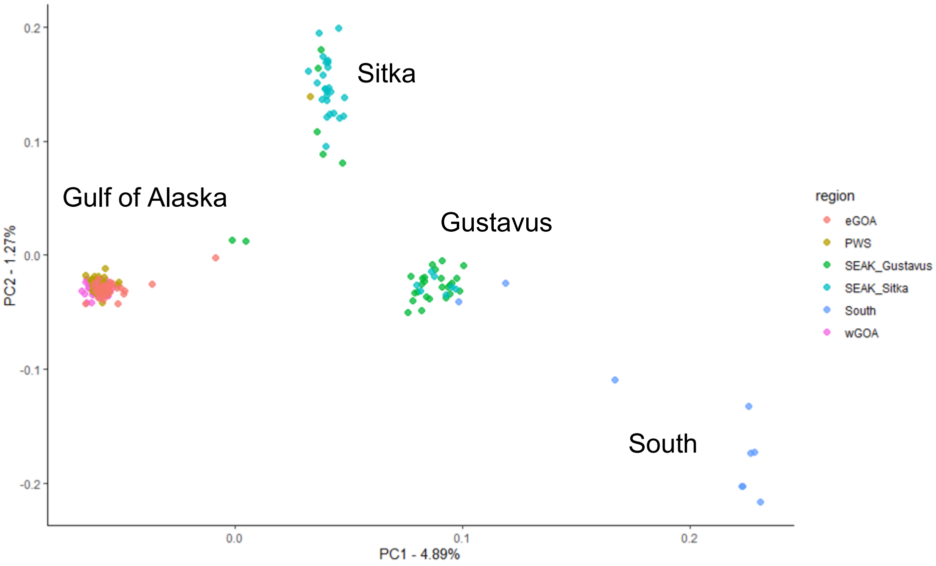
Demersal

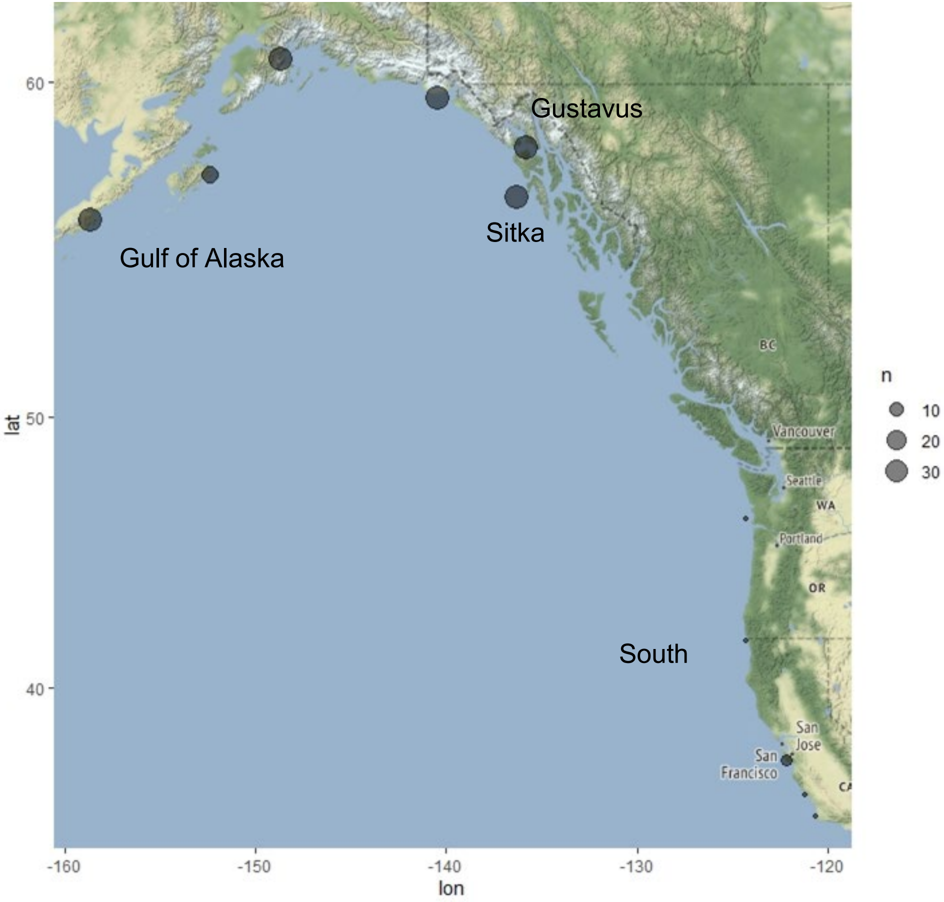
Pelagic

Patterns of population structure: hypotheses

- Adult movement is low and generally irrelevant. Population structure is driven by larval connectivity.
- Life history will influence population structure. Species with more structure:
  - Nearshore/inside waters-less larval connectivity
  - More specific habitat requirements (larvae & adults)
  - Shorter lifespan-smaller generation time
  - Smaller population sizes
- Cryptic diversity may exist and may not be easily related to phenotype

