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 the finalization of IPHC's five-year Biological and Ecosystem Science Research Plan (2017-21) and the start of the IPHC's five-year Program of Integrated Research and Monitoring (2022-2026).

BACKGROUND

The primary biological and ecological research activities at IPHC that follow Commission objectives are identified and described in the IPHC Five-Year Biological and Ecosystem Science Research Plan (2017-21). These activities are integrated with stock assessment and the management strategy evaluation processes (Appendix I) and are summarized in five main areas, as follows:

1) Migration and Distribution. Studies are aimed at further understanding reproductive migration and identification of spawning times and locations as well as larval and juvenile dispersal.
2) Reproduction. Studies are aimed at providing information on the sex ratio of the commercial catch and to improve current estimates of maturity.
3) Growth and Physiological Condition. Studies are aimed at describing the role of some of the factors responsible for the observed changes in size-at-age and to provide tools for measuring growth and physiological condition in Pacific halibut.
4) Discard Mortality Rates (DMRs) and Survival. Studies are aimed at providing updated estimates of DMRs in both the longline and the trawl fisheries.
5) Genetics and Genomics. Studies are aimed at describing the genetic structure of the Pacific halibut population and at providing the means to investigate rapid adaptive changes in response to fishery-dependent and fishery-independent influences.

A ranked list of biological uncertainties and parameters for stock assessment (Appendix II) and the management strategy evaluation 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 the following recommendations and requests in their report of SRB019 (IPHC-2021-SRB019-R):

*Recommendation 1 (*SRB019–Rec.09 (para. 43))

*"The SRB **RECOMMENDED** that the IPHC Secretariat consider the value of other opportunistically collected samples that would facilitate further downstream analyses in a cost effective manner."*

The IPHC Secretariat is maximizing opportunities for sample collection from fish encountered in experimental field trials as well as in the IPHC FISS. As an example, the IPHC Secretariat

will begin in 2022 the collection of fin clips of all Pacific halibut encountered in the FISS for future genetic analyses.

*Recommendation 2 (*SRB019–Rec.10 (para. 56))

*"The SRB **RECOMMENDED** that the IPHC Secretariat identify those research areas with uncertainty and indicate research questions that would require the SRB to provide input and/or decision in future documentation and presentations provided to the SRB."*

The Secretariat is working towards delineating research questions that address key areas of uncertainty for Stock Assessment and Management Strategy Evaluation.

*Request 1 (*SRB019–Req.06 (para. 46))

*"The SRB **NOTED** that the IPHC Secretariat is finalising a proposed sampling design for the collection of ovaries in the 2023 FISS, for providing precise estimates of fecundity and **REQUESTED** for SRB020 in June 2022, more detail on the considerations taken to ensure the sampling maximises the opportunity to address the objectives."*

The IPHC Secretariat is working towards selecting appropriate methods for fecundity estimations and towards devising a sampling strategy for 2023. This will be discussed during the IPHC Secretariat presentations during SRB020.

*Request 2 (*SRB019–Req.07 (para. 50))

*"The SRB **REQUESTED** that the IPHC Secretariat pause further pursuit of this research until it can articulate specifically how this approach will inform the stock assessment or MSE and why this approach is preferable to investigation of age-length-weight information which is available at a much broader geographic and temporal scale. "*

The IPHC Secretariat is complying with this request.

UPDATE ON PROGRESS ON THE MAIN RESEARCH ACTIVITIES

1. <u>Migration and Distribution</u>.

   Research activities in this Research Area aim at improving existing knowledge on Pacific halibut larval and juvenile distribution. The relevance of research outcomes from these activities for stock assessment (SA) is in the improvement of estimates of productivity. These research outcomes will be used to generate potential recruitment covariates and to inform minimum spawning biomass targets by Biological Region and represent one of the top three biological inputs into SA (<u>Appendix II</u>). The relevance of these research outcomes for the management and strategy evaluation (MSE) process is in the improvement of the parametrization of the Operating Model and represent the top ranked biological input into the MSE (<u>Appendix III</u>).

