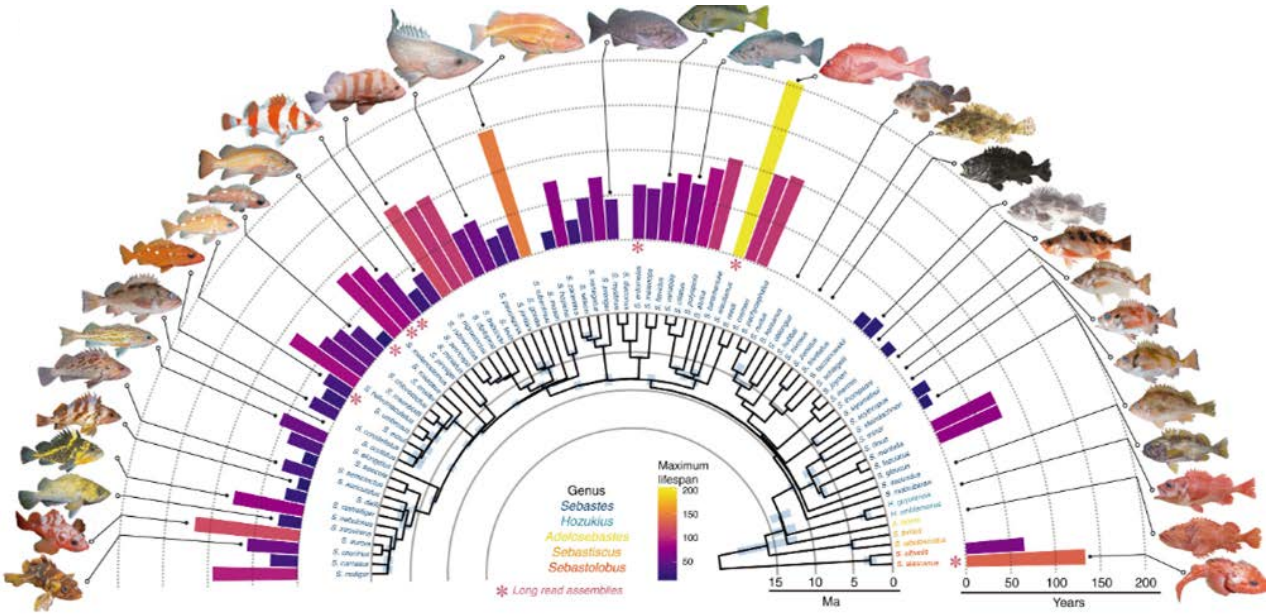
Genetic stock structure of multiple rockfish species in Alaska with a focus on Pacific ocean perch

Wes Larson
Laura Timm
Diana Baetscher
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

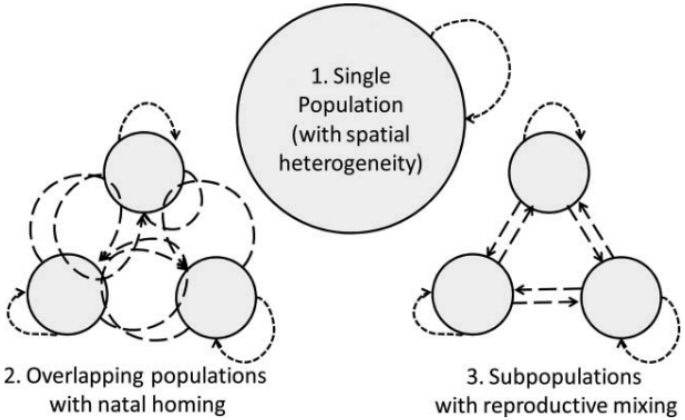


Kolora et al. 2021

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

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

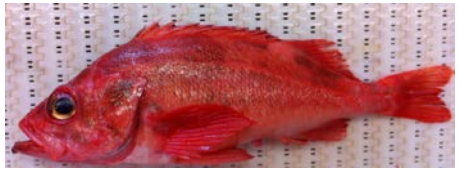
Study species

Shortspine thornyhead

Shortraker

Rougheye/
blackspotted

Yelloweye



Pacific Ocean Perch

Dusky

Northern

Dark

Black

Offshore

Nearshore

Demersal

Pelagic/schooling

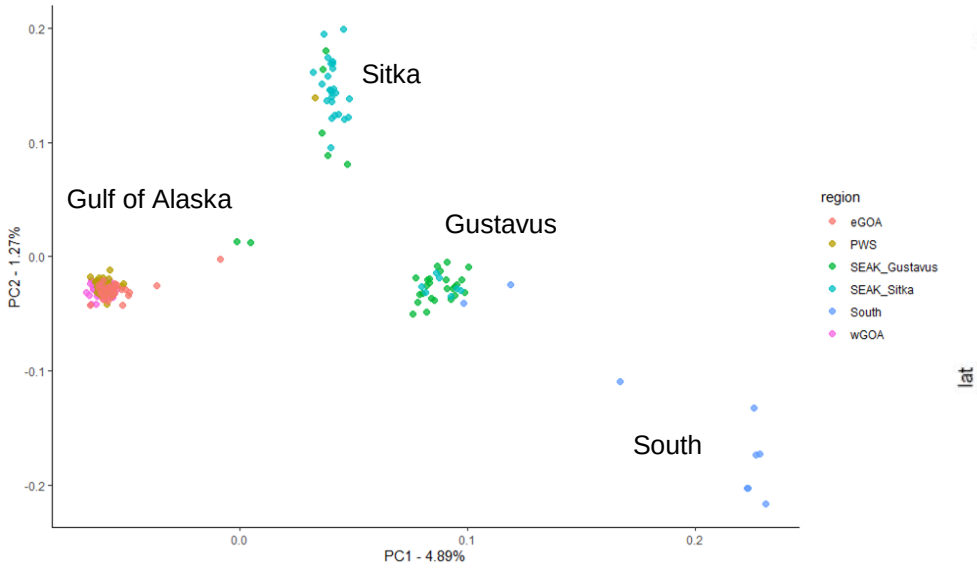
Patterns of population structure: hypotheses

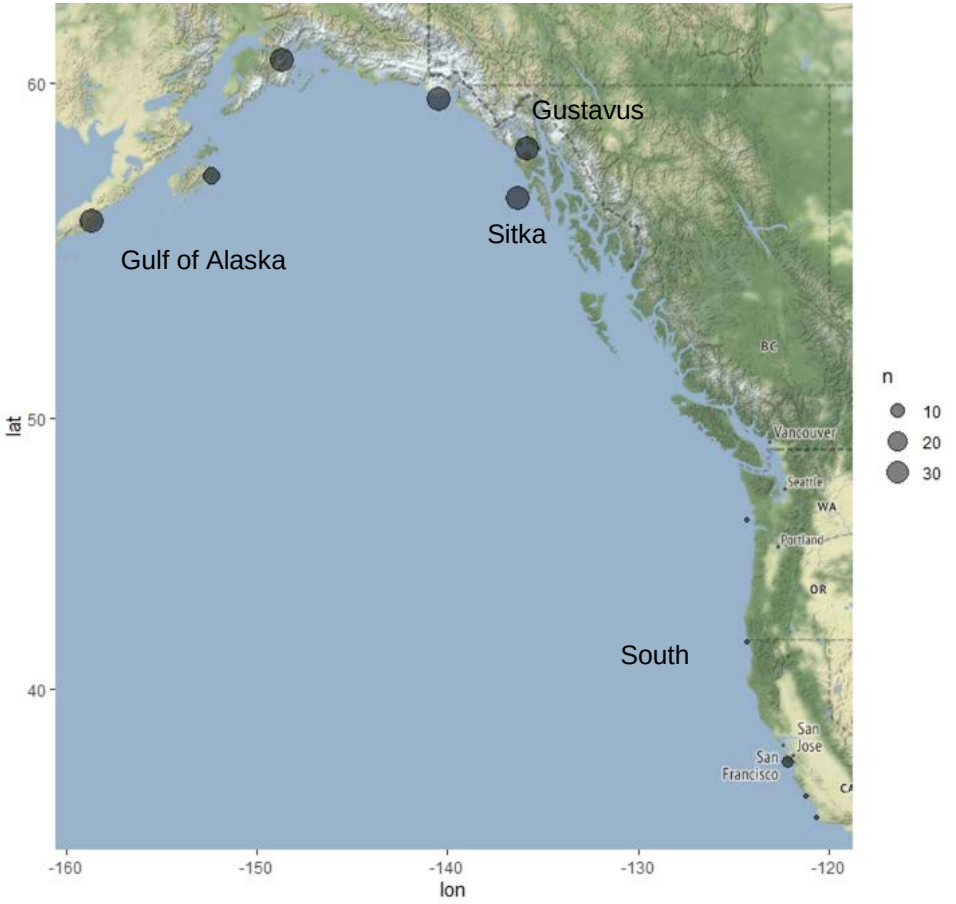
- Adult movement is generally low.
  Population structure is driven by larval connectivity.

- Life history will influence population structure.
  Species with more structure:
  - Nearshore/inside waters- limited long-distance larval connectivity
  - Spatially constrained habitat (juveniles & adults)
  - Shorter lifespan-shorter generation time
  - Smaller population sizes

- Cryptic diversity may exist and may not be easily related to phenotype

Black rockfish: nearshore, pelagic, high structure

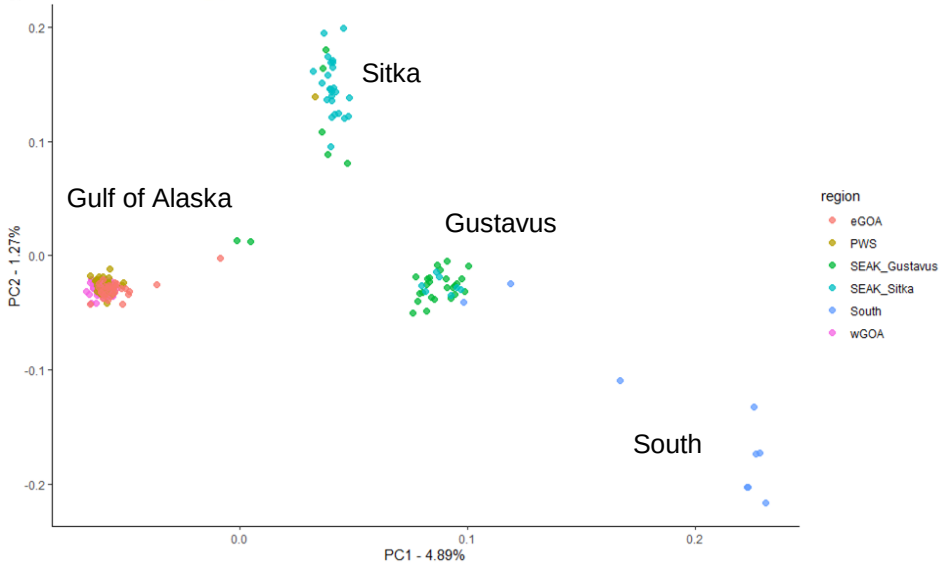




177 individuals

2.7 million (2,742,086) SNPs

Black rockfish: nearshore, pelagic, high structure

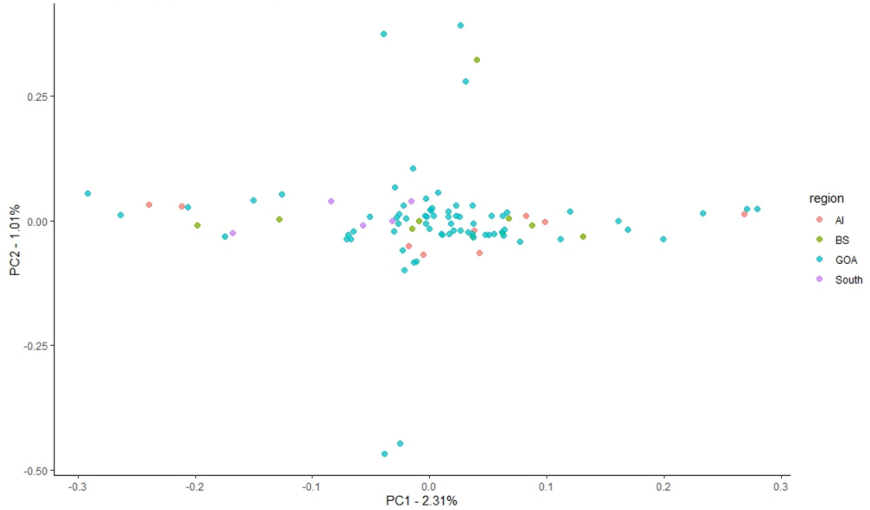


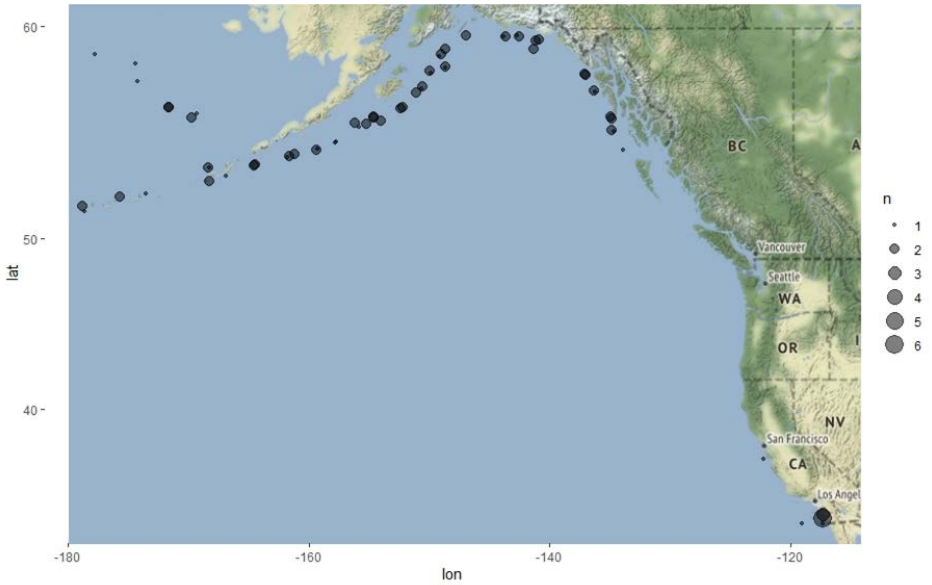
- Structure between inside and outside SE and between lower 48 and Alaska
- Low structure in central GOA
- Overall: some connectivity on regional scales, but high structure at larger scales and inside/outside waters
- Management: regional with consideration of oceanographically isolated populations with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

