INTERNATIONAL PACIFIC HALIBUT COMMISSION

Report on current and future Biological and Ecosystem Science Research activities

Agenda item: 4.1.1

IPHC-2026-SRB028-06

(J. Planas, C. Dykstra, A. Jasonowicz, C. Jones)

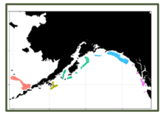
1. Migration and Population Dynamics

5-Yr Research Plan (2017-2021)

Multiple life-stage connectivity

Bering Sea

Gulf of Alaska



Genetic samples of spawning aggregations

Larval connectivity

- Larval catch and effort data
- Individual-based biophysical model
- Hydrographic ROMS model

→ Larval dispersal pathways → Inter-basin and intra-basin larval connectivity

Sadorus et al. (2021) *Fish. Oceanog*. ***30****: 174*

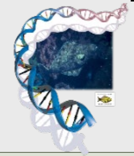
Juvenile connectivity

- NMFS trawl survey data
- Spatiotemporal model

→ Ontogenetic migration

Development and application of genomic approaches

Genome sequence



→ Population structure analyses

Jasonowicz et al. (2022) *Mol. Ecol. Res.* ***22****: 2685*

PIRM 2022-2026

- Climate effects on larval connectivity
- Connectivity with Western Pacific Ocean region
- Mapping of settlement/nursery areas
- Characterization of genetic composition/mixture of settlement areas
- 2 Manuscripts in preparation
- Stock composition: mixed stock analyses
- **Development of an epigenetic clock for aging Pacific halibut**

Relevance for stock assessment

- Generate potential recruitment covariates
- Define management targets for minimum spawning biomass by Biological Region

Improved estimates of productivity

In preparation

Genetic population structure

New bioinformatic method development

Final draft

arate assessments

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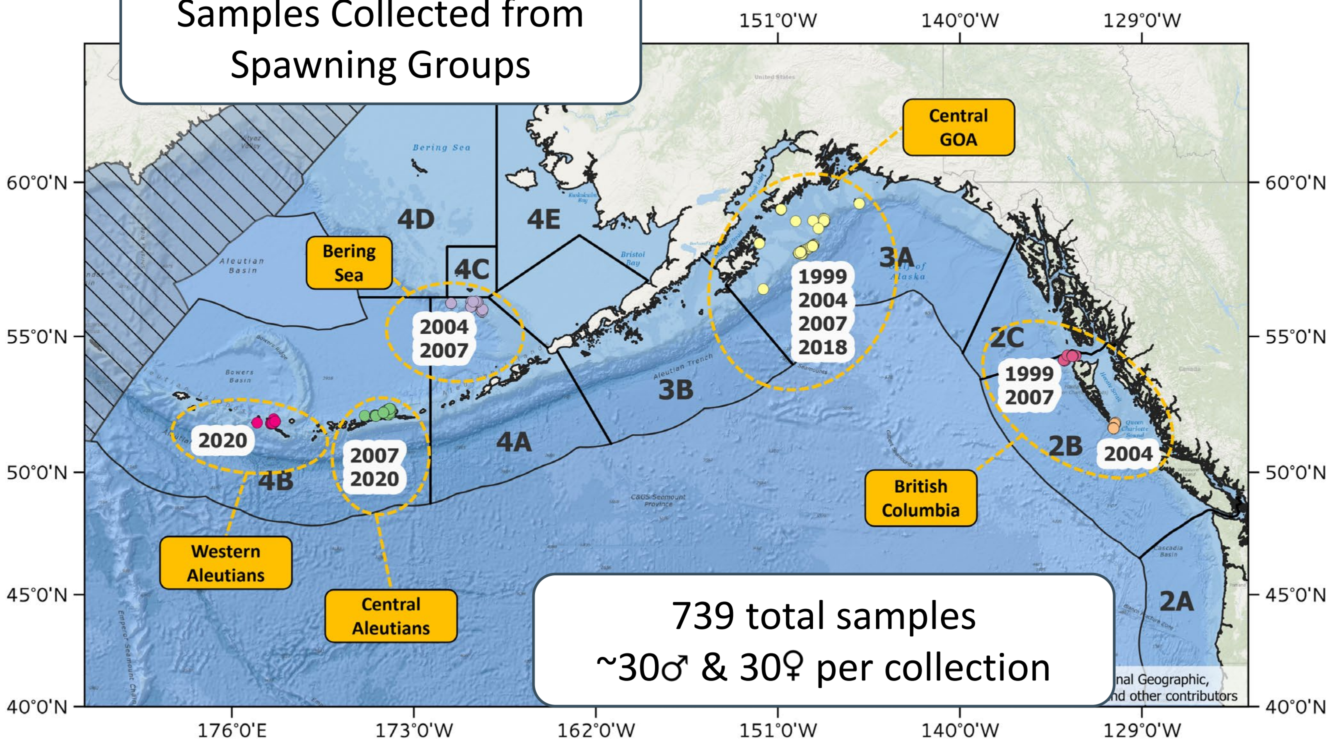
ck assessments

1. Migration and Population Dynamics

Development of a novel method for estimating genetic differentiation from genotype likelihoods

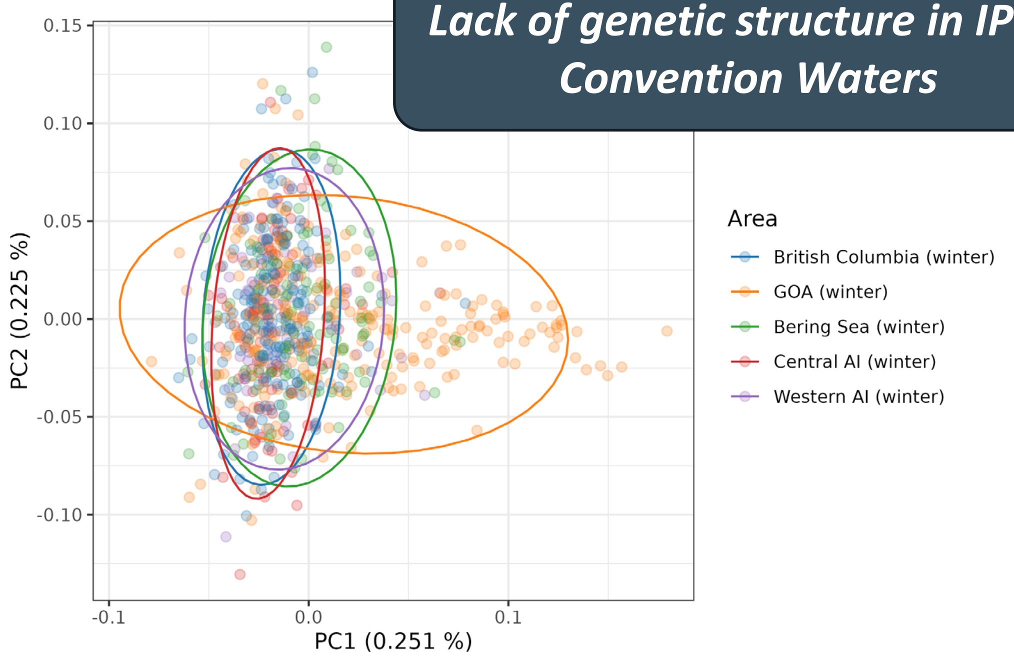
- Analysis of population structure among spawning groups
- **L**ow-**c**overage **w**hole **g**enome **r**esequencing (lcWGR)

Samples Collected from Spawning Groups



739 total samples
~30♂ & 30♀ per collection

Lack of genetic structure in IPHC Convention Waters

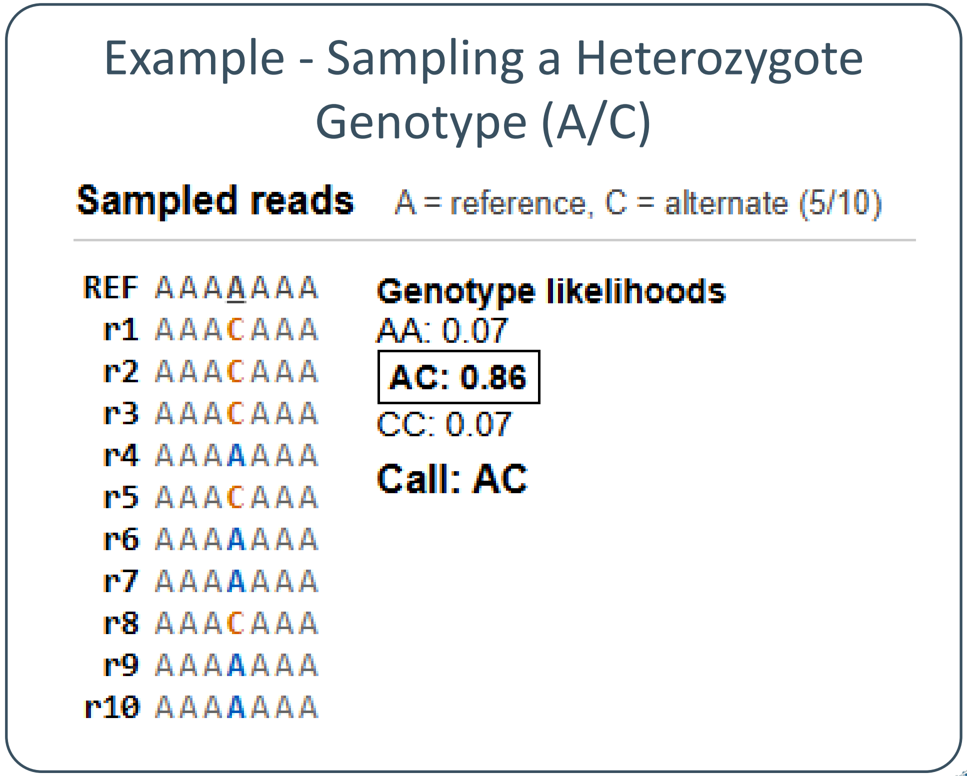


1. Migration and Population Dynamics

Development of a novel method for estimating genetic differentiation from genotype likelihoods

Motivation – Problem

- **L**ow-**c**overage **w**hole **g**enome **r**esequencing (lcWGR) – creates a sampling problem.
- At lower sequencing depths there is less certainty about an individual's genotype (e.g. A/A, A/C, or C/C).
- Genotype likelihood = the probability of the observed sequence data given a specific genotype.
- There is a limited number of tools that are designed to work with genotype likelihoods.