   1.1. <u>Larval distribution and connectivity between the Gulf of Alaska and Bering Sea</u>.

No updates to report.

1.2. Wire tagging of U32 Pacific halibut.

No updates to report.

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 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 finalized the processing of genetic samples from the 2020 aged commercial landings, completing four consecutive years of sex ratio information (2017-2020) and is currently processing genetic samples from the 2021 commercial landings.

2.2. Maturity assessment.

Recent sensitivity analyses have shown the importance of changes in spawning output due to skip spawning and/or changes in maturity schedules for stock assessment (Stewart and Hicks, 2018). Information of these key reproductive parameters provides direct input to stock assessment. For example, information on fecundity-at-age and –at-size could be used to replace spawning biomass with egg output as the metric of reproductive capability in the stock assessment and management reference points. This information highlights the need for a better understanding of factors influencing reproductive biology and success of Pacific halibut. In order to fill existing knowledge gaps related to the reproductive biology of female Pacific halibut, research efforts are devoted to characterize female maturity in this species. Specific objectives of current studies include: 1) histological assessment of the temporal progression of female developmental stages and reproductive phases throughout an entire reproductive cycle; 2) update of maturity schedules based on histological-based data; and, 3) fecundity determinations.

2.2.1. Histological assessment of the temporal progression of female developmental stages and reproductive phases throughout an entire reproductive cycle. The IPHC Secretariat has conducted the first detailed examination of temporal changes in female ovarian developmental stages, reproductive phases, and biological indicators of Pacific halibut reproductive development. The results obtained by ovarian histological examination indicate that female Pacific halibut

follow an annual reproductive cycle involving a clear progression of female developmental stages towards spawning within a single year. These results provide foundational information for future studies aimed at updating maturity ogives by histological assessment and at investigating fecundity in Pacific halibut. Furthermore, the potential use of easily-obtained biological indicators in predictive models to assign reproductive phase in Pacific halibut was demonstrated. The results of this study have been published in the journal *Frontiers in Marine Science* (Fish et al., 2022): https://doi.org/10.3389/fmars.2022.801759.

2.2.2. Update of maturity schedules based on histological-based data. The IPHC Secretariat is currently planning the collection of ovarian samples for histology during the 2022 FISS. Plans include the collection of 400 ovarian samples from Biological Region 3, 300 samples each from Biological Regions 2 and 4, and 250 samples from Biological Region 4B.

2.2.3. Fecundity estimations. Methods for fecundity determinations were investigated and, based on the current literature and recommendations from experts in the field, the auto-diametric method was selected as the method of choice (Witthames et al., 2009). The IPHC Secretariat is currently designing plans for ovarian sample collection for fecundity estimations within the 2023 FISS.

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.

No updates to report.

4. Discard Mortality Rates (DMRs) 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 in order 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).

