

## 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

## Research activity priorization

| Research areas | Research activities | Research outcomes | Relevance for stock assessment | Relevance for MSE | Specific analysis input | SA Rank | MSE Rank | Research priorization |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| $\begin{gathered} \text { Migration and } \\ \text { population dynamics } \end{gathered}$ | Population structure | Population structure in the Convention Area | Altered structure of future stock assessments | Improve parametization of the Operating Model | If $4 B$ is found to be functionally isolated, a separate assessment may be constructed for that IPHC Regulatory Area | 2. Biological input | 1. Biological parameterization and validation of movement estimates and recruitment distribution | 2 |
|  | Distribution | 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 | 3. Biological input |  | 2 |
|  | Larval and juvenile connectivity studies | Improved understanding of larval and juvenile distribution | Improve estimates of productivity |  | Will be used to generate potential recruitment covariates and to inform minimum spawning biomass targets by Biological Region | 3. Biological input | 1. Biological <br> parameterization and <br> validation of movement <br> estimates | 2 |
| Reproduction | Histological maturity assessment | Updated maturity schedule | Scale biomass and reference point estimates | Improve simulation of spawning biomass in the Operating Model | Will be included in the stock assessment, replacing the current schedule last updated in 2006 | 1. Biological input | 2. Biological parameterization and validation of recruitment variability and distribution | 1 |
|  | Examination of potential skip spawning | Incidence of skip spawning |  |  | 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 |  |  | 1 |
|  | Fecundity assessment | Fecundity-at-age and -size information |  |  | 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 |  |  | 1 |
|  | Examination of accuracy of <br> current field macroscopic maturity <br> classification | Revised field maturity classification |  |  | Revised time-series of historical (and future) maturity for input to the stock |  |  | 1 |
| Growth | Evaluation of somatic growthvariation as a driver for changes insize-at-age | Identification and application of markers for growth pattern evaluation | Scale stock productivity and reference point estimates | Improve simulation of variability and allow for scenarios investigating climate change | May inform yield-per-recruit and other spatial evaluations of productivity that support mortality limit-setting |  | 3. Biological parameterization and validation for growth projections | 5 |
|  |  | Environmental influences on growth patterns |  |  | May provide covariates for projecting short-term size-at-age. May help to delineate between effects due to fishing and those due to environment, thereby informing appropriate management response |  |  | 5 |
|  |  | Dietary influences on growth patterns and physiological condition |  |  | May provide covariates for projecting short-term size-at-age. May help to deleineate between effects due to fishing and those due to environment, thereby informing appropriate management response |  |  | 5 |
| Mortality and survivalassessment | Discard mortality rate estimate: longline fishery | $\underset{\substack{\text { Experimentally-derived } \\ \text { DMR }}}{ }$ | Improve trends in unobserved mortality | Improve estimates of stock productivity | Will improve estimates of discard mortality, reducing potential bias in stock assessment results and management of mortality limits | 1. Fishery yield | 1. Fishery parameterization | 4 |
|  | Discard mortality rate estimate: recreational fishery |  |  |  | Will improve estimates of discard mortality, reducing potential bias in stock assessment results and management of mortality limits |  |  | 4 |
|  | Best handling and release practices | Guidelines for reducing discard mortality |  |  | May reduce discard mortality, thereby increasing available yield for directed fisheries | 2. Fishery yield |  | 4 |
| Fishing technology | Whale depredation accounting and tools for avoidance | New tools for fishery avoidance/deterence; improved estimation of depredation mortality | Improve mortality accounting | Improve estimates of stock productivity | 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 | 1. Assessment data collection and processing |  | 3 |
|  | Bycatch reduction | Development of methods for reducing bycatch and better estimate mortality | Improve mortality accounting | Improve estimates of stock productivity | 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 | 1. Assessment data collection and processing |  | 3 |