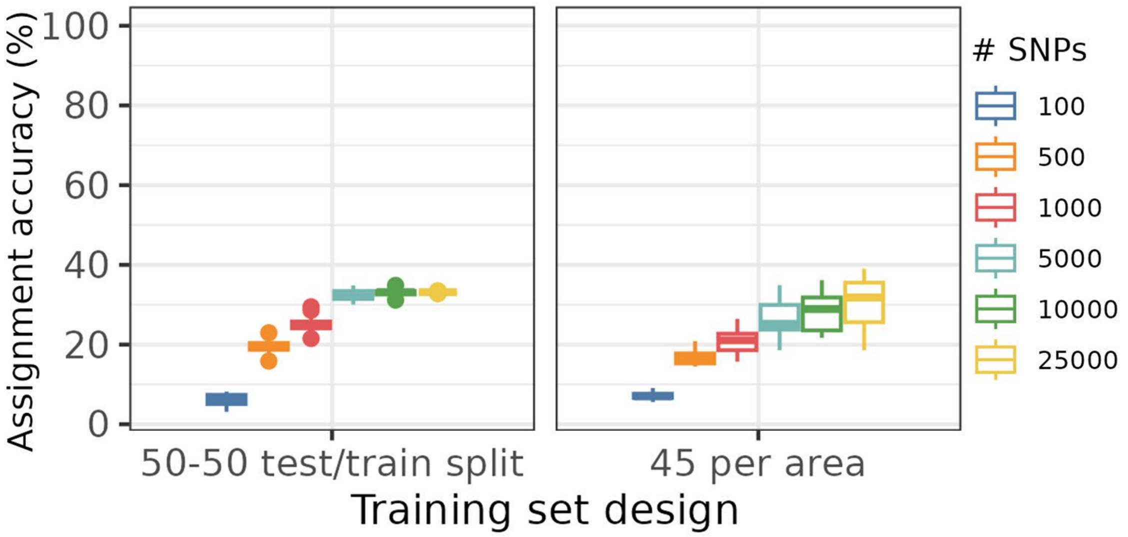


1. Migration and Population Dynamics

Development of a novel method for estimating genetic differentiation from genotype likelihoods

Motivation – Application

- Needed a way to repeatedly select SNPs for use in assignment testing.
  - Test/train split design testing – SNP panel size & training set design.
- Simplify SNP selection with global estimates of F_{ST} (vs. many pairwise comparisons).



Training Set	Test Set

SNP Selection

- Select the top *N* SNPs
  - *N*=100, 500, 1000, 5000, 10000, or 25000
- At least 10 KBp apart
- Estimate allele frequencies for reference populations

Population Assignment

- Assign individuals back to the reference populations
- Evaluate assignment accuracy with a set of "new" samples

Repeated 25 times for each scenario (Training set design & # of SNPs)

1. Migration and Population Dynamics

Development of a novel method for estimating genetic differentiation from genotype likelihoods

Methods – Implementation

- ***fst-gl*** - written in Nim programming language (nim-lang.org) – compiles to C
  - Leverages *hts-nim* library for parsing standardized file types associated with high throughput sequencing
  - *OpenMP* (www.openmp.org) - multicore processing
  - Uses an expectation-maximization (EM) algorithm for estimating allele and genotype frequencies from genotype likelihoods – these are used to calculate F_{ST}

1. Migration and Population Dynamics

Development of a novel method for estimating genetic differentiation from genotype likelihoods

Methods – Validation **-** Use both simulated data and empirical data for validation.

A

Individual based genetic simulations	Simulate sequence reads	Compare estimates of F_{ST}
Wright-Fisher based model (*SLiM*)	**Illumina Nova Seq Error Profile (*ReSeq*)**	**Between simulated genotypes and …**

Individual based genetic simulations – Wright-Fisher based model (*SLiM*)
- 2, 3, and 5 population scenarios
- Four different migration rates – (0.0, 0.01, 0.05, and 0.1)

Simulate sequence reads – Illumina Nova Seq Error Profile (*ReSeq*)
- Simulate reads to a depth of 20x
- Downsample to depths (0.1x, 0.5x, 2.5x, 5x, 10x, and 15x)

Compare estimates of F_{ST} – Between simulated genotypes and …
- new method
- hard called genotypes
- *angsd* (pairwise comparisons only)

B

Empirical Use Case

- Identification of sex associated region on chromosome 9 in Pacific halibut
- 30 males, 30 females – Portlock Bank (2018)
- Low coverage whole genome re-sequencing data (~2.9x)
  - 246,150 SNPs
  - Compare estimates of F_{ST} obtained with new method to *angsd*

Received: 10 December 2021 | Revised: 22 April 2022 | Accepted: 11 May 2022
DOI: 10.1111/1755-0998.13641
RESOURCE ARTICLE
MOLECULAR ECOLOGY RESOURCES WILEY

Generation of a chromosome-level genome assembly for Pacific halibut (*Hippoglossus stenolepis*) and characterization of its sex-determining genomic region

Andrew J. Jasonowicz[1] | Anna Simeon[1,2] | Margot Zahm[3] | Cédric Cabau[4] | Christophe Klopp[3] | Céline Roques[5] | Carole Iampietro[5] | Jérôme Lluch[5] | Cécile Donnadieu[5] | Hugues Parrinello[6] | Daniel P. Drinan[2] | Lorenz Hauser[2] | Yann Guiguen[7] | Josep V. Planas[1]

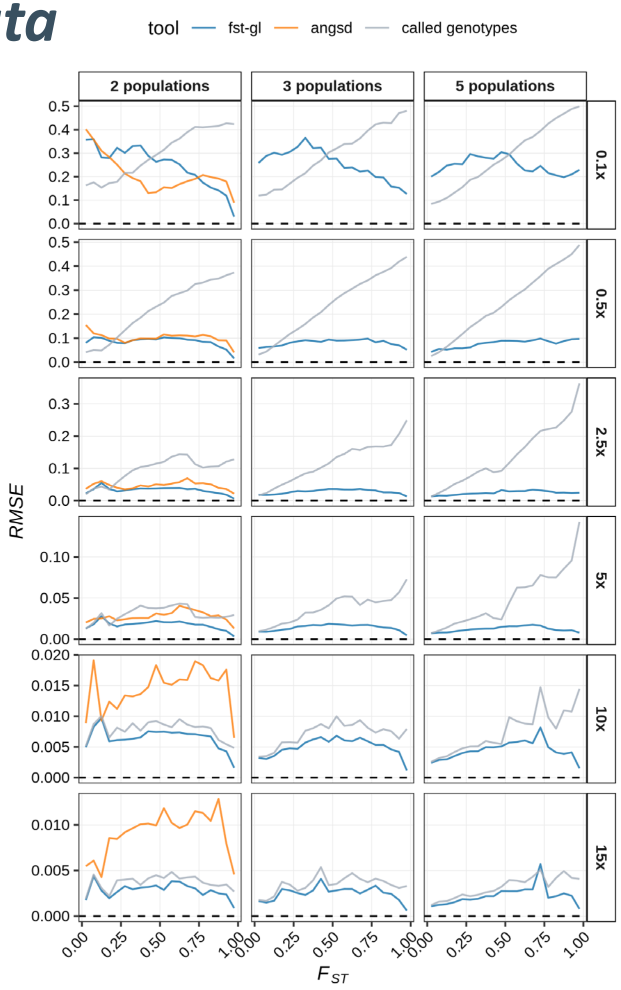
1. Migration and Population Dynamics

Development of a novel method for estimating genetic differentiation from genotype likelihoods

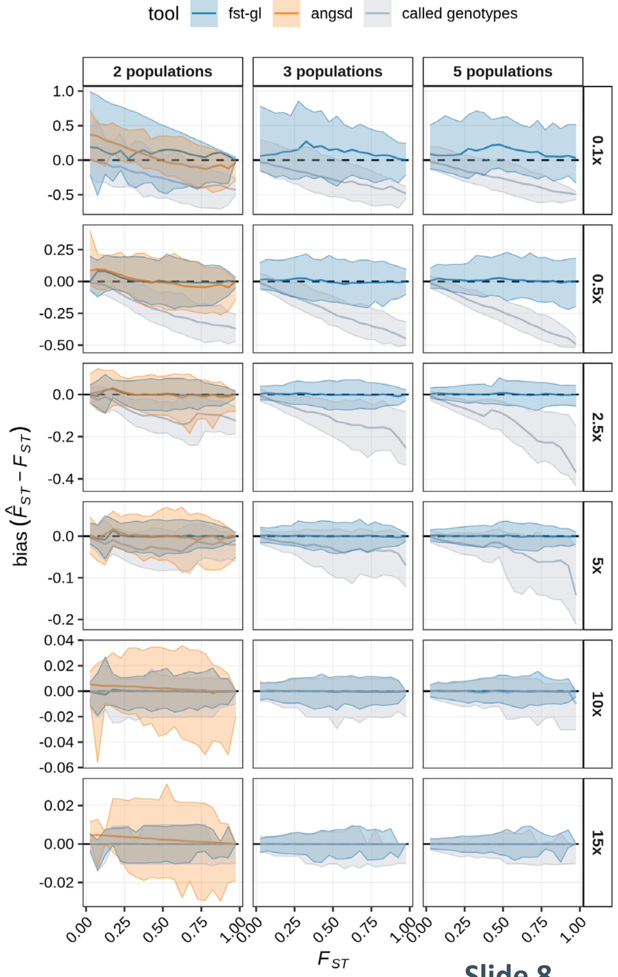
Results – Performance: simulated data

- More accurate than methods that use genotypes called from low-coverage data.
- At low depths – comparable to existing likelihood-based methods (*angsd*) for pairwise estimates.
- Faster – 69.7 – 94.0% reduction in wall time (real time) compared to *angsd*.