For this reason, the IPHC Secretariat is conducting two research projects to investigate the effects of capture and release on survival and to improve estimates of DMRs in the directed longline and guided recreational Pacific halibut fisheries:
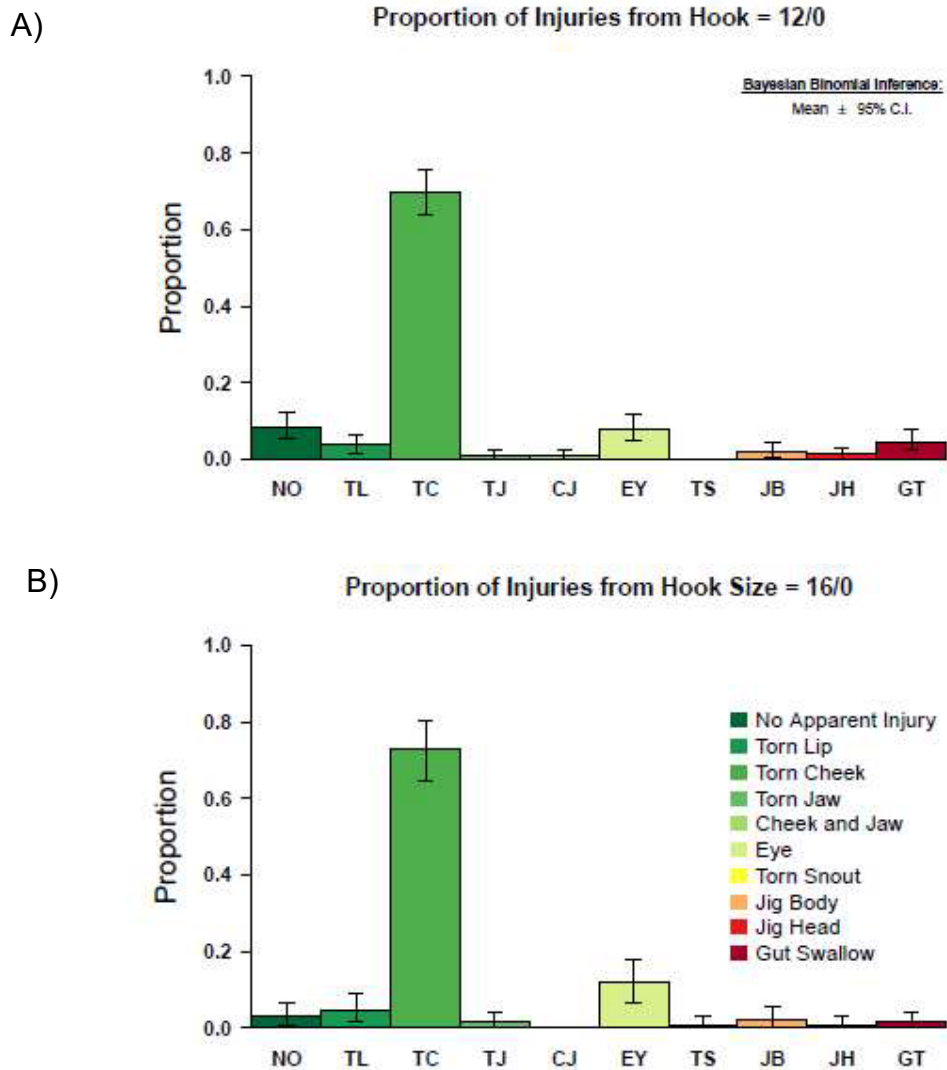
4.1. Evaluation of the effects of hook release techniques on injury levels and association with the physiological condition of captured Pacific halibut and estimation of discard mortality using remote-sensing techniques in the directed longline fishery.

A manuscript describing discard mortality rate estimations in the directed longline fishery has been published in the journal *North American Journal of Fisheries Management* (Loher et al., 2022). No other updates to report.

4.2. Estimation of discard mortality rates in the charter recreational sector.

The IPHC Secretariat is conducting a research project to better characterize the nature of charter recreational fisheries with the ultimate goal of better understanding discard practices relative to that which is employed in the directed longline fishery. This project has received funding from the National Fish and Wildlife Foundation and the North Pacific Research Board (Appendix IV) and the project narratives of both projects have been provided in previous meeting documentations. The experimental field components of this research project took place in Sitka, Alaska (IPHC Regulatory Area 2C) from 21-27 May 2021, and in Seward, Alaska (IPHC Regulatory Area 3A) from 11-16 June 2021, with methods and analyses detailed in the project narratives provided.

The fishing vessels were required to fish 6 rods at a time, three (3) rigged with 12/0 circle hooks and three (3) rigged with 16/0 circle hooks in order to establish a comparison of the two most common gear types used in the Alaskan Pacific halibut recreational fishery, as informed by the survey conducted in 2019 and subsequent discussions. The number of fish captured, sampled and released, as well as the size distribution of fish by tag type (wire tag or sPAT) was previously reported (IPHC-2021-SRB019-08).

