



IPHC 5-year Biological and Ecosystem Science Research Plan (2017-21): Update

PREPARED BY: IPHC SECRETARIAT (J. PLANAS, 15 DECEMBER 2020)

PURPOSE

To provide the Commission with a description of progress on the IPHC 5-year Biological and Ecosystem Science Research Plan (2017-21).

BACKGROUND

The main objectives of the Biological and Ecosystem Science Research at the IPHC are to:

- 1) identify and assess critical knowledge gaps in the biology of the Pacific halibut;
- 2) understand the influence of environmental conditions; and
- 3) apply the resulting knowledge to reduce uncertainty in current stock assessment models.

The primary biological 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 summarized in five broad research areas designed to provide inputs into stock assessment and the management strategy evaluation processes ([Appendix I](#)), as follows:

- 1) Migration. 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.

UPDATE ON PROGRESS ON THE MAIN RESEARCH ACTIVITIES

1. Migration.

Knowledge of Pacific halibut migration throughout all life stages is necessary in order to gain a complete understanding of stock distribution and the factors that influence it.

1.1. Larval distribution and connectivity between the Gulf of Alaska and Bering Sea.

Principal Investigator: Lauri Sadorus (M.Sc.)

Objective: To investigate larval and juvenile connectivity of Pacific halibut within and between the Gulf of Alaska and the Bering Sea.

Knowledge of the dispersal of Pacific halibut larvae and subsequent migration of young juveniles has remained elusive because traditional tagging methods are not effective on these life stages due to the small size of the fish. This larval connectivity project, in cooperation with NOAA EcoFOCI, used two recently developed modeling approaches to estimate dispersal and migration pathways in order to better understand the connectivity of populations both within and between the Gulf of Alaska (GOA) and Bering Sea (BS). A manuscript of the results has been recently published in the journal *Fisheries Oceanography* ([Sadorus et al., 2020](#)). In brief, to improve current understanding of larval dispersal pathways and migrations of young fish within and between GOA and BS, investigations were conducted to (1) examine pelagic larval dispersal and connectivity between the two basins using an individual-based biophysical model (IBM), and (2) track movement of fish up to age-6 years using annual age-based distributions and a spatio-temporal modeling approach. IBM results indicate that the Aleutian Islands constrain connectivity between GOA and BS, but that large island passes serve as pathways between these ecosystems. The degree of connectivity between GOA and BS is influenced by spawning location such that up to 50-60% of simulated larvae from the westernmost GOA spawning location arrive in the BS with progressively fewer larvae arriving proportional to distance from spawning grounds further east. There is also a large degree of connectivity between eastern and western GOA and between eastern and western BS. Spatial modeling of 2-6 year old fish shows ontogenetic migration from the inshore settlement areas of eastern BS towards Unimak Pass and GOA by age 4. The pattern of larval dispersal from GOA to BS, and subsequent post-settlement migrations back from BS toward GOA, provides evidence of circular, multiple life-stage, connectivity between these ecosystems, regardless of temperature stanza or year class strength. The results of these studies will improve estimates of productivity by contributing to the generation of potential recruitment covariates and by informing minimum spawning biomass targets by Biological Region. In addition, these results will assist in the biological parameterization and validation of movement estimates in the MSE Operating Model ([Appendix I](#)).

1.2. Wire tagging of U32 Pacific halibut.

Principal Investigator: Joan Forsberg (B.Sc.; Fisheries Statistics & Services Branch)

Objective: To investigate the migratory patterns of young Pacific halibut.

The patterns of movement of Pacific halibut among IPHC Regulatory Areas have important implications for management of the Pacific halibut fishery. The IPHC Secretariat has undertaken a long-term study of the migratory behavior of Pacific halibut through the use of externally visible tags (wire tags) on captured and released fish that must be retrieved and returned by workers in the fishing industry. In 2015, with the goal of gaining additional insight into movement and growth of young Pacific halibut (less than 32 inches [82 cm]; U32), the IPHC began wire-tagging small Pacific halibut encountered on the NOAA-Fisheries groundfish trawl survey and, beginning in 2016, on the IPHC Fishery-Independent Setline Survey (FISS). In 2019, a total of 821 Pacific halibut were tagged and released during the GOA trawl survey and 885 tags were released during the BS trawl survey. Through 2019, a total of 6,536 tags have been released in the NOAA-Fisheries groundfish trawl survey and, to date, 52 tags have been

