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Report on Current and Future Biological and Ecosystem Science Research Activities

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PURPOSE

To provide the Scientific Review Board with a description of progress towards research activities described in the IPHC's five-year Program of Integrated Research and Monitoring (2022-2026).

BACKGROUND

The primary biological and ecological research activities at the IPHC that follow Commission objectives are identified and described in the IPHC Five-Year Program of Integrated Research and Monitoring (2022-2026). These activities are integrated with stock assessment (SA) and the management strategy evaluation (MSE) processes (Appendix I) and are summarized in five main areas, as follows:

1) Migration and Population Dynamics. Studies are aimed at improving current knowledge of Pacific halibut migration and population dynamics throughout all life stages in order to achieve a complete understanding of stock structure and distribution across the entire distribution range of Pacific halibut in the North Pacific Ocean and the biotic and abiotic factors that influence it.
2) Reproduction. Studies are aimed at providing information on the sex ratio of the commercial catch and to improve current estimates of maturity and fecundity.
3) Growth. Studies are aimed at describing the role of factors responsible for the observed changes in size-at-age and at evaluating growth and physiological condition in Pacific halibut.
4) Mortality and Survival Assessment. Studies are aimed at providing updated estimates of discard mortality rates in the guided recreational fisheries and at evaluating methods for reducing mortality of Pacific halibut.
5) Fishing Technology. Studies are aimed at developing methods that involve modifications of fishing gear with the purpose of reducing Pacific halibut mortality due to depredation and bycatch.

A ranked list of biological uncertainties and parameters for SA (Appendix II) and the MSE process (Appendix III) and their links to research activities and outcomes derived from the five-year research plan are provided.

SRB RECOMMENDATIONS AND REQUESTS

The SRB issued several recommendations and requests in their report of SRB026 (IPHC-2025-SRB026-R) in relation to presentation IPHC-2025-SRB026-06:

SRB026–Rec.01 (para. 16). The SRB ***RECOMMENDED*** *that questions about stock structure should be deprioritized in future research plans, as this question has now been answered quite robustly.*

The IPHC Secretariat is currently preparing a manuscript intended for publication in a leading peer-review journal describing the results on genomic stock structure.

SRB026–Rec.02 (para. 18). The SRB ***RECOMMENDED*** *that the 2025 stock assessment incorporate the new maturity ogives, however, the incorporation of new fecundity information should be delayed until the next full stock assessment when more robust data and analysis of fecundity at age/weight information are available:*

The IPHC Secretariat has provided the new maturity ogives to be incorporated into the 2025 stock assessment and is initiating efforts to investigate fecundity.

SRB026–Rec.03 (para. 19). The SRB ***RECOMMENDED*** *that the Secretariat incorporate potential environmental causes (e.g. effects of temperature) of changing maturity ogives or other changing biological parameters in the next 5YPIRM.*

The IPHC Secretariat has incorporated potential environmental causes of changing biological parameters in the current draft of IPHC-2026-5YPIRM.

UPDATE ON PROGRESS ON THE MAIN RESEARCH ACTIVITIES

1. Migration and Population Dynamics.

   The IPHC Secretariat is currently focusing on studies that incorporate genomics approaches in order to produce useful information on population structure, distribution and connectivity of Pacific halibut. The relevance of research outcomes from these activities for stock assessment (SA) resides (1) in the introduction of possible changes in the structure of future stock assessments, as separate assessments may be constructed if functionally isolated components of the population are found (e.g. IPHC Regulatory Area 4B), and (2) in the improvement of productivity estimates, as this information may be used to define management targets for minimum spawning biomass by Biological Region. These research outcomes provide the second and third top ranked biological inputs into SA (Appendix II). Furthermore, the relevance of these research outcomes for the MSE process is in biological parameterization and validation of movement estimates, on one hand, and of recruitment distribution, on the other hand (Appendix III).