Black rockfish: nearshore, pelagic, high structure

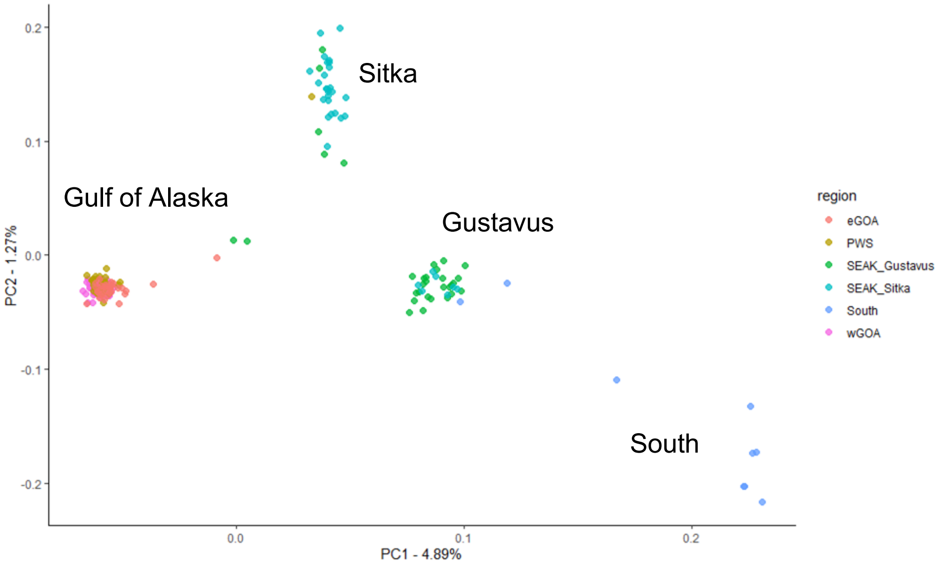




177 individuals

2.7 million (2,742,086) SNPs

Black rockfish: nearshore, pelagic, high structure

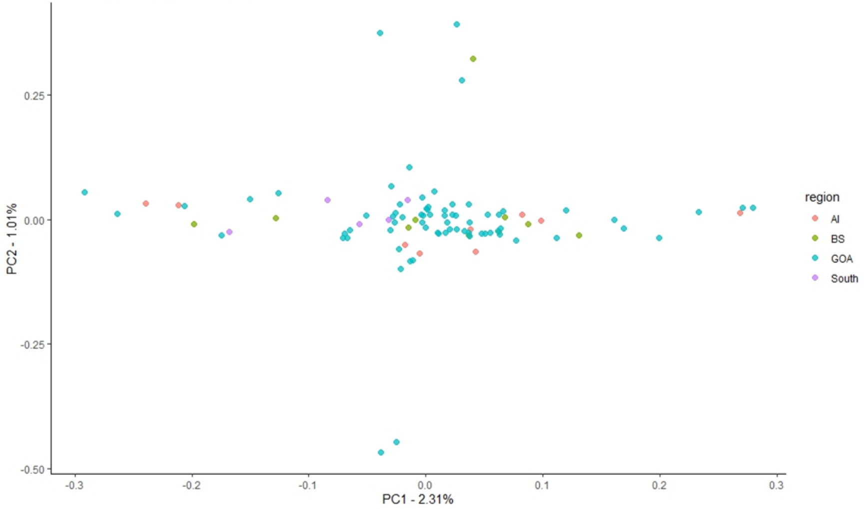


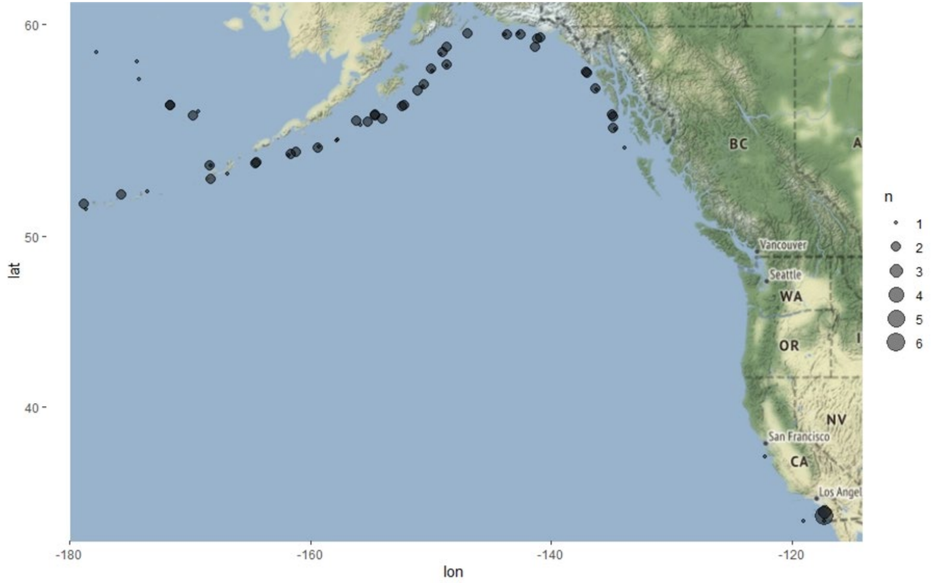
177 individuals

2.7 million (2,742,086) SNPs

- Connectivity in outside GOA (larval connectivity?)
- Structure between inside and outside SE and between lower 48 and Alaska
- Overall: some connectivity on regional scales, but high structure at larger scales and inside/outside waters
- Management: regional with consideration of oceanographically isolated populations with low larval connectivity

