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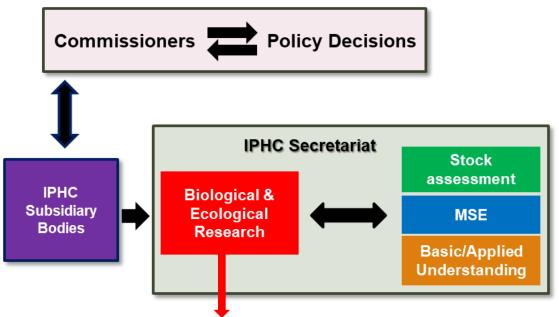


Report on current and future Biological and Ecosystem Science Research activities

Agenda item: 4.1.3 IPHC-2024-SRB024-09 (J. Planas, C. Dykstra, A. Jasonowicz, C. Jones)



Biological and Ecosystem Science Research



5 Yr – Program of Integrated Research and Monitoring (2022-2026)

Research Areas:

- Migration and Population Dynamics
 - Reproduction
 - Growth
 - Mortality and Survival Assessment
 - Fishing Technology



Top research priorities for stock assessment

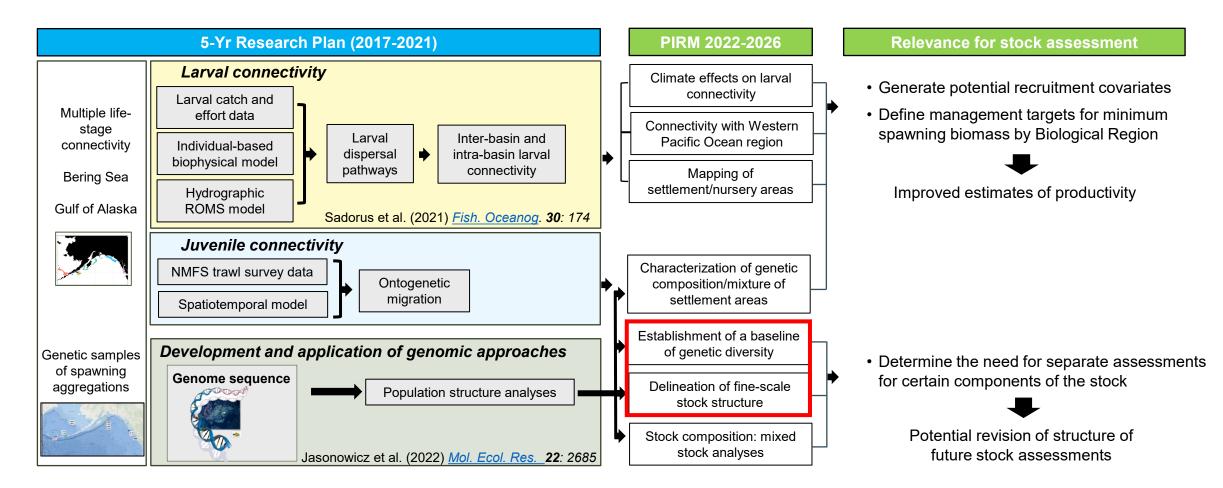
SA Rank	Research outcomes	Relevance for stock assessment	Specific analysis input	Research Area	Research activities	
	Updated maturity schedule		Will be included in the stock assessment, replacing the current schedule last updated in 2006		Histological maturity assessment	
	Incidence of skip spawning	Scale biomass and	Will be used to adjust the asymptote of the maturity schedule, if/when a time-series is available this will be used as a direct input to the stock assessment		Examination of potential skip spawning	
1. Biological input	Fecundity-at-age and -size information	reference point estimates	Will be used to move from spawning biomass to egg-output as the metric of reproductive capability in the stock assessment and management reference points	Reproduction	Fecundity assessment	
	Revised field maturity classification		Revised time-series of historical (and future) maturity for input to the stock assessment	*	Examination of accuracy of current field macroscopic maturity classification	
2. Biological input	Stock structure of IPHC Regulatory Area 4B relative to the rest of the Convention Area	Altered structure of future stock assessments	If 4B is found to be functionally isolated, a separate assessment may be constructed for that IPHC Regulatory Area		Population structure	
3. Biological input	Assignment of individuals to source populations and assessment of distribution changes	Improve estimates of productivity	Will be used to define management targets for minimum spawning biomass by Biological Region	Migration and population dynamics	Distribution	
	Improved understanding of larval and juvenile distribution	productivity	Will be used to generate potential recruitment covariates and to inform minimum spawning biomass targets by Biological Region		Larval and juvenile connectivity studies	
1. Assessment data	Sex ratio-at-age	Scale biomass and	Annual sex-ratio at age for the commercial fishery fit by the stock assessment	Dames duration	Sex ratio of current commercial landings	
collection and processing	Historical sex ratio-at-age	fishing intensity	Annual sex-ratio at age for the commercial fishery fit by the stock assessment	Reproduction	Historical sex ratios based on archived otolith DNA analyses	
2. Assessment data collection and processing	New tools for fishery avoidance/deterence; improved estimation of depredation mortality	Improve mortality accounting	May reduce depredation mortality, thereby increasing available yield for directed fisheries. May also be included as another explicit source of mortality in the stock assessment and mortality limit setting process depending on the estimated magnitude	Fishing technology	Whale depredation accounting and tools for avoidance	
1. Fishery yield	Physiological and behavioral responses to fishing gear	Reduce incidental mortality	May increase yield available to directed fisheries	Fishing technology	Biological interactions with fishing gear	
2. Fishery yield	Guidelines for reducing discard mortality	Improve estimates of unobserved mortality	May reduce discard mortality, thereby increasing available yield for directed fisheries	Mortality and Best handling practices: recreational fis		



Top research priorities for MSE

MSE Rank	Research outcomes	Relevance for MSE	Research Area	Research activities	
1. Biological parameterization and	Improved understanding of larval and juvenile distribution	Improve parametization of the		Larval and juvenile connectivity studies	
validation of movement estimates	Stock structure of IPHC Regulatory Area 4B relative to the rest of the Convention Area	Operating Model	Migration and population	Population structure	
2. Biological parameterization and validation of recruitment variability	Assignment of individuals to source populations and assessment of distribution changes	Improve simulation of recruitment variability and parametization of recruitment distribution in the Operating Model	dynamics	Distribution	
and distribution	Establishment of temporal and spatial maturity and spawning patterns	Improve simulation of recruitment variability and parametization of recruitment distribution in the Operating Model	Reproduction	Recruitment strength and variability	
	Identification and application of markers for growth pattern evaluation				
3. Biological parameterization and validation for growth projections	Environmental influences on growth patterns	Improve simulation of variability and allow for scenarios investigating climate change	Growth	Evaluation of somatic growth variation as a driver for changes in size-at-age	
	Dietary influences on growth patterns and physiological condition				
1. Fishery parameterization	Experimentally-derived DMRs	Improve estimates of stock productivity	Mortality and survival assessment	Discard mortality rate estimate: recreational fishery	