   1.1. Population genomics. The primary objective of these studies is to investigate the genetic structure of the Pacific halibut population and to conduct genetic analyses to inform on Pacific halibut population dynamics and distribution within the Convention Area

   Details on sample collection, sequencing, bioinformatic processing and proposed analyses utilizing low-coverage whole genome sequencing (lcWGR) to investigate Pacific halibut population structure were provided in documents IPHC-2021-SRB018-08, IPHC-2022-SRB021-09, IPHC-2023-SRB022-09, IPHC-2024-SRB024-09 and IPHC-2025-SRB026-06.

   Our results from the final genomics analyses using the complete set of baseline samples confirm our initial results regarding our inability to confidently identify the presence of discrete genetic groups using unsupervised clustering analyses. Furthermore, the lack of population structure limits our ability to assign samples back to the location from which they were sampled from. In summary, our results support the notion that a single genetic group of Pacific halibut is present in IPHC Convention Waters. We are currently preparing a manuscript for publication in a leading peer-reviewed journal describing these results.

1.2. Genomics-based method for estimating age of Pacific halibut. The primary objective of this project is to develop a genetic method for aging Pacific halibut using fin tissue, a sample that can be easily collected from either live or dead individuals. This method is based on the identification of DNA methylation patterns in fin tissue that are associated with age through the development of an age estimation model (i.e., an epigenetic clock) for Pacific halibut. The first epigenetic clock was developed for humans in 2013 (Horvath, 2013), and it predicted age with great accuracy (*r* = 0.96) and with a mean aging error (MAE) of 3.6 years. Subsequently, epigenetic clocks have been developed for several fish species that demonstrated improved accuracy (*r* between 0.84 and 0.99) and lower average MAE (0.87 years, or 3.5% of the total lifespan of the species examined) (reviewed in Piferrer and Anastasiadi, 2023).

Patterns of DNA methylation (i.e. a natural process of regulation of gene expression that consists in the covalent modification of the nucleobase cytosine) in Pacific halibut will be investigated by performing genome-wide DNA methylation at single base-pair resolution using reduced representation bisulfite sequencing (RRBS) by leveraging the high-quality genome assembly available for Pacific halibut (Jasonowicz et al. 2022). This is an efficient and cost-efficient method to identify methylation patterns (i.e., CpG sites) in DNA because it targets bisulfite sequencing to a well-defined set of genomic regions with high CpG density that can be sequenced at high read depth. Age-associated DNA methylation patterns will be modelled to generate an epigenetic age predictor (i.e., epigenetic clock) for Pacific halibut constructed using elastic net penalized regression models that select a group of CpG sites that have a monotonically increasing relationship with age in the selected training data set. By implementing these linear models that select and weight age-correlated CpG sites, chronological age of Pacific halibut will be estimated based on the percentage methylation at these key CpG sites in fin tissue samples.

1.2.1. Methods.

1.2.1.1. Genetic samples. For this project, we have selected fin clips from 250 individuals collected in the FISS seasons from 2021 to 2024. These genetic samples correspond to fish with known ages (read twice by the traditional break and bake aging method) between 6 to 30 years and include 10 individual samples (5 males and 5 females) for each of the 25 years of the sample collection.

1.2.1.2. Reduced representation bisulfite sequencing: library preparation and sequencing. High-quality genomic DNA will be extracted and purified using the DNeasy Blood and Tissue Kit (Qiagen) on a total of 250 individual samples (described above). Genomic DNA will be used to construct individual RRBS libraries using the Premium RRBS Kit V2 (Diagenode) following the manufacturer's specifications. In brief, RRBS libraries will be prepared by digesting genomic DNA with the methylation sensitive restriction enzyme *MspI*, and the resulting DNA fragments will be treated with bisulfite to convert non-methylated cytosines into uracils through chemical deamination, leaving methylated cytosines unaffected. A subsequent PCR amplification step will convert uracils into thymines. Constructed RRBS libraries will be first assessed for concentration and fragment size distribution by Bioanalyzer (Agilent) and, subsequently, libraries will be pooled and sequenced on an Illumina NovaSeq platform with 50 bp paired-end for 100 cycles at a commercial sequencing provider (Novagene). Two pools of 125 samples (individual libraries) each will be run on two NovaSeq S4 lanes with an estimated output of 2.5 bilion reads generated per lane to achieve an average sequencing depth of 20x per sample (i.e., 20x coverage). This assumes 1.4 million restriction sites based on an in silico digestion of the Pacific halibut genome using *MspI* (preliminary data) and a 25% phiX spike in and a 2% of the reads corresponding to the unmethylated E. coli control used to determine bisulfite conversion efficiency (Illumina).