177 individuals

2.7 million (2,742,086) SNPs

Shortspine thornyhead: offshore, demersal, no structure



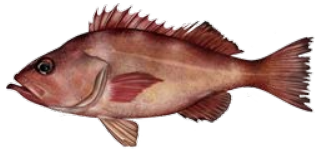


98 individuals

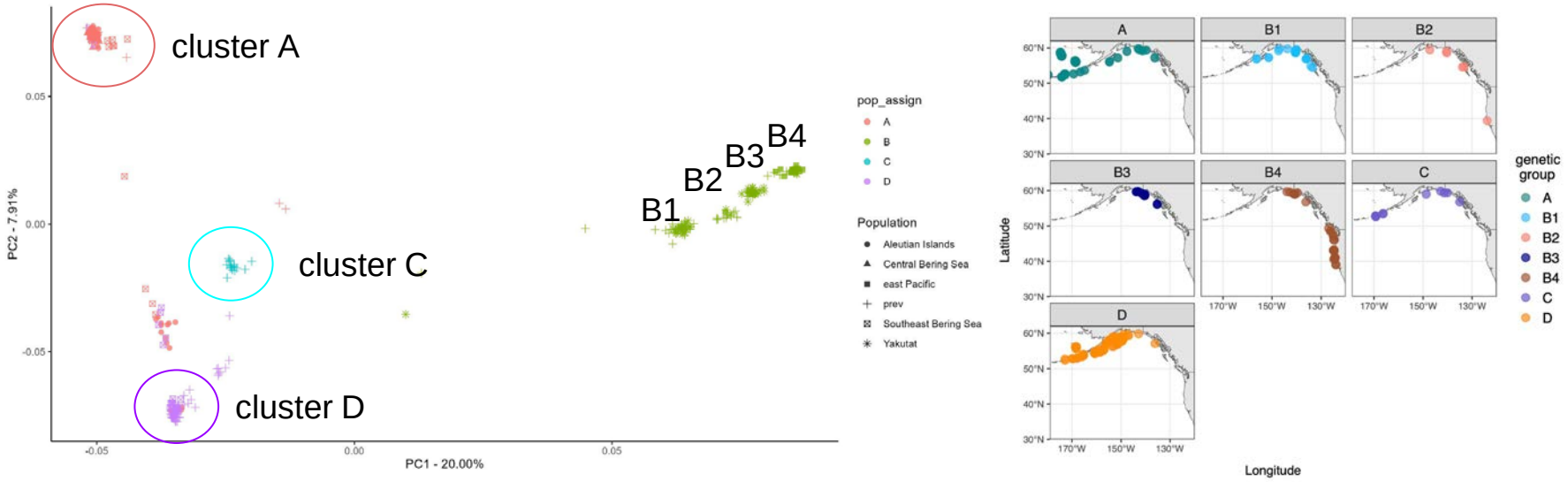
265,296 polymorphic sites

(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

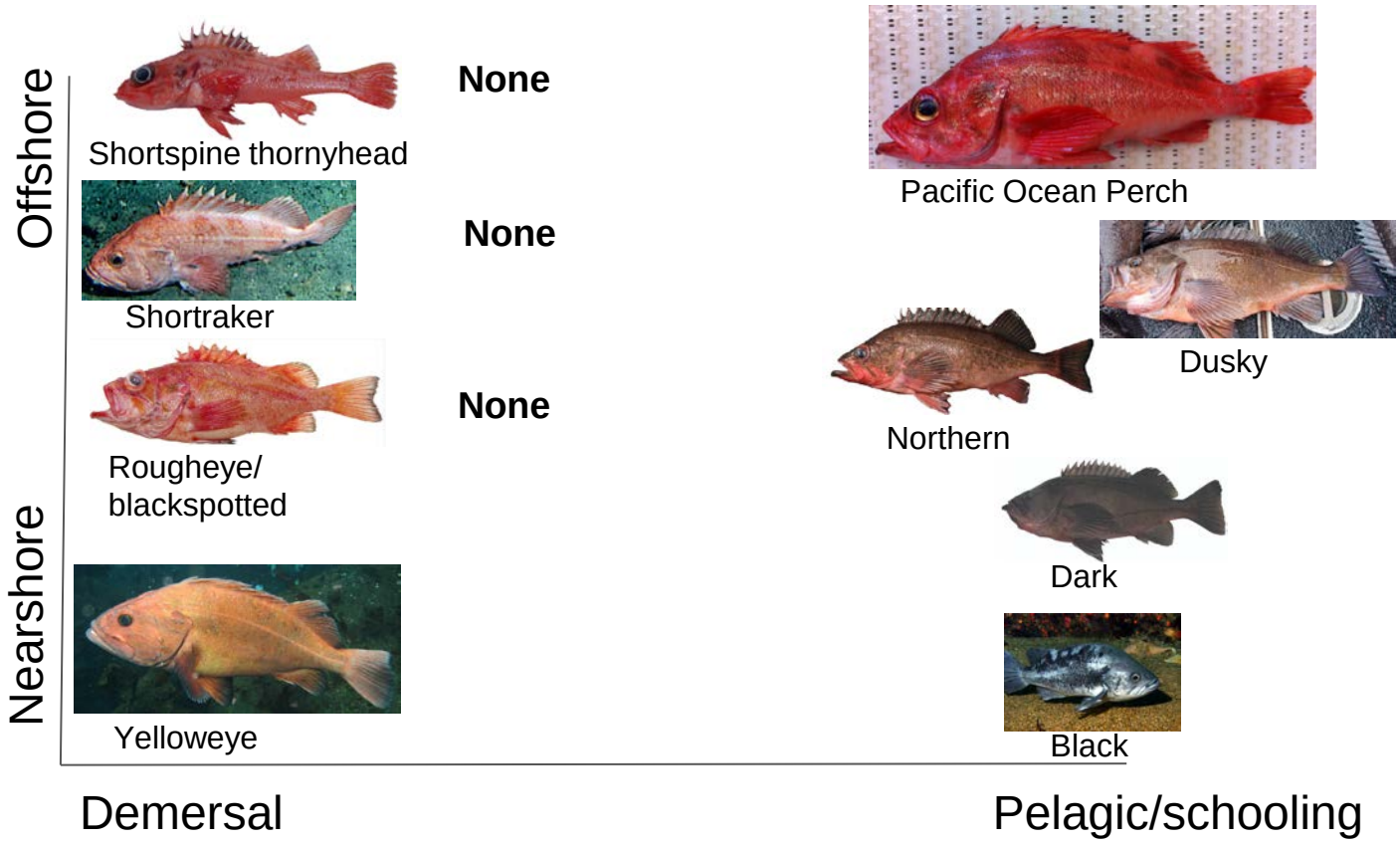


335 individuals

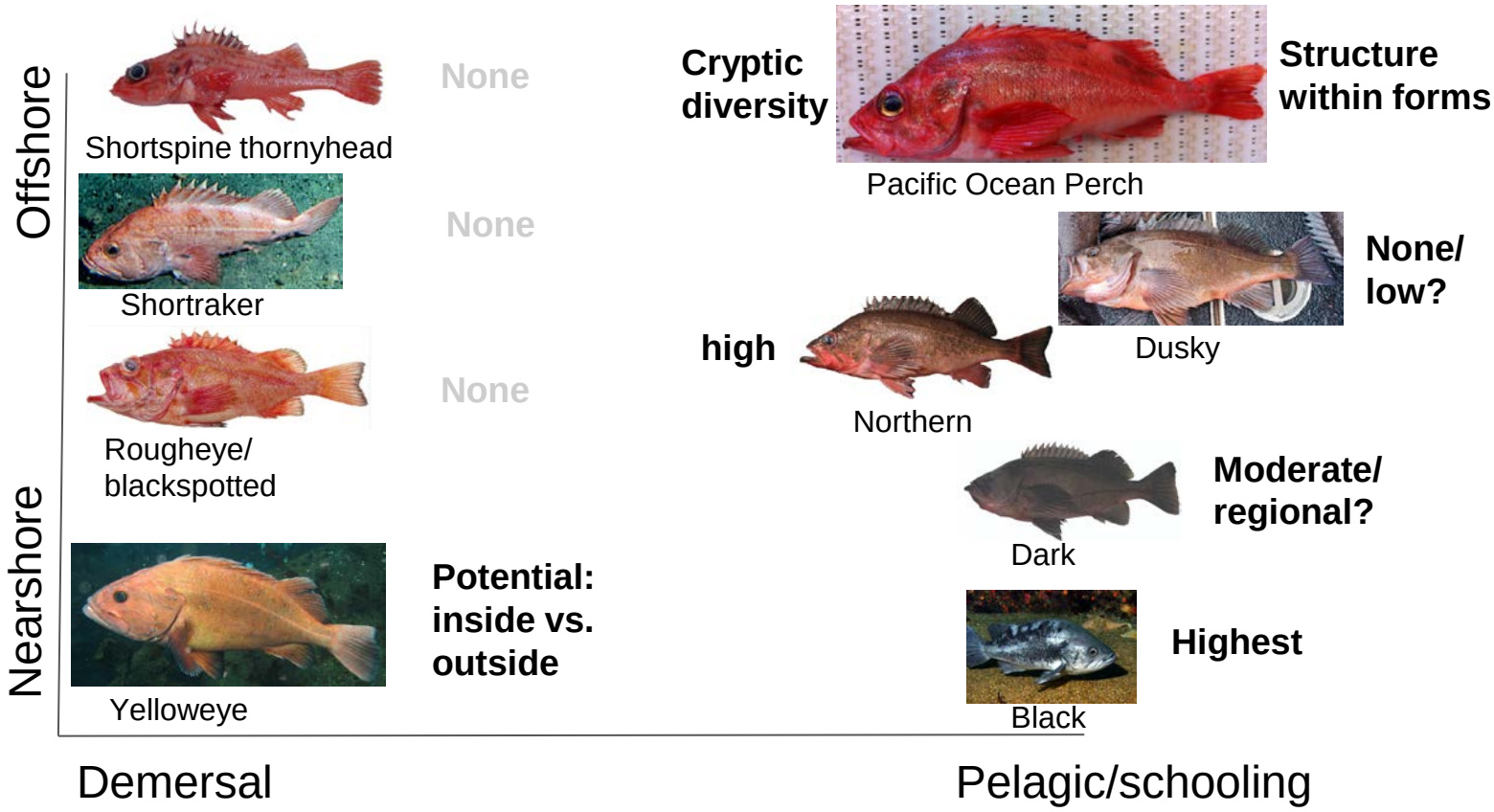
3.5 million (3,501,142) polymorphic sites

- Discrete genetic groups (PCA clusters)
- Spatial overlap among fish from multiple genetic groups

No structure in demersal/offshore species



More structure in nearshore/schooling species



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 spatial extent?
- Exceptions
  - Yelloweye-demersal but potential 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 spatial extent?
- Exceptions
  - Yelloweye-demersal but potential 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…

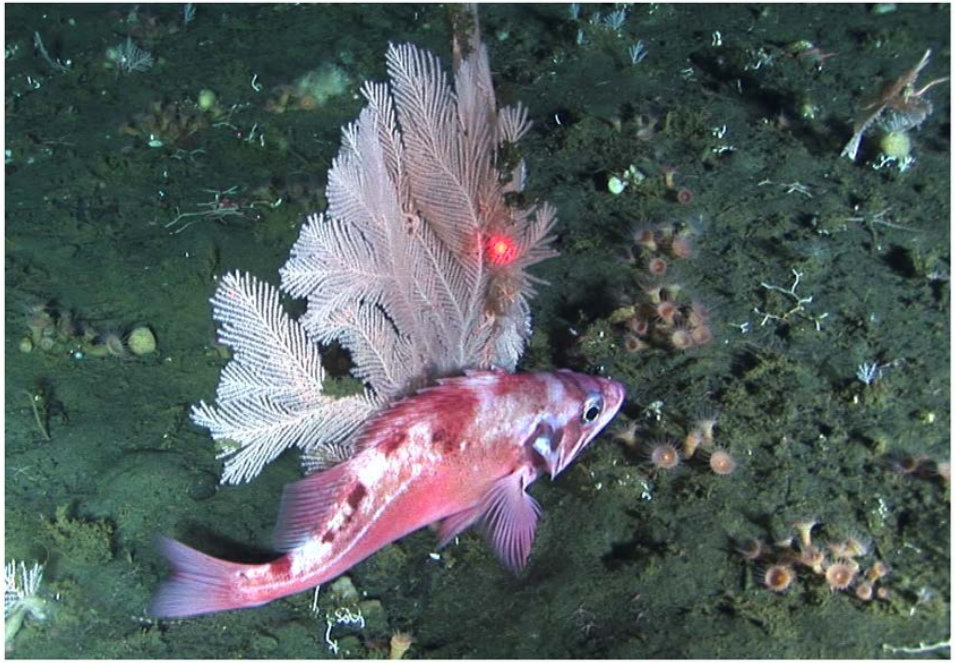
- Pelagic/schooling
- Nearshore
- Why?
  - Inshore settlement areas have discrete spatial distribution
  - More limited larval connectivity inshore (less long-distance exchange)
- Exceptions
  - POP: need to be evaluated as discrete forms
  - Northern: deeper dive into life history

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

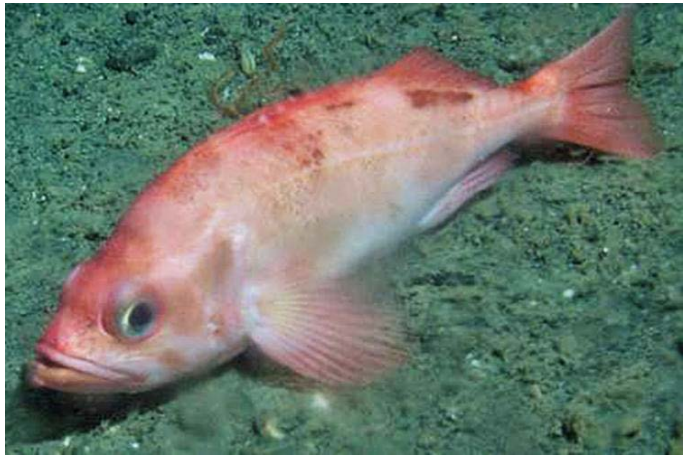
Management implications/future directions

- Rougheye, blackspotted, shortraker, and dusky show no evidence of structure across Alaska suggesting high gene flow
  - Regional assessments less important based on genetic data
- Northern shows strong structure and yelloweye shows potential structure
  - Spatial structure could be considered in assessments
- Additional sampling/sequencing to solidify patterns
  - More samples, including from the lower 48
  - New species: harlequin, others of interest?