Research activity priorization

| Research areas | Research activities | Research outcomes | Relevance for stock assessment | Relevance for MSE | Specific analysis input | SA Rank | MSE Rank | Research priorization |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Migration and population dynamics | Population structure | Population structure in the Convention Area | Altered structure of future stock assessments | Improve parametization of the Operating Model | If $4 B$ is found to be functionally isolated, a separate assessment may be constructed for that IPHC Regulatory Area | 2. Biological input | 1. Biological parameterization and validation of movement estimates and recruitment distribution | 2 |
|  | Distribution | 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 | 3. Biological input |  | 2 |
|  | Larval and juvenile connectivity studies | Improved understanding of larval and juvenile distribution | Improve estimates of productivity |  | Will be used to generate potential recruitment covariates and to inform minimum spawning biomass targets by Biological Region | 3. Biological input | 1. Biological parameterization and validation of movement estimates | 2 |
| Reproduction | Histological maturity assessment | Updated maturity schedule | Scale biomass and reference point estimates | Improve simulation of spawning biomass in the Operating Model | Will be included in the SA, replacing the current schedule last updated in 2006 | 1. Biological input | 2. Biological parameterization and validation of recruitment variability and distribution | 1 |
|  | Fecundity assessment | Fecundity-at-age and -size information |  |  | Will be used to move from spawning biomass to eggoutput as the metric of reproductive capability in the SA and management reference points |  |  | 1 |
|  | Examination of accuracy of current field macroscopic maturity classification | Revised field maturity classification |  |  | Revised time-series of historical (and future) maturity for input to the SA |  |  | 1 |
|  | Examination of potential skip spawning | Incidence of skip spawning |  |  | 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 SA |  |  | 1 |

international pacific
halibut commissian

## Top research priorities for stock assessment

| SA Rank | Research outcomes | Relevance for stock assessment | Specific analysis input | Research Area | Research activities |
| :---: | :---: | :---: | :---: | :---: | :---: |
| 1. Biological input | Updated maturity schedule | Scale biomass and reference point estimates | Will be included in the stock assessment, replacing the current schedule last updated in 2006 | Reproduction | Histological maturity assessment |
|  | Incidence of skip spawning |  | 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 |
|  | Fecundity-at-age and -size information |  | 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 |  | 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 $4 B$ is found to be functionally isolated, a separate assessment may be constructed for that IPHC Regulatory Area | Migration and population dynamics | 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 |  | Distribution |
|  | Improved understanding of larval and juvenile distribution |  | 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 collection and processing | Sex ratio-at-age | Scale biomass and fishing intensity | Annual sex-ratio at age for the commercial fishery fit by the stock assessment | Reproduction | Sex ratio of current commercial landings |
|  | Historical sex ratio-at-age |  | Annual sex-ratio at age for the commercial fishery fit by the stock assessment |  | 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 survival assessment | Best handling practices: recreational fishery |

International pacific
international pacific
Halibut Commission 100 years 2024

## Top research priorities for MSE

| MSE Rank | Research outcomes | Relevance for MSE | Research Area | Research activities |
| :---: | :---: | :---: | :---: | :---: |
| 1. Biological parameterization and validation of movement estimates | Improved understanding of larval and juvenile distribution | Improve parametization of the Operating Model | Migration and population dynamics | Larval and juvenile connectivity studies |
|  | Stock structure of IPHC Regulatory Area $4 B$ relative to the rest of the Convention Area |  |  | Population structure |
| 2. Biological parameterization and validation of recruitment variability and distribution | 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 |  | 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 |
| 3. Biological parameterization and validation for growth projections | Identification and application of markers for growth pattern evaluation | 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 |
|  | Environmental influences on growth patterns |  |  |  |
|  | 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 |

international pacific
Halibut Commission
100 years 2024

## Key research outputs informing management



## 1. Migration and Population Dynamics



- Substrate information: usSeabed database.
- B.C. substrate layer $100-\mathrm{m}$ resolution- provided by Dr. Dana Haggarty (DFO).
- Next step: bathymetry layer.



## 1. Migration and Population Dynamics

## 5-Yr Research Plan (2017-2021)

PIRM 2022-2026
Multiple life-
stage
connectivity
Bering Sea
Gulf of Alaska



## 1. Migration and Population Dynamics

## Population Genomics

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


NPRB Project 2110 (2022-2024)

- Low-coverage whole-genome resequencing (IcWGR)
- Allows for screening genomic variation at very high resolution
- Establish Genetic Baseline
- Identify potential local and/or environmental adaptations.
- 570 individuals ( $\sim 50$ /collection)
- 3 sequencing runs - Illumina NovaSeq S4
- Mean coverage - 3.5x
- 10,230,908 autosomal SNPs
- $4,725,899$ (minor allele frequency $\geq 0.05$ )