1.2.1.3. Sequencing data analysis and methylation calling. Prior to analysis, raw sequence reads will be quality checked using *FastQC* (Andrews et al., 2015) to ensure consistent quality across sequencing runs and to identify samples that may not be suitable for further analysis. Specifically, the raw base quality scores for each sample will be used to identify samples that were poorly sequenced and should be omitted from downstream analyses. Additionally, the presence of other sequencing artifacts may be detected at this step as well. The raw sequence reads will then be processed to remove Illumina adapter sequences and low quality reads using *Trim Galore!* (https://github.com/FelixKrueger/TrimGalore), a trimming tool designed specifically for RRBS data. Trimmed sequence reads will be aligned to a bisulfite converted index of the Pacific halibut reference genome (RefSeq assembly accession: GCF_022539355.2) excluding the sex chromosome (Chr09; Jasonowicz et al., 2022) to discard possible sex-associated methylation signals, using *bismark* (Krueger and Andrews, 2011) allowing for one mismatch. Having a high-quality reference genome available for Pacific halibut is a major benefit to this study as constructing one is costly and time consuming. Furthermore, the Pacific halibut genome has been annotated so that the locations and identity of genes are known, enabling the functional significance of methylated CpG sites present in protein coding gene regions to be inferred. The resulting sequence alignment map (SAM) files will be coordinate sorted and converted to the binary alignment map format (BAM) using *samtools* (Li et al., 2009). The methylation module in *BS-Seeker2* (Guo et al., 2013) with default settings will be used for methylation calling. For all identified CpG sites, percentage methylation will be calculated as the percentage of the number of methylated reads over the number of total reads with a 95% confidence interval. Typically, RRBS produces in the order of hundreds of thousands of CpGs (Anastasiadi and Piferrer, 2023). CpG sites with at least 20x coverage and with methylation levels in > 90% of the samples will be used for downstream analyses.

1.2.1.4. Development of an age predicting model for Pacific halibut. The sequenced genetic samples will be randomly assigned to a training (200 samples) or a testing data set (50 samples) following an 80/20 data split. Sample assignments will be conducted using *caret* to maintain equal sex ratios in each data set. The training set will be used to fit the model and the testing set will be an independent set of data that will be used to evaluate the model fit.

The relationship between otolith-derived age and percent methylation across age-correlated CpG sites in the training data set will be characterized by performing elastic net penalized regression analysis using the R package glmnet (Friedman et al., 2010) set to a 10-fold cross validation with an α-parameter of 0.5 and automatically selecting the optimal penalty parameter (λ). We expect that the age-predicting model will retain in the order of a few hundred CpG sites with a low λ value. The performance of the model in the training and testing data set will be evaluated using Pearson correlations (i.e. measuring the degree of correlation between chronological and estimated age) as a measure of accuracy, MAE as a measure of precision (i.e., how well the model fits the actual data), and relative error rates (Piferrer and Anastasiadi, 2023). Comparison of MAE between the training and testing data sets will inform on the potential overfit of the model constructed using the training data set. The linear relationship between predicted and chronological (i.e., otolith-derived) age will be visually represented and additional patterns in the data will be visualized using principal component analysis (PCA).

1.2.1.5. Identification of the genomic location of age markers. The Pacific halibut genome annotation (NCBI link) will also be used to determine if any functional genes are located within 400 bp of model selected CpG sites. This will inform whether clock CpG sites are proximal to specific annotated genes and whether methylation at those particular sites could have functional significance.