Shortspine thornyhead: offshore, demersal, no structure



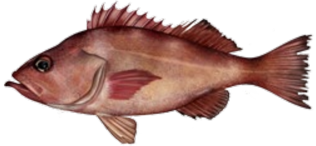


98 individuals

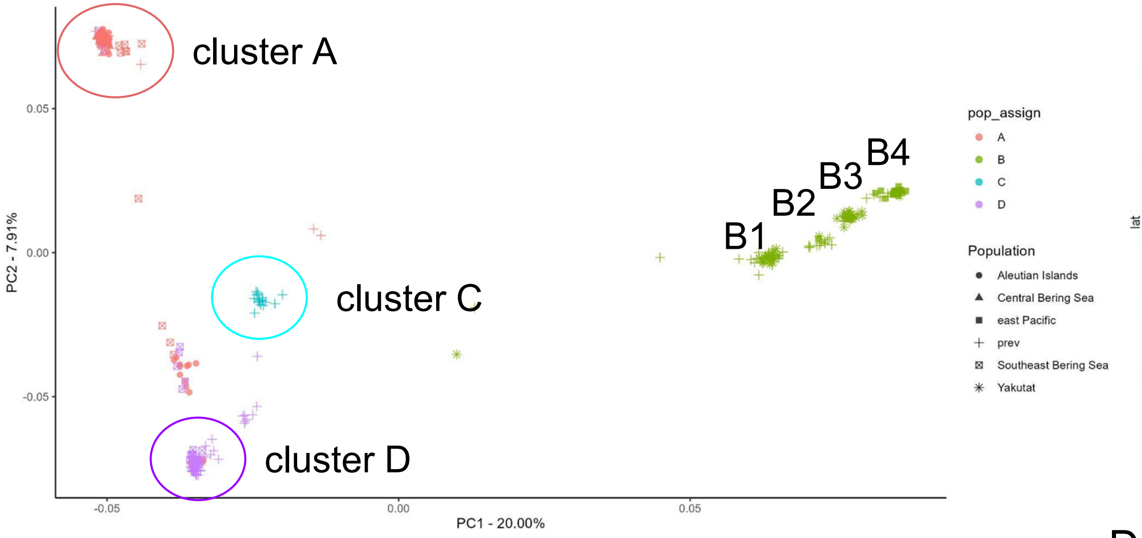
265,296 polymorphic sites

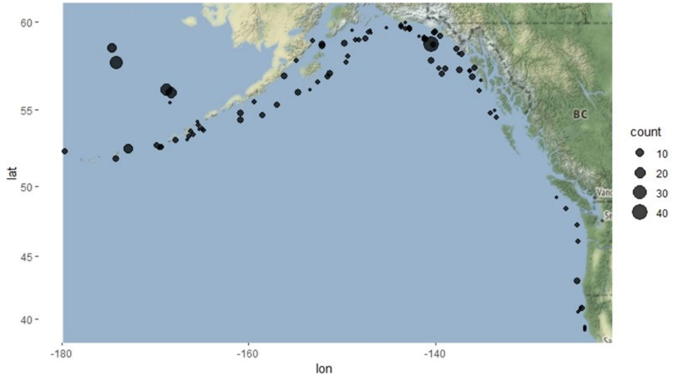
(likely due to distant reference genome)

- High larval connectivity
- Can settle in homogenous habitat
- Demersal habitats more similar across large geographic area (temperature, substrate)