Preliminary genetic analysis of Pacific Ocean Perch in Alaska

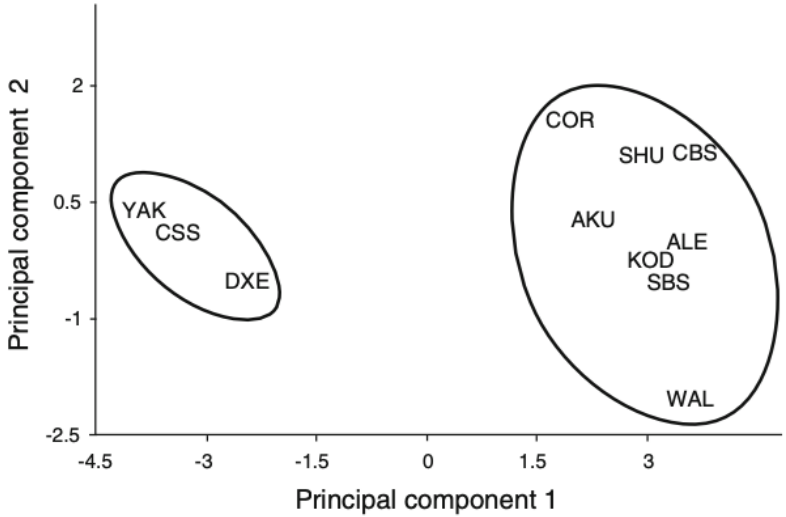


AFSC Genetics Program
Diana Baetscher, Laura Timm

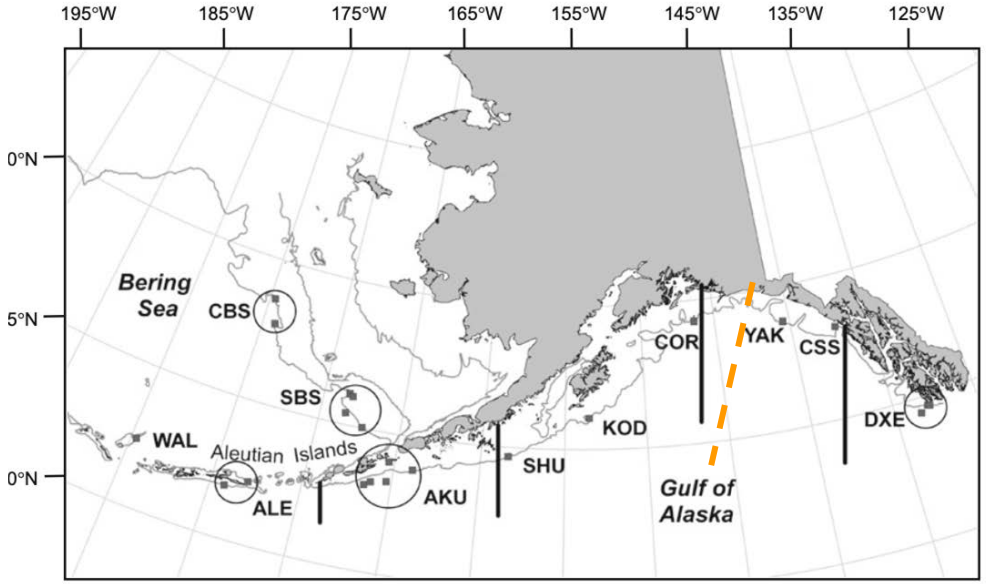


NOAA Fisheries photo

Background - POP structure with 14 microsatellites



From Palof et al., 2010 Marine Bio



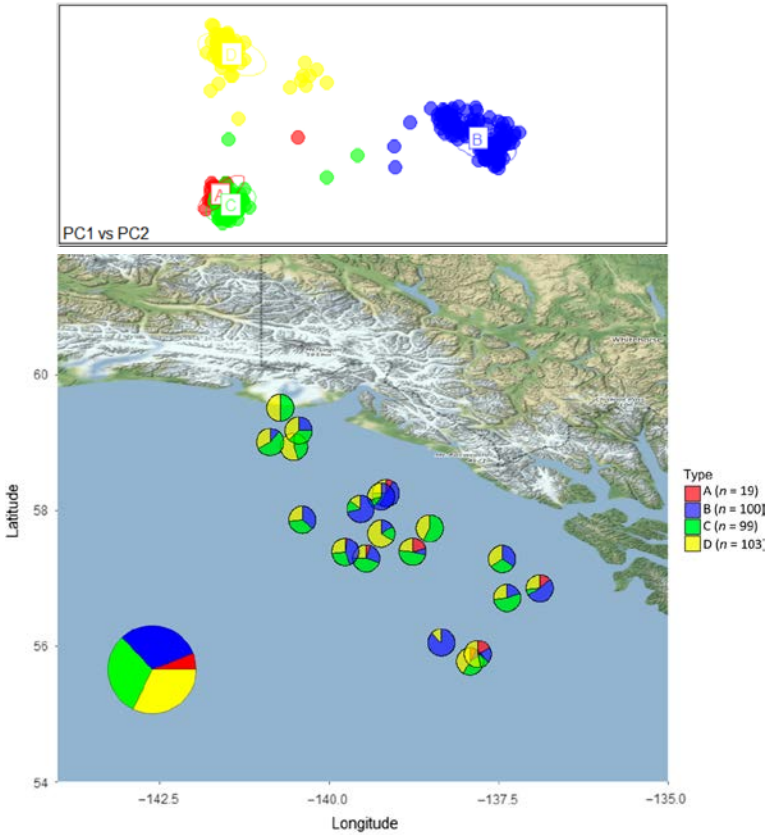
Large break ~Yakutat

Microsatellites-aggregated at the collection level, difficult to identify heterogeneity within collection

Background: multiple POP genetic groups with RADseq

- Four genetic groups identified among young-of-the-year POP in SE AK (RADseq 11,500 SNPs)

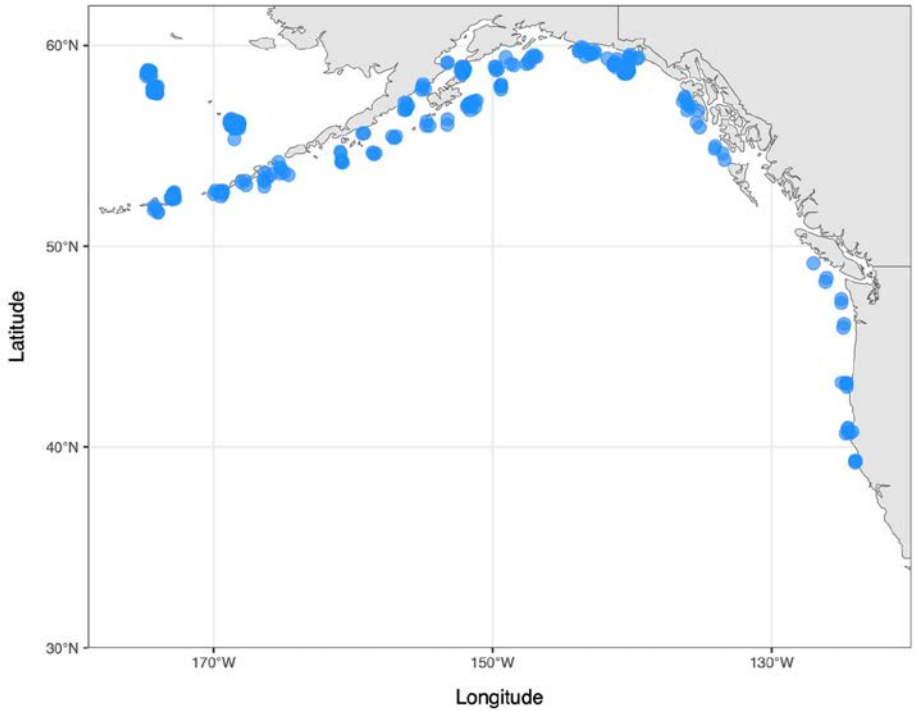
- Hypothesis:
  - Larval collections include multiple genetic groups because of pelagic dispersal
  - Adult collections likely more spatially separated



from Maselko et al., 2020 Ecol. Evol.

Low-coverage whole genome sequencing (2022-2023)

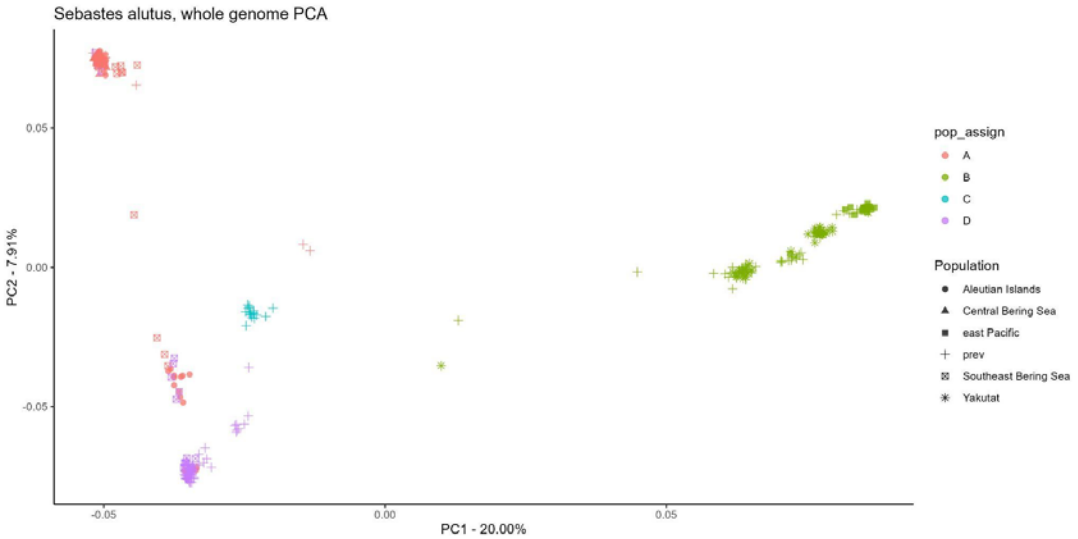
- 16 YOY samples from Maselko et al. (2020) study were sequenced **to define group membership**
- Other lcWGS samples chosen to maximize spatial distribution (collections from CA to AK)



321 adults, 3.5 million genetic markers

Low-coverage whole genome sequencing (2022-2023)

- Minimum of 4 and maximum of 8 genetic groups with varying levels of differentiation among them
- Some evidence of infrequent hybridization

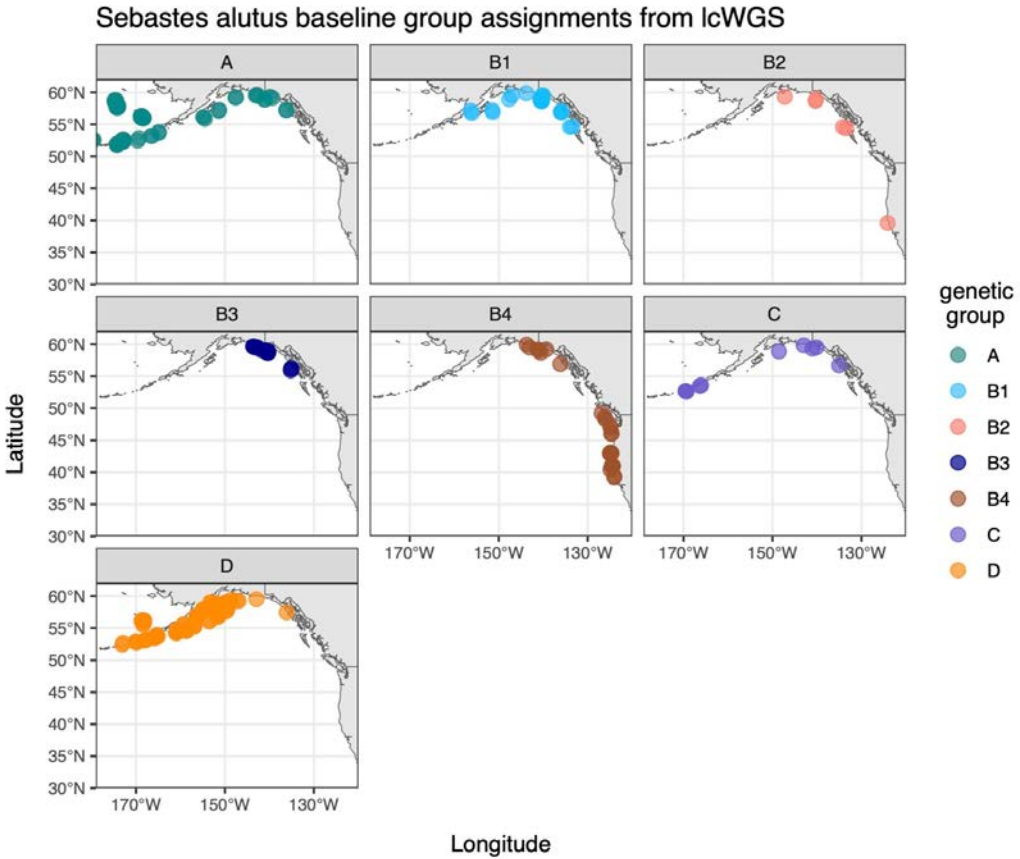


L. Timm

321 adults, 3.5 million genetic markers

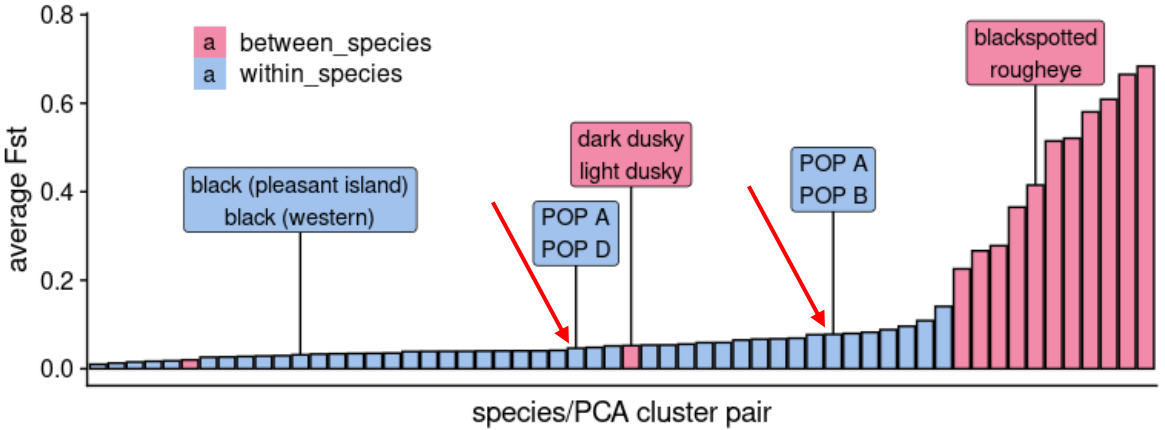
Genetic groups overlap in space

- B groups more prevalent in the south
- A, C, D groups more prevalent in the west
- Mixing zone in the central GOA