recovered. No U32 tagging on the NOAA-Fisheries groundfish trawl survey occurred in 2020 due its cancellation as a result of COVID-19. On the IPHC FISS, a total of 3,980 U32 Pacific halibut have been wire tagged are released and 74 of those have been recovered to date. In 2020, 868 U32 fish were wire-tagged and released: 321 fish in Regulatory Area 2B and 547 fish in Regulatory Area 3A. The distance traveled by recaptured fish from the release location was under 10 nm for 35% of the fish and between 11 and 50 nm for 25% of the fish. For example, of the 2,005 fish released in Reg Area 3A between 2015 and 2019, 31 of 32 recovered fish were recovered in the same area of release and within the first three years at liberty.

2. Reproduction.

Efforts at IPHC are currently underway to address two critical issues in stock assessment for estimating the female spawning biomass: the sex ratio of the commercial landings and maturity estimations.

2.1. Sex ratio of the commercial landings.

Principal Investigator: Anna Simeon (M.Sc.)

Objective: To provide information on the sex ratio of the commercial landings.

The sex ratio of the commercial fishery catch represents an extremely important source of uncertainty in the annual stock assessment (Stewart and Hicks, 2020). The IPHC has generated sex information of the entire set of aged commercial fishery samples collected in 2017 and in 2018 (>10,000 fin clips per year) using genetic techniques based on the identification of sex-specific single nucleotide polymorphisms (SNPs) (Drinan et al., 2018) using TaqMan qPCR assays conducted at the IPHC's Biological Laboratory. Therefore, for the first time, direct estimates of the sex-ratio at age for the directed commercial fishery have been available for stock assessment. Genetic analyses of commercial samples from 2017 showed that the proportion of females coastwide was high (82%), ranging from 65% to 92% depending on the biological region. Data from the 2018 commercial samples showed almost identical patterns, with females comprising 80% of the coastwide commercial landings (by number). Given that the sex-ratio data constitutes one of the two most important contributors to estimates of both population trend and scale, the inclusion of this information in the 2019 stock assessment resulted in higher spawning biomass. The IPHC Secretariat has recently completed the processing of genetic samples from the 2019 commercial landings and the results indicate that the percentage of females coastwide in the commercial catch is 78%, showing a continuous decline since 2017. Additional years of sex-ratio information of the commercial catch are likely to further inform selectivity parameters and cumulatively reduce uncertainty in future estimates of stock size, in addition to improving simulation of spawning biomass in the MSE Operating Model ([Appendix I](#)).

The IPHC Secretariat is also working towards providing information on sex ratios in years previous to 2017 through the use of genotyping techniques using historical samples of otoliths. The IPHC Secretariat has recently tested whether DNA can be extracted from otoliths and whether the extracted DNA is of sufficient quantity and quality to be used in the genotyping assays currently used with DNA derived from fin

clips. The results obtained indicate that DNA can be extracted from otoliths, albeit at low concentration, and that the genotyping assays can correctly identify the sex of the individual fish. Additional studies are underway to determine whether clean archived otoliths can also be used as a historical source of DNA for genotyping.

2.2. Maturity estimations.

Principal Investigator: Josep Planas (Ph.D.)

Objective: To characterize maturity and fecundity in female Pacific halibut.

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, 2020). These results highlight the need for a better understanding of factors influencing reproductive biology and success for 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) accurate description of oocyte developmental stages and their use to classify female maturity stages; 2) comparison of macroscopic (based on field observations) and microscopic (based on histological assessment) maturity stages and revision of maturity criteria; 3) revision of current estimates of female age-at-maturity; and 4) investigation of fecundity and skip-spawning in females.