A)

Proportion of Injuries from Hook = 12/0

Bayesian Binomial Inference:
Mean ± 95% C.I.

B)

Proportion of Injuries from Hook Size = 16/0

■ No Apparent Injury
■ Torn Lip
■ Torn Cheek
■ Torn Jaw
■ Cheek and Jaw
■ Eye
■ Torn Snout
■ Jig Body
■ Jig Head
■ Gut Swallow

Figure 1. Proportion of the different types of injuries in fish captured with 12/0 hooks (top) and 16/0 hooks (bottom). The legend of injury types corresponds to the abbreviations in the horizontal axis.

The proportion of the different types of injuries incurred over the hooking and release process were determined for Pacific halibut captured with 12/0 hooks and 16/0 hooks. For Pacific halibut captured with 12/0 hooks, approximately 70% of the fish had injuries corresponding to torn cheek, a type of minor injury that is incurred by the hook

penetrating the cheek musculature through a single location (Figure 1A) during the capture event. All other injuries were in much smaller proportion. Very similar distribution of injuries were observed in Pacific halibut captured with 16/0 hooks, again with a predominance of torn cheek injuries (Figure 1B). Overall, the predominant injury profile of Pacific halibut captured with either type of hook and subsequently released corresponded to relatively minor injuries.

To date, of the 281 fish that were tagged with opercular wire tags (243 fish in IPHC Regulatory Area 2C and 38 in IPHC Regulatory Area 3A) 27 tags have been recovered to date (25 from IPHC Regulatory Area 2C and 2 from IPHC Regulatory Area 3A).

In order to directly assess the survival of discarded fish, we tagged 80 with satellite-transmitting electronic archival tags equipped with accelerometers (sPAT tags). To date, 76 out of the 80 released sPAT tags provided data reports. Of the 4 sPAT tags that did not provide data, 2 sPAT tags never reported and 2 did not have sufficient data for successful interpretation. Therefore, 95% of the sPAT tags deployed provided survival information, a similar data transmission success as compared to our recently published report on the use of sPATs to evaluate survival of Pacific halibut discarded from the longline fishery (Loher et al. 2022). Of the 76 useable sPAT tags, 48 tags were at liberty for the full duration of the pre-programmed 96-day period, whereas 21 sPAT tags reported prematurely for unknown reasons, with an average time of at liberty reporting of 37.1 days (range of 3.6-76.8 days). The remaining 7 sPAT tags were physically recovered by fishery captures, with an average time at liberty of 58 days (range of 37.1-69.1 days). Of the physically recovered tags, one was recovered 2 Km from its release location, another one 16 Km from its release location and the remaining 5 tags were recovered less than 0.5 Km from their release location.

Preliminary analysis of the accelerometer data from all 76 tags that successfully reported data, following the survival criteria previously reported in Loher et al. (2022), indicates that only one discarded fish was confidently estimated to have died (its tag reported 8.3 days after deployment). Current analyses are devoted to evaluate whether a second potentially dead fish that reported 32.7 days after deployment fits the "dead" criteria. Therefore, preliminary estimates of discard mortality from the guided recreational fishery point towards a 1.3% discard mortality rate. The deduced preliminary discard mortality rate estimated in the present study is lower than the minimum 4.2% discard mortality rate recently estimated for Pacific halibut discarded from the longline fishery (Loher et al. 2022). The difference in estimated survival between Pacific halibut captured and discarded from the two types of fishery is consistent with the lower capture (hooking) and release time, under best practice handling conditions, of Pacific halibut captured by the recreational fishery. These results represent the first report of experimentally-derived estimates (albeit preliminary) of discard mortality of Pacific halibut captured and discarded in the recreational fishery.

5. <u>Genetics and genomics</u>. The IPHC Secretariat is conducting studies that incorporate genomics approaches in order to produce useful information on population structure and 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 management and strategy evaluation (MSE) process is in biological parametization and validation of movement estimates, on one hand, and of recruitment distribution, on the other hand (Appendix III).