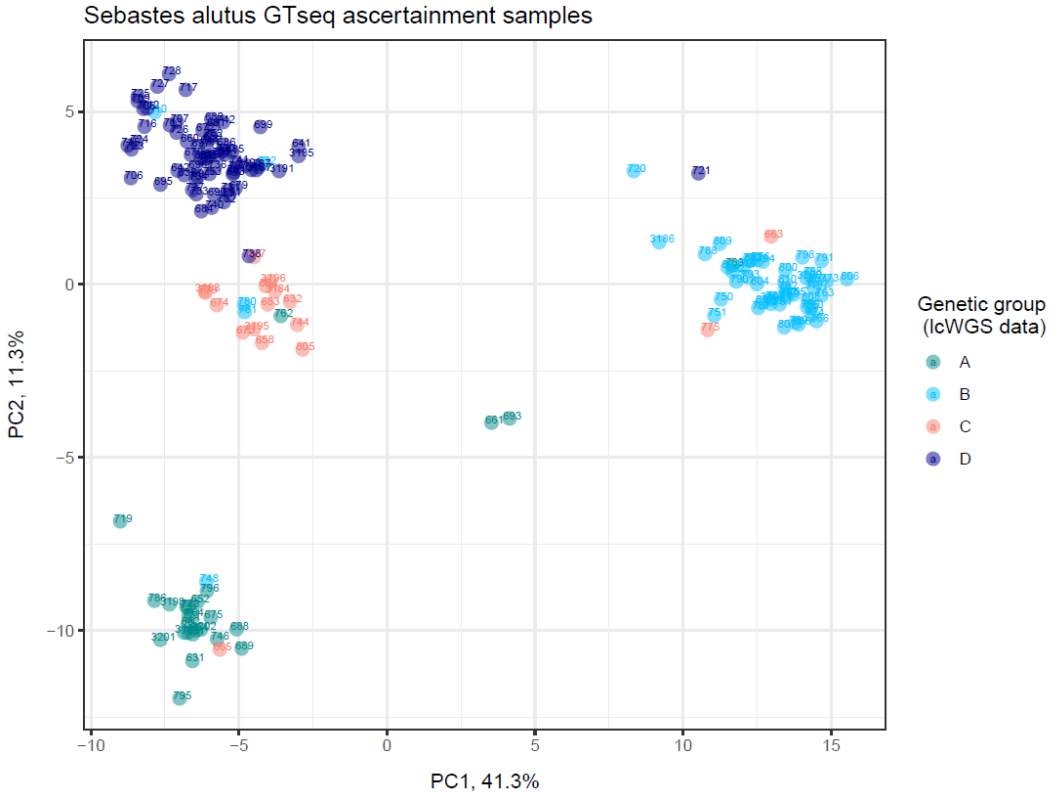
How different are POP genetic groups?

- POP groups A vs. B more differentiated than dark/dusky
- POP groups A vs D (sympatric):
  - F_{ST} higher than black rockfish - west/east GOA
  - Slightly lower but similar to dark vs. dusky
  - Much lower than rougheye vs. blackspotted



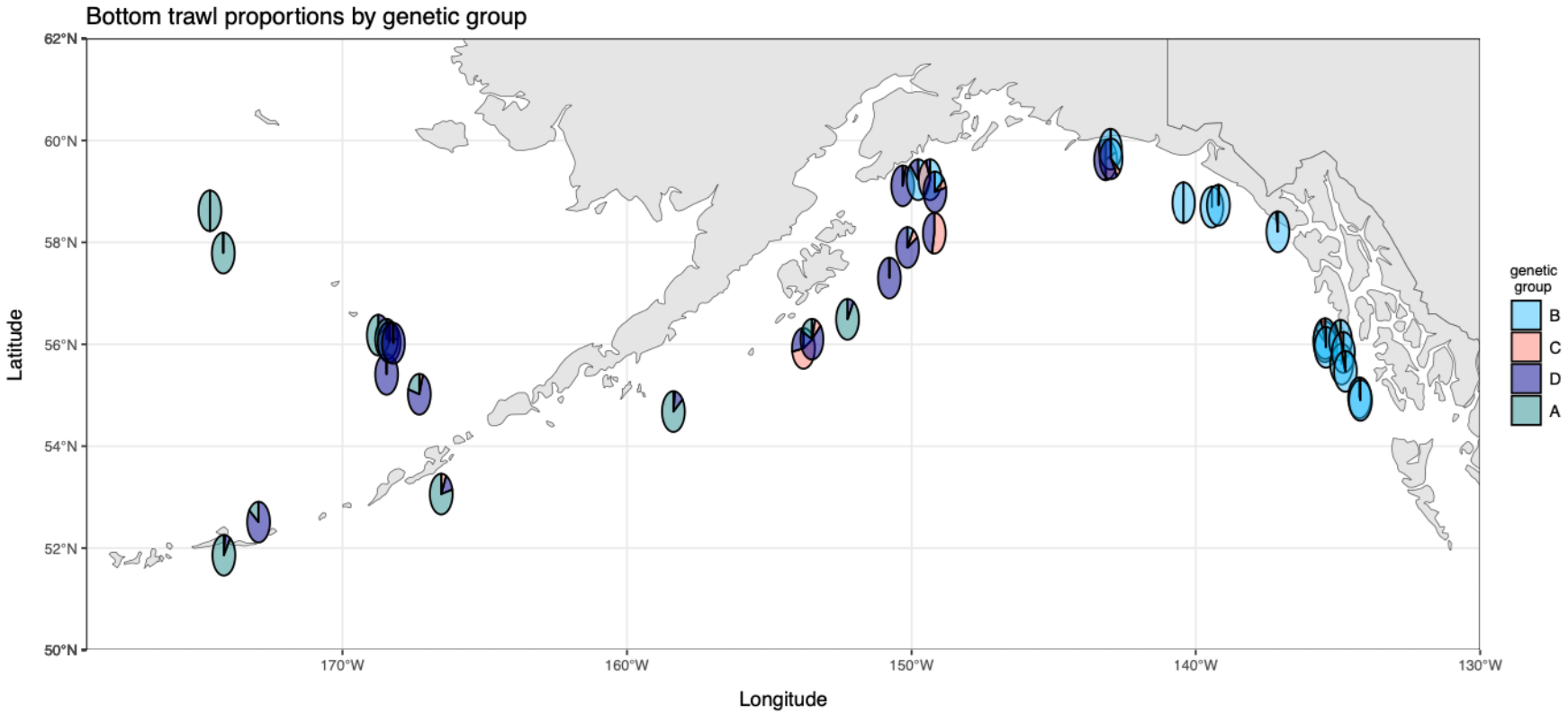
Designed high-throughput GTseq panel to better understand spatial distribution of groups

- For GTseq panel design, lcWGS samples were selected according to visual assessment of PCA
- 167 samples (18-68 per group)
- Panel facilitates accurate identification to group
- Cost effective, can be used to screen thousands of samples



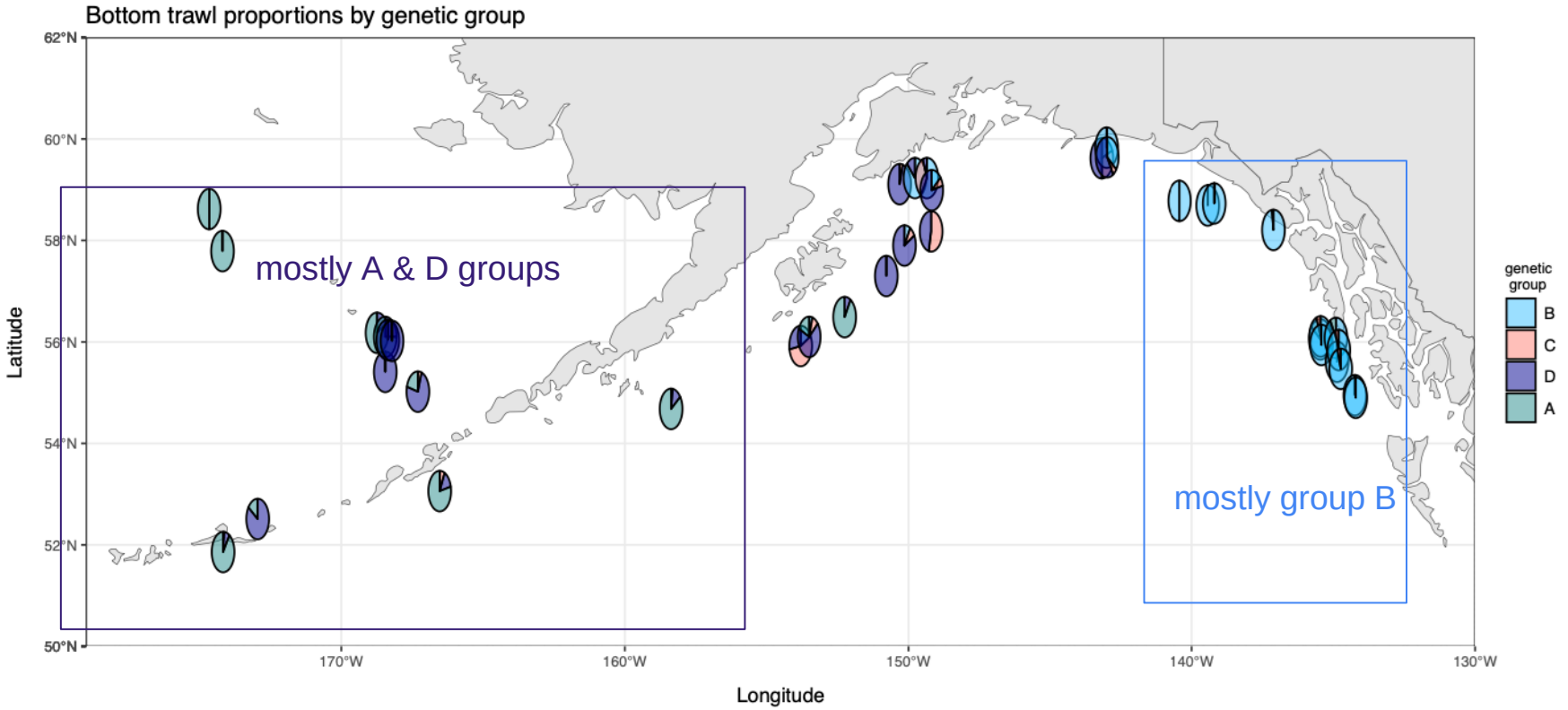
136 microhaplotype markers; 605 alleles

Genotyped 1,259 POP from BT to understand distribution of groups



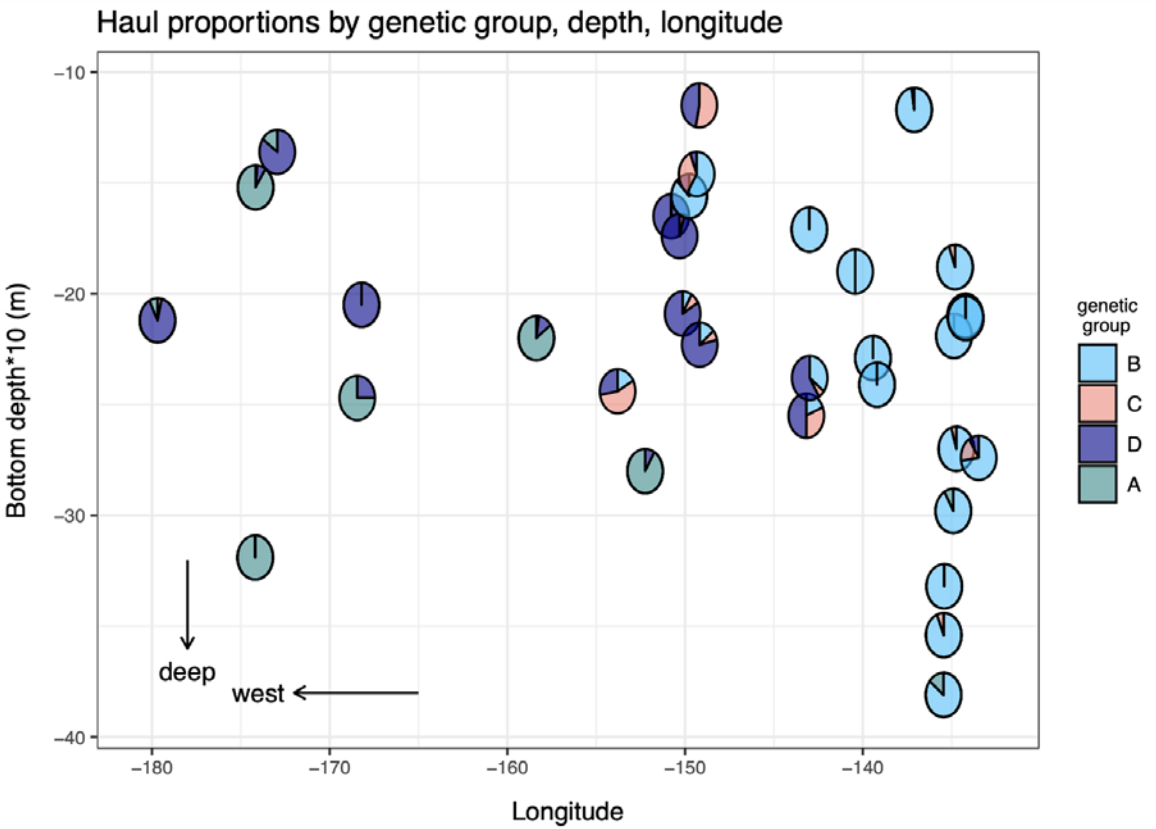
Intense sampling on small scales in central GOA