The IPHC Secretariat has described for the first time the different oocyte stages that are present in the ovary of female Pacific halibut and how these are used to classify females histologically to specific maturity stages. This information is contained in a manuscript that has been recently published in the *Journal of Fish Biology* ([Fish et al., 2020](#)). In brief, 8 different oocyte developmental stages have been described, from early primary growth oocytes until preovulatory oocytes, and their size and morphological characteristics established. Maturity classification was determined by assigning maturity status to the most advanced oocyte developmental stage present in ovarian tissue sections and 7 different microscopic maturity stages were established. Analysis of oocyte size frequency distribution among the seven different maturity stages provided evidence for the group-synchronous pattern of oocyte development and for the determinate fecundity reproductive strategy in female Pacific halibut. The results of this study will allow us to establish a comparison of the microscopic/histological and macroscopic/field classification criteria that are currently used to assign the maturity status of females that is used in stock assessment. The results of this study set the stage for an in-depth study on temporal changes in maturity, as assessed by microscopic observations of ovarian samples collected throughout an entire annual reproductive cycle, that is currently underway. Furthermore, the IPHC Secretariat is also establishing a comparison of the microscopic (e.g. histological) and macroscopic (e.g. visual) maturity classification criteria to determine whether field classification criteria that are currently used to assign the maturity status of females that is used in stock assessment needs to be revised in light of the improved knowledge on ovarian development.

In addition, the IPHC Secretariat is conducting temporal and spatial analyses of female maturity schedules through the collection of ovarian samples in FISS. For the temporal analysis of maturity, ovarian samples have been collected in the Portlock region (central Gulf of Alaska) during the same period (June-July) for 30 females (>90 cm length) for four consecutive years: 2017, 2018, 2019 and 2020. These ovarian samples have been processed for histology and microscopic maturity staging will be conducted to compare the maturity status over that time period. Furthermore, for the spatial analysis of maturity, ovarian samples from 30 females (>90 cm length) have been collected in the FISS in 5 different regions in the Gulf of Alaska in order to obtain preliminary information on potential spatial differences in maturity.

The results of these studies will be important for scaling biomass and reference point estimates and to improve simulation of spawning biomass in the MSE Operating Model ([Appendix I](#)).

3. Growth.

Principal Investigator: Josep Planas (Ph.D.)

Objective: To investigate somatic growth variation as a driver for changes in size-at-age.

Recent stock assessments conducted by the IPHC Secretariat have indicated that the Pacific halibut stock experienced a continuous coastwide decline from the late 1990s until approximately 2012 largely due to a decrease in size-at-age (SAA) (Stewart and Hicks, 2020). Current low values of SAA combined with low recruitment of cohorts spawned at the time of the initial decrease in SAA in the 1990s have contributed to a decrease in exploitable Pacific halibut biomass. Although the decrease in SAA has been hypothesized as being attributed to several potential causes, including environmental effects such as temperature or food availability, as well as ecological or fishery effects, our knowledge on the actual factors that influence SAA of Pacific halibut is still scarce. 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 are: 1) the identification and validation of physiological markers for somatic growth; and 2) the use of growth markers for evaluating growth patterns in the Pacific halibut population and the effects of environmental factors on somatic growth. In order to pursue these objectives, the IPHC Secretariat has investigate on the effects of temperature variation on growth performance, as well as on the effects of density, hierarchical dominance and handling stress on growth in juvenile Pacific halibut in captivity. These studies have been funded by a grant from the North Pacific Research Board to the IPHC (NPRB 1704; 2017-2020) ([Appendix II](#)).

The results on the effects of temperature on growth physiological indicators are being prepared for publication in a peer-reviewed journal (Planas et al., in preparation). In brief, juvenile Pacific halibut were subjected to temperature-induced growth manipulations, whereby somatic growth was suppressed by low temperature acclimation and stimulated by temperature-induced compensatory growth. Physiological signatures of growth suppression and growth stimulation were identified by a comparative transcriptomics and proteomics approach that identified genes and proteins, respectively, which experienced expression

changes in response to the two growth manipulations. The identified genes and proteins could potentially represent useful markers for growth in skeletal muscle. Currently, assays are being developed to test the validity of the identified molecular markers for growth on skeletal muscle samples from age-matched adult Pacific halibut of different sizes.

In addition to temperature-induced growth manipulations, the IPHC Secretariat is conducting similar studies to identify physiological growth markers that respond to density and stress-induced growth manipulations. On one hand, changes in SAA in Pacific halibut have been hypothesized, among other potential causes, to be the result of changes in population dynamics of the Pacific halibut stock due to a density effect, whereby high population densities would negatively affect growth. On the other hand, we hypothesize that stress responses associated with capture and release of discarded Pacific halibut may affect feeding and growth in the wild, therefore, addressing potential growth consequences related to capture and handling stress. Investigations related to the effects of density and stress exposure are currently underway.