5.1. <u>Population genomics</u>.

The primary objective of the studies that the IPHC Secretariat is currently conducting is to investigate the genetic structure of the Pacific halibut population and to conduct genetic analyses to inform on Pacific halibut movement and distribution within the Convention Area.

5.1.1. <u>Pacific halibut genome and characterization of the sex determining region in Pacific halibut</u>. The IPHC Secretariat has updated the Pacific halibut genome assembly. The updated Pacific halibut genome has an estimated size of 602 Mb, 24 chromosome-length scaffolds that contain 99.8% of the assembly and a N_{50} scaffold length of 27.3 Mb. The Pacific halibut whole genome sequencing data are openly available in NCBI at https://www.ncbi.nlm.nih.gov/bioproject/622249, under BioProject PRJNA622249, and the updated assembly is openly available in NCBI at https://www.ncbi.nlm.nih.gov/assembly/GCA_022539355.2/ with GenBank assembly accession number GCA_022539355.2. The master record for the whole genome shotgun sequencing project has been deposited at DDBJ/ENA/GenBank under the accession JAKRZP000000000 and is openly available in NCBI at https://www.ncbi.nlm.nih.gov/nuccore/JAKRZP000000000. Sample metadata is openly available in NCBI at https://www.ncbi.nlm.nih.gov/biosample?Db=biosample&DbFrom=bioproject&Cmd=Link&LinkName=bioproject_biosample&LinkReadableName=BioSample&ordinalpos=1&IdsFromResult=622249, under BioSamples SAMN14503176, SAMN25516224, SAMN25600010 and SAMN25600011.

Using the updated genome assembly, we conducted genome-wide analyses of sex-specific genetic variation by pool sequencing by mapping reads from male and female pools to the Pacific halibut genome assembly. We identified a potential sex-determining region in chromosome 9 of approximately 12 Mb containing a high density of female-specific SNPs. Within this sex-determining region, we identified among the annotated genes a potential candidate for the master sex-determining gene in Pacific halibut. Mapping of previously identified Pacific halibut RAD-tags associated with sex (Drinan et al., 2018) to the updated Pacific halibut genome assembly resulted in the alignment of 55 of the 56 RAD-tags, all of which mapped to the putative SD region, including the two tags
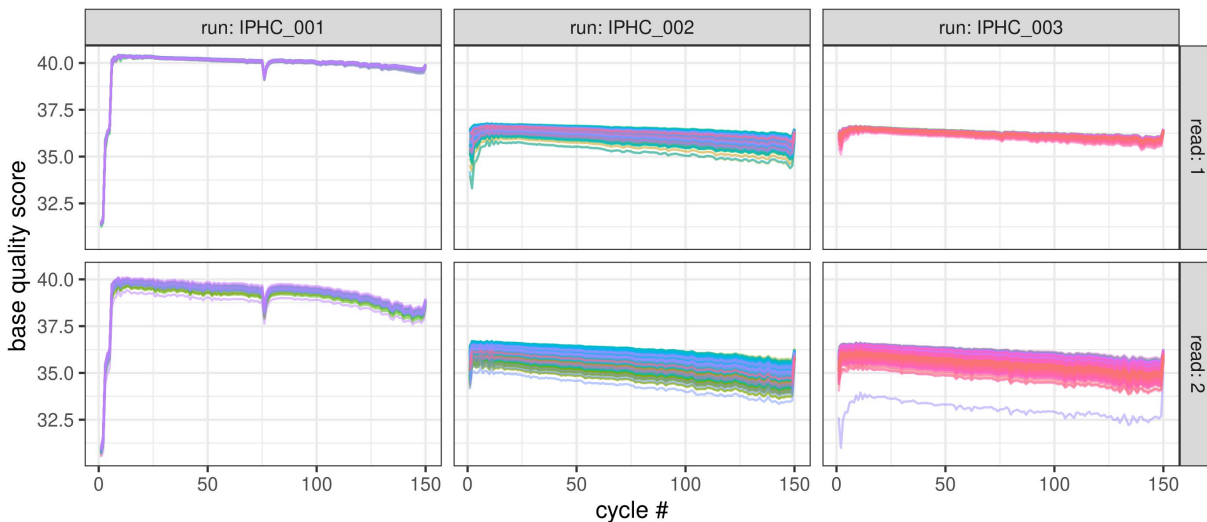
containing the sex-linked markers currently used for genetic sex identification (2.1.1). These results, together with data on the Pacific halibut genome sequencing and assembly, have been accepted for publication in the journal *Molecular Ecology Resources* (Jasonowicz et al., in press; provided separately).