1.2.2. Results.

All 250 aged fin clips have been processed for DNA extraction. The obtained genomic DNA has been quantified, and all samples yielded enough genomic DNA to proceed with individual library construction. Library preparation for the first set of 84 samples has been conducted and two library pools have been sent out for sequencing. Sequencing data will be processed as detailed in 1.2.1.3.

2. Reproduction.

Research activities in this Research Area aim at providing information on key biological processes related to reproduction in Pacific halibut (maturity and fecundity) and to provide sex ratio information of Pacific halibut commercial landings. The relevance of research outcomes from these activities for stock assessment (SA) is in the scaling of Pacific halibut biomass and in the estimation of reference points and fishing intensity. These research outputs will result in a revision of current maturity schedules and will be included as inputs into the SA (Appendix II), and represent some of the most important biological inputs for stock assessment (please see document IPHC-2021-SRB018-06). The relevance of these research outcomes for the management and strategy evaluation (MSE) process is in the improvement of the simulation of spawning biomass in the Operating Model (Appendix III).

2.1. Sex ratio of the commercial landings. The IPHC Secretariat is finalizing the processing of genetic samples from the 2024 aged commercial landings.

2.2. Reproductive assessment. Recent sensitivity analyses have shown the importance of changes in spawning output due to changes in maturity schedules and/or skip spawning and fecundity for SA (Stewart and Hicks, 2018). Information on these key reproductive parameters provides direct input to the SA. For example, information on fecundity-at-age and -size could be used to replace spawning biomass with egg output as the metric of reproductive capability in the SA and management reference points. This information highlights the need for a better understanding of factors influencing reproductive biology and success of Pacific halibut. To fill existing knowledge gaps related to the reproductive biology of female Pacific halibut, research efforts are devoted to characterizing female reproduction in this species. Specific objectives of current studies include: 1) update of maturity schedules based on histological-based data; and 2) calibration of historical visual maturity schedules using histological-based data.

2.2.1. Update of maturity schedules based on histological-based data. The IPHC Secretariat provided an update on temporal patterns in maturity ogives by Biological Region from 2022 to 2024, and a revised coastwide maturity ogive in IPHC-2025-SRB026-06. Furthermore, the IPHC Secretariat developed a calibration between histological and visual maturity curves from the 2022-2024 data and generated calibrated maturity ogives based on FISS visual maturity data from 2002 until 2024. At present, the IPHC Secretariat is preparing a manuscript for publication in a peer-reviewed journal describing the temporal and spatial changes in histology-derived maturity ogives and ovarian developmental stages.

2.2.2. Collection of samples for fecundity estimations. The IPHC Secretariat has initiated studies that are aimed at improving our understanding of Pacific halibut fecundity. This will allow us to estimate fecundity-at-size and -age and could be used to replace spawning biomass with egg output as the metric for reproductive capability in stock assessment and management reference points. Fecundity determinations will be conducted using the auto-diametric method (Thorsen and Kjesbu 2001; Witthames et al., 2009) and IPHC Secretariat staff received training on this method by experts in the field (NOAA Fisheries, Northeast Fisheries Science Center, Wood Hole, MA) in May 2023. Ovarian samples for the development and application of the auto-diametric method to estimate fecundity in female Pacific halibut were collected during the IPHC's FISS in 2023, 2024 and 2025. In 2023, sampling was conducted only in Biological Region 3, with a total of 456 fecundity samples collected. In 2024, sampling was conducted in Biological Regions 2 and 4, with 149 and 359 fecundity samples collected, respectively. In the Fall of 2024, 273 additional fecundity samples targeting large females (85-200+ cm in fork length) were collected in Biological Region 2. In 2025, in addition to samples collected in the FISS, fecundity samples were again collected in Biological Region 2 in a special project targeting large females. This comprehensive collection of ovarian samples will be used initially for the development of the auto-diametric method, followed by actual fecundity estimations by age and by size (length and weight).