## 1. Migration and Population Dynamics

## Pacific Halibut Reference Genome

- Version 2 - March 2022 (NCBI RefSeq: GCF 022539355.2)
- 602.2 Mbp (24 chromosomes)
- Fully Annotated (27,944 genes)
- Provide genetic basis for life-history traits (e.g., growth, maturity, migratory behavior, etc.).
- Large(12 Mbp) sex-associated region on Chr09

| Received: 10 December 2021 | Revised: 22 April 2022 | Accepted: 11 May 2022 |
| :--- | :--- | :--- |

DOI: 10.1111/1755-0998.13641
RESOURCE ARTICLE
MOLECULAR ECOLOGY

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 ${ }^{3}{ }^{\circ}$ | Cédric Cabau ${ }^{4}$ © | Christophe Klopp ${ }^{3}$ © | Céline Roques ${ }^{5}$ | Carole lampietro ${ }^{5}$ © | Jérôme Lluch ${ }^{5}$ | Cécile Donnadieu ${ }^{5}$ © | Hugues Parrinello ${ }^{6}$ © | Daniel P. Drinan ${ }^{2}$ | Lorenz Hauser ${ }^{2}$ | Yann Guiguen ${ }^{\text {© }}$ | Josep V. Planas ${ }^{1}$ ©

## INRAC <br> science for people, life \& earth

W
UNIVERSITY of WASHINGTON



## 1. Migration and Population Dynamics

## Bioinformatic Workflow

Figure 1. Proposed bioinformatic workflow for the interrogation of low-coverage whole-genome sequence data. This diagram tracks the flow of data through the main stages of this project:
(A) raw sequence read processing,
(B) alignment summaries,
(C) analysis of population structure,
(D) genomic analyses,
(E) quality control steps to be taken.


## 1. Migration and Population Dynamics

## Bioinformatic Workflow

Figure 1. Proposed bioinformatic workflow for the interrogation of low-coverage whole-genome sequence data. This diagram tracks the flow of data through the main stages of this project:
(A) raw sequence read processing,
(B) alignment summaries,
(C) analysis of population structure,
(D) genomic analyses,
(E) quality control steps to be taken.

## Additions since SRBO22

SRB022-Rec. 11 (c) - summary measures of genetic diversity SRB022-Rec. 20 (b) - population assignment testing


## 1. Migration and Population Dynamics

SRB022-Rec. 11 (para. 37) The SRB RECOMMENDED that the Secretariat include other genome-wide summary measures of diversity. Measures could include (a) measures of genome size, (b) percentages of genome as singleton and duplicated loci, (c) other summary measures of diversity including (i) number of loci with minor allele frequency (MAF)>0.01, (ii) number of loci with MAF>0.05, (iii) a measure of deviation of observed and expected heterozygosity (Fis), (iv) observed heterozygosity (Ho) and expected heterozygosity (He).

Table 1. Summary of diversity measures estimated from low coverage whole genome sequence data for sample collections of Pacific halibut. The table includes sample sizes ( N ), number of loci with minor allele frequency (MAF)>0.01, number of loci with MAF>0.05.

| Area | Collection Year | $\mathbf{N}$ | MAF $>\mathbf{0 . 0 1}$ | MAF $>\mathbf{0 . 0 5}$ | $\boldsymbol{F}_{\text {IS }}$ | $\boldsymbol{H}_{\boldsymbol{O}}$ | $\boldsymbol{H}_{\boldsymbol{E}}$ |
| ---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| British Columbia | 1999 | 49 | $8,958,267$ | $4,890,386$ | 0.109 | 0.154 | 0.158 |
|  | 2004 | 43 | $8,756,199$ | $4,995,125$ | 0.115 | 0.156 | 0.163 |
|  | 2007 | 50 | $8,939,078$ | $4,900,656$ | 0.120 | 0.154 | 0.157 |
|  | all years | 142 | $9,256,496$ | $4,762,476$ | 0.023 | 0.155 | 0.161 |
| Central Gulf of | 1999 | 50 | $9,131,547$ | $4,993,279$ | 0.049 | 0.158 | 0.171 |
| Alaska | 2004 | 50 | $9,065,567$ | $5,163,204$ | 0.029 | 0.162 | 0.189 |
|  | 2007 | 50 | $9,052,210$ | $5,052,609$ | 0.058 | 0.159 | 0.176 |
|  | 2018 | 49 | $8,627,118$ | $4,893,881$ | 0.172 | 0.153 | 0.153 |
|  | all years | 199 | $9,561,613$ | $4,862,986$ | -0.032 | 0.158 | 0.176 |
| Bering Sea | 2004 | 43 | $8,886,235$ | $5,007,451$ | 0.094 | 0.156 | 0.164 |
|  | 2007 | 50 | $9,057,451$ | $4,930,166$ | 0.089 | 0.155 | 0.162 |
|  | all years | 93 | $9,214,470$ | $4,851,360$ | 0.030 | 0.156 | 0.164 |
| Central Aleutian | 2007 | 37 | $8,464,803$ | $4,983,042$ | 0.150 | 0.154 | 0.157 |
| Islands | 2020 | 49 | $8,823,846$ | $4,904,749$ | 0.129 | 0.154 | 0.158 |
|  | all years | 86 | $8,921,876$ | $4,799,261$ | 0.066 | 0.154 | 0.159 |
| Western Aleutian | 2020 | 50 | $8,690,974$ | $4,893,669$ | 0.151 | 0.153 | 0.157 |
| Islands | all years | 50 | $8,690,974$ | $4,893,669$ | 0.151 | 0.153 | 0.157 |