RMSE



Median Bias
(2.5 & 97.5 percentiles)

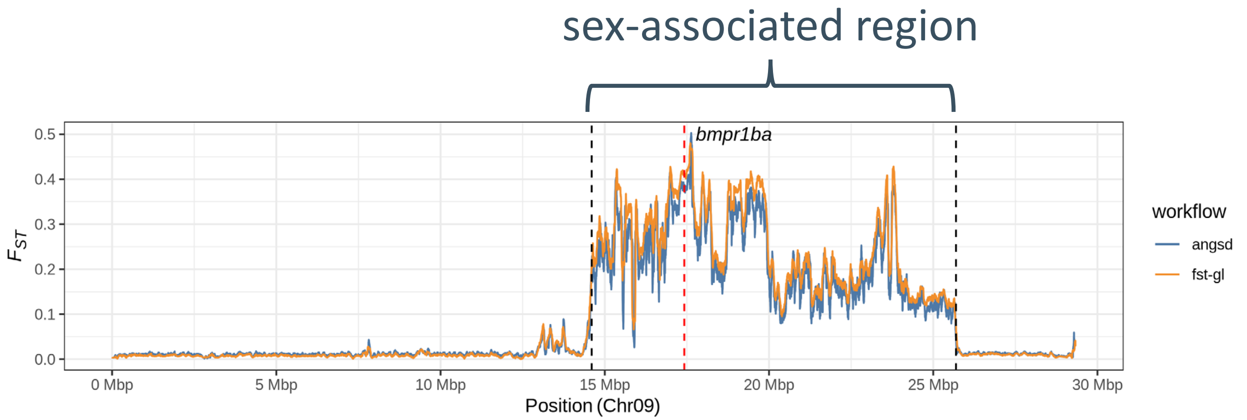


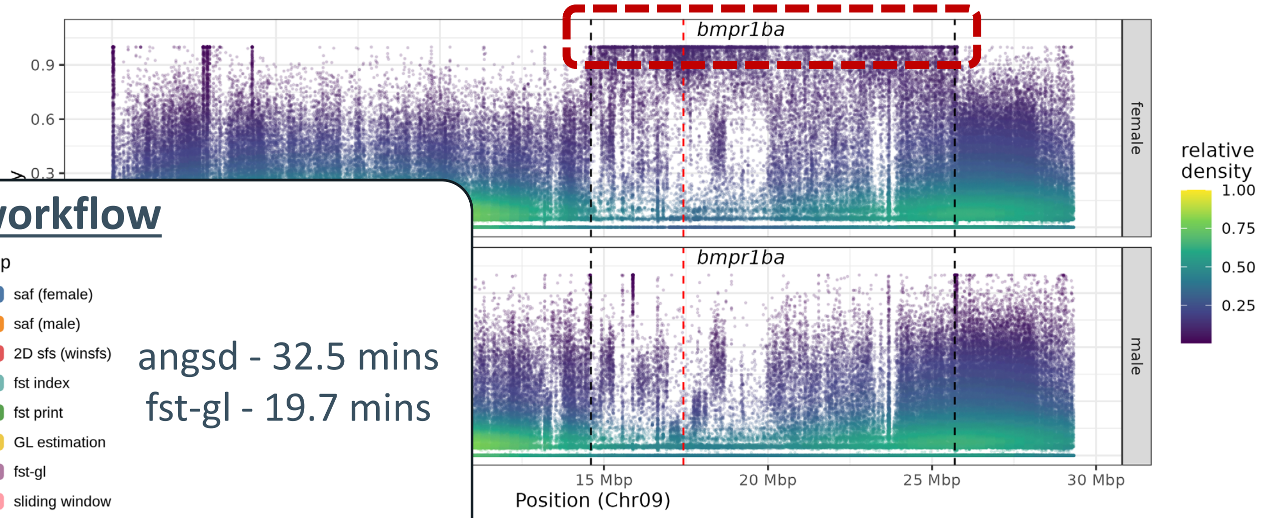
1. Migration and Population Dynamics

Development of a novel method for estimating genetic differentiation from genotype likelihoods

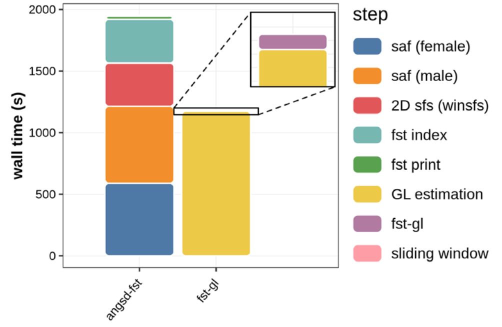
Results – Performance: empirical example

- Near identical signal detected with using *angsd* and new method.
- Elevated levels of F_{ST} detected in the sex-associated region on chromosome 9 previously identified using pooled sequencing.
- Fully heterozygous SNPs detected in females in this region (ZZ/ZW system).





Faster workflow



angsd - 32.5 mins
fst-gl - 19.7 mins

1. Migration and Population Dynamics

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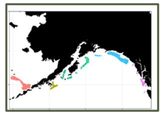

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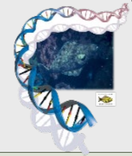

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1. Migration and Population Dynamics

Development of an epigenetic clock for aging Pacific halibut

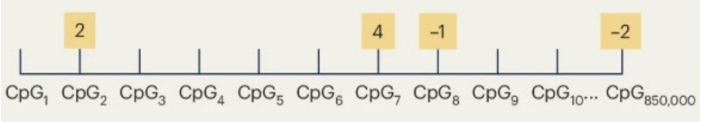
Objective: Develop a non-lethal genetic method for aging Pacific halibut using fin clips

- **Epigenetic clocks** are molecular ageing clocks: machine learning algorithms trained on epigenomic data from samples reflecting a wide range of ages.
- **Epigenetic clocks** use genome-wide DNA methylation features at cytosine-guanine (CpG) dinucleotide pairs in GC-rich regions of the genome (i.e. proportion of DNA molecules methylated at each CpG site for each individual) as input.

ID	Age	CpG_1	CpG_2	...	$CpG_{850,000}$
1	73	0.71	0.31		0.91
2	54	0.65	0.33		0.85
3	36	0.52	0.28		0.84
...					
10,000	64	0.68	0.30		0.95

Outcome: age
Predictors: CpG_1, CpG_2..., $CpG_{850,000}$

- **Age predicting models** (e.g. elastic net penalized regression models) rely on the weighed average of methylation across a subset of CpGs.



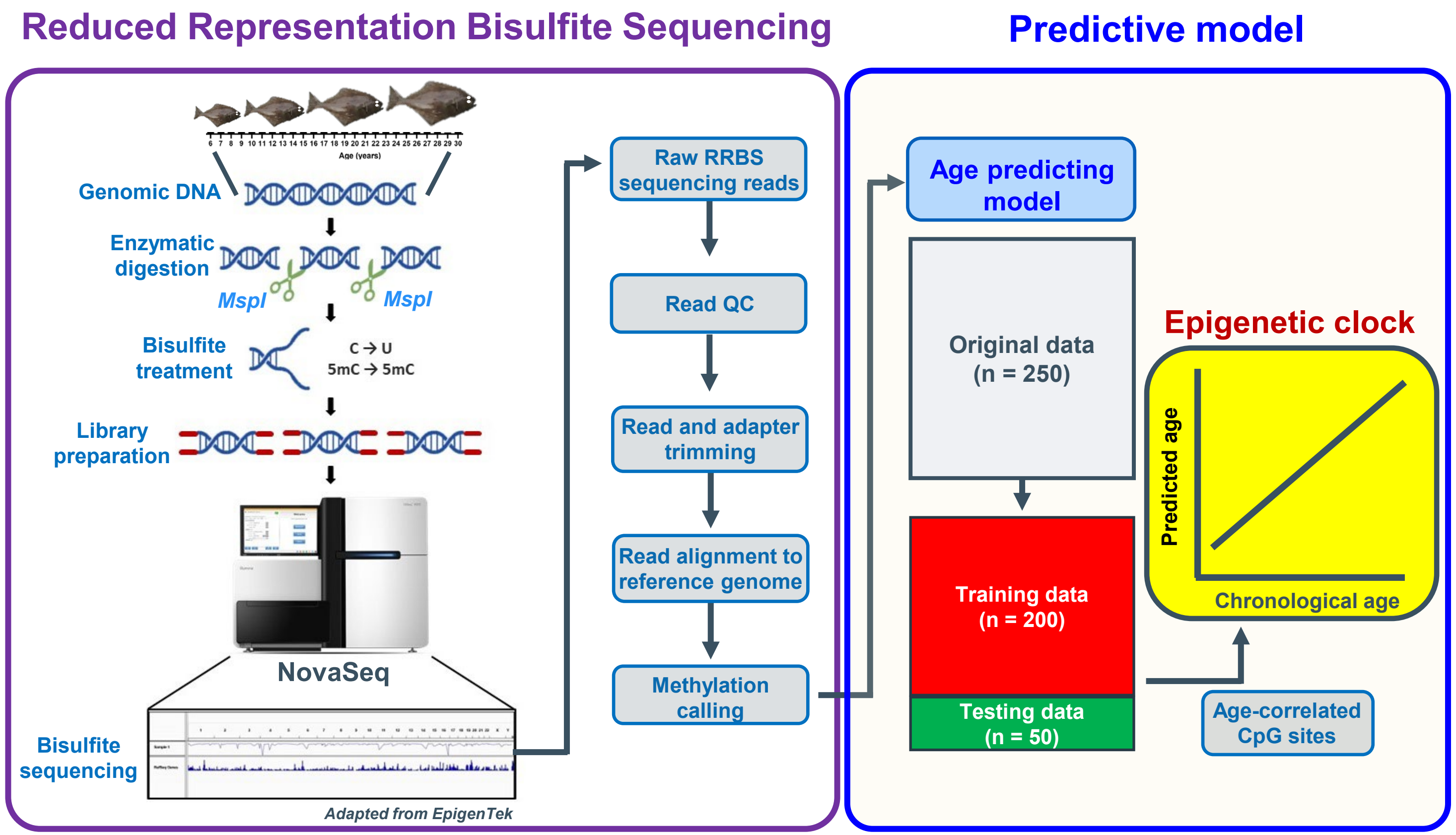
- **Test dataset** is used to validate and test the performance (e.g. Pearson correlation or median absolute error) of the epigenetic clock.