The results of these studies will inform scale stock productivity and reference point estimates, in addition to contributing to improve simulation of variability and allow for scenarios investigating climate change ([Appendix I](#)).

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 for 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. For this reason, the IPHC Secretariat is conducting investigations on the effects of capture and release on survival and on providing experimentally-derived estimates of DMRs in the directed longline and guided recreational Pacific halibut fisheries that will improve trends in unobserved mortality in stock assessment and that will be important for fishery parametrization ([Appendix I](#)):

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.

Principal Investigator: Claude Dykstra (B.Sc.)

Objective: To provide estimates of discard mortality and best-handling practices in the Pacific halibut directed fishery.

In order to better estimate post-release survival of Pacific halibut caught incidentally in the directed longline fishery, the IPHC Secretariat is conducting investigations to understand the relationship between fish handling practices and fish physical and

physiological condition and survival post-capture as assessed by electronic archival tagging. Currently, the IPHC assigns a 3.5% DMR to Pacific halibut released from longline gear with only minor injuries and a 16% DMR to the total estimated volume of U32 discards generated by the target fishery. The former was experimentally derived between 1958 and 1961, and the latter is a result of tagging studies in which the baseline DMR was used as a parameter in tag-recovery models that were used to estimate DMRs for fish returned to the water in relatively poorer condition than “minor”. As such, if the 3.5% is mis-specified, the subsequent rates that rest upon that value will be inaccurate, as will be our estimates of total discard mortality within the fishery. The baseline rate was generated from at-sea captive holding studies that reported that observed mortality patterns were, at least in part, due to fluctuating environmental conditions from which the fish could not escape, and for which they attempted to compensate analytically. Ambiguity therefore exists regarding the degree to which the baseline rate is accurate, necessitating additional studies in order to resolve this issue. For this reason, the IPHC Secretariat, with partial funding by a grant from the Saltonstall-Kennedy Grant Program NOAA (NA17NMF4270240; 2017-2020) ([Appendix II](#)), conducted studies to evaluate the effects of hook release techniques on injury levels, their association with the physiological condition of captured Pacific halibut and, importantly, generated experimentally-derived estimates of DMR in the directed longline fishery.

As part of this study, injury profiles and release viabilities for different release techniques (careful shake, gangion cutting, and hook stripping) have been developed. The results obtained indicate that injury patterns were similar for careful shake and gangion cutting, with most injuries being a small puncture to the cheek, and greater than 70% of the released fish were classified to be in excellent viability. The hook stripper produced more severe physical injuries with significantly greater numbers of fish classified as moderate or poor in viability condition upon release.

Blood glucose, lactate, and cortisol levels from all fish released have been determined using specific assays in the Biological Laboratory. Results are suggestive of a trend towards lower glucose and higher lactate blood levels in fish classified as dead in terms of the release condition. Cortisol levels do not show a significant trend across the release condition categories. Results on glucose, lactate, and cortisol plasma levels in fish according to physical injury code show a fair amount of variation within groups. The relationship of blood glucose, lactate, and cortisol levels to other measured parameters in discarded fish (fat levels, condition index, time out of water, temperature exposure, etc.) are under ongoing investigation.

Electronic monitoring (EM) systems were proven to be effective at accurately capturing the release method applied to each animal. Footage is now being reviewed to determine the ability of EM systems to provide length estimates of captured fish from the existing footage, and additional in season work on a FISS vessel is proposed.

4.2. Discard mortality rates of Pacific halibut in the charter recreational fishery.

Principal Investigator: Claude Dykstra (B.Sc.)

Objective: To provide estimates of discard mortality and best-handling practices in the Pacific halibut guided recreational fishery.