Population Genomics

Brief Background & Introduction

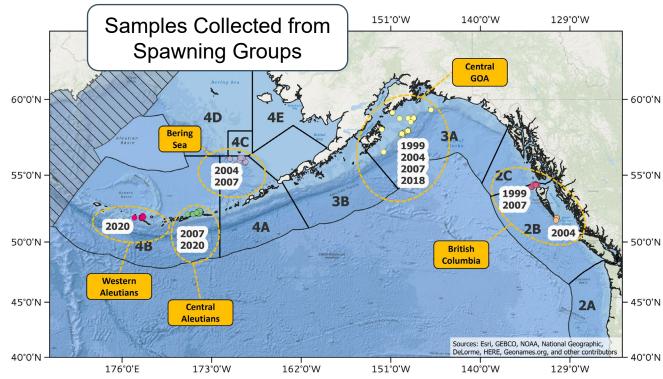
Results

- PCA & K-means clustering
- Admixture Unsupervised clustering (model based)
- Assignment Testing Supervised method Can we use a subset of SNPs to identify source populations of individuals?



Population Genomics

Objective: Resolve the genetic structure of the Pacific halibut stock in IPHC Convention Waters



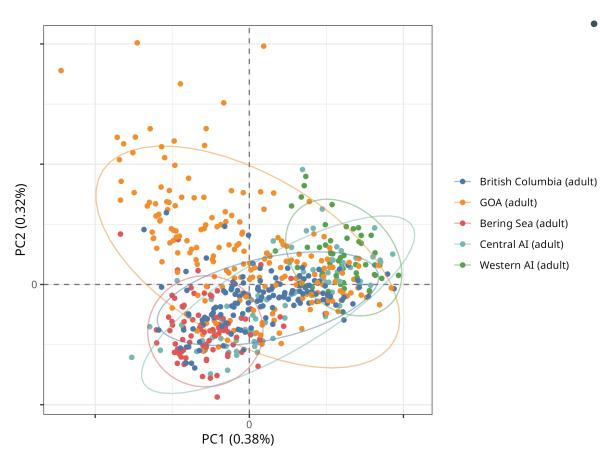


NPRB Project 2110 (2022-2024)

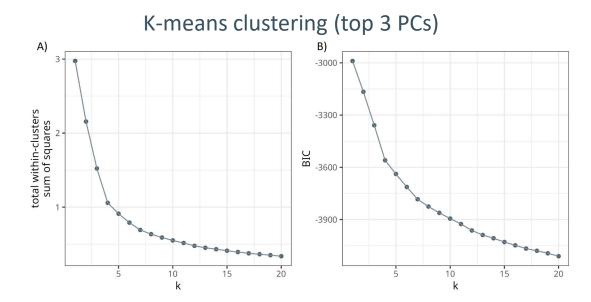
- Low-coverage whole-genome resequencing (lcWGR)
- Allows for screening genomic variation at very high resolution
- Establish genetic baseline
- Identify potential local and/or environmental adaptations.
 - 570 individuals (~ 50/collection)
 - 3 sequencing runs Illumina NovaSeq S4
 - Mean coverage 3.5x
 - 10,371,343 autosomal SNPs
 - 4,793,014 (minor allele frequency \geq 0.05)



Population Structure



- Principal components analysis (PCA)
 - Estimate covariance matrix from genotype likelihoods (*PCAngsd*)
 - 4,793,014 autosomal SNPs
 - Allele frequency ≥ 0.05
 - Eigendecomposition (R)
 - K-means clustering (R)





SRB023–Req.05 (para. 52) The SRB REQUESTED that admixture analyses and assignment testing be conducted and reported at SRB024, including estimates of assignment accuracy.

Admixture Analysis (NGSAdmix)

- Unsupervised model-based clustering (assumes HWE within clusters & SNPs are in linkage equilibrium)
 - Partition individuals into a pre-defined number of discrete populations (K)
 - Estimates allele frequencies for each cluster (F)
 - Estimates membership probabilities for each individual (Q) to each cluster

Assignment Testing (WGSassign)

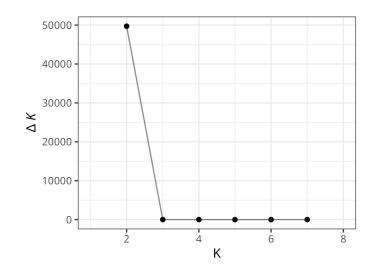
- Supervised method (pre-defined populations)
- What is the likelihood that an individual's genotype originates from a set of (predefined) reference populations?

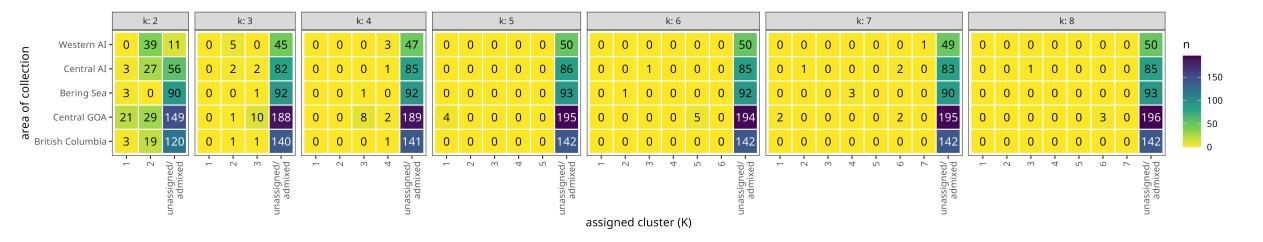


Admixture Analysis - NGSAdmix

- Ran model for K=2 to K=8 (5 replicates for each K)
- Required assignment probability of ≥ 0.8 to a single cluster for assignment.
- ΔK– to evaluate support for best K (Evanno at al. 2005)

Evanno, G., Regnaut, S., and Goudet, J. 2005. Detecting the number of clusters of individuals using the software structure: a simulation study. Mol. Ecol. **14**(8): 2611–2620. doi:10.1111/j.1365-294X.2005.02553.x.