1. Migration and Population Dynamics

Development of an epigenetic clock for aging Pacific halibut

Sea Grant ALASKA
Project R/2024-05 (2025-2027)

Project workflow

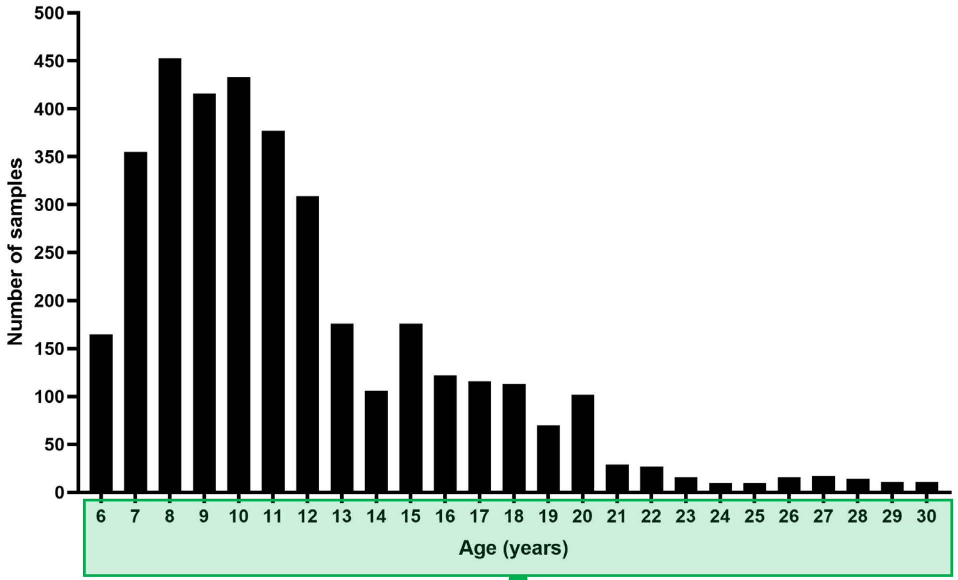


1. Migration and Population Dynamics

Development of an epigenetic clock for aging Pacific halibut

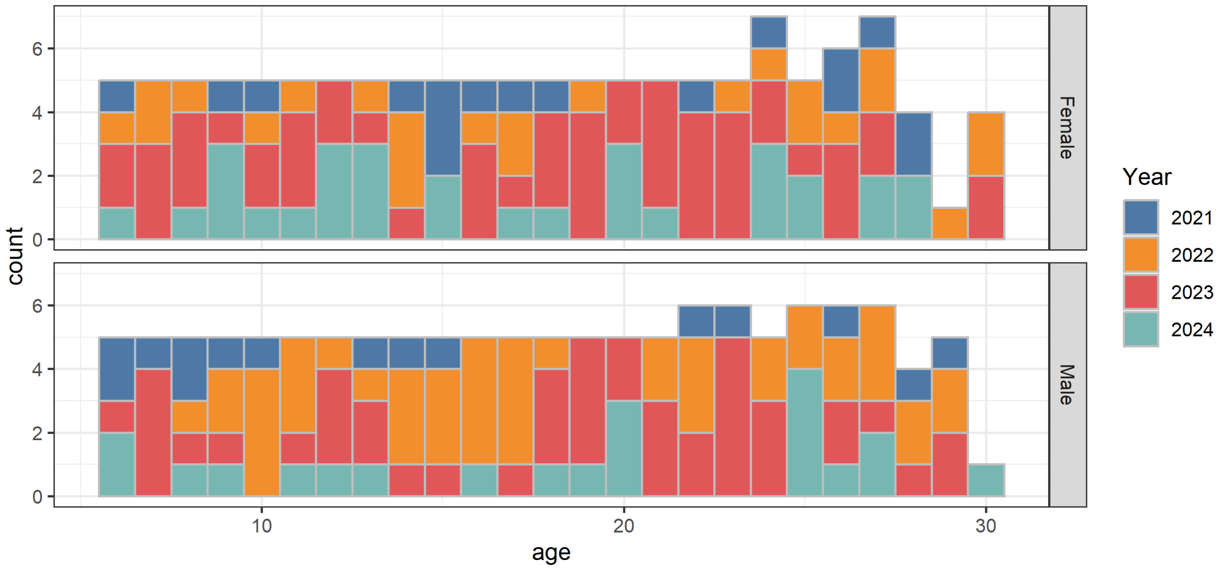
Genetic samples: aged fin clips

Year	2A	2B	2C	3A	3B	4A	4B	4D	Total
2021	1	12	12	3	0	3	1	0	32
2022	2	22	17	20	2	2	3	1	69
2023	16	32	25	14	10	0	0	0	97
2024	0	15	26	7	1	0	0	2	51
Total	**19**	**81**	**80**	**44**	**13**	**5**	**4**	**3**	**249**



5♂ and 5♀/age from 6 to 30 years of age
N = 249 samples

Ages of FISS Samples Selected for Epigenetic Clock Development (2021-2024)

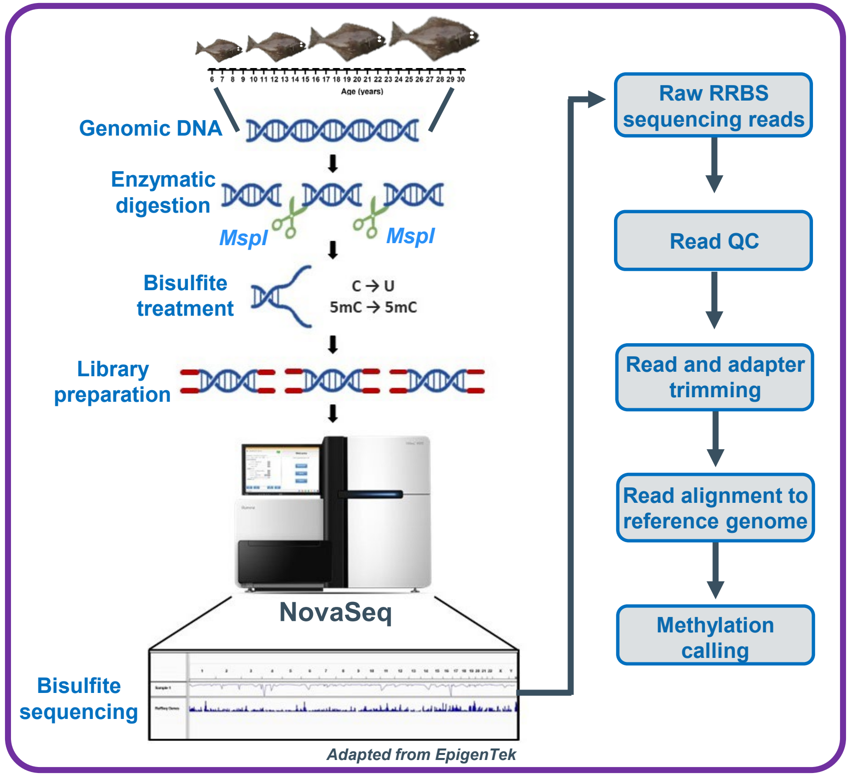


1. Migration and Population Dynamics

Development of an epigenetic clock for aging Pacific halibut

Sequencing results

Reduced Representation Bisulfite Sequencing



Adapted from EpigenTek

Pool	Number of samples processed	Average PCR duplication rate (%)	Average number of remaining reads/sample	Average of methylated control (%)	Average of unmethylated control (%)	Sum of deduplicated reads (reads remaining)
1	42	64.82	5,288,760	1.40	98.95	222,127,927
2	41	49.56	6,506,924	1.65	99.20	266,783,900
3	42	34.99	7,264,685	1.64	99.37	305,116,779
4	42	38.35	6,509,939	1.86	99.44	273,417,435
5	41	33.77	6,443,062	1.41	99.29	270,608,611
6	41	36.99	6,167,590	1.51	99.25	252,871,200
Total	**249**	**43.08**	**-**	**1.58**	**99.25**	**1,590,925,852**

- Sequencing completed
- Currently processing sequence data through bioinformatic pipeline

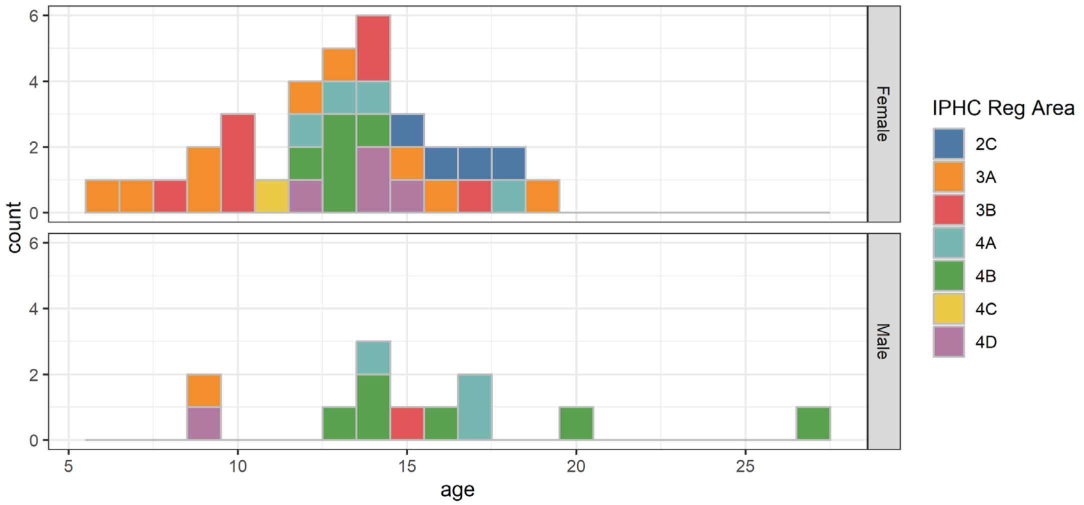
1. Migration and Population Dynamics

Development of an epigenetic clock for aging Pacific halibut

Recommendation from SRB027

SRB027–Rec.01 (para. 14). The SRB RECOMMENDED that that evaluation of epigenetic aging be expanded from random selection of cross-validation samples to include testing out-of-sample interannual predictive performance. That is, how well can an epigenetic aging method trained on data from one set of years predict age of individuals sampled in other years?