3. Growth.

   Research activities conducted in this Research Area aim at providing information on somatic growth processes driving size-at-age in Pacific halibut. The relevance of research outcomes from these activities for stock assessment (SA) resides, first, in their ability to inform yield-per-recruit and other spatial evaluations for productivity that support mortality limit-setting, and, second, in that they may provide covariates for projecting short-term size-at-age and may help delineate between fishery and environmental effects, thereby informing appropriate management responses (Appendix II). The relevance of these research outcomes for the management and strategy evaluation (MSE) process is in the improvement of the simulation of variability and to allow for scenarios investigating climate change (Appendix III).

   The IPHC Secretariat has conducted studies aimed at elucidating the drivers of somatic growth leading to the decline in SAA by investigating the physiological mechanisms that contribute to growth changes in the Pacific halibut. The two main objectives of these studies have been: 1) the identification and validation of physiological markers for somatic growth; and 2) the application of molecular growth markers for evaluating growth patterns in the Pacific halibut population.

   A manuscript describing the results of these studies has been submitted for publication to a peer-reviewed journal (Planas et al., in review).

4. Mortality and Survival Assessment.

   Information on all Pacific halibut removals is integrated by the IPHC Secretariat, providing annual estimates of total mortality from all sources for its stock assessment. Bycatch and wastage of Pacific halibut, as defined by the incidental catch of fish in non-target fisheries and by the mortality that occurs in the directed fishery (i.e. fish discarded for sublegal size or regulatory reasons), respectively, represent important sources of mortality that can result in significant reductions in exploitable yield in the directed fishery. Given that the incidental mortality from the commercial Pacific halibut fisheries and bycatch fisheries is included as part of the total removals that are accounted for in stock assessment, changes in the estimates of incidental mortality will influence the output of the stock assessment and, consequently, the catch levels of the directed fishery. Research activities conducted in this Research Area aim at providing information on discard mortality rates and producing guidelines for reducing discard mortality in Pacific halibut in the longline and recreational fisheries. The relevance of research outcomes from these activities for stock assessment (SA) resides in their ability to improve trends in unobserved mortality to improve estimates of stock productivity and represent the most important inputs in fishery yield for stock assessment (Appendix II). The relevance of these research outcomes for the management and strategy evaluation (MSE) process is in fishery parametrization (Appendix III).

   4.1. Estimation of discard mortality rates in the charter recreational sector. Results from a recently completed study investigating discard mortality rates and characteristics of fish captured and released using guided recreational fishery practices are currently being prepared for publication in a peer-reviewed journal.

5. Fishing technology.

The IPHC Secretariat has determined that research to provide the Pacific halibut fishery with tools to reduce whale depredation is considered a high priority (Appendix I). This research is now contemplated as one of the research areas of high priority within the 5-year Program of Integrated Research and Monitoring (2022-2026). Towards this goal, the IPHC secretariat has been investigating gear-based approaches to catch protection as a means for minimizing whale depredation in the Pacific halibut and other longline fisheries with funding from NOAA's Bycatch Research and Engineering Program (BREP) (NOAA Awards NA21NMF4720534 and NA23NMF4720414; Appendix IV). The results and outcomes of the initial pilot phase of this project were reported in the documentation provided for the previous SRB meetings: IPHC-2022-SRB020-08 and IPHC-2024-SRB024-09.

The second phase of this project focused on further refinement and performance characterization of the shuttle device in the presence of toothed whales in IPHC Regulatory Area 4A. Field operations occurred from 21-28 May 2025 aboard the F/V Oracle (Figure 1). Eighteen sets were successfully completed, generating 15 sets of shuttle and control catch comparison data along with close to 80 hours of underwater footage combined (control, shuttle exterior, shuttle interior). Depredating orcas were present at 6 of the paired sets. Data sets are currently being imported into IPHC databases or extracted from the video, and further field trials during a quota trip are in planning stages.