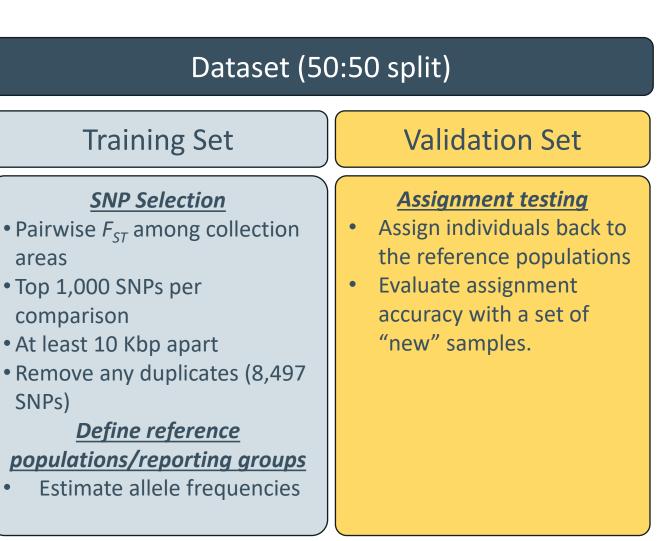


Assignment Testing - WGSassign

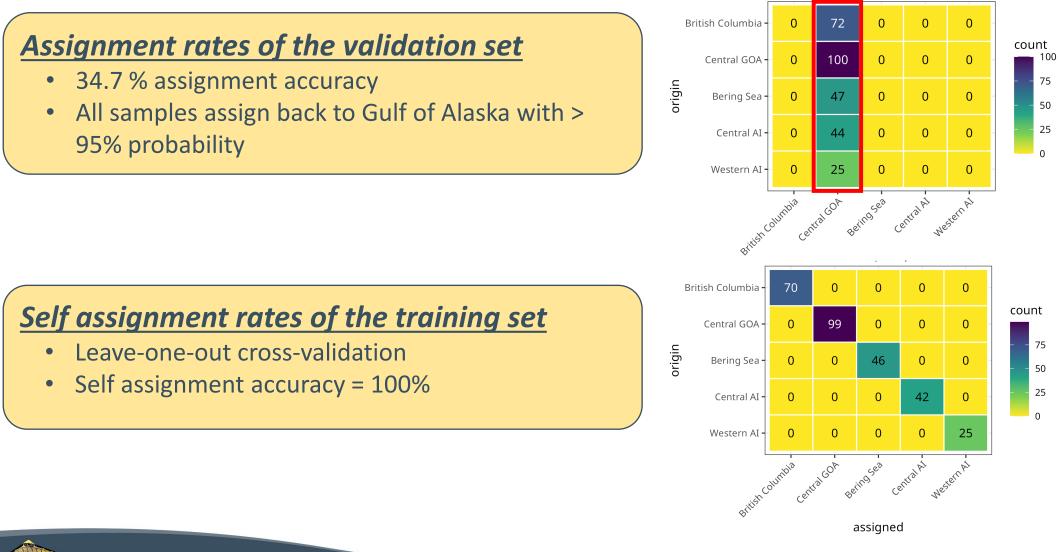
- Reference populations defined by geographic area
- Simple Training Holdout procedure
- Recommended approach by Anderson 2010 when selecting SNPs based on allele frequency
- Referred to as the "gold standard" by Anderson 2010 and Waples 2010

Anderson, E.C. 2010. Assessing the power of informative subsets of loci for population assignment: Standard methods are upwardly biased. Mol. Ecol. Resour. **10**(4): 701–710
Waples, R.S. 2010. High-grading bias: Subtle problems with assessing power of selected subsets of loci for

s, R.S. 2010. High-grading bias: Subtle problems with assessing power of selected subsets of lo population assignment. Mol. Ecol. **19**(13): 2599–2601.



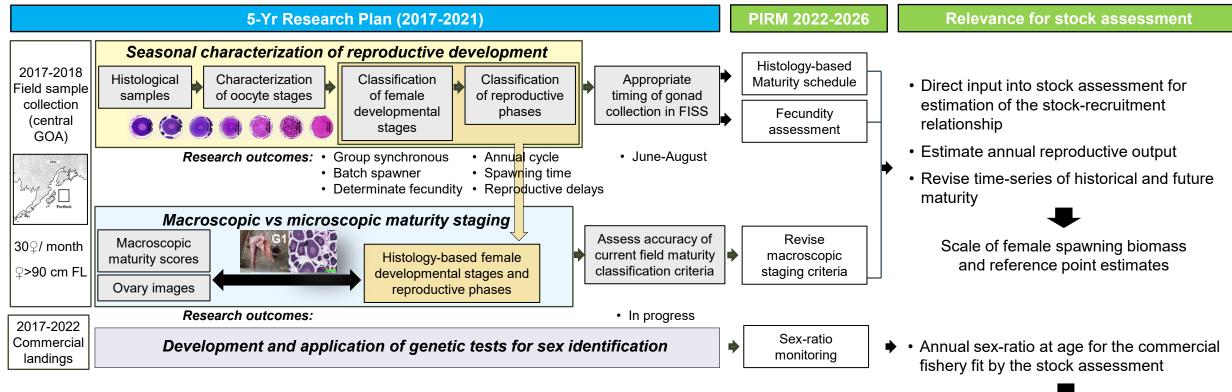




Conclusions

- Unsupervised clustering methods failed to identify discrete genetic groups of Pacific halibut.
- Limited ability to assign individuals back to the location in which they were sampled.
- Considerable geneflow lack of structure.
 - Tagging data 11% of Pacific halibut are recovered in a different IPHC Regulatory Area than they are released (Carpi et al. 2021).
 - Large amounts of larval exchange between Gulf of Alaska and the Bering Sea (Sadorus et al. 2021).
- Results are consistent with current assessment practices (modeled as a single coastwide stock).