- Selected 46 double-aged commercial genetic samples from 2017 to 2020
- Library construction completed and 1 library pool has been sequenced
- Sequencing data in process

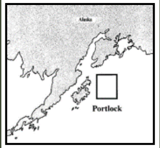


Year	2C	3A	3B	4A	4B	4C	4D	Total
2017	0	0	0	4	4	0	4	12
2018	1	3	2	0	5	0	1	12
2019	0	3	2	3	2	1	0	11
2020	3	4	4	0	0	0	0	11
Total	**4**	**10**	**8**	**7**	**11**	**1**	**5**	**46**

2. Reproduction

5-Yr Research Plan (2017-2021)	PIRM 2022-2026	Relevance for stock assessment

2017-2018 Field sample collection (central GOA)



30♀/ month

♀>90 cm FL

Seasonal characterization of reproductive development

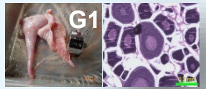
Histological samples → Characterization of oocyte stages → Classification of female developmental stages → Classification of reproductive phases → Appropriate timing of gonad collection in FISS

Research outcomes:
- Group synchronous
- Batch spawner
- Determinate fecundity
- Annual cycle
- Spawning time
- Reproductive delays
- June-August

Macroscopic vs microscopic maturity staging

Macroscopic maturity scores

Ovary images



Histology-based female developmental stages and reproductive phases

→ Assess accuracy of current field maturity classification criteria

Research outcomes:
- In progress

2017-2022 Commercial landings

Development and application of genetic tests for sex identification

PIRM 2022-2026:

- Manuscript in preparation
- Revised historical maturity ogives
- Fecundity assessment
- Male Reproductive Characterization
- Revise macroscopic staging criteria
- Sex-ratio monitoring

Relevance for stock assessment:

- Direct input into stock assessment for estimation of the stock-recruitment relationship
- Estimate annual reproductive output
- Revise time-series of historical and future maturity

Scale of female spawning biomass and reference point estimates

- Annual sex-ratio at age for the commercial fishery fit by the stock assessment

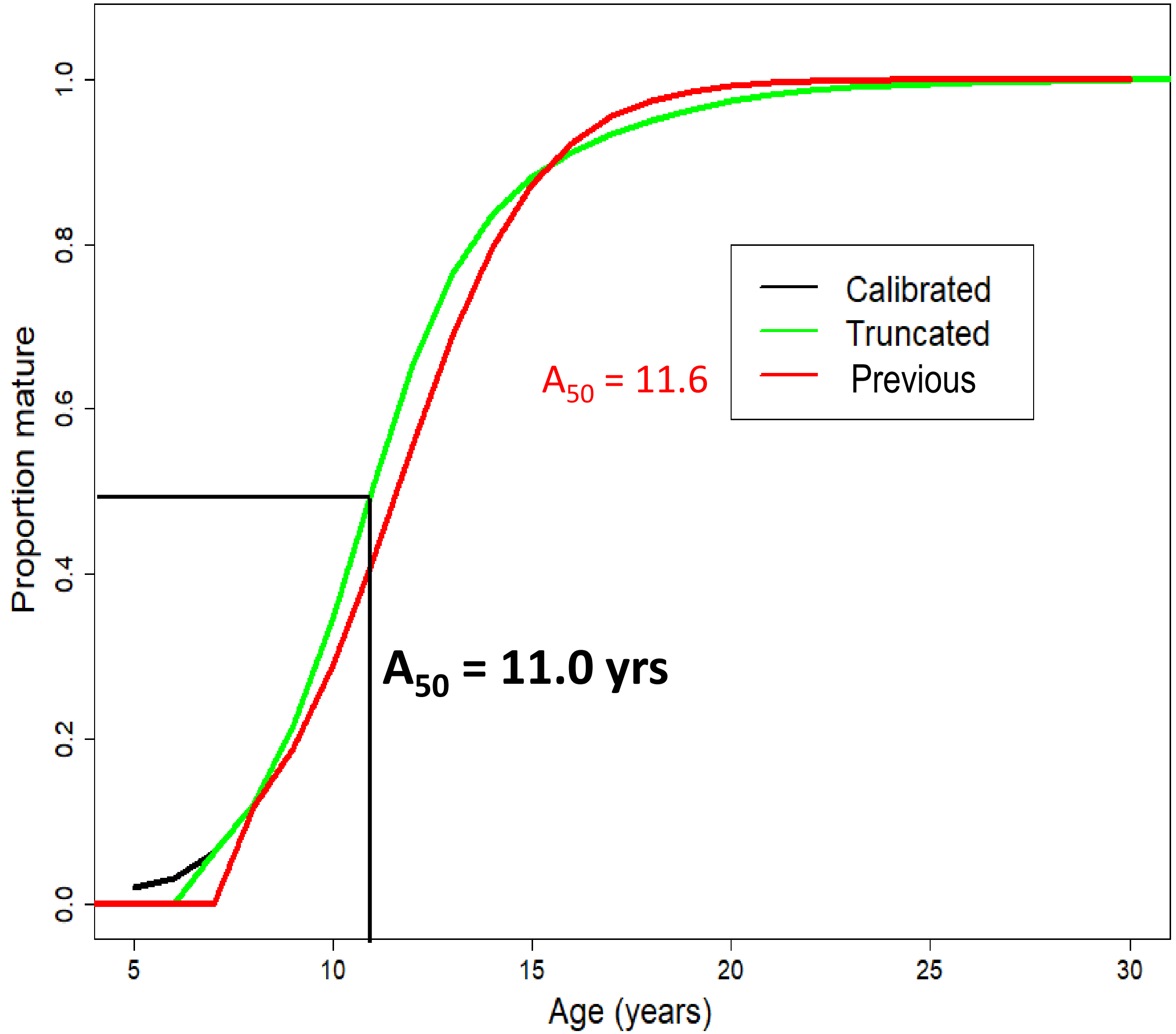
Reduce uncertainty in stock size and fishing intensity

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

2. Reproduction

New coastwide maturity ogive

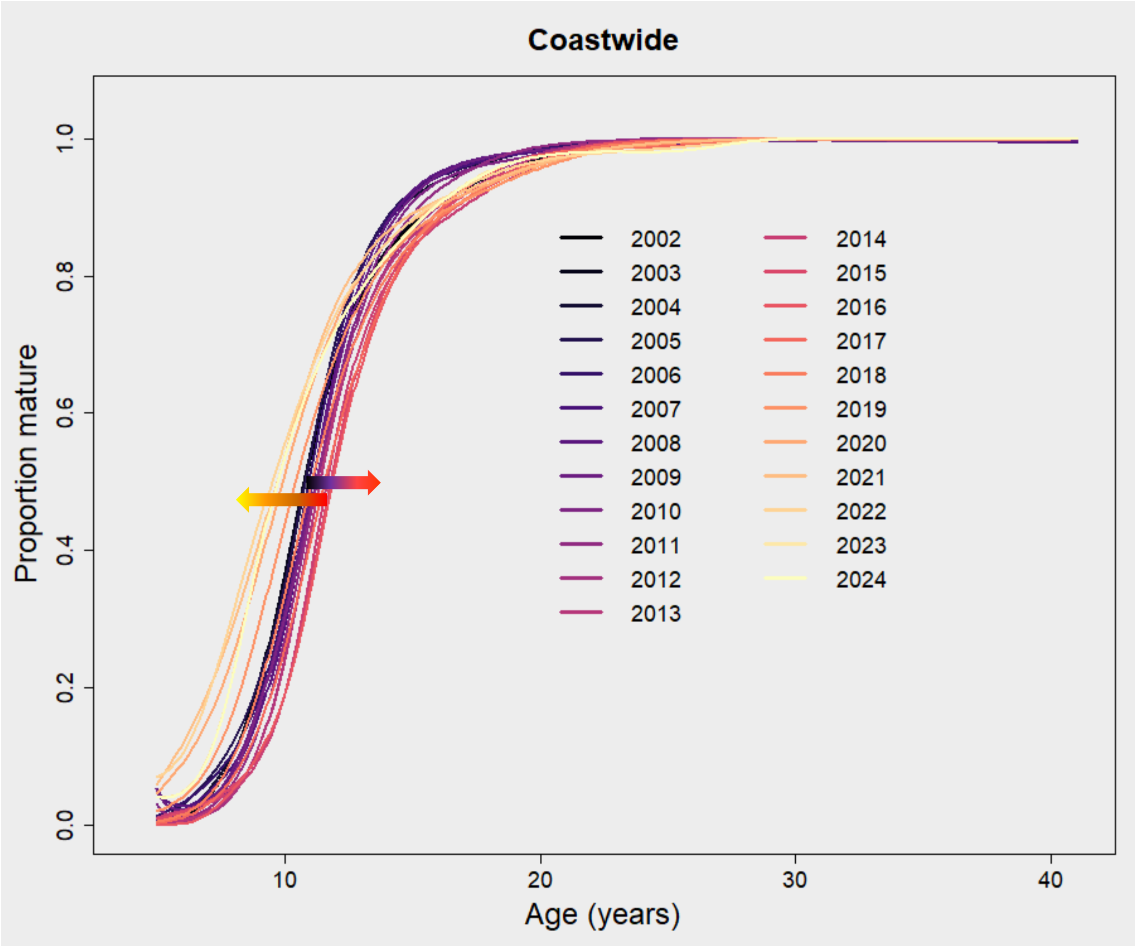
- A calibration between histological and visual maturity ogives with FISS-collected data from 2022-2024 was established.
- A **calibrated** coastwide maturity ogive was generated using visual maturity estimates from FISS (2002-2024)
- Maturity estimates from the average 2002-2024 calibrated coastwide ogive are shifted slightly to the left of **previous** assessment ogive (2002-2003)
- A_{50} is **0.6 yrs** lower
- Truncated to zero < Age 7
- **New coastwide maturity ogive used in the 2025 stock assessment**



2. Reproduction

Calibrated coastwide maturity ogives from 2002 to 2024

- GAM s(log(Age) * Region)
- Coastwide maturity ogive calculated from weighted regional ogives using average FISS space-time model abundance estimates from 2022-2024
- A calibration was developed between histological and visual maturity curves to estimate temporal patterns of age at maturity using the 2002-2024 time series of FISS visual maturity data
- Temporal shifts in maturity schedules are apparent