5.1.2. <u>Studies to resolve the genetic structure of the Pacific halibut population in the Convention Area</u>. This project has recently received funding from the North Pacific Research Board (NPRB Project No. 2110; <u>Appendix IV;</u> project narrative provided in the supplementary documentation). Details on sample collection, bioinformatic processing and proposed analyses utilizing low-coverage whole genome sequencing (lcWGR) to investigate Pacific halibut population structure were provided in document <u>IPHC-2021-SRB018-08</u>. The bioinformatic processing pipeline has been successfully migrated to Microsoft Azure cloud computing services and the raw sequence data from three sequencing runs totaling 536 samples have now been processed. This includes alignment to the Pacific halibut reference genome (version 1) and quality filters to ensure integrity of the data prior to analysis. On a per-sample basis, the data output of the sequencing runs is comparable (Table 1). However, we observed a difference in base quality scores between the two sequencing platforms used (Figure 2). This is likely a result of the different sequencing chemistry between the two sequencing platforms used. To mitigate the possibility of batch effects resulting from sequencing across different platforms and multiple runs, we have begun implementing strategies recommended by Lou and Therkildsen (2021) into our data processing workflow. Specifically, we used more stringent sequence read trimming using the sliding window option in Trimmomatic. Furthermore, samples with less than 1,000,000 sequence reads were omitted from any summaries, single nucleotide polymorphism (SNP) identification and downstream analyses.

Library	IPHC_001	IPHC_002	IPHC_003
Number of samples*	36 (35)	250 (249)	250 (249)
Sequencing Platform	Illumina HiSeq 4000	Illumina NovaSeq S4	Illumina NovaSeq S4
Raw Reads Per Sample (Millions)**	26.4 (21.8-42.9)	24.7 (10.7-47.2)	24.9 (13.0-51.6)
Reads Retained (%)**	58 (52-67)	62 (22-69)	61 (46-70)
Coverage Per Sample (x)**	2.5 (1.9-3.7)	3.0 (0.9-5.0)	3.0 (1.3-5.9)

Table 1. Summary of raw sequence data and genome alignments for two Pacific halibut lcWGR sequencing runs. *numbers in parenthesis indicate number of samples with > 1,000,000 raw sequence reads. **expressed as mean (min – max)
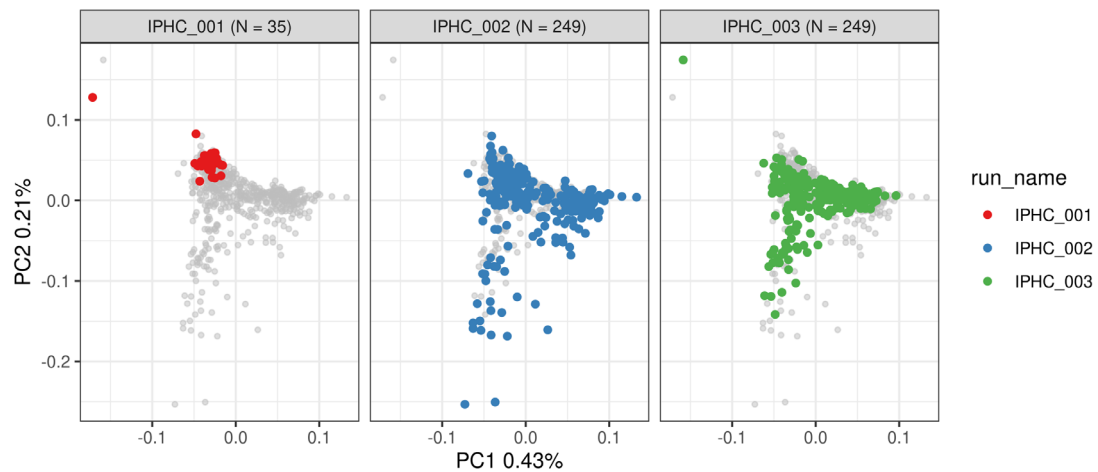
Figure 2. Average base quality score by sequencing cycle. Each sample is represented by a single line, facetted by sequencing run and read (1 = forward read, 2= reverse read).