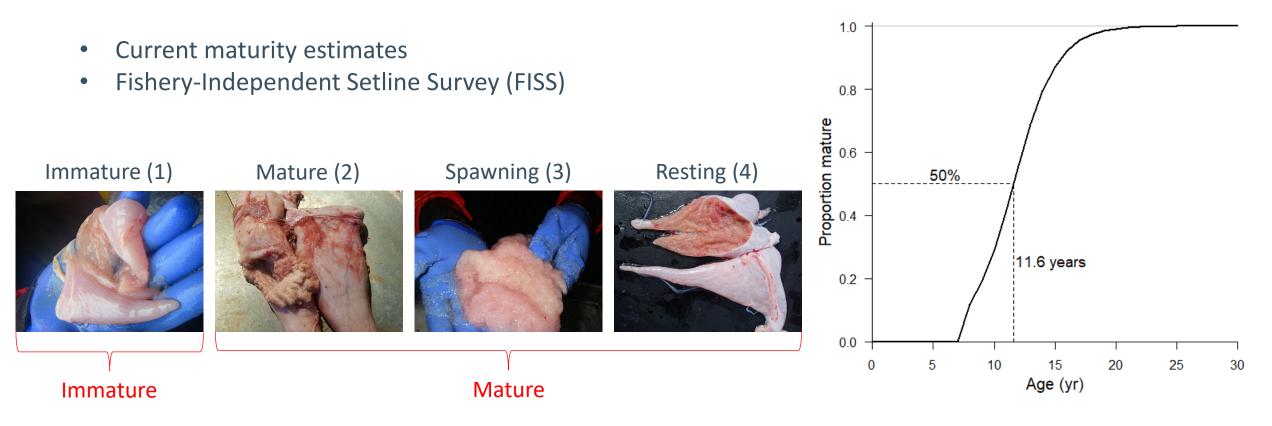


Publications: Fish et al. (2020) <u>J. Fish Biol.</u> **97**: 1880–1885 Fish et al. (2022) <u>Frontiers in Mar. Sci.</u> **9**: 801759 Simchick et al. (2024) <u>Gen. Comp. Endocrinol</u>. **347**: 114425

Reduce uncertainty in stock size and fishing intensity

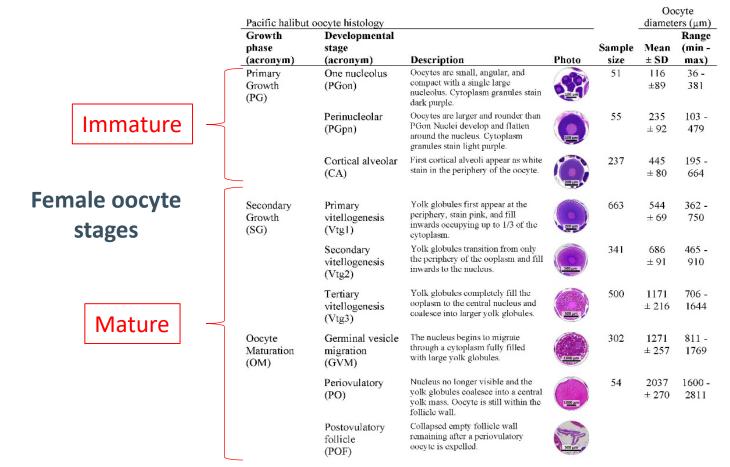


Female Maturity: visual assessment (macroscopic)





Histological (microscopic) maturity assessment

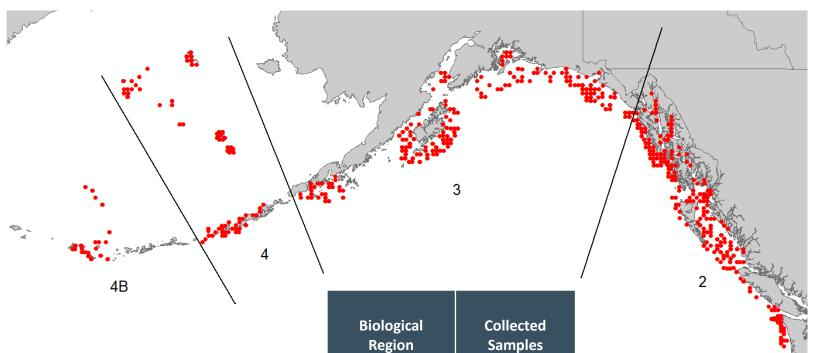


Females are assigned to a developmental stage based on the most advanced oocyte stage present