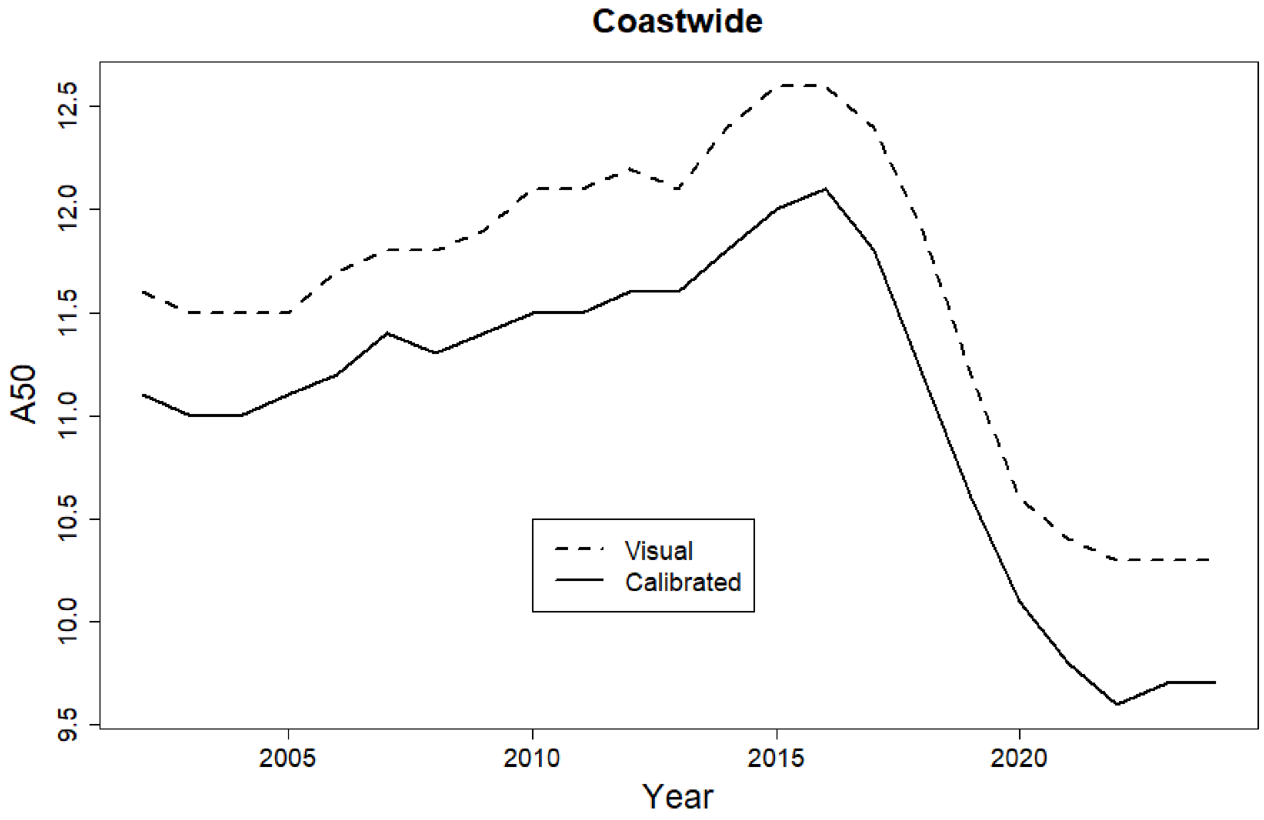


2. Reproduction

Historical coastwide maturity schedules

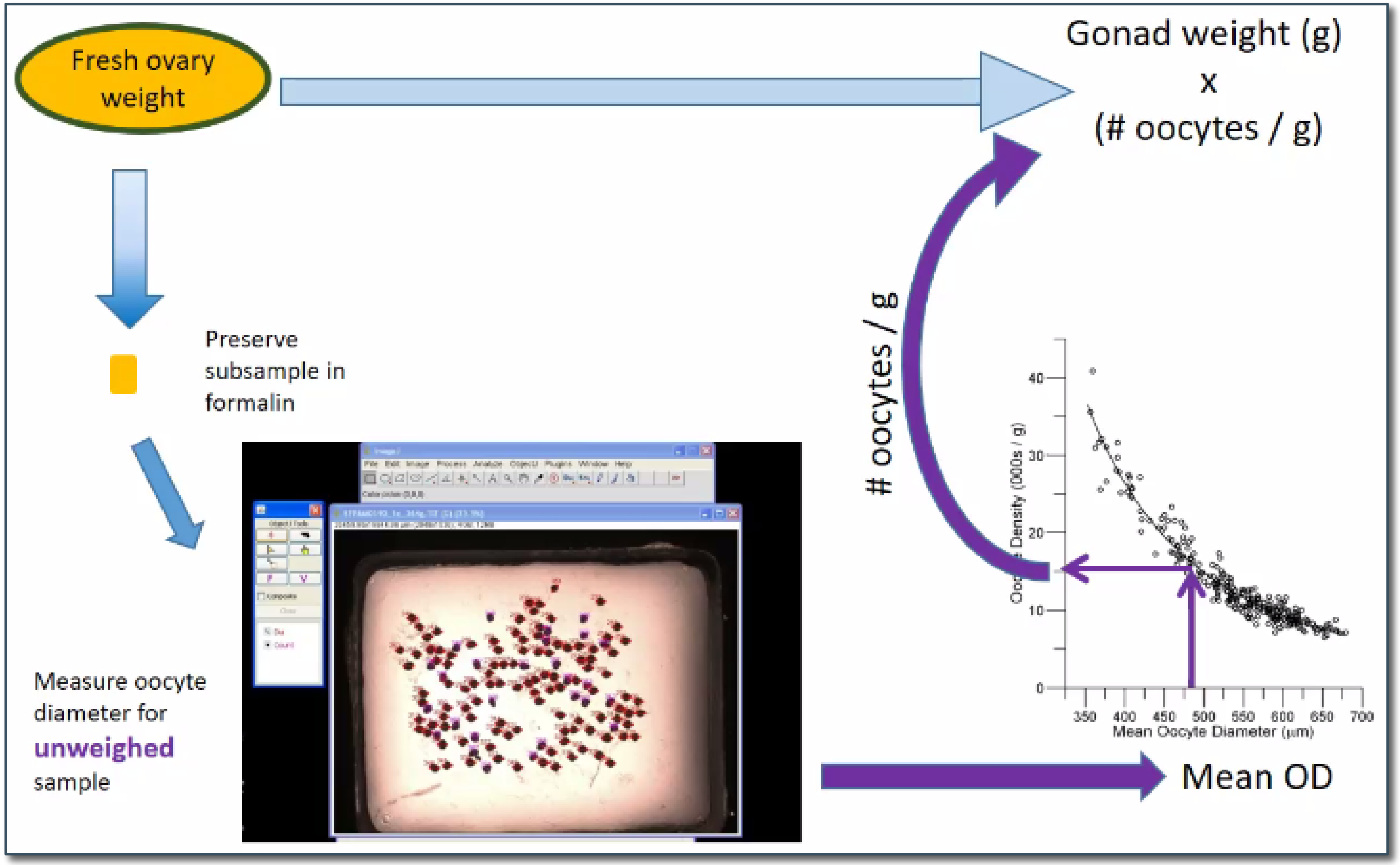
- 2002 - 2024
  - Raw visual data (dotted line)
  - Calibrated visual data using histology (solid line)

- Two temporal shifts
  - 2002 - 2016
  - 2017 - 2022



2. Reproduction

Fecundity estimation – Autodiametric method



➡

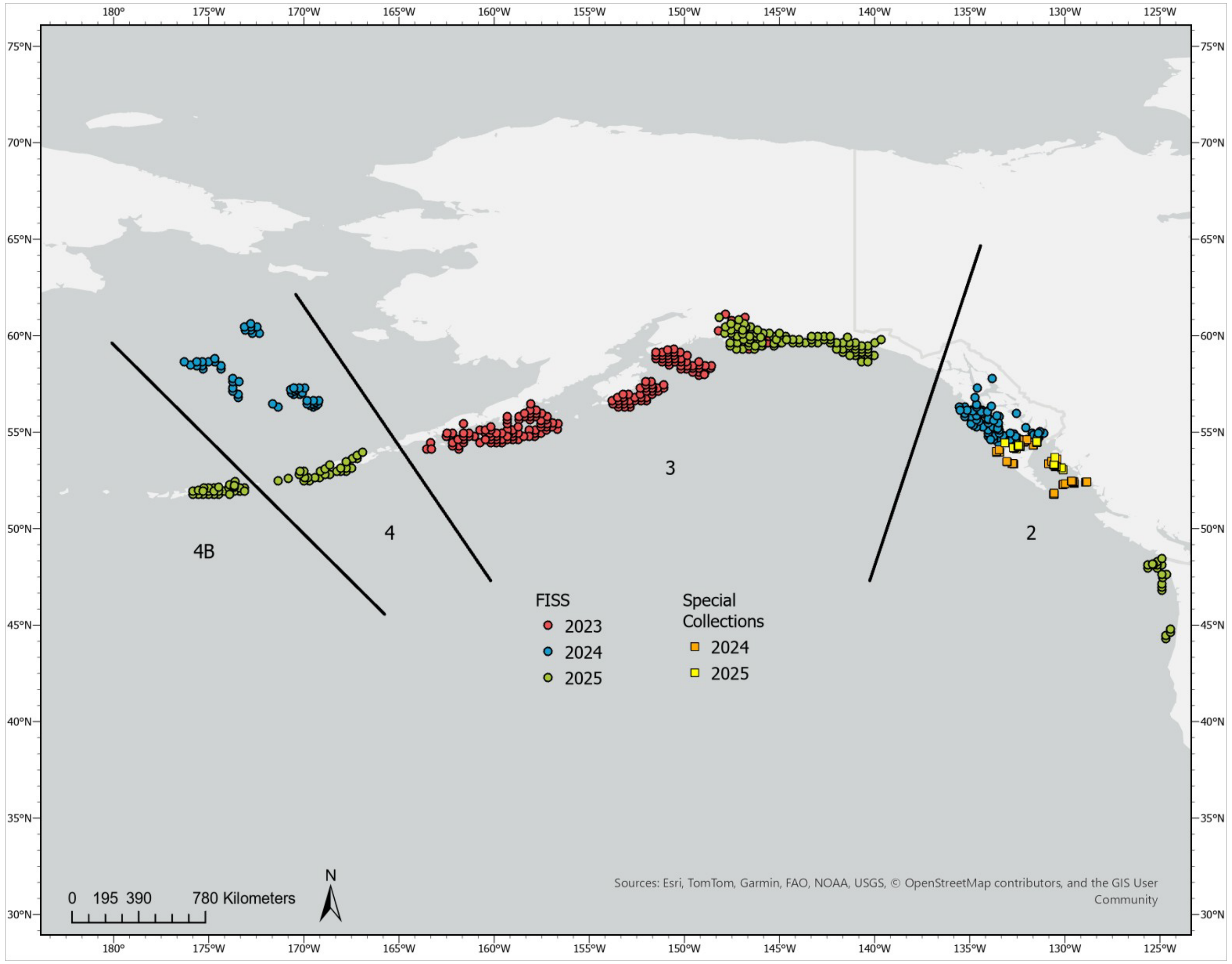
Potential Annual Fecundity (PAF) (Total # oocytes)