The IPHC has begun 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 ([Appendix II](#)). As an initial step in this project, information from the charter fleet on types of gear and fish handling practices used was collected through stakeholder meetings and on dock interviews with charter captains and operators. Results show that the guided recreational fleet predominantly uses circle hooks (75-100%), followed by jigs. Predominant hook release methods included reversing the hook (54%), or twisting the hook out with a gaff (40%), and the fish were generally handled by supporting both the head and tail (65%), while other common techniques included handling by the operculum (10%) or by the tail alone (10%). These results will inform the design of the experimental test fishing that will take place in Spring/Summer of 2021 and in which injury levels, fish condition and stress parameters will be evaluated to identify best practices intended to minimize discard mortality in this fishery and to provide direct estimates of discard survival.

5. Genetics and genomics. The IPHC Secretariat is exploring avenues for incorporating genetic approaches for a better understanding of population structure and distribution and is also building genomic resources to assist in genetics and molecular studies on Pacific halibut.

5.1. Genetics.

Principal Investigator: Andy Jasonowicz (M.Sc.)

Objective: To investigate the genetic structure of the Pacific halibut population and to conduct genetic analyses to inform on Pacific halibut movement and distribution in the eastern North Pacific Ocean. Two specific objectives are being pursued as follows:

- 5.1.1. Investigate the genetic structure of the Pacific halibut population in the North-eastern Pacific Ocean. Understanding population structure is imperative for sound management and conservation of natural resources (Hauser, 2008). Pacific halibut in Canadian and USA waters are managed by the International Pacific Halibut Commission (IPHC) as a single coastwide unit stock since 2006. The rationale behind this management approach is based on our current knowledge of the highly migratory nature of Pacific halibut as assessed by tagging studies (Webster et al., 2013) and of past analyses of genetic population structure that failed to demonstrate significant differentiation in the North-eastern Pacific Ocean population of Pacific halibut by allozyme (Grant, 1984) and small-scale microsatellite analyses (Bentzen, 1998; Nielsen *et al.*, 2010). However, more recent studies have reported slight genetic population structure on the basis of genetic analysis conducted with larger sets of microsatellites suggesting that Pacific halibut captured in the Aleutian Islands may be genetically distinct from other areas (Drinan et al., 2016). These findings of subtle

genetic structure in the Aleutian Island chain area are attributed to limited movement of adults and exchange of larvae between this area and the rest of the stock due to the presence of oceanographic barriers to larval and adult dispersal (i.e. Amchitka Pass) that could represent barriers to gene flow. Unfortunately, genetic studies suggesting subtle genetic structure (Drinan et al., 2016) were conducted based on a relatively limited set of microsatellite markers and, importantly, using genetic samples collected in the summer (i.e. non-spawning season) that may not be representative of the local spawning population. With the collection of winter (i.e. spawning season) genetic samples in the Aleutian Islands by the IPHC in early 2020, a collection of winter samples from 5 different geographic areas across the North-eastern Pacific Ocean (i.e. British Columbia, Central Gulf of Alaska, Bering Sea, Central and Western Aleutian Islands) is now available to re-examine the genetic structure of the Pacific halibut population. Importantly, novel, high-throughput and high-resolution genomics approaches are now available for use, such as low-coverage whole genome resequencing, in order to describe with unprecedented detail the genetic structure of the Pacific halibut population. The recently sequenced Pacific halibut genome ([Section 5.2](#)) will constitute an essential resource for the success of the whole genome resequencing approach. The results from the proposed genomic studies will provide important information on spawning structure and, consequently, on the genetic baselines of source populations. Importantly, the results from these studies will provide management advice regarding the relative justifiability for considering the western Aleutians as a genetically-distinct substock. These research outcomes will represent important avenues for improving estimates of productivity and parametrization of the MSE Operating Model ([Appendix I](#)).

- 5.1.2. Analysis of genetic variability among juvenile Pacific halibut in the Bering Sea and the Gulf of Alaska. The aim of this objective is to evaluate the genetic variability or genetic diversity among juvenile Pacific halibut in a given ocean basin in order to infer information on the potential contribution from fish spawned in different areas to that particular ocean basin. We hypothesize that genetic variability among juvenile Pacific halibut captured in one particular ocean basin (e.g. eastern Bering Sea) may be indicative of mixing of individuals originating in different spawning grounds and, therefore, of movement. By comparing the genetic variability of fish between two ocean basins (i.e. eastern Bering Sea and Gulf of Alaska), we will be able to evaluate the extent of the potential contribution from different sources (e.g. spawning groups) in each of the ocean basins and provide indications of relative movement of fish to these two different ocean basins. The use of genetic samples from juvenile Pacific halibut collected in the National Marine Fisheries Service trawl survey in the eastern Bering Sea and in the Gulf of Alaska, aged directly by otolith reading or indirectly through a length-age key, will allow us to provide information on genetic variability among fish that are at or near their settlement or nursery grounds. These studies will provide the ability to assign individual juvenile Pacific halibut to source populations (as established in 5.1.1) and genetic information on movement and distribution of juvenile Pacific halibut. These research outcomes will improve estimates of productivity and biological parametrization and validation of movement estimates and recruitment distribution in the MSE Operating Model ([Appendix I](#)).