Fish et al. (2020) J Fish Biol. 97:1880-1885



2022 FISS Ovary Sample Collection for Histological Assessment



2

3

4

4B

Total

440

351

181

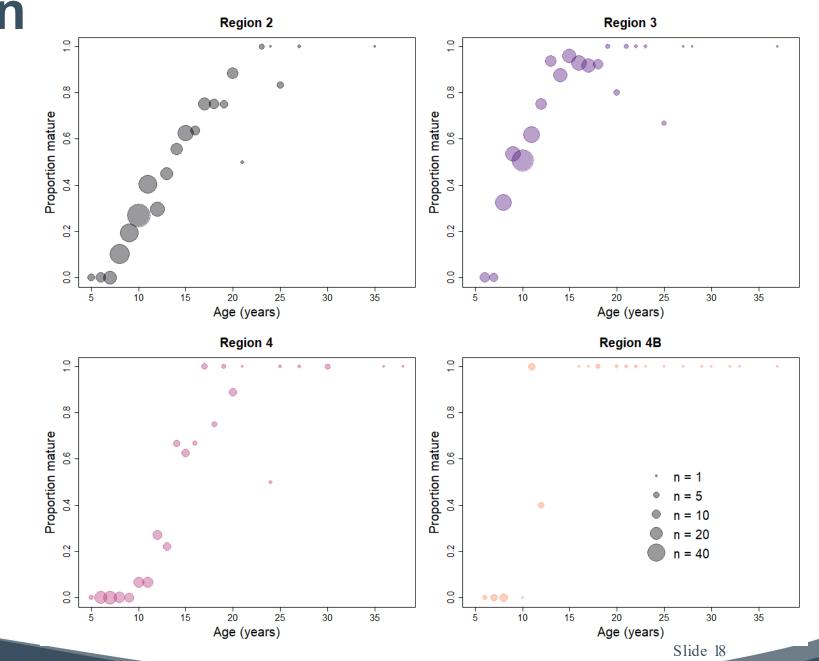
51

1023



Histological maturity assessment

- Raw data by Biological Region
- Each bubble represents an age



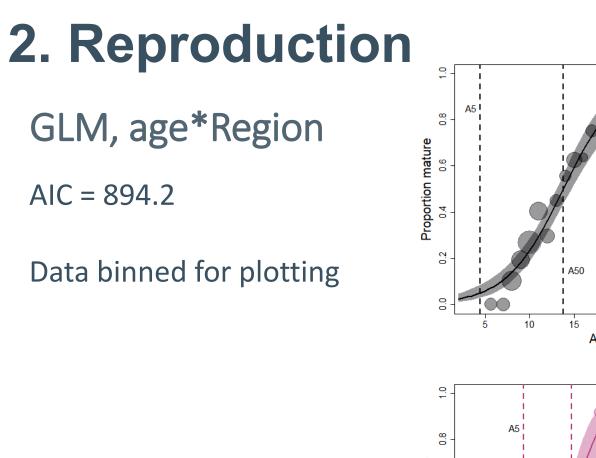


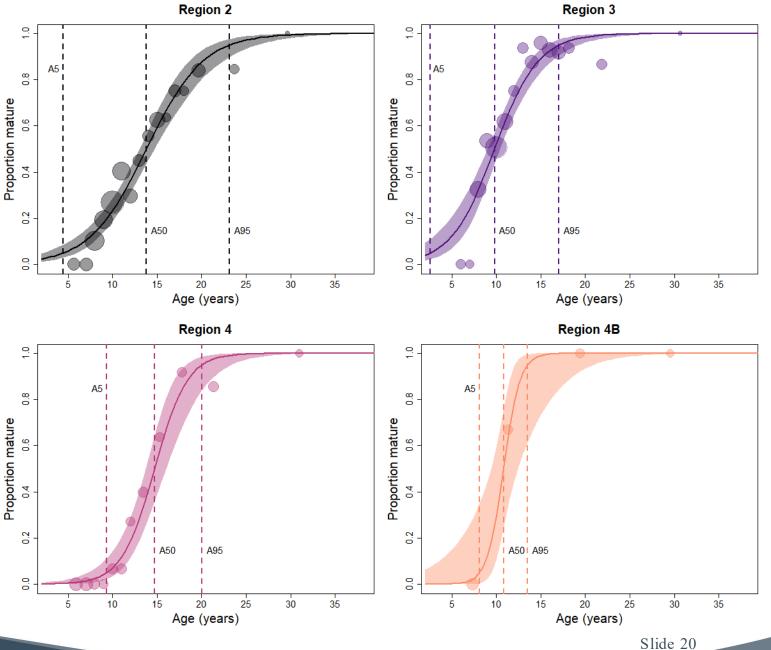
Maturity Model Comparisons

- Models with age and region
 - Logistic GLM: logit(P(mature)) ~ age*Region
 - Logistic GLM: logit(P(mature)) ~ log(age)*Region
 - Logistic GAM: logit(P(mature)) ~ s(log(age), by Region)
- Models with age for each region (single region models)
 - Logistic GLM with estimated breakpoint
 - Logistic GLM with breakpoint at A50

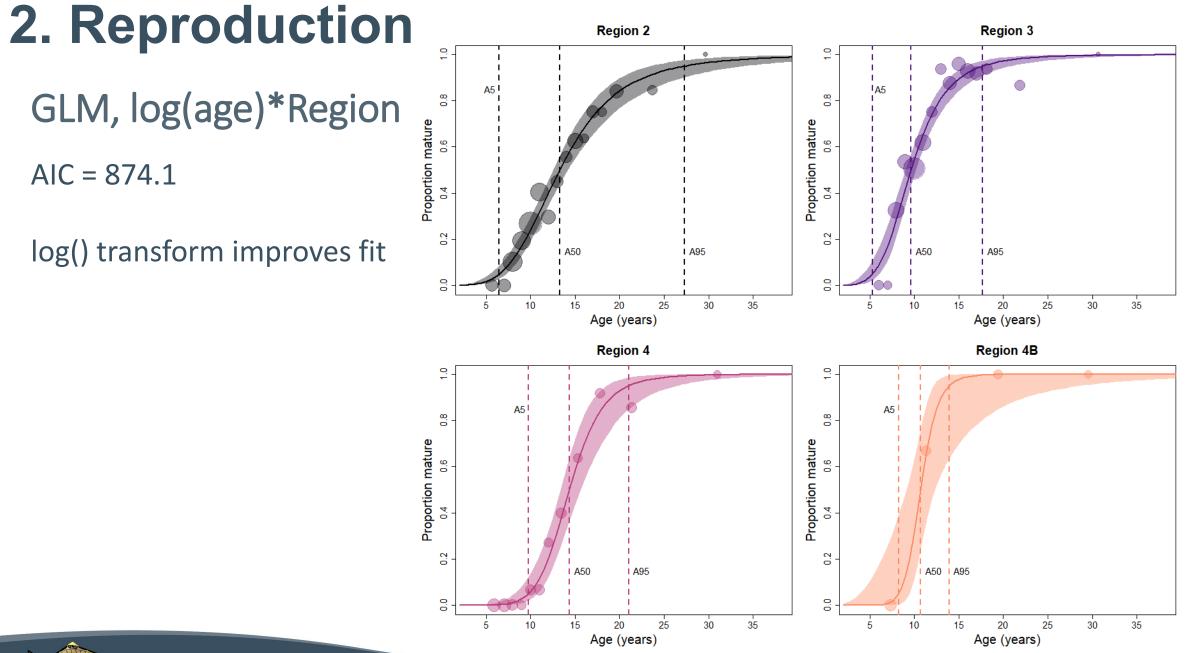
	Model	AIC	
	Age	995.99	
A a a	Age * Region	894.24	
Age	sqrt(Age) * Region	882.67	
	log(Age) * Region	874.06	
	Length	1038.99	
Length	Length * Region	944.53	
	log(Length) * Region	940.03	
	Weight	1082.99	
Weight	Weight * Region	983.65	
	log(Weight) * Region	956.41	









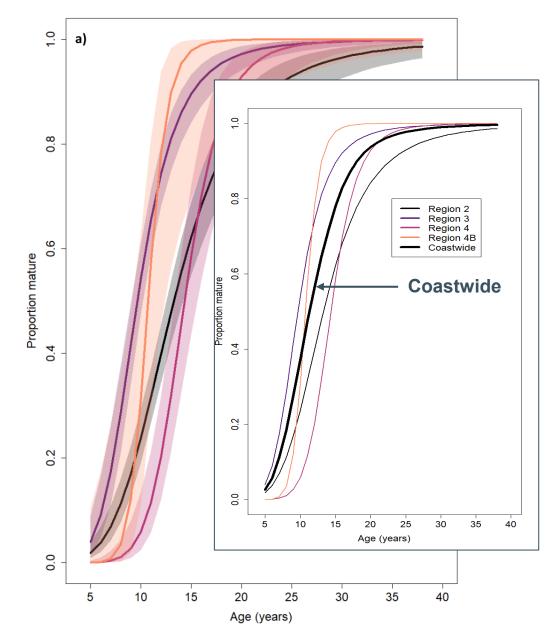


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Slide 21

GLM, log(age)*Region

- Coastwide ogive calculated from weighted regional ogives using FISS space-time model NPUE
- Coastwide ogive falls between Biological Regions 2 and 3
- A₅₀ = 11.3 yrs