Fishery focused mostly on A and D groups, some B and C in Central Gulf



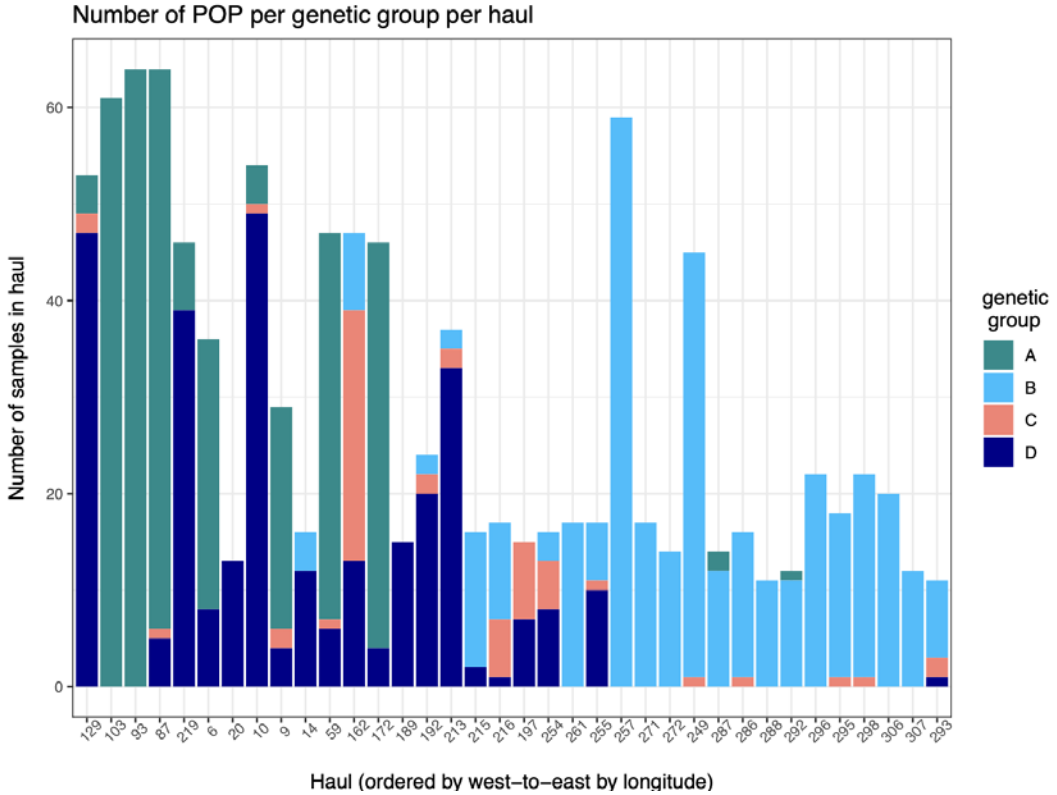
Are groups segregated by space or depth?

- West = groups A and D
- East = mostly B
- Central GOA = mixed hauls
- No clear segregation by depth
- Hauls less mixed than expected if distribution is random
- Driven by fine-scale habitat? Biogeographic breaks?



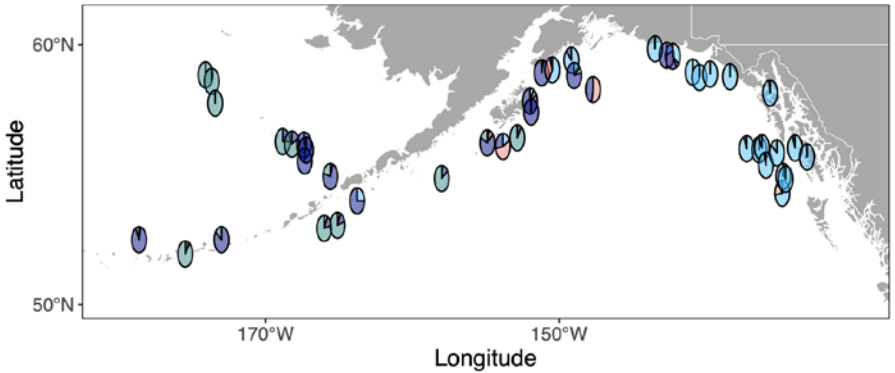
Hauls more homogenous than expected if groups fully mixed

- Many hauls with >1 group, but often hauls contain one primary group
- Hauls with different primary forms occur in close spatial proximity
- Fish in a single haul could be caught at multiple depths (on the way up/down)
- Do genetic groups school together?



Conclusions and management implications

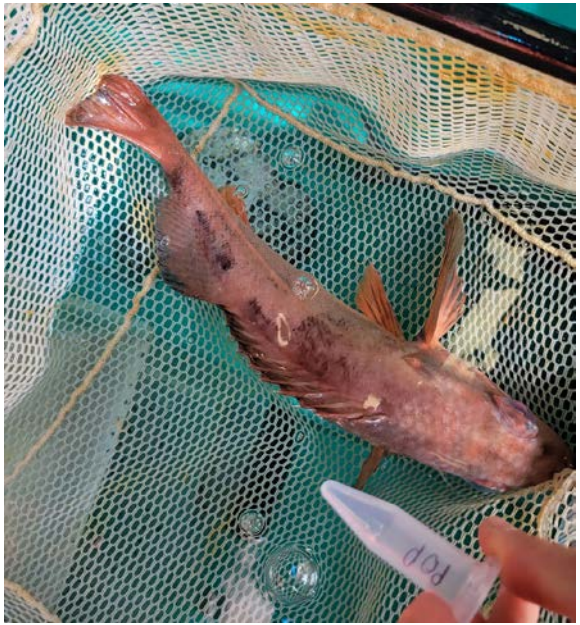
- Multiple genetic forms of POP
- Different spatial distributions
- Hauls contain multiple forms but include a single primary form
- Hauls of different forms occur close to each other
- Mechanisms driving segregation of forms unclear (future research)



- Fishery likely harvests primarily A and D, C in western GOA, some B in central GOA
- Unknown population sizes/abundances of genetic forms (is exploitation consistent with their relative abundances?)
- Explore ways to integrate genetic information into management

POP future directions

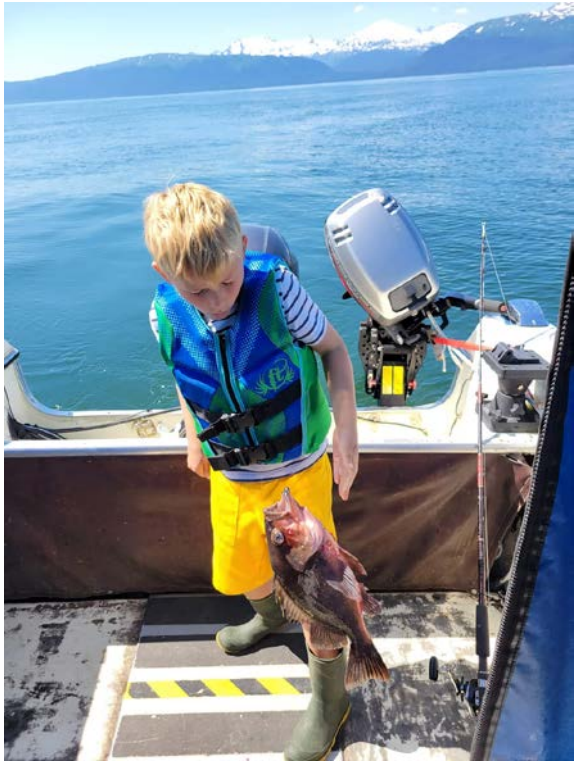
- Q: Do forms have morphological differences?
  - Collaboration with Sarah Friedman (samples collected)
- Q: Does habitat or fish size affect BT haul composition?
  - Explore BT strata characteristics, fish size as available
- Q: Do multiple genetic forms school together?
  - Work with industry to investigate genetic forms within individual schools of POP
  - Explore variation in the context of habitat
- Q: Do commercial catches resemble bottom trawl haul composition?
  - Genotype commercial catches



Acknowledgements

- Tony Gharrett-valuable insights and samples
- John Hyde and Matt Craig-access to amazing tissue database
- Sample collections: ADFG, NOAA
- ABL Genetics Team: Katie D'Amelio, Kirby Karpan, Charlotte Springer, Claire Tobin and Jackie Whittle
- NWFSC SEDNA computing support

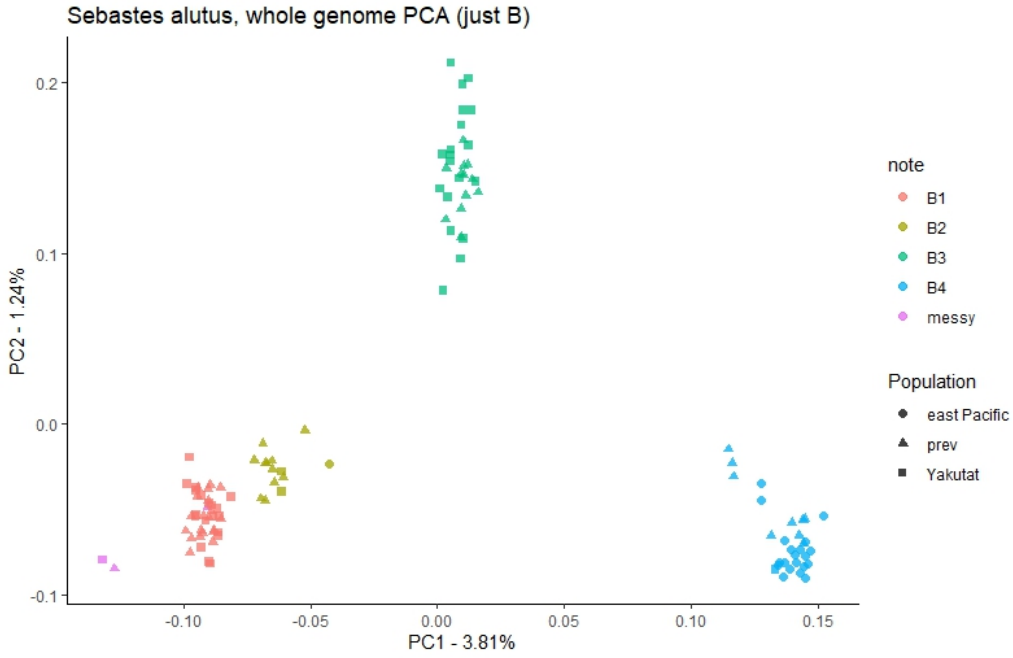
Questions



wes.larson@noaa.gov

Low-coverage whole genome sequencing (cont'd)

- Groups A and B are the most highly differentiated.
- PC1 explains 3.8% of the variation when just looking at individual data for the B group.
- The GTseq markers were chosen before group B was split into 4 separate groups. Unclear how effective the panel will be at separating B4 from B3, B2, and B1.