5.2. Genomics.

Principal Investigator: Josep Planas (Ph.D.)

Objective: To sequence the Pacific halibut genome as a key resource for genomic studies.

The IPHC Secretariat has recently completed conducting a project aimed at generating a first draft sequence of the Pacific halibut genome, the blueprint for all the genetic characteristics of the species. This project was conducted in collaboration with the French National Institute for Agricultural Research (INRA, Rennes, France). Briefly, the Pacific halibut genome has a size of 586 Mb and contains 24 chromosomes- covering 98.6% of the complete assembly with a N50 scaffold length of 25 Mb at a coverage of 91x. The Pacific halibut genome sequence has been submitted to the National Center for Biological Information (NCBI) with submission number SUB7094550 and with accession number [JABBIT000000000](#). Furthermore, the Pacific halibut genome has been annotated and is available in NCBI as [NCBI *Hippoglossus stenolepis* Annotation Release 100](#). The generated genomic resources will greatly assist current studies on the genetic structure of the Pacific halibut population, on the application of genetic signatures for assigning individuals to spawning populations and for a thorough characterization of regions of the genome or genes responsible for important traits of the species.

RECOMMENDATIONS

That the Commission **NOTE** paper IPHC-2021-AM097-10 which outlines progress on the [IPHC 5-year Biological and Ecosystem Science Research Plan](#).

References

- Bentzen, P., Britt, J., and Kwon, J., 1998. Genetic variation in Pacific halibut (*Hippoglossus stenolepis*) detected with novel microsatellite markers. Report of Assessment and Research Activities. International Pacific Halibut Commission, Seattle, WA, pp. 229–241.
- Drinan, D.P., Galindo, H.M., Loher, T., and Hauser, L., 2016. Subtle genetic population structure in Pacific halibut *Hippoglossus stenolepis*. *Journal of Fish Biology* 89, 2571-2594.
- Drinan, D.P., Loher, T., and Hauser, L., 2018. Identification of Genomic Regions Associated With Sex in Pacific Halibut. *Journal of Heredity* 109, 326-332.
- Fish, T., Wolf, N., Harris, B. P., and Planas, J. V. 2020. A comprehensive description of oocyte developmental stages in Pacific halibut, *Hippoglossus stenolepis*. *Journal of Fish Biology* 97, 1880-1885. <http://dx.doi.org/10.1111/jfb.14551>.
- Grant, W.S., Teel, D. J., and Kobayashi, T., 1984. Biochemical Population Genetics of Pacific Halibut (*Hippoglossus stenolepis*) and Comparison with Atlantic Halibut (*Hippoglossus hippoglossus*). *Canadian Journal of Fisheries and Aquatic Sciences* 41, 1083-1088.
- Hauser, L., and Carvalho, G. R., 2008. Paradigm shifts in marine fisheries genetics: ugly hypotheses slain by beautiful facts. *Fish and Fisheries* 9, 333-362.
- Nielsen, J.L., Graziano, S.L., Seitz, A.C., 2010. Fine-scale population genetic structure in Alaskan Pacific halibut (*Hippoglossus stenolepis*). *Conservation Genetics* 11, 999-1012.
- Planas, J.V., Jasonowicz, A., Simeon, A., Rudy, D., Timmins-Schiffman, E., Nunn, B.L., Kroska, A., Wolf, N., and Hurst, T.P. Physiological signatures of temperature-induced

growth manipulations in white skeletal muscle of juvenile Pacific halibut (*Hippoglossus stenolepis*). (In Preparation).