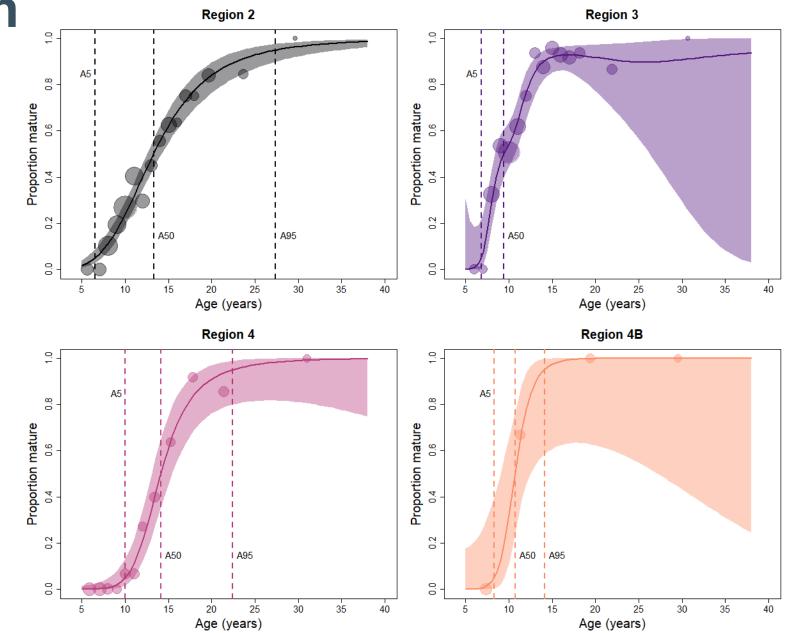
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GAM, s(log(age) by Region) AIC = 869.4

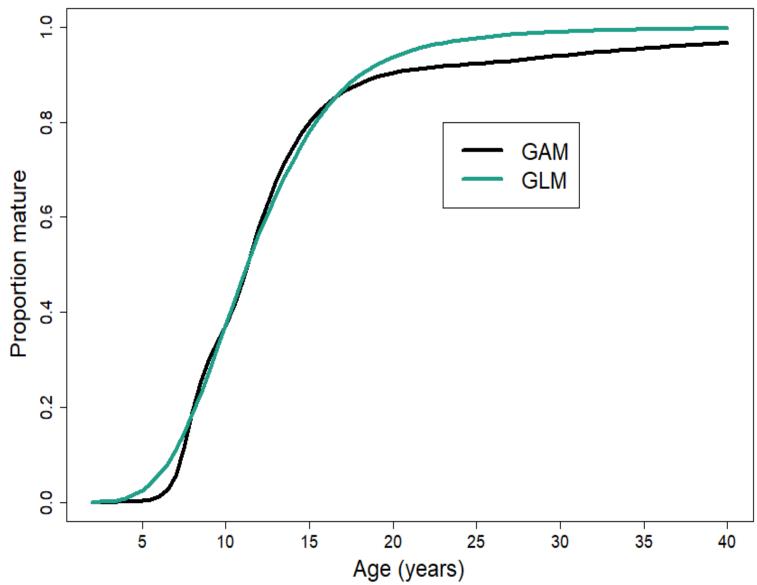
k = 14





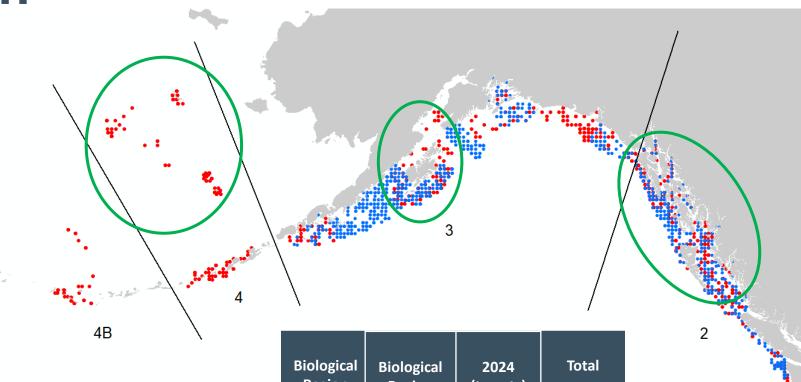
Coastwide Ogives

- GLM vs GAM
- GAM shows a steeper rise at younger ages and lower proportion mature for older individuals





2024 FISS Sample Collection



• 2023

• 2022

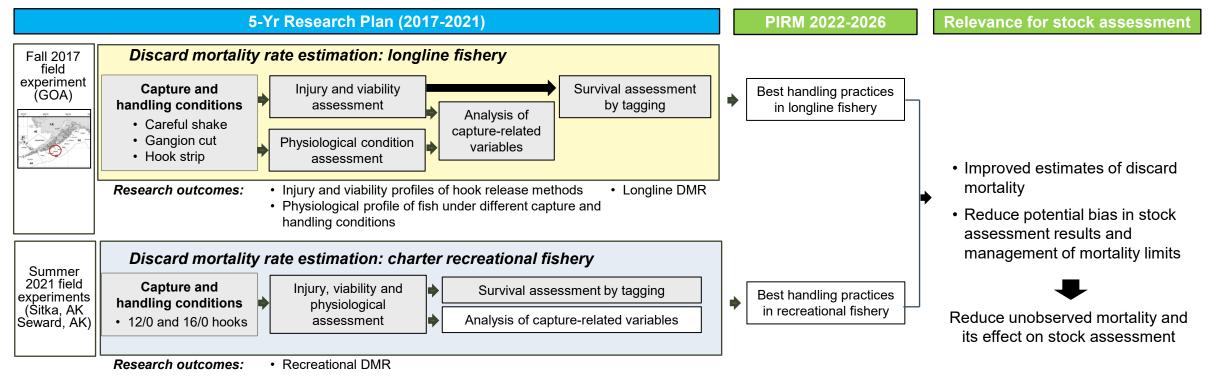
Biological Region	Biological Region	-	
2	2	400	843
3	3	400	1,059
4	4	552	181
4B	4B	-	51
Total	Total	1,352	2,134



Conclusions

- General modeling approach
 - log(age) transformation
 - GAM best fit model
 - Other suggestions?
- Coastwide ogive
 - Weighted regional ogives using FISS space-time model NPUE
 - GAM for combining regions to generate coastwide model?
- 2023 data currently being processed





External funding: Saltonstall-Kennedy NOAA (2017-2020); NFWF (2019-2021); NPRB#2009 (2021-2022)

Publications: Kroska et al. (2021) <u>Conservation Physiology</u> 9: coab001

Loher et al. (2022) North American Journal of Fisheries Management 42: 37-49

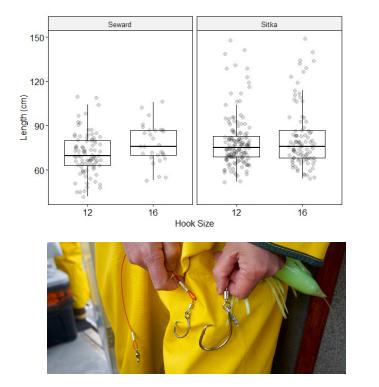
Dykstra et al. (2024) Ocean & Coastal Management. 249: 107018.