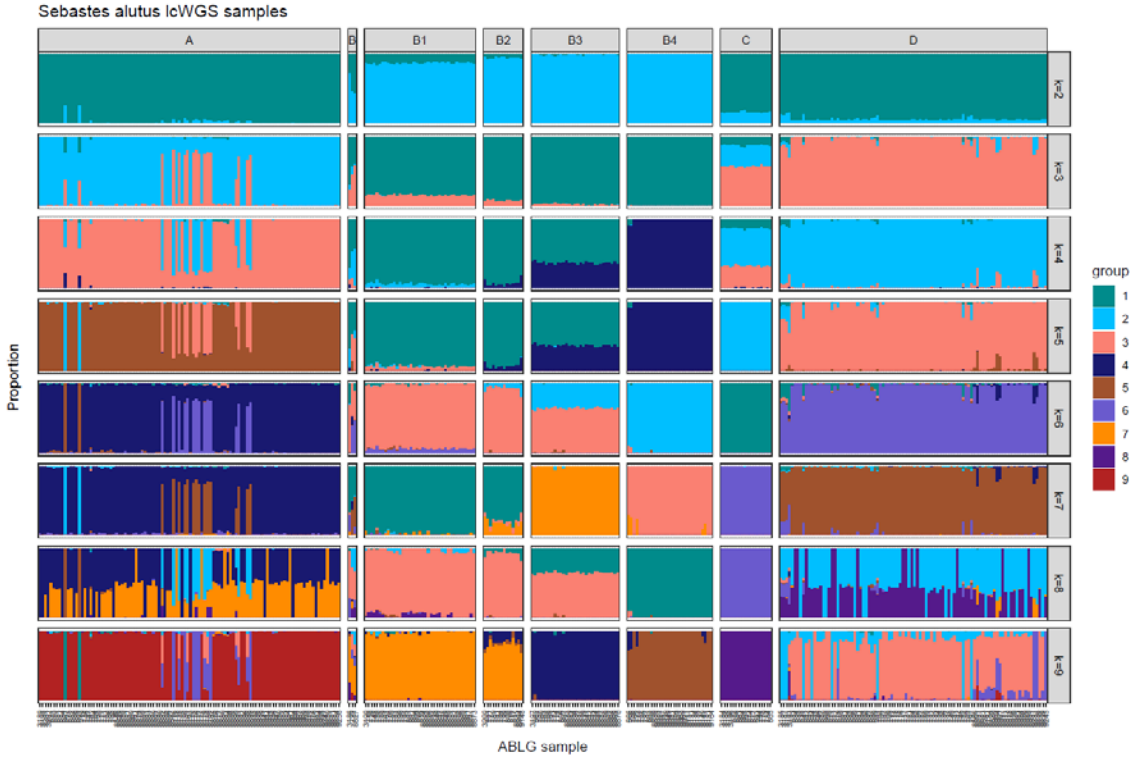


L. Timm

Low-coverage whole genome sequencing (cont'd)

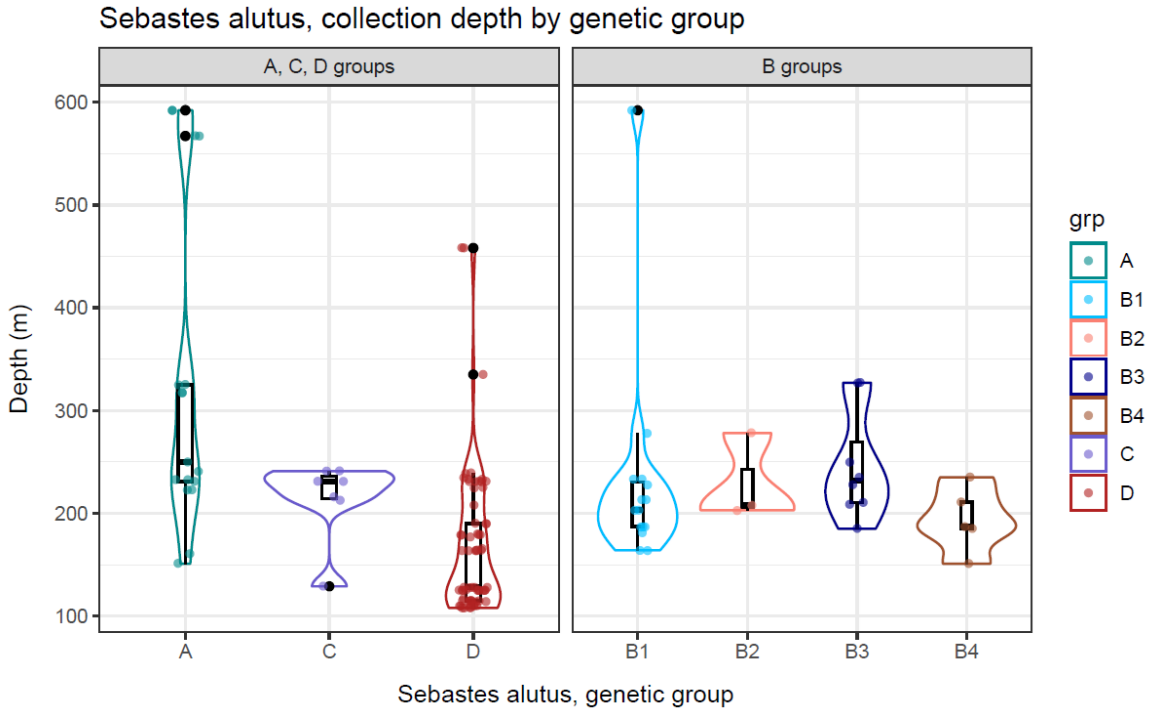
Admixed ancestry for a number of individuals grouped by PCA:

- individuals in group A are >50% admixed with group D
- groups B2 and B3 are admixed between B1 and B4 in different proportions
- group "B" consists of three highly admixed individuals
- group A includes two outliers that do not look like any other group

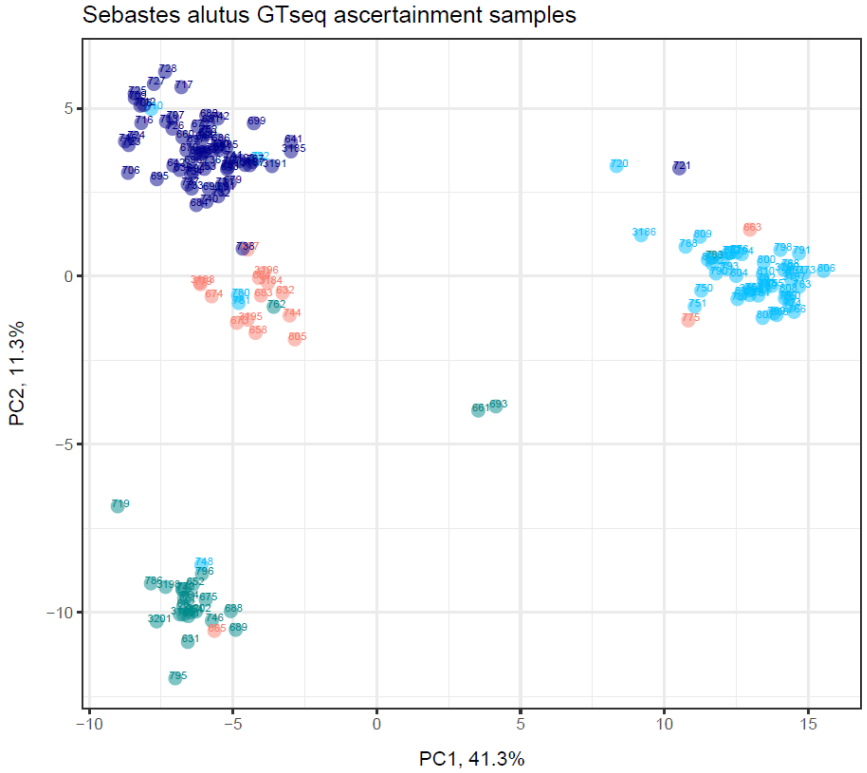


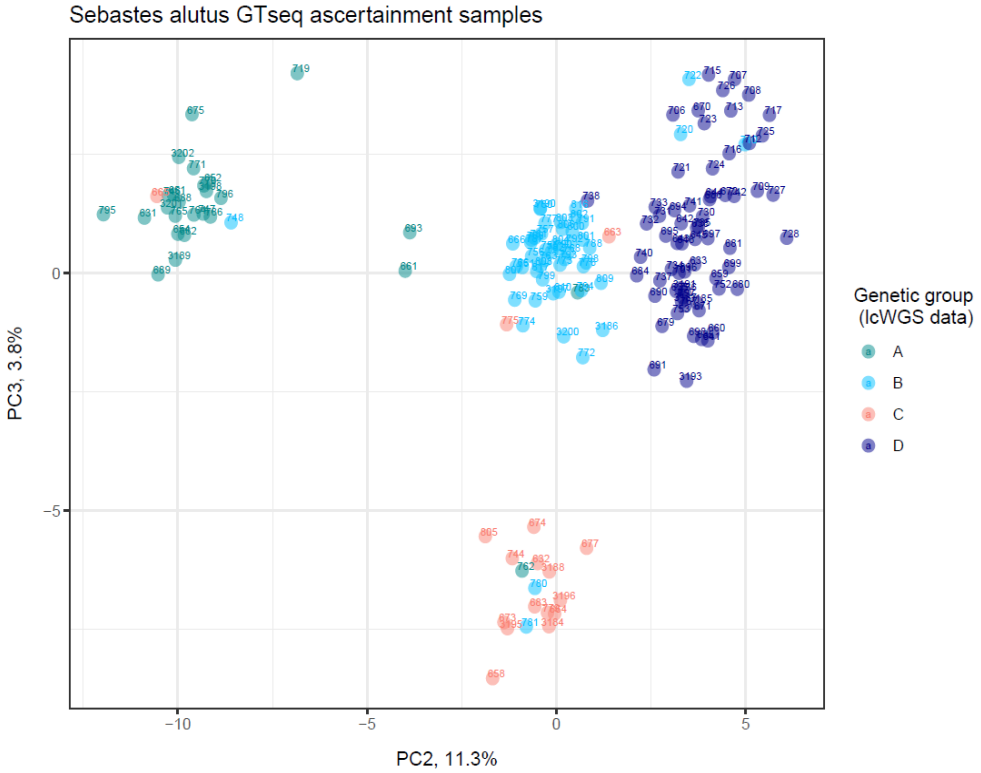
Depth distribution of lcWGS samples

- Potential depth differences between groups A, C, and D.
- No obvious difference among B groups.
- small sample sizes.



GTseq ascertainment panel, genotyped with GTseq panel





GTseq ascertainment panel, genotyped with GTseq panel

Admixed individuals evident in ascertainment samples genotyped with GTseq markers.

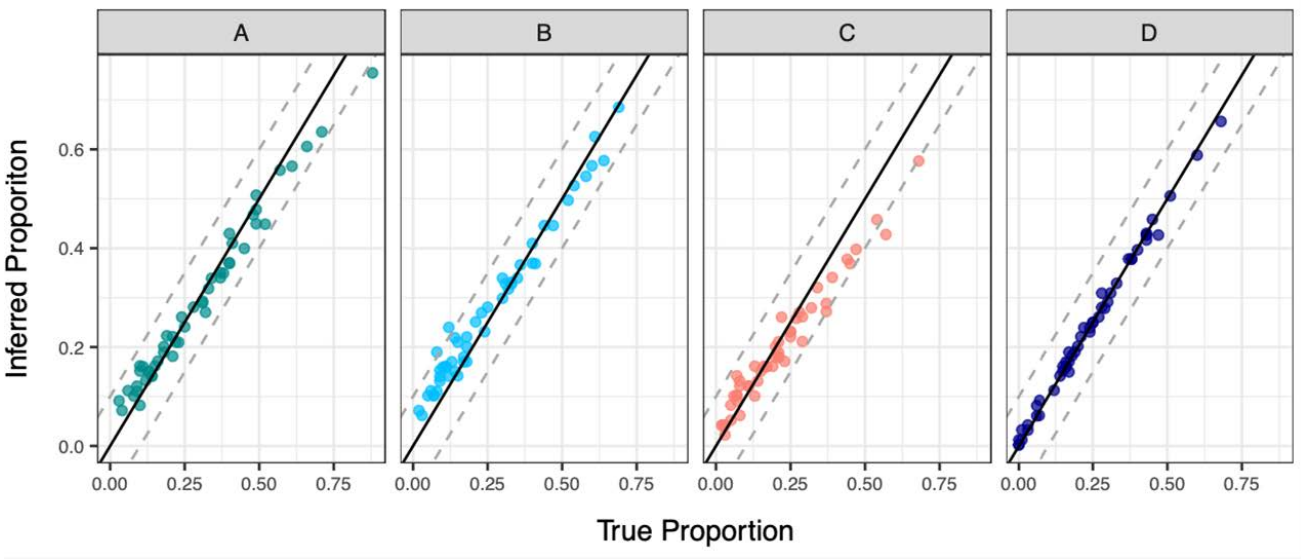
Why does this matter? Need a genetic reference baseline for mixture assignment (genetic stock identification).

- remove outliers
- remove group "B" (3 indivs)

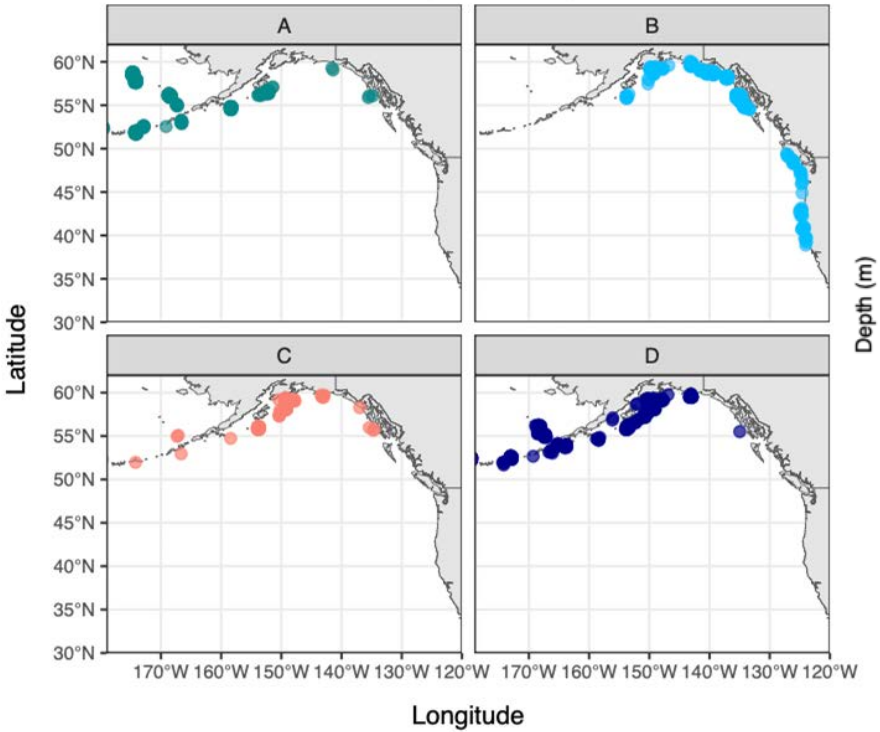
GTseq panel: Genetic stock identification (GSI)

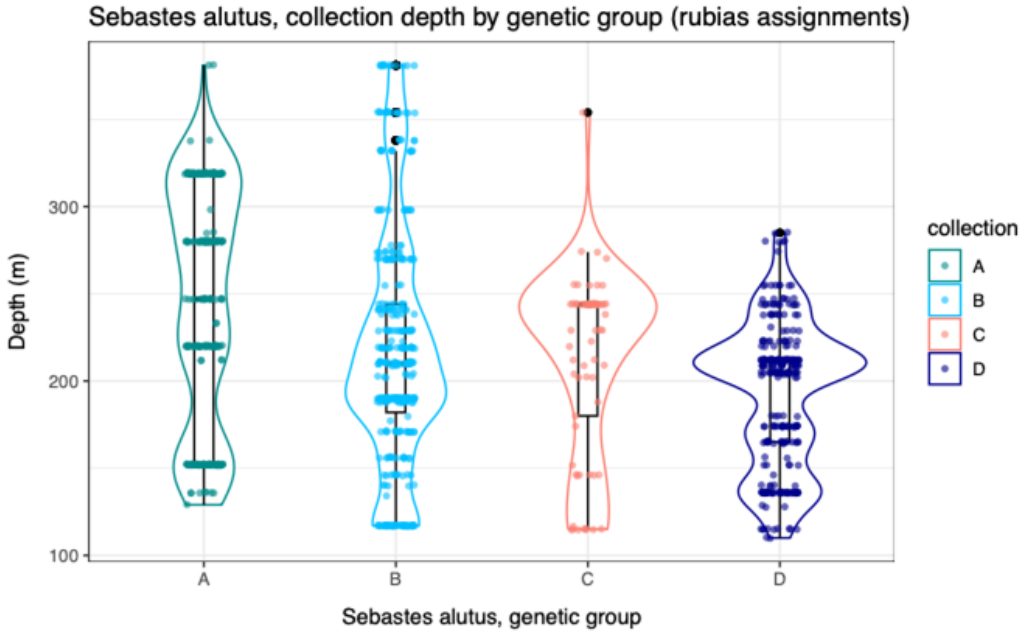
Ascertainment samples (with highly admixed samples removed) used to evaluate the GTseq dataset for GSI.