The sequence alignments were used to identify SNPs and estimate genotype likelihoods using the samtools model implemented in ANGSD (v0.934) (Korneliussen et al. 2014). A minimum base quality score of 20 (99% probability of correct base call) was required and SNPs were retained if they had a global minor allele frequency (MAF) ≥ 0.01 or greater, p-value of 1e-6 or less for a site being variable, and present in at least 402 out of 533 (75.4%) of the individuals. A total of 10,415,578 SNPs were identified using these parameters.

Principal component analysis was used to gain a preliminary look at the structure of the data set. Prior to this, the dataset was filtered to remove SNPs in any unplaced scaffolds, the mitochondrial genome, and chromosome 9 (RefSeq: NC_048935.1), which contains a large sex-associated region (Jasonowicz et al., in review). PCAngsd (v1.02) (Meisner and Albrechtsen 2018; Meisner et al. 2021) was run using default parameters (MAF ≥ 0.5 by default) to estimate a covariance matrix among individuals using genotype likelihoods for 533 Pacific halibut. Numpy (v1.21.2) (Harris et al. 2020) was then used to compute the eigenvalues and eigenvectors for the covariance matrix obtained using PCAngsd.

A total of 4,235,107 sites were retained by PCAngsd and, as recommended by Lou and Therkildsen (2021), individual points were colored by the sequencing run to visualize patterns of non-random groupings that may be indicative of quality differences in the sequencing runs. While there were no clear differences among the NovaSeq S4 runs (Figure 3), we have reserved space on the next sequencing run for resequencing the 36 samples in IPHC_001 (Table 1) on the NovaSeq S4.

Figure 3. Principal component analysis scores of genotype likelihoods from 4,235,107 SNPs in 533 Pacific halibut sequenced to date. Points are colored by sequencing run with the remaining samples colored in gray for comparison.

Currently, 75 samples are being prepared for inclusion in the next sequencing run. This will complete the sequencing phase of the project, with a total of 611 samples having been submitted for sequencing. Once this round of sequencing is complete, the raw reads for all samples will be re-processed using version 2 of the Pacific halibut reference genome.

6. Whale depredation avoidance strategies. The IPHC Secretariat has determined that research to provide the Pacific halibut fishery with tools to reduce whale depredation is considered a high priority. 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 recently obtained funding from NOAA's Bycatch Research and Engineering Program (BREP) to investigate gear-based approaches to catch protection as a means for minimizing whale depredation in the Pacific halibut and other longline fisheries (NOAA Award NA21NMF4720534; Appendix IV). The objectives of this study are to: 1) work with fishermen and gear manufacturers, via direct communication and through an international workshop, to identify effective methods for protecting hook-captured flatfish from depredation; and 2) develop and pilot test 2-3 simple, low-cost catch-protection designs that can be deployed effectively using current longline fishing techniques and on vessels currently operating in the Northeast Pacific Ocean.