## 1. Migration and Population Dynamics

PCA based analyses to address components of:
SRB022-Rec. 13 (para. 39): SNP outlier detection \& testing
SRB022-Rec. 14 (para. 40): Establish statistical significance of outlier loci

SRB022-Rec. 20 (para. 47): Unsupervised clustering


## 1. Migration and Population Dynamics

SRB022-Rec. 20 (para. 47) The SRB RECOMMENDED:
a) that the Secretariat move forward to stock discrimination to satisfy the Secretariat objective of using genetic data to define spatial structuring including unsupervised clustering methods (e.g. K-means, Structure, etc.) as well as PCA-based clustering (e.g. Discriminant Analysis of Principle Component) clustering;
b) using assignment testing and mixture analyses such as leave-one-out cross validation simulations to assess the potential accuracy of mixed stock analysis (MSA).

- PCA - 4,725,899 autosomal SNPs
- Retained top 3 PCs - Cattell's Rule

- K-means clustering in R
- tested K=1:20
- compared fit for each K using total within-cluster sum of squares and Bayesian Information Criterion (BIC)




## 1. Migration and Population Dynamics

SRB022-Rec. 13 (para. 39) NOTING that different outlier tests are based on different assumptions and statistical approaches, the SRB RECOMMENDED that the Secretariat implement more than one method. Selection of specific markers would appropriately be based on concordant designation of highly population discriminatory loci identify across methods. The Secretariat is likely to have greater confidence in assignment of 'outliers' based on principles of concordance using multiple and semi-independent software packages and statistical approaches.
SRB022-Rec. 14 (para. 40) The SRB RECOMMENDED that after statistical significance of SNP loci has been established, the Secretariat use gene set enrichment analyses to establish functional annotations for genes associated with SNPs.

- PCA based selection scan
- pcadapt test statistic implemented in PCAngsd (top 3 PCs)
- robust Mahalnobis distance ( $\chi^{2}$ distribution with K (3) degrees of freedom)
- false discovery rate level 0.001 (Benjamini-Hochberg procedure)
- 16,272 candidate SNPs



## 1. Migration and Population Dynamics

## Progress Update

Current Efforts (SRBO22-Rec. 13 \& 14):

- Establish statistical significance for the $F_{S T}$ based outlier scans
Next (SRB022-Rec. 20 a):
- Estimate individual admixture proportions NGSadmix
A) Sequence Read Processing


Map to Reference bwa-mem
 samtools $\downarrow$

 | Remove Duplic |
| :---: |
| picard | picard


B) Alignment Summary Statistics Sequencing Depth
mosdepth
 Sumpar Summary samtools


## 2. Reproduction

5-Yr Research Plan (2017-2021)

| 2017-2018 |
| :---: |
| Field sample |
| collection |
| (central |
| GOA) |

30\%/ month q $>90 \mathrm{~cm} \mathrm{FL}$

2017-2022 Commercial landings


## 2. Reproduction

## Microscopic maturity staging: histological oocyte stages



## 2. Reproduction FISS: ovarian sampling for histology-based maturity



## 2. Reproduction

## Maturity sample collection in FISS 2022/2023

Number of samples

| Biological <br> Region | $\mathbf{2 0 2 2}$ | $\mathbf{2 0 2 3}$ <br> (est.) | Total |
| :---: | :---: | :---: | :---: |
| $\mathbf{2}$ | 437 | 398 | 835 |
| $\mathbf{3}$ | 348 | 705 | 1,053 |
| $\mathbf{4}$ | 180 | - | 180 |
| $\mathbf{4 B}$ | 51 | - | 51 |
| Total | 1,016 | 1,103 | 2,119 |