Leave-one-out baseline evaluation.



GTseq panel: Genetic stock identification (GSI)

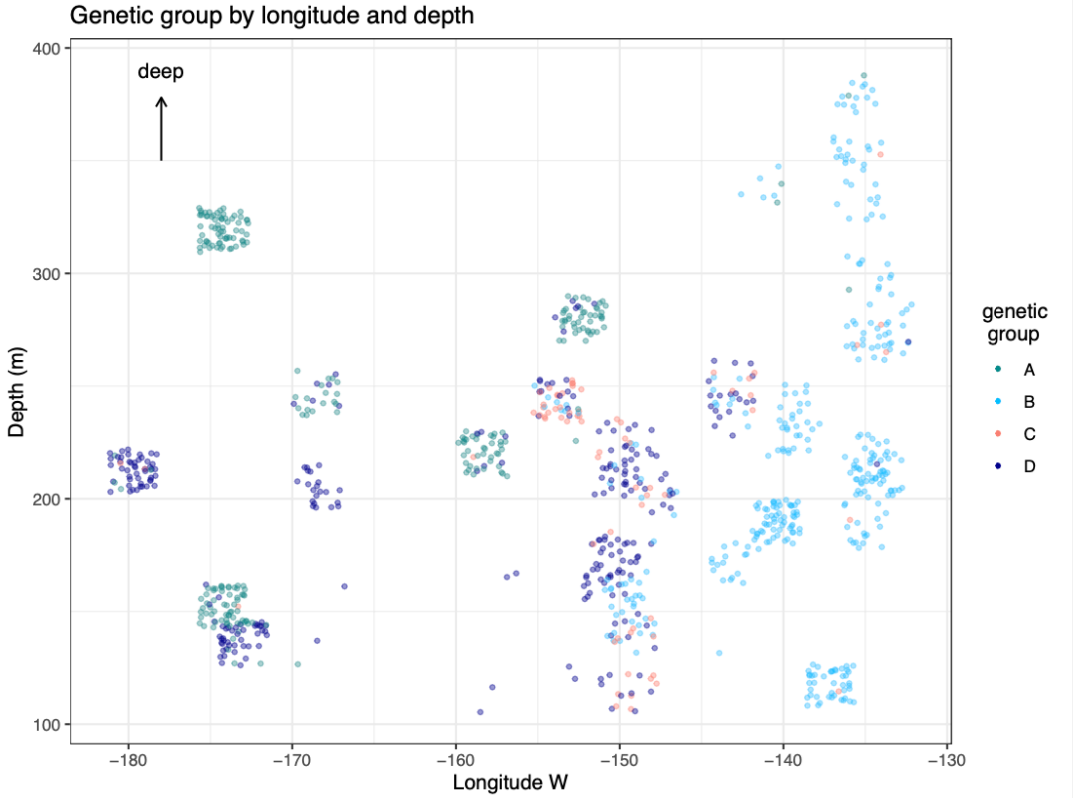


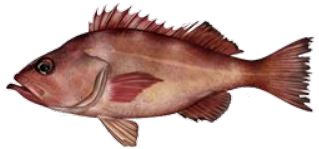


Mean bottom depth A (244 m) vs. D (192.8 m)
*POP are demersal, not benthic

Are multiple genetic groups captured in the same haul?

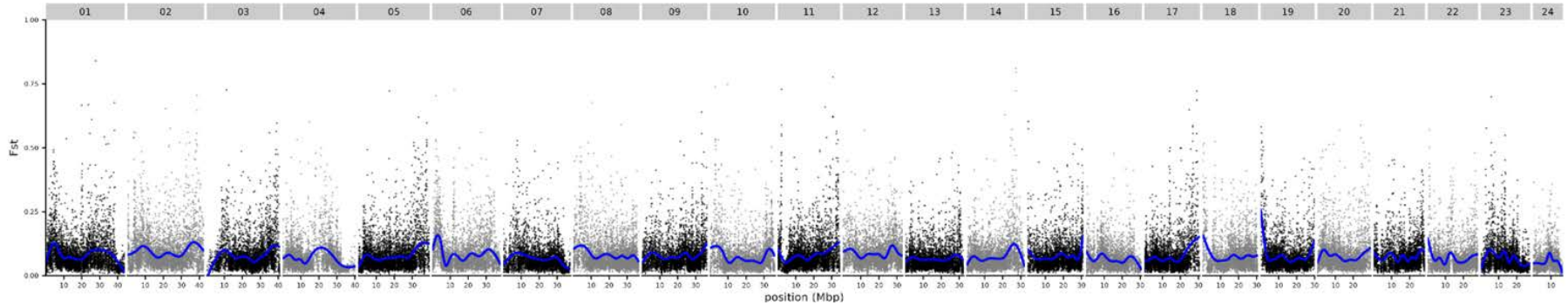
- west = mostly A&D
- east = mostly B
- mixed hauls in the central GOA and near Kodiak.



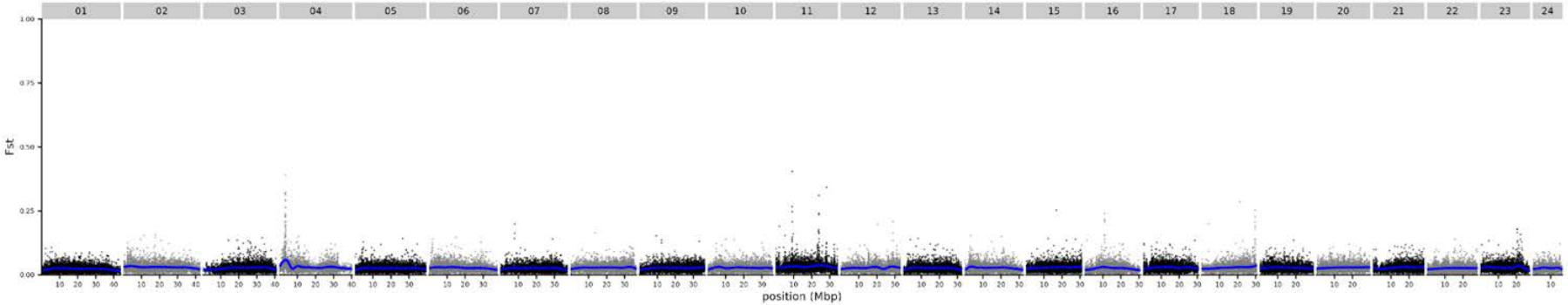


Pacific ocean perch forms: gradient of isolation

[1] "pop_a vs. pop_b"

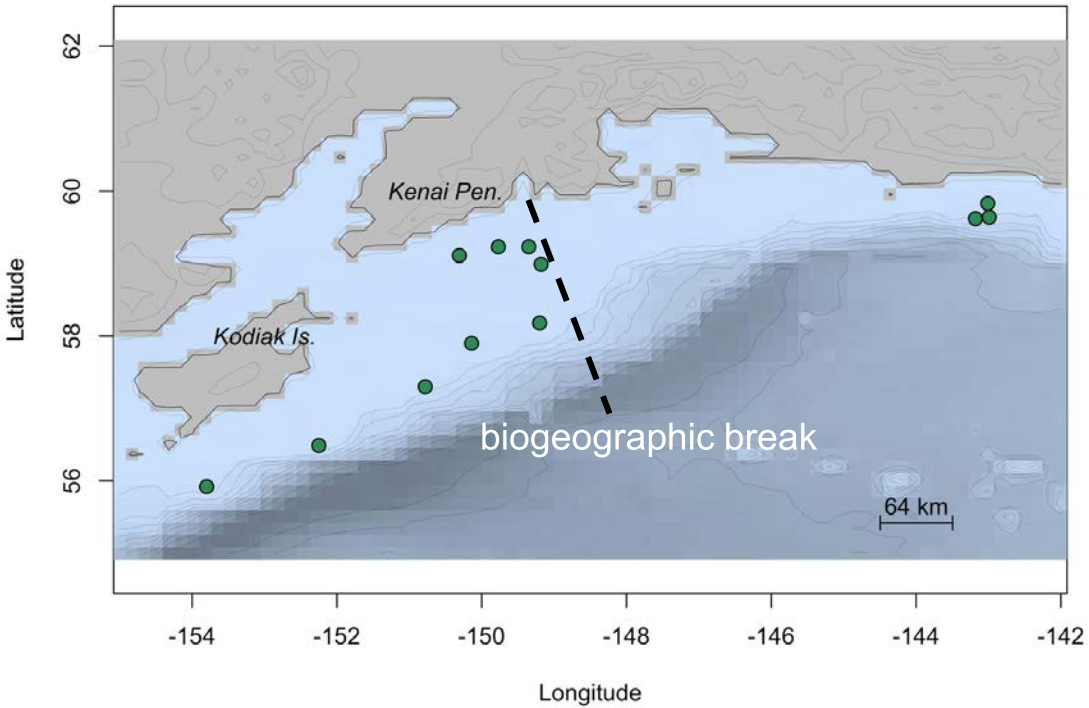


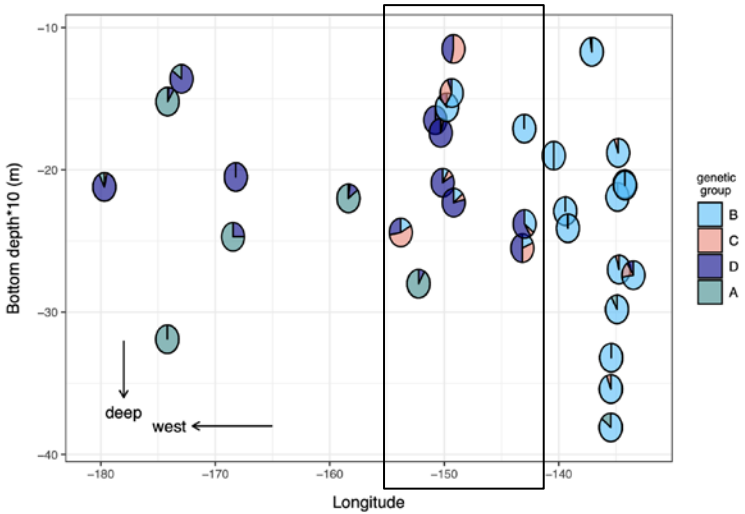
[1] "pop_b_1 vs. pop_b_3"



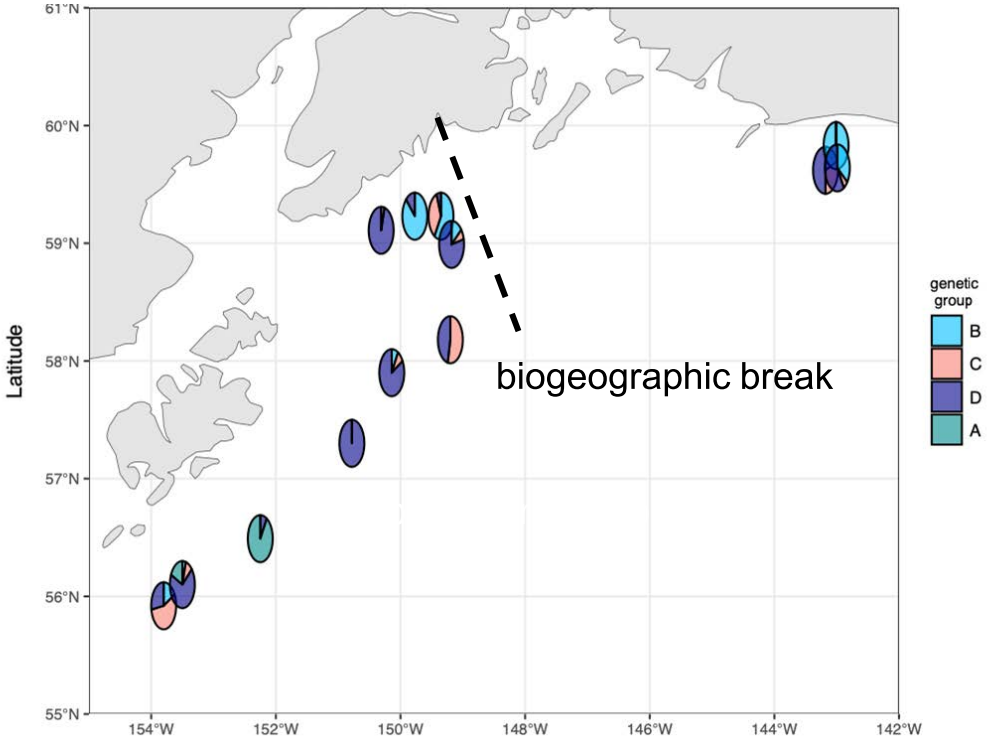
Differentiation across the genome indicates differing evolutionary histories