- Spatial management lower priority



Pacific ocean perch: offshore, pelagic

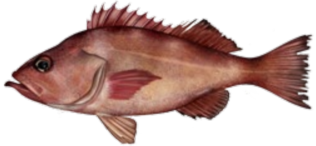




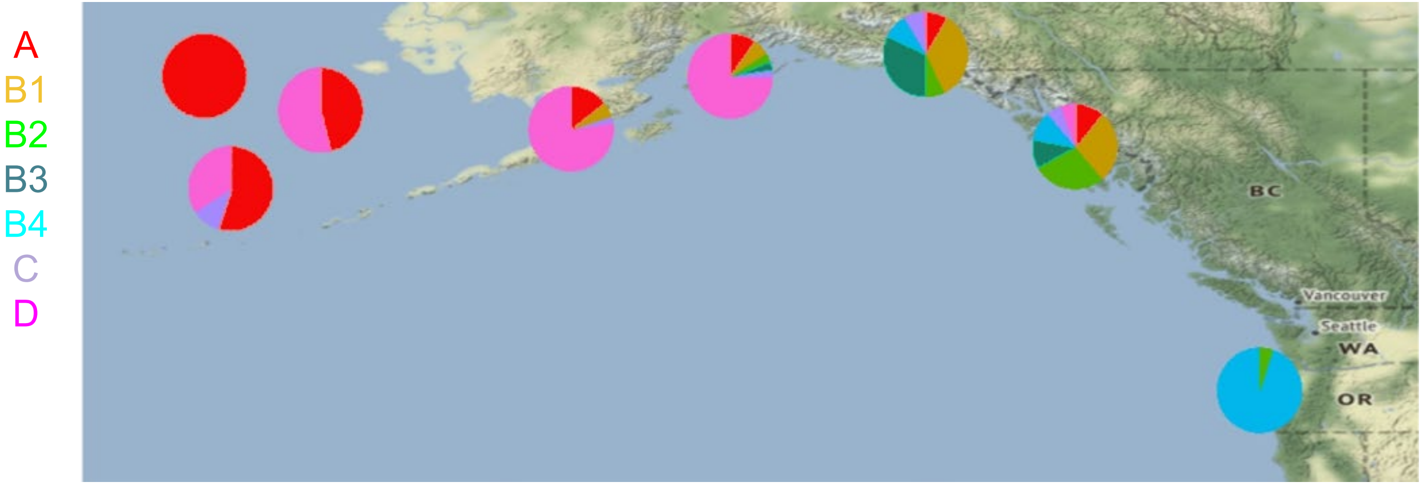
335 individuals

3.5 million (3,501,142) polymorphic sites

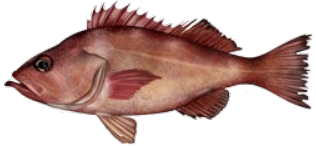
- Discrete genetic clusters that overlap in space but vary in frequency by geography
- Will be important to understand harvest patterns for different “forms”