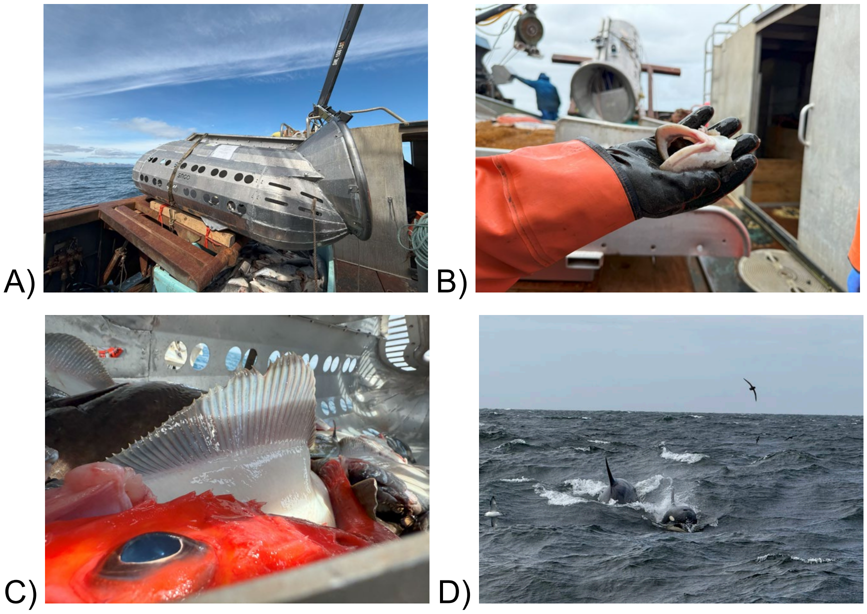

Figure 1. *A) Shuttle device in transport. B) Typical evidence (lips only) of depredation. C) Catch entrained within the shuttle. D). Killer whales rapidly approaching the hauling site.*

RECOMMENDATION/S

That the SRB:

a) **NOTE** paper IPHC-2025-SRB027-06 which provides a response to Recommendations and Requests from SRB026, and a report on current biological research activities contemplated within the IPHC's five-year Program of Integrated Research and Monitoring (2022-26).

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APPENDIX I

Integration of biological research, stock assessment (SA) and management strategy evaluation (MSE): rationale for biological research prioritization

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 4B 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 stock assessment, replacing the current schedule last updated in 2006	1. Biological input		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 current field macroscopic maturity classification	Revised field maturity classification			Revised time-series of historical (and future) maturity for input to the stock assessment			1
Growth	Evaluation of somatic growth variation as a driver for changes in size-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 survival assessment	Discard mortality rate estimate: longline fishery	Experimentally-derived 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

APPENDIX II

List of ranked biological uncertainties and parameters for stock assessment (SA) and their links to biological research areas and research activities

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 4B is found to be functionally isolated, a separate assessment may be constructed for that IPHC Regulatory Area	Genetics and Genomics	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	Migration	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	Mortality and survival assessment	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	Mortality and survival assessment	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

APPENDIX III

List of ranked biological uncertainties and parameters for management strategy evaluation (MSE) and their links to biological research areas and research activities

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	Larval and juvenile connectivity studies
	Stock structure of IPHC Regulatory Area 4B relative to the rest of the Convention Area		Genetics and Genomics	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

APPENDIX IV

Summary of current external research grants

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 (NA23NMF4720414)	IPHC	NOAA Fisheries - Alaska Fisheries Science Center (Seattle)	$199,870	Mortality estimations due to whale depredation	November 2023 – April 2026
2	**Alaska Sea Grant (pending award)**	Development of a non-lethal genetic-based method for aging Pacific halibut (R/2024-05)	IPHC, Alaska Pacific Univ. (APU)	Alaska Fisheries Science Center-NOAA (Juneau)	$60,374	Stock structure	December 2024-December 2026
Total awarded ($)					**$260,244**		