Sadorus, L.; Goldstein, E.; Webster, R.; Stockhausen, W.; Planas, J.V.; Duffy-Anderson, J. 2020. Multiple life-stage connectivity of Pacific halibut (*Hippoglossus stenolepis*) across the Bering Sea and Gulf of Alaska. Fisheries Oceanography (In press). <https://onlinelibrary.wiley.com/doi/abs/10.1111/fog.12512>

Stewart, I.J., and Hicks, A. 2020. Assessment of the Pacific halibut (*Hippoglossus stenolepis*) stock at the end of 2019. Int. Pac. Halibut Comm. Annual Meeting Report: IPHC-2020-SA-01.

Webster, R.A., Clark, W.G., Leaman, B.M., Forsberg, J.E., Hilborn, R., 2013. Pacific halibut on the move: a renewed understanding of adult migration from a coastwide tagging study. Canadian Journal of Fisheries and Aquatic Sciences 70, 642-653.

APPENDICES

Appendix I: Integration of ongoing biological research activities, stock assessment and management strategy evaluation.

Appendix II: Summary of awarded research grants current in 2020



APPENDIX I

Integration of ongoing biological research activities, stock assessment and management strategy evaluation

Research areas	Research activities	Research outcomes	Relevance for stock assessment	Relevance for MSE	Specific analysis input	SA Rank (Top 3)	MSE Rank (Top 3)
Migration	Larval and juvenile connectivity and early life history studies	Improved understanding of larval and juvenile distribution	Improve estimates of productivity	Improve parametrization of the Operating Model	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
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
	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		
	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		
	Examination of accuracy of current field macroscopic maturity classification	Revised field maturity classification	Scale biomass and fishing intensity		Revised time-series of historical (and future) maturity for input to the stock assessment	1. Assessment data collection and processing	
	Sex ratio of current commercial landings	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	Historical sex ratio-at-age	Annual sex-ratio at age for the commercial fishery fit by the stock assessment				
Recruitment strength and variability	Establishment of temporal and spatial maturity and spawning patterns	Improve stock-recruitment curve for more precise assessment	Improve simulation of recruitment variability and parametrization of recruitment distribution in the Operating Model	May be used to provide a weighted spawning biomass calculation and or inform targets for minimum spawning biomass by Biological Region			
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
		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		
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 parameterization	
	Discard mortality rate estimate: recreational fishery				Will improve estimates of discard mortality, reducing potential bias in stock assessment results and management of mortality limits		
	Best handling practices: longline fishery	Guidelines for reducing discard mortality			May reduce discard mortality, thereby increasing available yield for directed fisheries	2. Fishery parameterization	
	Best handling practices: recreational fishery	Guidelines for reducing discard mortality			May reduce discard mortality, thereby increasing available yield for directed fisheries		
Genetics and genomics	Population structure	Stock structure of IPHC Regulatory Area 4B relative to the rest of the Convention Area	Altered structure of future stock assessments	Improve parametrization 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.
	Distribution	Assignment of individuals to source populations and assessment of distribution changes			Will be used to define management targets for minimum spawning biomass by Biological Region	3. Biological input	2. Biological parameterization and validation of recruitment distribution



APPENDIX II
Summary of awarded research grants in 2020

Project #	Funding agency	Project title	PI	Partners	IPHC Budget (\$US)	Management implications	Grant period
1	Saltonstall-Kennedy NOAA	Improving discard mortality rate estimates in the Pacific halibut by integrating handling practices, physiological condition and post-release survival (Award No. NA17NMF4270240)	IPHC	Alaska Pacific University	\$286,121	Bycatch estimates	September 2017 – August 2020 (Finalized)
2	North Pacific Research Board	Somatic growth processes in the Pacific halibut (<i>Hippoglossus stenolepis</i>) and their response to temperature, density and stress manipulation effects (Award No. 1704)	IPHC	AFSC-NOAA-Newport, OR	\$131,891	Changes in biomass/size-at-age	September 2017 – February 2020 (Finalized)
3	National Fish & Wildlife Foundation	Improving the characterization of discard mortality of Pacific halibut in the recreational fisheries (Award No. 61484)	IPHC	Alaska Pacific University, U of A Fairbanks, charter industry	\$98,902	Bycatch estimates	April 2019 – June 2021
Total awarded (\$)					\$516,914		