2. Reproduction

Fecundity estimation – Sample collection

- FISS
  - 2023: Region 3
  - 2024: Region 2 and 4
  - 2025: All Regions

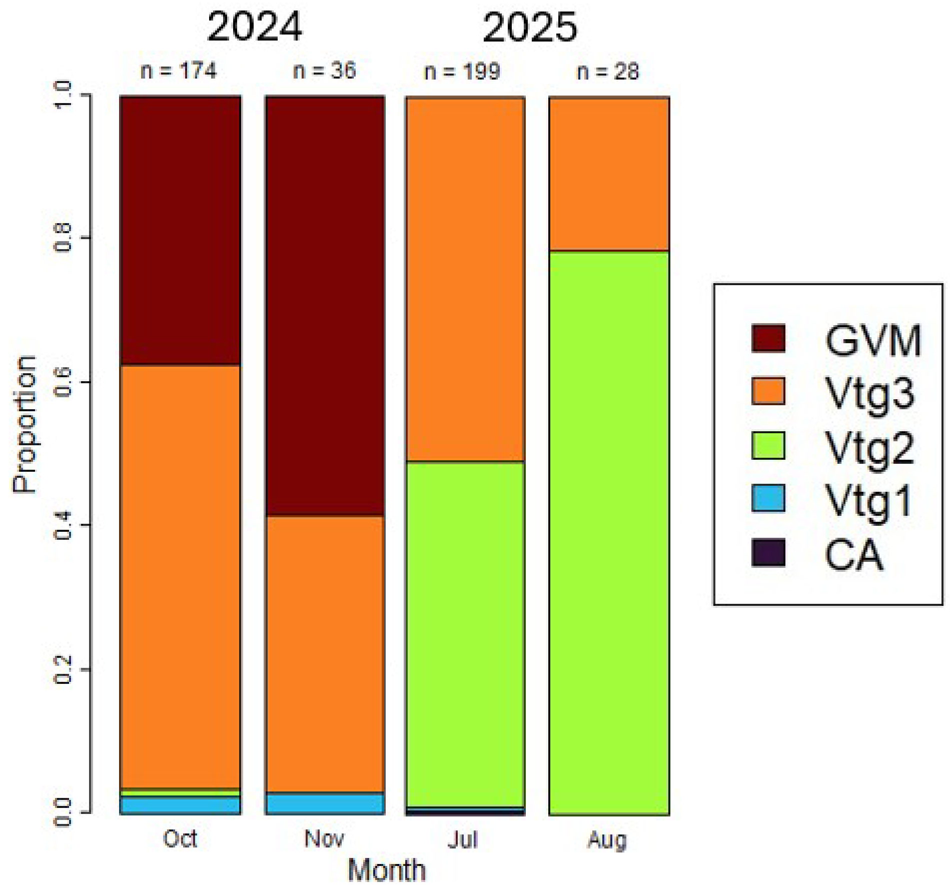
- Special Collections
  - 2024 and 2025
  - Region 2
  - ≥ 90 cm females



2. Reproduction

Fecundity estimation – Sample collection

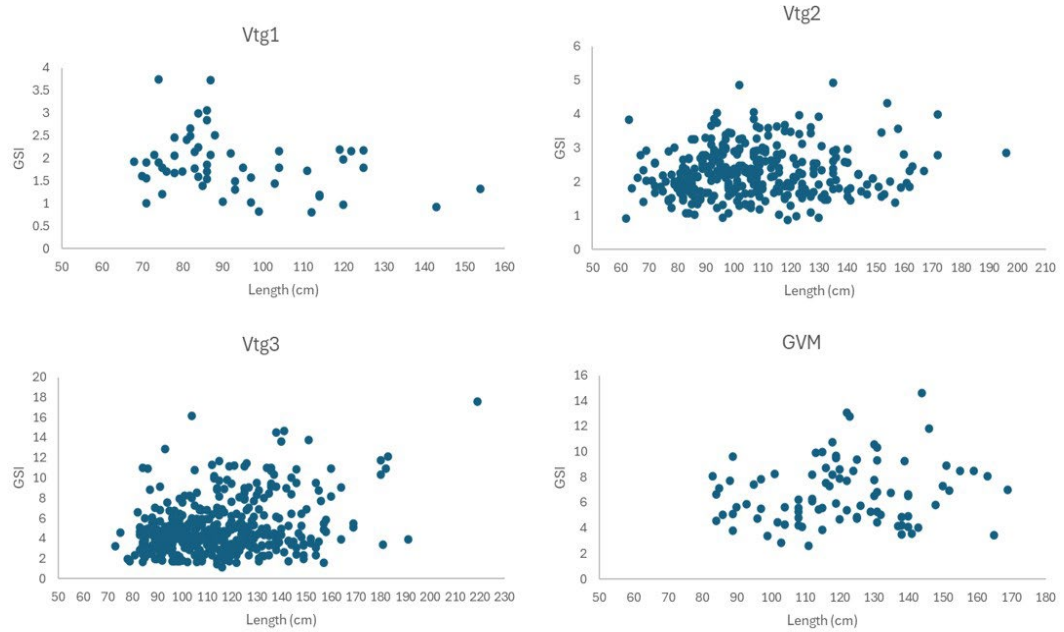
- Special collections (Region 2)
  - 2024: October / November
  - 2025: July / August
- 2024 – Vtg3 -> GVM
- 2025 – Vtg2 -> Vtg3



2. Reproduction

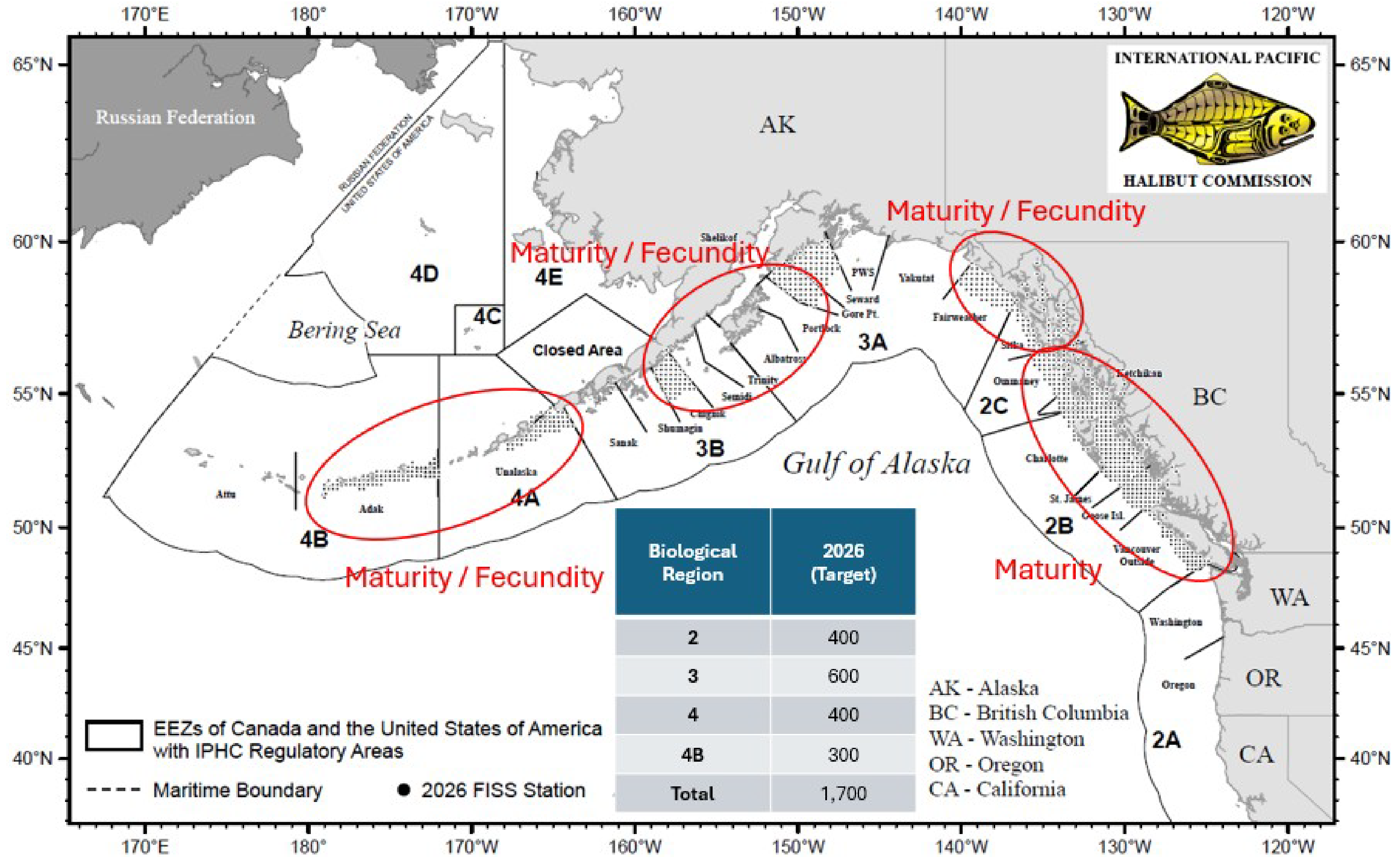
Fecundity estimation – GSI vs Age / Weight / Length

- 2023, 2024 FISS and All Special Collections have been scored for histology
- High variability in GSI
- Early indication of isometric relationship with weight or length



2. Reproduction

Maturity / Fecundity sampling – 2026 FISS



Biological Region	2026 (Target)
2	400
3	600
4	400
4B	300
Total	1,700

3. Growth

5-Yr Research Plan (2017-2021) | **(2022-2026)**

2016-2018
Age-0
summer
collection
(Kodiak)

Fish rearin
at Hatfiel
Marine
Science
Center
(Newport

Identification and validation of physiological growth markers

© 2025. Published by The Company of Biologists | Journal of Experimental Biology (2025) 228, jeb251013. doi:10.1242/jeb.251013

The Company of Biologists

RESEARCH ARTICLE

Mechanisms underlying thermally induced growth plasticity in juvenile Pacific halibut

Josep V. Planas[1,§], Andrew J. Jasonowicz[1], Anna Simeon[1,*], Crystal Simchick[1], Emma Timmins-Schiffman[2], Brook L. Nunn[2], Anita C. Kroska[3,‡], Nathan Wolf[3] and Thomas P. Hurst[4]

Research outcomes:
- Differentially-expressed genes
- Differentially-expressed proteins
- Validated growth markers

Environmental influences on growth patterns

Research outcomes:
- Effects of temperature on growth rates
- Temperature-specific molecular responses