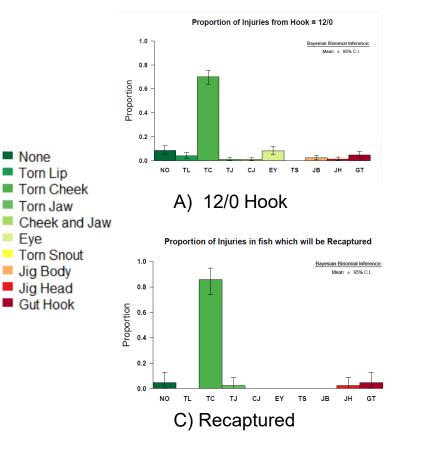


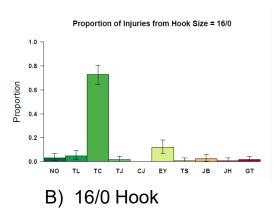
Characterization of discards in the charter recreational fishery

Effect of Hook Size on Fish Length

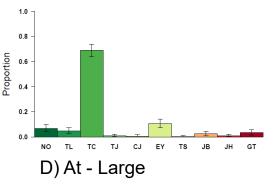
Injuries by Hook Size and Recovery Status





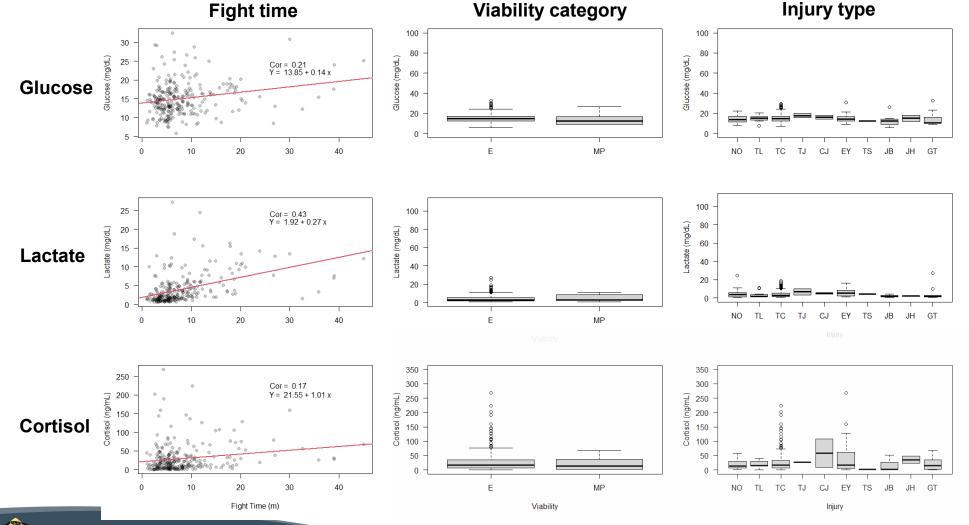


Proportion of Injuries in fish still At-Large



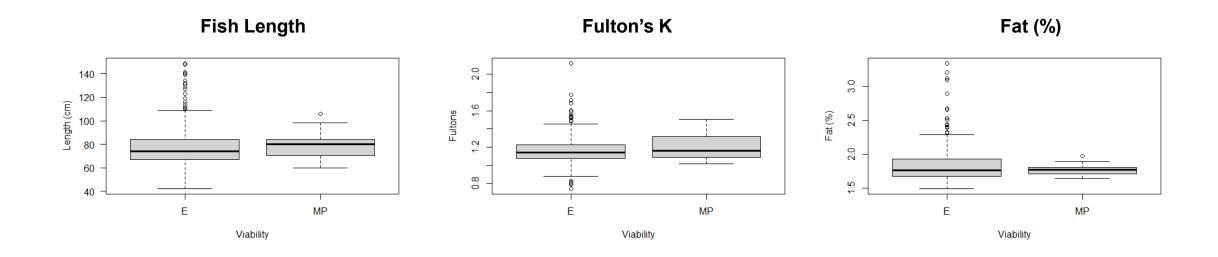


Characterization of discards: stress indicators in the blood





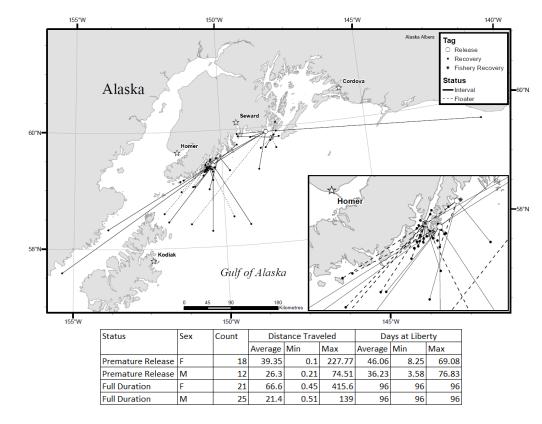
Characterization of discards: size and condition by viability



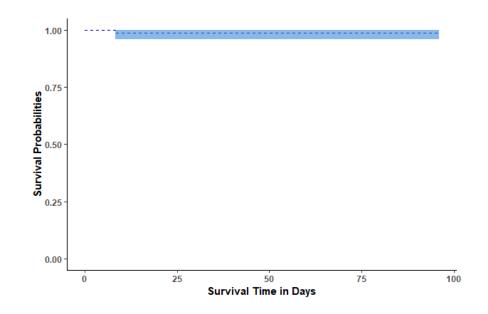


Characterization of discards: sPAT tagging

Behavior of sPAT taged fish (E viability, n = 76)



Survival probabilities



Discard mortality rate estimate: 1.35%
(95% CI of 0.00-3.95% for Excellent viability fish)