## 2. Reproduction

## Generating Maturity Ogives

- Logistic curve
- GLM with binomial distribution (mature or immature) and logit link function
- Length and age at $50 \%$ maturity calculated using dose.p function
- Proportion of mature individuals (p) set to 0.5
- Length and age will be examined coastwide and among IPHC biological regions based on data available
- MARVLS R code repository: https://github.com/MARVLS/Fish-GonadStaging/tree/main/analyses


## 2. Reproduction

## Fecundity sample collection in FISS 2023

## Biological Region 3

Total $=457$
Mature (field) $=299$
Ovary Weight $($ mature $)=255$


## 2. Reproduction

Fecundity: autodiametric method




Target:
$\mathrm{n}=\mathbf{2 5 0}-\mathbf{3 0 0}$ fish

## 2. Reproduction

Fecundity: autodiametric method

Potential Annual
Fecundity
(PAF)
(Total \# oocytes)

## 3. Mortality and Survival Assessment


international pacific
halibut Commission 100 years 2024
3. Mortality and Survival Assessment Characterization of discards in the directed longline fishery

3. Mortality and Survival Assessment

Characterization of discards in the directed longline fishery

- Hook Release Methods: Viabilities and Injuries


Min. DMR = 4.2\% (Loher et al. 2022)


Sustained Injury

Dykstra et al. (2023) Submitted

## 3. Mortality and Survival Assessment

## Characterization of discards in the directed longline fishery

- Stress Indicators in the Blood



## 4. Fishing technology <br> Reducing whale depredation by protecting longline catches

## Phase 1: International Workshop - 2022

Explore latest ideas in terminal gear modification and catch protection - an area previously identified as having the highest likelihood of 'breaking the reward cycle' in depredation.

- Refine attributes discussed into two viable approaches:
- Enclosing shuttles.
- Branchlines with shrouds.


## Phase 2: Field testing of catch protection devices - 2023

Tested selected devices for:

- Deployment / Retrieval logistics.
- Optimal configurations (weighting, attachments).
- Basic performance (species/sizes).


Shuttle


Shroud

## 4. Fishing technology <br> Reducing whale depredation by protecting longline catches

## Phase 2: Shuttle field testing



Preliminary conclusions

- Safely operational on a small vessel.
- Moderate learning curve to attach in-line during hauling event.
- Similar catch rates to standard gear.
- Groundline, gangion, hooks need refinement to minimize damage to fish.


## 4. Fishing technology <br> Reducing whale depredation by protecting longline catches

## Phase 2: Shroud field testing



## Preliminary conclusions

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


# 4. Fishing technology <br> <br> Reducing whale depredation by protecting longline catches 

 <br> <br> Reducing whale depredation by protecting longline catches}

## Phase 3a: Testing in presence of Orcas - 2024

Recently secured funding from NOAA BREP 2023 NA23NMF4720414

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


## Phase 3b: Testing in presence of Sperm whales

Pending funding

- Pre-proposal for funding submitted to Saltonstall-Kennedy - awaiting response.


## Summary of active research grants

| Project <br> \# | Grant agency | Project name | PI | Partners | IPHC <br> Budget (\$US) | Management implications | Grant period |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 1 | Bycatch <br> Reduction <br> Engineering <br> Program- <br> NOAA | Gear-based approaches to catch protection as a means for minimizing whale depredation in longline fisheries (NOAA Award Number NA21NMF4720534) | IPHC | Deep Sea <br> Fishermen's Union, Alaska Fisheries Science CenterNOAA, industry representatives | \$99,700 | Mortality estimations | 1 November 2021-31 <br> October 2023 |
| 2 | North Pacific <br> Research <br> Board | Pacific halibut population genomics (NPRB Award No. 2110) | IPHC | Alaska Fisheries Science CenterNOAA, Juneau, Seattle | \$193,685 | Stock structure | 1 December 2021-31 <br> January 2024 |
| Total awarded (\$) |  |  |  |  | \$293,385 |  |  |

## INTERNATIONAL PACIFIC



HALIBUT COMMISSION