Environmental influences on growth patterns

Dietary influences on growth patterns and physiological condition

Drivers of changes in size-at-age

External collaborators: Behavioral Ecology Program at AFSC-NOAA (Newport, OR), Alaska Pacific University, UW
External funding: NPRB Grant#1704 (Sept. 2017-Feb. 2020)
Publications: Planas et al. (2025)

4. Mortality and Survival Assessment

5-Yr Research Plan (2017-2021) | **PIRM 2022-2026** | **Relevance for stock assessment**

Fall 2017 field experiment (GOA)

Discard mortality rate estimation: longline fishery

Capture and handling conditions
- Careful shake
- Gangion cut
- Hook strip

→ Injury and viability assessment → Survival assessment by tagging

→ Physiological condition assessment → Analysis of capture-related variables

Research outcomes:
- Injury and viability profiles of hook release methods
- Physiological profile of fish under different capture and handling conditions
- Longline DMR

→ Best handling practices in longline fishery

Summer 2021 field experiments (Sitka, AK Seward, AK)

Discard mortality rate estimation: charter recreational fishery

Capture and handling conditions
- 12/0 and 16/0 hooks

→ Injury, viability and physiological assessment → Survival assessment by tagging; Analysis of capture-related variables

Research outcomes:
- Recreational DMR

→ Best handling practices in recreational fishery

- Improved estimates of discard mortality
- Reduce potential bias in stock assessment results and management of mortality limits

Reduce unobserved mortality and its effect on stock assessment

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

Publications: Kroska et al. (2021) *Conservation Physiology* ***9**: coab001*
Loher et al. (2022) *North American Journal of Fisheries Management* ***42**: 37-49*
Dykstra et al. (2024) *Ocean & Coastal Management*. ***249**: 107018.*
} Longline fishery

Dykstra et al. In Preparation } Recreational fishery

Manuscript in preparation

5. Fishing technology

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

Relevance for stock assessment

Summer 2023 pilot test

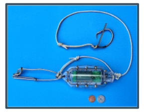
Investigate new methods for whale avoidance/deterrence to reduce whale depredation in the longline fishery

International Workshop on Protecting Fishery Catches from Whale Depredation → Catch protection device selection and production:
- Shuttle
- Slinky pot-Shroud

→ Pilot testing → Catch protection device refinement and improvement → Field testing in presence of whales:
- Killer whales (orcas)
- Sperm whales

Research outcomes:
- New tools for fishery avoidance and/or deterrence
- Improved estimation of depredation mortality

Collaboration with PSMFC



Investigate behavioral and physiological responses to fishing gear to reduce bycatch

Use of artificial illumination to reduce bycatch → Method refinement and improvement

Circle hook modifications to reduce rockfish bycatch → Method refinement and improvement

Research outcomes:
- New methods for reducing bycatch
- Improved estimation of bycatch mortality

- Increasing available yield for directed fishery.
- Reduce potential bias and uncertainty in the stock assessment.

Improve mortality accounting

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*

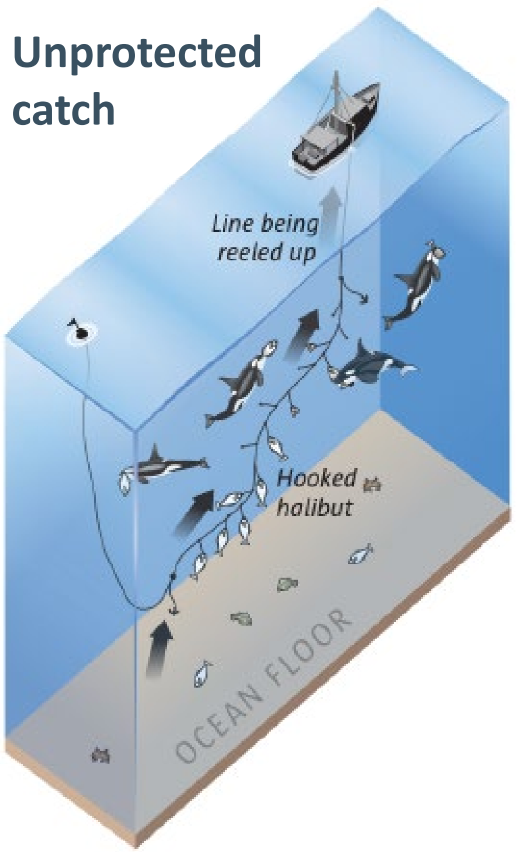
5. Fishing technology

Reducing whale depredation by protecting longline catches

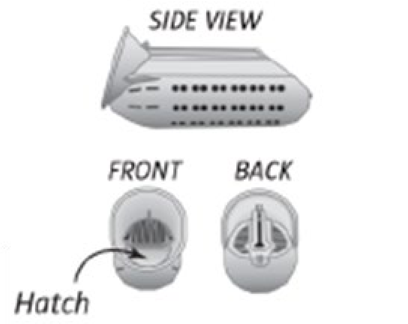
- Underwater Shuttle: Encapsulate the fish at depth – protect enroute to the surface

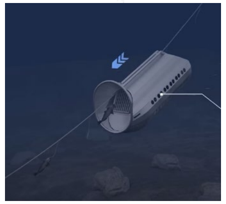
Bycatch Reduction Engineering Program (BREP) NA23NMF4720414

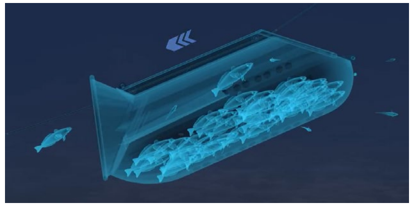
Unprotected catch

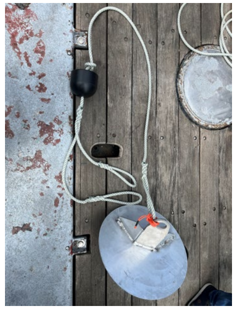


Sago Solutions shuttle



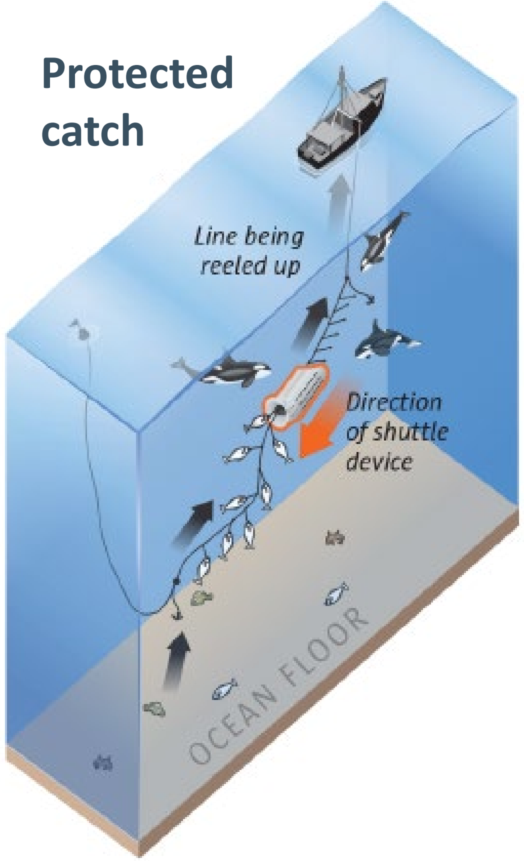






2.6 m x 0.8 m
100 kg empty

Protected catch



Emptying shuttle

Graphics by Mark Nowlin / The Seattle Times. Source materials: Alaska Sealife Center in Seward, NOAA, North Pacific Longline Association, Alaska Department of Fish and Game, Sago Solutions AS. Photos IPHC.

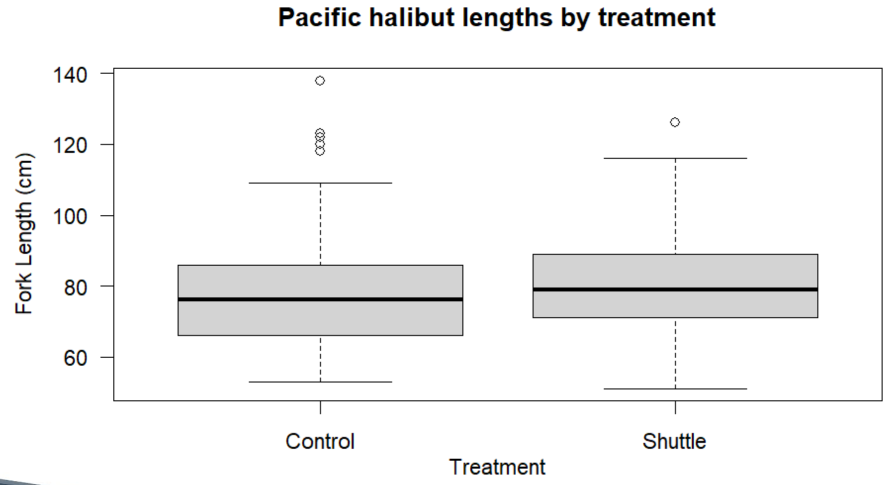
5. Fishing technology

Reducing whale depredation by protecting longline catches

- Preliminary Results: Retention trends in shuttle from analyzed video footage

Common Name	Encountered	Excluded	Entered and Escaped	Entered and Passed Through	Retained
Pacific halibut	**89**	**1 (1.1%)**	**0**	**8 (9.1%)**	**80 (90.9%)**
Sablefish	160	2 (1.3%)	45 (28.5%)	30 (19.0%)	83 (52.5%)
Pacific cod	124	3 (2.4%)	13 (10.7%)	6 (5.0%)	102 (84.3%)
Rockfish	16	7 (43.8%)	2 (22.2%)	1 (11.1%)	6 (66.7%)
Skate	18	3 (16.7%)	0	2 (13.3%)	13 (86.7%)

- Preliminary Results: Size of Pacific halibut retained by shuttle



5. Fishing technology

- F/V Oracle conducted two commercial trips in October 2025 in the Bering Sea:
  - One IPHC Field Specialist was deployed to collect biological information
  - Weather / lack of whales resulted in only 4 sets of effort

- This study effectively completed three field tests: pilot testing, testing in the presence of whales, and testing in commercial fishing

Conclusions

- Shuttle can be safely deployed and retrieved by vessels with a picking boom
- Shuttle has good retention in terms of numbers and size of Pacific halibut
- Continued interest from the fleet in this approach

Summary of awarded research grants to IPHC

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 2026
2	Alaska Sea Grant	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)	$60,374	Stock structure	January 2025-January 2027
				Total awarded ($)	**$260,244**		

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https://www.iphc.int/