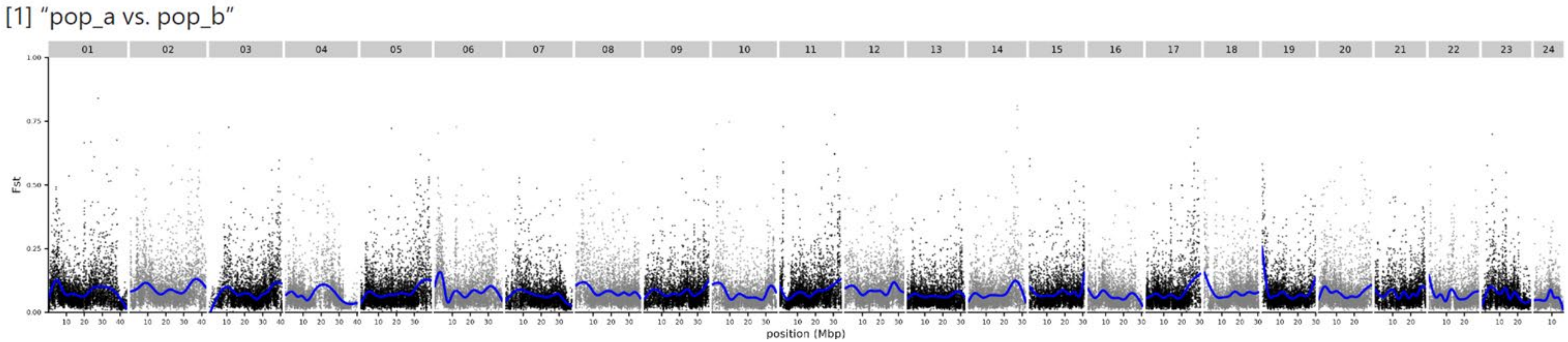
Pacific ocean perch: offshore, pelagic

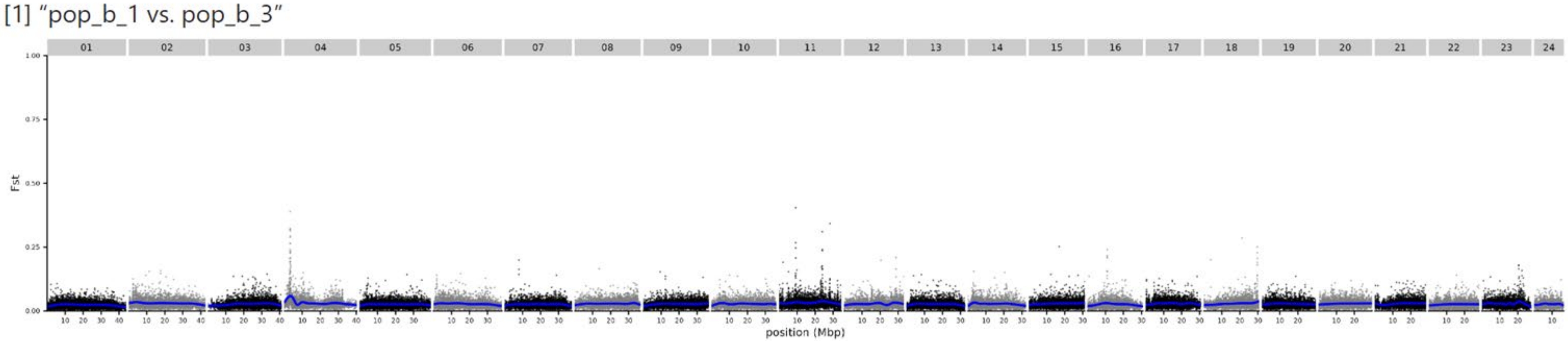


- A, C, and D dominate in the north (A is especially prevalent in the central Bering Sea)
- B1-B4 dominate in the south (B4 is especially prevalent along the northwest US coast)
- Central GOA is a mixing area
- Individuals from all clusters are found in SE Alaska



Pacific ocean perch forms: gradient of isolation





Differentiation across the genome indicates differing evolutionary histories

Structure by species

Offshore

Nearshore


Shortspine thornyhead

None


Shortraker

None


Rougheye/
blackspotted

None


Yelloweye

**Low:
inside vs
outside**

Cryptic diversity


Pacific Ocean Perch

Structure within forms?


Dusky

**None/
low?**

**Moderate
/high**


Northern


Dark

**Moderate/
regional?**


Black

Highest

Demersal

Pelagic

Preliminary conclusions

Species with low/no structure tend to be…

- Demersal
- Offshore and deeper (deep shelf and slope)
- Why: high larval connectivity, homogeneous habitat across large areas?
- Exceptions
  - Yelloweye-demersal but lack of connectivity with inside waters
  - Dusky-far enough offshore for larval exchange? Movement of inside water schools?