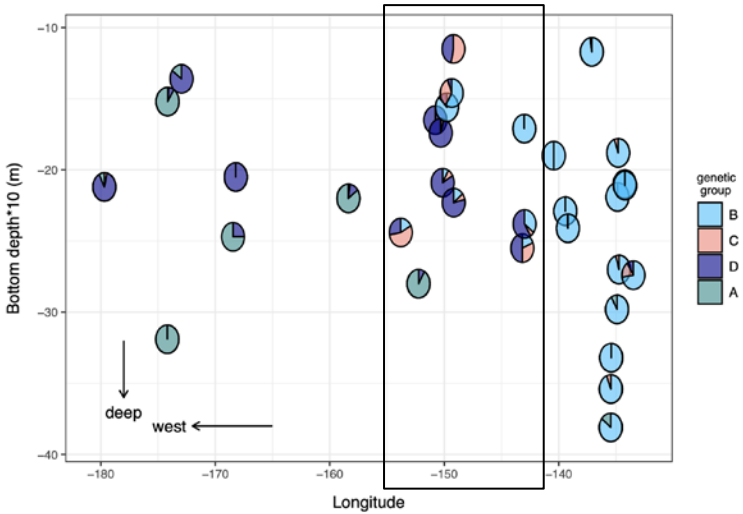
Take a closer look at geography/bathymetry near Kodiak





Take a closer look at geography/bathymetry near Kodiak





*different # of hauls in plots with depth because some hauls had no depth metadata

Take a closer look at geography/bathymetry near Kodiak

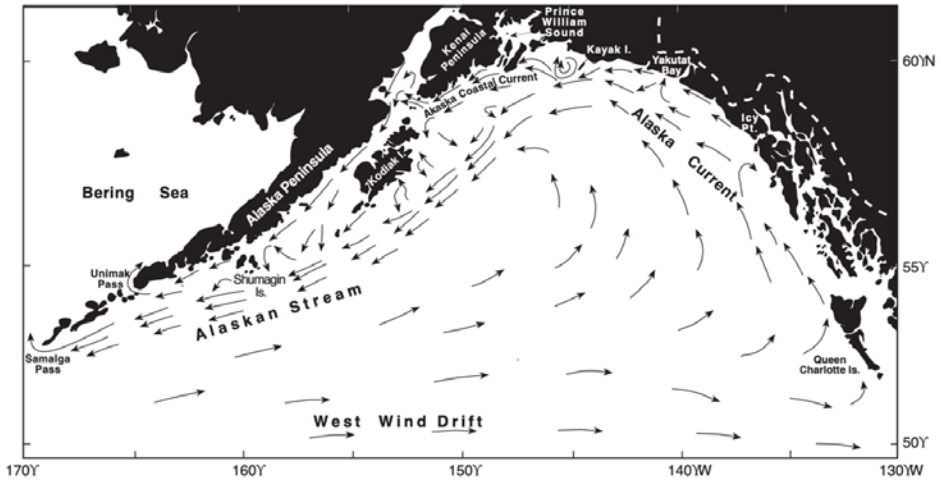
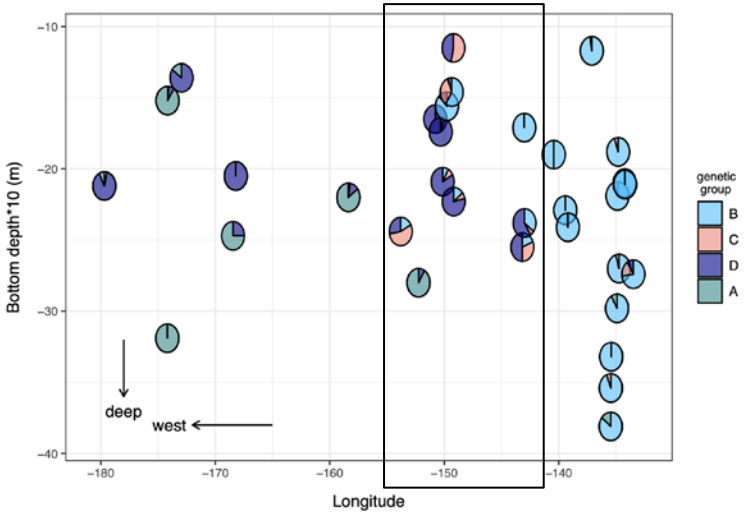


Fig. 1. Map of the Gulf of Alaska. The flow of the Alaska Coastal Current and subarctic gyre are indicated as are several geographic place names. (After Reed and Schumacher, 1986).



from Stabeno et al., 2004 Cont Shelf Res

Take a closer look at geography/bathymetry near Kodiak

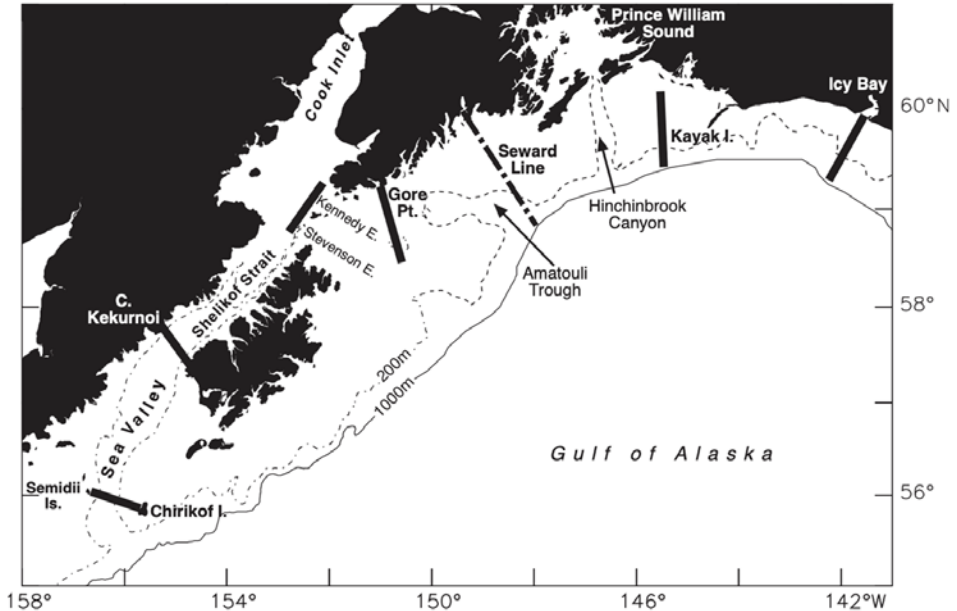
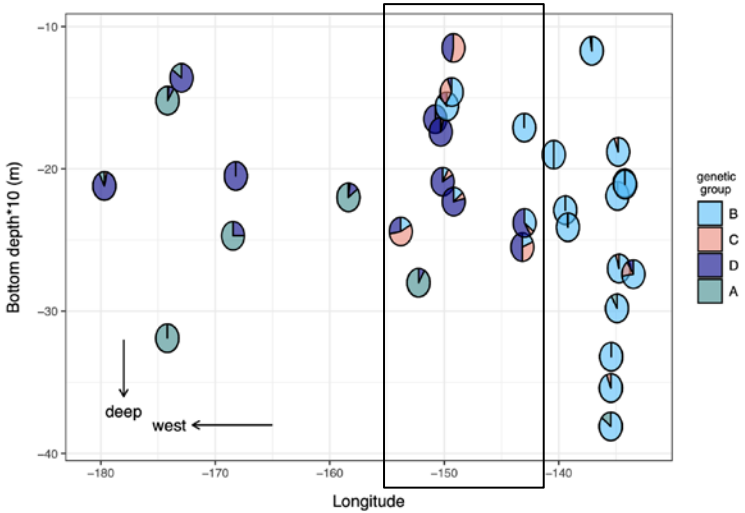


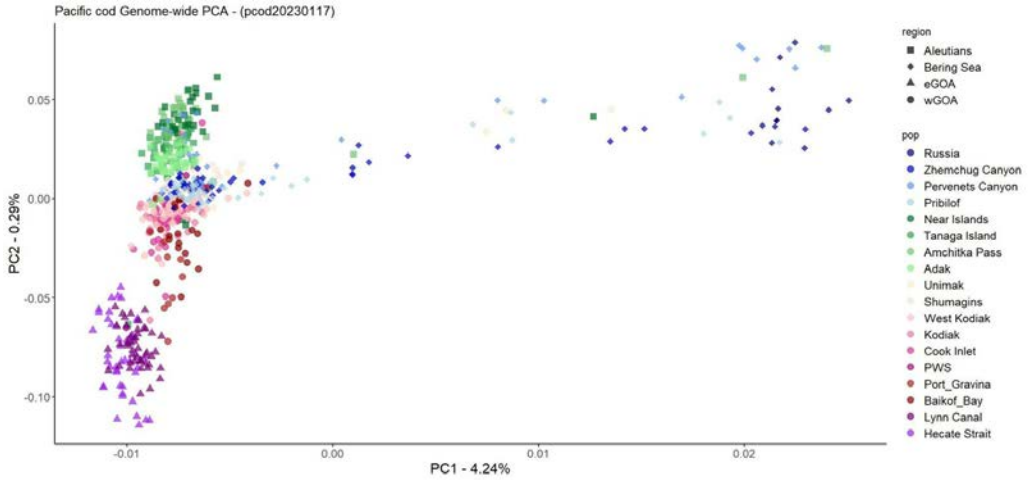
Fig. 2. Geographic place names and the locations of hydrographic sections (solid black lines) discussed in the paper. The Seward line is shown as a dashed line.

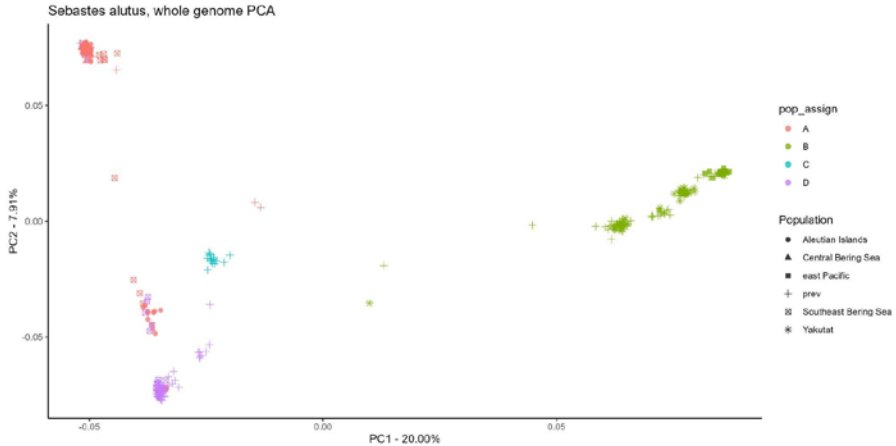


from Stabeno et al., 2004 Cont Shelf Res

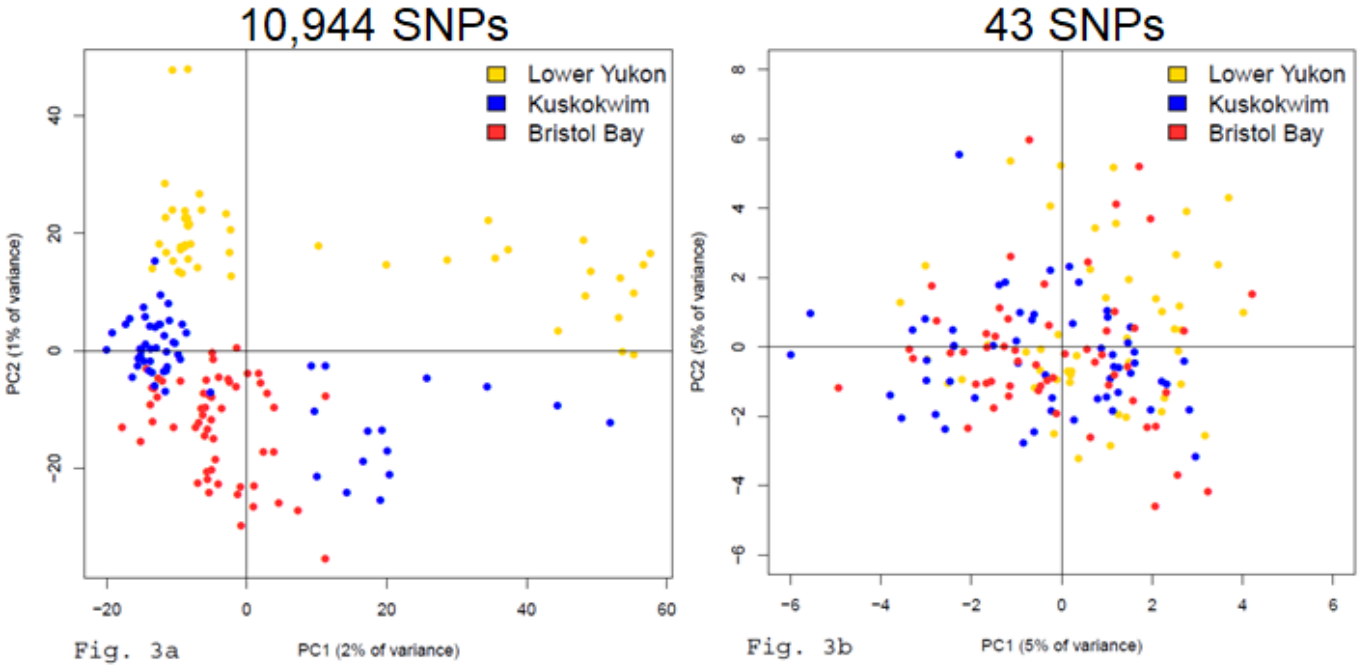
How different are POP genetic groups? Pcod vs POP

- Similar spatial scope of sampling, number of individuals, analysis methods
- Pcod-one of our more structured species, more typical IBD smear, POP much more discrete groups
- POP ~5 times the variation on PC1, ~ 25 times on PC2
- Pcod: individuals from a sample site are largely homogenous, POP are not





Transition to genomics: from populations to individuals



Lack of power requires aggregation into populations, within population heterogeneity cannot be observed

Larson et al. 2014