The first phase of this project consisted in recruiting participants for a catch protection workshop from the scientific community and from the harvesters active in the waters of Alaska, British Columbia and the U.S. west coast. Initial screening of research conducted around the world led to invitations to three different groups actively working on development of catch protection devices (Sago Solutions, Norway; National Institute for Sustainable Development (IRD) – Marine Biodiversity, Exploitation, and Conservation Unit (MARBEC), University of Montpellier – CNRS-INFREMER-IRD National Centre for Scientific Research, Centre d'Etudes Biologiques de Chisé, France; and Fish Tech Inc., United States). In parallel, harvesters active in the Pacific halibut and Greenland Turbot fisheries as well as scientists involved in marine mammal research were actively recruited for participation. The "1st International Workshop on Protecting Fishery Catches from Whale Depredation (WS001)" was held electronically on 9 February 2022. The Workshop brought together 74 participants from 6 countries, ranging from research scientists to active harvesters. A report summarizing material presented and discussions was produced and posted the IPHC's website along with video recordings of the entire workshop: https://www.iphc.int/venues/details/1st-international-workshop-on-protecting-fishery-catches-from-whale-depredation-ws001.

Current efforts are devoted to the development of designs for two devices for field testing in the second half of 2022.

RECOMMENDATION/S

That the SRB:

a) **NOTE** paper IPHC-2022-SRB020-08 which provides a response to requests from SRB019, and a report on current research activities contemplated within the IPHC Five-Year Biological and Ecosystem Science Research Plan (2017-2021).

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APPENDIX I

Integration of biological research, stock assessment and harvest strategy policy (2017-21)

Biological research		Stock assessment	Stock assessment MSE
Research areas	Research outcomes	Relevance for stock assessment	Inputs to stock assessment and MSE development
Reproduction	Sex ratio Spawning output Age at maturity	Spawning biomass scale and trend Stock productivity Recruitment variability	Sex ratio Maturity schedule Fecundity
Growth	Identification of growth patterns Environmental effects on growth Growth influence in size-at-age variation	Temporal and spatial variation in growth Yield calculations Effects of ecosystem conditions Effects of fishing	Predicted weight-at-age Mechanisms for changes in weight-at-age
Discard Survival	Bycatch survival estimates Discard mortality rate estimates	Scale and trend in mortality Scale and trend in productivity	Bycatch and discard mortality estimates Variability in bycatch and uncertainty in discard mortality estimates
Migration	Larval distribution Juvenile and adult migratory behavior and distribution	Geographical selectivity Stock distribution	Information for structural choices Recruitment indices Migration pathways and rates Timing of migration
Genetics and Genomics	Genetic structure of the population Sequencing of the Pacific halibut genome	Spatial dynamics Management units	Information for structural choices

APPENDIX II

List of ranked biological uncertainties and parameters for stock assessment (SA) and their links to potential research areas and research activities (2017-21)

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 potential links to research areas and research activities (2017-21)

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 active research grants during the reporting period

Project #	Grant agency	Project name	PI	Partners	IPHC Budget ($US)	Management implications	Grant period
1	**National Fish & Wildlife Foundation**	Improving the characterization of discard mortality of Pacific halibut in the recreational fisheries (NFWF No. 61484)	IPHC	Alaska Pacific University, U of A Fairbanks, charter industry	$98,902	Bycatch estimates	1 April 2019 – 1 November 2021
2	**North Pacific Research Board**	Pacific halibut discard mortality rates (NPRB No. 2009)	IPHC	Alaska Pacific University,	$210,502	Bycatch estimates	1 January 2021 – 31 March 2022
3	**Bycatch Reduction Engineering Program - NOAA**	Gear-based approaches to catch protection as a means for minimizing whale depredation in longline fisheries (NA21NMF4720534)	IPHC	Deep Sea Fishermen's Union, Alaska Fisheries Science Center-NOAA, industry representatives	$99,700	Mortality estimations due to whale depredation	November 2021 – October 2022
4	**North Pacific Research Board**	Pacific halibut population genomics (NPRB No. 2110)	IPHC	Alaska Fisheries Science Center-NOAA	$193,685	Stock structure	December 2021- January 2024
Total awarded ($)					**$602,789**		