[rougheye, blackspotted, shortraker, shortspine, dusky]

Preliminary conclusions

Species with low/no structure tend to be…

- Demersal
- Offshore and deeper (deep shelf and slope)
- Why: high larval connectivity, homogeneous habitat across large areas?
- Exceptions
  - Yelloweye-demersal but lack of connectivity with inside waters
  - Dusky-far enough offshore for larval exchange? Movement of inside water schools?

[rougheye, blackspotted, shortraker, shortspine, dusky]

Species with genetic structure tend to be…

- Pelagic/schooling
- Nearshore
- Why?
  - Inshore settlement areas are more specific
  - Lack of larval exchange in inshore waters
- Exceptions
  - POP: need to be evaluated as discrete forms
  - Northern: deeper dive into life history

[black, northern, dark, yelloweye, POP (sort of)]

Preliminary conclusions

Species with low/no structure tend to be…

- Demersal
- Offshore and deeper (deep shelf and slope)
- Why: high larval connectivity, homogeneous habitat across large areas?
- Exceptions
    - Yelloweye-demersal but lack of connectivity with inside waters
    - Dusky-far enough offshore for larval exchange? Movement of inside water schools?

[rougheye, blackspotted, shortraker, shortspine, dusky]

Species with genetic structure tend to be…

- Pelagic/schooling
- Nearshore
- Why?
    - Inshore settlement areas are more specific
    - Lack of larval exchange in inshore waters
- Exceptions
    - POP: need to be evaluated as discrete forms
    - Northern: deeper dive into life history

[black, northern, dark, yelloweye, POP (sort of)]

Does chaos reign supreme?

Future directions

- Additional sampling/sequencing to solidify patterns
- Analysis of ~1,500 POP to increase confidence in distribution of forms
- Pairing morphology and genetics in POP forms
- Larval species ID to improve knowledge of life history
- eDNA to better understand species distribution, abundance, habitat use (emphasis on untrawlable habitat and integration with other survey data)

Acknowledgements

- Tony Gharrett-valuable insights and samples
- John Hyde and Matt Craig-access to amazing tissue database
- Sample collections: ADFG, NOAA
- ABL Genetics Team especially Katie D’Amelio, Kirby Karpan, and Jackie Whittle: huge amount of laboratory work
- NWFSC SEDNA computing support

Cooperative Institute for
CLIMATE, OCEAN &
ECOSYSTEM STUDIES

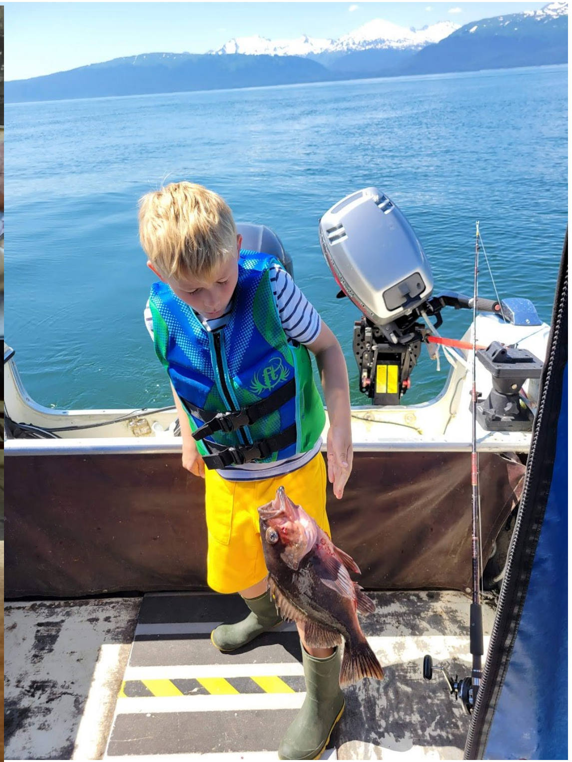
UAF
UNIVERSITY OF
ALASKA
FAIRBANKS
College of
Fisheries and
Ocean Sciences

Berkeley
UNIVERSITY OF CALIFORNIA

ALASKA
DEPARTMENT OF FISH AND GAME

University
of Victoria

Questions



wes.larson@noaa.gov