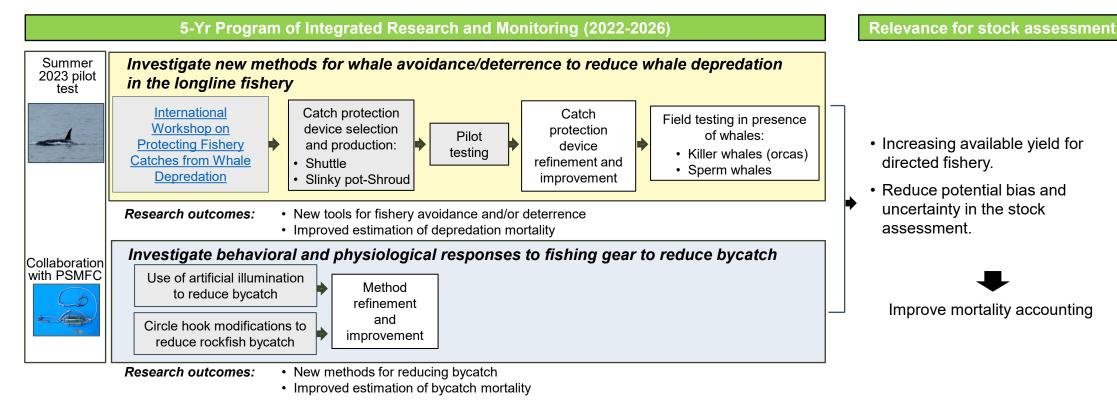
Characterization of discards in the charter recreational fishery

Conclusions

- Different hook sizes did not have different size selectivity in this study.
- The majority of injuries (~75%) were a simple torn cheek.
- Blood stress indicators increased with fight time but were not significantly different between viability or injury classifications.
- Fish size, fitness, and fat levels were similar across viability classifications.
- Estimated discard mortality estimates are very low (1.35%) for fish of Excellent viability in the charter recreational fishery.



4. Fishing technology



External funding: Bycatch Reduction Engineering Program NOAA NA21NMF4720534 (2021-2023), NA23NMF4720414 (2023-2025) Publications: Lomeli et al. (2021) *Fisheries Research* **233**: 105737 Lomeli et al. (2023) *Ocean & Coastal Management* 2**41**: 106664

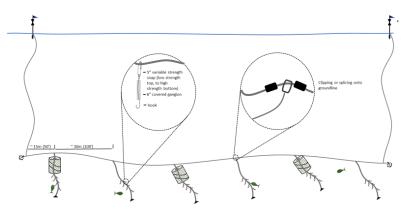


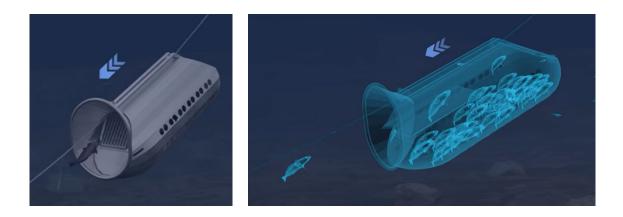




Reducing whale depredation by protecting longline catches

Devices selected for testing:





Branch lines with shrouds

Shuttle

Field testing of catch protection devices - 2023

Tested selected devices for:

- Deployment and retrieval logistics.
- Determine optimal configurations (weighting, attachments).
- Investigate basic performance characteristics (species/sizes).





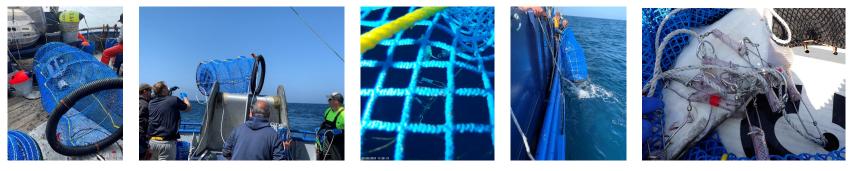


Reducing whale depredation by protecting longline catches

Shrouds

Planning required for general deployment, retrieval, safety

- Adjusted from 3 shrouds + 3 control branches to 2+2 with a blank in the middle
- Reduced hook spacing on branch line from 4 to 2 feet.



Results:

- Variable strength snaps allowed hooks to cluster.
- Shrouds generally slid down to cover the hooks but commonly with some snarling.
- Low catch rates in final configuration affected by small effective fishing footprint, and lots of hagfish.
- Basic concept works many logistical issues to sort out before scaling up to fishery level.



4. Fishing technology

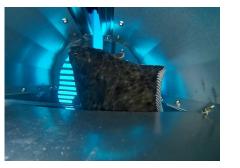


Reducing whale depredation by protecting longline catches

Shuttle

- Attach the device in-line during hauling event (1:30 min once technique established)
- Blank section of gear required to ensure unit is near bottom before encountering fish avoid moving them into the water column

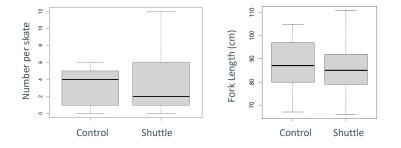






Results:

- Shuttle can be safely utilized on small vessels.
- Similar catch rates to standard gear.
- Comparable size categories of fish entrained.



Pacific Halibut Metrics - Shuttle







Reducing whale depredation by protecting longline catches

Next phase: Testing shuttle in the presence of depredators

Secured funding from NOAA BREP 2023 NA23NMF4720414

- Permit and vessel selection permitting:
- 10 days of fishing in presence of Orcas / Sperm whales.
- Further refinements (attachment protocols, gangion/hook strength).
- Catch rate comparisons with and without shuttle device.
- Catch composition details (size ranges, species, catch volume).
- Actively seeking vessels interested / available for the project.

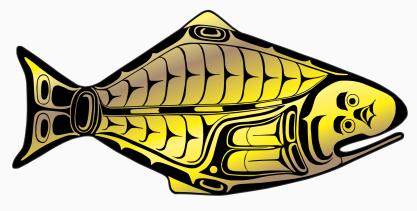


Summary of awarded research grants to IPHC current in 2024

Project #	Grant agency	Project name	PI	Partners	IPHC Budget (\$US)	Management implications	Grant period
1	Bycatch Reduction Engineering Program-NOAA	Full scale testing of devices to minimize whale depredation in longline fisheries (NOAA Award Number NA23NMF4720414)	IPHC	Alaska Fisheries Science Center-NOAA	\$199,870	Mortality estimations due to whale depredation	November 2023 – April 2025
2	Alaska Sea Grant (pending award)	Development of a non-lethal genetic- based method for aging Pacific halibut (R/2024-05)	IPHC, Alaska Pacific U. (APU)	Alaska Fisheries Science Center-NOAA (Juneau)	\$60,374	Stock structure	February 2024- January 2026
				Total awarded (\$)	\$260,244		



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